Table S1 - Set of 4,422 candidate genes identified in root and leaf tissues of the wheat cultivar MGS1 Aliança under drought.

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Contig00003	73	13	2.360	1.32E-10	No hit
Root	Contig00045	41987	39888	-0.055	7.57E-09	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Contig00046	62	3	4.240	1.60E-14	No hit
Root	Contig00054	764	863	-0.305	2.02E-05	CGD|CAL0002846 - symbol:CSA1 species:5476 "Candida albicans" [GO:0009277 "fungal-type cell wall" evidence=ISS;IDA] [GO:0009986 "cell surface" evidence=ISS;IDA] [GO:0020037 "heme binding" evidence=IGI] [GO:0006879 "cellular iron ion homeostasis" evidence=IMP] [GO:0005933 "cellular bud" evidence=IDA] [GO:0046658 "anchored to plasma membrane" evidence=ISS;IMP] [GO:0030446 "hyphal cell wall" evidence=IDA] [GO:0044011 "single-species biofilm formation on inanimate substrate" evidence=IMP] CGD:CAL0002846 EMBL:AACQ01000024 InterPro:IPR008427 Pfam:PF05730 RefSeq:XP_720404.1 RefSeq:XP_888643.1 GeneID:3638009 GeneID:3704110 KEGG:cal:CaO19.7114 KEGG:cal:CaO19_7114 InterPro:IPR014005 SMART:SM00747 Uniprot:G1UB63
Root	Contig00082	13319	12813	-0.073	3.05E-05	SGD|S000028422 - symbol:TAR1 "Mitochondrial protein potentially involved in respiratory metabolism" species:4932 "Saccharomyces cerevisiae" [GO:0003674 "molecular_function" evidence=ND] [GO:0043457 "regulation of cellular respiration" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IEA;IMP] SGD:S000028422 GO:GO:0005739 EMBL:BK006945 EMBL:U53879 GO:GO:0043457 EMBL:Z73326 EMBL:AF479964 RefSeq:NP_690845.1 ProteinModelPortal:Q8TGM6 STRING:Q8TGM6 EnsemblFungi:YLR154W-C GeneID:1466405 KEGG:sce:YLR154W-C CYGD:YLR154w-c eggNOG:NOG79861 OMA:SCSKEHR OrthoDB:EOG466ZX8 NextBio:967146 Genevestigator:Q8TGM6 GermOnline:YLR154W-C Uniprot:Q8TGM6
Root	Contig00147	634	25	4.536	1.69E-137	No hit
Root	Contig00175	1927	101	4.125	0	No hit
Root	Contig00293	562	24	4.420	9.88E-121	No hit
Root	Contig00426	13	0	4.571	0.000344357	No hit
Root	Contig00436	40	2	4.193	7.78E-10	No hit
Root	Contig00447	34	7	2.151	3.42E-05	UNIPROTKB|P17931 - symbol:LGALS3 "Galectin-3" species:9606 "Homo sapiens" [GO:0001501 "skeletal system development" evidence=IEA] [GO:0005515 "protein binding" evidence=IPI] [GO:0005578 "proteinaceous extracellular matrix" evidence=IEA] [GO:0005634 "nucleus" evidence=IDA] [GO:0005681 "spliceosomal complex" evidence=IEA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0005743 "mitochondrial inner membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=TAS] [GO:0006397 "mRNA processing" evidence=IEA] [GO:0008380 "RNA splicing" evidence=IEA] [GO:0019863 "IgE binding" evidence=IEA] [GO:0030154 "cell differentiation" evidence=IEA] [GO:0030198 "extracellular matrix organization" evidence=IEA] [GO:0031012 "extracellular matrix" evidence=IDA] [GO:0045087 "innate immune response" evidence=TAS] GO:GO:0005886 Reactome:REACT_6900 GO:GO:0030154 EMBL:CH471061 GO:GO:0008380 GO:GO:0005743 GO:GO:0005529 GO:GO:0006397 GO:GO:0045087 InterPro:IPR008985 InterPro:IPR013320 Gene3D:G3DSA:2.60.120.200 SUPFAM:SSF49899 HOVERGEN:HBG006255 InterPro:IPR001079 Pfam:PF00337 SMART:SM00908 SMART:SM00276 PROSITE:PS51304 GO:GO:0005681 Pathway_Interaction_DB:hedgehog_glipathway GO:GO:0019863 eggNOG:NOG312075 OrthoDB:EOG4C87TX InterPro:IPR015534 PANTHER:PTHR11346:SF26 EMBL:M57710 EMBL:M35368 EMBL:M36682 EMBL:M64303 EMBL:S59012 EMBL:AF031425 EMBL:AF031422 EMBL:AF031423 EMBL:AF031424 EMBL:AB006780 EMBL:AK314929 EMBL:CR456897 EMBL:AL139316 EMBL:BC001120 EMBL:BC053667 IPI:IPI00465431 PIR:A35820 RefSeq:NP_002297.2 UniGene:Hs.531081 PDB:1A3K PDB:1KJL PDB:1KJR PDB:2NMN PDB:2NMO PDB:2NN8 PDB:2XG3 PDB:3AYA PDB:3AYC PDB:3AYD PDB:3AYE PDB:3T1L PDB:3T1M PDB:3ZSJ PDB:3ZSK PDB:3ZSL PDB:3ZSM PDBsum:1A3K PDBsum:1KJL PDBsum:1KJR PDBsum:2NMN PDBsum:2NMO PDBsum:2NN8 PDBsum:2XG3 PDBsum:3AYA PDBsum:3AYC PDBsum:3AYD PDBsum:3AYE PDBsum:3T1L PDBsum:3T1M PDBsum:3ZSJ PDBsum:3ZSK PDBsum:3ZSL

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						PDBsum:3ZSM ProteinModelPortal:P17931 SMR:P17931 DIP:DIP-45623N IntAct:P17931 STRING:P17931 PhosphoSite:P17931 DMDM:215274262 DOSAC-COBS-2DPAGE:P17931 REPRODUCTION-2DPAGE:IPI00465431 UCD-2DPAGE:P17931 PRIDE:P17931 DNASU:3958 Ensembl:ENST00000254301 GeneID:3958 KEGG:hsa:3958 CTD:3958 GeneCards:GC14P055595 HGNC:HGNC:6563 HPA:CAB005191 HPA:HPA003162 MIM:153619 neXtProt:NX_P17931 PharmGKB:PA30340 GeneTree:ENSGT00630000089626 InParanoid:P17931 KO:K06831 OMA:QAPPGAY PhylomeDB:P17931 BindingDB:P17931 NextBio:15531 PMAP-CutDB:Q6IBA7 ArrayExpress:P17931 Bgee:P17931 CleanEx:HS_LGALS3 Genevestigator:P17931 GermOnline:ENSG00000131981 Uniprot:P17931
Root	Contig00455	36	0	6.041	1.05E-09	No hit
Root	Contig00496	31	3	3.240	8.04E-07	No hit
Root	Contig00498	60	2	4.778	8.85E-15	UNIPROTKB|P17931 - symbol:LGALS3 "Galectin-3" species:9606 "Homo sapiens" [GO:0001501 "skeletal system development" evidence=IEA] [GO:0005515 "protein binding" evidence=IPI] [GO:0005578 "proteinaceous extracellular matrix" evidence=IEA] [GO:0005634 "nucleus" evidence=IDA] [GO:0005681 "spliceosomal complex" evidence=IEA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0005743 "mitochondrial inner membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=TAS] [GO:0006397 "mRNA processing" evidence=IEA] [GO:0008380 "RNA splicing" evidence=IEA] [GO:0019863 "IgE binding" evidence=IEA] [GO:0030154 "cell differentiation" evidence=IEA] [GO:0030198 "extracellular matrix organization" evidence=IEA] [GO:0031012 "extracellular matrix" evidence=IDA] [GO:0045087 "innate immune response" evidence=TAS] GO:GO:0005886 Reactome:REACT_6900 GO:GO:0030154 EMBL:CH471061 GO:GO:0008380 GO:GO:0005743 GO:GO:0005529 GO:GO:0006397 GO:GO:0045087 InterPro:IPR008985 InterPro:IPR013320 Gene3D:G3DSA:2.60.120.200 SUPFAM:SSF49899 HOVERGEN:HBG006255 InterPro:IPR001079 Pfam:PF00337 SMART:SM00908 SMART:SM00276 PROSITE:PS51304 GO:GO:0005681 Pathway_Interaction_DB:hedgehog_glipathway GO:GO:0019863 eggNOG:NOG312075 OrthoDB:EOG4C87TX InterPro:IPR015534 PANTHER:PTHR11346:SF26 EMBL:M57710 EMBL:M35368 EMBL:M36682 EMBL:M64303 EMBL:S59012 EMBL:AF031425 EMBL:AF031422 EMBL:AF031423 EMBL:AF031424 EMBL:AB006780 EMBL:AK314929 EMBL:CR456897 EMBL:AL139316 EMBL:BC001120 EMBL:BC053667 IPI:IPI00465431 PIR:A35820 RefSeq:NP_002297.2 UniGene:Hs.531081 PDB:1A3K PDB:1KJL PDB:1KJR PDB:2NMN PDB:2NMO PDB:2NN8 PDB:2XG3 PDB:3AYA PDB:3AYC PDB:3AYD PDB:3AYE PDB:3T1L PDB:3T1M PDB:3ZSJ PDB:3ZSK PDB:3ZSL PDB:3ZSM PDBsum:1A3K PDBsum:1KJL PDBsum:1KJR PDBsum:2NMN PDBsum:2NMO PDBsum:2NN8 PDBsum:2XG3 PDBsum:3AYA PDBsum:3AYC PDBsum:3AYD PDBsum:3AYE PDBsum:3T1L PDBsum:3T1M PDBsum:3ZSJ PDBsum:3ZSK PDBsum:3ZSL PDBsum:3ZSM ProteinModelPortal:P17931 SMR:P17931 DIP:DIP-45623N IntAct:P17931 STRING:P17931 PhosphoSite:P17931 DMDM:215274262 DOSAC-COBS-2DPAGE:P17931 REPRODUCTION-2DPAGE:IPI00465431 UCD-2DPAGE:P17931 PRIDE:P17931 DNASU:3958 Ensembl:ENST00000254301 GeneID:3958 KEGG:hsa:3958 CTD:3958 GeneCards:GC14P055595 HGNC:HGNC:6563 HPA:CAB005191 HPA:HPA003162 MIM:153619 neXtProt:NX_P17931 PharmGKB:PA30340 GeneTree:ENSGT00630000089626 InParanoid:P17931 KO:K06831 OMA:QAPPGAY PhylomeDB:P17931 BindingDB:P17931 NextBio:15531 PMAP-CutDB:Q6IBA7 ArrayExpress:P17931 Bgee:P17931 CleanEx:HS_LGALS3 Genevestigator:P17931 GermOnline:ENSG00000131981 Uniprot:P17931
Root	Contig00507	108	12	3.041	3.63E-19	UNIPROTKB|Q8NEZ4 - symbol:MLL3 "Histone-lysine N-methyltransferase MLL3" species:9606 "Homo sapiens" [GO:0003677 "DNA binding" evidence=IEA] [GO:0005515 "protein binding" evidence=IPI] [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0008270 "zinc ion binding" evidence=IEA] [GO:0035097 "histone methyltransferase complex" evidence=IEA] [GO:0035556 "intracellular signal transduction" evidence=IEA] [GO:0042800 "histone methyltransferase activity (H3-K4 specific)" evidence=IEA] InterPro:IPR001841 Pfam:PF00856 InterPro:IPR009071 InterPro:IPR000637 InterPro:IPR001214 InterPro:IPR001594 InterPro:IPR001965 InterPro:IPR002219 InterPro:IPR003888 InterPro:IPR003889 InterPro:IPR017956 InterPro:IPR019787 Pfam:PF00628 Pfam:PF05964 Pfam:PF05965 PROSITE:PS00354 PROSITE:PS50016 PROSITE:PS50089 PROSITE:PS50216 PROSITE:PS50280 PROSITE:PS51542 PROSITE:PS51543 SMART:SM00109 SMART:SM00184 SMART:SM00249 SMART:SM00317 SMART:SM00384 SMART:SM00398 SMART:SM00541 SMART:SM00542 InterPro:IPR011011 InterPro:IPR018516 InterPro:IPR018518 GO:GO:0035556 GO:GO:0005515 GO:GO:0006355 GO:GO:0003677 GO:GO:0008270 GO:GO:0006351 InterPro:IPR013083 Gene3D:G3DSA:3.30.40.10 SUPFAM:SSF57903 PROSITE:PS01359 eggNOG:COG2940 InterPro:IPR003616 SMART:SM00508

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						PROSITE:PS50868 EMBL:AC005631 EMBL:AC006017 GeneTree:ENSGT00650000093319 EMBL:AY024361 EMBL:AF264750 EMBL:AC104692 EMBL:AB040939 EMBL:AK022687 EMBL:AK075113 EMBL:AL833924 IPI:IPI00168806 IPI:IPI00375729 IPI:IPI00916332 RefSeq:NP_733751.2 UniGene:Hs.647120 PDB:2YSM PDB:2YUK PDB:3UVL PDBsum:2YSM PDBsum:2YUK PDBsum:3UVL ProteinModelPortal:Q8NEZ4 SMR:Q8NEZ4 DIP:DIP-48649N IntAct:Q8NEZ4 STRING:Q8NEZ4 PhosphoSite:Q8NEZ4 DMDM:221222521 PRIDE:Q8NEZ4 Ensembl:ENST00000262189 GeneID:58508 KEGG:hsa:58508 UCSC:uc003wla.1 CTD:58508 GeneCards:GC07M151832 H-InvDB:HIX0007238 HGNC:HGNC:13726 MIM:606833 neXtProt:NX_Q8NEZ4 PharmGKB:PA30847 HOVERGEN:HBG045586 InParanoid:Q8NEZ4 KO:K09188 OMA:DTSRQNK PhylomeDB:Q8NEZ4 NextBio:65023 ArrayExpress:Q8NEZ4 Bgee:Q8NEZ4 CleanEx:HS_MLL3 Genevestigator:Q8NEZ4 GermOnline:ENSG00000055609 Uniprot:Q8NEZ4
Root	Isotig00001	302	169	0.709	1.75E-07	TAIR|locus:2061310 - symbol:GUN1 "AT2G31400" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0031930 "mitochondria-nucleus signaling pathway" evidence=IMP] [GO:0010019 "chloroplast-nucleus signaling pathway" evidence=IMP] InterPro:IPR011990 InterPro:IPR002885 INTERPRO:IPR002625 GO:GO:0009507 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0003677 GO:GO:0031930 Gene3D:G3DSA:1.25.40.10 EMBL:AC007169 PROSITE:PS51375 Pfam:PF01535 Pfam:PF13812 TIGRFAMs:TIGR00756 SMART:SM00463 PROSITE:PS50828 GO:GO:0010019 Pfam:PF13041 EMBL:BX819946 IPI:IPI00538422 PIR:C84720 RefSeq:NP_180698.1 UniGene:At.20815 ProteinModelPortal:Q9SIC9 SMR:Q9SIC9 PRIDE:Q9SIC9 EnsemblPlants:AT2G31400.1 GeneID:817698 KEGG:ath:AT2G31400 GeneFarm:4937 TAIR:At2g31400 eggNOG:NOG313285 HOGENOM:HBG319251 InParanoid:Q9SIC9 OMA:GNTVYAF PhylomeDB:Q9SIC9 ProtClustDB:CLSN2683142 ArrayExpress:Q9SIC9 Genevestigator:Q9SIC9 Uniprot:Q9SIC9
Root	Isotig00002	706	384	0.750	4.73E-17	TAIR|locus:2061310 - symbol:GUN1 "AT2G31400" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0031930 "mitochondria-nucleus signaling pathway" evidence=IMP] [GO:0010019 "chloroplast-nucleus signaling pathway" evidence=IMP] InterPro:IPR011990 InterPro:IPR002885 INTERPRO:IPR002625 GO:GO:0009507 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0003677 GO:GO:0031930 Gene3D:G3DSA:1.25.40.10 EMBL:AC007169 PROSITE:PS51375 Pfam:PF01535 Pfam:PF13812 TIGRFAMs:TIGR00756 SMART:SM00463 PROSITE:PS50828 GO:GO:0010019 Pfam:PF13041 EMBL:BX819946 IPI:IPI00538422 PIR:C84720 RefSeq:NP_180698.1 UniGene:At.20815 ProteinModelPortal:Q9SIC9 SMR:Q9SIC9 PRIDE:Q9SIC9 EnsemblPlants:AT2G31400.1 GeneID:817698 KEGG:ath:AT2G31400 GeneFarm:4937 TAIR:At2g31400 eggNOG:NOG313285 HOGENOM:HBG319251 InParanoid:Q9SIC9 OMA:GNTVYAF PhylomeDB:Q9SIC9 ProtClustDB:CLSN2683142 ArrayExpress:Q9SIC9 Genevestigator:Q9SIC9 Uniprot:Q9SIC9
Root	Isotig00003	767	92	2.931	2.11E-121	TAIR|locus:2061310 - symbol:GUN1 "AT2G31400" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0031930 "mitochondria-nucleus signaling pathway" evidence=IMP] [GO:0010019 "chloroplast-nucleus signaling pathway" evidence=IMP] InterPro:IPR011990 InterPro:IPR002885 INTERPRO:IPR002625 GO:GO:0009507 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0003677 GO:GO:0031930 Gene3D:G3DSA:1.25.40.10 EMBL:AC007169 PROSITE:PS51375 Pfam:PF01535 Pfam:PF13812 TIGRFAMs:TIGR00756 SMART:SM00463 PROSITE:PS50828 GO:GO:0010019 Pfam:PF13041 EMBL:BX819946 IPI:IPI00538422 PIR:C84720 RefSeq:NP_180698.1 UniGene:At.20815 ProteinModelPortal:Q9SIC9 SMR:Q9SIC9 PRIDE:Q9SIC9 EnsemblPlants:AT2G31400.1 GeneID:817698 KEGG:ath:AT2G31400 GeneFarm:4937 TAIR:At2g31400 eggNOG:NOG313285 HOGENOM:HBG319251 InParanoid:Q9SIC9 OMA:GNTVYAF PhylomeDB:Q9SIC9 ProtClustDB:CLSN2683142 ArrayExpress:Q9SIC9 Genevestigator:Q9SIC9 Uniprot:Q9SIC9
Root	Isotig00004	767	92	2.931	2.11E-121	TAIR|locus:2061310 - symbol:GUN1 "AT2G31400" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0031930 "mitochondria-nucleus signaling pathway" evidence=IMP] [GO:0010019 "chloroplast-nucleus signaling pathway" evidence=IMP] InterPro:IPR011990 InterPro:IPR002885 INTERPRO:IPR002625 GO:GO:0009507 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0003677 GO:GO:0031930 Gene3D:G3DSA:1.25.40.10 EMBL:AC007169 PROSITE:PS51375 Pfam:PF01535 Pfam:PF13812 TIGRFAMs:TIGR00756 SMART:SM00463 PROSITE:PS50828 GO:GO:0010019 Pfam:PF13041 EMBL:BX819946 IPI:IPI00538422 PIR:C84720 RefSeq:NP_180698.1 UniGene:At.20815 ProteinModelPortal:Q9SIC9 SMR:Q9SIC9 PRIDE:Q9SIC9 EnsemblPlants:AT2G31400.1 GeneID:817698 KEGG:ath:AT2G31400 GeneFarm:4937 TAIR:At2g31400 eggNOG:NOG313285 HOGENOM:HBG319251

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						InParanoid:Q9SIC9 OMA:GNTVYAF PhylomeDB:Q9SIC9 ProtClustDB:CLSN2683142 ArrayExpress:Q9SIC9 Genevestigator:Q9SIC9 Uniprot:Q9SIC9
Root	Isotig00005	767	92	2.931	2.11E-121	TAIR|locus:2061310 - symbol:GUN1 "AT2G31400" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0031930 "mitochondria-nucleus signaling pathway" evidence=IMP] [GO:0010019 "chloroplast-nucleus signaling pathway" evidence=IMP] InterPro:IPR011990 InterPro:IPR002885 INTERPRO:IPR002625 GO:GO:0009507 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0003677 GO:GO:0031930 Gene3D:G3DSA:1.25.40.10 EMBL:AC007169 PROSITE:PS51375 Pfam:PF01535 Pfam:PF13812 TIGRFAMs:TIGR00756 SMART:SM00463 PROSITE:PS50828 GO:GO:0010019 Pfam:PF13041 EMBL:BX819946 IPI:IPI00538422 PIR:C84720 RefSeq:NP_180698.1 UniGene:At.20815 ProteinModelPortal:Q9SIC9 SMR:Q9SIC9 PRIDE:Q9SIC9 EnsemblPlants:AT2G31400.1 GeneID:817698 KEGG:ath:AT2G31400 GeneFarm:4937 TAIR:At2g31400 eggNOG:NOG313285 HOGENOM:HBG319251 InParanoid:Q9SIC9 OMA:GNTVYAF PhylomeDB:Q9SIC9 ProtClustDB:CLSN2683142 ArrayExpress:Q9SIC9 Genevestigator:Q9SIC9 Uniprot:Q9SIC9
Root	Isotig00006	766	92	2.929	3.59E-121	TAIR|locus:2061310 - symbol:GUN1 "AT2G31400" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0031930 "mitochondria-nucleus signaling pathway" evidence=IMP] [GO:0010019 "chloroplast-nucleus signaling pathway" evidence=IMP] InterPro:IPR011990 InterPro:IPR002885 INTERPRO:IPR002625 GO:GO:0009507 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0003677 GO:GO:0031930 Gene3D:G3DSA:1.25.40.10 EMBL:AC007169 PROSITE:PS51375 Pfam:PF01535 Pfam:PF13812 TIGRFAMs:TIGR00756 SMART:SM00463 PROSITE:PS50828 GO:GO:0010019 Pfam:PF13041 EMBL:BX819946 IPI:IPI00538422 PIR:C84720 RefSeq:NP_180698.1 UniGene:At.20815 ProteinModelPortal:Q9SIC9 SMR:Q9SIC9 PRIDE:Q9SIC9 EnsemblPlants:AT2G31400.1 GeneID:817698 KEGG:ath:AT2G31400 GeneFarm:4937 TAIR:At2g31400 eggNOG:NOG313285 HOGENOM:HBG319251 InParanoid:Q9SIC9 OMA:GNTVYAF PhylomeDB:Q9SIC9 ProtClustDB:CLSN2683142 ArrayExpress:Q9SIC9 Genevestigator:Q9SIC9 Uniprot:Q9SIC9
Root	Isotig00007	766	92	2.929	3.59E-121	TAIR|locus:2061310 - symbol:GUN1 "AT2G31400" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0031930 "mitochondria-nucleus signaling pathway" evidence=IMP] [GO:0010019 "chloroplast-nucleus signaling pathway" evidence=IMP] InterPro:IPR011990 InterPro:IPR002885 INTERPRO:IPR002625 GO:GO:0009507 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0003677 GO:GO:0031930 Gene3D:G3DSA:1.25.40.10 EMBL:AC007169 PROSITE:PS51375 Pfam:PF01535 Pfam:PF13812 TIGRFAMs:TIGR00756 SMART:SM00463 PROSITE:PS50828 GO:GO:0010019 Pfam:PF13041 EMBL:BX819946 IPI:IPI00538422 PIR:C84720 RefSeq:NP_180698.1 UniGene:At.20815 ProteinModelPortal:Q9SIC9 SMR:Q9SIC9 PRIDE:Q9SIC9 EnsemblPlants:AT2G31400.1 GeneID:817698 KEGG:ath:AT2G31400 GeneFarm:4937 TAIR:At2g31400 eggNOG:NOG313285 HOGENOM:HBG319251 InParanoid:Q9SIC9 OMA:GNTVYAF PhylomeDB:Q9SIC9 ProtClustDB:CLSN2683142 ArrayExpress:Q9SIC9 Genevestigator:Q9SIC9 Uniprot:Q9SIC9
Root	Isotig00008	591	44	3.619	1.75E-112	TAIR|locus:2061310 - symbol:GUN1 "AT2G31400" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0031930 "mitochondria-nucleus signaling pathway" evidence=IMP] [GO:0010019 "chloroplast-nucleus signaling pathway" evidence=IMP] InterPro:IPR011990 InterPro:IPR002885 INTERPRO:IPR002625 GO:GO:0009507 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0003677 GO:GO:0031930 Gene3D:G3DSA:1.25.40.10 EMBL:AC007169 PROSITE:PS51375 Pfam:PF01535 Pfam:PF13812 TIGRFAMs:TIGR00756 SMART:SM00463 PROSITE:PS50828 GO:GO:0010019 Pfam:PF13041 EMBL:BX819946 IPI:IPI00538422 PIR:C84720 RefSeq:NP_180698.1 UniGene:At.20815 ProteinModelPortal:Q9SIC9 SMR:Q9SIC9 PRIDE:Q9SIC9 EnsemblPlants:AT2G31400.1 GeneID:817698 KEGG:ath:AT2G31400 GeneFarm:4937 TAIR:At2g31400 eggNOG:NOG313285 HOGENOM:HBG319251 InParanoid:Q9SIC9 OMA:GNTVYAF PhylomeDB:Q9SIC9 ProtClustDB:CLSN2683142 ArrayExpress:Q9SIC9 Genevestigator:Q9SIC9 Uniprot:Q9SIC9
Root	Isotig00009	766	92	2.929	3.59E-121	TAIR|locus:2061310 - symbol:GUN1 "AT2G31400" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0031930 "mitochondria-nucleus signaling pathway" evidence=IMP] [GO:0010019 "chloroplast-nucleus signaling pathway" evidence=IMP] InterPro:IPR011990 InterPro:IPR002885 INTERPRO:IPR002625 GO:GO:0009507 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0003677 GO:GO:0031930 Gene3D:G3DSA:1.25.40.10 EMBL:AC007169 PROSITE:PS51375 Pfam:PF01535 Pfam:PF13812 TIGRFAMs:TIGR00756 SMART:SM00463 PROSITE:PS50828 GO:GO:0010019

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						Pfam:PF13041 EMBL:BX819946 IPI:IPI00538422 PIR:C84720 RefSeq:NP_180698.1 UniGene:At.20815 ProteinModelPortal:Q9SIC9 SMR:Q9SIC9 PRIDE:Q9SIC9 EnsemblPlants:AT2G31400.1 GeneID:817698 KEGG:ath:AT2G31400 GeneFarm:4937 TAIR:At2g31400 eggNOG:NOG313285 HOGENOM:HBG319251 InParanoid:Q9SIC9 OMA:GNTVYAF PhylomeDB:Q9SIC9 ProtClustDB:CLSN2683142 ArrayExpress:Q9SIC9 Genevestigator:Q9SIC9 Uniprot:Q9SIC9
Root	Isotig00010	181	240	-0.536	0.000147189	TAIR|locus:2061310 - symbol:GUN1 "AT2G31400" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0031930 "mitochondria-nucleus signaling pathway" evidence=IMP] [GO:0010019 "chloroplast-nucleus signaling pathway" evidence=IMP] InterPro:IPR011990 InterPro:IPR002885 INTERPRO:IPR002625 GO:GO:0009507 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0003677 GO:GO:0031930 Gene3D:G3DSA:1.25.40.10 EMBL:AC007169 PROSITE:PS51375 Pfam:PF01535 Pfam:PF13812 TIGRFAMs:TIGR00756 SMART:SM00463 PROSITE:PS50828 GO:GO:0010019 Pfam:PF13041 EMBL:BX819946 IPI:IPI00538422 PIR:C84720 RefSeq:NP_180698.1 UniGene:At.20815 ProteinModelPortal:Q9SIC9 SMR:Q9SIC9 PRIDE:Q9SIC9 EnsemblPlants:AT2G31400.1 GeneID:817698 KEGG:ath:AT2G31400 GeneFarm:4937 TAIR:At2g31400 eggNOG:NOG313285 HOGENOM:HBG319251 InParanoid:Q9SIC9 OMA:GNTVYAF PhylomeDB:Q9SIC9 ProtClustDB:CLSN2683142 ArrayExpress:Q9SIC9 Genevestigator:Q9SIC9 Uniprot:Q9SIC9
Root	Isotig00011	181	240	-0.536	0.000147189	TAIR|locus:2061310 - symbol:GUN1 "AT2G31400" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0031930 "mitochondria-nucleus signaling pathway" evidence=IMP] [GO:0010019 "chloroplast-nucleus signaling pathway" evidence=IMP] InterPro:IPR011990 InterPro:IPR002885 INTERPRO:IPR002625 GO:GO:0009507 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0003677 GO:GO:0031930 Gene3D:G3DSA:1.25.40.10 EMBL:AC007169 PROSITE:PS51375 Pfam:PF01535 Pfam:PF13812 TIGRFAMs:TIGR00756 SMART:SM00463 PROSITE:PS50828 GO:GO:0010019 Pfam:PF13041 EMBL:BX819946 IPI:IPI00538422 PIR:C84720 RefSeq:NP_180698.1 UniGene:At.20815 ProteinModelPortal:Q9SIC9 SMR:Q9SIC9 PRIDE:Q9SIC9 EnsemblPlants:AT2G31400.1 GeneID:817698 KEGG:ath:AT2G31400 GeneFarm:4937 TAIR:At2g31400 eggNOG:NOG313285 HOGENOM:HBG319251 InParanoid:Q9SIC9 OMA:GNTVYAF PhylomeDB:Q9SIC9 ProtClustDB:CLSN2683142 ArrayExpress:Q9SIC9 Genevestigator:Q9SIC9 Uniprot:Q9SIC9
Root	Isotig00012	616	79	2.834	1.03E-94	TAIR|locus:2061310 - symbol:GUN1 "AT2G31400" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0031930 "mitochondria-nucleus signaling pathway" evidence=IMP] [GO:0010019 "chloroplast-nucleus signaling pathway" evidence=IMP] InterPro:IPR011990 InterPro:IPR002885 INTERPRO:IPR002625 GO:GO:0009507 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0003677 GO:GO:0031930 Gene3D:G3DSA:1.25.40.10 EMBL:AC007169 PROSITE:PS51375 Pfam:PF01535 Pfam:PF13812 TIGRFAMs:TIGR00756 SMART:SM00463 PROSITE:PS50828 GO:GO:0010019 Pfam:PF13041 EMBL:BX819946 IPI:IPI00538422 PIR:C84720 RefSeq:NP_180698.1 UniGene:At.20815 ProteinModelPortal:Q9SIC9 SMR:Q9SIC9 PRIDE:Q9SIC9 EnsemblPlants:AT2G31400.1 GeneID:817698 KEGG:ath:AT2G31400 GeneFarm:4937 TAIR:At2g31400 eggNOG:NOG313285 HOGENOM:HBG319251 InParanoid:Q9SIC9 OMA:GNTVYAF PhylomeDB:Q9SIC9 ProtClustDB:CLSN2683142 ArrayExpress:Q9SIC9 Genevestigator:Q9SIC9 Uniprot:Q9SIC9
Root	Isotig00013	616	79	2.834	1.03E-94	TAIR|locus:2061310 - symbol:GUN1 "AT2G31400" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0031930 "mitochondria-nucleus signaling pathway" evidence=IMP] [GO:0010019 "chloroplast-nucleus signaling pathway" evidence=IMP] InterPro:IPR011990 InterPro:IPR002885 INTERPRO:IPR002625 GO:GO:0009507 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0003677 GO:GO:0031930 Gene3D:G3DSA:1.25.40.10 EMBL:AC007169 PROSITE:PS51375 Pfam:PF01535 Pfam:PF13812 TIGRFAMs:TIGR00756 SMART:SM00463 PROSITE:PS50828 GO:GO:0010019 Pfam:PF13041 EMBL:BX819946 IPI:IPI00538422 PIR:C84720 RefSeq:NP_180698.1 UniGene:At.20815 ProteinModelPortal:Q9SIC9 SMR:Q9SIC9 PRIDE:Q9SIC9 EnsemblPlants:AT2G31400.1 GeneID:817698 KEGG:ath:AT2G31400 GeneFarm:4937 TAIR:At2g31400 eggNOG:NOG313285 HOGENOM:HBG319251 InParanoid:Q9SIC9 OMA:GNTVYAF PhylomeDB:Q9SIC9 ProtClustDB:CLSN2683142 ArrayExpress:Q9SIC9 Genevestigator:Q9SIC9 Uniprot:Q9SIC9
Root	Isotig00014	616	79	2.834	1.03E-94	TAIR|locus:2061310 - symbol:GUN1 "AT2G31400" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0031930 "mitochondria-nucleus signaling pathway" evidence=IMP] [GO:0010019 "chloroplast-nucleus signaling pathway" evidence=IMP] InterPro:IPR011990

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						InterPro:IPR002885 INTERPRO:IPR002625 GO:GO:0009507 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0003677 GO:GO:0031930 Gene3D:G3DSA:1.25.40.10 EMBL:AC007169 PROSITE:PS51375 Pfam:PF01535 Pfam:PF13812 TIGRFAMs:TIGR00756 SMART:SM00463 PROSITE:PS50828 GO:GO:0010019 Pfam:PF13041 EMBL:BX819946 IPI:IPI00538422 PIR:C84720 RefSeq:NP_180698.1 UniGene:At.20815 ProteinModelPortal:Q9SIC9 SMR:Q9SIC9 PRIDE:Q9SIC9 EnsemblPlants:AT2G31400.1 GeneID:817698 KEGG:ath:AT2G31400 GeneFarm:4937 TAIR:At2g31400 eggNOG:NOG313285 HOGENOM:HBG319251 InParanoid:Q9SIC9 OMA:GNTVYAF PhylomeDB:Q9SIC9 ProtClustDB:CLSN2683142 ArrayExpress:Q9SIC9 Genevestigator:Q9SIC9 Uniprot:Q9SIC9
Root	Isotig00015	182	60	1.472	1.59E-13	TAIR|locus:2061310 - symbol:GUN1 "AT2G31400" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0031930 "mitochondria-nucleus signaling pathway" evidence=IMP] [GO:0010019 "chloroplast-nucleus signaling pathway" evidence=IMP] InterPro:IPR011990 InterPro:IPR002885 INTERPRO:IPR002625 GO:GO:0009507 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0003677 GO:GO:0031930 Gene3D:G3DSA:1.25.40.10 EMBL:AC007169 PROSITE:PS51375 Pfam:PF01535 Pfam:PF13812 TIGRFAMs:TIGR00756 SMART:SM00463 PROSITE:PS50828 GO:GO:0010019 Pfam:PF13041 EMBL:BX819946 IPI:IPI00538422 PIR:C84720 RefSeq:NP_180698.1 UniGene:At.20815 ProteinModelPortal:Q9SIC9 SMR:Q9SIC9 PRIDE:Q9SIC9 EnsemblPlants:AT2G31400.1 GeneID:817698 KEGG:ath:AT2G31400 GeneFarm:4937 TAIR:At2g31400 eggNOG:NOG313285 HOGENOM:HBG319251 InParanoid:Q9SIC9 OMA:GNTVYAF PhylomeDB:Q9SIC9 ProtClustDB:CLSN2683142 ArrayExpress:Q9SIC9 Genevestigator:Q9SIC9 Uniprot:Q9SIC9
Root	Isotig00016	295	160	0.754	5.06E-08	SGD|S000028422 - symbol:TAR1 "Mitochondrial protein potentially involved in respiratory metabolism" species:4932 "Saccharomyces cerevisiae" [GO:0003674 "molecular_function" evidence=ND] [GO:0043457 "regulation of cellular respiration" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IEA;IMP] SGD:S000028422 GO:GO:0005739 EMBL:BK006945 EMBL:U53879 GO:GO:0043457 EMBL:Z73326 EMBL:AF479964 RefSeq:NP_690845.1 ProteinModelPortal:Q8TGM6 STRING:Q8TGM6 EnsemblFungi:YLR154W-C GeneID:1466405 KEGG:sce:YLR154W-C CYGD:YLR154w-c eggNOG:NOG79861 OMA:SCSKEHR OrthoDB:EOG466ZX8 NextBio:967146 Genevestigator:Q8TGM6 GermOnline:YLR154W-C Uniprot:Q8TGM6
Root	Isotig00017	699	375	0.769	1.31E-17	SGD|S000028422 - symbol:TAR1 "Mitochondrial protein potentially involved in respiratory metabolism" species:4932 "Saccharomyces cerevisiae" [GO:0003674 "molecular_function" evidence=ND] [GO:0043457 "regulation of cellular respiration" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IEA;IMP] SGD:S000028422 GO:GO:0005739 EMBL:BK006945 EMBL:U53879 GO:GO:0043457 EMBL:Z73326 EMBL:AF479964 RefSeq:NP_690845.1 ProteinModelPortal:Q8TGM6 STRING:Q8TGM6 EnsemblFungi:YLR154W-C GeneID:1466405 KEGG:sce:YLR154W-C CYGD:YLR154w-c eggNOG:NOG79861 OMA:SCSKEHR OrthoDB:EOG466ZX8 NextBio:967146 Genevestigator:Q8TGM6 GermOnline:YLR154W-C Uniprot:Q8TGM6
Root	Isotig00018	760	83	3.066	1.49E-125	SGD|S000028422 - symbol:TAR1 "Mitochondrial protein potentially involved in respiratory metabolism" species:4932 "Saccharomyces cerevisiae" [GO:0003674 "molecular_function" evidence=ND] [GO:0043457 "regulation of cellular respiration" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IEA;IMP] SGD:S000028422 GO:GO:0005739 EMBL:BK006945 EMBL:U53879 GO:GO:0043457 EMBL:Z73326 EMBL:AF479964 RefSeq:NP_690845.1 ProteinModelPortal:Q8TGM6 STRING:Q8TGM6 EnsemblFungi:YLR154W-C GeneID:1466405 KEGG:sce:YLR154W-C CYGD:YLR154w-c eggNOG:NOG79861 OMA:SCSKEHR OrthoDB:EOG466ZX8 NextBio:967146 Genevestigator:Q8TGM6 GermOnline:YLR154W-C Uniprot:Q8TGM6
Root	Isotig00019	760	83	3.066	1.49E-125	SGD|S000028422 - symbol:TAR1 "Mitochondrial protein potentially involved in respiratory metabolism" species:4932 "Saccharomyces cerevisiae" [GO:0003674 "molecular_function" evidence=ND] [GO:0043457 "regulation of cellular respiration" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IEA;IMP] SGD:S000028422 GO:GO:0005739 EMBL:BK006945 EMBL:U53879 GO:GO:0043457 EMBL:Z73326 EMBL:AF479964 RefSeq:NP_690845.1 ProteinModelPortal:Q8TGM6 STRING:Q8TGM6 EnsemblFungi:YLR154W-C GeneID:1466405 KEGG:sce:YLR154W-C CYGD:YLR154w-c eggNOG:NOG79861 OMA:SCSKEHR OrthoDB:EOG466ZX8 NextBio:967146 Genevestigator:Q8TGM6 GermOnline:YLR154W-C Uniprot:Q8TGM6
Root	Isotig00020	760	83	3.066	1.49E-125	SGD|S000028422 - symbol:TAR1 "Mitochondrial protein potentially involved in respiratory metabolism" species:4932 "Saccharomyces cerevisiae" [GO:0003674 "molecular_function" evidence=ND] [GO:0043457 "regulation of cellular respiration" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IEA;IMP] SGD:S000028422 GO:GO:0005739 EMBL:BK006945 EMBL:U53879 GO:GO:0043457 EMBL:Z73326 EMBL:AF479964 RefSeq:NP_690845.1 ProteinModelPortal:Q8TGM6 STRING:Q8TGM6 EnsemblFungi:YLR154W-

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						C GeneID:1466405 KEGG:sce:YLR154W-C CYGD:YLR154w-c eggNOG:NOG79861 OMA:SCSKEHR OrthoDB:EOG466ZX8 NextBio:967146 Genevestigator:Q8TGM6 GermOnline:YLR154W-C Uniprot:Q8TGM6
Root	Isotig00021	759	83	3.064	2.55E-125	SGD|S000028422 - symbol:TAR1 "Mitochondrial protein potentially involved in respiratory metabolism" species:4932 "Saccharomyces cerevisiae" [GO:0003674 "molecular_function" evidence=ND] [GO:0043457 "regulation of cellular respiration" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IEA;IMP] SGD:S000028422 GO:GO:0005739 EMBL:BK006945 EMBL:U53879 GO:GO:0043457 EMBL:Z73326 EMBL:AF479964 RefSeq:NP_690845.1 ProteinModelPortal:Q8TGM6 STRING:Q8TGM6 EnsemblFungi:YLR154W-C GeneID:1466405 KEGG:sce:YLR154W-C CYGD:YLR154w-c eggNOG:NOG79861 OMA:SCSKEHR OrthoDB:EOG466ZX8 NextBio:967146 Genevestigator:Q8TGM6 GermOnline:YLR154W-C Uniprot:Q8TGM6
Root	Isotig00022	759	83	3.064	2.55E-125	SGD|S000028422 - symbol:TAR1 "Mitochondrial protein potentially involved in respiratory metabolism" species:4932 "Saccharomyces cerevisiae" [GO:0003674 "molecular_function" evidence=ND] [GO:0043457 "regulation of cellular respiration" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IEA;IMP] SGD:S000028422 GO:GO:0005739 EMBL:BK006945 EMBL:U53879 GO:GO:0043457 EMBL:Z73326 EMBL:AF479964 RefSeq:NP_690845.1 ProteinModelPortal:Q8TGM6 STRING:Q8TGM6 EnsemblFungi:YLR154W-C GeneID:1466405 KEGG:sce:YLR154W-C CYGD:YLR154w-c eggNOG:NOG79861 OMA:SCSKEHR OrthoDB:EOG466ZX8 NextBio:967146 Genevestigator:Q8TGM6 GermOnline:YLR154W-C Uniprot:Q8TGM6
Root	Isotig00023	584	35	3.932	1.26E-117	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00024	759	83	3.064	2.55E-125	SGD|S000028422 - symbol:TAR1 "Mitochondrial protein potentially involved in respiratory metabolism" species:4932 "Saccharomyces cerevisiae" [GO:0003674 "molecular_function" evidence=ND] [GO:0043457 "regulation of cellular respiration" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IEA;IMP] SGD:S000028422 GO:GO:0005739 EMBL:BK006945 EMBL:U53879 GO:GO:0043457 EMBL:Z73326 EMBL:AF479964 RefSeq:NP_690845.1 ProteinModelPortal:Q8TGM6 STRING:Q8TGM6 EnsemblFungi:YLR154W-C GeneID:1466405 KEGG:sce:YLR154W-C CYGD:YLR154w-c eggNOG:NOG79861 OMA:SCSKEHR OrthoDB:EOG466ZX8 NextBio:967146 Genevestigator:Q8TGM6 GermOnline:YLR154W-C Uniprot:Q8TGM6
Root	Isotig00025	92	40	1.073	4.18E-05	TAIR|locus:2061310 - symbol:GUN1 "AT2G31400" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0031930 "mitochondria-nucleus signaling pathway" evidence=IMP] [GO:0010019 "chloroplast-nucleus signaling pathway" evidence=IMP] InterPro:IPR011990 InterPro:IPR002885 INTERPRO:IPR002625 GO:GO:0009507 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0003677 GO:GO:0031930 Gene3D:G3DSA:1.25.40.10 EMBL:AC007169 PROSITE:PS51375 Pfam:PF01535 Pfam:PF13812 TIGRFAMs:TIGR00756 SMART:SM00463 PROSITE:PS50828 GO:GO:0010019 Pfam:PF13041 EMBL:BX819946 IPI:IPI00538422 PIR:C84720 RefSeq:NP_180698.1 UniGene:At.20815 ProteinModelPortal:Q9SIC9 SMR:Q9SIC9 PRIDE:Q9SIC9 EnsemblPlants:AT2G31400.1 GeneID:817698 KEGG:ath:AT2G31400 GeneFarm:4937 TAIR:At2g31400 eggNOG:NOG313285 HOGENOM:HBG319251 InParanoid:Q9SIC9 OMA:GNTVYAF PhylomeDB:Q9SIC9 ProtClustDB:CLSN2683142 ArrayExpress:Q9SIC9 Genevestigator:Q9SIC9 Uniprot:Q9SIC9
Root	Isotig00026	172	45	1.805	9.97E-17	TAIR|locus:2061310 - symbol:GUN1 "AT2G31400" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0031930 "mitochondria-nucleus signaling pathway" evidence=IMP] [GO:0010019 "chloroplast-nucleus signaling pathway" evidence=IMP] InterPro:IPR011990 InterPro:IPR002885 INTERPRO:IPR002625 GO:GO:0009507 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0003677 GO:GO:0031930 Gene3D:G3DSA:1.25.40.10 EMBL:AC007169 PROSITE:PS51375 Pfam:PF01535 Pfam:PF13812 TIGRFAMs:TIGR00756 SMART:SM00463 PROSITE:PS50828 GO:GO:0010019 Pfam:PF13041 EMBL:BX819946 IPI:IPI00538422 PIR:C84720 RefSeq:NP_180698.1 UniGene:At.20815 ProteinModelPortal:Q9SIC9 SMR:Q9SIC9 PRIDE:Q9SIC9 EnsemblPlants:AT2G31400.1 GeneID:817698 KEGG:ath:AT2G31400 GeneFarm:4937 TAIR:At2g31400 eggNOG:NOG313285 HOGENOM:HBG319251

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						InParanoid:Q9SIC9 OMA:GNTVYAF PhylomeDB:Q9SIC9 ProtClustDB:CLSN2683142 ArrayExpress:Q9SIC9 Genevestigator:Q9SIC9 Uniprot:Q9SIC9
Root	Isotig00027	174	231	-0.538	0.000187739	SGD|S000028422 - symbol:TAR1 "Mitochondrial protein potentially involved in respiratory metabolism" species:4932 "Saccharomyces cerevisiae" [GO:0003674 "molecular_function" evidence=ND] [GO:0043457 "regulation of cellular respiration" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IEA;IMP] SGD:S000028422 GO:GO:0005739 EMBL:BK006945 EMBL:U53879 GO:GO:0043457 EMBL:Z73326 EMBL:AF479964 RefSeq:NP_690845.1 ProteinModelPortal:Q8TGM6 STRING:Q8TGM6 EnsemblFungi:YLR154W-C GeneID:1466405 KEGG:sce:YLR154W-C CYGD:YLR154w-c eggNOG:NOG79861 OMA:SCSKEHR OrthoDB:EOG466ZX8 NextBio:967146 Genevestigator:Q8TGM6 GermOnline:YLR154W-C Uniprot:Q8TGM6
Root	Isotig00028	174	231	-0.538	0.000187739	SGD|S000028422 - symbol:TAR1 "Mitochondrial protein potentially involved in respiratory metabolism" species:4932 "Saccharomyces cerevisiae" [GO:0003674 "molecular_function" evidence=ND] [GO:0043457 "regulation of cellular respiration" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IEA;IMP] SGD:S000028422 GO:GO:0005739 EMBL:BK006945 EMBL:U53879 GO:GO:0043457 EMBL:Z73326 EMBL:AF479964 RefSeq:NP_690845.1 ProteinModelPortal:Q8TGM6 STRING:Q8TGM6 EnsemblFungi:YLR154W-C GeneID:1466405 KEGG:sce:YLR154W-C CYGD:YLR154w-c eggNOG:NOG79861 OMA:SCSKEHR OrthoDB:EOG466ZX8 NextBio:967146 Genevestigator:Q8TGM6 GermOnline:YLR154W-C Uniprot:Q8TGM6
Root	Isotig00029	609	70	2.992	1.02E-98	SGD|S000028422 - symbol:TAR1 "Mitochondrial protein potentially involved in respiratory metabolism" species:4932 "Saccharomyces cerevisiae" [GO:0003674 "molecular_function" evidence=ND] [GO:0043457 "regulation of cellular respiration" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IEA;IMP] SGD:S000028422 GO:GO:0005739 EMBL:BK006945 EMBL:U53879 GO:GO:0043457 EMBL:Z73326 EMBL:AF479964 RefSeq:NP_690845.1 ProteinModelPortal:Q8TGM6 STRING:Q8TGM6 EnsemblFungi:YLR154W-C GeneID:1466405 KEGG:sce:YLR154W-C CYGD:YLR154w-c eggNOG:NOG79861 OMA:SCSKEHR OrthoDB:EOG466ZX8 NextBio:967146 Genevestigator:Q8TGM6 GermOnline:YLR154W-C Uniprot:Q8TGM6
Root	Isotig00030	609	70	2.992	1.02E-98	SGD|S000028422 - symbol:TAR1 "Mitochondrial protein potentially involved in respiratory metabolism" species:4932 "Saccharomyces cerevisiae" [GO:0003674 "molecular_function" evidence=ND] [GO:0043457 "regulation of cellular respiration" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IEA;IMP] SGD:S000028422 GO:GO:0005739 EMBL:BK006945 EMBL:U53879 GO:GO:0043457 EMBL:Z73326 EMBL:AF479964 RefSeq:NP_690845.1 ProteinModelPortal:Q8TGM6 STRING:Q8TGM6 EnsemblFungi:YLR154W-C GeneID:1466405 KEGG:sce:YLR154W-C CYGD:YLR154w-c eggNOG:NOG79861 OMA:SCSKEHR OrthoDB:EOG466ZX8 NextBio:967146 Genevestigator:Q8TGM6 GermOnline:YLR154W-C Uniprot:Q8TGM6
Root	Isotig00031	609	70	2.992	1.02E-98	SGD|S000028422 - symbol:TAR1 "Mitochondrial protein potentially involved in respiratory metabolism" species:4932 "Saccharomyces cerevisiae" [GO:0003674 "molecular_function" evidence=ND] [GO:0043457 "regulation of cellular respiration" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IEA;IMP] SGD:S000028422 GO:GO:0005739 EMBL:BK006945 EMBL:U53879 GO:GO:0043457 EMBL:Z73326 EMBL:AF479964 RefSeq:NP_690845.1 ProteinModelPortal:Q8TGM6 STRING:Q8TGM6 EnsemblFungi:YLR154W-C GeneID:1466405 KEGG:sce:YLR154W-C CYGD:YLR154w-c eggNOG:NOG79861 OMA:SCSKEHR OrthoDB:EOG466ZX8 NextBio:967146 Genevestigator:Q8TGM6 GermOnline:YLR154W-C Uniprot:Q8TGM6
Root	Isotig00032	100	41	1.157	5.58E-06	TAIR|locus:2061310 - symbol:GUN1 "AT2G31400" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0031930 "mitochondria-nucleus signaling pathway" evidence=IMP] [GO:0010019 "chloroplast-nucleus signaling pathway" evidence=IMP] InterPro:IPR011990 InterPro:IPR002885 INTERPRO:IPR002625 GO:GO:0009507 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0003677 GO:GO:0031930 Gene3D:G3DSA:1.25.40.10 EMBL:AC007169 PROSITE:PS51375 Pfam:PF01535 Pfam:PF13812 TIGRFAMs:TIGR00756 SMART:SM00463 PROSITE:PS50828 GO:GO:0010019 Pfam:PF13041 EMBL:BX819946 IPI:IPI00538422 PIR:C84720 RefSeq:NP_180698.1 UniGene:At.20815 ProteinModelPortal:Q9SIC9 SMR:Q9SIC9 PRIDE:Q9SIC9 EnsemblPlants:AT2G31400.1 GeneID:817698 KEGG:ath:AT2G31400 GeneFarm:4937 TAIR:At2g31400 eggNOG:NOG313285 HOGENOM:HBG319251 InParanoid:Q9SIC9 OMA:GNTVYAF PhylomeDB:Q9SIC9 ProtClustDB:CLSN2683142 ArrayExpress:Q9SIC9 Genevestigator:Q9SIC9 Uniprot:Q9SIC9
Root	Isotig00033	175	51	1.650	3.71E-15	SGD|S000028422 - symbol:TAR1 "Mitochondrial protein potentially involved in respiratory metabolism" species:4932 "Saccharomyces cerevisiae" [GO:0003674 "molecular_function" evidence=ND] [GO:0043457 "regulation of cellular respiration" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IEA;IMP] SGD:S000028422 GO:GO:0005739 EMBL:BK006945 EMBL:U53879 GO:GO:0043457 EMBL:Z73326

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
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Root	Isotig00034	85	31	1.326	3.17E-06	SGD|S000028422 - symbol:TAR1 "Mitochondrial protein potentially involved in respiratory metabolism" species:4932 "Saccharomyces cerevisiae" [GO:0003674 "molecular_function" evidence=ND] [GO:0043457 "regulation of cellular respiration" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IEA;IMP] SGD:S000028422 GO:GO:0005739 EMBL:BK006945 EMBL:U53879 GO:GO:0043457 EMBL:Z73326 EMBL:AF479964 RefSeq:NP_690845.1 ProteinModelPortal:Q8TGM6 STRING:Q8TGM6 EnsemblFungi:YLR154W-C GeneID:1466405 KEGG:sce:YLR154W-C CYGD:YLR154w-c eggNOG:NOG79861 OMA:SCSKEHR OrthoDB:EOG466ZX8 NextBio:967146 Genevestigator:Q8TGM6 GermOnline:YLR154W-C Uniprot:Q8TGM6
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Root	Isotig00037	93	32	1.410	3.26E-07	SGD|S000028422 - symbol:TAR1 "Mitochondrial protein potentially involved in respiratory metabolism" species:4932 "Saccharomyces cerevisiae" [GO:0003674 "molecular_function" evidence=ND] [GO:0043457 "regulation of cellular respiration" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IEA;IMP] SGD:S000028422 GO:GO:0005739 EMBL:BK006945 EMBL:U53879 GO:GO:0043457 EMBL:Z73326 EMBL:AF479964 RefSeq:NP_690845.1 ProteinModelPortal:Q8TGM6 STRING:Q8TGM6 EnsemblFungi:YLR154W-C GeneID:1466405 KEGG:sce:YLR154W-C CYGD:YLR154w-c eggNOG:NOG79861 OMA:SCSKEHR OrthoDB:EOG466ZX8 NextBio:967146 Genevestigator:Q8TGM6 GermOnline:YLR154W-C Uniprot:Q8TGM6
Root	Isotig00038	409	168	1.155	4.71E-20	No hit
Root	Isotig00039	419	177	1.114	1.88E-19	No hit
Root	Isotig00040	406	168	1.144	1.20E-19	No hit
Root	Isotig00041	410	168	1.158	3.45E-20	No hit
Root	Isotig00042	407	165	1.174	1.91E-20	No hit
Root	Isotig00043	416	177	1.104	4.66E-19	No hit
Root	Isotig00044	420	177	1.118	1.39E-19	No hit
Root	Isotig00045	417	174	1.132	7.96E-20	No hit
Root	Isotig00046	407	168	1.148	8.77E-20	No hit
Root	Isotig00047	404	165	1.163	4.90E-20	No hit
Root	Isotig00048	417	177	1.107	3.45E-19	No hit
Root	Isotig00049	414	174	1.122	1.99E-19	No hit
Root	Isotig00050	387	161	1.136	1.29E-18	SGD|S000028422 - symbol:TAR1 "Mitochondrial protein potentially involved in respiratory metabolism" species:4932 "Saccharomyces cerevisiae" [GO:0003674 "molecular_function" evidence=ND] [GO:0043457 "regulation of cellular respiration" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IEA;IMP] SGD:S000028422 GO:GO:0005739 EMBL:BK006945 EMBL:U53879 GO:GO:0043457 EMBL:Z73326 EMBL:AF479964 RefSeq:NP_690845.1 ProteinModelPortal:Q8TGM6 STRING:Q8TGM6 EnsemblFungi:YLR154W-C GeneID:1466405 KEGG:sce:YLR154W-C CYGD:YLR154w-c eggNOG:NOG79861 OMA:SCSKEHR OrthoDB:EOG466ZX8 NextBio:967146 Genevestigator:Q8TGM6 GermOnline:YLR154W-C Uniprot:Q8TGM6
Root	Isotig00051	386	159	1.151	6.47E-19	SGD|S000028422 - symbol:TAR1 "Mitochondrial protein potentially involved in respiratory metabolism" species:4932 "Saccharomyces cerevisiae" [GO:0003674 "molecular_function" evidence=ND] [GO:0043457 "regulation of cellular respiration" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IEA;IMP] SGD:S000028422 GO:GO:0005739 EMBL:BK006945 EMBL:U53879 GO:GO:0043457 EMBL:Z73326 EMBL:AF479964 RefSeq:NP_690845.1 ProteinModelPortal:Q8TGM6 STRING:Q8TGM6 EnsemblFungi:YLR154W-C GeneID:1466405 KEGG:sce:YLR154W-C CYGD:YLR154w-c eggNOG:NOG79861 OMA:SCSKEHR OrthoDB:EOG466ZX8 NextBio:967146 Genevestigator:Q8TGM6 GermOnline:YLR154W-C Uniprot:Q8TGM6
Root	Isotig00052	387	161	1.136	1.29E-18	No hit

<table>
<tr><th>Tissue</th><th>Identification</th><th># of reads (stress)</th><th># of reads (control)</th><th>Fold Change</th><th>p-value</th><th>Description</th></tr>
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<tr><td>Root</td><td>Isotig00058</td><td>388</td><td>161</td><td>1.140</td><td>9.49E-19</td><td>SGD|S000028422 - symbol:TAR1 "Mitochondrial protein potentially involved in respiratory metabolism" species:4932 "Saccharomyces cerevisiae" [GO:0003674 "molecular_function" evidence=ND] [GO:0043457 "regulation of cellular respiration" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IEA;IMP] SGD:S000028422 GO:GO:0005739 EMBL:BK006945 EMBL:U53879 GO:GO:0043457 EMBL:Z73326 EMBL:AF479964 RefSeq:NP_690845.1 ProteinModelPortal:Q8TGM6 STRING:Q8TGM6 EnsemblFungi:YLR154W-C GeneID:1466405 KEGG:sce:YLR154W-C CYGD:YLR154w-c eggNOG:NOG79861 OMA:SCSKEHR OrthoDB:EOG466ZX8 NextBio:967146 Genevestigator:Q8TGM6 GermOnline:YLR154W-C Uniprot:Q8TGM6</td></tr>
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<tr><td>Root</td><td>Isotig00060</td><td>387</td><td>159</td><td>1.154</td><td>4.74E-19</td><td>SGD|S000028422 - symbol:TAR1 "Mitochondrial protein potentially involved in respiratory metabolism" species:4932 "Saccharomyces cerevisiae" [GO:0003674 "molecular_function" evidence=ND] [GO:0043457 "regulation of cellular respiration" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IEA;IMP] SGD:S000028422 GO:GO:0005739 EMBL:BK006945 EMBL:U53879 GO:GO:0043457 EMBL:Z73326 EMBL:AF479964 RefSeq:NP_690845.1 ProteinModelPortal:Q8TGM6 STRING:Q8TGM6 EnsemblFungi:YLR154W-C GeneID:1466405 KEGG:sce:YLR154W-C CYGD:YLR154w-c eggNOG:NOG79861 OMA:SCSKEHR OrthoDB:EOG466ZX8 NextBio:967146 Genevestigator:Q8TGM6 GermOnline:YLR154W-C Uniprot:Q8TGM6</td></tr>
<tr><td>Root</td><td>Isotig00061</td><td>384</td><td>156</td><td>1.171</td><td>2.63E-19</td><td>SGD|S000028422 - symbol:TAR1 "Mitochondrial protein potentially involved in respiratory metabolism" species:4932 "Saccharomyces cerevisiae" [GO:0003674 "molecular_function" evidence=ND] [GO:0043457 "regulation of cellular respiration" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IEA;IMP] SGD:S000028422 GO:GO:0005739 EMBL:BK006945 EMBL:U53879 GO:GO:0043457 EMBL:Z73326 EMBL:AF479964 RefSeq:NP_690845.1 ProteinModelPortal:Q8TGM6 STRING:Q8TGM6 EnsemblFungi:YLR154W-C GeneID:1466405 KEGG:sce:YLR154W-C CYGD:YLR154w-c eggNOG:NOG79861 OMA:SCSKEHR OrthoDB:EOG466ZX8 NextBio:967146 Genevestigator:Q8TGM6 GermOnline:YLR154W-C Uniprot:Q8TGM6</td></tr>
<tr><td>Root</td><td>Isotig00062</td><td>388</td><td>161</td><td>1.140</td><td>9.49E-19</td><td>No hit</td></tr>
<tr><td>Root</td><td>Isotig00063</td><td>385</td><td>158</td><td>1.156</td><td>5.33E-19</td><td>No hit</td></tr>
<tr><td>Root</td><td>Isotig00064</td><td>387</td><td>159</td><td>1.154</td><td>4.74E-19</td><td>No hit</td></tr>
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<tr><td>Root</td><td>Isotig00066</td><td>398</td><td>170</td><td>1.098</td><td>3.66E-18</td><td>SGD|S000028422 - symbol:TAR1 "Mitochondrial protein potentially involved in respiratory metabolism" species:4932 "Saccharomyces cerevisiae" [GO:0003674 "molecular_function" evidence=ND] [GO:0043457 "regulation of cellular respiration" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IEA;IMP]</td></tr>
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Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
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Root	Isotig00067	395	167	1.113	2.13E-18	SGD|S000028422 - symbol:TAR1 "Mitochondrial protein potentially involved in respiratory metabolism" species:4932 "Saccharomyces cerevisiae" [GO:0003674 "molecular_function" evidence=ND] [GO:0043457 "regulation of cellular respiration" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IEA;IMP] SGD:S000028422 GO:GO:0005739 EMBL:BK006945 EMBL:U53879 GO:GO:0043457 EMBL:Z73326 EMBL:AF479964 RefSeq:NP_690845.1 ProteinModelPortal:Q8TGM6 STRING:Q8TGM6 EnsemblFungi:YLR154W-C GeneID:1466405 KEGG:sce:YLR154W-C CYGD:YLR154w-c eggNOG:NOG79861 OMA:SCSKEHR OrthoDB:EOG466ZX8 NextBio:967146 Genevestigator:Q8TGM6 GermOnline:YLR154W-C Uniprot:Q8TGM6
Root	Isotig00068	397	168	1.112	1.89E-18	SGD|S000028422 - symbol:TAR1 "Mitochondrial protein potentially involved in respiratory metabolism" species:4932 "Saccharomyces cerevisiae" [GO:0003674 "molecular_function" evidence=ND] [GO:0043457 "regulation of cellular respiration" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IEA;IMP] SGD:S000028422 GO:GO:0005739 EMBL:BK006945 EMBL:U53879 GO:GO:0043457 EMBL:Z73326 EMBL:AF479964 RefSeq:NP_690845.1 ProteinModelPortal:Q8TGM6 STRING:Q8TGM6 EnsemblFungi:YLR154W-C GeneID:1466405 KEGG:sce:YLR154W-C CYGD:YLR154w-c eggNOG:NOG79861 OMA:SCSKEHR OrthoDB:EOG466ZX8 NextBio:967146 Genevestigator:Q8TGM6 GermOnline:YLR154W-C Uniprot:Q8TGM6
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Root	Isotig00070	398	170	1.098	3.66E-18	No hit
Root	Isotig00071	395	167	1.113	2.13E-18	No hit
Root	Isotig00072	397	168	1.112	1.89E-18	No hit
Root	Isotig00073	394	165	1.127	1.09E-18	No hit
Root	Isotig00078	180	75	1.134	2.03E-09	No hit
Root	Isotig00079	190	84	1.049	7.45E-09	No hit
Root	Isotig00082	202	80	1.207	2.45E-11	SGD|S000028422 - symbol:TAR1 "Mitochondrial protein potentially involved in respiratory metabolism" species:4932 "Saccharomyces cerevisiae" [GO:0003674 "molecular_function" evidence=ND] [GO:0043457 "regulation of cellular respiration" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IEA;IMP] SGD:S000028422 GO:GO:0005739 EMBL:BK006945 EMBL:U53879 GO:GO:0043457 EMBL:Z73326 EMBL:AF479964 RefSeq:NP_690845.1 ProteinModelPortal:Q8TGM6 STRING:Q8TGM6 EnsemblFungi:YLR154W-C GeneID:1466405 KEGG:sce:YLR154W-C CYGD:YLR154w-c eggNOG:NOG79861 OMA:SCSKEHR OrthoDB:EOG466ZX8 NextBio:967146 Genevestigator:Q8TGM6 GermOnline:YLR154W-C Uniprot:Q8TGM6
Root	Isotig00083	199	80	1.186	6.47E-11	No hit
Root	Isotig00084	180	73	1.173	7.29E-10	SGD|S000028422 - symbol:TAR1 "Mitochondrial protein potentially involved in respiratory metabolism" species:4932 "Saccharomyces cerevisiae" [GO:0003674 "molecular_function" evidence=ND] [GO:0043457 "regulation of cellular respiration" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IEA;IMP] SGD:S000028422 GO:GO:0005739 EMBL:BK006945 EMBL:U53879 GO:GO:0043457 EMBL:Z73326 EMBL:AF479964 RefSeq:NP_690845.1 ProteinModelPortal:Q8TGM6 STRING:Q8TGM6 EnsemblFungi:YLR154W-C GeneID:1466405 KEGG:sce:YLR154W-C CYGD:YLR154w-c eggNOG:NOG79861 OMA:SCSKEHR OrthoDB:EOG466ZX8 NextBio:967146 Genevestigator:Q8TGM6 GermOnline:YLR154W-C Uniprot:Q8TGM6
Root	Isotig00085	179	71	1.205	3.49E-10	SGD|S000028422 - symbol:TAR1 "Mitochondrial protein potentially involved in respiratory metabolism" species:4932 "Saccharomyces cerevisiae" [GO:0003674 "molecular_function" evidence=ND] [GO:0043457 "regulation of cellular respiration" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IEA;IMP] SGD:S000028422 GO:GO:0005739 EMBL:BK006945 EMBL:U53879 GO:GO:0043457 EMBL:Z73326 EMBL:AF479964 RefSeq:NP_690845.1 ProteinModelPortal:Q8TGM6 STRING:Q8TGM6 EnsemblFungi:YLR154W-

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						C GeneID:1466405 KEGG:sce:YLR154W-C CYGD:YLR154w-c eggNOG:NOG79861 OMA:SCSKEHR OrthoDB:EOG466ZX8 NextBio:967146 Genevestigator:Q8TGM6 GermOnline:YLR154W-C Uniprot:Q8TGM6
Root	Isotig00086	180	73	1.173	7.29E-10	No hit
Root	Isotig00087	179	71	1.205	3.49E-10	No hit
Root	Isotig00088	2770	3117	-0.299	1.40E-15	SGD|S000028422 - symbol:TAR1 "Mitochondrial protein potentially involved in respiratory metabolism" species:4932 "Saccharomyces cerevisiae" [GO:0003674 "molecular_function" evidence=ND] [GO:0043457 "regulation of cellular respiration" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IEA;IMP] SGD:S000028422 GO:GO:0005739 EMBL:BK006945 EMBL:U53879 GO:GO:0043457 EMBL:Z73326 EMBL:AF479964 RefSeq:NP_690845.1 ProteinModelPortal:Q8TGM6 STRING:Q8TGM6 EnsemblFungi:YLR154W-C GeneID:1466405 KEGG:sce:YLR154W-C CYGD:YLR154w-c eggNOG:NOG79861 OMA:SCSKEHR OrthoDB:EOG466ZX8 NextBio:967146 Genevestigator:Q8TGM6 GermOnline:YLR154W-C Uniprot:Q8TGM6
Root	Isotig00089	2770	3116	-0.299	1.55E-15	SGD|S000028422 - symbol:TAR1 "Mitochondrial protein potentially involved in respiratory metabolism" species:4932 "Saccharomyces cerevisiae" [GO:0003674 "molecular_function" evidence=ND] [GO:0043457 "regulation of cellular respiration" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IEA;IMP] SGD:S000028422 GO:GO:0005739 EMBL:BK006945 EMBL:U53879 GO:GO:0043457 EMBL:Z73326 EMBL:AF479964 RefSeq:NP_690845.1 ProteinModelPortal:Q8TGM6 STRING:Q8TGM6 EnsemblFungi:YLR154W-C GeneID:1466405 KEGG:sce:YLR154W-C CYGD:YLR154w-c eggNOG:NOG79861 OMA:SCSKEHR OrthoDB:EOG466ZX8 NextBio:967146 Genevestigator:Q8TGM6 GermOnline:YLR154W-C Uniprot:Q8TGM6
Root	Isotig00090	2770	3117	-0.299	1.40E-15	SGD|S000028422 - symbol:TAR1 "Mitochondrial protein potentially involved in respiratory metabolism" species:4932 "Saccharomyces cerevisiae" [GO:0003674 "molecular_function" evidence=ND] [GO:0043457 "regulation of cellular respiration" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IEA;IMP] SGD:S000028422 GO:GO:0005739 EMBL:BK006945 EMBL:U53879 GO:GO:0043457 EMBL:Z73326 EMBL:AF479964 RefSeq:NP_690845.1 ProteinModelPortal:Q8TGM6 STRING:Q8TGM6 EnsemblFungi:YLR154W-C GeneID:1466405 KEGG:sce:YLR154W-C CYGD:YLR154w-c eggNOG:NOG79861 OMA:SCSKEHR OrthoDB:EOG466ZX8 NextBio:967146 Genevestigator:Q8TGM6 GermOnline:YLR154W-C Uniprot:Q8TGM6
Root	Isotig00091	2689	3059	-0.315	1.01E-16	TAIR|locus:2825935 - symbol:AT1G28135 "AT1G28135" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002684 GenomeReviews:CT485782_GR EMBL:BT010779 EMBL:BT014675 IPI:IPI00538576 RefSeq:NP_174135.1 UniGene:At.48243 IntAct:Q6IDD0 PRIDE:Q6IDD0 EnsemblPlants:AT1G28135.1 GeneID:839707 KEGG:ath:AT1G28135 TAIR:At1g28135 Genevestigator:Q6IDD0 Uniprot:Q6IDD0
Root	Isotig00092	2688	3060	-0.316	8.11E-17	TAIR|locus:2825935 - symbol:AT1G28135 "AT1G28135" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002684 GenomeReviews:CT485782_GR EMBL:BT010779 EMBL:BT014675 IPI:IPI00538576 RefSeq:NP_174135.1 UniGene:At.48243 IntAct:Q6IDD0 PRIDE:Q6IDD0 EnsemblPlants:AT1G28135.1 GeneID:839707 KEGG:ath:AT1G28135 TAIR:At1g28135 Genevestigator:Q6IDD0 Uniprot:Q6IDD0
Root	Isotig00093	2338	1619	0.401	3.31E-18	SGD|S000028422 - symbol:TAR1 "Mitochondrial protein potentially involved in respiratory metabolism" species:4932 "Saccharomyces cerevisiae" [GO:0003674 "molecular_function" evidence=ND] [GO:0043457 "regulation of cellular respiration" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IEA;IMP] SGD:S000028422 GO:GO:0005739 EMBL:BK006945 EMBL:U53879 GO:GO:0043457 EMBL:Z73326 EMBL:AF479964 RefSeq:NP_690845.1 ProteinModelPortal:Q8TGM6 STRING:Q8TGM6 EnsemblFungi:YLR154W-C GeneID:1466405 KEGG:sce:YLR154W-C CYGD:YLR154w-c eggNOG:NOG79861 OMA:SCSKEHR OrthoDB:EOG466ZX8 NextBio:967146 Genevestigator:Q8TGM6 GermOnline:YLR154W-C Uniprot:Q8TGM6
Root	Isotig00094	2338	1618	0.402	2.82E-18	SGD|S000028422 - symbol:TAR1 "Mitochondrial protein potentially involved in respiratory metabolism" species:4932 "Saccharomyces cerevisiae" [GO:0003674 "molecular_function" evidence=ND] [GO:0043457 "regulation of cellular respiration" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IEA;IMP] SGD:S000028422 GO:GO:0005739 EMBL:BK006945 EMBL:U53879 GO:GO:0043457 EMBL:Z73326 EMBL:AF479964 RefSeq:NP_690845.1 ProteinModelPortal:Q8TGM6 STRING:Q8TGM6 EnsemblFungi:YLR154W-C GeneID:1466405 KEGG:sce:YLR154W-C CYGD:YLR154w-c eggNOG:NOG79861 OMA:SCSKEHR OrthoDB:EOG466ZX8 NextBio:967146 Genevestigator:Q8TGM6 GermOnline:YLR154W-C Uniprot:Q8TGM6
Root	Isotig00095	2338	1619	0.401	3.31E-18	SGD|S000028422 - symbol:TAR1 "Mitochondrial protein potentially involved in respiratory metabolism" species:4932 "Saccharomyces cerevisiae" [GO:0003674 "molecular_function" evidence=ND] [GO:0043457 "regulation of cellular respiration" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IEA;IMP]

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						SGD:S000028422 GO:GO:0005739 EMBL:BK006945 EMBL:U53879 GO:GO:0043457 EMBL:Z73326 EMBL:AF479964 RefSeq:NP_690845.1 ProteinModelPortal:Q8TGM6 STRING:Q8TGM6 EnsemblFungi:YLR154W-C GeneID:1466405 KEGG:sce:YLR154W-C CYGD:YLR154w-c eggNOG:NOG79861 OMA:SCSKEHR OrthoDB:EOG466ZX8 NextBio:967146 Genevestigator:Q8TGM6 GermOnline:YLR154W-C Uniprot:Q8TGM6
Root	Isotig00096	2257	1561	0.403	9.29E-18	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00097	2256	1562	0.401	1.24E-17	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00098	1982	1295	0.485	1.42E-21	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00106	659	438	0.460	1.64E-07	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00109	414	157	1.270	2.61E-23	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00110	415	157	1.273	1.87E-23	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig00111	392	148	1.276	2.57E-22	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00112	393	148	1.280	1.84E-22	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00113	401	155	1.242	6.42E-22	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00114	404	156	1.244	4.15E-22	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00115	377	149	1.210	6.26E-20	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00116	414	157	1.270	2.61E-23	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00117	414	157	1.270	2.61E-23	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00118	379	146	1.247	6.38E-21	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00119	382	147	1.249	4.11E-21	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00120	378	149	1.214	4.53E-20	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00121	415	157	1.273	1.87E-23	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00122	355	140	1.213	6.28E-19	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00123	415	157	1.273	1.87E-23	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig00124	392	148	1.276	2.57E-22	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00125	392	148	1.276	2.57E-22	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00126	356	140	1.217	4.54E-19	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00127	364	147	1.179	1.41E-18	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00128	367	148	1.181	9.11E-19	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00129	393	148	1.280	1.84E-22	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00130	401	155	1.242	6.42E-22	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00131	404	156	1.244	4.15E-22	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00132	393	148	1.280	1.84E-22	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00133	401	155	1.242	6.42E-22	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00134	404	156	1.244	4.15E-22	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00135	342	138	1.180	1.42E-17	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00136	345	139	1.183	9.18E-18	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig00137	379	146	1.247	6.38E-21	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00138	382	147	1.249	4.11E-21	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00139	379	146	1.247	6.38E-21	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00140	382	147	1.249	4.11E-21	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00141	317	126	1.202	7.71E-17	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00142	318	126	1.207	5.58E-17	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00143	295	117	1.205	7.78E-16	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00144	296	117	1.210	5.63E-16	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00145	304	124	1.165	1.71E-15	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00146	307	125	1.167	1.11E-15	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00147	386	147	1.264	1.09E-21	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00148	282	115	1.165	1.74E-14	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00149	285	116	1.168	1.13E-14	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig00150	387	147	1.268	7.80E-22	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00151	373	145	1.234	2.65E-20	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00152	376	146	1.236	1.71E-20	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00153	349	139	1.199	2.56E-18	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00154	386	147	1.264	1.09E-21	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00155	386	147	1.264	1.09E-21	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00156	350	139	1.203	1.85E-18	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00157	387	147	1.268	7.80E-22	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00158	387	147	1.268	7.80E-22	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00159	336	137	1.165	5.64E-17	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00160	339	138	1.168	3.66E-17	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00161	373	145	1.234	2.65E-20	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00162	376	146	1.236	1.71E-20	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig00163	373	145	1.234	2.65E-20	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00164	376	146	1.236	1.71E-20	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00165	289	116	1.188	3.16E-15	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00166	290	116	1.193	2.29E-15	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00167	229	83	1.335	1.48E-14	SGD|S000028422 - symbol:TAR1 "Mitochondrial protein potentially involved in respiratory metabolism" species:4932 "Saccharomyces cerevisiae" [GO:0003674 "molecular_function" evidence=ND] [GO:0043457 "regulation of cellular respiration" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IEA;IMP] SGD:S000028422 GO:GO:0005739 EMBL:BK006945 EMBL:U53879 GO:GO:0043457 EMBL:Z73326 EMBL:AF479964 RefSeq:NP_690845.1 ProteinModelPortal:Q8TGM6 STRING:Q8TGM6 EnsemblFungi:YLR154W-C GeneID:1466405 KEGG:sce:YLR154W-C CYGD:YLR154w-c eggNOG:NOG79861 OMA:SCSKEHR OrthoDB:EOG466ZX8 NextBio:967146 Genevestigator:Q8TGM6 GermOnline:YLR154W-C Uniprot:Q8TGM6
Root	Isotig00168	276	114	1.147	6.85E-14	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00169	279	115	1.150	4.45E-14	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00170	175	73	1.132	3.54E-09	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00171	207	74	1.355	1.43E-13	SGD|S000028422 - symbol:TAR1 "Mitochondrial protein potentially involved in respiratory metabolism" species:4932 "Saccharomyces cerevisiae" [GO:0003674 "molecular_function" evidence=ND] [GO:0043457 "regulation of cellular respiration" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IEA;IMP] SGD:S000028422 GO:GO:0005739 EMBL:BK006945 EMBL:U53879 GO:GO:0043457 EMBL:Z73326 EMBL:AF479964 RefSeq:NP_690845.1 ProteinModelPortal:Q8TGM6 STRING:Q8TGM6 EnsemblFungi:YLR154W-C GeneID:1466405 KEGG:sce:YLR154W-C CYGD:YLR154w-c eggNOG:NOG79861 OMA:SCSKEHR OrthoDB:EOG466ZX8 NextBio:967146 Genevestigator:Q8TGM6 GermOnline:YLR154W-C Uniprot:Q8TGM6
Root	Isotig00172	138	65	0.957	4.91E-06	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00173	175	73	1.132	3.54E-09	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00174	175	73	1.132	3.54E-09	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00176	201	73	1.332	6.41E-13	RGD|727924 - symbol:LOC257642 "rRNA promoter binding protein" species:10116 "Rattus norvegicus" [GO:0003690 "double-stranded DNA binding" evidence=IDA] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=IDA] [GO:0008134 "transcription factor binding" evidence=IDA] [GO:0008283 "cell proliferation" evidence=IDA] [GO:0009303 "rRNA transcription" evidence=IDA] RGD:727924 GO:GO:0008134 GO:GO:0008283 GO:GO:0003700 GO:GO:0003690 GO:GO:0009303 EMBL:U77931 IPI:IPI00195015 RefSeq:NP_671477.1 GeneID:257642 KEGG:rno:257642 NextBio:624170 Genevestigator:Q99JC0 Uniprot:Q99JC0
Root	Isotig00177	92	26	1.694	6.24E-09	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00178	92	26	1.694	6.24E-09	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00179	92	26	1.694	6.24E-09	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00180	94	188	-1.129	1.72E-10	TAIR|locus:2120532 - symbol:CSLC12 "AT4G07960" species:3702 "Arabidopsis thaliana" [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0016759 "cellulose synthase activity" evidence=ISS] [GO:0009506 "plasmodesma" evidence=IDA] GO:GO:0016021 GO:GO:0009506 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0000139 GO:GO:0007047 GO:GO:0016757 CAZy:GT2 eggNOG:COG1215 HOGENOM:HBG602904 EMBL:AC006266 EMBL:AL161508 EMBL:AK118480 EMBL:AY087066 EMBL:BT008770 IPI:IPI00545815 PIR:B85078 RefSeq:NP_192536.1 UniGene:At.33785 ProteinModelPortal:Q9ZQB9 STRING:Q9ZQB9 PRIDE:Q9ZQB9 EnsemblPlants:AT4G07960.1 GeneID:826301 KEGG:ath:AT4G07960 TAIR:At4g07960 InParanoid:Q9ZQB9 OMA:FEIAAYF PhylomeDB:Q9ZQB9 ProtClustDB:CLSN2685849 ArrayExpress:Q9ZQB9 Genevestigator:Q9ZQB9 Uniprot:Q9ZQB9
Root	Isotig00181	94	188	-1.129	1.72E-10	TAIR|locus:2120532 - symbol:CSLC12 "AT4G07960" species:3702 "Arabidopsis thaliana" [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0016759 "cellulose synthase activity" evidence=ISS] [GO:0009506 "plasmodesma" evidence=IDA] GO:GO:0016021 GO:GO:0009506 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0000139 GO:GO:0007047 GO:GO:0016757 CAZy:GT2 eggNOG:COG1215 HOGENOM:HBG602904 EMBL:AC006266 EMBL:AL161508 EMBL:AK118480 EMBL:AY087066 EMBL:BT008770 IPI:IPI00545815 PIR:B85078 RefSeq:NP_192536.1 UniGene:At.33785 ProteinModelPortal:Q9ZQB9 STRING:Q9ZQB9 PRIDE:Q9ZQB9 EnsemblPlants:AT4G07960.1 GeneID:826301 KEGG:ath:AT4G07960 TAIR:At4g07960 InParanoid:Q9ZQB9 OMA:FEIAAYF PhylomeDB:Q9ZQB9 ProtClustDB:CLSN2685849 ArrayExpress:Q9ZQB9 Genevestigator:Q9ZQB9 Uniprot:Q9ZQB9
Root	Isotig00182	94	188	-1.129	1.72E-10	TAIR|locus:2120532 - symbol:CSLC12 "AT4G07960" species:3702 "Arabidopsis thaliana" [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0016759 "cellulose synthase activity" evidence=ISS] [GO:0009506 "plasmodesma" evidence=IDA] GO:GO:0016021 GO:GO:0009506 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0000139 GO:GO:0007047 GO:GO:0016757 CAZy:GT2 eggNOG:COG1215 HOGENOM:HBG602904 EMBL:AC006266 EMBL:AL161508 EMBL:AK118480 EMBL:AY087066 EMBL:BT008770 IPI:IPI00545815 PIR:B85078 RefSeq:NP_192536.1 UniGene:At.33785 ProteinModelPortal:Q9ZQB9 STRING:Q9ZQB9 PRIDE:Q9ZQB9 EnsemblPlants:AT4G07960.1 GeneID:826301 KEGG:ath:AT4G07960 TAIR:At4g07960 InParanoid:Q9ZQB9 OMA:FEIAAYF PhylomeDB:Q9ZQB9 ProtClustDB:CLSN2685849 ArrayExpress:Q9ZQB9 Genevestigator:Q9ZQB9 Uniprot:Q9ZQB9
Root	Isotig00183	94	189	-1.137	1.23E-10	TAIR|locus:2120532 - symbol:CSLC12 "AT4G07960" species:3702 "Arabidopsis thaliana" [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0016759 "cellulose synthase activity" evidence=ISS] [GO:0009506 "plasmodesma" evidence=IDA] GO:GO:0016021 GO:GO:0009506 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0000139 GO:GO:0007047 GO:GO:0016757 CAZy:GT2 eggNOG:COG1215 HOGENOM:HBG602904 EMBL:AC006266 EMBL:AL161508 EMBL:AK118480

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EMBL:AY087066 EMBL:BT008770 IPI:IPI00545815 PIR:B85078 RefSeq:NP_192536.1 UniGene:At.33785 ProteinModelPortal:Q9ZQB9 STRING:Q9ZQB9 PRIDE:Q9ZQB9 EnsemblPlants:AT4G07960.1 GeneID:826301 KEGG:ath:AT4G07960 TAIR:At4g07960 InParanoid:Q9ZQB9 OMA:FEIAAYF PhylomeDB:Q9ZQB9 ProtClustDB:CLSN2685849 ArrayExpress:Q9ZQB9 Genevestigator:Q9ZQB9 Uniprot:Q9ZQB9
Root	Isotig00184	94	189	-1.137	1.23E-10	TAIR|locus:2120532 - symbol:CSLC12 "AT4G07960" species:3702 "Arabidopsis thaliana" [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0016759 "cellulose synthase activity" evidence=ISS] [GO:0009506 "plasmodesma" evidence=IDA] GO:GO:0016021 GO:GO:0009506 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0000139 GO:GO:0007047 GO:GO:0016757 CAZy:GT2 eggNOG:COG1215 HOGENOM:HBG602904 EMBL:AC006266 EMBL:AL161508 EMBL:AK118480 EMBL:AY087066 EMBL:BT008770 IPI:IPI00545815 PIR:B85078 RefSeq:NP_192536.1 UniGene:At.33785 ProteinModelPortal:Q9ZQB9 STRING:Q9ZQB9 PRIDE:Q9ZQB9 EnsemblPlants:AT4G07960.1 GeneID:826301 KEGG:ath:AT4G07960 TAIR:At4g07960 InParanoid:Q9ZQB9 OMA:FEIAAYF PhylomeDB:Q9ZQB9 ProtClustDB:CLSN2685849 ArrayExpress:Q9ZQB9 Genevestigator:Q9ZQB9 Uniprot:Q9ZQB9
Root	Isotig00185	90	179	-1.121	5.87E-10	TAIR|locus:2120532 - symbol:CSLC12 "AT4G07960" species:3702 "Arabidopsis thaliana" [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0016759 "cellulose synthase activity" evidence=ISS] [GO:0009506 "plasmodesma" evidence=IDA] GO:GO:0016021 GO:GO:0009506 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0000139 GO:GO:0007047 GO:GO:0016757 CAZy:GT2 eggNOG:COG1215 HOGENOM:HBG602904 EMBL:AC006266 EMBL:AL161508 EMBL:AK118480 EMBL:AY087066 EMBL:BT008770 IPI:IPI00545815 PIR:B85078 RefSeq:NP_192536.1 UniGene:At.33785 ProteinModelPortal:Q9ZQB9 STRING:Q9ZQB9 PRIDE:Q9ZQB9 EnsemblPlants:AT4G07960.1 GeneID:826301 KEGG:ath:AT4G07960 TAIR:At4g07960 InParanoid:Q9ZQB9 OMA:FEIAAYF PhylomeDB:Q9ZQB9 ProtClustDB:CLSN2685849 ArrayExpress:Q9ZQB9 Genevestigator:Q9ZQB9 Uniprot:Q9ZQB9
Root	Isotig00186	90	179	-1.121	5.87E-10	TAIR|locus:2120532 - symbol:CSLC12 "AT4G07960" species:3702 "Arabidopsis thaliana" [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0016759 "cellulose synthase activity" evidence=ISS] [GO:0009506 "plasmodesma" evidence=IDA] GO:GO:0016021 GO:GO:0009506 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0000139 GO:GO:0007047 GO:GO:0016757 CAZy:GT2 eggNOG:COG1215 HOGENOM:HBG602904 EMBL:AC006266 EMBL:AL161508 EMBL:AK118480 EMBL:AY087066 EMBL:BT008770 IPI:IPI00545815 PIR:B85078 RefSeq:NP_192536.1 UniGene:At.33785 ProteinModelPortal:Q9ZQB9 STRING:Q9ZQB9 PRIDE:Q9ZQB9 EnsemblPlants:AT4G07960.1 GeneID:826301 KEGG:ath:AT4G07960 TAIR:At4g07960 InParanoid:Q9ZQB9 OMA:FEIAAYF PhylomeDB:Q9ZQB9 ProtClustDB:CLSN2685849 ArrayExpress:Q9ZQB9 Genevestigator:Q9ZQB9 Uniprot:Q9ZQB9
Root	Isotig00187	90	179	-1.121	5.87E-10	TAIR|locus:2120532 - symbol:CSLC12 "AT4G07960" species:3702 "Arabidopsis thaliana" [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0016759 "cellulose synthase activity" evidence=ISS] [GO:0009506 "plasmodesma" evidence=IDA] GO:GO:0016021 GO:GO:0009506 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0000139 GO:GO:0007047 GO:GO:0016757 CAZy:GT2 eggNOG:COG1215 HOGENOM:HBG602904 EMBL:AC006266 EMBL:AL161508 EMBL:AK118480 EMBL:AY087066 EMBL:BT008770 IPI:IPI00545815 PIR:B85078 RefSeq:NP_192536.1 UniGene:At.33785 ProteinModelPortal:Q9ZQB9 STRING:Q9ZQB9 PRIDE:Q9ZQB9 EnsemblPlants:AT4G07960.1 GeneID:826301 KEGG:ath:AT4G07960 TAIR:At4g07960 InParanoid:Q9ZQB9 OMA:FEIAAYF PhylomeDB:Q9ZQB9 ProtClustDB:CLSN2685849 ArrayExpress:Q9ZQB9 Genevestigator:Q9ZQB9 Uniprot:Q9ZQB9
Root	Isotig00188	90	180	-1.129	4.19E-10	TAIR|locus:2120532 - symbol:CSLC12 "AT4G07960" species:3702 "Arabidopsis thaliana" [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0016759 "cellulose synthase activity" evidence=ISS] [GO:0009506 "plasmodesma" evidence=IDA] GO:GO:0016021 GO:GO:0009506 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0000139 GO:GO:0007047 GO:GO:0016757 CAZy:GT2 eggNOG:COG1215 HOGENOM:HBG602904 EMBL:AC006266 EMBL:AL161508 EMBL:AK118480 EMBL:AY087066 EMBL:BT008770 IPI:IPI00545815 PIR:B85078 RefSeq:NP_192536.1 UniGene:At.33785 ProteinModelPortal:Q9ZQB9 STRING:Q9ZQB9 PRIDE:Q9ZQB9 EnsemblPlants:AT4G07960.1 GeneID:826301 KEGG:ath:AT4G07960 TAIR:At4g07960 InParanoid:Q9ZQB9 OMA:FEIAAYF PhylomeDB:Q9ZQB9 ProtClustDB:CLSN2685849 ArrayExpress:Q9ZQB9 Genevestigator:Q9ZQB9 Uniprot:Q9ZQB9
Root	Isotig00189	91	185	-1.153	1.20E-10	TAIR|locus:2120532 - symbol:CSLC12 "AT4G07960" species:3702 "Arabidopsis thaliana" [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0016759 "cellulose synthase activity" evidence=ISS] [GO:0009506 "plasmodesma" evidence=IDA] GO:GO:0016021 GO:GO:0009506 EMBL:CP002687

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GenomeReviews:CT486007_GR GO:GO:0000139 GO:GO:0007047 GO:GO:0016757 CAZy:GT2 eggNOG:COG1215 HOGENOM:HBG602904 EMBL:AC006266 EMBL:AL161508 EMBL:AK118480 EMBL:AY087066 EMBL:BT008770 IPI:IPI00545815 PIR:B85078 RefSeq:NP_192536.1 UniGene:At.33785 ProteinModelPortal:Q9ZQB9 STRING:Q9ZQB9 PRIDE:Q9ZQB9 EnsemblPlants:AT4G07960.1 GeneID:826301 KEGG:ath:AT4G07960 TAIR:At4g07960 InParanoid:Q9ZQB9 OMA:FEIAAYF PhylomeDB:Q9ZQB9 ProtClustDB:CLSN2685849 ArrayExpress:Q9ZQB9 Genevestigator:Q9ZQB9 Uniprot:Q9ZQB9
Root	Isotig00190	90	180	-1.129	4.19E-10	TAIR|locus:2120532 - symbol:CSLC12 "AT4G07960" species:3702 "Arabidopsis thaliana" [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0016759 "cellulose synthase activity" evidence=ISS] [GO:0009506 "plasmodesma" evidence=IDA] GO:GO:0016021 GO:GO:0009506 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0000139 GO:GO:0007047 GO:GO:0016757 CAZy:GT2 eggNOG:COG1215 HOGENOM:HBG602904 EMBL:AC006266 EMBL:AL161508 EMBL:AK118480 EMBL:AY087066 EMBL:BT008770 IPI:IPI00545815 PIR:B85078 RefSeq:NP_192536.1 UniGene:At.33785 ProteinModelPortal:Q9ZQB9 STRING:Q9ZQB9 PRIDE:Q9ZQB9 EnsemblPlants:AT4G07960.1 GeneID:826301 KEGG:ath:AT4G07960 TAIR:At4g07960 InParanoid:Q9ZQB9 OMA:FEIAAYF PhylomeDB:Q9ZQB9 ProtClustDB:CLSN2685849 ArrayExpress:Q9ZQB9 Genevestigator:Q9ZQB9 Uniprot:Q9ZQB9
Root	Isotig00191	87	176	-1.145	4.12E-10	TAIR|locus:2120532 - symbol:CSLC12 "AT4G07960" species:3702 "Arabidopsis thaliana" [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0016759 "cellulose synthase activity" evidence=ISS] [GO:0009506 "plasmodesma" evidence=IDA] GO:GO:0016021 GO:GO:0009506 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0000139 GO:GO:0007047 GO:GO:0016757 CAZy:GT2 eggNOG:COG1215 HOGENOM:HBG602904 EMBL:AC006266 EMBL:AL161508 EMBL:AK118480 EMBL:AY087066 EMBL:BT008770 IPI:IPI00545815 PIR:B85078 RefSeq:NP_192536.1 UniGene:At.33785 ProteinModelPortal:Q9ZQB9 STRING:Q9ZQB9 PRIDE:Q9ZQB9 EnsemblPlants:AT4G07960.1 GeneID:826301 KEGG:ath:AT4G07960 TAIR:At4g07960 InParanoid:Q9ZQB9 OMA:FEIAAYF PhylomeDB:Q9ZQB9 ProtClustDB:CLSN2685849 ArrayExpress:Q9ZQB9 Genevestigator:Q9ZQB9 Uniprot:Q9ZQB9
Root	Isotig00192	94	187	-1.121	2.42E-10	TAIR|locus:2120532 - symbol:CSLC12 "AT4G07960" species:3702 "Arabidopsis thaliana" [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0016759 "cellulose synthase activity" evidence=ISS] [GO:0009506 "plasmodesma" evidence=IDA] GO:GO:0016021 GO:GO:0009506 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0000139 GO:GO:0007047 GO:GO:0016757 CAZy:GT2 eggNOG:COG1215 HOGENOM:HBG602904 EMBL:AC006266 EMBL:AL161508 EMBL:AK118480 EMBL:AY087066 EMBL:BT008770 IPI:IPI00545815 PIR:B85078 RefSeq:NP_192536.1 UniGene:At.33785 ProteinModelPortal:Q9ZQB9 STRING:Q9ZQB9 PRIDE:Q9ZQB9 EnsemblPlants:AT4G07960.1 GeneID:826301 KEGG:ath:AT4G07960 TAIR:At4g07960 InParanoid:Q9ZQB9 OMA:FEIAAYF PhylomeDB:Q9ZQB9 ProtClustDB:CLSN2685849 ArrayExpress:Q9ZQB9 Genevestigator:Q9ZQB9 Uniprot:Q9ZQB9
Root	Isotig00193	94	187	-1.121	2.42E-10	TAIR|locus:2120532 - symbol:CSLC12 "AT4G07960" species:3702 "Arabidopsis thaliana" [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0016759 "cellulose synthase activity" evidence=ISS] [GO:0009506 "plasmodesma" evidence=IDA] GO:GO:0016021 GO:GO:0009506 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0000139 GO:GO:0007047 GO:GO:0016757 CAZy:GT2 eggNOG:COG1215 HOGENOM:HBG602904 EMBL:AC006266 EMBL:AL161508 EMBL:AK118480 EMBL:AY087066 EMBL:BT008770 IPI:IPI00545815 PIR:B85078 RefSeq:NP_192536.1 UniGene:At.33785 ProteinModelPortal:Q9ZQB9 STRING:Q9ZQB9 PRIDE:Q9ZQB9 EnsemblPlants:AT4G07960.1 GeneID:826301 KEGG:ath:AT4G07960 TAIR:At4g07960 InParanoid:Q9ZQB9 OMA:FEIAAYF PhylomeDB:Q9ZQB9 ProtClustDB:CLSN2685849 ArrayExpress:Q9ZQB9 Genevestigator:Q9ZQB9 Uniprot:Q9ZQB9
Root	Isotig00194	94	187	-1.121	2.42E-10	TAIR|locus:2120532 - symbol:CSLC12 "AT4G07960" species:3702 "Arabidopsis thaliana" [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0016759 "cellulose synthase activity" evidence=ISS] [GO:0009506 "plasmodesma" evidence=IDA] GO:GO:0016021 GO:GO:0009506 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0000139 GO:GO:0007047 GO:GO:0016757 CAZy:GT2 eggNOG:COG1215 HOGENOM:HBG602904 EMBL:AC006266 EMBL:AL161508 EMBL:AK118480 EMBL:AY087066 EMBL:BT008770 IPI:IPI00545815 PIR:B85078 RefSeq:NP_192536.1 UniGene:At.33785 ProteinModelPortal:Q9ZQB9 STRING:Q9ZQB9 PRIDE:Q9ZQB9 EnsemblPlants:AT4G07960.1 GeneID:826301 KEGG:ath:AT4G07960 TAIR:At4g07960 InParanoid:Q9ZQB9 OMA:FEIAAYF PhylomeDB:Q9ZQB9 ProtClustDB:CLSN2685849 ArrayExpress:Q9ZQB9 Genevestigator:Q9ZQB9 Uniprot:Q9ZQB9

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig00195	94	188	-1.129	1.72E-10	TAIR|locus:2120532 - symbol:CSLC12 "AT4G07960" species:3702 "Arabidopsis thaliana" [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0016759 "cellulose synthase activity" evidence=ISS] [GO:0009506 "plasmodesma" evidence=IDA] GO:GO:0016021 GO:GO:0009506 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0000139 GO:GO:0007047 GO:GO:0016757 CAZy:GT2 eggNOG:COG1215 HOGENOM:HBG602904 EMBL:AC006266 EMBL:AL161508 EMBL:AK118480 EMBL:AY087066 EMBL:BT008770 IPI:IPI00545815 PIR:B85078 RefSeq:NP_192536.1 UniGene:At.33785 ProteinModelPortal:Q9ZQB9 STRING:Q9ZQB9 PRIDE:Q9ZQB9 EnsemblPlants:AT4G07960.1 GeneID:826301 KEGG:ath:AT4G07960 TAIR:At4g07960 InParanoid:Q9ZQB9 OMA:FEIAAYF PhylomeDB:Q9ZQB9 ProtClustDB:CLSN2685849 ArrayExpress:Q9ZQB9 Genevestigator:Q9ZQB9 Uniprot:Q9ZQB9
Root	Isotig00196	94	188	-1.129	1.72E-10	TAIR|locus:2120532 - symbol:CSLC12 "AT4G07960" species:3702 "Arabidopsis thaliana" [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0016759 "cellulose synthase activity" evidence=ISS] [GO:0009506 "plasmodesma" evidence=IDA] GO:GO:0016021 GO:GO:0009506 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0000139 GO:GO:0007047 GO:GO:0016757 CAZy:GT2 eggNOG:COG1215 HOGENOM:HBG602904 EMBL:AC006266 EMBL:AL161508 EMBL:AK118480 EMBL:AY087066 EMBL:BT008770 IPI:IPI00545815 PIR:B85078 RefSeq:NP_192536.1 UniGene:At.33785 ProteinModelPortal:Q9ZQB9 STRING:Q9ZQB9 PRIDE:Q9ZQB9 EnsemblPlants:AT4G07960.1 GeneID:826301 KEGG:ath:AT4G07960 TAIR:At4g07960 InParanoid:Q9ZQB9 OMA:FEIAAYF PhylomeDB:Q9ZQB9 ProtClustDB:CLSN2685849 ArrayExpress:Q9ZQB9 Genevestigator:Q9ZQB9 Uniprot:Q9ZQB9
Root	Isotig00197	91	184	-1.145	1.70E-10	TAIR|locus:2120532 - symbol:CSLC12 "AT4G07960" species:3702 "Arabidopsis thaliana" [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0016759 "cellulose synthase activity" evidence=ISS] [GO:0009506 "plasmodesma" evidence=IDA] GO:GO:0016021 GO:GO:0009506 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0000139 GO:GO:0007047 GO:GO:0016757 CAZy:GT2 eggNOG:COG1215 HOGENOM:HBG602904 EMBL:AC006266 EMBL:AL161508 EMBL:AK118480 EMBL:AY087066 EMBL:BT008770 IPI:IPI00545815 PIR:B85078 RefSeq:NP_192536.1 UniGene:At.33785 ProteinModelPortal:Q9ZQB9 STRING:Q9ZQB9 PRIDE:Q9ZQB9 EnsemblPlants:AT4G07960.1 GeneID:826301 KEGG:ath:AT4G07960 TAIR:At4g07960 InParanoid:Q9ZQB9 OMA:FEIAAYF PhylomeDB:Q9ZQB9 ProtClustDB:CLSN2685849 ArrayExpress:Q9ZQB9 Genevestigator:Q9ZQB9 Uniprot:Q9ZQB9
Root	Isotig00198	94	187	-1.121	2.42E-10	TAIR|locus:2120532 - symbol:CSLC12 "AT4G07960" species:3702 "Arabidopsis thaliana" [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0016759 "cellulose synthase activity" evidence=ISS] [GO:0009506 "plasmodesma" evidence=IDA] GO:GO:0016021 GO:GO:0009506 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0000139 GO:GO:0007047 GO:GO:0016757 CAZy:GT2 eggNOG:COG1215 HOGENOM:HBG602904 EMBL:AC006266 EMBL:AL161508 EMBL:AK118480 EMBL:AY087066 EMBL:BT008770 IPI:IPI00545815 PIR:B85078 RefSeq:NP_192536.1 UniGene:At.33785 ProteinModelPortal:Q9ZQB9 STRING:Q9ZQB9 PRIDE:Q9ZQB9 EnsemblPlants:AT4G07960.1 GeneID:826301 KEGG:ath:AT4G07960 TAIR:At4g07960 InParanoid:Q9ZQB9 OMA:FEIAAYF PhylomeDB:Q9ZQB9 ProtClustDB:CLSN2685849 ArrayExpress:Q9ZQB9 Genevestigator:Q9ZQB9 Uniprot:Q9ZQB9
Root	Isotig00199	94	187	-1.121	2.42E-10	TAIR|locus:2120532 - symbol:CSLC12 "AT4G07960" species:3702 "Arabidopsis thaliana" [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0016759 "cellulose synthase activity" evidence=ISS] [GO:0009506 "plasmodesma" evidence=IDA] GO:GO:0016021 GO:GO:0009506 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0000139 GO:GO:0007047 GO:GO:0016757 CAZy:GT2 eggNOG:COG1215 HOGENOM:HBG602904 EMBL:AC006266 EMBL:AL161508 EMBL:AK118480 EMBL:AY087066 EMBL:BT008770 IPI:IPI00545815 PIR:B85078 RefSeq:NP_192536.1 UniGene:At.33785 ProteinModelPortal:Q9ZQB9 STRING:Q9ZQB9 PRIDE:Q9ZQB9 EnsemblPlants:AT4G07960.1 GeneID:826301 KEGG:ath:AT4G07960 TAIR:At4g07960 InParanoid:Q9ZQB9 OMA:FEIAAYF PhylomeDB:Q9ZQB9 ProtClustDB:CLSN2685849 ArrayExpress:Q9ZQB9 Genevestigator:Q9ZQB9 Uniprot:Q9ZQB9
Root	Isotig00200	94	187	-1.121	2.42E-10	TAIR|locus:2120532 - symbol:CSLC12 "AT4G07960" species:3702 "Arabidopsis thaliana" [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0016759 "cellulose synthase activity" evidence=ISS] [GO:0009506 "plasmodesma" evidence=IDA] GO:GO:0016021 GO:GO:0009506 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0000139 GO:GO:0007047 GO:GO:0016757 CAZy:GT2 eggNOG:COG1215 HOGENOM:HBG602904 EMBL:AC006266 EMBL:AL161508 EMBL:AK118480 EMBL:AY087066 EMBL:BT008770 IPI:IPI00545815 PIR:B85078 RefSeq:NP_192536.1 UniGene:At.33785 ProteinModelPortal:Q9ZQB9 STRING:Q9ZQB9 PRIDE:Q9ZQB9 EnsemblPlants:AT4G07960.1 GeneID:826301

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						KEGG:ath:AT4G07960 TAIR:At4g07960 InParanoid:Q9ZQB9 OMA:FEIAAYF PhylomeDB:Q9ZQB9 ProtClustDB:CLSN2685849 ArrayExpress:Q9ZQB9 Genevestigator:Q9ZQB9 Uniprot:Q9ZQB9
Root	Isotig00201	94	188	-1.129	1.72E-10	TAIR|locus:2120532 - symbol:CSLC12 "AT4G07960" species:3702 "Arabidopsis thaliana" [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0016759 "cellulose synthase activity" evidence=ISS] [GO:0009506 "plasmodesma" evidence=IDA] GO:GO:0016021 GO:GO:0009506 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0000139 GO:GO:0007047 GO:GO:0016757 CAZy:GT2 eggNOG:COG1215 HOGENOM:HBG602904 EMBL:AC006266 EMBL:AL161508 EMBL:AK118480 EMBL:AY087066 EMBL:BT008770 IPI:IPI00545815 PIR:B85078 RefSeq:NP_192536.1 UniGene:At.33785 ProteinModelPortal:Q9ZQB9 STRING:Q9ZQB9 PRIDE:Q9ZQB9 EnsemblPlants:AT4G07960.1 GeneID:826301 KEGG:ath:AT4G07960 TAIR:At4g07960 InParanoid:Q9ZQB9 OMA:FEIAAYF PhylomeDB:Q9ZQB9 ProtClustDB:CLSN2685849 ArrayExpress:Q9ZQB9 Genevestigator:Q9ZQB9 Uniprot:Q9ZQB9
Root	Isotig00202	94	188	-1.129	1.72E-10	TAIR|locus:2120532 - symbol:CSLC12 "AT4G07960" species:3702 "Arabidopsis thaliana" [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0016759 "cellulose synthase activity" evidence=ISS] [GO:0009506 "plasmodesma" evidence=IDA] GO:GO:0016021 GO:GO:0009506 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0000139 GO:GO:0007047 GO:GO:0016757 CAZy:GT2 eggNOG:COG1215 HOGENOM:HBG602904 EMBL:AC006266 EMBL:AL161508 EMBL:AK118480 EMBL:AY087066 EMBL:BT008770 IPI:IPI00545815 PIR:B85078 RefSeq:NP_192536.1 UniGene:At.33785 ProteinModelPortal:Q9ZQB9 STRING:Q9ZQB9 PRIDE:Q9ZQB9 EnsemblPlants:AT4G07960.1 GeneID:826301 KEGG:ath:AT4G07960 TAIR:At4g07960 InParanoid:Q9ZQB9 OMA:FEIAAYF PhylomeDB:Q9ZQB9 ProtClustDB:CLSN2685849 ArrayExpress:Q9ZQB9 Genevestigator:Q9ZQB9 Uniprot:Q9ZQB9
Root	Isotig00203	91	184	-1.145	1.70E-10	TAIR|locus:2120532 - symbol:CSLC12 "AT4G07960" species:3702 "Arabidopsis thaliana" [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0016759 "cellulose synthase activity" evidence=ISS] [GO:0009506 "plasmodesma" evidence=IDA] GO:GO:0016021 GO:GO:0009506 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0000139 GO:GO:0007047 GO:GO:0016757 CAZy:GT2 eggNOG:COG1215 HOGENOM:HBG602904 EMBL:AC006266 EMBL:AL161508 EMBL:AK118480 EMBL:AY087066 EMBL:BT008770 IPI:IPI00545815 PIR:B85078 RefSeq:NP_192536.1 UniGene:At.33785 ProteinModelPortal:Q9ZQB9 STRING:Q9ZQB9 PRIDE:Q9ZQB9 EnsemblPlants:AT4G07960.1 GeneID:826301 KEGG:ath:AT4G07960 TAIR:At4g07960 InParanoid:Q9ZQB9 OMA:FEIAAYF PhylomeDB:Q9ZQB9 ProtClustDB:CLSN2685849 ArrayExpress:Q9ZQB9 Genevestigator:Q9ZQB9 Uniprot:Q9ZQB9
Root	Isotig00204	91	185	-1.153	1.20E-10	TAIR|locus:2120532 - symbol:CSLC12 "AT4G07960" species:3702 "Arabidopsis thaliana" [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0016759 "cellulose synthase activity" evidence=ISS] [GO:0009506 "plasmodesma" evidence=IDA] GO:GO:0016021 GO:GO:0009506 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0000139 GO:GO:0007047 GO:GO:0016757 CAZy:GT2 eggNOG:COG1215 HOGENOM:HBG602904 EMBL:AC006266 EMBL:AL161508 EMBL:AK118480 EMBL:AY087066 EMBL:BT008770 IPI:IPI00545815 PIR:B85078 RefSeq:NP_192536.1 UniGene:At.33785 ProteinModelPortal:Q9ZQB9 STRING:Q9ZQB9 PRIDE:Q9ZQB9 EnsemblPlants:AT4G07960.1 GeneID:826301 KEGG:ath:AT4G07960 TAIR:At4g07960 InParanoid:Q9ZQB9 OMA:FEIAAYF PhylomeDB:Q9ZQB9 ProtClustDB:CLSN2685849 ArrayExpress:Q9ZQB9 Genevestigator:Q9ZQB9 Uniprot:Q9ZQB9
Root	Isotig00205	87	176	-1.145	4.12E-10	TAIR|locus:2120532 - symbol:CSLC12 "AT4G07960" species:3702 "Arabidopsis thaliana" [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0016759 "cellulose synthase activity" evidence=ISS] [GO:0009506 "plasmodesma" evidence=IDA] GO:GO:0016021 GO:GO:0009506 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0000139 GO:GO:0007047 GO:GO:0016757 CAZy:GT2 eggNOG:COG1215 HOGENOM:HBG602904 EMBL:AC006266 EMBL:AL161508 EMBL:AK118480 EMBL:AY087066 EMBL:BT008770 IPI:IPI00545815 PIR:B85078 RefSeq:NP_192536.1 UniGene:At.33785 ProteinModelPortal:Q9ZQB9 STRING:Q9ZQB9 PRIDE:Q9ZQB9 EnsemblPlants:AT4G07960.1 GeneID:826301 KEGG:ath:AT4G07960 TAIR:At4g07960 InParanoid:Q9ZQB9 OMA:FEIAAYF PhylomeDB:Q9ZQB9 ProtClustDB:CLSN2685849 ArrayExpress:Q9ZQB9 Genevestigator:Q9ZQB9 Uniprot:Q9ZQB9
Root	Isotig00206	91	184	-1.145	1.70E-10	TAIR|locus:2120532 - symbol:CSLC12 "AT4G07960" species:3702 "Arabidopsis thaliana" [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0016759 "cellulose synthase activity" evidence=ISS] [GO:0009506 "plasmodesma" evidence=IDA] GO:GO:0016021 GO:GO:0009506 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0000139 GO:GO:0007047 GO:GO:0016757 CAZy:GT2 eggNOG:COG1215 HOGENOM:HBG602904 EMBL:AC006266 EMBL:AL161508 EMBL:AK118480

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EMBL:AY087066 EMBL:BT008770 IPI:IPI00545815 PIR:B85078 RefSeq:NP_192536.1 UniGene:At.33785 ProteinModelPortal:Q9ZQB9 STRING:Q9ZQB9 PRIDE:Q9ZQB9 EnsemblPlants:AT4G07960.1 GeneID:826301 KEGG:ath:AT4G07960 TAIR:At4g07960 InParanoid:Q9ZQB9 OMA:FEIAAYF PhylomeDB:Q9ZQB9 ProtClustDB:CLSN2685849 ArrayExpress:Q9ZQB9 Genevestigator:Q9ZQB9 Uniprot:Q9ZQB9
Root	Isotig00207	91	184	-1.145	1.70E-10	TAIR|locus:2120532 - symbol:CSLC12 "AT4G07960" species:3702 "Arabidopsis thaliana" [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0016759 "cellulose synthase activity" evidence=ISS] [GO:0009506 "plasmodesma" evidence=IDA] GO:GO:0016021 GO:GO:0009506 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0000139 GO:GO:0007047 GO:GO:0016757 CAZy:GT2 eggNOG:COG1215 HOGENOM:HBG602904 EMBL:AC006266 EMBL:AL161508 EMBL:AK118480 EMBL:AY087066 EMBL:BT008770 IPI:IPI00545815 PIR:B85078 RefSeq:NP_192536.1 UniGene:At.33785 ProteinModelPortal:Q9ZQB9 STRING:Q9ZQB9 PRIDE:Q9ZQB9 EnsemblPlants:AT4G07960.1 GeneID:826301 KEGG:ath:AT4G07960 TAIR:At4g07960 InParanoid:Q9ZQB9 OMA:FEIAAYF PhylomeDB:Q9ZQB9 ProtClustDB:CLSN2685849 ArrayExpress:Q9ZQB9 Genevestigator:Q9ZQB9 Uniprot:Q9ZQB9
Root	Isotig00219	21	62	-1.691	6.33E-07	TAIR|locus:2159143 - symbol:AT5G13980 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=IEA] [GO:0004559 "alpha-mannosidase activity" evidence=IEA;ISS] [GO:0005975 "carbohydrate metabolic process" evidence=IEA] [GO:0006013 "mannose metabolic process" evidence=IEA] [GO:0008270 "zinc ion binding" evidence=IEA] [GO:0015923 "mannosidase activity" evidence=IEA] [GO:0030246 "carbohydrate binding" evidence=IEA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0009505 "plant-type cell wall" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] InterPro:IPR000602 InterPro:IPR011013 InterPro:IPR011330 InterPro:IPR011682 InterPro:IPR013780 InterPro:IPR015341 Pfam:PF01074 Pfam:PF07748 Pfam:PF09261 SMART:SM00872 GO:GO:0048046 GO:GO:0005774 EMBL:CP002688 Gene3D:G3DSA:2.60.40.1180 GO:GO:0008270 GO:GO:0009505 GO:GO:0030246 SUPFAM:SSF74650 SUPFAM:SSF88713 GO:GO:0006013 CAZy:GH38 GO:GO:0004559 Gene3D:G3DSA:3.20.110.10 HSSP:Q29451 OMA:SPVVQDD ProtClustDB:CLSN2684873 EMBL:AY099704 EMBL:BT000301 IPI:IPI00529830 RefSeq:NP_196902.2 RefSeq:NP_851037.2 UniGene:At.19885 ProteinModelPortal:Q8LPJ3 SMR:Q8LPJ3 PRIDE:Q8LPJ3 EnsemblPlants:AT5G13980.1 EnsemblPlants:AT5G13980.2 GeneID:831246 KEGG:ath:AT5G13980 TAIR:At5g13980 InParanoid:Q8LPJ3 PhylomeDB:Q8LPJ3 ArrayExpress:Q8LPJ3 Genevestigator:Q8LPJ3 Uniprot:Q8LPJ3
Root	Isotig00220	21	62	-1.691	6.33E-07	TAIR|locus:2159143 - symbol:AT5G13980 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=IEA] [GO:0004559 "alpha-mannosidase activity" evidence=IEA;ISS] [GO:0005975 "carbohydrate metabolic process" evidence=IEA] [GO:0006013 "mannose metabolic process" evidence=IEA] [GO:0008270 "zinc ion binding" evidence=IEA] [GO:0015923 "mannosidase activity" evidence=IEA] [GO:0030246 "carbohydrate binding" evidence=IEA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0009505 "plant-type cell wall" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] InterPro:IPR000602 InterPro:IPR011013 InterPro:IPR011330 InterPro:IPR011682 InterPro:IPR013780 InterPro:IPR015341 Pfam:PF01074 Pfam:PF07748 Pfam:PF09261 SMART:SM00872 GO:GO:0048046 GO:GO:0005774 EMBL:CP002688 Gene3D:G3DSA:2.60.40.1180 GO:GO:0008270 GO:GO:0009505 GO:GO:0030246 SUPFAM:SSF74650 SUPFAM:SSF88713 GO:GO:0006013 CAZy:GH38 GO:GO:0004559 Gene3D:G3DSA:3.20.110.10 HSSP:Q29451 OMA:SPVVQDD ProtClustDB:CLSN2684873 EMBL:AY099704 EMBL:BT000301 IPI:IPI00529830 RefSeq:NP_196902.2 RefSeq:NP_851037.2 UniGene:At.19885 ProteinModelPortal:Q8LPJ3 SMR:Q8LPJ3 PRIDE:Q8LPJ3 EnsemblPlants:AT5G13980.1 EnsemblPlants:AT5G13980.2 GeneID:831246 KEGG:ath:AT5G13980 TAIR:At5g13980 InParanoid:Q8LPJ3 PhylomeDB:Q8LPJ3 ArrayExpress:Q8LPJ3 Genevestigator:Q8LPJ3 Uniprot:Q8LPJ3
Root	Isotig00221	21	61	-1.667	9.99E-07	TAIR|locus:2159143 - symbol:AT5G13980 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=IEA] [GO:0004559 "alpha-mannosidase activity" evidence=IEA;ISS] [GO:0005975 "carbohydrate metabolic process" evidence=IEA] [GO:0006013 "mannose metabolic process" evidence=IEA] [GO:0008270 "zinc ion binding" evidence=IEA] [GO:0015923 "mannosidase activity" evidence=IEA] [GO:0030246 "carbohydrate binding" evidence=IEA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0009505 "plant-type cell wall" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA]

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						InterPro:IPR000602 InterPro:IPR011013 InterPro:IPR011330 InterPro:IPR011682 InterPro:IPR013780 InterPro:IPR015341 Pfam:PF01074 Pfam:PF07748 Pfam:PF09261 SMART:SM00872 GO:GO:0048046 GO:GO:0005774 EMBL:CP002688 Gene3D:G3DSA:2.60.40.1180 GO:GO:0008270 GO:GO:0009505 GO:GO:0030246 SUPFAM:SSF74650 SUPFAM:SSF88713 GO:GO:0006013 CAZy:GH38 GO:GO:0004559 Gene3D:G3DSA:3.20.110.10 HSSP:Q29451 OMA:SPVVQDD ProtClustDB:CLSN2684873 EMBL:AY099704 EMBL:BT000301 IPI:IPI00529830 RefSeq:NP_196902.2 RefSeq:NP_851037.2 UniGene:At.19885 ProteinModelPortal:Q8LPJ3 SMR:Q8LPJ3 PRIDE:Q8LPJ3 EnsemblPlants:AT5G13980.1 EnsemblPlants:AT5G13980.2 GeneID:831246 KEGG:ath:AT5G13980 TAIR:At5g13980 InParanoid:Q8LPJ3 PhylomeDB:Q8LPJ3 ArrayExpress:Q8LPJ3 Genevestigator:Q8LPJ3 Uniprot:Q8LPJ3
Root	Isotig00222	21	61	-1.667	9.99E-07	TAIR|locus:2159143 - symbol:AT5G13980 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=IEA] [GO:0004559 "alpha-mannosidase activity" evidence=IEA;ISS] [GO:0005975 "carbohydrate metabolic process" evidence=IEA] [GO:0006013 "mannose metabolic process" evidence=IEA] [GO:0008270 "zinc ion binding" evidence=IEA] [GO:0015923 "mannosidase activity" evidence=IEA] [GO:0030246 "carbohydrate binding" evidence=IEA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0009505 "plant-type cell wall" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] InterPro:IPR000602 InterPro:IPR011013 InterPro:IPR011330 InterPro:IPR011682 InterPro:IPR013780 InterPro:IPR015341 Pfam:PF01074 Pfam:PF07748 Pfam:PF09261 SMART:SM00872 GO:GO:0048046 GO:GO:0005774 EMBL:CP002688 Gene3D:G3DSA:2.60.40.1180 GO:GO:0008270 GO:GO:0009505 GO:GO:0030246 SUPFAM:SSF74650 SUPFAM:SSF88713 GO:GO:0006013 CAZy:GH38 GO:GO:0004559 Gene3D:G3DSA:3.20.110.10 HSSP:Q29451 OMA:SPVVQDD ProtClustDB:CLSN2684873 EMBL:AY099704 EMBL:BT000301 IPI:IPI00529830 RefSeq:NP_196902.2 RefSeq:NP_851037.2 UniGene:At.19885 ProteinModelPortal:Q8LPJ3 SMR:Q8LPJ3 PRIDE:Q8LPJ3 EnsemblPlants:AT5G13980.1 EnsemblPlants:AT5G13980.2 GeneID:831246 KEGG:ath:AT5G13980 TAIR:At5g13980 InParanoid:Q8LPJ3 PhylomeDB:Q8LPJ3 ArrayExpress:Q8LPJ3 Genevestigator:Q8LPJ3 Uniprot:Q8LPJ3
Root	Isotig00223	20	59	-1.690	1.19E-06	TAIR|locus:2159143 - symbol:AT5G13980 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=IEA] [GO:0004559 "alpha-mannosidase activity" evidence=IEA;ISS] [GO:0005975 "carbohydrate metabolic process" evidence=IEA] [GO:0006013 "mannose metabolic process" evidence=IEA] [GO:0008270 "zinc ion binding" evidence=IEA] [GO:0015923 "mannosidase activity" evidence=IEA] [GO:0030246 "carbohydrate binding" evidence=IEA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0009505 "plant-type cell wall" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] InterPro:IPR000602 InterPro:IPR011013 InterPro:IPR011330 InterPro:IPR011682 InterPro:IPR013780 InterPro:IPR015341 Pfam:PF01074 Pfam:PF07748 Pfam:PF09261 SMART:SM00872 GO:GO:0048046 GO:GO:0005774 EMBL:CP002688 Gene3D:G3DSA:2.60.40.1180 GO:GO:0008270 GO:GO:0009505 GO:GO:0030246 SUPFAM:SSF74650 SUPFAM:SSF88713 GO:GO:0006013 CAZy:GH38 GO:GO:0004559 Gene3D:G3DSA:3.20.110.10 HSSP:Q29451 OMA:SPVVQDD ProtClustDB:CLSN2684873 EMBL:AY099704 EMBL:BT000301 IPI:IPI00529830 RefSeq:NP_196902.2 RefSeq:NP_851037.2 UniGene:At.19885 ProteinModelPortal:Q8LPJ3 SMR:Q8LPJ3 PRIDE:Q8LPJ3 EnsemblPlants:AT5G13980.1 EnsemblPlants:AT5G13980.2 GeneID:831246 KEGG:ath:AT5G13980 TAIR:At5g13980 InParanoid:Q8LPJ3 PhylomeDB:Q8LPJ3 ArrayExpress:Q8LPJ3 Genevestigator:Q8LPJ3 Uniprot:Q8LPJ3
Root	Isotig00224	20	59	-1.690	1.19E-06	TAIR|locus:2159143 - symbol:AT5G13980 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=IEA] [GO:0004559 "alpha-mannosidase activity" evidence=IEA;ISS] [GO:0005975 "carbohydrate metabolic process" evidence=IEA] [GO:0006013 "mannose metabolic process" evidence=IEA] [GO:0008270 "zinc ion binding" evidence=IEA] [GO:0015923 "mannosidase activity" evidence=IEA] [GO:0030246 "carbohydrate binding" evidence=IEA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0009505 "plant-type cell wall" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] InterPro:IPR000602 InterPro:IPR011013 InterPro:IPR011330 InterPro:IPR011682 InterPro:IPR013780 InterPro:IPR015341 Pfam:PF01074 Pfam:PF07748 Pfam:PF09261 SMART:SM00872 GO:GO:0048046 GO:GO:0005774 EMBL:CP002688 Gene3D:G3DSA:2.60.40.1180 GO:GO:0008270 GO:GO:0009505 GO:GO:0030246 SUPFAM:SSF74650 SUPFAM:SSF88713 GO:GO:0006013 CAZy:GH38 GO:GO:0004559

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						Gene3D:G3DSA:3.20.110.10 HSSP:Q29451 OMA:SPVVQDD ProtClustDB:CLSN2684873 EMBL:AY099704 EMBL:BT000301 IPI:IPI00529830 RefSeq:NP_196902.2 RefSeq:NP_851037.2 UniGene:At.19885 ProteinModelPortal:Q8LPJ3 SMR:Q8LPJ3 PRIDE:Q8LPJ3 EnsemblPlants:AT5G13980.1 EnsemblPlants:AT5G13980.2 GeneID:831246 KEGG:ath:AT5G13980 TAIR:At5g13980 InParanoid:Q8LPJ3 PhylomeDB:Q8LPJ3 ArrayExpress:Q8LPJ3 Genevestigator:Q8LPJ3 Uniprot:Q8LPJ3
Root	Isotig00225	20	59	-1.690	1.19E-06	TAIR|locus:2159143 - symbol:AT5G13980 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=IEA] [GO:0004559 "alpha-mannosidase activity" evidence=IEA;ISS] [GO:0005975 "carbohydrate metabolic process" evidence=IEA] [GO:0006013 "mannose metabolic process" evidence=IEA] [GO:0008270 "zinc ion binding" evidence=IEA] [GO:0015923 "mannosidase activity" evidence=IEA] [GO:0030246 "carbohydrate binding" evidence=IEA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0009505 "plant-type cell wall" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] InterPro:IPR000602 InterPro:IPR011013 InterPro:IPR011330 InterPro:IPR011682 InterPro:IPR013780 InterPro:IPR015341 Pfam:PF01074 Pfam:PF07748 Pfam:PF09261 SMART:SM00872 GO:GO:0048046 GO:GO:0005774 EMBL:CP002688 Gene3D:G3DSA:2.60.40.1180 GO:GO:0008270 GO:GO:0009505 GO:GO:0030246 SUPFAM:SSF74650 SUPFAM:SSF88713 GO:GO:0006013 CAZy:GH38 GO:GO:0004559 Gene3D:G3DSA:3.20.110.10 HSSP:Q29451 OMA:SPVVQDD ProtClustDB:CLSN2684873 EMBL:AY099704 EMBL:BT000301 IPI:IPI00529830 RefSeq:NP_196902.2 RefSeq:NP_851037.2 UniGene:At.19885 ProteinModelPortal:Q8LPJ3 SMR:Q8LPJ3 PRIDE:Q8LPJ3 EnsemblPlants:AT5G13980.1 EnsemblPlants:AT5G13980.2 GeneID:831246 KEGG:ath:AT5G13980 TAIR:At5g13980 InParanoid:Q8LPJ3 PhylomeDB:Q8LPJ3 ArrayExpress:Q8LPJ3 Genevestigator:Q8LPJ3 Uniprot:Q8LPJ3
Root	Isotig00226	20	59	-1.690	1.19E-06	TAIR|locus:2159143 - symbol:AT5G13980 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=IEA] [GO:0004559 "alpha-mannosidase activity" evidence=IEA;ISS] [GO:0005975 "carbohydrate metabolic process" evidence=IEA] [GO:0006013 "mannose metabolic process" evidence=IEA] [GO:0008270 "zinc ion binding" evidence=IEA] [GO:0015923 "mannosidase activity" evidence=IEA] [GO:0030246 "carbohydrate binding" evidence=IEA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0009505 "plant-type cell wall" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] InterPro:IPR000602 InterPro:IPR011013 InterPro:IPR011330 InterPro:IPR011682 InterPro:IPR013780 InterPro:IPR015341 Pfam:PF01074 Pfam:PF07748 Pfam:PF09261 SMART:SM00872 GO:GO:0048046 GO:GO:0005774 EMBL:CP002688 Gene3D:G3DSA:2.60.40.1180 GO:GO:0008270 GO:GO:0009505 GO:GO:0030246 SUPFAM:SSF74650 SUPFAM:SSF88713 GO:GO:0006013 CAZy:GH38 GO:GO:0004559 Gene3D:G3DSA:3.20.110.10 HSSP:Q29451 OMA:SPVVQDD ProtClustDB:CLSN2684873 EMBL:AY099704 EMBL:BT000301 IPI:IPI00529830 RefSeq:NP_196902.2 RefSeq:NP_851037.2 UniGene:At.19885 ProteinModelPortal:Q8LPJ3 SMR:Q8LPJ3 PRIDE:Q8LPJ3 EnsemblPlants:AT5G13980.1 EnsemblPlants:AT5G13980.2 GeneID:831246 KEGG:ath:AT5G13980 TAIR:At5g13980 InParanoid:Q8LPJ3 PhylomeDB:Q8LPJ3 ArrayExpress:Q8LPJ3 Genevestigator:Q8LPJ3 Uniprot:Q8LPJ3
Root	Isotig00227	12	48	-2.129	3.14E-07	TAIR|locus:2159143 - symbol:AT5G13980 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=IEA] [GO:0004559 "alpha-mannosidase activity" evidence=IEA;ISS] [GO:0005975 "carbohydrate metabolic process" evidence=IEA] [GO:0006013 "mannose metabolic process" evidence=IEA] [GO:0008270 "zinc ion binding" evidence=IEA] [GO:0015923 "mannosidase activity" evidence=IEA] [GO:0030246 "carbohydrate binding" evidence=IEA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0009505 "plant-type cell wall" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] InterPro:IPR000602 InterPro:IPR011013 InterPro:IPR011330 InterPro:IPR011682 InterPro:IPR013780 InterPro:IPR015341 Pfam:PF01074 Pfam:PF07748 Pfam:PF09261 SMART:SM00872 GO:GO:0048046 GO:GO:0005774 EMBL:CP002688 Gene3D:G3DSA:2.60.40.1180 GO:GO:0008270 GO:GO:0009505 GO:GO:0030246 SUPFAM:SSF74650 SUPFAM:SSF88713 GO:GO:0006013 CAZy:GH38 GO:GO:0004559 Gene3D:G3DSA:3.20.110.10 HSSP:Q29451 OMA:SPVVQDD ProtClustDB:CLSN2684873 EMBL:AY099704 EMBL:BT000301 IPI:IPI00529830 RefSeq:NP_196902.2 RefSeq:NP_851037.2 UniGene:At.19885 ProteinModelPortal:Q8LPJ3 SMR:Q8LPJ3 PRIDE:Q8LPJ3 EnsemblPlants:AT5G13980.1

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EnsemblPlants:AT5G13980.2 GeneID:831246 KEGG:ath:AT5G13980 TAIR:At5g13980 InParanoid:Q8LPJ3 PhylomeDB:Q8LPJ3 ArrayExpress:Q8LPJ3 Genevestigator:Q8LPJ3 Uniprot:Q8LPJ3
Root	Isotig00228	12	48	-2.129	3.14E-07	TAIR|locus:2159143 - symbol:AT5G13980 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=IEA] [GO:0004559 "alpha-mannosidase activity" evidence=IEA;ISS] [GO:0005975 "carbohydrate metabolic process" evidence=IEA] [GO:0006013 "mannose metabolic process" evidence=IEA] [GO:0008270 "zinc ion binding" evidence=IEA] [GO:0015923 "mannosidase activity" evidence=IEA] [GO:0030246 "carbohydrate binding" evidence=IEA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0009505 "plant-type cell wall" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] InterPro:IPR000602 InterPro:IPR011013 InterPro:IPR011330 InterPro:IPR011682 InterPro:IPR013780 InterPro:IPR015341 Pfam:PF01074 Pfam:PF07748 Pfam:PF09261 SMART:SM00872 GO:GO:0048046 GO:GO:0005774 EMBL:CP002688 Gene3D:G3DSA:2.60.40.1180 GO:GO:0008270 GO:GO:0009505 GO:GO:0030246 SUPFAM:SSF74650 SUPFAM:SSF88713 GO:GO:0006013 CAZy:GH38 GO:GO:0004559 Gene3D:G3DSA:3.20.110.10 HSSP:Q29451 OMA:SPVVQDD ProtClustDB:CLSN2684873 EMBL:AY099704 EMBL:BT000301 IPI:IPI00529830 RefSeq:NP_196902.2 RefSeq:NP_851037.2 UniGene:At.19885 ProteinModelPortal:Q8LPJ3 SMR:Q8LPJ3 PRIDE:Q8LPJ3 EnsemblPlants:AT5G13980.1 EnsemblPlants:AT5G13980.2 GeneID:831246 KEGG:ath:AT5G13980 TAIR:At5g13980 InParanoid:Q8LPJ3 PhylomeDB:Q8LPJ3 ArrayExpress:Q8LPJ3 Genevestigator:Q8LPJ3 Uniprot:Q8LPJ3
Root	Isotig00229	1	34	-5.216	6.54E-10	TAIR|locus:2090817 - symbol:AT3G26720 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=IEA] [GO:0004559 "alpha-mannosidase activity" evidence=IEA;ISS] [GO:0005975 "carbohydrate metabolic process" evidence=IEA] [GO:0006013 "mannose metabolic process" evidence=IEA] [GO:0008270 "zinc ion binding" evidence=IEA] [GO:0015923 "mannosidase activity" evidence=IEA] [GO:0030246 "carbohydrate binding" evidence=IEA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0009505 "plant-type cell wall" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] InterPro:IPR000602 InterPro:IPR011013 InterPro:IPR011330 InterPro:IPR011682 InterPro:IPR013780 InterPro:IPR015341 Pfam:PF01074 Pfam:PF07748 Pfam:PF09261 SMART:SM00872 GO:GO:0005774 EMBL:CP002686 Gene3D:G3DSA:2.60.40.1180 GO:GO:0008270 GO:GO:0009505 GO:GO:0030246 SUPFAM:SSF74650 SUPFAM:SSF88713 EMBL:X98130 EMBL:AB026648 GO:GO:0006013 CAZy:GH38 GO:GO:0004559 Gene3D:G3DSA:3.20.110.10 HOGENOM:HBG718615 OMA:DSAPLNE KO:K01191 HSSP:Q29451 EMBL:AY039536 EMBL:AY113006 EMBL:Y11767 IPI:IPI00531647 RefSeq:NP_189306.1 UniGene:At.21651 ProteinModelPortal:P94078 SMR:P94078 PRIDE:P94078 EnsemblPlants:AT3G26720.1 GeneID:822284 KEGG:ath:AT3G26720 TAIR:At3g26720 InParanoid:P94078 PhylomeDB:P94078 ProtClustDB:CLSN2684873 Genevestigator:P94078 Uniprot:P94078
Root	Isotig00230	1	34	-5.216	6.54E-10	TAIR|locus:2090817 - symbol:AT3G26720 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=IEA] [GO:0004559 "alpha-mannosidase activity" evidence=IEA;ISS] [GO:0005975 "carbohydrate metabolic process" evidence=IEA] [GO:0006013 "mannose metabolic process" evidence=IEA] [GO:0008270 "zinc ion binding" evidence=IEA] [GO:0015923 "mannosidase activity" evidence=IEA] [GO:0030246 "carbohydrate binding" evidence=IEA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0009505 "plant-type cell wall" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] InterPro:IPR000602 InterPro:IPR011013 InterPro:IPR011330 InterPro:IPR011682 InterPro:IPR013780 InterPro:IPR015341 Pfam:PF01074 Pfam:PF07748 Pfam:PF09261 SMART:SM00872 GO:GO:0005774 EMBL:CP002686 Gene3D:G3DSA:2.60.40.1180 GO:GO:0008270 GO:GO:0009505 GO:GO:0030246 SUPFAM:SSF74650 SUPFAM:SSF88713 EMBL:X98130 EMBL:AB026648 GO:GO:0006013 CAZy:GH38 GO:GO:0004559 Gene3D:G3DSA:3.20.110.10 HOGENOM:HBG718615 OMA:DSAPLNE KO:K01191 HSSP:Q29451 EMBL:AY039536 EMBL:AY113006 EMBL:Y11767 IPI:IPI00531647 RefSeq:NP_189306.1 UniGene:At.21651 ProteinModelPortal:P94078 SMR:P94078 PRIDE:P94078 EnsemblPlants:AT3G26720.1 GeneID:822284 KEGG:ath:AT3G26720 TAIR:At3g26720 InParanoid:P94078 PhylomeDB:P94078 ProtClustDB:CLSN2684873 Genevestigator:P94078 Uniprot:P94078
Root	Isotig00312	95	137	-0.657	0.000576456	ZFIN|ZDB-GENE-030131-8278 - symbol:eef1a1a "eukaryotic translation elongation factor 1 alpha 1a" species:7955 "Danio rerio" [GO:0003924 "GTPase activity" evidence=IEA] [GO:0005525 "GTP binding" evidence=IEA] [GO:0006414 "translational elongation" evidence=IEA] [GO:0003746 "translation elongation factor activity" evidence=IEA] [GO:0005737 "cytoplasm" evidence=IEA] [GO:0000166 "nucleotide binding" evidence=IEA]

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						InterPro:IPR000795 InterPro:IPR004160 InterPro:IPR004161 InterPro:IPR004539 Pfam:PF00009 Pfam:PF03143 Pfam:PF03144 PRINTS:PR00315 PROSITE:PS00301 ZFIN:ZDB-GENE-030131-8278 GO:GO:0005525 GO:GO:0005737 GO:GO:0003924 GO:GO:0003746 GeneTree:ENSGT00570000078778 InterPro:IPR009001 InterPro:IPR009000 SUPFAM:SSF50465 SUPFAM:SSF50447 HOGENOM:HBG307581 HOVERGEN:HBG000179 KO:K03231 OMA:SIETHHM OrthoDB:EOG40K7ZP TIGRFAMs:TIGR00483 HSSP:P02994 HAMAP:MF_00118_A EMBL:BX323884 EMBL:BC060907 IPI:IPI00485902 RefSeq:NP_956303.1 UniGene:Dr.159839 UniGene:Dr.80241 ProteinModelPortal:Q6P969 SMR:Q6P969 STRING:Q6P969 PRIDE:Q6P969 Ensembl:ENSDART00000128726 GeneID:336334 KEGG:dre:336334 CTD:336334 InParanoid:Q6P969 PhylomeDB:Q6P969 ArrayExpress:Q6P969 Bgee:Q6P969 Uniprot:Q6P969
Root	Isotig00313	94	144	-0.744	8.23E-05	TAIR|locus:2175118 - symbol:AT5G60390 "AT5G60390" species:3702 "Arabidopsis thaliana" [GO:0003746 "translation elongation factor activity" evidence=ISS] [GO:0006414 "translational elongation" evidence=IEA] [GO:0005516 "calmodulin binding" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] PROSITE:PS00301 EMBL:CP002684 EMBL:U63815 EMBL:AC026875 EMBL:X16430 EMBL:AY039583 EMBL:BT000595 IPI:IPI00548618 PIR:S06724 UniGene:At.69737 UniGene:At.74830 EnsemblPlants:AT1G07940.1 EnsemblPlants:AT1G07940.2 TAIR:At1g07940 OMA:FLKAGDA GermOnline:AT1G07940 Uniprot:P0DH99
Root	Isotig00321	186	13	3.710	2.83E-37	TAIR|locus:2163153 - symbol:NAC100 "AT5G61430" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0007275 "multicellular organismal development" evidence=ISS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] InterPro:IPR003441 Pfam:PF02365 PROSITE:PS51005 GO:GO:0005634 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0006355 GO:GO:0003677 GO:GO:0006351 EMBL:AB010073 HSSP:Q9C932 SUPFAM:SSF101941 EMBL:AY054644 EMBL:AY081496 EMBL:AY085102 IPI:IPI00529416 RefSeq:NP_200951.1 UniGene:At.7461 ProteinModelPortal:Q9FLJ2 SMR:Q9FLJ2 PRIDE:Q9FLJ2 DNASU:836264 EnsemblPlants:AT5G61430.1 GeneID:836264 KEGG:ath:AT5G61430 TAIR:At5g61430 eggNOG:NOG255211 InParanoid:Q9FLJ2 OMA:HAMIENN PhylomeDB:Q9FLJ2 ProtClustDB:CLSN2686918 Genevestigator:Q9FLJ2 Uniprot:Q9FLJ2
Root	Isotig00322	185	13	3.702	4.97E-37	TAIR|locus:2163153 - symbol:NAC100 "AT5G61430" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0007275 "multicellular organismal development" evidence=ISS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] InterPro:IPR003441 Pfam:PF02365 PROSITE:PS51005 GO:GO:0005634 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0006355 GO:GO:0003677 GO:GO:0006351 EMBL:AB010073 HSSP:Q9C932 SUPFAM:SSF101941 EMBL:AY054644 EMBL:AY081496 EMBL:AY085102 IPI:IPI00529416 RefSeq:NP_200951.1 UniGene:At.7461 ProteinModelPortal:Q9FLJ2 SMR:Q9FLJ2 PRIDE:Q9FLJ2 DNASU:836264 EnsemblPlants:AT5G61430.1 GeneID:836264 KEGG:ath:AT5G61430 TAIR:At5g61430 eggNOG:NOG255211 InParanoid:Q9FLJ2 OMA:HAMIENN PhylomeDB:Q9FLJ2 ProtClustDB:CLSN2686918 Genevestigator:Q9FLJ2 Uniprot:Q9FLJ2
Root	Isotig00323	186	13	3.710	2.83E-37	TAIR|locus:2163153 - symbol:NAC100 "AT5G61430" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0007275 "multicellular organismal development" evidence=ISS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] InterPro:IPR003441 Pfam:PF02365 PROSITE:PS51005 GO:GO:0005634 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0006355 GO:GO:0003677 GO:GO:0006351 EMBL:AB010073 HSSP:Q9C932 SUPFAM:SSF101941 EMBL:AY054644 EMBL:AY081496 EMBL:AY085102 IPI:IPI00529416 RefSeq:NP_200951.1 UniGene:At.7461 ProteinModelPortal:Q9FLJ2 SMR:Q9FLJ2 PRIDE:Q9FLJ2 DNASU:836264 EnsemblPlants:AT5G61430.1 GeneID:836264 KEGG:ath:AT5G61430 TAIR:At5g61430 eggNOG:NOG255211 InParanoid:Q9FLJ2 OMA:HAMIENN PhylomeDB:Q9FLJ2 ProtClustDB:CLSN2686918 Genevestigator:Q9FLJ2 Uniprot:Q9FLJ2
Root	Isotig00324	185	13	3.702	4.97E-37	TAIR|locus:2163153 - symbol:NAC100 "AT5G61430" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0007275 "multicellular organismal development" evidence=ISS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] InterPro:IPR003441 Pfam:PF02365 PROSITE:PS51005

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0005634 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0006355 GO:GO:0003677 GO:GO:0006351 EMBL:AB010073 HSSP:Q9C932 SUPFAM:SSF101941 EMBL:AY054644 EMBL:AY081496 EMBL:AY085102 IPI:IPI00529416 RefSeq:NP_200951.1 UniGene:At.7461 ProteinModelPortal:Q9FLJ2 SMR:Q9FLJ2 PRIDE:Q9FLJ2 DNASU:836264 EnsemblPlants:AT5G61430.1 GeneID:836264 KEGG:ath:AT5G61430 TAIR:At5g61430 eggNOG:NOG255211 InParanoid:Q9FLJ2 OMA:HAMIENN PhylomeDB:Q9FLJ2 ProtClustDB:CLSN2686918 Genevestigator:Q9FLJ2 Uniprot:Q9FLJ2
Root	Isotig00325	176	12	3.745	1.37E-35	TAIR|locus:2163153 - symbol:NAC100 "AT5G61430" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0007275 "multicellular organismal development" evidence=ISS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] InterPro:IPR003441 Pfam:PF02365 PROSITE:PS51005 GO:GO:0005634 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0006355 GO:GO:0003677 GO:GO:0006351 EMBL:AB010073 HSSP:Q9C932 SUPFAM:SSF101941 EMBL:AY054644 EMBL:AY081496 EMBL:AY085102 IPI:IPI00529416 RefSeq:NP_200951.1 UniGene:At.7461 ProteinModelPortal:Q9FLJ2 SMR:Q9FLJ2 PRIDE:Q9FLJ2 DNASU:836264 EnsemblPlants:AT5G61430.1 GeneID:836264 KEGG:ath:AT5G61430 TAIR:At5g61430 eggNOG:NOG255211 InParanoid:Q9FLJ2 OMA:HAMIENN PhylomeDB:Q9FLJ2 ProtClustDB:CLSN2686918 Genevestigator:Q9FLJ2 Uniprot:Q9FLJ2
Root	Isotig00326	176	12	3.745	1.37E-35	TAIR|locus:2163153 - symbol:NAC100 "AT5G61430" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0007275 "multicellular organismal development" evidence=ISS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] InterPro:IPR003441 Pfam:PF02365 PROSITE:PS51005 GO:GO:0005634 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0006355 GO:GO:0003677 GO:GO:0006351 EMBL:AB010073 HSSP:Q9C932 SUPFAM:SSF101941 EMBL:AY054644 EMBL:AY081496 EMBL:AY085102 IPI:IPI00529416 RefSeq:NP_200951.1 UniGene:At.7461 ProteinModelPortal:Q9FLJ2 SMR:Q9FLJ2 PRIDE:Q9FLJ2 DNASU:836264 EnsemblPlants:AT5G61430.1 GeneID:836264 KEGG:ath:AT5G61430 TAIR:At5g61430 eggNOG:NOG255211 InParanoid:Q9FLJ2 OMA:HAMIENN PhylomeDB:Q9FLJ2 ProtClustDB:CLSN2686918 Genevestigator:Q9FLJ2 Uniprot:Q9FLJ2
Root	Isotig00327	186	8	4.410	3.90E-41	TAIR|locus:2163153 - symbol:NAC100 "AT5G61430" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0007275 "multicellular organismal development" evidence=ISS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] InterPro:IPR003441 Pfam:PF02365 PROSITE:PS51005 GO:GO:0005634 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0006355 GO:GO:0003677 GO:GO:0006351 EMBL:AB010073 HSSP:Q9C932 SUPFAM:SSF101941 EMBL:AY054644 EMBL:AY081496 EMBL:AY085102 IPI:IPI00529416 RefSeq:NP_200951.1 UniGene:At.7461 ProteinModelPortal:Q9FLJ2 SMR:Q9FLJ2 PRIDE:Q9FLJ2 DNASU:836264 EnsemblPlants:AT5G61430.1 GeneID:836264 KEGG:ath:AT5G61430 TAIR:At5g61430 eggNOG:NOG255211 InParanoid:Q9FLJ2 OMA:HAMIENN PhylomeDB:Q9FLJ2 ProtClustDB:CLSN2686918 Genevestigator:Q9FLJ2 Uniprot:Q9FLJ2
Root	Isotig00328	185	8	4.402	6.85E-41	TAIR|locus:2163153 - symbol:NAC100 "AT5G61430" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0007275 "multicellular organismal development" evidence=ISS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] InterPro:IPR003441 Pfam:PF02365 PROSITE:PS51005 GO:GO:0005634 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0006355 GO:GO:0003677 GO:GO:0006351 EMBL:AB010073 HSSP:Q9C932 SUPFAM:SSF101941 EMBL:AY054644 EMBL:AY081496 EMBL:AY085102 IPI:IPI00529416 RefSeq:NP_200951.1 UniGene:At.7461 ProteinModelPortal:Q9FLJ2 SMR:Q9FLJ2 PRIDE:Q9FLJ2 DNASU:836264 EnsemblPlants:AT5G61430.1 GeneID:836264 KEGG:ath:AT5G61430 TAIR:At5g61430 eggNOG:NOG255211 InParanoid:Q9FLJ2 OMA:HAMIENN PhylomeDB:Q9FLJ2 ProtClustDB:CLSN2686918 Genevestigator:Q9FLJ2 Uniprot:Q9FLJ2
Root	Isotig00329	176	7	4.523	1.91E-39	TAIR|locus:2163153 - symbol:NAC100 "AT5G61430" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0007275 "multicellular organismal development" evidence=ISS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] InterPro:IPR003441 Pfam:PF02365 PROSITE:PS51005 GO:GO:0005634 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0006355 GO:GO:0003677 GO:GO:0006351 EMBL:AB010073 HSSP:Q9C932 SUPFAM:SSF101941 EMBL:AY054644 EMBL:AY081496

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EMBL:AY085102 IPI:IPI00529416 RefSeq:NP_200951.1 UniGene:At.7461 ProteinModelPortal:Q9FLJ2 SMR:Q9FLJ2 PRIDE:Q9FLJ2 DNASU:836264 EnsemblPlants:AT5G61430.1 GeneID:836264 KEGG:ath:AT5G61430 TAIR:At5g61430 eggNOG:NOG255211 InParanoid:Q9FLJ2 OMA:HAMIENN PhylomeDB:Q9FLJ2 ProtClustDB:CLSN2686918 Genevestigator:Q9FLJ2 Uniprot:Q9FLJ2
Root	Isotig00330	187	2	6.418	1.45E-43	TAIR|locus:2034640 - symbol:ARK3 "armadillo repeat kinesin 3" species:3702 "Arabidopsis thaliana" [GO:0003777 "microtubule motor activity" evidence=IEA;ISS] [GO:0005524 "ATP binding" evidence=IEA] [GO:0007018 "microtubule-based movement" evidence=IEA] [GO:0009574 "preprophase band" evidence=IDA] InterPro:IPR000225 InterPro:IPR001752 InterPro:IPR011989 InterPro:IPR016024 InterPro:IPR019821 Pfam:PF00225 Pfam:PF00514 PRINTS:PR00380 PROSITE:PS00411 PROSITE:PS50067 PROSITE:PS50176 SMART:SM00129 SMART:SM00185 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005524 SUPFAM:SSF48371 Gene3D:G3DSA:1.25.10.10 eggNOG:COG5059 GO:GO:0005874 GO:GO:0003777 HSSP:P17119 HOGENOM:HBG319705 GO:GO:0007018 Gene3D:G3DSA:3.40.850.10 EMBL:AB290930 EMBL:AF159052 EMBL:AC025416 IPI:IPI00543027 RefSeq:NP_563908.1 UniGene:At.16100 ProteinModelPortal:Q9FZ06 SMR:Q9FZ06 PRIDE:Q9FZ06 EnsemblPlants:AT1G12430.1 GeneID:837799 KEGG:ath:AT1G12430 GeneFarm:2953 TAIR:At1g12430 InParanoid:Q9FZ06 OMA:HAILMVN PhylomeDB:Q9FZ06 Genevestigator:Q9FZ06 GO:GO:0009574 Uniprot:Q9FZ06
Root	Isotig00331	186	2	6.410	2.37E-43	TAIR|locus:2034640 - symbol:ARK3 "armadillo repeat kinesin 3" species:3702 "Arabidopsis thaliana" [GO:0003777 "microtubule motor activity" evidence=IEA;ISS] [GO:0005524 "ATP binding" evidence=IEA] [GO:0007018 "microtubule-based movement" evidence=IEA] [GO:0009574 "preprophase band" evidence=IDA] InterPro:IPR000225 InterPro:IPR001752 InterPro:IPR011989 InterPro:IPR016024 InterPro:IPR019821 Pfam:PF00225 Pfam:PF00514 PRINTS:PR00380 PROSITE:PS00411 PROSITE:PS50067 PROSITE:PS50176 SMART:SM00129 SMART:SM00185 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005524 SUPFAM:SSF48371 Gene3D:G3DSA:1.25.10.10 eggNOG:COG5059 GO:GO:0005874 GO:GO:0003777 HSSP:P17119 HOGENOM:HBG319705 GO:GO:0007018 Gene3D:G3DSA:3.40.850.10 EMBL:AB290930 EMBL:AF159052 EMBL:AC025416 IPI:IPI00543027 RefSeq:NP_563908.1 UniGene:At.16100 ProteinModelPortal:Q9FZ06 SMR:Q9FZ06 PRIDE:Q9FZ06 EnsemblPlants:AT1G12430.1 GeneID:837799 KEGG:ath:AT1G12430 GeneFarm:2953 TAIR:At1g12430 InParanoid:Q9FZ06 OMA:HAILMVN PhylomeDB:Q9FZ06 Genevestigator:Q9FZ06 GO:GO:0009574 Uniprot:Q9FZ06
Root	Isotig00332	186	2	6.410	2.37E-43	TAIR|locus:2034640 - symbol:ARK3 "armadillo repeat kinesin 3" species:3702 "Arabidopsis thaliana" [GO:0003777 "microtubule motor activity" evidence=IEA;ISS] [GO:0005524 "ATP binding" evidence=IEA] [GO:0007018 "microtubule-based movement" evidence=IEA] [GO:0009574 "preprophase band" evidence=IDA] InterPro:IPR000225 InterPro:IPR001752 InterPro:IPR011989 InterPro:IPR016024 InterPro:IPR019821 Pfam:PF00225 Pfam:PF00514 PRINTS:PR00380 PROSITE:PS00411 PROSITE:PS50067 PROSITE:PS50176 SMART:SM00129 SMART:SM00185 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005524 SUPFAM:SSF48371 Gene3D:G3DSA:1.25.10.10 eggNOG:COG5059 GO:GO:0005874 GO:GO:0003777 HSSP:P17119 HOGENOM:HBG319705 GO:GO:0007018 Gene3D:G3DSA:3.40.850.10 EMBL:AB290930 EMBL:AF159052 EMBL:AC025416 IPI:IPI00543027 RefSeq:NP_563908.1 UniGene:At.16100 ProteinModelPortal:Q9FZ06 SMR:Q9FZ06 PRIDE:Q9FZ06 EnsemblPlants:AT1G12430.1 GeneID:837799 KEGG:ath:AT1G12430 GeneFarm:2953 TAIR:At1g12430 InParanoid:Q9FZ06 OMA:HAILMVN PhylomeDB:Q9FZ06 Genevestigator:Q9FZ06 GO:GO:0009574 Uniprot:Q9FZ06
Root	Isotig00333	185	2	6.402	3.87E-43	TAIR|locus:2034640 - symbol:ARK3 "armadillo repeat kinesin 3" species:3702 "Arabidopsis thaliana" [GO:0003777 "microtubule motor activity" evidence=IEA;ISS] [GO:0005524 "ATP binding" evidence=IEA] [GO:0007018 "microtubule-based movement" evidence=IEA] [GO:0009574 "preprophase band" evidence=IDA] InterPro:IPR000225 InterPro:IPR001752 InterPro:IPR011989 InterPro:IPR016024 InterPro:IPR019821 Pfam:PF00225 Pfam:PF00514 PRINTS:PR00380 PROSITE:PS00411 PROSITE:PS50067 PROSITE:PS50176 SMART:SM00129 SMART:SM00185 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005524 SUPFAM:SSF48371 Gene3D:G3DSA:1.25.10.10 eggNOG:COG5059 GO:GO:0005874 GO:GO:0003777 HSSP:P17119 HOGENOM:HBG319705 GO:GO:0007018 Gene3D:G3DSA:3.40.850.10 EMBL:AB290930 EMBL:AF159052 EMBL:AC025416 IPI:IPI00543027 RefSeq:NP_563908.1 UniGene:At.16100 ProteinModelPortal:Q9FZ06 SMR:Q9FZ06 PRIDE:Q9FZ06 EnsemblPlants:AT1G12430.1 GeneID:837799 KEGG:ath:AT1G12430 GeneFarm:2953 TAIR:At1g12430 InParanoid:Q9FZ06 OMA:HAILMVN PhylomeDB:Q9FZ06 Genevestigator:Q9FZ06 GO:GO:0009574 Uniprot:Q9FZ06

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig00334	177	1	7.339	2.33E-39	UNIPROTKB|F1MI03 - symbol:SRRM2 "Uncharacterized protein" species:9913 "Bos taurus" [GO:0015030 "Cajal body" evidence=IEA] [GO:0016607 "nuclear speck" evidence=IEA] [GO:0047485 "protein N-terminus binding" evidence=IEA] [GO:0070742 "C2H2 zinc finger domain binding" evidence=IEA] [GO:0071013 "catalytic step 2 spliceosome" evidence=IEA] InterPro:IPR024945 SMART:SM01104 InterPro:IPR013170 Pfam:PF08312 GeneTree:ENSGT00650000093061 OMA:TSPAPWK EMBL:DAAA02057317 EMBL:DAAA02057318 IPI:IPI00688395 Ensembl:ENSBTAT00000037527 Uniprot:F1MI03
Root	Isotig00336	176	1	7.330	3.60E-39	UNIPROTKB|F1MI03 - symbol:SRRM2 "Uncharacterized protein" species:9913 "Bos taurus" [GO:0015030 "Cajal body" evidence=IEA] [GO:0016607 "nuclear speck" evidence=IEA] [GO:0047485 "protein N-terminus binding" evidence=IEA] [GO:0070742 "C2H2 zinc finger domain binding" evidence=IEA] [GO:0071013 "catalytic step 2 spliceosome" evidence=IEA] InterPro:IPR024945 SMART:SM01104 InterPro:IPR013170 Pfam:PF08312 GeneTree:ENSGT00650000093061 OMA:TSPAPWK EMBL:DAAA02057317 EMBL:DAAA02057318 IPI:IPI00688395 Ensembl:ENSBTAT00000037527 Uniprot:F1MI03
Root	Isotig00342	193	10	4.142	2.62E-41	No hit
Root	Isotig00343	185	9	4.232	4.02E-40	No hit
Root	Isotig00344	190	9	4.271	2.39E-41	UNIPROTKB|E1BE02 - symbol:E2F7 "Uncharacterized protein" species:9913 "Bos taurus" [GO:0003677 "DNA binding" evidence=IEA] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=IEA] [GO:0005667 "transcription factor complex" evidence=IEA] [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0008285 "negative regulation of cell proliferation" evidence=IEA] [GO:0042802 "identical protein binding" evidence=IEA] InterPro:IPR003316 Pfam:PF02319 GO:GO:0003677 GO:GO:0006351 InterPro:IPR011991 Gene3D:G3DSA:1.10.10.10 GO:GO:0005667 InterPro:IPR015633 PANTHER:PTHR12081 GeneTree:ENSGT00530000063616 OMA:QRKVNSE EMBL:DAAA02012389 EMBL:DAAA02012390 IPI:IPI00691572 Ensembl:ENSBTAT00000022518 PhylomeDB:E1BE02 Uniprot:E1BE02
Root	Isotig00345	94	5	4.104	7.25E-21	No hit
Root	Isotig00346	92	5	4.073	2.26E-20	ZFIN|ZDB-GENE-990415-15 - symbol:arx "aristaless related homeobox" species:7955 "Danio rerio" [GO:0043565 "sequence-specific DNA binding" evidence=IEA] [GO:0005634 "nucleus" evidence=IEA] [GO:0003677 "DNA binding" evidence=IEA] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=IEA] [GO:0007275 "multicellular organismal development" evidence=IEA] [GO:0006351 "transcription, DNA-dependent" evidence=IEA] InterPro:IPR001356 InterPro:IPR009057 InterPro:IPR017970 Pfam:PF00046 PROSITE:PS00027 PROSITE:PS50071 SMART:SM00389 InterPro:IPR003654 ZFIN:ZDB-GENE-990415-15 GO:GO:0007275 GO:GO:0005634 GO:GO:0043565 GO:GO:0003700 GO:GO:0006351 Gene3D:G3DSA:1.10.10.60 SUPFAM:SSF46689 Pfam:PF03826 PROSITE:PS50803 eggNOG:NOG313402 GeneTree:ENSGT00650000092984 KO:K09452 EMBL:AB006104 IPI:IPI00502004 RefSeq:NP_571459.1 UniGene:Dr.9011 ProteinModelPortal:O42115 SMR:O42115 STRING:O42115 PRIDE:O42115 Ensembl:ENSDART00000080810 GeneID:30657 KEGG:dre:30657 CTD:170302 HOGENOM:HBG715732 HOVERGEN:HBG004285 InParanoid:O42115 OMA:RRSPCKV OrthoDB:EOG43TZW9 PhylomeDB:O42115 ArrayExpress:O42115 Bgee:O42115 Uniprot:O42115
Root	Isotig00347	133	8	3.926	3.96E-28	MGI|MGI:2144837 - symbol:Ptpn23 "protein tyrosine phosphatase, non-receptor type 23" species:10090 "Mus musculus" [GO:0005634 "nucleus" evidence=ISO] [GO:0005737 "cytoplasm" evidence=ISO] [GO:0005768 "endosome" evidence=ISO] [GO:0016311 "dephosphorylation" evidence=IEA] [GO:0016791 "phosphatase activity" evidence=IEA] [GO:0004725 "protein tyrosine phosphatase activity" evidence=IEA] [GO:0005932 "microtubule basal body" evidence=ISO] [GO:0005856 "cytoskeleton" evidence=IEA] [GO:0016787 "hydrolase activity" evidence=IEA] [GO:0030030 "cell projection organization" evidence=IEA] [GO:0004721 "phosphoprotein phosphatase activity" evidence=IEA] [GO:0005929 "cilium" evidence=IEA] [GO:0031410 "cytoplasmic vesicle" evidence=IEA] [GO:0042995 "cell projection" evidence=IEA] [GO:0006470 "protein dephosphorylation" evidence=IEA] [GO:0060271 "cilium morphogenesis" evidence=ISO] InterPro:IPR000242 InterPro:IPR000387 InterPro:IPR016130 InterPro:IPR025304 Pfam:PF00102 Pfam:PF13949 PRINTS:PR00700 PROSITE:PS00383 PROSITE:PS50005 PROSITE:PS50055 PROSITE:PS50056 PROSITE:PS50293 SMART:SM00194 MGI:MGI:2144837 GO:GO:0005634 GO:GO:0005768 GO:GO:0016023 GO:GO:0005929 GO:GO:0005932 InterPro:IPR004328 Gene3D:G3DSA:1.25.40.280 Pfam:PF03097 SMART:SM01041 PROSITE:PS51180 GeneTree:ENSGT00650000093161 GO:GO:0060271 GO:GO:0004725 eggNOG:COG5599 KO:K01104 PDB:2W10 PDBsum:2W10 CTD:25930 HOVERGEN:HBG082231 OMA:GPGPHYL EMBL:BY750106 EMBL:CF734421 EMBL:CB248963 EMBL:BC006582 EMBL:BC022721 EMBL:BC059902 EMBL:AK173178 IPI:IPI00464166

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						IPI:IPI00606716 RefSeq:NP_001074512.1 UniGene:Mm.335477 ProteinModelPortal:Q6PB44 SMR:Q6PB44 DIP:DIP-48351N IntAct:Q6PB44 STRING:Q6PB44 PhosphoSite:Q6PB44 PRIDE:Q6PB44 Ensembl:ENSMUST00000040021 GeneID:104831 KEGG:mmu:104831 UCSC:uc009rty.1 UCSC:uc012hbi.1 HOGENOM:HBG444522 InParanoid:Q6PB44 OrthoDB:EOG4NCMBX PhylomeDB:Q6PB44 NextBio:357310 ArrayExpress:Q6PB44 Bgee:Q6PB44 Genevestigator:Q6PB44 GermOnline:ENSMUSG00000036057 Uniprot:Q6PB44
Root	Isotig00348	123	6	4.229	3.15E-27	No hit
Root	Isotig00349	114	6	4.119	5.16E-25	No hit
Root	Isotig00351	30	3	3.193	1.42E-06	MGI|MGI:2144837 - symbol:Ptpn23 "protein tyrosine phosphatase, non-receptor type 23" species:10090 "Mus musculus" [GO:0005634 "nucleus" evidence=ISO] [GO:0005737 "cytoplasm" evidence=ISO] [GO:0005768 "endosome" evidence=ISO] [GO:0016311 "dephosphorylation" evidence=IEA] [GO:0016791 "phosphatase activity" evidence=IEA] [GO:0004725 "protein tyrosine phosphatase activity" evidence=IEA] [GO:0005932 "microtubule basal body" evidence=ISO] [GO:0005856 "cytoskeleton" evidence=IEA] [GO:0016787 "hydrolase activity" evidence=IEA] [GO:0030030 "cell projection organization" evidence=IEA] [GO:0004721 "phosphoprotein phosphatase activity" evidence=IEA] [GO:0005929 "cilium" evidence=IEA] [GO:0031410 "cytoplasmic vesicle" evidence=IEA] [GO:0042995 "cell projection" evidence=IEA] [GO:0006470 "protein dephosphorylation" evidence=IEA] [GO:0060271 "cilium morphogenesis" evidence=ISO] InterPro:IPR000242 InterPro:IPR000387 InterPro:IPR016130 InterPro:IPR025304 Pfam:PF00102 Pfam:PF13949 PRINTS:PR00700 PROSITE:PS00383 PROSITE:PS50005 PROSITE:PS50055 PROSITE:PS50056 PROSITE:PS50293 SMART:SM00194 MGI:MGI:2144837 GO:GO:0005634 GO:GO:0005768 GO:GO:0016023 GO:GO:0005929 GO:GO:0005932 InterPro:IPR004328 Gene3D:G3DSA:1.25.40.280 Pfam:PF03097 SMART:SM01041 PROSITE:PS51180 GeneTree:ENSGT00650000093161 GO:GO:0060271 GO:GO:0004725 eggNOG:COG5599 KO:K01104 PDB:2W10 PDBsum:2W10 CTD:25930 HOVERGEN:HBG082231 OMA:GPGPHYL EMBL:BY750106 EMBL:CF734421 EMBL:CB248963 EMBL:BC006582 EMBL:BC022721 EMBL:BC059902 EMBL:AK173178 IPI:IPI00464166 IPI:IPI00606716 RefSeq:NP_001074512.1 UniGene:Mm.335477 ProteinModelPortal:Q6PB44 SMR:Q6PB44 DIP:DIP-48351N IntAct:Q6PB44 STRING:Q6PB44 PhosphoSite:Q6PB44 PRIDE:Q6PB44 Ensembl:ENSMUST00000040021 GeneID:104831 KEGG:mmu:104831 UCSC:uc009rty.1 UCSC:uc012hbi.1 HOGENOM:HBG444522 InParanoid:Q6PB44 OrthoDB:EOG4NCMBX PhylomeDB:Q6PB44 NextBio:357310 ArrayExpress:Q6PB44 Bgee:Q6PB44 Genevestigator:Q6PB44 GermOnline:ENSMUSG00000036057 Uniprot:Q6PB44
Root	Isotig00352	13	1	3.571	0.000882483	UNIPROTKB|E2R9J1 - symbol:HEYL "Uncharacterized protein" species:9615 "Canis lupus familiaris" [GO:0003677 "DNA binding" evidence=IEA] [GO:0005634 "nucleus" evidence=IEA] [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] InterPro:IPR003650 Pfam:PF07527 PROSITE:PS51054 InterPro:IPR011598 Pfam:PF00010 GO:GO:0005634 GO:GO:0006355 GO:GO:0003677 GO:GO:0006351 Gene3D:G3DSA:4.10.280.10 SMART:SM00353 SUPFAM:SSF47459 PROSITE:PS50888 InterPro:IPR018352 SMART:SM00511 GeneTree:ENSGT00510000046466 KO:K09091 CTD:26508 OMA:WVSEITE RefSeq:XP_849702.1 Ensembl:ENSCAFT00000004941 GeneID:607804 KEGG:cfa:607804 Uniprot:E2R9J1
Root	Isotig00353	28	3	3.093	4.38E-06	MGI|MGI:2144837 - symbol:Ptpn23 "protein tyrosine phosphatase, non-receptor type 23" species:10090 "Mus musculus" [GO:0005634 "nucleus" evidence=ISO] [GO:0005737 "cytoplasm" evidence=ISO] [GO:0005768 "endosome" evidence=ISO] [GO:0016311 "dephosphorylation" evidence=IEA] [GO:0016791 "phosphatase activity" evidence=IEA] [GO:0004725 "protein tyrosine phosphatase activity" evidence=IEA] [GO:0005932 "microtubule basal body" evidence=ISO] [GO:0005856 "cytoskeleton" evidence=IEA] [GO:0016787 "hydrolase activity" evidence=IEA] [GO:0030030 "cell projection organization" evidence=IEA] [GO:0004721 "phosphoprotein phosphatase activity" evidence=IEA] [GO:0005929 "cilium" evidence=IEA] [GO:0031410 "cytoplasmic vesicle" evidence=IEA] [GO:0042995 "cell projection" evidence=IEA] [GO:0006470 "protein dephosphorylation" evidence=IEA] [GO:0060271 "cilium morphogenesis" evidence=ISO] InterPro:IPR000242 InterPro:IPR000387 InterPro:IPR016130 InterPro:IPR025304 Pfam:PF00102 Pfam:PF13949 PRINTS:PR00700 PROSITE:PS00383 PROSITE:PS50005 PROSITE:PS50055 PROSITE:PS50056 PROSITE:PS50293 SMART:SM00194 MGI:MGI:2144837 GO:GO:0005634 GO:GO:0005768 GO:GO:0016023 GO:GO:0005929 GO:GO:0005932 InterPro:IPR004328 Gene3D:G3DSA:1.25.40.280 Pfam:PF03097 SMART:SM01041 PROSITE:PS51180 GeneTree:ENSGT00650000093161 GO:GO:0060271 GO:GO:0004725 eggNOG:COG5599 KO:K01104 PDB:2W10

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						PDBsum:2W10 CTD:25930 HOVERGEN:HBG082231 OMA:GPGPHYL EMBL:BY750106 EMBL:CF734421 EMBL:CB248963 EMBL:BC006582 EMBL:BC022721 EMBL:BC059902 EMBL:AK173178 IPI:IPI00464166 IPI:IPI00606716 RefSeq:NP_001074512.1 UniGene:Mm.335477 ProteinModelPortal:Q6PB44 SMR:Q6PB44 DIP:DIP-48351N IntAct:Q6PB44 STRING:Q6PB44 PhosphoSite:Q6PB44 PRIDE:Q6PB44 Ensembl:ENSMUST00000040021 GeneID:104831 KEGG:mmu:104831 UCSC:uc009rty.1 UCSC:uc012hbi.1 HOGENOM:HBG444522 InParanoid:Q6PB44 OrthoDB:EOG4NCMBX PhylomeDB:Q6PB44 NextBio:357310 ArrayExpress:Q6PB44 Bgee:Q6PB44 Genevestigator:Q6PB44 GermOnline:ENSMUSG00000036057 Uniprot:Q6PB44
Root	Isotig00354	13	1	3.571	0.000882483	UNIPROTKB|E2R9J1 - symbol:HEYL "Uncharacterized protein" species:9615 "Canis lupus familiaris" [GO:0003677 "DNA binding" evidence=IEA] [GO:0005634 "nucleus" evidence=IEA] [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] InterPro:IPR003650 Pfam:PF07527 PROSITE:PS51054 InterPro:IPR011598 Pfam:PF00010 GO:GO:0005634 GO:GO:0006355 GO:GO:0003677 GO:GO:0006351 Gene3D:G3DSA:4.10.280.10 SMART:SM00353 SUPFAM:SSF47459 PROSITE:PS50888 InterPro:IPR018352 SMART:SM00511 GeneTree:ENSGT00510000046466 KO:K09091 CTD:26508 OMA:WVSEITE RefSeq:XP_849702.1 Ensembl:ENSCAFT00000004941 GeneID:607804 KEGG:cfa:607804 Uniprot:E2R9J1
Root	Isotig00366	24	78	-1.829	3.61E-09	TAIR|locus:2079834 - symbol:AAO2 "aldehyde oxidase 2" species:3702 "Arabidopsis thaliana" [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0004031 "aldehyde oxidase activity" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001041 InterPro:IPR002346 InterPro:IPR002888 InterPro:IPR006058 InterPro:IPR008274 InterPro:IPR016166 InterPro:IPR016169 InterPro:IPR016208 Pfam:PF00111 Pfam:PF00941 Pfam:PF01799 Pfam:PF02738 PIRSF:PIRSF000127 PROSITE:PS00197 PROSITE:PS00559 PROSITE:PS51085 PROSITE:PS51387 InterPro:IPR000674 Pfam:PF01315 GO:GO:0005829 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005506 GO:GO:0009055 GO:GO:0050660 SUPFAM:SSF56176 GO:GO:0004031 eggNOG:COG4630 GO:GO:0051537 InterPro:IPR012675 InterPro:IPR005107 Gene3D:G3DSA:1.10.150.120 Gene3D:G3DSA:3.30.365.10 Gene3D:G3DSA:3.90.1170.50 Gene3D:G3DSA:3.30.390.50 Gene3D:G3DSA:3.30.465.10 Gene3D:G3DSA:3.10.20.30 Pfam:PF03450 SMART:SM01008 SMART:SM01092 SUPFAM:SSF47741 SUPFAM:SSF56003 SUPFAM:SSF54665 SUPFAM:SSF55447 SUPFAM:SSF54292 HOGENOM:HBG746468 ProtClustDB:PLN00192 EMBL:AB005805 EMBL:AL391734 EMBL:AF039896 IPI:IPI00529435 PIR:T51623 PIR:T52050 RefSeq:NP_189946.1 UniGene:At.462 ProteinModelPortal:Q7G192 SMR:Q7G192 STRING:Q7G192 PRIDE:Q7G192 EnsemblPlants:AT3G43600.1 GeneID:823457 KEGG:ath:AT3G43600 GeneFarm:4893 TAIR:At3g43600 InParanoid:Q7G192 OMA:ILYDCGK PhylomeDB:Q7G192 BioCyc:ARA:AT3G43600-MONOMER BioCyc:MetaCyc:AT3G43600-MONOMER Genevestigator:Q7G192 GermOnline:AT3G43600 GO:GO:0016614 Uniprot:Q7G192
Root	Isotig00367	24	78	-1.829	3.61E-09	TAIR|locus:2079834 - symbol:AAO2 "aldehyde oxidase 2" species:3702 "Arabidopsis thaliana" [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0004031 "aldehyde oxidase activity" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001041 InterPro:IPR002346 InterPro:IPR002888 InterPro:IPR006058 InterPro:IPR008274 InterPro:IPR016166 InterPro:IPR016169 InterPro:IPR016208 Pfam:PF00111 Pfam:PF00941 Pfam:PF01799 Pfam:PF02738 PIRSF:PIRSF000127 PROSITE:PS00197 PROSITE:PS00559 PROSITE:PS51085 PROSITE:PS51387 InterPro:IPR000674 Pfam:PF01315 GO:GO:0005829 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005506 GO:GO:0009055 GO:GO:0050660 SUPFAM:SSF56176 GO:GO:0004031 eggNOG:COG4630 GO:GO:0051537 InterPro:IPR012675 InterPro:IPR005107 Gene3D:G3DSA:1.10.150.120 Gene3D:G3DSA:3.30.365.10 Gene3D:G3DSA:3.90.1170.50 Gene3D:G3DSA:3.30.390.50 Gene3D:G3DSA:3.30.465.10 Gene3D:G3DSA:3.10.20.30 Pfam:PF03450 SMART:SM01008 SMART:SM01092 SUPFAM:SSF47741 SUPFAM:SSF56003 SUPFAM:SSF54665 SUPFAM:SSF55447 SUPFAM:SSF54292 HOGENOM:HBG746468 ProtClustDB:PLN00192 EMBL:AB005805 EMBL:AL391734 EMBL:AF039896 IPI:IPI00529435 PIR:T51623 PIR:T52050 RefSeq:NP_189946.1 UniGene:At.462 ProteinModelPortal:Q7G192 SMR:Q7G192 STRING:Q7G192 PRIDE:Q7G192 EnsemblPlants:AT3G43600.1 GeneID:823457 KEGG:ath:AT3G43600 GeneFarm:4893 TAIR:At3g43600 InParanoid:Q7G192 OMA:ILYDCGK PhylomeDB:Q7G192 BioCyc:ARA:AT3G43600-MONOMER BioCyc:MetaCyc:AT3G43600-MONOMER Genevestigator:Q7G192 GermOnline:AT3G43600 GO:GO:0016614 Uniprot:Q7G192
Root	Isotig00368	19	84	-2.273	1.83E-12	TAIR|locus:2079834 - symbol:AAO2 "aldehyde oxidase 2" species:3702 "Arabidopsis thaliana" [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0004031 "aldehyde oxidase activity" evidence=IDA] [GO:0005829

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						"cytosol" evidence=IDA] InterPro:IPR001041 InterPro:IPR002346 InterPro:IPR002888 InterPro:IPR006058 InterPro:IPR008274 InterPro:IPR016166 InterPro:IPR016169 InterPro:IPR016208 Pfam:PF00111 Pfam:PF00941 Pfam:PF01799 Pfam:PF02738 PIRSF:PIRSF000127 PROSITE:PS00197 PROSITE:PS00559 PROSITE:PS51085 PROSITE:PS51387 InterPro:IPR000674 Pfam:PF01315 GO:GO:0005829 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005506 GO:GO:0009055 GO:GO:0050660 SUPFAM:SSF56176 GO:GO:0004031 eggNOG:COG4630 GO:GO:0051537 InterPro:IPR012675 InterPro:IPR005107 Gene3D:G3DSA:1.10.150.120 Gene3D:G3DSA:3.30.365.10 Gene3D:G3DSA:3.90.1170.50 Gene3D:G3DSA:3.30.390.50 Gene3D:G3DSA:3.30.465.10 Gene3D:G3DSA:3.10.20.30 Pfam:PF03450 SMART:SM01008 SMART:SM01092 SUPFAM:SSF47741 SUPFAM:SSF56003 SUPFAM:SSF54665 SUPFAM:SSF55447 SUPFAM:SSF54292 HOGENOM:HBG746468 ProtClustDB:PLN00192 EMBL:AB005805 EMBL:AL391734 EMBL:AF039896 IPI:IPI00529435 PIR:T51623 PIR:T52050 RefSeq:NP_189946.1 UniGene:At.462 ProteinModelPortal:Q7G192 SMR:Q7G192 STRING:Q7G192 PRIDE:Q7G192 EnsemblPlants:AT3G43600.1 GeneID:823457 KEGG:ath:AT3G43600 GeneFarm:4893 TAIR:At3g43600 InParanoid:Q7G192 OMA:ILYDCGK PhylomeDB:Q7G192 BioCyc:ARA:AT3G43600-MONOMER BioCyc:MetaCyc:AT3G43600-MONOMER Genevestigator:Q7G192 GermOnline:AT3G43600 GO:GO:0016614 Uniprot:Q7G192
Root	Isotig00369	24	78	-1.829	3.61E-09	TAIR|locus:2079834 - symbol:AAO2 "aldehyde oxidase 2" species:3702 "Arabidopsis thaliana" [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0004031 "aldehyde oxidase activity" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001041 InterPro:IPR002346 InterPro:IPR002888 InterPro:IPR006058 InterPro:IPR008274 InterPro:IPR016166 InterPro:IPR016169 InterPro:IPR016208 Pfam:PF00111 Pfam:PF00941 Pfam:PF01799 Pfam:PF02738 PIRSF:PIRSF000127 PROSITE:PS00197 PROSITE:PS00559 PROSITE:PS51085 PROSITE:PS51387 InterPro:IPR000674 Pfam:PF01315 GO:GO:0005829 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005506 GO:GO:0009055 GO:GO:0050660 SUPFAM:SSF56176 GO:GO:0004031 eggNOG:COG4630 GO:GO:0051537 InterPro:IPR012675 InterPro:IPR005107 Gene3D:G3DSA:1.10.150.120 Gene3D:G3DSA:3.30.365.10 Gene3D:G3DSA:3.90.1170.50 Gene3D:G3DSA:3.30.390.50 Gene3D:G3DSA:3.30.465.10 Gene3D:G3DSA:3.10.20.30 Pfam:PF03450 SMART:SM01008 SMART:SM01092 SUPFAM:SSF47741 SUPFAM:SSF56003 SUPFAM:SSF54665 SUPFAM:SSF55447 SUPFAM:SSF54292 HOGENOM:HBG746468 ProtClustDB:PLN00192 EMBL:AB005805 EMBL:AL391734 EMBL:AF039896 IPI:IPI00529435 PIR:T51623 PIR:T52050 RefSeq:NP_189946.1 UniGene:At.462 ProteinModelPortal:Q7G192 SMR:Q7G192 STRING:Q7G192 PRIDE:Q7G192 EnsemblPlants:AT3G43600.1 GeneID:823457 KEGG:ath:AT3G43600 GeneFarm:4893 TAIR:At3g43600 InParanoid:Q7G192 OMA:ILYDCGK PhylomeDB:Q7G192 BioCyc:ARA:AT3G43600-MONOMER BioCyc:MetaCyc:AT3G43600-MONOMER Genevestigator:Q7G192 GermOnline:AT3G43600 GO:GO:0016614 Uniprot:Q7G192
Root	Isotig00370	24	78	-1.829	3.61E-09	TAIR|locus:2079834 - symbol:AAO2 "aldehyde oxidase 2" species:3702 "Arabidopsis thaliana" [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0004031 "aldehyde oxidase activity" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001041 InterPro:IPR002346 InterPro:IPR002888 InterPro:IPR006058 InterPro:IPR008274 InterPro:IPR016166 InterPro:IPR016169 InterPro:IPR016208 Pfam:PF00111 Pfam:PF00941 Pfam:PF01799 Pfam:PF02738 PIRSF:PIRSF000127 PROSITE:PS00197 PROSITE:PS00559 PROSITE:PS51085 PROSITE:PS51387 InterPro:IPR000674 Pfam:PF01315 GO:GO:0005829 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005506 GO:GO:0009055 GO:GO:0050660 SUPFAM:SSF56176 GO:GO:0004031 eggNOG:COG4630 GO:GO:0051537 InterPro:IPR012675 InterPro:IPR005107 Gene3D:G3DSA:1.10.150.120 Gene3D:G3DSA:3.30.365.10 Gene3D:G3DSA:3.90.1170.50 Gene3D:G3DSA:3.30.390.50 Gene3D:G3DSA:3.30.465.10 Gene3D:G3DSA:3.10.20.30 Pfam:PF03450 SMART:SM01008 SMART:SM01092 SUPFAM:SSF47741 SUPFAM:SSF56003 SUPFAM:SSF54665 SUPFAM:SSF55447 SUPFAM:SSF54292 HOGENOM:HBG746468 ProtClustDB:PLN00192 EMBL:AB005805 EMBL:AL391734 EMBL:AF039896 IPI:IPI00529435 PIR:T51623 PIR:T52050 RefSeq:NP_189946.1 UniGene:At.462 ProteinModelPortal:Q7G192 SMR:Q7G192 STRING:Q7G192 PRIDE:Q7G192 EnsemblPlants:AT3G43600.1 GeneID:823457 KEGG:ath:AT3G43600 GeneFarm:4893 TAIR:At3g43600 InParanoid:Q7G192 OMA:ILYDCGK PhylomeDB:Q7G192 BioCyc:ARA:AT3G43600-MONOMER BioCyc:MetaCyc:AT3G43600-MONOMER Genevestigator:Q7G192 GermOnline:AT3G43600 GO:GO:0016614 Uniprot:Q7G192
Root	Isotig00371	19	84	-2.273	1.83E-12	TAIR|locus:2079834 - symbol:AAO2 "aldehyde oxidase 2" species:3702 "Arabidopsis thaliana" [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0004031 "aldehyde oxidase activity" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001041 InterPro:IPR002346 InterPro:IPR002888 InterPro:IPR006058

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						InterPro:IPR008274 InterPro:IPR016166 InterPro:IPR016169 InterPro:IPR016208 Pfam:PF00111 Pfam:PF00941 Pfam:PF01799 Pfam:PF02738 PIRSF:PIRSF000127 PROSITE:PS00197 PROSITE:PS00559 PROSITE:PS51085 PROSITE:PS51387 InterPro:IPR000674 Pfam:PF01315 GO:GO:0005829 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005506 GO:GO:0009055 GO:GO:0050660 SUPFAM:SSF56176 GO:GO:0004031 eggNOG:COG4630 GO:GO:0051537 InterPro:IPR012675 InterPro:IPR005107 Gene3D:G3DSA:1.10.150.120 Gene3D:G3DSA:3.30.365.10 Gene3D:G3DSA:3.90.1170.50 Gene3D:G3DSA:3.30.390.50 Gene3D:G3DSA:3.30.465.10 Gene3D:G3DSA:3.10.20.30 Pfam:PF03450 SMART:SM01008 SMART:SM01092 SUPFAM:SSF47741 SUPFAM:SSF56003 SUPFAM:SSF54665 SUPFAM:SSF55447 SUPFAM:SSF54292 HOGENOM:HBG746468 ProtClustDB:PLN00192 EMBL:AB005805 EMBL:AL391734 EMBL:AF039896 IPI:IPI00529435 PIR:T51623 PIR:T52050 RefSeq:NP_189946.1 UniGene:At.462 ProteinModelPortal:Q7G192 SMR:Q7G192 STRING:Q7G192 PRIDE:Q7G192 EnsemblPlants:AT3G43600.1 GeneID:823457 KEGG:ath:AT3G43600 GeneFarm:4893 TAIR:At3g43600 InParanoid:Q7G192 OMA:ILYDCGK PhylomeDB:Q7G192 BioCyc:ARA:AT3G43600-MONOMER BioCyc:MetaCyc:AT3G43600-MONOMER Genevestigator:Q7G192 GermOnline:AT3G43600 GO:GO:0016614 Uniprot:Q7G192
Root	Isotig00372	19	84	-2.273	1.83E-12	TAIR|locus:2079834 - symbol:AAO2 "aldehyde oxidase 2" species:3702 "Arabidopsis thaliana" [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0004031 "aldehyde oxidase activity" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001041 InterPro:IPR002346 InterPro:IPR002888 InterPro:IPR006058 InterPro:IPR008274 InterPro:IPR016166 InterPro:IPR016169 InterPro:IPR016208 Pfam:PF00111 Pfam:PF00941 Pfam:PF01799 Pfam:PF02738 PIRSF:PIRSF000127 PROSITE:PS00197 PROSITE:PS00559 PROSITE:PS51085 PROSITE:PS51387 InterPro:IPR000674 Pfam:PF01315 GO:GO:0005829 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005506 GO:GO:0009055 GO:GO:0050660 SUPFAM:SSF56176 GO:GO:0004031 eggNOG:COG4630 GO:GO:0051537 InterPro:IPR012675 InterPro:IPR005107 Gene3D:G3DSA:1.10.150.120 Gene3D:G3DSA:3.30.365.10 Gene3D:G3DSA:3.90.1170.50 Gene3D:G3DSA:3.30.390.50 Gene3D:G3DSA:3.30.465.10 Gene3D:G3DSA:3.10.20.30 Pfam:PF03450 SMART:SM01008 SMART:SM01092 SUPFAM:SSF47741 SUPFAM:SSF56003 SUPFAM:SSF54665 SUPFAM:SSF55447 SUPFAM:SSF54292 HOGENOM:HBG746468 ProtClustDB:PLN00192 EMBL:AB005805 EMBL:AL391734 EMBL:AF039896 IPI:IPI00529435 PIR:T51623 PIR:T52050 RefSeq:NP_189946.1 UniGene:At.462 ProteinModelPortal:Q7G192 SMR:Q7G192 STRING:Q7G192 PRIDE:Q7G192 EnsemblPlants:AT3G43600.1 GeneID:823457 KEGG:ath:AT3G43600 GeneFarm:4893 TAIR:At3g43600 InParanoid:Q7G192 OMA:ILYDCGK PhylomeDB:Q7G192 BioCyc:ARA:AT3G43600-MONOMER BioCyc:MetaCyc:AT3G43600-MONOMER Genevestigator:Q7G192 GermOnline:AT3G43600 GO:GO:0016614 Uniprot:Q7G192
Root	Isotig00373	19	84	-2.273	1.83E-12	TAIR|locus:2079834 - symbol:AAO2 "aldehyde oxidase 2" species:3702 "Arabidopsis thaliana" [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0004031 "aldehyde oxidase activity" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001041 InterPro:IPR002346 InterPro:IPR002888 InterPro:IPR006058 InterPro:IPR008274 InterPro:IPR016166 InterPro:IPR016169 InterPro:IPR016208 Pfam:PF00111 Pfam:PF00941 Pfam:PF01799 Pfam:PF02738 PIRSF:PIRSF000127 PROSITE:PS00197 PROSITE:PS00559 PROSITE:PS51085 PROSITE:PS51387 InterPro:IPR000674 Pfam:PF01315 GO:GO:0005829 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005506 GO:GO:0009055 GO:GO:0050660 SUPFAM:SSF56176 GO:GO:0004031 eggNOG:COG4630 GO:GO:0051537 InterPro:IPR012675 InterPro:IPR005107 Gene3D:G3DSA:1.10.150.120 Gene3D:G3DSA:3.30.365.10 Gene3D:G3DSA:3.90.1170.50 Gene3D:G3DSA:3.30.390.50 Gene3D:G3DSA:3.30.465.10 Gene3D:G3DSA:3.10.20.30 Pfam:PF03450 SMART:SM01008 SMART:SM01092 SUPFAM:SSF47741 SUPFAM:SSF56003 SUPFAM:SSF54665 SUPFAM:SSF55447 SUPFAM:SSF54292 HOGENOM:HBG746468 ProtClustDB:PLN00192 EMBL:AB005805 EMBL:AL391734 EMBL:AF039896 IPI:IPI00529435 PIR:T51623 PIR:T52050 RefSeq:NP_189946.1 UniGene:At.462 ProteinModelPortal:Q7G192 SMR:Q7G192 STRING:Q7G192 PRIDE:Q7G192 EnsemblPlants:AT3G43600.1 GeneID:823457 KEGG:ath:AT3G43600 GeneFarm:4893 TAIR:At3g43600 InParanoid:Q7G192 OMA:ILYDCGK PhylomeDB:Q7G192 BioCyc:ARA:AT3G43600-MONOMER BioCyc:MetaCyc:AT3G43600-MONOMER Genevestigator:Q7G192 GermOnline:AT3G43600 GO:GO:0016614 Uniprot:Q7G192
Root	Isotig00374	24	73	-1.734	3.78E-08	TAIR|locus:2079834 - symbol:AAO2 "aldehyde oxidase 2" species:3702 "Arabidopsis thaliana" [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0004031 "aldehyde oxidase activity" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001041 InterPro:IPR002346 InterPro:IPR002888 InterPro:IPR006058 InterPro:IPR008274 InterPro:IPR016166 InterPro:IPR016169 InterPro:IPR016208 Pfam:PF00111 Pfam:PF00941

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						Pfam:PF01799 Pfam:PF02738 PIRSF:PIRSF000127 PROSITE:PS00197 PROSITE:PS00559 PROSITE:PS51085 PROSITE:PS51387 InterPro:IPR000674 Pfam:PF01315 GO:GO:0005829 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005506 GO:GO:0009055 GO:GO:0050660 SUPFAM:SSF56176 GO:GO:0004031 eggNOG:COG4630 GO:GO:0051537 InterPro:IPR012675 InterPro:IPR005107 Gene3D:G3DSA:1.10.150.120 Gene3D:G3DSA:3.30.365.10 Gene3D:G3DSA:3.90.1170.50 Gene3D:G3DSA:3.30.390.50 Gene3D:G3DSA:3.30.465.10 Gene3D:G3DSA:3.10.20.30 Pfam:PF03450 SMART:SM01008 SMART:SM01092 SUPFAM:SSF47741 SUPFAM:SSF56003 SUPFAM:SSF54665 SUPFAM:SSF55447 SUPFAM:SSF54292 HOGENOM:HBG746468 ProtClustDB:PLN00192 EMBL:AB005805 EMBL:AL391734 EMBL:AF039896 IPI:IPI00529435 PIR:T51623 PIR:T52050 RefSeq:NP_189946.1 UniGene:At.462 ProteinModelPortal:Q7G192 SMR:Q7G192 STRING:Q7G192 PRIDE:Q7G192 EnsemblPlants:AT3G43600.1 GeneID:823457 KEGG:ath:AT3G43600 GeneFarm:4893 TAIR:At3g43600 InParanoid:Q7G192 OMA:ILYDCGK PhylomeDB:Q7G192 BioCyc:ARA:AT3G43600-MONOMER BioCyc:MetaCyc:AT3G43600-MONOMER Genevestigator:Q7G192 GermOnline:AT3G43600 GO:GO:0016614 Uniprot:Q7G192
Root	Isotig00375	24	73	-1.734	3.78E-08	TAIR|locus:2079834 - symbol:AAO2 "aldehyde oxidase 2" species:3702 "Arabidopsis thaliana" [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0004031 "aldehyde oxidase activity" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001041 InterPro:IPR002346 InterPro:IPR002888 InterPro:IPR006058 InterPro:IPR008274 InterPro:IPR016166 InterPro:IPR016169 InterPro:IPR016208 Pfam:PF00111 Pfam:PF00941 Pfam:PF01799 Pfam:PF02738 PIRSF:PIRSF000127 PROSITE:PS00197 PROSITE:PS00559 PROSITE:PS51085 PROSITE:PS51387 InterPro:IPR000674 Pfam:PF01315 GO:GO:0005829 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005506 GO:GO:0009055 GO:GO:0050660 SUPFAM:SSF56176 GO:GO:0004031 eggNOG:COG4630 GO:GO:0051537 InterPro:IPR012675 InterPro:IPR005107 Gene3D:G3DSA:1.10.150.120 Gene3D:G3DSA:3.30.365.10 Gene3D:G3DSA:3.90.1170.50 Gene3D:G3DSA:3.30.390.50 Gene3D:G3DSA:3.30.465.10 Gene3D:G3DSA:3.10.20.30 Pfam:PF03450 SMART:SM01008 SMART:SM01092 SUPFAM:SSF47741 SUPFAM:SSF56003 SUPFAM:SSF54665 SUPFAM:SSF55447 SUPFAM:SSF54292 HOGENOM:HBG746468 ProtClustDB:PLN00192 EMBL:AB005805 EMBL:AL391734 EMBL:AF039896 IPI:IPI00529435 PIR:T51623 PIR:T52050 RefSeq:NP_189946.1 UniGene:At.462 ProteinModelPortal:Q7G192 SMR:Q7G192 STRING:Q7G192 PRIDE:Q7G192 EnsemblPlants:AT3G43600.1 GeneID:823457 KEGG:ath:AT3G43600 GeneFarm:4893 TAIR:At3g43600 InParanoid:Q7G192 OMA:ILYDCGK PhylomeDB:Q7G192 BioCyc:ARA:AT3G43600-MONOMER BioCyc:MetaCyc:AT3G43600-MONOMER Genevestigator:Q7G192 GermOnline:AT3G43600 GO:GO:0016614 Uniprot:Q7G192
Root	Isotig00376	19	79	-2.185	2.58E-11	TAIR|locus:2079834 - symbol:AAO2 "aldehyde oxidase 2" species:3702 "Arabidopsis thaliana" [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0004031 "aldehyde oxidase activity" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001041 InterPro:IPR002346 InterPro:IPR002888 InterPro:IPR006058 InterPro:IPR008274 InterPro:IPR016166 InterPro:IPR016169 InterPro:IPR016208 Pfam:PF00111 Pfam:PF00941 Pfam:PF01799 Pfam:PF02738 PIRSF:PIRSF000127 PROSITE:PS00197 PROSITE:PS00559 PROSITE:PS51085 PROSITE:PS51387 InterPro:IPR000674 Pfam:PF01315 GO:GO:0005829 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005506 GO:GO:0009055 GO:GO:0050660 SUPFAM:SSF56176 GO:GO:0004031 eggNOG:COG4630 GO:GO:0051537 InterPro:IPR012675 InterPro:IPR005107 Gene3D:G3DSA:1.10.150.120 Gene3D:G3DSA:3.30.365.10 Gene3D:G3DSA:3.90.1170.50 Gene3D:G3DSA:3.30.390.50 Gene3D:G3DSA:3.30.465.10 Gene3D:G3DSA:3.10.20.30 Pfam:PF03450 SMART:SM01008 SMART:SM01092 SUPFAM:SSF47741 SUPFAM:SSF56003 SUPFAM:SSF54665 SUPFAM:SSF55447 SUPFAM:SSF54292 HOGENOM:HBG746468 ProtClustDB:PLN00192 EMBL:AB005805 EMBL:AL391734 EMBL:AF039896 IPI:IPI00529435 PIR:T51623 PIR:T52050 RefSeq:NP_189946.1 UniGene:At.462 ProteinModelPortal:Q7G192 SMR:Q7G192 STRING:Q7G192 PRIDE:Q7G192 EnsemblPlants:AT3G43600.1 GeneID:823457 KEGG:ath:AT3G43600 GeneFarm:4893 TAIR:At3g43600 InParanoid:Q7G192 OMA:ILYDCGK PhylomeDB:Q7G192 BioCyc:ARA:AT3G43600-MONOMER BioCyc:MetaCyc:AT3G43600-MONOMER Genevestigator:Q7G192 GermOnline:AT3G43600 GO:GO:0016614 Uniprot:Q7G192
Root	Isotig00377	24	73	-1.734	3.78E-08	TAIR|locus:2079834 - symbol:AAO2 "aldehyde oxidase 2" species:3702 "Arabidopsis thaliana" [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0004031 "aldehyde oxidase activity" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001041 InterPro:IPR002346 InterPro:IPR002888 InterPro:IPR006058 InterPro:IPR008274 InterPro:IPR016166 InterPro:IPR016169 InterPro:IPR016208 Pfam:PF00111 Pfam:PF00941 Pfam:PF01799 Pfam:PF02738 PIRSF:PIRSF000127 PROSITE:PS00197 PROSITE:PS00559 PROSITE:PS51085

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						PROSITE:PS51387 InterPro:IPR000674 Pfam:PF01315 GO:GO:0005829 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005506 GO:GO:0009055 GO:GO:0050660 SUPFAM:SSF56176 GO:GO:0004031 eggNOG:COG4630 GO:GO:0051537 InterPro:IPR012675 InterPro:IPR005107 Gene3D:G3DSA:1.10.150.120 Gene3D:G3DSA:3.30.365.10 Gene3D:G3DSA:3.90.1170.50 Gene3D:G3DSA:3.30.390.50 Gene3D:G3DSA:3.30.465.10 Gene3D:G3DSA:3.10.20.30 Pfam:PF03450 SMART:SM01008 SMART:SM01092 SUPFAM:SSF47741 SUPFAM:SSF56003 SUPFAM:SSF54665 SUPFAM:SSF55447 SUPFAM:SSF54292 HOGENOM:HBG746468 ProtClustDB:PLN00192 EMBL:AB005805 EMBL:AL391734 EMBL:AF039896 IPI:IPI00529435 PIR:T51623 PIR:T52050 RefSeq:NP_189946.1 UniGene:At.462 ProteinModelPortal:Q7G192 SMR:Q7G192 STRING:Q7G192 PRIDE:Q7G192 EnsemblPlants:AT3G43600.1 GeneID:823457 KEGG:ath:AT3G43600 GeneFarm:4893 TAIR:At3g43600 InParanoid:Q7G192 OMA:ILYDCGK PhylomeDB:Q7G192 BioCyc:ARA:AT3G43600-MONOMER BioCyc:MetaCyc:AT3G43600-MONOMER Genevestigator:Q7G192 GermOnline:AT3G43600 GO:GO:0016614 Uniprot:Q7G192
Root	Isotig00378	24	73	-1.734	3.78E-08	TAIR|locus:2079834 - symbol:AAO2 "aldehyde oxidase 2" species:3702 "Arabidopsis thaliana" [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0004031 "aldehyde oxidase activity" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001041 InterPro:IPR002346 InterPro:IPR002888 InterPro:IPR006058 InterPro:IPR008274 InterPro:IPR016166 InterPro:IPR016169 InterPro:IPR016208 Pfam:PF00111 Pfam:PF00941 Pfam:PF01799 Pfam:PF02738 PIRSF:PIRSF000127 PROSITE:PS00197 PROSITE:PS00559 PROSITE:PS51085 PROSITE:PS51387 InterPro:IPR000674 Pfam:PF01315 GO:GO:0005829 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005506 GO:GO:0009055 GO:GO:0050660 SUPFAM:SSF56176 GO:GO:0004031 eggNOG:COG4630 GO:GO:0051537 InterPro:IPR012675 InterPro:IPR005107 Gene3D:G3DSA:1.10.150.120 Gene3D:G3DSA:3.30.365.10 Gene3D:G3DSA:3.90.1170.50 Gene3D:G3DSA:3.30.390.50 Gene3D:G3DSA:3.30.465.10 Gene3D:G3DSA:3.10.20.30 Pfam:PF03450 SMART:SM01008 SMART:SM01092 SUPFAM:SSF47741 SUPFAM:SSF56003 SUPFAM:SSF54665 SUPFAM:SSF55447 SUPFAM:SSF54292 HOGENOM:HBG746468 ProtClustDB:PLN00192 EMBL:AB005805 EMBL:AL391734 EMBL:AF039896 IPI:IPI00529435 PIR:T51623 PIR:T52050 RefSeq:NP_189946.1 UniGene:At.462 ProteinModelPortal:Q7G192 SMR:Q7G192 STRING:Q7G192 PRIDE:Q7G192 EnsemblPlants:AT3G43600.1 GeneID:823457 KEGG:ath:AT3G43600 GeneFarm:4893 TAIR:At3g43600 InParanoid:Q7G192 OMA:ILYDCGK PhylomeDB:Q7G192 BioCyc:ARA:AT3G43600-MONOMER BioCyc:MetaCyc:AT3G43600-MONOMER Genevestigator:Q7G192 GermOnline:AT3G43600 GO:GO:0016614 Uniprot:Q7G192
Root	Isotig00379	19	79	-2.185	2.58E-11	TAIR|locus:2079834 - symbol:AAO2 "aldehyde oxidase 2" species:3702 "Arabidopsis thaliana" [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0004031 "aldehyde oxidase activity" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001041 InterPro:IPR002346 InterPro:IPR002888 InterPro:IPR006058 InterPro:IPR008274 InterPro:IPR016166 InterPro:IPR016169 InterPro:IPR016208 Pfam:PF00111 Pfam:PF00941 Pfam:PF01799 Pfam:PF02738 PIRSF:PIRSF000127 PROSITE:PS00197 PROSITE:PS00559 PROSITE:PS51085 PROSITE:PS51387 InterPro:IPR000674 Pfam:PF01315 GO:GO:0005829 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005506 GO:GO:0009055 GO:GO:0050660 SUPFAM:SSF56176 GO:GO:0004031 eggNOG:COG4630 GO:GO:0051537 InterPro:IPR012675 InterPro:IPR005107 Gene3D:G3DSA:1.10.150.120 Gene3D:G3DSA:3.30.365.10 Gene3D:G3DSA:3.90.1170.50 Gene3D:G3DSA:3.30.390.50 Gene3D:G3DSA:3.30.465.10 Gene3D:G3DSA:3.10.20.30 Pfam:PF03450 SMART:SM01008 SMART:SM01092 SUPFAM:SSF47741 SUPFAM:SSF56003 SUPFAM:SSF54665 SUPFAM:SSF55447 SUPFAM:SSF54292 HOGENOM:HBG746468 ProtClustDB:PLN00192 EMBL:AB005805 EMBL:AL391734 EMBL:AF039896 IPI:IPI00529435 PIR:T51623 PIR:T52050 RefSeq:NP_189946.1 UniGene:At.462 ProteinModelPortal:Q7G192 SMR:Q7G192 STRING:Q7G192 PRIDE:Q7G192 EnsemblPlants:AT3G43600.1 GeneID:823457 KEGG:ath:AT3G43600 GeneFarm:4893 TAIR:At3g43600 InParanoid:Q7G192 OMA:ILYDCGK PhylomeDB:Q7G192 BioCyc:ARA:AT3G43600-MONOMER BioCyc:MetaCyc:AT3G43600-MONOMER Genevestigator:Q7G192 GermOnline:AT3G43600 GO:GO:0016614 Uniprot:Q7G192
Root	Isotig00380	19	79	-2.185	2.58E-11	TAIR|locus:2079834 - symbol:AAO2 "aldehyde oxidase 2" species:3702 "Arabidopsis thaliana" [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0004031 "aldehyde oxidase activity" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001041 InterPro:IPR002346 InterPro:IPR002888 InterPro:IPR006058 InterPro:IPR008274 InterPro:IPR016166 InterPro:IPR016169 InterPro:IPR016208 Pfam:PF00111 Pfam:PF00941 Pfam:PF01799 Pfam:PF02738 PIRSF:PIRSF000127 PROSITE:PS00197 PROSITE:PS00559 PROSITE:PS51085 PROSITE:PS51387 InterPro:IPR000674 Pfam:PF01315 GO:GO:0005829 EMBL:CP002686

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GenomeReviews:BA000014_GR GO:GO:0005506 GO:GO:0009055 GO:GO:0050660 SUPFAM:SSF56176 GO:GO:0004031 eggNOG:COG4630 GO:GO:0051537 InterPro:IPR012675 InterPro:IPR005107 Gene3D:G3DSA:1.10.150.120 Gene3D:G3DSA:3.30.365.10 Gene3D:G3DSA:3.90.1170.50 Gene3D:G3DSA:3.30.390.50 Gene3D:G3DSA:3.30.465.10 Gene3D:G3DSA:3.10.20.30 Pfam:PF03450 SMART:SM01008 SMART:SM01092 SUPFAM:SSF47741 SUPFAM:SSF56003 SUPFAM:SSF54665 SUPFAM:SSF55447 SUPFAM:SSF54292 HOGENOM:HBG746468 ProtClustDB:PLN00192 EMBL:AB005805 EMBL:AL391734 EMBL:AF039896 IPI:IPI00529435 PIR:T51623 PIR:T52050 RefSeq:NP_189946.1 UniGene:At.462 ProteinModelPortal:Q7G192 SMR:Q7G192 STRING:Q7G192 PRIDE:Q7G192 EnsemblPlants:AT3G43600.1 GeneID:823457 KEGG:ath:AT3G43600 GeneFarm:4893 TAIR:At3g43600 InParanoid:Q7G192 OMA:ILYDCGK PhylomeDB:Q7G192 BioCyc:ARA:AT3G43600-MONOMER BioCyc:MetaCyc:AT3G43600-MONOMER Genevestigator:Q7G192 GermOnline:AT3G43600 GO:GO:0016614 Uniprot:Q7G192
Root	Isotig00381	19	79	-2.185	2.58E-11	TAIR|locus:2079834 - symbol:AAO2 "aldehyde oxidase 2" species:3702 "Arabidopsis thaliana" [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0004031 "aldehyde oxidase activity" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001041 InterPro:IPR002346 InterPro:IPR002888 InterPro:IPR006058 InterPro:IPR008274 InterPro:IPR016166 InterPro:IPR016169 InterPro:IPR016208 Pfam:PF00111 Pfam:PF00941 Pfam:PF01799 Pfam:PF02738 PIRSF:PIRSF000127 PROSITE:PS00197 PROSITE:PS00559 PROSITE:PS51085 PROSITE:PS51387 InterPro:IPR000674 Pfam:PF01315 GO:GO:0005829 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005506 GO:GO:0009055 GO:GO:0050660 SUPFAM:SSF56176 GO:GO:0004031 eggNOG:COG4630 GO:GO:0051537 InterPro:IPR012675 InterPro:IPR005107 Gene3D:G3DSA:1.10.150.120 Gene3D:G3DSA:3.30.365.10 Gene3D:G3DSA:3.90.1170.50 Gene3D:G3DSA:3.30.390.50 Gene3D:G3DSA:3.30.465.10 Gene3D:G3DSA:3.10.20.30 Pfam:PF03450 SMART:SM01008 SMART:SM01092 SUPFAM:SSF47741 SUPFAM:SSF56003 SUPFAM:SSF54665 SUPFAM:SSF55447 SUPFAM:SSF54292 HOGENOM:HBG746468 ProtClustDB:PLN00192 EMBL:AB005805 EMBL:AL391734 EMBL:AF039896 IPI:IPI00529435 PIR:T51623 PIR:T52050 RefSeq:NP_189946.1 UniGene:At.462 ProteinModelPortal:Q7G192 SMR:Q7G192 STRING:Q7G192 PRIDE:Q7G192 EnsemblPlants:AT3G43600.1 GeneID:823457 KEGG:ath:AT3G43600 GeneFarm:4893 TAIR:At3g43600 InParanoid:Q7G192 OMA:ILYDCGK PhylomeDB:Q7G192 BioCyc:ARA:AT3G43600-MONOMER BioCyc:MetaCyc:AT3G43600-MONOMER Genevestigator:Q7G192 GermOnline:AT3G43600 GO:GO:0016614 Uniprot:Q7G192
Root	Isotig00382	19	77	-2.148	7.31E-11	TAIR|locus:2079834 - symbol:AAO2 "aldehyde oxidase 2" species:3702 "Arabidopsis thaliana" [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0004031 "aldehyde oxidase activity" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001041 InterPro:IPR002346 InterPro:IPR002888 InterPro:IPR006058 InterPro:IPR008274 InterPro:IPR016166 InterPro:IPR016169 InterPro:IPR016208 Pfam:PF00111 Pfam:PF00941 Pfam:PF01799 Pfam:PF02738 PIRSF:PIRSF000127 PROSITE:PS00197 PROSITE:PS00559 PROSITE:PS51085 PROSITE:PS51387 InterPro:IPR000674 Pfam:PF01315 GO:GO:0005829 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005506 GO:GO:0009055 GO:GO:0050660 SUPFAM:SSF56176 GO:GO:0004031 eggNOG:COG4630 GO:GO:0051537 InterPro:IPR012675 InterPro:IPR005107 Gene3D:G3DSA:1.10.150.120 Gene3D:G3DSA:3.30.365.10 Gene3D:G3DSA:3.90.1170.50 Gene3D:G3DSA:3.30.390.50 Gene3D:G3DSA:3.30.465.10 Gene3D:G3DSA:3.10.20.30 Pfam:PF03450 SMART:SM01008 SMART:SM01092 SUPFAM:SSF47741 SUPFAM:SSF56003 SUPFAM:SSF54665 SUPFAM:SSF55447 SUPFAM:SSF54292 HOGENOM:HBG746468 ProtClustDB:PLN00192 EMBL:AB005805 EMBL:AL391734 EMBL:AF039896 IPI:IPI00529435 PIR:T51623 PIR:T52050 RefSeq:NP_189946.1 UniGene:At.462 ProteinModelPortal:Q7G192 SMR:Q7G192 STRING:Q7G192 PRIDE:Q7G192 EnsemblPlants:AT3G43600.1 GeneID:823457 KEGG:ath:AT3G43600 GeneFarm:4893 TAIR:At3g43600 InParanoid:Q7G192 OMA:ILYDCGK PhylomeDB:Q7G192 BioCyc:ARA:AT3G43600-MONOMER BioCyc:MetaCyc:AT3G43600-MONOMER Genevestigator:Q7G192 GermOnline:AT3G43600 GO:GO:0016614 Uniprot:Q7G192
Root	Isotig00383	19	77	-2.148	7.31E-11	TAIR|locus:2079834 - symbol:AAO2 "aldehyde oxidase 2" species:3702 "Arabidopsis thaliana" [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0004031 "aldehyde oxidase activity" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001041 InterPro:IPR002346 InterPro:IPR002888 InterPro:IPR006058 InterPro:IPR008274 InterPro:IPR016166 InterPro:IPR016169 InterPro:IPR016208 Pfam:PF00111 Pfam:PF00941 Pfam:PF01799 Pfam:PF02738 PIRSF:PIRSF000127 PROSITE:PS00197 PROSITE:PS00559 PROSITE:PS51085 PROSITE:PS51387 InterPro:IPR000674 Pfam:PF01315 GO:GO:0005829 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005506 GO:GO:0009055 GO:GO:0050660 SUPFAM:SSF56176

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0004031 eggNOG:COG4630 GO:GO:0051537 InterPro:IPR012675 InterPro:IPR005107 Gene3D:G3DSA:1.10.150.120 Gene3D:G3DSA:3.30.365.10 Gene3D:G3DSA:3.90.1170.50 Gene3D:G3DSA:3.30.390.50 Gene3D:G3DSA:3.30.465.10 Gene3D:G3DSA:3.10.20.30 Pfam:PF03450 SMART:SM01008 SMART:SM01092 SUPFAM:SSF47741 SUPFAM:SSF56003 SUPFAM:SSF54665 SUPFAM:SSF55447 SUPFAM:SSF54292 HOGENOM:HBG746468 ProtClustDB:PLN00192 EMBL:AB005805 EMBL:AL391734 EMBL:AF039896 IPI:IPI00529435 PIR:T51623 PIR:T52050 RefSeq:NP_189946.1 UniGene:At.462 ProteinModelPortal:Q7G192 SMR:Q7G192 STRING:Q7G192 PRIDE:Q7G192 EnsemblPlants:AT3G43600.1 GeneID:823457 KEGG:ath:AT3G43600 GeneFarm:4893 TAIR:At3g43600 InParanoid:Q7G192 OMA:ILYDCGK PhylomeDB:Q7G192 BioCyc:ARA:AT3G43600-MONOMER BioCyc:MetaCyc:AT3G43600-MONOMER Genevestigator:Q7G192 GermOnline:AT3G43600 GO:GO:0016614 Uniprot:Q7G192
Root	Isotig00384	19	64	-1.881	5.11E-08	TAIR|locus:2045149 - symbol:AAO3 "AT2G27150" species:3702 "Arabidopsis thaliana" [GO:0004031 "aldehyde oxidase activity" evidence=IDA] [GO:0050302 "indole-3-acetaldehyde oxidase activity" evidence=IDA] [GO:0009688 "abscisic acid biosynthetic process" evidence=IMP] [GO:0010293 "abscisic aldehyde oxidase activity" evidence=IDA] [GO:0031625 "ubiquitin protein ligase binding" evidence=IPI] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001041 InterPro:IPR002346 InterPro:IPR002888 InterPro:IPR006058 InterPro:IPR008274 InterPro:IPR016166 InterPro:IPR016169 InterPro:IPR016208 Pfam:PF00111 Pfam:PF00941 Pfam:PF01799 Pfam:PF02738 PIRSF:PIRSF000127 PROSITE:PS00197 PROSITE:PS00559 PROSITE:PS51085 PROSITE:PS51387 InterPro:IPR000674 Pfam:PF01315 GO:GO:0005829 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0005506 GO:GO:0009055 GO:GO:0050660 GO:GO:0009688 GO:GO:0031625 SUPFAM:SSF56176 eggNOG:COG4630 GO:GO:0051537 InterPro:IPR012675 InterPro:IPR005107 Gene3D:G3DSA:1.10.150.120 Gene3D:G3DSA:3.30.365.10 Gene3D:G3DSA:3.90.1170.50 Gene3D:G3DSA:3.30.390.50 Gene3D:G3DSA:3.30.465.10 Gene3D:G3DSA:3.10.20.30 Pfam:PF03450 SMART:SM01008 SMART:SM01092 SUPFAM:SSF47741 SUPFAM:SSF56003 SUPFAM:SSF54665 SUPFAM:SSF55447 SUPFAM:SSF54292 HOGENOM:HBG746468 ProtClustDB:PLN00192 GO:GO:0050302 GO:GO:0009851 GO:GO:0016614 EMBL:AB016622 EMBL:AC007154 EMBL:AB010080 IPI:IPI00517261 PIR:D84669 PIR:T52176 RefSeq:NP_001077966.1 RefSeq:NP_180283.1 UniGene:At.20239 ProteinModelPortal:Q7G9P4 SMR:Q7G9P4 STRING:Q7G9P4 PRIDE:Q7G9P4 EnsemblPlants:AT2G27150.1 EnsemblPlants:AT2G27150.2 GeneID:817257 KEGG:ath:AT2G27150 GeneFarm:4894 TAIR:At2g27150 InParanoid:Q7G9P4 KO:K09842 OMA:ADELTRC PhylomeDB:Q7G9P4 BioCyc:ARA:AT2G27150-MONOMER BioCyc:MetaCyc:AT2G27150-MONOMER BRENDA:1.2.3.14 ArrayExpress:Q7G9P4 Genevestigator:Q7G9P4 GermOnline:AT2G27150 GO:GO:0010293 Uniprot:Q7G9P4
Root	Isotig00385	19	64	-1.881	5.11E-08	TAIR|locus:2045149 - symbol:AAO3 "AT2G27150" species:3702 "Arabidopsis thaliana" [GO:0004031 "aldehyde oxidase activity" evidence=IDA] [GO:0050302 "indole-3-acetaldehyde oxidase activity" evidence=IDA] [GO:0009688 "abscisic acid biosynthetic process" evidence=IMP] [GO:0010293 "abscisic aldehyde oxidase activity" evidence=IDA] [GO:0031625 "ubiquitin protein ligase binding" evidence=IPI] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001041 InterPro:IPR002346 InterPro:IPR002888 InterPro:IPR006058 InterPro:IPR008274 InterPro:IPR016166 InterPro:IPR016169 InterPro:IPR016208 Pfam:PF00111 Pfam:PF00941 Pfam:PF01799 Pfam:PF02738 PIRSF:PIRSF000127 PROSITE:PS00197 PROSITE:PS00559 PROSITE:PS51085 PROSITE:PS51387 InterPro:IPR000674 Pfam:PF01315 GO:GO:0005829 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0005506 GO:GO:0009055 GO:GO:0050660 GO:GO:0009688 GO:GO:0031625 SUPFAM:SSF56176 eggNOG:COG4630 GO:GO:0051537 InterPro:IPR012675 InterPro:IPR005107 Gene3D:G3DSA:1.10.150.120 Gene3D:G3DSA:3.30.365.10 Gene3D:G3DSA:3.90.1170.50 Gene3D:G3DSA:3.30.390.50 Gene3D:G3DSA:3.30.465.10 Gene3D:G3DSA:3.10.20.30 Pfam:PF03450 SMART:SM01008 SMART:SM01092 SUPFAM:SSF47741 SUPFAM:SSF56003 SUPFAM:SSF54665 SUPFAM:SSF55447 SUPFAM:SSF54292 HOGENOM:HBG746468 ProtClustDB:PLN00192 GO:GO:0050302 GO:GO:0009851 GO:GO:0016614 EMBL:AB016622 EMBL:AC007154 EMBL:AB010080 IPI:IPI00517261 PIR:D84669 PIR:T52176 RefSeq:NP_001077966.1 RefSeq:NP_180283.1 UniGene:At.20239 ProteinModelPortal:Q7G9P4 SMR:Q7G9P4 STRING:Q7G9P4 PRIDE:Q7G9P4 EnsemblPlants:AT2G27150.1 EnsemblPlants:AT2G27150.2 GeneID:817257 KEGG:ath:AT2G27150 GeneFarm:4894 TAIR:At2g27150 InParanoid:Q7G9P4 KO:K09842 OMA:ADELTRC PhylomeDB:Q7G9P4 BioCyc:ARA:AT2G27150-MONOMER BioCyc:MetaCyc:AT2G27150-MONOMER BRENDA:1.2.3.14 ArrayExpress:Q7G9P4 Genevestigator:Q7G9P4 GermOnline:AT2G27150 GO:GO:0010293 Uniprot:Q7G9P4

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig00386	14	70	-2.451	1.76E-11	TAIR|locus:2079834 - symbol:AAO2 "aldehyde oxidase 2" species:3702 "Arabidopsis thaliana" [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0004031 "aldehyde oxidase activity" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001041 InterPro:IPR002346 InterPro:IPR002888 InterPro:IPR006058 InterPro:IPR008274 InterPro:IPR016166 InterPro:IPR016169 InterPro:IPR016208 Pfam:PF00111 Pfam:PF00941 Pfam:PF01799 Pfam:PF02738 PIRSF:PIRSF000127 PROSITE:PS00197 PROSITE:PS00559 PROSITE:PS51085 PROSITE:PS51387 InterPro:IPR000674 Pfam:PF01315 GO:GO:0005829 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005506 GO:GO:0009055 GO:GO:0050660 SUPFAM:SSF56176 GO:GO:0004031 eggNOG:COG4630 GO:GO:0051537 InterPro:IPR012675 InterPro:IPR005107 Gene3D:G3DSA:1.10.150.120 Gene3D:G3DSA:3.30.365.10 Gene3D:G3DSA:3.90.1170.50 Gene3D:G3DSA:3.30.390.50 Gene3D:G3DSA:3.30.465.10 Gene3D:G3DSA:3.10.20.30 Pfam:PF03450 SMART:SM01008 SMART:SM01092 SUPFAM:SSF47741 SUPFAM:SSF56003 SUPFAM:SSF54665 SUPFAM:SSF55447 SUPFAM:SSF54292 HOGENOM:HBG746468 ProtClustDB:PLN00192 EMBL:AB005805 EMBL:AL391734 EMBL:AF039896 IPI:IPI00529435 PIR:T51623 PIR:T52050 RefSeq:NP_189946.1 UniGene:At.462 ProteinModelPortal:Q7G192 SMR:Q7G192 STRING:Q7G192 PRIDE:Q7G192 EnsemblPlants:AT3G43600.1 GeneID:823457 KEGG:ath:AT3G43600 GeneFarm:4893 TAIR:At3g43600 InParanoid:Q7G192 OMA:ILYDCGK PhylomeDB:Q7G192 BioCyc:ARA:AT3G43600-MONOMER BioCyc:MetaCyc:AT3G43600-MONOMER Genevestigator:Q7G192 GermOnline:AT3G43600 GO:GO:0016614 Uniprot:Q7G192
Root	Isotig00387	19	64	-1.881	5.11E-08	TAIR|locus:2045149 - symbol:AAO3 "AT2G27150" species:3702 "Arabidopsis thaliana" [GO:0004031 "aldehyde oxidase activity" evidence=IDA] [GO:0050302 "indole-3-acetaldehyde oxidase activity" evidence=IDA] [GO:0009688 "abscisic acid biosynthetic process" evidence=IMP] [GO:0010293 "abscisic aldehyde oxidase activity" evidence=IDA] [GO:0031625 "ubiquitin protein ligase binding" evidence=IPI] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001041 InterPro:IPR002346 InterPro:IPR002888 InterPro:IPR006058 InterPro:IPR008274 InterPro:IPR016166 InterPro:IPR016169 InterPro:IPR016208 Pfam:PF00111 Pfam:PF00941 Pfam:PF01799 Pfam:PF02738 PIRSF:PIRSF000127 PROSITE:PS00197 PROSITE:PS00559 PROSITE:PS51085 PROSITE:PS51387 InterPro:IPR000674 Pfam:PF01315 GO:GO:0005829 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0005506 GO:GO:0009055 GO:GO:0050660 GO:GO:0009688 GO:GO:0031625 SUPFAM:SSF56176 eggNOG:COG4630 GO:GO:0051537 InterPro:IPR012675 InterPro:IPR005107 Gene3D:G3DSA:1.10.150.120 Gene3D:G3DSA:3.30.365.10 Gene3D:G3DSA:3.90.1170.50 Gene3D:G3DSA:3.30.390.50 Gene3D:G3DSA:3.30.465.10 Gene3D:G3DSA:3.10.20.30 Pfam:PF03450 SMART:SM01008 SMART:SM01092 SUPFAM:SSF47741 SUPFAM:SSF56003 SUPFAM:SSF54665 SUPFAM:SSF55447 SUPFAM:SSF54292 HOGENOM:HBG746468 ProtClustDB:PLN00192 GO:GO:0050302 GO:GO:0009851 GO:GO:0016614 EMBL:AB016622 EMBL:AC007154 EMBL:AB010080 IPI:IPI00517261 PIR:D84669 PIR:T52176 RefSeq:NP_001077966.1 RefSeq:NP_180283.1 UniGene:At.20239 ProteinModelPortal:Q7G9P4 SMR:Q7G9P4 STRING:Q7G9P4 PRIDE:Q7G9P4 EnsemblPlants:AT2G27150.1 EnsemblPlants:AT2G27150.2 GeneID:817257 KEGG:ath:AT2G27150 GeneFarm:4894 TAIR:At2g27150 InParanoid:Q7G9P4 KO:K09842 OMA:ADELTRC PhylomeDB:Q7G9P4 BioCyc:ARA:AT2G27150-MONOMER BioCyc:MetaCyc:AT2G27150-MONOMER BRENDA:1.2.3.14 ArrayExpress:Q7G9P4 Genevestigator:Q7G9P4 GermOnline:AT2G27150 GO:GO:0010293 Uniprot:Q7G9P4
Root	Isotig00388	19	64	-1.881	5.11E-08	TAIR|locus:2045149 - symbol:AAO3 "AT2G27150" species:3702 "Arabidopsis thaliana" [GO:0004031 "aldehyde oxidase activity" evidence=IDA] [GO:0050302 "indole-3-acetaldehyde oxidase activity" evidence=IDA] [GO:0009688 "abscisic acid biosynthetic process" evidence=IMP] [GO:0010293 "abscisic aldehyde oxidase activity" evidence=IDA] [GO:0031625 "ubiquitin protein ligase binding" evidence=IPI] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001041 InterPro:IPR002346 InterPro:IPR002888 InterPro:IPR006058 InterPro:IPR008274 InterPro:IPR016166 InterPro:IPR016169 InterPro:IPR016208 Pfam:PF00111 Pfam:PF00941 Pfam:PF01799 Pfam:PF02738 PIRSF:PIRSF000127 PROSITE:PS00197 PROSITE:PS00559 PROSITE:PS51085 PROSITE:PS51387 InterPro:IPR000674 Pfam:PF01315 GO:GO:0005829 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0005506 GO:GO:0009055 GO:GO:0050660 GO:GO:0009688 GO:GO:0031625 SUPFAM:SSF56176 eggNOG:COG4630 GO:GO:0051537 InterPro:IPR012675 InterPro:IPR005107 Gene3D:G3DSA:1.10.150.120 Gene3D:G3DSA:3.30.365.10 Gene3D:G3DSA:3.90.1170.50 Gene3D:G3DSA:3.30.390.50 Gene3D:G3DSA:3.30.465.10 Gene3D:G3DSA:3.10.20.30 Pfam:PF03450 SMART:SM01008 SMART:SM01092 SUPFAM:SSF47741 SUPFAM:SSF56003 SUPFAM:SSF54665 SUPFAM:SSF55447 SUPFAM:SSF54292 HOGENOM:HBG746468 ProtClustDB:PLN00192 GO:GO:0050302 GO:GO:0009851 GO:GO:0016614 EMBL:AB016622 EMBL:AC007154 EMBL:AB010080 IPI:IPI00517261

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						PIR:D84669 PIR:T52176 RefSeq:NP_001077966.1 RefSeq:NP_180283.1 UniGene:At.20239 ProteinModelPortal:Q7G9P4 SMR:Q7G9P4 STRING:Q7G9P4 PRIDE:Q7G9P4 EnsemblPlants:AT2G27150.1 EnsemblPlants:AT2G27150.2 GeneID:817257 KEGG:ath:AT2G27150 GeneFarm:4894 TAIR:At2g27150 InParanoid:Q7G9P4 KO:K09842 OMA:ADELTRC PhylomeDB:Q7G9P4 BioCyc:ARA:AT2G27150-MONOMER BioCyc:MetaCyc:AT2G27150-MONOMER BRENDA:1.2.3.14 ArrayExpress:Q7G9P4 Genevestigator:Q7G9P4 GermOnline:AT2G27150 GO:GO:0010293 Uniprot:Q7G9P4
Root	Isotig00389	14	70	-2.451	1.76E-11	TAIR|locus:2079834 - symbol:AAO2 "aldehyde oxidase 2" species:3702 "Arabidopsis thaliana" [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0004031 "aldehyde oxidase activity" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001041 InterPro:IPR002346 InterPro:IPR002888 InterPro:IPR006058 InterPro:IPR008274 InterPro:IPR016166 InterPro:IPR016169 InterPro:IPR016208 Pfam:PF00111 Pfam:PF00941 Pfam:PF01799 Pfam:PF02738 PIRSF:PIRSF000127 PROSITE:PS00197 PROSITE:PS00559 PROSITE:PS51085 PROSITE:PS51387 InterPro:IPR000674 Pfam:PF01315 GO:GO:0005829 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005506 GO:GO:0009055 GO:GO:0050660 SUPFAM:SSF56176 GO:GO:0004031 eggNOG:COG4630 GO:GO:0051537 InterPro:IPR012675 InterPro:IPR005107 Gene3D:G3DSA:1.10.150.120 Gene3D:G3DSA:3.30.365.10 Gene3D:G3DSA:3.90.1170.50 Gene3D:G3DSA:3.30.390.50 Gene3D:G3DSA:3.30.465.10 Gene3D:G3DSA:3.10.20.30 Pfam:PF03450 SMART:SM01008 SMART:SM01092 SUPFAM:SSF47741 SUPFAM:SSF56003 SUPFAM:SSF54665 SUPFAM:SSF55447 SUPFAM:SSF54292 HOGENOM:HBG746468 ProtClustDB:PLN00192 EMBL:AB005805 EMBL:AL391734 EMBL:AF039896 IPI:IPI00529435 PIR:T51623 PIR:T52050 RefSeq:NP_189946.1 UniGene:At.462 ProteinModelPortal:Q7G192 SMR:Q7G192 STRING:Q7G192 PRIDE:Q7G192 EnsemblPlants:AT3G43600.1 GeneID:823457 KEGG:ath:AT3G43600 GeneFarm:4893 TAIR:At3g43600 InParanoid:Q7G192 OMA:ILYDCGK PhylomeDB:Q7G192 BioCyc:ARA:AT3G43600-MONOMER BioCyc:MetaCyc:AT3G43600-MONOMER Genevestigator:Q7G192 GermOnline:AT3G43600 GO:GO:0016614 Uniprot:Q7G192
Root	Isotig00390	14	70	-2.451	1.76E-11	TAIR|locus:2147127 - symbol:AO1 "AT5G20960" species:3702 "Arabidopsis thaliana" [GO:0004031 "aldehyde oxidase activity" evidence=IDA] [GO:0050302 "indole-3-acetaldehyde oxidase activity" evidence=IDA] [GO:0009851 "auxin biosynthetic process" evidence=IMP] InterPro:IPR001041 InterPro:IPR002346 InterPro:IPR002888 InterPro:IPR006058 InterPro:IPR008274 InterPro:IPR016166 InterPro:IPR016167 InterPro:IPR016169 InterPro:IPR016208 Pfam:PF00111 Pfam:PF00941 Pfam:PF01799 Pfam:PF02738 PIRSF:PIRSF000127 PROSITE:PS00197 PROSITE:PS00559 PROSITE:PS51085 PROSITE:PS51387 InterPro:IPR000674 Pfam:PF01315 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005506 GO:GO:0009055 GO:GO:0050660 GO:GO:0009688 GO:GO:0008762 Gene3D:G3DSA:3.30.43.10 SUPFAM:SSF56176 eggNOG:COG4630 GO:GO:0051537 InterPro:IPR012675 InterPro:IPR005107 Gene3D:G3DSA:1.10.150.120 Gene3D:G3DSA:3.30.365.10 Gene3D:G3DSA:3.90.1170.50 Gene3D:G3DSA:3.30.390.50 Gene3D:G3DSA:3.30.465.10 Gene3D:G3DSA:3.10.20.30 Pfam:PF03450 SMART:SM01008 SMART:SM01092 SUPFAM:SSF47741 SUPFAM:SSF56003 SUPFAM:SSF54665 SUPFAM:SSF55447 SUPFAM:SSF54292 EMBL:AF296834 EMBL:AF039895 EMBL:AB005804 IPI:IPI00532267 PIR:T51622 PIR:T52049 RefSeq:NP_568407.2 RefSeq:NP_851049.1 UniGene:At.19954 ProteinModelPortal:Q7G193 SMR:Q7G193 IntAct:Q7G193 STRING:Q7G193 PRIDE:Q7G193 EnsemblPlants:AT5G20960.1 EnsemblPlants:AT5G20960.2 GeneID:832221 KEGG:ath:AT5G20960 GeneFarm:4892 TAIR:At5g20960 HOGENOM:HBG746468 InParanoid:Q7G193 KO:K11817 OMA:ADSQKHA PhylomeDB:Q7G193 ProtClustDB:PLN00192 Genevestigator:Q7G193 GermOnline:AT5G20960 GO:GO:0050302 GO:GO:0009851 Uniprot:Q7G193
Root	Isotig00391	14	70	-2.451	1.76E-11	TAIR|locus:2147127 - symbol:AO1 "AT5G20960" species:3702 "Arabidopsis thaliana" [GO:0004031 "aldehyde oxidase activity" evidence=IDA] [GO:0050302 "indole-3-acetaldehyde oxidase activity" evidence=IDA] [GO:0009851 "auxin biosynthetic process" evidence=IMP] InterPro:IPR001041 InterPro:IPR002346 InterPro:IPR002888 InterPro:IPR006058 InterPro:IPR008274 InterPro:IPR016166 InterPro:IPR016167 InterPro:IPR016169 InterPro:IPR016208 Pfam:PF00111 Pfam:PF00941 Pfam:PF01799 Pfam:PF02738 PIRSF:PIRSF000127 PROSITE:PS00197 PROSITE:PS00559 PROSITE:PS51085 PROSITE:PS51387 InterPro:IPR000674 Pfam:PF01315 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005506 GO:GO:0009055 GO:GO:0050660 GO:GO:0009688 GO:GO:0008762 Gene3D:G3DSA:3.30.43.10 SUPFAM:SSF56176 eggNOG:COG4630 GO:GO:0051537 InterPro:IPR012675 InterPro:IPR005107 Gene3D:G3DSA:1.10.150.120 Gene3D:G3DSA:3.30.365.10 Gene3D:G3DSA:3.90.1170.50 Gene3D:G3DSA:3.30.390.50 Gene3D:G3DSA:3.30.465.10 Gene3D:G3DSA:3.10.20.30 Pfam:PF03450 SMART:SM01008 SMART:SM01092

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						SUPFAM:SSF47741 SUPFAM:SSF56003 SUPFAM:SSF54665 SUPFAM:SSF55447 SUPFAM:SSF54292 EMBL:AF296834 EMBL:AF039895 EMBL:AB005804 IPI:IPI00532267 PIR:T51622 PIR:T52049 RefSeq:NP_568407.2 RefSeq:NP_851049.1 UniGene:At.19954 ProteinModelPortal:Q7G193 SMR:Q7G193 IntAct:Q7G193 STRING:Q7G193 PRIDE:Q7G193 EnsemblPlants:AT5G20960.1 EnsemblPlants:AT5G20960.2 GeneID:832221 KEGG:ath:AT5G20960 GeneFarm:4892 TAIR:At5g20960 HOGENOM:HBG746468 InParanoid:Q7G193 KO:K11817 OMA:ADSQKHA PhylomeDB:Q7G193 ProtClustDB:PLN00192 Genevestigator:Q7G193 GermOnline:AT5G20960 GO:GO:0050302 GO:GO:0009851 Uniprot:Q7G193
Root	Isotig00392	19	72	-2.051	9.54E-10	TAIR|locus:2147127 - symbol:AO1 "AT5G20960" species:3702 "Arabidopsis thaliana" [GO:0004031 "aldehyde oxidase activity" evidence=IDA] [GO:0050302 "indole-3-acetaldehyde oxidase activity" evidence=IDA] [GO:0009851 "auxin biosynthetic process" evidence=IMP] InterPro:IPR001041 InterPro:IPR002346 InterPro:IPR002888 InterPro:IPR006058 InterPro:IPR008274 InterPro:IPR016166 InterPro:IPR016167 InterPro:IPR016169 InterPro:IPR016208 Pfam:PF00111 Pfam:PF00941 Pfam:PF01799 Pfam:PF02738 PIRSF:PIRSF000127 PROSITE:PS00197 PROSITE:PS00559 PROSITE:PS51085 PROSITE:PS51387 InterPro:IPR000674 Pfam:PF01315 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005506 GO:GO:0009055 GO:GO:0050660 GO:GO:0009688 GO:GO:0008762 Gene3D:G3DSA:3.30.43.10 SUPFAM:SSF56176 eggNOG:COG4630 GO:GO:0051537 InterPro:IPR012675 InterPro:IPR005107 Gene3D:G3DSA:1.10.150.120 Gene3D:G3DSA:3.30.365.10 Gene3D:G3DSA:3.90.1170.50 Gene3D:G3DSA:3.30.390.50 Gene3D:G3DSA:3.30.465.10 Gene3D:G3DSA:3.10.20.30 Pfam:PF03450 SMART:SM01008 SMART:SM01092 SUPFAM:SSF47741 SUPFAM:SSF56003 SUPFAM:SSF54665 SUPFAM:SSF55447 SUPFAM:SSF54292 EMBL:AF296834 EMBL:AF039895 EMBL:AB005804 IPI:IPI00532267 PIR:T51622 PIR:T52049 RefSeq:NP_568407.2 RefSeq:NP_851049.1 UniGene:At.19954 ProteinModelPortal:Q7G193 SMR:Q7G193 IntAct:Q7G193 STRING:Q7G193 PRIDE:Q7G193 EnsemblPlants:AT5G20960.1 EnsemblPlants:AT5G20960.2 GeneID:832221 KEGG:ath:AT5G20960 GeneFarm:4892 TAIR:At5g20960 HOGENOM:HBG746468 InParanoid:Q7G193 KO:K11817 OMA:ADSQKHA PhylomeDB:Q7G193 ProtClustDB:PLN00192 Genevestigator:Q7G193 GermOnline:AT5G20960 GO:GO:0050302 GO:GO:0009851 Uniprot:Q7G193
Root	Isotig00393	19	72	-2.051	9.54E-10	TAIR|locus:2147127 - symbol:AO1 "AT5G20960" species:3702 "Arabidopsis thaliana" [GO:0004031 "aldehyde oxidase activity" evidence=IDA] [GO:0050302 "indole-3-acetaldehyde oxidase activity" evidence=IDA] [GO:0009851 "auxin biosynthetic process" evidence=IMP] InterPro:IPR001041 InterPro:IPR002346 InterPro:IPR002888 InterPro:IPR006058 InterPro:IPR008274 InterPro:IPR016166 InterPro:IPR016167 InterPro:IPR016169 InterPro:IPR016208 Pfam:PF00111 Pfam:PF00941 Pfam:PF01799 Pfam:PF02738 PIRSF:PIRSF000127 PROSITE:PS00197 PROSITE:PS00559 PROSITE:PS51085 PROSITE:PS51387 InterPro:IPR000674 Pfam:PF01315 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005506 GO:GO:0009055 GO:GO:0050660 GO:GO:0009688 GO:GO:0008762 Gene3D:G3DSA:3.30.43.10 SUPFAM:SSF56176 eggNOG:COG4630 GO:GO:0051537 InterPro:IPR012675 InterPro:IPR005107 Gene3D:G3DSA:1.10.150.120 Gene3D:G3DSA:3.30.365.10 Gene3D:G3DSA:3.90.1170.50 Gene3D:G3DSA:3.30.390.50 Gene3D:G3DSA:3.30.465.10 Gene3D:G3DSA:3.10.20.30 Pfam:PF03450 SMART:SM01008 SMART:SM01092 SUPFAM:SSF47741 SUPFAM:SSF56003 SUPFAM:SSF54665 SUPFAM:SSF55447 SUPFAM:SSF54292 EMBL:AF296834 EMBL:AF039895 EMBL:AB005804 IPI:IPI00532267 PIR:T51622 PIR:T52049 RefSeq:NP_568407.2 RefSeq:NP_851049.1 UniGene:At.19954 ProteinModelPortal:Q7G193 SMR:Q7G193 IntAct:Q7G193 STRING:Q7G193 PRIDE:Q7G193 EnsemblPlants:AT5G20960.1 EnsemblPlants:AT5G20960.2 GeneID:832221 KEGG:ath:AT5G20960 GeneFarm:4892 TAIR:At5g20960 HOGENOM:HBG746468 InParanoid:Q7G193 KO:K11817 OMA:ADSQKHA PhylomeDB:Q7G193 ProtClustDB:PLN00192 Genevestigator:Q7G193 GermOnline:AT5G20960 GO:GO:0050302 GO:GO:0009851 Uniprot:Q7G193
Root	Isotig00394	14	63	-2.299	8.06E-10	TAIR|locus:2079834 - symbol:AAO2 "aldehyde oxidase 2" species:3702 "Arabidopsis thaliana" [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0004031 "aldehyde oxidase activity" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001041 InterPro:IPR002346 InterPro:IPR002888 InterPro:IPR006058 InterPro:IPR008274 InterPro:IPR016166 InterPro:IPR016169 InterPro:IPR016208 Pfam:PF00111 Pfam:PF00941 Pfam:PF01799 Pfam:PF02738 PIRSF:PIRSF000127 PROSITE:PS00197 PROSITE:PS00559 PROSITE:PS51085 PROSITE:PS51387 InterPro:IPR000674 Pfam:PF01315 GO:GO:0005829 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005506 GO:GO:0009055 GO:GO:0050660 SUPFAM:SSF56176 GO:GO:0004031 eggNOG:COG4630 GO:GO:0051537 InterPro:IPR012675 InterPro:IPR005107 Gene3D:G3DSA:1.10.150.120 Gene3D:G3DSA:3.30.365.10 Gene3D:G3DSA:3.90.1170.50

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						Gene3D:G3DSA:3.30.390.50 Gene3D:G3DSA:3.30.465.10 Gene3D:G3DSA:3.10.20.30 Pfam:PF03450 SMART:SM01008 SMART:SM01092 SUPFAM:SSF47741 SUPFAM:SSF56003 SUPFAM:SSF54665 SUPFAM:SSF55447 SUPFAM:SSF54292 HOGENOM:HBG746468 ProtClustDB:PLN00192 EMBL:AB005805 EMBL:AL391734 EMBL:AF039896 IPI:IPI00529435 PIR:T51623 PIR:T52050 RefSeq:NP_189946.1 UniGene:At.462 ProteinModelPortal:Q7G192 SMR:Q7G192 STRING:Q7G192 PRIDE:Q7G192 EnsemblPlants:AT3G43600.1 GeneID:823457 KEGG:ath:AT3G43600 GeneFarm:4893 TAIR:At3g43600 InParanoid:Q7G192 OMA:ILYDCGK PhylomeDB:Q7G192 BioCyc:ARA:AT3G43600-MONOMER BioCyc:MetaCyc:AT3G43600-MONOMER Genevestigator:Q7G192 GermOnline:AT3G43600 GO:GO:0016614 Uniprot:Q7G192
Root	Isotig00395	14	63	-2.299	8.06E-10	TAIR|locus:2079834 - symbol:AAO2 "aldehyde oxidase 2" species:3702 "Arabidopsis thaliana" [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0004031 "aldehyde oxidase activity" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001041 InterPro:IPR002346 InterPro:IPR002888 InterPro:IPR006058 InterPro:IPR008274 InterPro:IPR016166 InterPro:IPR016169 InterPro:IPR016208 Pfam:PF00111 Pfam:PF00941 Pfam:PF01799 Pfam:PF02738 PIRSF:PIRSF000127 PROSITE:PS00197 PROSITE:PS00559 PROSITE:PS51085 PROSITE:PS51387 InterPro:IPR000674 Pfam:PF01315 GO:GO:0005829 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005506 GO:GO:0009055 GO:GO:0050660 SUPFAM:SSF56176 GO:GO:0004031 eggNOG:COG4630 GO:GO:0051537 InterPro:IPR012675 InterPro:IPR005107 Gene3D:G3DSA:1.10.150.120 Gene3D:G3DSA:3.30.365.10 Gene3D:G3DSA:3.90.1170.50 Gene3D:G3DSA:3.30.390.50 Gene3D:G3DSA:3.30.465.10 Gene3D:G3DSA:3.10.20.30 Pfam:PF03450 SMART:SM01008 SMART:SM01092 SUPFAM:SSF47741 SUPFAM:SSF56003 SUPFAM:SSF54665 SUPFAM:SSF55447 SUPFAM:SSF54292 HOGENOM:HBG746468 ProtClustDB:PLN00192 EMBL:AB005805 EMBL:AL391734 EMBL:AF039896 IPI:IPI00529435 PIR:T51623 PIR:T52050 RefSeq:NP_189946.1 UniGene:At.462 ProteinModelPortal:Q7G192 SMR:Q7G192 STRING:Q7G192 PRIDE:Q7G192 EnsemblPlants:AT3G43600.1 GeneID:823457 KEGG:ath:AT3G43600 GeneFarm:4893 TAIR:At3g43600 InParanoid:Q7G192 OMA:ILYDCGK PhylomeDB:Q7G192 BioCyc:ARA:AT3G43600-MONOMER BioCyc:MetaCyc:AT3G43600-MONOMER Genevestigator:Q7G192 GermOnline:AT3G43600 GO:GO:0016614 Uniprot:Q7G192
Root	Isotig00411	191	13	3.748	1.70E-38	No hit
Root	Isotig00412	193	13	3.763	5.51E-39	No hit
Root	Isotig00413	191	13	3.748	1.70E-38	No hit
Root	Isotig00414	193	13	3.763	5.51E-39	FB|FBgn0003372 - symbol:Sgs1 "Salivary gland secretion 1" species:7227 "Drosophila melanogaster" [GO:0005198 "structural molecule activity" evidence=TAS] [GO:0005576 "extracellular region" evidence=TAS] [GO:0007594 "puparial adhesion" evidence=TAS] EMBL:AE014134 GeneTree:ENSGT00650000092999 RefSeq:NP_523475.3 UniGene:Dm.23846 ProteinModelPortal:Q9VR49 STRING:Q9VR49 EnsemblMetazoa:FBtr0077393 GeneID:33701 KEGG:dme:Dmel_CG3047 UCSC:CG3047-RA CTD:33701 FlyBase:FBgn0003372 eggNOG:NOG124330 OMA:RSTTTTC OrthoDB:EOG41VHM9 NextBio:784856 ArrayExpress:Q9VR49 Bgee:Q9VR49 Uniprot:Q9VR49
Root	Isotig00415	191	13	3.748	1.70E-38	No hit
Root	Isotig00416	191	13	3.748	1.70E-38	No hit
Root	Isotig00417	191	13	3.748	1.70E-38	No hit
Root	Isotig00418	193	13	3.763	5.51E-39	No hit
Root	Isotig00419	191	13	3.748	1.70E-38	No hit
Root	Isotig00420	196	11	4.026	2.89E-41	No hit
Root	Isotig00421	193	13	3.763	5.51E-39	No hit
Root	Isotig00422	198	11	4.041	9.34E-42	No hit
Root	Isotig00423	191	13	3.748	1.70E-38	No hit
Root	Isotig00424	193	13	3.763	5.51E-39	No hit
Root	Isotig00425	191	13	3.748	1.70E-38	No hit
Root	Isotig00426	191	13	3.748	1.70E-38	No hit
Root	Isotig00427	193	13	3.763	5.51E-39	No hit
Root	Isotig00428	191	13	3.748	1.70E-38	No hit
Root	Isotig00429	196	11	4.026	2.89E-41	No hit
Root	Isotig00430	191	13	3.748	1.70E-38	No hit

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig00431	191	13	3.748	1.70E-38	No hit
Root	Isotig00432	163	9	4.050	1.01E-34	No hit
Root	Isotig00433	165	9	4.067	3.26E-35	FB|FBgn0003372 - symbol:Sgs1 "Salivary gland secretion 1" species:7227 "Drosophila melanogaster" [GO:0005198 "structural molecule activity" evidence=TAS] [GO:0005576 "extracellular region" evidence=TAS] [GO:0007594 "puparial adhesion" evidence=TAS] EMBL:AE014134 GeneTree:ENSGT00650000092999 RefSeq:NP_523475.3 UniGene:Dm.23846 ProteinModelPortal:Q9VR49 STRING:Q9VR49 EnsemblMetazoa:FBtr0077393 GeneID:33701 KEGG:dme:Dmel_CG3047 UCSC:CG3047-RA CTD:33701 FlyBase:FBgn0003372 eggNOG:NOG124330 OMA:RSTTTTC OrthoDB:EOG41VHM9 NextBio:784856 ArrayExpress:Q9VR49 Bgee:Q9VR49 Uniprot:Q9VR49
Root	Isotig00434	163	9	4.050	1.01E-34	No hit
Root	Isotig00435	114	8	3.704	1.83E-23	No hit
Root	Isotig00442	19	3	2.534	0.000639389	No hit
Root	Isotig00443	19	3	2.534	0.000639389	No hit
Root	Isotig00450	28	55	-1.103	0.00070297	TAIR|locus:2051789 - symbol:MTHFR2 "methylenetetrahydrofolate reductase 2" species:3702 "Arabidopsis thaliana" [GO:0004489 "methylenetetrahydrofolate reductase (NADPH) activity" evidence=IEA;ISS] [GO:0006555 "methionine metabolic process" evidence=IEA;ISS] [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR003171 InterPro:IPR004621 Pfam:PF02219 GO:GO:0005829 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0006555 EMBL:AC004005 eggNOG:COG0685 HOGENOM:HBG649727 KO:K00297 GO:GO:0004489 UniGene:At.23509 ProtClustDB:PLN02540 TIGRFAMs:TIGR00677 EMBL:AJ245414 EMBL:AF181967 EMBL:AY050434 EMBL:AF370515 EMBL:AK220952 IPI:IPI00541304 PIR:T00696 RefSeq:NP_566011.1 UniGene:At.11693 ProteinModelPortal:O80585 SMR:O80585 IntAct:O80585 STRING:O80585 PRIDE:O80585 ProMEX:O80585 EnsemblPlants:AT2G44160.1 GeneID:819022 KEGG:ath:AT2G44160 GeneFarm:5158 TAIR:At2g44160 InParanoid:O80585 OMA:MIDESKI PhylomeDB:O80585 ArrayExpress:O80585 Genevestigator:O80585 GermOnline:AT2G44160 Uniprot:O80585
Root	Isotig00451	13	40	-1.750	4.15E-05	TAIR|locus:2051789 - symbol:MTHFR2 "methylenetetrahydrofolate reductase 2" species:3702 "Arabidopsis thaliana" [GO:0004489 "methylenetetrahydrofolate reductase (NADPH) activity" evidence=IEA;ISS] [GO:0006555 "methionine metabolic process" evidence=IEA;ISS] [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR003171 InterPro:IPR004621 Pfam:PF02219 GO:GO:0005829 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0006555 EMBL:AC004005 eggNOG:COG0685 HOGENOM:HBG649727 KO:K00297 GO:GO:0004489 UniGene:At.23509 ProtClustDB:PLN02540 TIGRFAMs:TIGR00677 EMBL:AJ245414 EMBL:AF181967 EMBL:AY050434 EMBL:AF370515 EMBL:AK220952 IPI:IPI00541304 PIR:T00696 RefSeq:NP_566011.1 UniGene:At.11693 ProteinModelPortal:O80585 SMR:O80585 IntAct:O80585 STRING:O80585 PRIDE:O80585 ProMEX:O80585 EnsemblPlants:AT2G44160.1 GeneID:819022 KEGG:ath:AT2G44160 GeneFarm:5158 TAIR:At2g44160 InParanoid:O80585 OMA:MIDESKI PhylomeDB:O80585 ArrayExpress:O80585 Genevestigator:O80585 GermOnline:AT2G44160 Uniprot:O80585
Root	Isotig00453	18	43	-1.385	0.000339352	TAIR|locus:2051789 - symbol:MTHFR2 "methylenetetrahydrofolate reductase 2" species:3702 "Arabidopsis thaliana" [GO:0004489 "methylenetetrahydrofolate reductase (NADPH) activity" evidence=IEA;ISS] [GO:0006555 "methionine metabolic process" evidence=IEA;ISS] [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR003171 InterPro:IPR004621 Pfam:PF02219 GO:GO:0005829 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0006555 EMBL:AC004005 eggNOG:COG0685 HOGENOM:HBG649727 KO:K00297 GO:GO:0004489 UniGene:At.23509 ProtClustDB:PLN02540 TIGRFAMs:TIGR00677 EMBL:AJ245414 EMBL:AF181967 EMBL:AY050434 EMBL:AF370515 EMBL:AK220952 IPI:IPI00541304 PIR:T00696 RefSeq:NP_566011.1 UniGene:At.11693 ProteinModelPortal:O80585 SMR:O80585 IntAct:O80585 STRING:O80585 PRIDE:O80585 ProMEX:O80585 EnsemblPlants:AT2G44160.1 GeneID:819022 KEGG:ath:AT2G44160 GeneFarm:5158 TAIR:At2g44160 InParanoid:O80585 OMA:MIDESKI PhylomeDB:O80585 ArrayExpress:O80585 Genevestigator:O80585 GermOnline:AT2G44160 Uniprot:O80585
Root	Isotig00454	25	113	-2.305	1.69E-16	TAIR|locus:2130419 - symbol:OASA1 "AT4G14880" species:3702 "Arabidopsis thaliana" [GO:0004124 "cysteine synthase activity" evidence=IGI;IDA] [GO:0005829 "cytosol" evidence=ISS;IDA] [GO:0006535 "cysteine biosynthetic process from serine" evidence=TAS] [GO:0046686 "response to cadmium ion" evidence=IEP;IMP;IDA] [GO:0007568 "aging" evidence=IMP] [GO:0005634 "nucleus" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005777 "peroxisome" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0019344 "cysteine

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						biosynthetic process" evidence=IMP] [GO:0048046 "apoplast" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0009570 "chloroplast stroma" evidence=IDA] InterPro:IPR001216 InterPro:IPR001926 InterPro:IPR005856 InterPro:IPR005859 Pfam:PF00291 PROSITE:PS00901 GO:GO:0005829 GO:GO:0005886 EMBL:CP002687 GO:GO:0048046 GO:GO:0009570 GO:GO:0005634 GO:GO:0046686 GO:GO:0005774 GO:GO:0005515 GO:GO:0030170 SUPFAM:SSF53686 GO:GO:0005777 GO:GO:0007568 GO:GO:0016740 EMBL:AL161540 EMBL:Z97337 eggNOG:COG0031 GO:GO:0006535 UniGene:At.34389 GO:GO:0004124 EMBL:X80376 EMBL:X84097 EMBL:AJ272027 EMBL:AY045825 EMBL:BT025878 IPI:IPI00519731 PIR:A71412 PIR:S48694 RefSeq:NP_001190732.1 RefSeq:NP_001190733.1 RefSeq:NP_193224.1 RefSeq:NP_849386.1 UniGene:At.30 PDB:1Z7W PDB:1Z7Y PDB:2ISQ PDBsum:1Z7W PDBsum:1Z7Y PDBsum:2ISQ ProteinModelPortal:P47998 SMR:P47998 IntAct:P47998 STRING:P47998 PRIDE:P47998 EnsemblPlants:AT4G14880.1 EnsemblPlants:AT4G14880.2 EnsemblPlants:AT4G14880.3 EnsemblPlants:AT4G14880.4 GeneID:827145 KEGG:ath:AT4G14880 TAIR:At4g14880 InParanoid:P47998 KO:K01738 OMA:SCGERYM PhylomeDB:P47998 ProtClustDB:PLN02565 ArrayExpress:P47998 Genevestigator:P47998 GermOnline:AT4G14880 TIGRFAMs:TIGR01139 TIGRFAMs:TIGR01136 Uniprot:P47998
Root	Isotig00456	12	69	-2.653	3.00E-12	TAIR|locus:2183139 - symbol:SULTR3;5 "sulfate transporter 3;5" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=IEA] [GO:0008272 "sulfate transport" evidence=IEA] [GO:0015116 "sulfate transmembrane transporter activity" evidence=ISS] [GO:0016020 "membrane" evidence=IEA] [GO:0016021 "integral to membrane" evidence=IEA] [GO:0055085 "transmembrane transport" evidence=IEA] InterPro:IPR001902 InterPro:IPR011547 InterPro:IPR018045 Pfam:PF00916 PROSITE:PS01130 GO:GO:0016021 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0015293 GO:GO:0008271 InterPro:IPR002645 Gene3D:G3DSA:3.30.750.24 SUPFAM:SSF52091 PROSITE:PS50801 EMBL:AF296838 eggNOG:COG0659 Pfam:PF01740 TIGRFAMs:TIGR00815 HOGENOM:HBG554309 ProtClustDB:CLSN2685981 EMBL:AB061739 IPI:IPI00538924 RefSeq:NP_568377.1 UniGene:At.10546 ProteinModelPortal:Q94LW6 SMR:Q94LW6 PRIDE:Q94LW6 EnsemblPlants:AT5G19600.1 GeneID:832080 KEGG:ath:AT5G19600 GeneFarm:2700 TAIR:At5g19600 InParanoid:Q94LW6 OMA:CKETFFP PhylomeDB:Q94LW6 ArrayExpress:Q94LW6 Genevestigator:Q94LW6 GermOnline:AT5G19600 Uniprot:Q94LW6
Root	Isotig00457	12	69	-2.653	3.00E-12	TAIR|locus:2183139 - symbol:SULTR3;5 "sulfate transporter 3;5" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=IEA] [GO:0008272 "sulfate transport" evidence=IEA] [GO:0015116 "sulfate transmembrane transporter activity" evidence=ISS] [GO:0016020 "membrane" evidence=IEA] [GO:0016021 "integral to membrane" evidence=IEA] [GO:0055085 "transmembrane transport" evidence=IEA] InterPro:IPR001902 InterPro:IPR011547 InterPro:IPR018045 Pfam:PF00916 PROSITE:PS01130 GO:GO:0016021 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0015293 GO:GO:0008271 InterPro:IPR002645 Gene3D:G3DSA:3.30.750.24 SUPFAM:SSF52091 PROSITE:PS50801 EMBL:AF296838 eggNOG:COG0659 Pfam:PF01740 TIGRFAMs:TIGR00815 HOGENOM:HBG554309 ProtClustDB:CLSN2685981 EMBL:AB061739 IPI:IPI00538924 RefSeq:NP_568377.1 UniGene:At.10546 ProteinModelPortal:Q94LW6 SMR:Q94LW6 PRIDE:Q94LW6 EnsemblPlants:AT5G19600.1 GeneID:832080 KEGG:ath:AT5G19600 GeneFarm:2700 TAIR:At5g19600 InParanoid:Q94LW6 OMA:CKETFFP PhylomeDB:Q94LW6 ArrayExpress:Q94LW6 Genevestigator:Q94LW6 GermOnline:AT5G19600 Uniprot:Q94LW6
Root	Isotig00458	12	67	-2.610	9.38E-12	TAIR|locus:2183139 - symbol:SULTR3;5 "sulfate transporter 3;5" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=IEA] [GO:0008272 "sulfate transport" evidence=IEA] [GO:0015116 "sulfate transmembrane transporter activity" evidence=ISS] [GO:0016020 "membrane" evidence=IEA] [GO:0016021 "integral to membrane" evidence=IEA] [GO:0055085 "transmembrane transport" evidence=IEA] InterPro:IPR001902 InterPro:IPR011547 InterPro:IPR018045 Pfam:PF00916 PROSITE:PS01130 GO:GO:0016021 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0015293 GO:GO:0008271 InterPro:IPR002645 Gene3D:G3DSA:3.30.750.24 SUPFAM:SSF52091 PROSITE:PS50801 EMBL:AF296838 eggNOG:COG0659 Pfam:PF01740 TIGRFAMs:TIGR00815 HOGENOM:HBG554309 ProtClustDB:CLSN2685981 EMBL:AB061739 IPI:IPI00538924 RefSeq:NP_568377.1 UniGene:At.10546 ProteinModelPortal:Q94LW6 SMR:Q94LW6 PRIDE:Q94LW6 EnsemblPlants:AT5G19600.1 GeneID:832080 KEGG:ath:AT5G19600 GeneFarm:2700 TAIR:At5g19600 InParanoid:Q94LW6 OMA:CKETFFP PhylomeDB:Q94LW6 ArrayExpress:Q94LW6 Genevestigator:Q94LW6 GermOnline:AT5G19600 Uniprot:Q94LW6
Root	Isotig00459	12	67	-2.610	9.38E-12	TAIR|locus:2183139 - symbol:SULTR3;5 "sulfate transporter 3;5" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=IEA] [GO:0008272 "sulfate transport" evidence=IEA] [GO:0015116 "sulfate transmembrane

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						transporter activity" evidence=ISS] [GO:0016020 "membrane" evidence=IEA] [GO:0016021 "integral to membrane" evidence=IEA] [GO:0055085 "transmembrane transport" evidence=IEA] InterPro:IPR001902 InterPro:IPR011547 InterPro:IPR018045 Pfam:PF00916 PROSITE:PS01130 GO:GO:0016021 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0015293 GO:GO:0008271 InterPro:IPR002645 Gene3D:G3DSA:3.30.750.24 SUPFAM:SSF52091 PROSITE:PS50801 EMBL:AF296838 eggNOG:COG0659 Pfam:PF01740 TIGRFAMs:TIGR00815 HOGENOM:HBG554309 ProtClustDB:CLSN2685981 EMBL:AB061739 IPI:IPI00538924 RefSeq:NP_568377.1 UniGene:At.10546 ProteinModelPortal:Q94LW6 SMR:Q94LW6 PRIDE:Q94LW6 EnsemblPlants:AT5G19600.1 GeneID:832080 KEGG:ath:AT5G19600 GeneFarm:2700 TAIR:At5g19600 InParanoid:Q94LW6 OMA:CKETFFP PhylomeDB:Q94LW6 ArrayExpress:Q94LW6 Genevestigator:Q94LW6 GermOnline:AT5G19600 Uniprot:Q94LW6
Root	Isotig00460	12	67	-2.610	9.38E-12	TAIR|locus:2183139 - symbol:SULTR3;5 "sulfate transporter 3;5" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=IEA] [GO:0008272 "sulfate transport" evidence=IEA] [GO:0015116 "sulfate transmembrane transporter activity" evidence=ISS] [GO:0016020 "membrane" evidence=IEA] [GO:0016021 "integral to membrane" evidence=IEA] [GO:0055085 "transmembrane transport" evidence=IEA] InterPro:IPR001902 InterPro:IPR011547 InterPro:IPR018045 Pfam:PF00916 PROSITE:PS01130 GO:GO:0016021 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0015293 GO:GO:0008271 InterPro:IPR002645 Gene3D:G3DSA:3.30.750.24 SUPFAM:SSF52091 PROSITE:PS50801 EMBL:AF296838 eggNOG:COG0659 Pfam:PF01740 TIGRFAMs:TIGR00815 HOGENOM:HBG554309 ProtClustDB:CLSN2685981 EMBL:AB061739 IPI:IPI00538924 RefSeq:NP_568377.1 UniGene:At.10546 ProteinModelPortal:Q94LW6 SMR:Q94LW6 PRIDE:Q94LW6 EnsemblPlants:AT5G19600.1 GeneID:832080 KEGG:ath:AT5G19600 GeneFarm:2700 TAIR:At5g19600 InParanoid:Q94LW6 OMA:CKETFFP PhylomeDB:Q94LW6 ArrayExpress:Q94LW6 Genevestigator:Q94LW6 GermOnline:AT5G19600 Uniprot:Q94LW6
Root	Isotig00461	12	67	-2.610	9.38E-12	TAIR|locus:2183139 - symbol:SULTR3;5 "sulfate transporter 3;5" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=IEA] [GO:0008272 "sulfate transport" evidence=IEA] [GO:0015116 "sulfate transmembrane transporter activity" evidence=ISS] [GO:0016020 "membrane" evidence=IEA] [GO:0016021 "integral to membrane" evidence=IEA] [GO:0055085 "transmembrane transport" evidence=IEA] InterPro:IPR001902 InterPro:IPR011547 InterPro:IPR018045 Pfam:PF00916 PROSITE:PS01130 GO:GO:0016021 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0015293 GO:GO:0008271 InterPro:IPR002645 Gene3D:G3DSA:3.30.750.24 SUPFAM:SSF52091 PROSITE:PS50801 EMBL:AF296838 eggNOG:COG0659 Pfam:PF01740 TIGRFAMs:TIGR00815 HOGENOM:HBG554309 ProtClustDB:CLSN2685981 EMBL:AB061739 IPI:IPI00538924 RefSeq:NP_568377.1 UniGene:At.10546 ProteinModelPortal:Q94LW6 SMR:Q94LW6 PRIDE:Q94LW6 EnsemblPlants:AT5G19600.1 GeneID:832080 KEGG:ath:AT5G19600 GeneFarm:2700 TAIR:At5g19600 InParanoid:Q94LW6 OMA:CKETFFP PhylomeDB:Q94LW6 ArrayExpress:Q94LW6 Genevestigator:Q94LW6 GermOnline:AT5G19600 Uniprot:Q94LW6
Root	Isotig00462	3	52	-4.244	1.90E-13	TAIR|locus:2183139 - symbol:SULTR3;5 "sulfate transporter 3;5" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=IEA] [GO:0008272 "sulfate transport" evidence=IEA] [GO:0015116 "sulfate transmembrane transporter activity" evidence=ISS] [GO:0016020 "membrane" evidence=IEA] [GO:0016021 "integral to membrane" evidence=IEA] [GO:0055085 "transmembrane transport" evidence=IEA] InterPro:IPR001902 InterPro:IPR011547 InterPro:IPR018045 Pfam:PF00916 PROSITE:PS01130 GO:GO:0016021 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0015293 GO:GO:0008271 InterPro:IPR002645 Gene3D:G3DSA:3.30.750.24 SUPFAM:SSF52091 PROSITE:PS50801 EMBL:AF296838 eggNOG:COG0659 Pfam:PF01740 TIGRFAMs:TIGR00815 HOGENOM:HBG554309 ProtClustDB:CLSN2685981 EMBL:AB061739 IPI:IPI00538924 RefSeq:NP_568377.1 UniGene:At.10546 ProteinModelPortal:Q94LW6 SMR:Q94LW6 PRIDE:Q94LW6 EnsemblPlants:AT5G19600.1 GeneID:832080 KEGG:ath:AT5G19600 GeneFarm:2700 TAIR:At5g19600 InParanoid:Q94LW6 OMA:CKETFFP PhylomeDB:Q94LW6 ArrayExpress:Q94LW6 Genevestigator:Q94LW6 GermOnline:AT5G19600 Uniprot:Q94LW6
Root	Isotig00463	3	42	-3.936	9.98E-11	TAIR|locus:2183139 - symbol:SULTR3;5 "sulfate transporter 3;5" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=IEA] [GO:0008272 "sulfate transport" evidence=IEA] [GO:0015116 "sulfate transmembrane transporter activity" evidence=ISS] [GO:0016020 "membrane" evidence=IEA] [GO:0016021 "integral to membrane" evidence=IEA] [GO:0055085 "transmembrane transport" evidence=IEA] InterPro:IPR001902 InterPro:IPR011547 InterPro:IPR018045 Pfam:PF00916 PROSITE:PS01130 GO:GO:0016021 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0015293 GO:GO:0008271 InterPro:IPR002645

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						Gene3D:G3DSA:3.30.750.24 SUPFAM:SSF52091 PROSITE:PS50801 EMBL:AF296838 eggNOG:COG0659 Pfam:PF01740 TIGRFAMs:TIGR00815 HOGENOM:HBG554309 ProtClustDB:CLSN2685981 EMBL:AB061739 IPI:IPI00538924 RefSeq:NP_568377.1 UniGene:At.10546 ProteinModelPortal:Q94LW6 SMR:Q94LW6 PRIDE:Q94LW6 EnsemblPlants:AT5G19600.1 GeneID:832080 KEGG:ath:AT5G19600 GeneFarm:2700 TAIR:At5g19600 InParanoid:Q94LW6 OMA:CKETFFP PhylomeDB:Q94LW6 ArrayExpress:Q94LW6 Genevestigator:Q94LW6 GermOnline:AT5G19600 Uniprot:Q94LW6
Root	Isotig00464	3	50	-4.188	6.62E-13	TAIR|locus:2183139 - symbol:SULTR3;5 "sulfate transporter 3;5" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=IEA] [GO:0008272 "sulfate transport" evidence=IEA] [GO:0015116 "sulfate transmembrane transporter activity" evidence=ISS] [GO:0016020 "membrane" evidence=IEA] [GO:0016021 "integral to membrane" evidence=IEA] [GO:0055085 "transmembrane transport" evidence=IEA] InterPro:IPR001902 InterPro:IPR011547 InterPro:IPR018045 Pfam:PF00916 PROSITE:PS01130 GO:GO:0016021 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0015293 GO:GO:0008271 InterPro:IPR002645 Gene3D:G3DSA:3.30.750.24 SUPFAM:SSF52091 PROSITE:PS50801 EMBL:AF296838 eggNOG:COG0659 Pfam:PF01740 TIGRFAMs:TIGR00815 HOGENOM:HBG554309 ProtClustDB:CLSN2685981 EMBL:AB061739 IPI:IPI00538924 RefSeq:NP_568377.1 UniGene:At.10546 ProteinModelPortal:Q94LW6 SMR:Q94LW6 PRIDE:Q94LW6 EnsemblPlants:AT5G19600.1 GeneID:832080 KEGG:ath:AT5G19600 GeneFarm:2700 TAIR:At5g19600 InParanoid:Q94LW6 OMA:CKETFFP PhylomeDB:Q94LW6 ArrayExpress:Q94LW6 Genevestigator:Q94LW6 GermOnline:AT5G19600 Uniprot:Q94LW6
Root	Isotig00465	9	31	-1.913	0.000125821	TAIR|locus:3437527 - symbol:SULTR3;1 "sulfate transporter 3;1" species:3702 "Arabidopsis thaliana" [GO:0005215 "transporter activity" evidence=IEA] [GO:0006810 "transport" evidence=IEA] [GO:0008271 "secondary active sulfate transmembrane transporter activity" evidence=IEA] [GO:0008272 "sulfate transport" evidence=IEA;ISS] [GO:0015116 "sulfate transmembrane transporter activity" evidence=ISS] [GO:0055085 "transmembrane transport" evidence=IEA] InterPro:IPR001902 InterPro:IPR011547 InterPro:IPR018045 Pfam:PF00916 PROSITE:PS01130 GO:GO:0016021 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0006950 GO:GO:0015293 EMBL:AF049236 EMBL:AL049711 GO:GO:0008271 InterPro:IPR002645 Gene3D:G3DSA:3.30.750.24 SUPFAM:SSF52091 PROSITE:PS50801 eggNOG:COG0659 Pfam:PF01740 TIGRFAMs:TIGR00815 HOGENOM:HBG554309 ProtClustDB:CLSN2685981 EMBL:D89631 EMBL:AB012048 EMBL:AY099873 IPI:IPI00533966 PIR:T48901 PIR:T48902 PIR:T49069 PIR:T51161 RefSeq:NP_190758.2 UniGene:At.11928 ProteinModelPortal:Q9SV13 SMR:Q9SV13 PRIDE:Q9SV13 EnsemblPlants:AT3G51895.1 GeneID:824353 KEGG:ath:AT3G51895 GeneFarm:2359 TAIR:At3g51895 InParanoid:Q9SV13 PhylomeDB:Q9SV13 ArrayExpress:Q9SV13 Genevestigator:Q9SV13 GermOnline:AT3G51895 Uniprot:Q9SV13
Root	Isotig00466	3	50	-4.188	6.62E-13	TAIR|locus:2183139 - symbol:SULTR3;5 "sulfate transporter 3;5" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=IEA] [GO:0008272 "sulfate transport" evidence=IEA] [GO:0015116 "sulfate transmembrane transporter activity" evidence=ISS] [GO:0016020 "membrane" evidence=IEA] [GO:0016021 "integral to membrane" evidence=IEA] [GO:0055085 "transmembrane transport" evidence=IEA] InterPro:IPR001902 InterPro:IPR011547 InterPro:IPR018045 Pfam:PF00916 PROSITE:PS01130 GO:GO:0016021 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0015293 GO:GO:0008271 InterPro:IPR002645 Gene3D:G3DSA:3.30.750.24 SUPFAM:SSF52091 PROSITE:PS50801 EMBL:AF296838 eggNOG:COG0659 Pfam:PF01740 TIGRFAMs:TIGR00815 HOGENOM:HBG554309 ProtClustDB:CLSN2685981 EMBL:AB061739 IPI:IPI00538924 RefSeq:NP_568377.1 UniGene:At.10546 ProteinModelPortal:Q94LW6 SMR:Q94LW6 PRIDE:Q94LW6 EnsemblPlants:AT5G19600.1 GeneID:832080 KEGG:ath:AT5G19600 GeneFarm:2700 TAIR:At5g19600 InParanoid:Q94LW6 OMA:CKETFFP PhylomeDB:Q94LW6 ArrayExpress:Q94LW6 Genevestigator:Q94LW6 GermOnline:AT5G19600 Uniprot:Q94LW6
Root	Isotig00467	9	31	-1.913	0.000125821	TAIR|locus:3437527 - symbol:SULTR3;1 "sulfate transporter 3;1" species:3702 "Arabidopsis thaliana" [GO:0005215 "transporter activity" evidence=IEA] [GO:0006810 "transport" evidence=IEA] [GO:0008271 "secondary active sulfate transmembrane transporter activity" evidence=IEA] [GO:0008272 "sulfate transport" evidence=IEA;ISS] [GO:0015116 "sulfate transmembrane transporter activity" evidence=ISS] [GO:0055085 "transmembrane transport" evidence=IEA] InterPro:IPR001902 InterPro:IPR011547 InterPro:IPR018045 Pfam:PF00916 PROSITE:PS01130 GO:GO:0016021 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0006950 GO:GO:0015293 EMBL:AF049236 EMBL:AL049711 GO:GO:0008271 InterPro:IPR002645 Gene3D:G3DSA:3.30.750.24 SUPFAM:SSF52091 PROSITE:PS50801 eggNOG:COG0659 Pfam:PF01740 TIGRFAMs:TIGR00815 HOGENOM:HBG554309 ProtClustDB:CLSN2685981 EMBL:D89631 EMBL:AB012048 EMBL:AY099873

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						IPI:IPI00533966 PIR:T48901 PIR:T48902 PIR:T49069 PIR:T51161 RefSeq:NP_190758.2 UniGene:At.11928 ProteinModelPortal:Q9SV13 SMR:Q9SV13 PRIDE:Q9SV13 EnsemblPlants:AT3G51895.1 GeneID:824353 KEGG:ath:AT3G51895 GeneFarm:2359 TAIR:At3g51895 InParanoid:Q9SV13 PhylomeDB:Q9SV13 ArrayExpress:Q9SV13 Genevestigator:Q9SV13 GermOnline:AT3G51895 Uniprot:Q9SV13
Root	Isotig00468	3	40	-3.866	3.51E-10	TAIR|locus:2183139 - symbol:SULTR3;5 "sulfate transporter 3;5" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=IEA] [GO:0008272 "sulfate transport" evidence=IEA] [GO:0015116 "sulfate transmembrane transporter activity" evidence=ISS] [GO:0016020 "membrane" evidence=IEA] [GO:0016021 "integral to membrane" evidence=IEA] [GO:0055085 "transmembrane transport" evidence=IEA] InterPro:IPR001902 InterPro:IPR011547 InterPro:IPR018045 Pfam:PF00916 PROSITE:PS01130 GO:GO:0016021 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0015293 GO:GO:0008271 InterPro:IPR002645 Gene3D:G3DSA:3.30.750.24 SUPFAM:SSF52091 PROSITE:PS50801 EMBL:AF296838 eggNOG:COG0659 Pfam:PF01740 TIGRFAMs:TIGR00815 HOGENOM:HBG554309 ProtClustDB:CLSN2685981 EMBL:AB061739 IPI:IPI00538924 RefSeq:NP_568377.1 UniGene:At.10546 ProteinModelPortal:Q94LW6 SMR:Q94LW6 PRIDE:Q94LW6 EnsemblPlants:AT5G19600.1 GeneID:832080 KEGG:ath:AT5G19600 GeneFarm:2700 TAIR:At5g19600 InParanoid:Q94LW6 OMA:CKETFFP PhylomeDB:Q94LW6 ArrayExpress:Q94LW6 Genevestigator:Q94LW6 GermOnline:AT5G19600 Uniprot:Q94LW6
Root	Isotig00469	3	40	-3.866	3.51E-10	TAIR|locus:2183139 - symbol:SULTR3;5 "sulfate transporter 3;5" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=IEA] [GO:0008272 "sulfate transport" evidence=IEA] [GO:0015116 "sulfate transmembrane transporter activity" evidence=ISS] [GO:0016020 "membrane" evidence=IEA] [GO:0016021 "integral to membrane" evidence=IEA] [GO:0055085 "transmembrane transport" evidence=IEA] InterPro:IPR001902 InterPro:IPR011547 InterPro:IPR018045 Pfam:PF00916 PROSITE:PS01130 GO:GO:0016021 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0015293 GO:GO:0008271 InterPro:IPR002645 Gene3D:G3DSA:3.30.750.24 SUPFAM:SSF52091 PROSITE:PS50801 EMBL:AF296838 eggNOG:COG0659 Pfam:PF01740 TIGRFAMs:TIGR00815 HOGENOM:HBG554309 ProtClustDB:CLSN2685981 EMBL:AB061739 IPI:IPI00538924 RefSeq:NP_568377.1 UniGene:At.10546 ProteinModelPortal:Q94LW6 SMR:Q94LW6 PRIDE:Q94LW6 EnsemblPlants:AT5G19600.1 GeneID:832080 KEGG:ath:AT5G19600 GeneFarm:2700 TAIR:At5g19600 InParanoid:Q94LW6 OMA:CKETFFP PhylomeDB:Q94LW6 ArrayExpress:Q94LW6 Genevestigator:Q94LW6 GermOnline:AT5G19600 Uniprot:Q94LW6
Root	Isotig00471	0	14	-4.936	8.24E-05	TAIR|locus:2183139 - symbol:SULTR3;5 "sulfate transporter 3;5" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=IEA] [GO:0008272 "sulfate transport" evidence=IEA] [GO:0015116 "sulfate transmembrane transporter activity" evidence=ISS] [GO:0016020 "membrane" evidence=IEA] [GO:0016021 "integral to membrane" evidence=IEA] [GO:0055085 "transmembrane transport" evidence=IEA] InterPro:IPR001902 InterPro:IPR011547 InterPro:IPR018045 Pfam:PF00916 PROSITE:PS01130 GO:GO:0016021 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0015293 GO:GO:0008271 InterPro:IPR002645 Gene3D:G3DSA:3.30.750.24 SUPFAM:SSF52091 PROSITE:PS50801 EMBL:AF296838 eggNOG:COG0659 Pfam:PF01740 TIGRFAMs:TIGR00815 HOGENOM:HBG554309 ProtClustDB:CLSN2685981 EMBL:AB061739 IPI:IPI00538924 RefSeq:NP_568377.1 UniGene:At.10546 ProteinModelPortal:Q94LW6 SMR:Q94LW6 PRIDE:Q94LW6 EnsemblPlants:AT5G19600.1 GeneID:832080 KEGG:ath:AT5G19600 GeneFarm:2700 TAIR:At5g19600 InParanoid:Q94LW6 OMA:CKETFFP PhylomeDB:Q94LW6 ArrayExpress:Q94LW6 Genevestigator:Q94LW6 GermOnline:AT5G19600 Uniprot:Q94LW6
Root	Isotig00473	5	74	-4.016	5.70E-18	TAIR|locus:2203221 - symbol:NIA1 "AT1G77760" species:3702 "Arabidopsis thaliana" [GO:0006809 "nitric oxide biosynthetic process" evidence=IMP] [GO:0005829 "cytosol" evidence=TAS] [GO:0009416 "response to light stimulus" evidence=IMP] [GO:0005515 "protein binding" evidence=IPI] [GO:0008940 "nitrate reductase activity" evidence=IMP] [GO:0042128 "nitrate assimilation" evidence=IMP] InterPro:IPR000572 InterPro:IPR001199 InterPro:IPR001433 InterPro:IPR001709 InterPro:IPR001834 InterPro:IPR005066 InterPro:IPR008335 InterPro:IPR012137 InterPro:IPR017927 InterPro:IPR017938 InterPro:IPR018506 InterPro:IPR022407 Pfam:PF00173 Pfam:PF00174 Pfam:PF00175 Pfam:PF03404 PIRSF:PIRSF000233 PRINTS:PR00363 PRINTS:PR00371 PRINTS:PR00406 PRINTS:PR00407 PROSITE:PS00191 PROSITE:PS00559 PROSITE:PS50255 PROSITE:PS51384 InterPro:IPR008333 Pfam:PF00970 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0005515 GO:GO:0009635 GO:GO:0009055 GO:GO:0050660 GO:GO:0020037 GO:GO:0009416 Gene3D:G3DSA:3.10.120.10 SUPFAM:SSF55856 InterPro:IPR014756 SUPFAM:SSF81296 GO:GO:0043546 eggNOG:COG0543 SUPFAM:SSF63380

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0006809 GO:GO:0042128 EMBL:AC012193 GO:GO:0030151 KO:K00360 EMBL:Z19050 EMBL:AY090950 EMBL:AF424624 EMBL:BT000989 EMBL:X13434 EMBL:X13436 IPI:IPI00518959 PIR:E96807 PIR:S35228 RefSeq:NP_177899.1 UniGene:At.17771 ProteinModelPortal:P11832 SMR:P11832 IntAct:P11832 STRING:P11832 PRIDE:P11832 EnsemblPlants:AT1G77760.1 GeneID:844112 KEGG:ath:AT1G77760 TAIR:At1g77760 HOGENOM:HBG326850 InParanoid:P11832 OMA:HGAVPKA PhylomeDB:P11832 ProtClustDB:PLN02252 ArrayExpress:P11832 Genevestigator:P11832 GermOnline:AT1G77760 GO:GO:0009703 Gene3D:G3DSA:2.60.40.650 Gene3D:G3DSA:3.90.420.10 SUPFAM:SSF56524 Uniprot:P11832
Root	Isotig00474	5	74	-4.016	5.70E-18	TAIR|locus:2203221 - symbol:NIA1 "AT1G77760" species:3702 "Arabidopsis thaliana" [GO:0006809 "nitric oxide biosynthetic process" evidence=IMP] [GO:0005829 "cytosol" evidence=TAS] [GO:0009416 "response to light stimulus" evidence=IMP] [GO:0005515 "protein binding" evidence=IPI] [GO:0008940 "nitrate reductase activity" evidence=IMP] [GO:0042128 "nitrate assimilation" evidence=IMP] InterPro:IPR000572 InterPro:IPR001199 InterPro:IPR001433 InterPro:IPR001709 InterPro:IPR001834 InterPro:IPR005066 InterPro:IPR008335 InterPro:IPR012137 InterPro:IPR017927 InterPro:IPR017938 InterPro:IPR018506 InterPro:IPR022407 Pfam:PF00173 Pfam:PF00174 Pfam:PF00175 Pfam:PF03404 PIRSF:PIRSF000233 PRINTS:PR00363 PRINTS:PR00371 PRINTS:PR00406 PRINTS:PR00407 PROSITE:PS00191 PROSITE:PS00559 PROSITE:PS50255 PROSITE:PS51384 InterPro:IPR008333 Pfam:PF00970 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0005515 GO:GO:0009635 GO:GO:0009055 GO:GO:0050660 GO:GO:0020037 GO:GO:0009416 Gene3D:G3DSA:3.10.120.10 SUPFAM:SSF55856 InterPro:IPR014756 SUPFAM:SSF81296 GO:GO:0043546 eggNOG:COG0543 SUPFAM:SSF63380 GO:GO:0006809 GO:GO:0042128 EMBL:AC012193 GO:GO:0030151 KO:K00360 EMBL:Z19050 EMBL:AY090950 EMBL:AF424624 EMBL:BT000989 EMBL:X13434 EMBL:X13436 IPI:IPI00518959 PIR:E96807 PIR:S35228 RefSeq:NP_177899.1 UniGene:At.17771 ProteinModelPortal:P11832 SMR:P11832 IntAct:P11832 STRING:P11832 PRIDE:P11832 EnsemblPlants:AT1G77760.1 GeneID:844112 KEGG:ath:AT1G77760 TAIR:At1g77760 HOGENOM:HBG326850 InParanoid:P11832 OMA:HGAVPKA PhylomeDB:P11832 ProtClustDB:PLN02252 ArrayExpress:P11832 Genevestigator:P11832 GermOnline:AT1G77760 GO:GO:0009703 Gene3D:G3DSA:2.60.40.650 Gene3D:G3DSA:3.90.420.10 SUPFAM:SSF56524 Uniprot:P11832
Root	Isotig00475	4	75	-4.358	5.91E-19	TAIR|locus:2203221 - symbol:NIA1 "AT1G77760" species:3702 "Arabidopsis thaliana" [GO:0006809 "nitric oxide biosynthetic process" evidence=IMP] [GO:0005829 "cytosol" evidence=TAS] [GO:0009416 "response to light stimulus" evidence=IMP] [GO:0005515 "protein binding" evidence=IPI] [GO:0008940 "nitrate reductase activity" evidence=IMP] [GO:0042128 "nitrate assimilation" evidence=IMP] InterPro:IPR000572 InterPro:IPR001199 InterPro:IPR001433 InterPro:IPR001709 InterPro:IPR001834 InterPro:IPR005066 InterPro:IPR008335 InterPro:IPR012137 InterPro:IPR017927 InterPro:IPR017938 InterPro:IPR018506 InterPro:IPR022407 Pfam:PF00173 Pfam:PF00174 Pfam:PF00175 Pfam:PF03404 PIRSF:PIRSF000233 PRINTS:PR00363 PRINTS:PR00371 PRINTS:PR00406 PRINTS:PR00407 PROSITE:PS00191 PROSITE:PS00559 PROSITE:PS50255 PROSITE:PS51384 InterPro:IPR008333 Pfam:PF00970 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0005515 GO:GO:0009635 GO:GO:0009055 GO:GO:0050660 GO:GO:0020037 GO:GO:0009416 Gene3D:G3DSA:3.10.120.10 SUPFAM:SSF55856 InterPro:IPR014756 SUPFAM:SSF81296 GO:GO:0043546 eggNOG:COG0543 SUPFAM:SSF63380 GO:GO:0006809 GO:GO:0042128 EMBL:AC012193 GO:GO:0030151 KO:K00360 EMBL:Z19050 EMBL:AY090950 EMBL:AF424624 EMBL:BT000989 EMBL:X13434 EMBL:X13436 IPI:IPI00518959 PIR:E96807 PIR:S35228 RefSeq:NP_177899.1 UniGene:At.17771 ProteinModelPortal:P11832 SMR:P11832 IntAct:P11832 STRING:P11832 PRIDE:P11832 EnsemblPlants:AT1G77760.1 GeneID:844112 KEGG:ath:AT1G77760 TAIR:At1g77760 HOGENOM:HBG326850 InParanoid:P11832 OMA:HGAVPKA PhylomeDB:P11832 ProtClustDB:PLN02252 ArrayExpress:P11832 Genevestigator:P11832 GermOnline:AT1G77760 GO:GO:0009703 Gene3D:G3DSA:2.60.40.650 Gene3D:G3DSA:3.90.420.10 SUPFAM:SSF56524 Uniprot:P11832
Root	Isotig00476	5	74	-4.016	5.70E-18	TAIR|locus:2203221 - symbol:NIA1 "AT1G77760" species:3702 "Arabidopsis thaliana" [GO:0006809 "nitric oxide biosynthetic process" evidence=IMP] [GO:0005829 "cytosol" evidence=TAS] [GO:0009416 "response to light stimulus" evidence=IMP] [GO:0005515 "protein binding" evidence=IPI] [GO:0008940 "nitrate reductase activity" evidence=IMP] [GO:0042128 "nitrate assimilation" evidence=IMP] InterPro:IPR000572 InterPro:IPR001199 InterPro:IPR001433 InterPro:IPR001709 InterPro:IPR001834 InterPro:IPR005066 InterPro:IPR008335 InterPro:IPR012137 InterPro:IPR017927 InterPro:IPR017938 InterPro:IPR018506 InterPro:IPR022407 Pfam:PF00173 Pfam:PF00174 Pfam:PF00175 Pfam:PF03404 PIRSF:PIRSF000233 PRINTS:PR00363

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						PRINTS:PR00371 PRINTS:PR00406 PRINTS:PR00407 PROSITE:PS00191 PROSITE:PS00559 PROSITE:PS50255 PROSITE:PS51384 InterPro:IPR008333 Pfam:PF00970 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0005515 GO:GO:0009635 GO:GO:0009055 GO:GO:0050660 GO:GO:0020037 GO:GO:0009416 Gene3D:G3DSA:3.10.120.10 SUPFAM:SSF55856 InterPro:IPR014756 SUPFAM:SSF81296 GO:GO:0043546 eggNOG:COG0543 SUPFAM:SSF63380 GO:GO:0006809 GO:GO:0042128 EMBL:AC012193 GO:GO:0030151 KO:K00360 EMBL:Z19050 EMBL:AY090950 EMBL:AF424624 EMBL:BT000989 EMBL:X13434 EMBL:X13436 IPI:IPI00518959 PIR:E96807 PIR:S35228 RefSeq:NP_177899.1 UniGene:At.17771 ProteinModelPortal:P11832 SMR:P11832 IntAct:P11832 STRING:P11832 PRIDE:P11832 EnsemblPlants:AT1G77760.1 GeneID:844112 KEGG:ath:AT1G77760 TAIR:At1g77760 HOGENOM:HBG326850 InParanoid:P11832 OMA:HGAVPKA PhylomeDB:P11832 ProtClustDB:PLN02252 ArrayExpress:P11832 Genevestigator:P11832 GermOnline:AT1G77760 GO:GO:0009703 Gene3D:G3DSA:2.60.40.650 Gene3D:G3DSA:3.90.420.10 SUPFAM:SSF56524 Uniprot:P11832
Root	Isotig00477	5	74	-4.016	5.70E-18	TAIR|locus:2203221 - symbol:NIA1 "AT1G77760" species:3702 "Arabidopsis thaliana" [GO:0006809 "nitric oxide biosynthetic process" evidence=IMP] [GO:0005829 "cytosol" evidence=TAS] [GO:0009416 "response to light stimulus" evidence=IMP] [GO:0005515 "protein binding" evidence=IPI] [GO:0008940 "nitrate reductase activity" evidence=IMP] [GO:0042128 "nitrate assimilation" evidence=IMP] InterPro:IPR000572 InterPro:IPR001199 InterPro:IPR001433 InterPro:IPR001709 InterPro:IPR001834 InterPro:IPR005066 InterPro:IPR008335 InterPro:IPR012137 InterPro:IPR017927 InterPro:IPR017938 InterPro:IPR018506 InterPro:IPR022407 Pfam:PF00173 Pfam:PF00174 Pfam:PF00175 Pfam:PF03404 PIRSF:PIRSF000233 PRINTS:PR00363 PRINTS:PR00371 PRINTS:PR00406 PRINTS:PR00407 PROSITE:PS00191 PROSITE:PS00559 PROSITE:PS50255 PROSITE:PS51384 InterPro:IPR008333 Pfam:PF00970 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0005515 GO:GO:0009635 GO:GO:0009055 GO:GO:0050660 GO:GO:0020037 GO:GO:0009416 Gene3D:G3DSA:3.10.120.10 SUPFAM:SSF55856 InterPro:IPR014756 SUPFAM:SSF81296 GO:GO:0043546 eggNOG:COG0543 SUPFAM:SSF63380 GO:GO:0006809 GO:GO:0042128 EMBL:AC012193 GO:GO:0030151 KO:K00360 EMBL:Z19050 EMBL:AY090950 EMBL:AF424624 EMBL:BT000989 EMBL:X13434 EMBL:X13436 IPI:IPI00518959 PIR:E96807 PIR:S35228 RefSeq:NP_177899.1 UniGene:At.17771 ProteinModelPortal:P11832 SMR:P11832 IntAct:P11832 STRING:P11832 PRIDE:P11832 EnsemblPlants:AT1G77760.1 GeneID:844112 KEGG:ath:AT1G77760 TAIR:At1g77760 HOGENOM:HBG326850 InParanoid:P11832 OMA:HGAVPKA PhylomeDB:P11832 ProtClustDB:PLN02252 ArrayExpress:P11832 Genevestigator:P11832 GermOnline:AT1G77760 GO:GO:0009703 Gene3D:G3DSA:2.60.40.650 Gene3D:G3DSA:3.90.420.10 SUPFAM:SSF56524 Uniprot:P11832
Root	Isotig00478	4	75	-4.358	5.91E-19	TAIR|locus:2203221 - symbol:NIA1 "AT1G77760" species:3702 "Arabidopsis thaliana" [GO:0006809 "nitric oxide biosynthetic process" evidence=IMP] [GO:0005829 "cytosol" evidence=TAS] [GO:0009416 "response to light stimulus" evidence=IMP] [GO:0005515 "protein binding" evidence=IPI] [GO:0008940 "nitrate reductase activity" evidence=IMP] [GO:0042128 "nitrate assimilation" evidence=IMP] InterPro:IPR000572 InterPro:IPR001199 InterPro:IPR001433 InterPro:IPR001709 InterPro:IPR001834 InterPro:IPR005066 InterPro:IPR008335 InterPro:IPR012137 InterPro:IPR017927 InterPro:IPR017938 InterPro:IPR018506 InterPro:IPR022407 Pfam:PF00173 Pfam:PF00174 Pfam:PF00175 Pfam:PF03404 PIRSF:PIRSF000233 PRINTS:PR00363 PRINTS:PR00371 PRINTS:PR00406 PRINTS:PR00407 PROSITE:PS00191 PROSITE:PS00559 PROSITE:PS50255 PROSITE:PS51384 InterPro:IPR008333 Pfam:PF00970 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0005515 GO:GO:0009635 GO:GO:0009055 GO:GO:0050660 GO:GO:0020037 GO:GO:0009416 Gene3D:G3DSA:3.10.120.10 SUPFAM:SSF55856 InterPro:IPR014756 SUPFAM:SSF81296 GO:GO:0043546 eggNOG:COG0543 SUPFAM:SSF63380 GO:GO:0006809 GO:GO:0042128 EMBL:AC012193 GO:GO:0030151 KO:K00360 EMBL:Z19050 EMBL:AY090950 EMBL:AF424624 EMBL:BT000989 EMBL:X13434 EMBL:X13436 IPI:IPI00518959 PIR:E96807 PIR:S35228 RefSeq:NP_177899.1 UniGene:At.17771 ProteinModelPortal:P11832 SMR:P11832 IntAct:P11832 STRING:P11832 PRIDE:P11832 EnsemblPlants:AT1G77760.1 GeneID:844112 KEGG:ath:AT1G77760 TAIR:At1g77760 HOGENOM:HBG326850 InParanoid:P11832 OMA:HGAVPKA PhylomeDB:P11832 ProtClustDB:PLN02252 ArrayExpress:P11832 Genevestigator:P11832 GermOnline:AT1G77760 GO:GO:0009703 Gene3D:G3DSA:2.60.40.650 Gene3D:G3DSA:3.90.420.10 SUPFAM:SSF56524 Uniprot:P11832
Root	Isotig00479	5	72	-3.977	1.98E-17	TAIR|locus:2203221 - symbol:NIA1 "AT1G77760" species:3702 "Arabidopsis thaliana" [GO:0006809 "nitric oxide biosynthetic process" evidence=IMP] [GO:0005829 "cytosol" evidence=TAS] [GO:0009416 "response to light

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						stimulus" evidence=IMP] [GO:0005515 "protein binding" evidence=IPI] [GO:0008940 "nitrate reductase activity" evidence=IMP] [GO:0042128 "nitrate assimilation" evidence=IMP] InterPro:IPR000572 InterPro:IPR001199 InterPro:IPR001433 InterPro:IPR001709 InterPro:IPR001834 InterPro:IPR005066 InterPro:IPR008335 InterPro:IPR012137 InterPro:IPR017927 InterPro:IPR017938 InterPro:IPR018506 InterPro:IPR022407 Pfam:PF00173 Pfam:PF00174 Pfam:PF00175 Pfam:PF03404 PIRSF:PIRSF000233 PRINTS:PR00363 PRINTS:PR00371 PRINTS:PR00406 PRINTS:PR00407 PROSITE:PS00191 PROSITE:PS00559 PROSITE:PS50255 PROSITE:PS51384 InterPro:IPR008333 Pfam:PF00970 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0005515 GO:GO:0009635 GO:GO:0009055 GO:GO:0050660 GO:GO:0020037 GO:GO:0009416 Gene3D:G3DSA:3.10.120.10 SUPFAM:SSF55856 InterPro:IPR014756 SUPFAM:SSF81296 GO:GO:0043546 eggNOG:COG0543 SUPFAM:SSF63380 GO:GO:0006809 GO:GO:0042128 EMBL:AC012193 GO:GO:0030151 KO:K00360 EMBL:Z19050 EMBL:AY090950 EMBL:AF424624 EMBL:BT000989 EMBL:X13434 EMBL:X13436 IPI:IPI00518959 PIR:E96807 PIR:S35228 RefSeq:NP_177899.1 UniGene:At.17771 ProteinModelPortal:P11832 SMR:P11832 IntAct:P11832 STRING:P11832 PRIDE:P11832 EnsemblPlants:AT1G77760.1 GeneID:844112 KEGG:ath:AT1G77760 TAIR:At1g77760 HOGENOM:HBG326850 InParanoid:P11832 OMA:HGAVPKA PhylomeDB:P11832 ProtClustDB:PLN02252 ArrayExpress:P11832 Genevestigator:P11832 GermOnline:AT1G77760 GO:GO:0009703 Gene3D:G3DSA:2.60.40.650 Gene3D:G3DSA:3.90.420.10 SUPFAM:SSF56524 Uniprot:P11832
Root	Isotig00480	5	72	-3.977	1.98E-17	TAIR|locus:2203221 - symbol:NIA1 "AT1G77760" species:3702 "Arabidopsis thaliana" [GO:0006809 "nitric oxide biosynthetic process" evidence=IMP] [GO:0005829 "cytosol" evidence=TAS] [GO:0009416 "response to light stimulus" evidence=IMP] [GO:0005515 "protein binding" evidence=IPI] [GO:0008940 "nitrate reductase activity" evidence=IMP] [GO:0042128 "nitrate assimilation" evidence=IMP] InterPro:IPR000572 InterPro:IPR001199 InterPro:IPR001433 InterPro:IPR001709 InterPro:IPR001834 InterPro:IPR005066 InterPro:IPR008335 InterPro:IPR012137 InterPro:IPR017927 InterPro:IPR017938 InterPro:IPR018506 InterPro:IPR022407 Pfam:PF00173 Pfam:PF00174 Pfam:PF00175 Pfam:PF03404 PIRSF:PIRSF000233 PRINTS:PR00363 PRINTS:PR00371 PRINTS:PR00406 PRINTS:PR00407 PROSITE:PS00191 PROSITE:PS00559 PROSITE:PS50255 PROSITE:PS51384 InterPro:IPR008333 Pfam:PF00970 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0005515 GO:GO:0009635 GO:GO:0009055 GO:GO:0050660 GO:GO:0020037 GO:GO:0009416 Gene3D:G3DSA:3.10.120.10 SUPFAM:SSF55856 InterPro:IPR014756 SUPFAM:SSF81296 GO:GO:0043546 eggNOG:COG0543 SUPFAM:SSF63380 GO:GO:0006809 GO:GO:0042128 EMBL:AC012193 GO:GO:0030151 KO:K00360 EMBL:Z19050 EMBL:AY090950 EMBL:AF424624 EMBL:BT000989 EMBL:X13434 EMBL:X13436 IPI:IPI00518959 PIR:E96807 PIR:S35228 RefSeq:NP_177899.1 UniGene:At.17771 ProteinModelPortal:P11832 SMR:P11832 IntAct:P11832 STRING:P11832 PRIDE:P11832 EnsemblPlants:AT1G77760.1 GeneID:844112 KEGG:ath:AT1G77760 TAIR:At1g77760 HOGENOM:HBG326850 InParanoid:P11832 OMA:HGAVPKA PhylomeDB:P11832 ProtClustDB:PLN02252 ArrayExpress:P11832 Genevestigator:P11832 GermOnline:AT1G77760 GO:GO:0009703 Gene3D:G3DSA:2.60.40.650 Gene3D:G3DSA:3.90.420.10 SUPFAM:SSF56524 Uniprot:P11832
Root	Isotig00481	4	73	-4.319	2.04E-18	TAIR|locus:2203221 - symbol:NIA1 "AT1G77760" species:3702 "Arabidopsis thaliana" [GO:0006809 "nitric oxide biosynthetic process" evidence=IMP] [GO:0005829 "cytosol" evidence=TAS] [GO:0009416 "response to light stimulus" evidence=IMP] [GO:0005515 "protein binding" evidence=IPI] [GO:0008940 "nitrate reductase activity" evidence=IMP] [GO:0042128 "nitrate assimilation" evidence=IMP] InterPro:IPR000572 InterPro:IPR001199 InterPro:IPR001433 InterPro:IPR001709 InterPro:IPR001834 InterPro:IPR005066 InterPro:IPR008335 InterPro:IPR012137 InterPro:IPR017927 InterPro:IPR017938 InterPro:IPR018506 InterPro:IPR022407 Pfam:PF00173 Pfam:PF00174 Pfam:PF00175 Pfam:PF03404 PIRSF:PIRSF000233 PRINTS:PR00363 PRINTS:PR00371 PRINTS:PR00406 PRINTS:PR00407 PROSITE:PS00191 PROSITE:PS00559 PROSITE:PS50255 PROSITE:PS51384 InterPro:IPR008333 Pfam:PF00970 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0005515 GO:GO:0009635 GO:GO:0009055 GO:GO:0050660 GO:GO:0020037 GO:GO:0009416 Gene3D:G3DSA:3.10.120.10 SUPFAM:SSF55856 InterPro:IPR014756 SUPFAM:SSF81296 GO:GO:0043546 eggNOG:COG0543 SUPFAM:SSF63380 GO:GO:0006809 GO:GO:0042128 EMBL:AC012193 GO:GO:0030151 KO:K00360 EMBL:Z19050 EMBL:AY090950 EMBL:AF424624 EMBL:BT000989 EMBL:X13434 EMBL:X13436 IPI:IPI00518959 PIR:E96807 PIR:S35228 RefSeq:NP_177899.1 UniGene:At.17771 ProteinModelPortal:P11832 SMR:P11832 IntAct:P11832 STRING:P11832 PRIDE:P11832 EnsemblPlants:AT1G77760.1 GeneID:844112 KEGG:ath:AT1G77760 TAIR:At1g77760 HOGENOM:HBG326850 InParanoid:P11832 OMA:HGAVPKA PhylomeDB:P11832 ProtClustDB:PLN02252

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						ArrayExpress:P11832 Genevestigator:P11832 GermOnline:AT1G77760 GO:GO:0009703 Gene3D:G3DSA:2.60.40.650 Gene3D:G3DSA:3.90.420.10 SUPFAM:SSF56524 Uniprot:P11832
Root	Isotig00482	5	72	-3.977	1.98E-17	TAIR|locus:2203221 - symbol:NIA1 "AT1G77760" species:3702 "Arabidopsis thaliana" [GO:0006809 "nitric oxide biosynthetic process" evidence=IMP] [GO:0005829 "cytosol" evidence=TAS] [GO:0009416 "response to light stimulus" evidence=IMP] [GO:0005515 "protein binding" evidence=IPI] [GO:0008940 "nitrate reductase activity" evidence=IMP] [GO:0042128 "nitrate assimilation" evidence=IMP] InterPro:IPR000572 InterPro:IPR001199 InterPro:IPR001433 InterPro:IPR001709 InterPro:IPR001834 InterPro:IPR005066 InterPro:IPR008335 InterPro:IPR012137 InterPro:IPR017927 InterPro:IPR017938 InterPro:IPR018506 InterPro:IPR022407 Pfam:PF00173 Pfam:PF00174 Pfam:PF00175 Pfam:PF03404 PIRSF:PIRSF000233 PRINTS:PR00363 PRINTS:PR00371 PRINTS:PR00406 PRINTS:PR00407 PROSITE:PS00191 PROSITE:PS00559 PROSITE:PS50255 PROSITE:PS51384 InterPro:IPR008333 Pfam:PF00970 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0005515 GO:GO:0009635 GO:GO:0009055 GO:GO:0050660 GO:GO:0020037 GO:GO:0009416 Gene3D:G3DSA:3.10.120.10 SUPFAM:SSF55856 InterPro:IPR014756 SUPFAM:SSF81296 GO:GO:0043546 eggNOG:COG0543 SUPFAM:SSF63380 GO:GO:0006809 GO:GO:0042128 EMBL:AC012193 GO:GO:0030151 KO:K00360 EMBL:Z19050 EMBL:AY090950 EMBL:AF424624 EMBL:BT000989 EMBL:X13434 EMBL:X13436 IPI:IPI00518959 PIR:E96807 PIR:S35228 RefSeq:NP_177899.1 UniGene:At.17771 ProteinModelPortal:P11832 SMR:P11832 IntAct:P11832 STRING:P11832 PRIDE:P11832 EnsemblPlants:AT1G77760.1 GeneID:844112 KEGG:ath:AT1G77760 TAIR:At1g77760 HOGENOM:HBG326850 InParanoid:P11832 OMA:HGAVPKA PhylomeDB:P11832 ProtClustDB:PLN02252 ArrayExpress:P11832 Genevestigator:P11832 GermOnline:AT1G77760 GO:GO:0009703 Gene3D:G3DSA:2.60.40.650 Gene3D:G3DSA:3.90.420.10 SUPFAM:SSF56524 Uniprot:P11832
Root	Isotig00483	5	72	-3.977	1.98E-17	TAIR|locus:2203221 - symbol:NIA1 "AT1G77760" species:3702 "Arabidopsis thaliana" [GO:0006809 "nitric oxide biosynthetic process" evidence=IMP] [GO:0005829 "cytosol" evidence=TAS] [GO:0009416 "response to light stimulus" evidence=IMP] [GO:0005515 "protein binding" evidence=IPI] [GO:0008940 "nitrate reductase activity" evidence=IMP] [GO:0042128 "nitrate assimilation" evidence=IMP] InterPro:IPR000572 InterPro:IPR001199 InterPro:IPR001433 InterPro:IPR001709 InterPro:IPR001834 InterPro:IPR005066 InterPro:IPR008335 InterPro:IPR012137 InterPro:IPR017927 InterPro:IPR017938 InterPro:IPR018506 InterPro:IPR022407 Pfam:PF00173 Pfam:PF00174 Pfam:PF00175 Pfam:PF03404 PIRSF:PIRSF000233 PRINTS:PR00363 PRINTS:PR00371 PRINTS:PR00406 PRINTS:PR00407 PROSITE:PS00191 PROSITE:PS00559 PROSITE:PS50255 PROSITE:PS51384 InterPro:IPR008333 Pfam:PF00970 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0005515 GO:GO:0009635 GO:GO:0009055 GO:GO:0050660 GO:GO:0020037 GO:GO:0009416 Gene3D:G3DSA:3.10.120.10 SUPFAM:SSF55856 InterPro:IPR014756 SUPFAM:SSF81296 GO:GO:0043546 eggNOG:COG0543 SUPFAM:SSF63380 GO:GO:0006809 GO:GO:0042128 EMBL:AC012193 GO:GO:0030151 KO:K00360 EMBL:Z19050 EMBL:AY090950 EMBL:AF424624 EMBL:BT000989 EMBL:X13434 EMBL:X13436 IPI:IPI00518959 PIR:E96807 PIR:S35228 RefSeq:NP_177899.1 UniGene:At.17771 ProteinModelPortal:P11832 SMR:P11832 IntAct:P11832 STRING:P11832 PRIDE:P11832 EnsemblPlants:AT1G77760.1 GeneID:844112 KEGG:ath:AT1G77760 TAIR:At1g77760 HOGENOM:HBG326850 InParanoid:P11832 OMA:HGAVPKA PhylomeDB:P11832 ProtClustDB:PLN02252 ArrayExpress:P11832 Genevestigator:P11832 GermOnline:AT1G77760 GO:GO:0009703 Gene3D:G3DSA:2.60.40.650 Gene3D:G3DSA:3.90.420.10 SUPFAM:SSF56524 Uniprot:P11832
Root	Isotig00484	4	73	-4.319	2.04E-18	TAIR|locus:2203221 - symbol:NIA1 "AT1G77760" species:3702 "Arabidopsis thaliana" [GO:0006809 "nitric oxide biosynthetic process" evidence=IMP] [GO:0005829 "cytosol" evidence=TAS] [GO:0009416 "response to light stimulus" evidence=IMP] [GO:0005515 "protein binding" evidence=IPI] [GO:0008940 "nitrate reductase activity" evidence=IMP] [GO:0042128 "nitrate assimilation" evidence=IMP] InterPro:IPR000572 InterPro:IPR001199 InterPro:IPR001433 InterPro:IPR001709 InterPro:IPR001834 InterPro:IPR005066 InterPro:IPR008335 InterPro:IPR012137 InterPro:IPR017927 InterPro:IPR017938 InterPro:IPR018506 InterPro:IPR022407 Pfam:PF00173 Pfam:PF00174 Pfam:PF00175 Pfam:PF03404 PIRSF:PIRSF000233 PRINTS:PR00363 PRINTS:PR00371 PRINTS:PR00406 PRINTS:PR00407 PROSITE:PS00191 PROSITE:PS00559 PROSITE:PS50255 PROSITE:PS51384 InterPro:IPR008333 Pfam:PF00970 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0005515 GO:GO:0009635 GO:GO:0009055 GO:GO:0050660 GO:GO:0020037 GO:GO:0009416 Gene3D:G3DSA:3.10.120.10 SUPFAM:SSF55856 InterPro:IPR014756 SUPFAM:SSF81296 GO:GO:0043546 eggNOG:COG0543 SUPFAM:SSF63380

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0006809 GO:GO:0042128 EMBL:AC012193 GO:GO:0030151 KO:K00360 EMBL:Z19050 EMBL:AY090950 EMBL:AF424624 EMBL:BT000989 EMBL:X13434 EMBL:X13436 IPI:IPI00518959 PIR:E96807 PIR:S35228 RefSeq:NP_177899.1 UniGene:At.17771 ProteinModelPortal:P11832 SMR:P11832 IntAct:P11832 STRING:P11832 PRIDE:P11832 EnsemblPlants:AT1G77760.1 GeneID:844112 KEGG:ath:AT1G77760 TAIR:At1g77760 HOGENOM:HBG326850 InParanoid:P11832 OMA:HGAVPKA PhylomeDB:P11832 ProtClustDB:PLN02252 ArrayExpress:P11832 Genevestigator:P11832 GermOnline:AT1G77760 GO:GO:0009703 Gene3D:G3DSA:2.60.40.650 Gene3D:G3DSA:3.90.420.10 SUPFAM:SSF56524 Uniprot:P11832
Root	Isotig00485	1	27	-4.884	4.78E-08	TAIR|locus:2203221 - symbol:NIA1 "AT1G77760" species:3702 "Arabidopsis thaliana" [GO:0006809 "nitric oxide biosynthetic process" evidence=IMP] [GO:0005829 "cytosol" evidence=TAS] [GO:0009416 "response to light stimulus" evidence=IMP] [GO:0005515 "protein binding" evidence=IPI] [GO:0008940 "nitrate reductase activity" evidence=IMP] [GO:0042128 "nitrate assimilation" evidence=IMP] InterPro:IPR000572 InterPro:IPR001199 InterPro:IPR001433 InterPro:IPR001709 InterPro:IPR001834 InterPro:IPR005066 InterPro:IPR008335 InterPro:IPR012137 InterPro:IPR017927 InterPro:IPR017938 InterPro:IPR018506 InterPro:IPR022407 Pfam:PF00173 Pfam:PF00174 Pfam:PF00175 Pfam:PF03404 PIRSF:PIRSF000233 PRINTS:PR00363 PRINTS:PR00371 PRINTS:PR00406 PRINTS:PR00407 PROSITE:PS00191 PROSITE:PS00559 PROSITE:PS50255 PROSITE:PS51384 InterPro:IPR008333 Pfam:PF00970 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0005515 GO:GO:0009635 GO:GO:0009055 GO:GO:0050660 GO:GO:0020037 GO:GO:0009416 Gene3D:G3DSA:3.10.120.10 SUPFAM:SSF55856 InterPro:IPR014756 SUPFAM:SSF81296 GO:GO:0043546 eggNOG:COG0543 SUPFAM:SSF63380 GO:GO:0006809 GO:GO:0042128 EMBL:AC012193 GO:GO:0030151 KO:K00360 EMBL:Z19050 EMBL:AY090950 EMBL:AF424624 EMBL:BT000989 EMBL:X13434 EMBL:X13436 IPI:IPI00518959 PIR:E96807 PIR:S35228 RefSeq:NP_177899.1 UniGene:At.17771 ProteinModelPortal:P11832 SMR:P11832 IntAct:P11832 STRING:P11832 PRIDE:P11832 EnsemblPlants:AT1G77760.1 GeneID:844112 KEGG:ath:AT1G77760 TAIR:At1g77760 HOGENOM:HBG326850 InParanoid:P11832 OMA:HGAVPKA PhylomeDB:P11832 ProtClustDB:PLN02252 ArrayExpress:P11832 Genevestigator:P11832 GermOnline:AT1G77760 GO:GO:0009703 Gene3D:G3DSA:2.60.40.650 Gene3D:G3DSA:3.90.420.10 SUPFAM:SSF56524 Uniprot:P11832
Root	Isotig00486	1	25	-4.773	1.66E-07	TAIR|locus:2203221 - symbol:NIA1 "AT1G77760" species:3702 "Arabidopsis thaliana" [GO:0006809 "nitric oxide biosynthetic process" evidence=IMP] [GO:0005829 "cytosol" evidence=TAS] [GO:0009416 "response to light stimulus" evidence=IMP] [GO:0005515 "protein binding" evidence=IPI] [GO:0008940 "nitrate reductase activity" evidence=IMP] [GO:0042128 "nitrate assimilation" evidence=IMP] InterPro:IPR000572 InterPro:IPR001199 InterPro:IPR001433 InterPro:IPR001709 InterPro:IPR001834 InterPro:IPR005066 InterPro:IPR008335 InterPro:IPR012137 InterPro:IPR017927 InterPro:IPR017938 InterPro:IPR018506 InterPro:IPR022407 Pfam:PF00173 Pfam:PF00174 Pfam:PF00175 Pfam:PF03404 PIRSF:PIRSF000233 PRINTS:PR00363 PRINTS:PR00371 PRINTS:PR00406 PRINTS:PR00407 PROSITE:PS00191 PROSITE:PS00559 PROSITE:PS50255 PROSITE:PS51384 InterPro:IPR008333 Pfam:PF00970 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0005515 GO:GO:0009635 GO:GO:0009055 GO:GO:0050660 GO:GO:0020037 GO:GO:0009416 Gene3D:G3DSA:3.10.120.10 SUPFAM:SSF55856 InterPro:IPR014756 SUPFAM:SSF81296 GO:GO:0043546 eggNOG:COG0543 SUPFAM:SSF63380 GO:GO:0006809 GO:GO:0042128 EMBL:AC012193 GO:GO:0030151 KO:K00360 EMBL:Z19050 EMBL:AY090950 EMBL:AF424624 EMBL:BT000989 EMBL:X13434 EMBL:X13436 IPI:IPI00518959 PIR:E96807 PIR:S35228 RefSeq:NP_177899.1 UniGene:At.17771 ProteinModelPortal:P11832 SMR:P11832 IntAct:P11832 STRING:P11832 PRIDE:P11832 EnsemblPlants:AT1G77760.1 GeneID:844112 KEGG:ath:AT1G77760 TAIR:At1g77760 HOGENOM:HBG326850 InParanoid:P11832 OMA:HGAVPKA PhylomeDB:P11832 ProtClustDB:PLN02252 ArrayExpress:P11832 Genevestigator:P11832 GermOnline:AT1G77760 GO:GO:0009703 Gene3D:G3DSA:2.60.40.650 Gene3D:G3DSA:3.90.420.10 SUPFAM:SSF56524 Uniprot:P11832
Root	Isotig00490	34	8	1.958	9.61E-05	TAIR|locus:2011656 - symbol:HMG1 "AT1G76490" species:3702 "Arabidopsis thaliana" [GO:0016126 "sterol biosynthetic process" evidence=IMP] [GO:0005777 "peroxisome" evidence=IDA] [GO:0009536 "plastid" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0005789 "endoplasmic reticulum membrane" evidence=IDA] [GO:0019287 "isopentenyl diphosphate biosynthetic process, mevalonate pathway" evidence=IDA] [GO:0042282 "hydroxymethylglutaryl-CoA reductase activity" evidence=IGI;ISS;IDA] [GO:0060964 "regulation of gene silencing by miRNA" evidence=IMP] [GO:0008299 "isoprenoid biosynthetic process" evidence=ISS;TAS] [GO:0016020 "membrane" evidence=TAS] [GO:0005783 "endoplasmic reticulum" evidence=IDA]

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						InterPro:IPR002202 InterPro:IPR004554 InterPro:IPR009023 InterPro:IPR009029 InterPro:IPR023074 InterPro:IPR023076 InterPro:IPR023282 Pfam:PF00368 PRINTS:PR00071 PROSITE:PS00066 PROSITE:PS00318 PROSITE:PS01192 PROSITE:PS50065 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005515 GO:GO:0005789 GO:GO:0050661 GO:GO:0016126 GO:GO:0015936 EMBL:AC012394 EMBL:AC015450 GO:GO:0019287 EMBL:X15032 EMBL:J04537 EMBL:L19261 EMBL:AY488113 EMBL:AF385690 EMBL:BT000703 EMBL:BT010468 IPI:IPI00545411 IPI:IPI01018461 PIR:A32107 RefSeq:NP_177775.2 UniGene:At.22772 ProteinModelPortal:P14891 SMR:P14891 STRING:P14891 PRIDE:P14891 GeneID:843982 KEGG:ath:AT1G76490 TAIR:At1g76490 eggNOG:COG1257 InParanoid:P14891 KO:K00021 PhylomeDB:P14891 ProtClustDB:CLSN2683887 BioCyc:ARA:AT1G76490-MONOMER BioCyc:MetaCyc:AT1G76490-MONOMER Genevestigator:P14891 GO:GO:0004420 GO:GO:0042282 Gene3D:G3DSA:3.30.70.420 Gene3D:G3DSA:3.90.770.10 Gene3D:G3DSA:1.10.3270.10 PANTHER:PTHR10572 SUPFAM:SSF55035 SUPFAM:SSF56542 TIGRFAMs:TIGR00533 Uniprot:P14891
Root	Isotig00491	40	11	1.734	9.88E-05	TAIR|locus:2011656 - symbol:HMG1 "AT1G76490" species:3702 "Arabidopsis thaliana" [GO:0016126 "sterol biosynthetic process" evidence=IMP] [GO:0005777 "peroxisome" evidence=IDA] [GO:0009536 "plastid" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0005789 "endoplasmic reticulum membrane" evidence=IDA] [GO:0019287 "isopentenyl diphosphate biosynthetic process, mevalonate pathway" evidence=IDA] [GO:0042282 "hydroxymethylglutaryl-CoA reductase activity" evidence=IGI;ISS;IDA] [GO:0060964 "regulation of gene silencing by miRNA" evidence=IMP] [GO:0008299 "isoprenoid biosynthetic process" evidence=ISS;TAS] [GO:0016020 "membrane" evidence=TAS] [GO:0005783 "endoplasmic reticulum" evidence=IDA] InterPro:IPR002202 InterPro:IPR004554 InterPro:IPR009023 InterPro:IPR009029 InterPro:IPR023074 InterPro:IPR023076 InterPro:IPR023282 Pfam:PF00368 PRINTS:PR00071 PROSITE:PS00066 PROSITE:PS00318 PROSITE:PS01192 PROSITE:PS50065 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005515 GO:GO:0005789 GO:GO:0050661 GO:GO:0016126 GO:GO:0015936 EMBL:AC012394 EMBL:AC015450 GO:GO:0019287 EMBL:X15032 EMBL:J04537 EMBL:L19261 EMBL:AY488113 EMBL:AF385690 EMBL:BT000703 EMBL:BT010468 IPI:IPI00545411 IPI:IPI01018461 PIR:A32107 RefSeq:NP_177775.2 UniGene:At.22772 ProteinModelPortal:P14891 SMR:P14891 STRING:P14891 PRIDE:P14891 GeneID:843982 KEGG:ath:AT1G76490 TAIR:At1g76490 eggNOG:COG1257 InParanoid:P14891 KO:K00021 PhylomeDB:P14891 ProtClustDB:CLSN2683887 BioCyc:ARA:AT1G76490-MONOMER BioCyc:MetaCyc:AT1G76490-MONOMER Genevestigator:P14891 GO:GO:0004420 GO:GO:0042282 Gene3D:G3DSA:3.30.70.420 Gene3D:G3DSA:3.90.770.10 Gene3D:G3DSA:1.10.3270.10 PANTHER:PTHR10572 SUPFAM:SSF55035 SUPFAM:SSF56542 TIGRFAMs:TIGR00533 Uniprot:P14891
Root	Isotig00493	40	11	1.734	9.88E-05	TAIR|locus:2011656 - symbol:HMG1 "AT1G76490" species:3702 "Arabidopsis thaliana" [GO:0016126 "sterol biosynthetic process" evidence=IMP] [GO:0005777 "peroxisome" evidence=IDA] [GO:0009536 "plastid" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0005789 "endoplasmic reticulum membrane" evidence=IDA] [GO:0019287 "isopentenyl diphosphate biosynthetic process, mevalonate pathway" evidence=IDA] [GO:0042282 "hydroxymethylglutaryl-CoA reductase activity" evidence=IGI;ISS;IDA] [GO:0060964 "regulation of gene silencing by miRNA" evidence=IMP] [GO:0008299 "isoprenoid biosynthetic process" evidence=ISS;TAS] [GO:0016020 "membrane" evidence=TAS] [GO:0005783 "endoplasmic reticulum" evidence=IDA] InterPro:IPR002202 InterPro:IPR004554 InterPro:IPR009023 InterPro:IPR009029 InterPro:IPR023074 InterPro:IPR023076 InterPro:IPR023282 Pfam:PF00368 PRINTS:PR00071 PROSITE:PS00066 PROSITE:PS00318 PROSITE:PS01192 PROSITE:PS50065 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005515 GO:GO:0005789 GO:GO:0050661 GO:GO:0016126 GO:GO:0015936 EMBL:AC012394 EMBL:AC015450 GO:GO:0019287 EMBL:X15032 EMBL:J04537 EMBL:L19261 EMBL:AY488113 EMBL:AF385690 EMBL:BT000703 EMBL:BT010468 IPI:IPI00545411 IPI:IPI01018461 PIR:A32107 RefSeq:NP_177775.2 UniGene:At.22772 ProteinModelPortal:P14891 SMR:P14891 STRING:P14891 PRIDE:P14891 GeneID:843982 KEGG:ath:AT1G76490 TAIR:At1g76490 eggNOG:COG1257 InParanoid:P14891 KO:K00021 PhylomeDB:P14891 ProtClustDB:CLSN2683887 BioCyc:ARA:AT1G76490-MONOMER BioCyc:MetaCyc:AT1G76490-MONOMER Genevestigator:P14891 GO:GO:0004420 GO:GO:0042282 Gene3D:G3DSA:3.30.70.420 Gene3D:G3DSA:3.90.770.10 Gene3D:G3DSA:1.10.3270.10 PANTHER:PTHR10572 SUPFAM:SSF55035 SUPFAM:SSF56542 TIGRFAMs:TIGR00533 Uniprot:P14891
Root	Isotig00494	33	7	2.108	5.57E-05	TAIR|locus:2011656 - symbol:HMG1 "AT1G76490" species:3702 "Arabidopsis thaliana" [GO:0016126 "sterol biosynthetic process" evidence=IMP] [GO:0005777 "peroxisome" evidence=IDA] [GO:0009536 "plastid"

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0005789 "endoplasmic reticulum membrane" evidence=IDA] [GO:0019287 "isopentenyl diphosphate biosynthetic process, mevalonate pathway" evidence=IDA] [GO:0042282 "hydroxymethylglutaryl-CoA reductase activity" evidence=IGI;ISS;IDA] [GO:0060964 "regulation of gene silencing by miRNA" evidence=IMP] [GO:0008299 "isoprenoid biosynthetic process" evidence=ISS;TAS] [GO:0016020 "membrane" evidence=TAS] [GO:0005783 "endoplasmic reticulum" evidence=IDA] InterPro:IPR002202 InterPro:IPR004554 InterPro:IPR009023 InterPro:IPR009029 InterPro:IPR023074 InterPro:IPR023076 InterPro:IPR023282 Pfam:PF00368 PRINTS:PR00071 PROSITE:PS00066 PROSITE:PS00318 PROSITE:PS01192 PROSITE:PS50065 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005515 GO:GO:0005789 GO:GO:0050661 GO:GO:0016126 GO:GO:0015936 EMBL:AC012394 EMBL:AC015450 GO:GO:0019287 EMBL:X15032 EMBL:J04537 EMBL:L19261 EMBL:AY488113 EMBL:AF385690 EMBL:BT000703 EMBL:BT010468 IPI:IPI00545411 IPI:IPI01018461 PIR:A32107 RefSeq:NP_177775.2 UniGene:At.22772 ProteinModelPortal:P14891 SMR:P14891 STRING:P14891 PRIDE:P14891 GeneID:843982 KEGG:ath:AT1G76490 TAIR:At1g76490 eggNOG:COG1257 InParanoid:P14891 KO:K00021 PhylomeDB:P14891 ProtClustDB:CLSN2683887 BioCyc:ARA:AT1G76490-MONOMER BioCyc:MetaCyc:AT1G76490-MONOMER Genevestigator:P14891 GO:GO:0004420 GO:GO:0042282 Gene3D:G3DSA:3.30.70.420 Gene3D:G3DSA:3.90.770.10 Gene3D:G3DSA:1.10.3270.10 PANTHER:PTHR10572 SUPFAM:SSF55035 SUPFAM:SSF56542 TIGRFAMs:TIGR00533 Uniprot:P14891
Root	Isotig00495	39	10	1.835	6.39E-05	TAIR|locus:2011656 - symbol:HMG1 "AT1G76490" species:3702 "Arabidopsis thaliana" [GO:0016126 "sterol biosynthetic process" evidence=IMP] [GO:0005777 "peroxisome" evidence=IDA] [GO:0009536 "plastid" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0005789 "endoplasmic reticulum membrane" evidence=IDA] [GO:0019287 "isopentenyl diphosphate biosynthetic process, mevalonate pathway" evidence=IDA] [GO:0042282 "hydroxymethylglutaryl-CoA reductase activity" evidence=IGI;ISS;IDA] [GO:0060964 "regulation of gene silencing by miRNA" evidence=IMP] [GO:0008299 "isoprenoid biosynthetic process" evidence=ISS;TAS] [GO:0016020 "membrane" evidence=TAS] [GO:0005783 "endoplasmic reticulum" evidence=IDA] InterPro:IPR002202 InterPro:IPR004554 InterPro:IPR009023 InterPro:IPR009029 InterPro:IPR023074 InterPro:IPR023076 InterPro:IPR023282 Pfam:PF00368 PRINTS:PR00071 PROSITE:PS00066 PROSITE:PS00318 PROSITE:PS01192 PROSITE:PS50065 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005515 GO:GO:0005789 GO:GO:0050661 GO:GO:0016126 GO:GO:0015936 EMBL:AC012394 EMBL:AC015450 GO:GO:0019287 EMBL:X15032 EMBL:J04537 EMBL:L19261 EMBL:AY488113 EMBL:AF385690 EMBL:BT000703 EMBL:BT010468 IPI:IPI00545411 IPI:IPI01018461 PIR:A32107 RefSeq:NP_177775.2 UniGene:At.22772 ProteinModelPortal:P14891 SMR:P14891 STRING:P14891 PRIDE:P14891 GeneID:843982 KEGG:ath:AT1G76490 TAIR:At1g76490 eggNOG:COG1257 InParanoid:P14891 KO:K00021 PhylomeDB:P14891 ProtClustDB:CLSN2683887 BioCyc:ARA:AT1G76490-MONOMER BioCyc:MetaCyc:AT1G76490-MONOMER Genevestigator:P14891 GO:GO:0004420 GO:GO:0042282 Gene3D:G3DSA:3.30.70.420 Gene3D:G3DSA:3.90.770.10 Gene3D:G3DSA:1.10.3270.10 PANTHER:PTHR10572 SUPFAM:SSF55035 SUPFAM:SSF56542 TIGRFAMs:TIGR00533 Uniprot:P14891
Root	Isotig00496	39	10	1.835	6.39E-05	TAIR|locus:2011656 - symbol:HMG1 "AT1G76490" species:3702 "Arabidopsis thaliana" [GO:0016126 "sterol biosynthetic process" evidence=IMP] [GO:0005777 "peroxisome" evidence=IDA] [GO:0009536 "plastid" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0005789 "endoplasmic reticulum membrane" evidence=IDA] [GO:0019287 "isopentenyl diphosphate biosynthetic process, mevalonate pathway" evidence=IDA] [GO:0042282 "hydroxymethylglutaryl-CoA reductase activity" evidence=IGI;ISS;IDA] [GO:0060964 "regulation of gene silencing by miRNA" evidence=IMP] [GO:0008299 "isoprenoid biosynthetic process" evidence=ISS;TAS] [GO:0016020 "membrane" evidence=TAS] [GO:0005783 "endoplasmic reticulum" evidence=IDA] InterPro:IPR002202 InterPro:IPR004554 InterPro:IPR009023 InterPro:IPR009029 InterPro:IPR023074 InterPro:IPR023076 InterPro:IPR023282 Pfam:PF00368 PRINTS:PR00071 PROSITE:PS00066 PROSITE:PS00318 PROSITE:PS01192 PROSITE:PS50065 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005515 GO:GO:0005789 GO:GO:0050661 GO:GO:0016126 GO:GO:0015936 EMBL:AC012394 EMBL:AC015450 GO:GO:0019287 EMBL:X15032 EMBL:J04537 EMBL:L19261 EMBL:AY488113 EMBL:AF385690 EMBL:BT000703 EMBL:BT010468 IPI:IPI00545411 IPI:IPI01018461 PIR:A32107 RefSeq:NP_177775.2 UniGene:At.22772 ProteinModelPortal:P14891 SMR:P14891 STRING:P14891 PRIDE:P14891 GeneID:843982 KEGG:ath:AT1G76490 TAIR:At1g76490 eggNOG:COG1257 InParanoid:P14891 KO:K00021 PhylomeDB:P14891 ProtClustDB:CLSN2683887 BioCyc:ARA:AT1G76490-MONOMER BioCyc:MetaCyc:AT1G76490-MONOMER Genevestigator:P14891 GO:GO:0004420 GO:GO:0042282 Gene3D:G3DSA:3.30.70.420

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						Gene3D:G3DSA:3.90.770.10 Gene3D:G3DSA:1.10.3270.10 PANTHER:PTHR10572 SUPFAM:SSF55035 SUPFAM:SSF56542 TIGRFAMs:TIGR00533 Uniprot:P14891
Root	Isotig00520	19	3	2.534	0.000639389	No hit
Root	Isotig00521	16	2	2.871	0.000812389	No hit
Root	Isotig00522	19	2	3.119	0.000146225	No hit
Root	Isotig00524	19	3	2.534	0.000639389	No hit
Root	Isotig00526	16	2	2.871	0.000812389	No hit
Root	Isotig00527	19	2	3.119	0.000146225	No hit
Root	Isotig00529	18	2	3.041	0.000259481	No hit
Root	Isotig00530	17	2	2.958	0.000459627	No hit
Root	Isotig00532	15	1	3.778	0.000266457	No hit
Root	Isotig00533	18	1	4.041	4.47E-05	No hit
Root	Isotig00534	15	1	3.778	0.000266457	No hit
Root	Isotig00537	48	5	3.134	1.46E-09	TAIR|locus:2027549 - symbol:GolS2 "AT1G56600" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0016051 "carbohydrate biosynthetic process" evidence=ISS] [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0016758 "transferase activity, transferring hexosyl groups" evidence=ISS] [GO:0006012 "galactose metabolic process" evidence=IDA] [GO:0006979 "response to oxidative stress" evidence=IEP] [GO:0009409 "response to cold" evidence=IMP] [GO:0009651 "response to salt stress" evidence=IMP] [GO:0047216 "inositol 3-alpha-galactosyltransferase activity" evidence=IDA] [GO:0009414 "response to water deprivation" evidence=IEP] InterPro:IPR002495 Pfam:PF01501 EMBL:CP002684 GO:GO:0006979 GO:GO:0009409 GO:GO:0009651 GO:GO:0009414 GO:GO:0006012 EMBL:AC009323 CAZy:GT8 OMA:DSQDAAN ProtClustDB:PLN00176 GO:GO:0047216 EMBL:AY050410 EMBL:AY058238 EMBL:AB062849 IPI:IPI00517274 PIR:G96607 RefSeq:NP_176053.1 UniGene:At.19795 ProteinModelPortal:Q9FXB2 SMR:Q9FXB2 STRING:Q9FXB2 PRIDE:Q9FXB2 EnsemblPlants:AT1G56600.1 GeneID:842114 KEGG:ath:AT1G56600 TAIR:At1g56600 InParanoid:Q9FXB2 PhylomeDB:Q9FXB2 Genevestigator:Q9FXB2 Uniprot:Q9FXB2
Root	Isotig00538	47	4	3.426	4.96E-10	TAIR|locus:2027549 - symbol:GolS2 "AT1G56600" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0016051 "carbohydrate biosynthetic process" evidence=ISS] [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0016758 "transferase activity, transferring hexosyl groups" evidence=ISS] [GO:0006012 "galactose metabolic process" evidence=IDA] [GO:0006979 "response to oxidative stress" evidence=IEP] [GO:0009409 "response to cold" evidence=IMP] [GO:0009651 "response to salt stress" evidence=IMP] [GO:0047216 "inositol 3-alpha-galactosyltransferase activity" evidence=IDA] [GO:0009414 "response to water deprivation" evidence=IEP] InterPro:IPR002495 Pfam:PF01501 EMBL:CP002684 GO:GO:0006979 GO:GO:0009409 GO:GO:0009651 GO:GO:0009414 GO:GO:0006012 EMBL:AC009323 CAZy:GT8 OMA:DSQDAAN ProtClustDB:PLN00176 GO:GO:0047216 EMBL:AY050410 EMBL:AY058238 EMBL:AB062849 IPI:IPI00517274 PIR:G96607 RefSeq:NP_176053.1 UniGene:At.19795 ProteinModelPortal:Q9FXB2 SMR:Q9FXB2 STRING:Q9FXB2 PRIDE:Q9FXB2 EnsemblPlants:AT1G56600.1 GeneID:842114 KEGG:ath:AT1G56600 TAIR:At1g56600 InParanoid:Q9FXB2 PhylomeDB:Q9FXB2 Genevestigator:Q9FXB2 Uniprot:Q9FXB2
Root	Isotig00539	46	4	3.395	8.74E-10	TAIR|locus:2027549 - symbol:GolS2 "AT1G56600" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0016051 "carbohydrate biosynthetic process" evidence=ISS] [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0016758 "transferase activity, transferring hexosyl groups" evidence=ISS] [GO:0006012 "galactose metabolic process" evidence=IDA] [GO:0006979 "response to oxidative stress" evidence=IEP] [GO:0009409 "response to cold" evidence=IMP] [GO:0009651 "response to salt stress" evidence=IMP] [GO:0047216 "inositol 3-alpha-galactosyltransferase activity" evidence=IDA] [GO:0009414 "response to water deprivation" evidence=IEP] InterPro:IPR002495 Pfam:PF01501 EMBL:CP002684 GO:GO:0006979 GO:GO:0009409 GO:GO:0009651 GO:GO:0009414 GO:GO:0006012 EMBL:AC009323 CAZy:GT8 OMA:DSQDAAN ProtClustDB:PLN00176 GO:GO:0047216 EMBL:AY050410 EMBL:AY058238 EMBL:AB062849 IPI:IPI00517274 PIR:G96607 RefSeq:NP_176053.1 UniGene:At.19795 ProteinModelPortal:Q9FXB2 SMR:Q9FXB2 STRING:Q9FXB2 PRIDE:Q9FXB2 EnsemblPlants:AT1G56600.1 GeneID:842114 KEGG:ath:AT1G56600 TAIR:At1g56600 InParanoid:Q9FXB2 PhylomeDB:Q9FXB2 Genevestigator:Q9FXB2 Uniprot:Q9FXB2

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig00540	47	4	3.426	4.96E-10	TAIR|locus:2027549 - symbol:GolS2 "AT1G56600" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0016051 "carbohydrate biosynthetic process" evidence=ISS] [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0016758 "transferase activity, transferring hexosyl groups" evidence=ISS] [GO:0006012 "galactose metabolic process" evidence=IDA] [GO:0006979 "response to oxidative stress" evidence=IEP] [GO:0009409 "response to cold" evidence=IMP] [GO:0009651 "response to salt stress" evidence=IMP] [GO:0047216 "inositol 3-alpha-galactosyltransferase activity" evidence=IDA] [GO:0009414 "response to water deprivation" evidence=IEP] InterPro:IPR002495 Pfam:PF01501 EMBL:CP002684 GO:GO:0006979 GO:GO:0009409 GO:GO:0009651 GO:GO:0009414 GO:GO:0006012 EMBL:AC009323 CAZy:GT8 OMA:DSQDAAN ProtClustDB:PLN00176 GO:GO:0047216 EMBL:AY050410 EMBL:AY058238 EMBL:AB062849 IPI:IPI00517274 PIR:G96607 RefSeq:NP_176053.1 UniGene:At.19795 ProteinModelPortal:Q9FXB2 SMR:Q9FXB2 STRING:Q9FXB2 PRIDE:Q9FXB2 EnsemblPlants:AT1G56600.1 GeneID:842114 KEGG:ath:AT1G56600 TAIR:At1g56600 InParanoid:Q9FXB2 PhylomeDB:Q9FXB2 Genevestigator:Q9FXB2 Uniprot:Q9FXB2
Root	Isotig00541	46	4	3.395	8.74E-10	TAIR|locus:2027549 - symbol:GolS2 "AT1G56600" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0016051 "carbohydrate biosynthetic process" evidence=ISS] [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0016758 "transferase activity, transferring hexosyl groups" evidence=ISS] [GO:0006012 "galactose metabolic process" evidence=IDA] [GO:0006979 "response to oxidative stress" evidence=IEP] [GO:0009409 "response to cold" evidence=IMP] [GO:0009651 "response to salt stress" evidence=IMP] [GO:0047216 "inositol 3-alpha-galactosyltransferase activity" evidence=IDA] [GO:0009414 "response to water deprivation" evidence=IEP] InterPro:IPR002495 Pfam:PF01501 EMBL:CP002684 GO:GO:0006979 GO:GO:0009409 GO:GO:0009651 GO:GO:0009414 GO:GO:0006012 EMBL:AC009323 CAZy:GT8 OMA:DSQDAAN ProtClustDB:PLN00176 GO:GO:0047216 EMBL:AY050410 EMBL:AY058238 EMBL:AB062849 IPI:IPI00517274 PIR:G96607 RefSeq:NP_176053.1 UniGene:At.19795 ProteinModelPortal:Q9FXB2 SMR:Q9FXB2 STRING:Q9FXB2 PRIDE:Q9FXB2 EnsemblPlants:AT1G56600.1 GeneID:842114 KEGG:ath:AT1G56600 TAIR:At1g56600 InParanoid:Q9FXB2 PhylomeDB:Q9FXB2 Genevestigator:Q9FXB2 Uniprot:Q9FXB2
Root	Isotig00542	42	1	5.263	5.01E-11	TAIR|locus:2027549 - symbol:GolS2 "AT1G56600" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0016051 "carbohydrate biosynthetic process" evidence=ISS] [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0016758 "transferase activity, transferring hexosyl groups" evidence=ISS] [GO:0006012 "galactose metabolic process" evidence=IDA] [GO:0006979 "response to oxidative stress" evidence=IEP] [GO:0009409 "response to cold" evidence=IMP] [GO:0009651 "response to salt stress" evidence=IMP] [GO:0047216 "inositol 3-alpha-galactosyltransferase activity" evidence=IDA] [GO:0009414 "response to water deprivation" evidence=IEP] InterPro:IPR002495 Pfam:PF01501 EMBL:CP002684 GO:GO:0006979 GO:GO:0009409 GO:GO:0009651 GO:GO:0009414 GO:GO:0006012 EMBL:AC009323 CAZy:GT8 OMA:DSQDAAN ProtClustDB:PLN00176 GO:GO:0047216 EMBL:AY050410 EMBL:AY058238 EMBL:AB062849 IPI:IPI00517274 PIR:G96607 RefSeq:NP_176053.1 UniGene:At.19795 ProteinModelPortal:Q9FXB2 SMR:Q9FXB2 STRING:Q9FXB2 PRIDE:Q9FXB2 EnsemblPlants:AT1G56600.1 GeneID:842114 KEGG:ath:AT1G56600 TAIR:At1g56600 InParanoid:Q9FXB2 PhylomeDB:Q9FXB2 Genevestigator:Q9FXB2 Uniprot:Q9FXB2
Root	Isotig00543	41	0	6.229	8.08E-11	TAIR|locus:2027549 - symbol:GolS2 "AT1G56600" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0016051 "carbohydrate biosynthetic process" evidence=ISS] [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0016758 "transferase activity, transferring hexosyl groups" evidence=ISS] [GO:0006012 "galactose metabolic process" evidence=IDA] [GO:0006979 "response to oxidative stress" evidence=IEP] [GO:0009409 "response to cold" evidence=IMP] [GO:0009651 "response to salt stress" evidence=IMP] [GO:0047216 "inositol 3-alpha-galactosyltransferase activity" evidence=IDA] [GO:0009414 "response to water deprivation" evidence=IEP] InterPro:IPR002495 Pfam:PF01501 EMBL:CP002684 GO:GO:0006979 GO:GO:0009409 GO:GO:0009651 GO:GO:0009414 GO:GO:0006012 EMBL:AC009323 CAZy:GT8 OMA:DSQDAAN ProtClustDB:PLN00176 GO:GO:0047216 EMBL:AY050410 EMBL:AY058238 EMBL:AB062849 IPI:IPI00517274 PIR:G96607 RefSeq:NP_176053.1 UniGene:At.19795 ProteinModelPortal:Q9FXB2 SMR:Q9FXB2 STRING:Q9FXB2 PRIDE:Q9FXB2 EnsemblPlants:AT1G56600.1 GeneID:842114 KEGG:ath:AT1G56600 TAIR:At1g56600 InParanoid:Q9FXB2 PhylomeDB:Q9FXB2 Genevestigator:Q9FXB2 Uniprot:Q9FXB2

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig00544	40	0	6.193	1.34E-10	TAIR|locus:2027549 - symbol:GolS2 "AT1G56600" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0016051 "carbohydrate biosynthetic process" evidence=ISS] [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0016758 "transferase activity, transferring hexosyl groups" evidence=ISS] [GO:0006012 "galactose metabolic process" evidence=IDA] [GO:0006979 "response to oxidative stress" evidence=IEP] [GO:0009409 "response to cold" evidence=IMP] [GO:0009651 "response to salt stress" evidence=IMP] [GO:0047216 "inositol 3-alpha-galactosyltransferase activity" evidence=IDA] [GO:0009414 "response to water deprivation" evidence=IEP] InterPro:IPR002495 Pfam:PF01501 EMBL:CP002684 GO:GO:0006979 GO:GO:0009409 GO:GO:0009651 GO:GO:0009414 GO:GO:0006012 EMBL:AC009323 CAZy:GT8 OMA:DSQDAAN ProtClustDB:PLN00176 GO:GO:0047216 EMBL:AY050410 EMBL:AY058238 EMBL:AB062849 IPI:IPI00517274 PIR:G96607 RefSeq:NP_176053.1 UniGene:At.19795 ProteinModelPortal:Q9FXB2 SMR:Q9FXB2 STRING:Q9FXB2 PRIDE:Q9FXB2 EnsemblPlants:AT1G56600.1 GeneID:842114 KEGG:ath:AT1G56600 TAIR:At1g56600 InParanoid:Q9FXB2 PhylomeDB:Q9FXB2 Genevestigator:Q9FXB2 Uniprot:Q9FXB2
Root	Isotig00545	41	0	6.229	8.08E-11	TAIR|locus:2027549 - symbol:GolS2 "AT1G56600" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0016051 "carbohydrate biosynthetic process" evidence=ISS] [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0016758 "transferase activity, transferring hexosyl groups" evidence=ISS] [GO:0006012 "galactose metabolic process" evidence=IDA] [GO:0006979 "response to oxidative stress" evidence=IEP] [GO:0009409 "response to cold" evidence=IMP] [GO:0009651 "response to salt stress" evidence=IMP] [GO:0047216 "inositol 3-alpha-galactosyltransferase activity" evidence=IDA] [GO:0009414 "response to water deprivation" evidence=IEP] InterPro:IPR002495 Pfam:PF01501 EMBL:CP002684 GO:GO:0006979 GO:GO:0009409 GO:GO:0009651 GO:GO:0009414 GO:GO:0006012 EMBL:AC009323 CAZy:GT8 OMA:DSQDAAN ProtClustDB:PLN00176 GO:GO:0047216 EMBL:AY050410 EMBL:AY058238 EMBL:AB062849 IPI:IPI00517274 PIR:G96607 RefSeq:NP_176053.1 UniGene:At.19795 ProteinModelPortal:Q9FXB2 SMR:Q9FXB2 STRING:Q9FXB2 PRIDE:Q9FXB2 EnsemblPlants:AT1G56600.1 GeneID:842114 KEGG:ath:AT1G56600 TAIR:At1g56600 InParanoid:Q9FXB2 PhylomeDB:Q9FXB2 Genevestigator:Q9FXB2 Uniprot:Q9FXB2
Root	Isotig00546	40	0	6.193	1.34E-10	TAIR|locus:2027549 - symbol:GolS2 "AT1G56600" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0016051 "carbohydrate biosynthetic process" evidence=ISS] [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0016758 "transferase activity, transferring hexosyl groups" evidence=ISS] [GO:0006012 "galactose metabolic process" evidence=IDA] [GO:0006979 "response to oxidative stress" evidence=IEP] [GO:0009409 "response to cold" evidence=IMP] [GO:0009651 "response to salt stress" evidence=IMP] [GO:0047216 "inositol 3-alpha-galactosyltransferase activity" evidence=IDA] [GO:0009414 "response to water deprivation" evidence=IEP] InterPro:IPR002495 Pfam:PF01501 EMBL:CP002684 GO:GO:0006979 GO:GO:0009409 GO:GO:0009651 GO:GO:0009414 GO:GO:0006012 EMBL:AC009323 CAZy:GT8 OMA:DSQDAAN ProtClustDB:PLN00176 GO:GO:0047216 EMBL:AY050410 EMBL:AY058238 EMBL:AB062849 IPI:IPI00517274 PIR:G96607 RefSeq:NP_176053.1 UniGene:At.19795 ProteinModelPortal:Q9FXB2 SMR:Q9FXB2 STRING:Q9FXB2 PRIDE:Q9FXB2 EnsemblPlants:AT1G56600.1 GeneID:842114 KEGG:ath:AT1G56600 TAIR:At1g56600 InParanoid:Q9FXB2 PhylomeDB:Q9FXB2 Genevestigator:Q9FXB2 Uniprot:Q9FXB2
Root	Isotig00570	31	110	-1.956	2.29E-13	TAIR|locus:2031855 - symbol:PBE1 "20S proteasome beta subunit E1" species:3702 "Arabidopsis thaliana" [GO:0004175 "endopeptidase activity" evidence=IEA] [GO:0004298 "threonine-type endopeptidase activity" evidence=IEA] [GO:0008233 "peptidase activity" evidence=ISS] [GO:0006511 "ubiquitin-dependent protein catabolic process" evidence=TAS] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0000502 "proteasome complex" evidence=IDA] [GO:0005839 "proteasome core complex" evidence=TAS] InterPro:IPR000243 InterPro:IPR001353 InterPro:IPR016050 InterPro:IPR023333 Pfam:PF00227 PRINTS:PR00141 PROSITE:PS00854 PROSITE:PS51476 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005634 GO:GO:0046686 GO:GO:0005737 EMBL:AC007357 GO:GO:0004298 GO:GO:0051603 GO:GO:0005839 eggNOG:COG0638 HOGENOM:HBG499923 EMBL:Y13695 EMBL:AF043536 EMBL:AF348579 EMBL:AY050871 EMBL:AY150473 IPI:IPI00544396 PIR:F86264 RefSeq:NP_172765.1 UniGene:At.22436 ProteinModelPortal:O23717 SMR:O23717 STRING:O23717 PRIDE:O23717 EnsemblPlants:AT1G13060.1 GeneID:837863 KEGG:ath:AT1G13060 TAIR:At1g13060 InParanoid:O23717 KO:K02737 OMA:QTFAYGV PhylomeDB:O23717 ProtClustDB:CLSN2682489 Genevestigator:O23717 Uniprot:O23717

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig00571	35	112	-1.807	2.35E-12	TAIR|locus:2031855 - symbol:PBE1 "20S proteasome beta subunit E1" species:3702 "Arabidopsis thaliana" [GO:0004175 "endopeptidase activity" evidence=IEA] [GO:0004298 "threonine-type endopeptidase activity" evidence=IEA] [GO:0008233 "peptidase activity" evidence=ISS] [GO:0006511 "ubiquitin-dependent protein catabolic process" evidence=TAS] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0000502 "proteasome complex" evidence=IDA] [GO:0005839 "proteasome core complex" evidence=TAS] InterPro:IPR000243 InterPro:IPR001353 InterPro:IPR016050 InterPro:IPR023333 Pfam:PF00227 PRINTS:PR00141 PROSITE:PS00854 PROSITE:PS51476 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005634 GO:GO:0046686 GO:GO:0005737 EMBL:AC007357 GO:GO:0004298 GO:GO:0051603 GO:GO:0005839 eggNOG:COG0638 HOGENOM:HBG499923 EMBL:Y13695 EMBL:AF043536 EMBL:AF348579 EMBL:AY050871 EMBL:AY150473 IPI:IPI00544396 PIR:F86264 RefSeq:NP_172765.1 UniGene:At.22436 ProteinModelPortal:O23717 SMR:O23717 STRING:O23717 PRIDE:O23717 EnsemblPlants:AT1G13060.1 GeneID:837863 KEGG:ath:AT1G13060 TAIR:At1g13060 InParanoid:O23717 KO:K02737 OMA:QTFAYGV PhylomeDB:O23717 ProtClustDB:CLSN2682489 Genevestigator:O23717 Uniprot:O23717
Root	Isotig00574	9	53	-2.687	7.37E-10	TAIR|locus:2177003 - symbol:TUB6 "AT5G12250" species:3702 "Arabidopsis thaliana" [GO:0009409 "response to cold" evidence=IEP] [GO:0005200 "structural constituent of cytoskeleton" evidence=ISS] [GO:0007017 "microtubule-based process" evidence=ISS] [GO:0015630 "microtubule cytoskeleton" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] InterPro:IPR000217 InterPro:IPR002453 InterPro:IPR003008 InterPro:IPR008280 InterPro:IPR017975 InterPro:IPR018316 Pfam:PF00091 Pfam:PF03953 PRINTS:PR01161 PRINTS:PR01163 PROSITE:PS00227 SMART:SM00864 SMART:SM00865 GO:GO:0005525 GO:GO:0005886 GO:GO:0005737 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005198 GO:GO:0003924 GO:GO:0009409 GO:GO:0009651 GO:GO:0005874 GO:GO:0051258 Gene3D:G3DSA:3.40.50.1440 SUPFAM:SSF52490 GO:GO:0007018 EMBL:AB007727 Gene3D:G3DSA:3.30.1330.20 SUPFAM:SSF55307 HOGENOM:HBG750007 InterPro:IPR023123 Gene3D:G3DSA:1.10.287.600 PANTHER:PTHR11588 InterPro:IPR013838 KO:K07375 ProtClustDB:PLN00220 PROSITE:PS00228 OMA:EVINDEH EMBL:M84703 EMBL:AF360260 EMBL:AY040074 IPI:IPI00545934 PIR:JQ1590 RefSeq:NP_196786.1 UniGene:At.23425 UniGene:At.72672 UniGene:At.74848 ProteinModelPortal:P29514 SMR:P29514 STRING:P29514 PRIDE:P29514 EnsemblPlants:AT5G12250.1 GeneID:831100 KEGG:ath:AT5G12250 TAIR:At5g12250 InParanoid:P29514 PhylomeDB:P29514 ArrayExpress:P29514 Genevestigator:P29514 GermOnline:AT5G12250 Uniprot:P29514
Root	Isotig00605	2	15	-3.036	0.000493759	No hit
Root	Isotig00607	2	14	-2.936	0.000925454	No hit
Root	Isotig00608	2	15	-3.036	0.000493759	No hit
Root	Isotig00609	51	10	2.222	2.25E-07	No hit
Root	Isotig00610	46	11	1.935	6.77E-06	No hit
Root	Isotig00611	52	11	2.112	4.08E-07	No hit
Root	Isotig00615	37	9	1.911	6.27E-05	No hit
Root	Isotig00617	38	10	1.797	9.99E-05	No hit
Root	Isotig00618	29	8	1.729	0.000936087	No hit
Root	Isotig00621	49	18	1.316	0.000437347	TAIR|locus:2123782 - symbol:GAMMA-VPE "AT4G32940" species:3702 "Arabidopsis thaliana" [GO:0004197 "cysteine-type endopeptidase activity" evidence=ISS;IDA] [GO:0006508 "proteolysis" evidence=ISS] [GO:0000323 "lytic vacuole" evidence=IDA] [GO:0006624 "vacuolar protein processing" evidence=ISS] InterPro:IPR001096 Pfam:PF01650 PIRSF:PIRSF019663 PRINTS:PR00776 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0004197 GO:GO:0006508 EMBL:AL031804 EMBL:AL161582 eggNOG:COG5206 PANTHER:PTHR12000 KO:K01369 HOGENOM:HBG318720 GO:GO:0000323 ProtClustDB:CLSN2682340 EMBL:D61395 EMBL:AF370160 EMBL:AF424619 EMBL:AY059104 EMBL:AY133531 IPI:IPI00537536 PIR:T05302 RefSeq:NP_195020.1 UniGene:At.21567 UniGene:At.48929 UniGene:At.75206 ProteinModelPortal:Q39119 STRING:Q39119 MEROPS:C13.006 PRIDE:Q39119 EnsemblPlants:AT4G32940.1 GeneID:829431 KEGG:ath:AT4G32940 TAIR:At4g32940 InParanoid:Q39119 OMA:ICHAYQL PhylomeDB:Q39119 Genevestigator:Q39119 Uniprot:Q39119
Root	Isotig00622	49	18	1.316	0.000437347	TAIR|locus:2123782 - symbol:GAMMA-VPE "AT4G32940" species:3702 "Arabidopsis thaliana" [GO:0004197 "cysteine-type endopeptidase activity" evidence=ISS;IDA] [GO:0006508 "proteolysis" evidence=ISS] [GO:0000323 "lytic vacuole" evidence=IDA] [GO:0006624 "vacuolar protein processing" evidence=ISS] InterPro:IPR001096

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						Pfam:PF01650 PIRSF:PIRSF019663 PRINTS:PR00776 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0004197 GO:GO:0006508 EMBL:AL031804 EMBL:AL161582 eggNOG:COG5206 PANTHER:PTHR12000 KO:K01369 HOGENOM:HBG318720 GO:GO:0000323 ProtClustDB:CLSN2682340 EMBL:D61395 EMBL:AF370160 EMBL:AF424619 EMBL:AY059104 EMBL:AY133531 IPI:IPI00537536 PIR:T05302 RefSeq:NP_195020.1 UniGene:At.21567 UniGene:At.48929 UniGene:At.75206 ProteinModelPortal:Q39119 STRING:Q39119 MEROPS:C13.006 PRIDE:Q39119 EnsemblPlants:AT4G32940.1 GeneID:829431 KEGG:ath:AT4G32940 TAIR:At4g32940 InParanoid:Q39119 OMA:ICHAYQL PhylomeDB:Q39119 Genevestigator:Q39119 Uniprot:Q39119
Root	Isotig00625	49	16	1.486	0.000115562	TAIR|locus:2123782 - symbol:GAMMA-VPE "AT4G32940" species:3702 "Arabidopsis thaliana" [GO:0004197 "cysteine-type endopeptidase activity" evidence=ISS;IDA] [GO:0006508 "proteolysis" evidence=ISS] [GO:0000323 "lytic vacuole" evidence=IDA] [GO:0006624 "vacuolar protein processing" evidence=ISS] InterPro:IPR001096 Pfam:PF01650 PIRSF:PIRSF019663 PRINTS:PR00776 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0004197 GO:GO:0006508 EMBL:AL031804 EMBL:AL161582 eggNOG:COG5206 PANTHER:PTHR12000 KO:K01369 HOGENOM:HBG318720 GO:GO:0000323 ProtClustDB:CLSN2682340 EMBL:D61395 EMBL:AF370160 EMBL:AF424619 EMBL:AY059104 EMBL:AY133531 IPI:IPI00537536 PIR:T05302 RefSeq:NP_195020.1 UniGene:At.21567 UniGene:At.48929 UniGene:At.75206 ProteinModelPortal:Q39119 STRING:Q39119 MEROPS:C13.006 PRIDE:Q39119 EnsemblPlants:AT4G32940.1 GeneID:829431 KEGG:ath:AT4G32940 TAIR:At4g32940 InParanoid:Q39119 OMA:ICHAYQL PhylomeDB:Q39119 Genevestigator:Q39119 Uniprot:Q39119
Root	Isotig00626	49	16	1.486	0.000115562	TAIR|locus:2123782 - symbol:GAMMA-VPE "AT4G32940" species:3702 "Arabidopsis thaliana" [GO:0004197 "cysteine-type endopeptidase activity" evidence=ISS;IDA] [GO:0006508 "proteolysis" evidence=ISS] [GO:0000323 "lytic vacuole" evidence=IDA] [GO:0006624 "vacuolar protein processing" evidence=ISS] InterPro:IPR001096 Pfam:PF01650 PIRSF:PIRSF019663 PRINTS:PR00776 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0004197 GO:GO:0006508 EMBL:AL031804 EMBL:AL161582 eggNOG:COG5206 PANTHER:PTHR12000 KO:K01369 HOGENOM:HBG318720 GO:GO:0000323 ProtClustDB:CLSN2682340 EMBL:D61395 EMBL:AF370160 EMBL:AF424619 EMBL:AY059104 EMBL:AY133531 IPI:IPI00537536 PIR:T05302 RefSeq:NP_195020.1 UniGene:At.21567 UniGene:At.48929 UniGene:At.75206 ProteinModelPortal:Q39119 STRING:Q39119 MEROPS:C13.006 PRIDE:Q39119 EnsemblPlants:AT4G32940.1 GeneID:829431 KEGG:ath:AT4G32940 TAIR:At4g32940 InParanoid:Q39119 OMA:ICHAYQL PhylomeDB:Q39119 Genevestigator:Q39119 Uniprot:Q39119
Root	Isotig00645	54	8	2.626	4.34E-09	TAIR|locus:2051008 - symbol:AT2G33590 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0009809 "lignin biosynthetic process" evidence=ISS] [GO:0016621 "cinnamoyl-CoA reductase activity" evidence=ISS] [GO:0050662 "coenzyme binding" evidence=IEA] [GO:0046686 "response to cadmium ion" evidence=IEP] InterPro:IPR001509 InterPro:IPR016040 Pfam:PF01370 GO:GO:0046686 EMBL:CP002685 GenomeReviews:CT485783_GR eggNOG:COG0451 GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 HOGENOM:HBG755066 GO:GO:0003824 GO:GO:0044237 GO:GO:0050662 EMBL:AC002332 EMBL:AY120714 EMBL:AY084584 EMBL:BT000055 IPI:IPI00536249 PIR:D84747 RefSeq:NP_180917.1 UniGene:At.19951 ProteinModelPortal:O22809 SMR:O22809 STRING:O22809 PRIDE:O22809 EnsemblPlants:AT2G33590.1 GeneID:817925 KEGG:ath:AT2G33590 TAIR:At2g33590 InParanoid:O22809 OMA:CLAKTRA PhylomeDB:O22809 ProtClustDB:CLSN2683499 ArrayExpress:O22809 Genevestigator:O22809 Uniprot:O22809
Root	Isotig00646	55	8	2.652	2.57E-09	TAIR|locus:2051008 - symbol:AT2G33590 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0009809 "lignin biosynthetic process" evidence=ISS] [GO:0016621 "cinnamoyl-CoA reductase activity" evidence=ISS] [GO:0050662 "coenzyme binding" evidence=IEA] [GO:0046686 "response to cadmium ion" evidence=IEP] InterPro:IPR001509 InterPro:IPR016040 Pfam:PF01370 GO:GO:0046686 EMBL:CP002685 GenomeReviews:CT485783_GR eggNOG:COG0451 GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 HOGENOM:HBG755066 GO:GO:0003824 GO:GO:0044237 GO:GO:0050662 EMBL:AC002332 EMBL:AY120714 EMBL:AY084584 EMBL:BT000055 IPI:IPI00536249 PIR:D84747 RefSeq:NP_180917.1 UniGene:At.19951 ProteinModelPortal:O22809 SMR:O22809 STRING:O22809 PRIDE:O22809 EnsemblPlants:AT2G33590.1 GeneID:817925 KEGG:ath:AT2G33590 TAIR:At2g33590 InParanoid:O22809 OMA:CLAKTRA PhylomeDB:O22809 ProtClustDB:CLSN2683499 ArrayExpress:O22809 Genevestigator:O22809 Uniprot:O22809

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig00647	53	4	3.599	1.65E-11	SGD|S000028422 - symbol:TAR1 "Mitochondrial protein potentially involved in respiratory metabolism" species:4932 "Saccharomyces cerevisiae" [GO:0003674 "molecular_function" evidence=ND] [GO:0043457 "regulation of cellular respiration" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IEA;IMP] SGD:S000028422 GO:GO:0005739 EMBL:BK006945 EMBL:U53879 GO:GO:0043457 EMBL:Z73326 EMBL:AF479964 RefSeq:NP_690845.1 ProteinModelPortal:Q8TGM6 STRING:Q8TGM6 EnsemblFungi:YLR154W-C GeneID:1466405 KEGG:sce:YLR154W-C CYGD:YLR154w-c eggNOG:NOG79861 OMA:SCSKEHR OrthoDB:EOG466ZX8 NextBio:967146 Genevestigator:Q8TGM6 GermOnline:YLR154W-C Uniprot:Q8TGM6
Root	Isotig00648	49	2	4.486	4.48E-12	SGD|S000028422 - symbol:TAR1 "Mitochondrial protein potentially involved in respiratory metabolism" species:4932 "Saccharomyces cerevisiae" [GO:0003674 "molecular_function" evidence=ND] [GO:0043457 "regulation of cellular respiration" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IEA;IMP] SGD:S000028422 GO:GO:0005739 EMBL:BK006945 EMBL:U53879 GO:GO:0043457 EMBL:Z73326 EMBL:AF479964 RefSeq:NP_690845.1 ProteinModelPortal:Q8TGM6 STRING:Q8TGM6 EnsemblFungi:YLR154W-C GeneID:1466405 KEGG:sce:YLR154W-C CYGD:YLR154w-c eggNOG:NOG79861 OMA:SCSKEHR OrthoDB:EOG466ZX8 NextBio:967146 Genevestigator:Q8TGM6 GermOnline:YLR154W-C Uniprot:Q8TGM6
Root	Isotig00649	30	8	1.778	0.000599962	TAIR|locus:2051008 - symbol:AT2G33590 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0009809 "lignin biosynthetic process" evidence=ISS] [GO:0016621 "cinnamoyl-CoA reductase activity" evidence=ISS] [GO:0050662 "coenzyme binding" evidence=IEA] [GO:0046686 "response to cadmium ion" evidence=IEP] InterPro:IPR001509 InterPro:IPR016040 Pfam:PF01370 GO:GO:0046686 EMBL:CP002685 GenomeReviews:CT485783_GR eggNOG:COG0451 GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 HOGENOM:HBG755066 GO:GO:0003824 GO:GO:0044237 GO:GO:0050662 EMBL:AC002332 EMBL:AY120714 EMBL:AY084584 EMBL:BT000055 IPI:IPI00536249 PIR:D84747 RefSeq:NP_180917.1 UniGene:At.19951 ProteinModelPortal:O22809 SMR:O22809 STRING:O22809 PRIDE:O22809 EnsemblPlants:AT2G33590.1 GeneID:817925 KEGG:ath:AT2G33590 TAIR:At2g33590 InParanoid:O22809 OMA:CLAKTRA PhylomeDB:O22809 ProtClustDB:CLSN2683499 ArrayExpress:O22809 Genevestigator:O22809 Uniprot:O22809
Root	Isotig00651	31	8	1.825	0.000382406	TAIR|locus:2051008 - symbol:AT2G33590 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0009809 "lignin biosynthetic process" evidence=ISS] [GO:0016621 "cinnamoyl-CoA reductase activity" evidence=ISS] [GO:0050662 "coenzyme binding" evidence=IEA] [GO:0046686 "response to cadmium ion" evidence=IEP] InterPro:IPR001509 InterPro:IPR016040 Pfam:PF01370 GO:GO:0046686 EMBL:CP002685 GenomeReviews:CT485783_GR eggNOG:COG0451 GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 HOGENOM:HBG755066 GO:GO:0003824 GO:GO:0044237 GO:GO:0050662 EMBL:AC002332 EMBL:AY120714 EMBL:AY084584 EMBL:BT000055 IPI:IPI00536249 PIR:D84747 RefSeq:NP_180917.1 UniGene:At.19951 ProteinModelPortal:O22809 SMR:O22809 STRING:O22809 PRIDE:O22809 EnsemblPlants:AT2G33590.1 GeneID:817925 KEGG:ath:AT2G33590 TAIR:At2g33590 InParanoid:O22809 OMA:CLAKTRA PhylomeDB:O22809 ProtClustDB:CLSN2683499 ArrayExpress:O22809 Genevestigator:O22809 Uniprot:O22809
Root	Isotig00654	29	4	2.729	1.12E-05	RGD|727924 - symbol:LOC257642 "rRNA promoter binding protein" species:10116 "Rattus norvegicus" [GO:0003690 "double-stranded DNA binding" evidence=IDA] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=IDA] [GO:0008134 "transcription factor binding" evidence=IDA] [GO:0008283 "cell proliferation" evidence=IDA] [GO:0009303 "rRNA transcription" evidence=IDA] RGD:727924 GO:GO:0008134 GO:GO:0008283 GO:GO:0003700 GO:GO:0003690 GO:GO:0009303 EMBL:U77931 IPI:IPI00195015 RefSeq:NP_671477.1 GeneID:257642 KEGG:rno:257642 NextBio:624170 Genevestigator:Q99JC0 Uniprot:Q99JC0
Root	Isotig00655	25	2	3.515	4.58E-06	RGD|727924 - symbol:LOC257642 "rRNA promoter binding protein" species:10116 "Rattus norvegicus" [GO:0003690 "double-stranded DNA binding" evidence=IDA] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=IDA] [GO:0008134 "transcription factor binding" evidence=IDA] [GO:0008283 "cell proliferation" evidence=IDA] [GO:0009303 "rRNA transcription" evidence=IDA] RGD:727924 GO:GO:0008134 GO:GO:0008283 GO:GO:0003700 GO:GO:0003690 GO:GO:0009303 EMBL:U77931 IPI:IPI00195015 RefSeq:NP_671477.1 GeneID:257642 KEGG:rno:257642 NextBio:624170 Genevestigator:Q99JC0 Uniprot:Q99JC0
Root	Isotig00656	21	54	-1.492	2.19E-05	TAIR|locus:2159223 - symbol:CNX1 "calnexin 1" species:3702 "Arabidopsis thaliana" [GO:0005509 "calcium ion binding" evidence=IEA] [GO:0006457 "protein folding" evidence=IEA] [GO:0051082 "unfolded protein binding" evidence=IEA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0009505 "plant-type cell wall" evidence=IDA] [GO:0005783 "endoplasmic reticulum" evidence=IDA] [GO:0005774 "vacuolar

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] [GO:0005792 "microsome" evidence=IDA] InterPro:IPR001580 InterPro:IPR009033 InterPro:IPR018124 Pfam:PF00262 PRINTS:PR00626 PROSITE:PS00803 PROSITE:PS00804 PROSITE:PS00805 GO:GO:0016021 GO:GO:0005739 GO:GO:0005886 GO:GO:0009506 GO:GO:0005774 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009507 GO:GO:0005509 GO:GO:0006457 GO:GO:0005789 GO:GO:0005529 GO:GO:0051082 EMBL:AB010069 InterPro:IPR008985 InterPro:IPR013320 Gene3D:G3DSA:2.60.120.200 SUPFAM:SSF49899 GO:GO:0009505 eggNOG:NOG305105 HOGENOM:HBG444251 PANTHER:PTHR11073 SUPFAM:SSF63887 EMBL:Z18242 EMBL:AY059880 EMBL:AY114669 EMBL:AY086864 IPI:IPI00539561 PIR:JN0597 RefSeq:NP_200987.1 UniGene:At.21770 ProteinModelPortal:P29402 SMR:P29402 STRING:P29402 PRIDE:P29402 EnsemblPlants:AT5G61790.1 GeneID:836301 KEGG:ath:AT5G61790 TAIR:At5g61790 InParanoid:P29402 KO:K08054 OMA:DYKGIWK PhylomeDB:P29402 ProtClustDB:CLSN2686945 ArrayExpress:P29402 Genevestigator:P29402 GermOnline:AT5G61790 Gene3D:G3DSA:2.10.250.10 Uniprot:P29402
Root	Isotig00657	21	54	-1.492	2.19E-05	TAIR|locus:2159223 - symbol:CNX1 "calnexin 1" species:3702 "Arabidopsis thaliana" [GO:0005509 "calcium ion binding" evidence=IEA] [GO:0006457 "protein folding" evidence=IEA] [GO:0051082 "unfolded protein binding" evidence=IEA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0009505 "plant-type cell wall" evidence=IDA] [GO:0005783 "endoplasmic reticulum" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] [GO:0005792 "microsome" evidence=IDA] InterPro:IPR001580 InterPro:IPR009033 InterPro:IPR018124 Pfam:PF00262 PRINTS:PR00626 PROSITE:PS00803 PROSITE:PS00804 PROSITE:PS00805 GO:GO:0016021 GO:GO:0005739 GO:GO:0005886 GO:GO:0009506 GO:GO:0005774 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009507 GO:GO:0005509 GO:GO:0006457 GO:GO:0005789 GO:GO:0005529 GO:GO:0051082 EMBL:AB010069 InterPro:IPR008985 InterPro:IPR013320 Gene3D:G3DSA:2.60.120.200 SUPFAM:SSF49899 GO:GO:0009505 eggNOG:NOG305105 HOGENOM:HBG444251 PANTHER:PTHR11073 SUPFAM:SSF63887 EMBL:Z18242 EMBL:AY059880 EMBL:AY114669 EMBL:AY086864 IPI:IPI00539561 PIR:JN0597 RefSeq:NP_200987.1 UniGene:At.21770 ProteinModelPortal:P29402 SMR:P29402 STRING:P29402 PRIDE:P29402 EnsemblPlants:AT5G61790.1 GeneID:836301 KEGG:ath:AT5G61790 TAIR:At5g61790 InParanoid:P29402 KO:K08054 OMA:DYKGIWK PhylomeDB:P29402 ProtClustDB:CLSN2686945 ArrayExpress:P29402 Genevestigator:P29402 GermOnline:AT5G61790 Gene3D:G3DSA:2.10.250.10 Uniprot:P29402
Root	Isotig00658	23	52	-1.306	0.000165922	TAIR|locus:2159223 - symbol:CNX1 "calnexin 1" species:3702 "Arabidopsis thaliana" [GO:0005509 "calcium ion binding" evidence=IEA] [GO:0006457 "protein folding" evidence=IEA] [GO:0051082 "unfolded protein binding" evidence=IEA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0009505 "plant-type cell wall" evidence=IDA] [GO:0005783 "endoplasmic reticulum" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] [GO:0005792 "microsome" evidence=IDA] InterPro:IPR001580 InterPro:IPR009033 InterPro:IPR018124 Pfam:PF00262 PRINTS:PR00626 PROSITE:PS00803 PROSITE:PS00804 PROSITE:PS00805 GO:GO:0016021 GO:GO:0005739 GO:GO:0005886 GO:GO:0009506 GO:GO:0005774 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009507 GO:GO:0005509 GO:GO:0006457 GO:GO:0005789 GO:GO:0005529 GO:GO:0051082 EMBL:AB010069 InterPro:IPR008985 InterPro:IPR013320 Gene3D:G3DSA:2.60.120.200 SUPFAM:SSF49899 GO:GO:0009505 eggNOG:NOG305105 HOGENOM:HBG444251 PANTHER:PTHR11073 SUPFAM:SSF63887 EMBL:Z18242 EMBL:AY059880 EMBL:AY114669 EMBL:AY086864 IPI:IPI00539561 PIR:JN0597 RefSeq:NP_200987.1 UniGene:At.21770 ProteinModelPortal:P29402 SMR:P29402 STRING:P29402 PRIDE:P29402 EnsemblPlants:AT5G61790.1 GeneID:836301 KEGG:ath:AT5G61790 TAIR:At5g61790 InParanoid:P29402 KO:K08054 OMA:DYKGIWK PhylomeDB:P29402 ProtClustDB:CLSN2686945 ArrayExpress:P29402 Genevestigator:P29402 GermOnline:AT5G61790 Gene3D:G3DSA:2.10.250.10 Uniprot:P29402
Root	Isotig00659	23	52	-1.306	0.000165922	TAIR|locus:2159223 - symbol:CNX1 "calnexin 1" species:3702 "Arabidopsis thaliana" [GO:0005509 "calcium ion binding" evidence=IEA] [GO:0006457 "protein folding" evidence=IEA] [GO:0051082 "unfolded protein binding"

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						evidence=IEA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0009505 "plant-type cell wall" evidence=IDA] [GO:0005783 "endoplasmic reticulum" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] [GO:0005792 "microsome" evidence=IDA] InterPro:IPR001580 InterPro:IPR009033 InterPro:IPR018124 Pfam:PF00262 PRINTS:PR00626 PROSITE:PS00803 PROSITE:PS00804 PROSITE:PS00805 GO:GO:0016021 GO:GO:0005739 GO:GO:0005886 GO:GO:0009506 GO:GO:0005774 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009507 GO:GO:0005509 GO:GO:0006457 GO:GO:0005789 GO:GO:0005529 GO:GO:0051082 EMBL:AB010069 InterPro:IPR008985 InterPro:IPR013320 Gene3D:G3DSA:2.60.120.200 SUPFAM:SSF49899 GO:GO:0009505 eggNOG:NOG305105 HOGENOM:HBG444251 PANTHER:PTHR11073 SUPFAM:SSF63887 EMBL:Z18242 EMBL:AY059880 EMBL:AY114669 EMBL:AY086864 IPI:IPI00539561 PIR:JN0597 RefSeq:NP_200987.1 UniGene:At.21770 ProteinModelPortal:P29402 SMR:P29402 STRING:P29402 PRIDE:P29402 EnsemblPlants:AT5G61790.1 GeneID:836301 KEGG:ath:AT5G61790 TAIR:At5g61790 InParanoid:P29402 KO:K08054 OMA:DYKGIWK PhylomeDB:P29402 ProtClustDB:CLSN2686945 ArrayExpress:P29402 Genevestigator:P29402 GermOnline:AT5G61790 Gene3D:G3DSA:2.10.250.10 Uniprot:P29402
Root	Isotig00660	23	52	-1.306	0.000165922	TAIR|locus:2159223 - symbol:CNX1 "calnexin 1" species:3702 "Arabidopsis thaliana" [GO:0005509 "calcium ion binding" evidence=IEA] [GO:0006457 "protein folding" evidence=IEA] [GO:0051082 "unfolded protein binding" evidence=IEA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0009505 "plant-type cell wall" evidence=IDA] [GO:0005783 "endoplasmic reticulum" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] [GO:0005792 "microsome" evidence=IDA] InterPro:IPR001580 InterPro:IPR009033 InterPro:IPR018124 Pfam:PF00262 PRINTS:PR00626 PROSITE:PS00803 PROSITE:PS00804 PROSITE:PS00805 GO:GO:0016021 GO:GO:0005739 GO:GO:0005886 GO:GO:0009506 GO:GO:0005774 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009507 GO:GO:0005509 GO:GO:0006457 GO:GO:0005789 GO:GO:0005529 GO:GO:0051082 EMBL:AB010069 InterPro:IPR008985 InterPro:IPR013320 Gene3D:G3DSA:2.60.120.200 SUPFAM:SSF49899 GO:GO:0009505 eggNOG:NOG305105 HOGENOM:HBG444251 PANTHER:PTHR11073 SUPFAM:SSF63887 EMBL:Z18242 EMBL:AY059880 EMBL:AY114669 EMBL:AY086864 IPI:IPI00539561 PIR:JN0597 RefSeq:NP_200987.1 UniGene:At.21770 ProteinModelPortal:P29402 SMR:P29402 STRING:P29402 PRIDE:P29402 EnsemblPlants:AT5G61790.1 GeneID:836301 KEGG:ath:AT5G61790 TAIR:At5g61790 InParanoid:P29402 KO:K08054 OMA:DYKGIWK PhylomeDB:P29402 ProtClustDB:CLSN2686945 ArrayExpress:P29402 Genevestigator:P29402 GermOnline:AT5G61790 Gene3D:G3DSA:2.10.250.10 Uniprot:P29402
Root	Isotig00661	23	52	-1.306	0.000165922	TAIR|locus:2159223 - symbol:CNX1 "calnexin 1" species:3702 "Arabidopsis thaliana" [GO:0005509 "calcium ion binding" evidence=IEA] [GO:0006457 "protein folding" evidence=IEA] [GO:0051082 "unfolded protein binding" evidence=IEA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0009505 "plant-type cell wall" evidence=IDA] [GO:0005783 "endoplasmic reticulum" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] [GO:0005792 "microsome" evidence=IDA] InterPro:IPR001580 InterPro:IPR009033 InterPro:IPR018124 Pfam:PF00262 PRINTS:PR00626 PROSITE:PS00803 PROSITE:PS00804 PROSITE:PS00805 GO:GO:0016021 GO:GO:0005739 GO:GO:0005886 GO:GO:0009507 GO:GO:0005509 GO:GO:0006457 GO:GO:0005789 GO:GO:0005529 GO:GO:0051082 EMBL:AB010069 InterPro:IPR008985 InterPro:IPR013320 Gene3D:G3DSA:2.60.120.200 SUPFAM:SSF49899 GO:GO:0009505 eggNOG:NOG305105 HOGENOM:HBG444251 PANTHER:PTHR11073 SUPFAM:SSF63887 EMBL:Z18242 EMBL:AY059880 EMBL:AY114669 EMBL:AY086864 IPI:IPI00539561 PIR:JN0597 RefSeq:NP_200987.1 UniGene:At.21770 ProteinModelPortal:P29402 SMR:P29402 STRING:P29402 PRIDE:P29402 EnsemblPlants:AT5G61790.1 GeneID:836301 KEGG:ath:AT5G61790 TAIR:At5g61790 InParanoid:P29402 KO:K08054 OMA:DYKGIWK PhylomeDB:P29402 ProtClustDB:CLSN2686945 ArrayExpress:P29402 Genevestigator:P29402 GermOnline:AT5G61790 Gene3D:G3DSA:2.10.250.10 Uniprot:P29402

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig00674	438	101	1.988	2.18E-45	TAIR|locus:505006460 - symbol:AHL20 "AT4G14465" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0042742 "defense response to bacterium" evidence=IMP] EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0042742 HOGENOM:HBG748911 InterPro:IPR005175 InterPro:IPR014476 Pfam:PF03479 PIRSF:PIRSF016021 EMBL:BT006423 EMBL:AK118702 EMBL:AK227935 EMBL:BR000356 IPI:IPI00521749 RefSeq:NP_567432.1 UniGene:At.33280 UniGene:At.67625 ProteinModelPortal:Q8GWQ2 SMR:Q8GWQ2 IntAct:Q8GWQ2 PRIDE:Q8GWQ2 EnsemblPlants:AT4G14465.1 GeneID:827093 KEGG:ath:AT4G14465 TAIR:At4g14465 eggNOG:NOG328801 InParanoid:Q8GWQ2 OMA:YAWAHAR PhylomeDB:Q8GWQ2 ProtClustDB:CLSN2917544 Genevestigator:Q8GWQ2 Uniprot:Q8GWQ2
Root	Isotig00675	438	101	1.988	2.18E-45	TAIR|locus:505006460 - symbol:AHL20 "AT4G14465" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0042742 "defense response to bacterium" evidence=IMP] EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0042742 HOGENOM:HBG748911 InterPro:IPR005175 InterPro:IPR014476 Pfam:PF03479 PIRSF:PIRSF016021 EMBL:BT006423 EMBL:AK118702 EMBL:AK227935 EMBL:BR000356 IPI:IPI00521749 RefSeq:NP_567432.1 UniGene:At.33280 UniGene:At.67625 ProteinModelPortal:Q8GWQ2 SMR:Q8GWQ2 IntAct:Q8GWQ2 PRIDE:Q8GWQ2 EnsemblPlants:AT4G14465.1 GeneID:827093 KEGG:ath:AT4G14465 TAIR:At4g14465 eggNOG:NOG328801 InParanoid:Q8GWQ2 OMA:YAWAHAR PhylomeDB:Q8GWQ2 ProtClustDB:CLSN2917544 Genevestigator:Q8GWQ2 Uniprot:Q8GWQ2
Root	Isotig00676	469	144	1.575	1.37E-35	UNIPROTKB|Q70KG5 - symbol:RAFTIN1A "Protein RAFTIN 1A" species:4565 "Triticum aestivum" [GO:0009555 "pollen development" evidence=ISS] [GO:0043668 "exine" evidence=IDA] GO:GO:0009555 InterPro:IPR004873 Pfam:PF03181 PROSITE:PS51277 EMBL:AJ575662 EMBL:AJ575663 UniGene:Ta.56095 Gramene:Q70KG5 GO:GO:0043668 Uniprot:Q70KG5
Root	Isotig00677	55	11	2.193	9.64E-08	TAIR|locus:2156997 - symbol:AT5G49690 species:3702 "Arabidopsis thaliana" [GO:0008152 "metabolic process" evidence=IEA] [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR002213 Pfam:PF00201 PROSITE:PS00375 GO:GO:0005829 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0016758 CAZy:GT1 PANTHER:PTHR11926 EMBL:AB025613 HOGENOM:HBG749942 eggNOG:NOG271171 EMBL:AK117150 EMBL:BT005390 IPI:IPI00525933 RefSeq:NP_199780.1 UniGene:At.29773 UniGene:At.75314 ProteinModelPortal:Q9LTA3 SMR:Q9LTA3 IntAct:Q9LTA3 PRIDE:Q9LTA3 EnsemblPlants:AT5G49690.1 GeneID:835032 KEGG:ath:AT5G49690 TAIR:At5g49690 InParanoid:Q9LTA3 OMA:YDYASHW PhylomeDB:Q9LTA3 ProtClustDB:PLN02670 Genevestigator:Q9LTA3 Uniprot:Q9LTA3
Root	Isotig00678	40	0	6.193	1.34E-10	TAIR|locus:2156997 - symbol:AT5G49690 species:3702 "Arabidopsis thaliana" [GO:0008152 "metabolic process" evidence=IEA] [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR002213 Pfam:PF00201 PROSITE:PS00375 GO:GO:0005829 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0016758 CAZy:GT1 PANTHER:PTHR11926 EMBL:AB025613 HOGENOM:HBG749942 eggNOG:NOG271171 EMBL:AK117150 EMBL:BT005390 IPI:IPI00525933 RefSeq:NP_199780.1 UniGene:At.29773 UniGene:At.75314 ProteinModelPortal:Q9LTA3 SMR:Q9LTA3 IntAct:Q9LTA3 PRIDE:Q9LTA3 EnsemblPlants:AT5G49690.1 GeneID:835032 KEGG:ath:AT5G49690 TAIR:At5g49690 InParanoid:Q9LTA3 OMA:YDYASHW PhylomeDB:Q9LTA3 ProtClustDB:PLN02670 Genevestigator:Q9LTA3 Uniprot:Q9LTA3
Root	Isotig00683	44	16	1.330	0.000777292	TAIR|locus:2222607 - symbol:AT5G14520 "AT5G14520" species:3702 "Arabidopsis thaliana" [GO:0003713 "transcription coactivator activity" evidence=ISS] [GO:0005622 "intracellular" evidence=IEA;ISS] [GO:0005730 "nucleolus" evidence=IEA] [GO:0008283 "cell proliferation" evidence=IEA] InterPro:IPR001357 InterPro:IPR010613 Pfam:PF00533 Pfam:PF06732 PROSITE:PS50172 SMART:SM00292 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005730 SUPFAM:SSF52113 GO:GO:0006364 EMBL:AL163792 eggNOG:COG5163 HOGENOM:HBG410102 KO:K14843 OMA:SIKGVYY HSSP:P18887 IPI:IPI00522738 PIR:T48625 RefSeq:NP_196956.1 UniGene:At.50457 ProteinModelPortal:Q9LYK7 SMR:Q9LYK7 STRING:Q9LYK7 PRIDE:Q9LYK7 EnsemblPlants:AT5G14520.1 GeneID:831303 KEGG:ath:AT5G14520 TAIR:At5g14520 InParanoid:Q9LYK7 PhylomeDB:Q9LYK7 ProtClustDB:CLSN2687226 Genevestigator:Q9LYK7 Uniprot:Q9LYK7
Root	Isotig00684	44	16	1.330	0.000777292	TAIR|locus:2222607 - symbol:AT5G14520 "AT5G14520" species:3702 "Arabidopsis thaliana" [GO:0003713 "transcription coactivator activity" evidence=ISS] [GO:0005622 "intracellular" evidence=IEA;ISS] [GO:0005730 "nucleolus" evidence=IEA] [GO:0008283 "cell proliferation" evidence=IEA] InterPro:IPR001357 InterPro:IPR010613

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						Pfam:PF00533 Pfam:PF06732 PROSITE:PS50172 SMART:SM00292 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005730 SUPFAM:SSF52113 GO:GO:0006364 EMBL:AL163792 eggNOG:COG5163 HOGENOM:HBG410102 KO:K14843 OMA:SIKGVYY HSSP:P18887 IPI:IPI00522738 PIR:T48625 RefSeq:NP_196956.1 UniGene:At.50457 ProteinModelPortal:Q9LYK7 SMR:Q9LYK7 STRING:Q9LYK7 PRIDE:Q9LYK7 EnsemblPlants:AT5G14520.1 GeneID:831303 KEGG:ath:AT5G14520 TAIR:At5g14520 InParanoid:Q9LYK7 PhylomeDB:Q9LYK7 ProtClustDB:CLSN2687226 Genevestigator:Q9LYK7 Uniprot:Q9LYK7
Root	Isotig00688	20	3	2.608	0.000371713	TAIR|locus:2119971 - symbol:AT4G28990 "AT4G28990" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0008270 "zinc ion binding" evidence=IEA] InterPro:IPR001876 PROSITE:PS01358 PROSITE:PS50199 SMART:SM00547 EMBL:CP002687 GO:GO:0008270 GO:GO:0005622 EMBL:AL078470 EMBL:AL161574 EMBL:BT029205 IPI:IPI00536508 PIR:T08954 RefSeq:NP_194628.1 UniGene:At.31966 ProteinModelPortal:Q9SZD0 SMR:Q9SZD0 PRIDE:Q9SZD0 EnsemblPlants:AT4G28990.1 GeneID:829020 KEGG:ath:AT4G28990 TAIR:At4g28990 InParanoid:Q9SZD0 OMA:FARREYC PhylomeDB:Q9SZD0 ProtClustDB:CLSN2916031 ArrayExpress:Q9SZD0 Genevestigator:Q9SZD0 Uniprot:Q9SZD0
Root	Isotig00693	33	4	2.915	1.26E-06	No hit
Root	Isotig00694	33	4	2.915	1.26E-06	TAIR|locus:2036467 - symbol:ETFALPHA "AT1G50940" species:3702 "Arabidopsis thaliana" [GO:0005739 "mitochondrion" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] InterPro:IPR001308 PIRSF:PIRSF000089 Pfam:PF01012 Pfam:PF00766 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009055 GO:GO:0050660 GO:GO:0005759 GO:GO:0006810 GO:GO:0005507 GO:GO:0022900 InterPro:IPR014729 Gene3D:G3DSA:3.40.50.620 EMBL:AC079284 EMBL:BT004989 EMBL:AK117515 IPI:IPI00542927 PIR:E96546 RefSeq:NP_175507.1 UniGene:At.21003 UniGene:At.66968 HSSP:P13804 ProteinModelPortal:Q9C6I6 SMR:Q9C6I6 IntAct:Q9C6I6 STRING:Q9C6I6 PRIDE:Q9C6I6 EnsemblPlants:AT1G50940.1 GeneID:841516 KEGG:ath:AT1G50940 GeneFarm:2340 TAIR:At1g50940 eggNOG:COG2025 HOGENOM:HBG615986 InParanoid:Q9C6I6 KO:K03522 OMA:TIRSTSF PhylomeDB:Q9C6I6 ProtClustDB:PLN00022 ArrayExpress:Q9C6I6 Genevestigator:Q9C6I6 InterPro:IPR014730 InterPro:IPR014731 InterPro:IPR018206 SMART:SM00893 PROSITE:PS00696 Uniprot:Q9C6I6
Root	Isotig00695	28	4	2.678	1.93E-05	No hit
Root	Isotig00696	17	1	3.958	8.09E-05	No hit
Root	Isotig00697	17	1	3.958	8.09E-05	TAIR|locus:2036467 - symbol:ETFALPHA "AT1G50940" species:3702 "Arabidopsis thaliana" [GO:0005739 "mitochondrion" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] InterPro:IPR001308 PIRSF:PIRSF000089 Pfam:PF01012 Pfam:PF00766 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009055 GO:GO:0050660 GO:GO:0005759 GO:GO:0006810 GO:GO:0005507 GO:GO:0022900 InterPro:IPR014729 Gene3D:G3DSA:3.40.50.620 EMBL:AC079284 EMBL:BT004989 EMBL:AK117515 IPI:IPI00542927 PIR:E96546 RefSeq:NP_175507.1 UniGene:At.21003 UniGene:At.66968 HSSP:P13804 ProteinModelPortal:Q9C6I6 SMR:Q9C6I6 IntAct:Q9C6I6 STRING:Q9C6I6 PRIDE:Q9C6I6 EnsemblPlants:AT1G50940.1 GeneID:841516 KEGG:ath:AT1G50940 GeneFarm:2340 TAIR:At1g50940 eggNOG:COG2025 HOGENOM:HBG615986 InParanoid:Q9C6I6 KO:K03522 OMA:TIRSTSF PhylomeDB:Q9C6I6 ProtClustDB:PLN00022 ArrayExpress:Q9C6I6 Genevestigator:Q9C6I6 InterPro:IPR014730 InterPro:IPR014731 InterPro:IPR018206 SMART:SM00893 PROSITE:PS00696 Uniprot:Q9C6I6
Root	Isotig00698	274	118	1.086	8.96E-13	TAIR|locus:2165512 - symbol:PAF1 "proteasome alpha subunit F1" species:3702 "Arabidopsis thaliana" [GO:0004175 "endopeptidase activity" evidence=IEA] [GO:0004298 "threonine-type endopeptidase activity" evidence=IEA] [GO:0008233 "peptidase activity" evidence=ISS] [GO:0006511 "ubiquitin-dependent protein catabolic process" evidence=TAS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0046685 "response to arsenic-containing substance" evidence=IMP] [GO:0000502 "proteasome complex" evidence=ISS;IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0030163 "protein catabolic process" evidence=ISS] [GO:0005839 "proteasome core complex" evidence=TAS] InterPro:IPR000426 InterPro:IPR001353 InterPro:IPR023332 Pfam:PF00227 Pfam:PF10584 PROSITE:PS00388 PROSITE:PS51475 SMART:SM00948 GO:GO:0005829 GO:GO:0005886 GO:GO:0005634 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0046685 GO:GO:0006511 GO:GO:0004298 EMBL:AB007647 EMBL:M98495 EMBL:AF043526 EMBL:AF375447 EMBL:AY058128 EMBL:AY113047 EMBL:AY085017 IPI:IPI00525551 PIR:S39900 PIR:T51974 RefSeq:NP_199093.1 UniGene:At.23724 ProteinModelPortal:P34066 SMR:P34066 IntAct:P34066 STRING:P34066 PRIDE:P34066 EnsemblPlants:AT5G42790.1 GeneID:834290 KEGG:ath:AT5G42790 TAIR:At5g42790 eggNOG:COG0638 HOGENOM:HBG499923 InParanoid:P34066 KO:K02725 OMA:DVAPMEM PhylomeDB:P34066

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						ProtClustDB:CLSN2681914 ArrayExpress:P34066 Genevestigator:P34066 GermOnline:AT5G42790 GO:GO:0019773 Uniprot:P34066
Root	Isotig00699	255	105	1.151	5.11E-13	TAIR|locus:2157869 - symbol:PNG1 "AT5G49570" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=ISS] [GO:0000224 "peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase activity" evidence=IGI;IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009751 "response to salicylic acid stimulus" evidence=IEP] [GO:0010188 "response to microbial phytotoxin" evidence=IEP] [GO:0010193 "response to ozone" evidence=IEP] InterPro:IPR018325 Pfam:PF03835 GO:GO:0005829 GO:GO:0005634 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0046872 GO:GO:0003684 GO:GO:0010193 GO:GO:0009751 InterPro:IPR008979 SUPFAM:SSF49785 GO:GO:0006289 EMBL:AB023033 InterPro:IPR002931 GO:GO:0010188 SMART:SM00460 KO:K01456 GO:GO:0000224 HSSP:Q8K113 eggNOG:NOG307426 EMBL:AY140065 EMBL:BT003161 EMBL:BT003398 EMBL:AK228156 IPI:IPI00533409 RefSeq:NP_199768.1 UniGene:At.27656 UniGene:At.29778 ProteinModelPortal:Q9FGY9 SMR:Q9FGY9 STRING:Q9FGY9 PRIDE:Q9FGY9 EnsemblPlants:AT5G49570.1 GeneID:835019 KEGG:ath:AT5G49570 TAIR:At5g49570 HOGENOM:HBG316986 InParanoid:Q9FGY9 OMA:QLLFWFK PhylomeDB:Q9FGY9 ProtClustDB:CLSN2686981 Genevestigator:Q9FGY9 GermOnline:AT5G49570 Uniprot:Q9FGY9
Root	Isotig00700	250	101	1.179	3.17E-13	No hit
Root	Isotig00701	247	98	1.205	1.71E-13	No hit
Root	Isotig00702	242	97	1.190	5.03E-13	No hit
Root	Isotig00703	242	101	1.132	3.91E-12	No hit
Root	Isotig00718	55	17	1.565	2.20E-05	No hit
Root	Isotig00719	56	17	1.591	1.47E-05	No hit
Root	Isotig00720	59	17	1.666	4.26E-06	No hit
Root	Isotig00721	55	17	1.565	2.20E-05	TIGR_CMR|GSU_1062 - symbol:GSU_1062 "cytochrome c family protein, putative" species:243231 "Geobacter sulfurreducens PCA" [GO:0009055 "electron carrier activity" evidence=ISS] EMBL:AE017180 GenomeReviews:AE017180_GR RefSeq:NP_952115.1 GeneID:2688672 KEGG:gsu:GSU1062 PATRIC:22024890 TIGR:GSU1062 HOGENOM:HBG090252 OMA:RIPELND ProtClustDB:CLSK743107 Uniprot:Q74EA1
Root	Isotig00722	60	17	1.690	2.80E-06	No hit
Root	Isotig00723	55	17	1.565	2.20E-05	No hit
Root	Isotig00724	60	17	1.690	2.80E-06	No hit
Root	Isotig00725	59	17	1.666	4.26E-06	TIGR_CMR|GSU_1062 - symbol:GSU_1062 "cytochrome c family protein, putative" species:243231 "Geobacter sulfurreducens PCA" [GO:0009055 "electron carrier activity" evidence=ISS] EMBL:AE017180 GenomeReviews:AE017180_GR RefSeq:NP_952115.1 GeneID:2688672 KEGG:gsu:GSU1062 PATRIC:22024890 TIGR:GSU1062 HOGENOM:HBG090252 OMA:RIPELND ProtClustDB:CLSK743107 Uniprot:Q74EA1
Root	Isotig00726	61	17	1.714	1.84E-06	No hit
Root	Isotig00727	59	17	1.666	4.26E-06	No hit
Root	Isotig00728	60	17	1.690	2.80E-06	TIGR_CMR|GSU_1062 - symbol:GSU_1062 "cytochrome c family protein, putative" species:243231 "Geobacter sulfurreducens PCA" [GO:0009055 "electron carrier activity" evidence=ISS] EMBL:AE017180 GenomeReviews:AE017180_GR RefSeq:NP_952115.1 GeneID:2688672 KEGG:gsu:GSU1062 PATRIC:22024890 TIGR:GSU1062 HOGENOM:HBG090252 OMA:RIPELND ProtClustDB:CLSK743107 Uniprot:Q74EA1
Root	Isotig00729	60	17	1.690	2.80E-06	No hit
Root	Isotig00730	55	17	1.565	2.20E-05	No hit
Root	Isotig00731	59	17	1.666	4.26E-06	No hit
Root	Isotig00732	60	17	1.690	2.80E-06	No hit
Root	Isotig00733	317	824	-1.507	9.46E-63	SGD|S000028422 - symbol:TAR1 "Mitochondrial protein potentially involved in respiratory metabolism" species:4932 "Saccharomyces cerevisiae" [GO:0003674 "molecular_function" evidence=ND] [GO:0043457 "regulation of cellular respiration" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IEA;IMP] SGD:S000028422 GO:GO:0005739 EMBL:BK006945 EMBL:U53879 GO:GO:0043457 EMBL:Z73326 EMBL:AF479964 RefSeq:NP_690845.1 ProteinModelPortal:Q8TGM6 STRING:Q8TGM6 EnsemblFungi:YLR154W-C GeneID:1466405 KEGG:sce:YLR154W-C CYGD:YLR154w-c eggNOG:NOG79861 OMA:SCSKEHR OrthoDB:EOG466ZX8 NextBio:967146 Genevestigator:Q8TGM6 GermOnline:YLR154W-C Uniprot:Q8TGM6

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig00734	353	959	-1.571	3.54E-77	SGD|S000028422 - symbol:TAR1 "Mitochondrial protein potentially involved in respiratory metabolism" species:4932 "Saccharomyces cerevisiae" [GO:0003674 "molecular_function" evidence=ND] [GO:0043457 "regulation of cellular respiration" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IEA;IMP] SGD:S000028422 GO:GO:0005739 EMBL:BK006945 EMBL:U53879 GO:GO:0043457 EMBL:Z73326 EMBL:AF479964 RefSeq:NP_690845.1 ProteinModelPortal:Q8TGM6 STRING:Q8TGM6 EnsemblFungi:YLR154W-C GeneID:1466405 KEGG:sce:YLR154W-C CYGD:YLR154w-c eggNOG:NOG79861 OMA:SCSKEHR OrthoDB:EOG466ZX8 NextBio:967146 Genevestigator:Q8TGM6 GermOnline:YLR154W-C Uniprot:Q8TGM6
Root	Isotig00735	353	959	-1.571	3.54E-77	SGD|S000028422 - symbol:TAR1 "Mitochondrial protein potentially involved in respiratory metabolism" species:4932 "Saccharomyces cerevisiae" [GO:0003674 "molecular_function" evidence=ND] [GO:0043457 "regulation of cellular respiration" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IEA;IMP] SGD:S000028422 GO:GO:0005739 EMBL:BK006945 EMBL:U53879 GO:GO:0043457 EMBL:Z73326 EMBL:AF479964 RefSeq:NP_690845.1 ProteinModelPortal:Q8TGM6 STRING:Q8TGM6 EnsemblFungi:YLR154W-C GeneID:1466405 KEGG:sce:YLR154W-C CYGD:YLR154w-c eggNOG:NOG79861 OMA:SCSKEHR OrthoDB:EOG466ZX8 NextBio:967146 Genevestigator:Q8TGM6 GermOnline:YLR154W-C Uniprot:Q8TGM6
Root	Isotig00736	353	959	-1.571	3.54E-77	SGD|S000028422 - symbol:TAR1 "Mitochondrial protein potentially involved in respiratory metabolism" species:4932 "Saccharomyces cerevisiae" [GO:0003674 "molecular_function" evidence=ND] [GO:0043457 "regulation of cellular respiration" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IEA;IMP] SGD:S000028422 GO:GO:0005739 EMBL:BK006945 EMBL:U53879 GO:GO:0043457 EMBL:Z73326 EMBL:AF479964 RefSeq:NP_690845.1 ProteinModelPortal:Q8TGM6 STRING:Q8TGM6 EnsemblFungi:YLR154W-C GeneID:1466405 KEGG:sce:YLR154W-C CYGD:YLR154w-c eggNOG:NOG79861 OMA:SCSKEHR OrthoDB:EOG466ZX8 NextBio:967146 Genevestigator:Q8TGM6 GermOnline:YLR154W-C Uniprot:Q8TGM6
Root	Isotig00737	252	576	-1.322	1.03E-36	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00738	200	434	-1.247	8.89E-26	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00739	200	434	-1.247	8.89E-26	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00740	200	434	-1.247	8.89E-26	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00741	242	562	-1.345	8.92E-37	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00742	278	697	-1.455	1.01E-50	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00743	278	697	-1.455	1.01E-50	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00744	278	697	-1.455	1.01E-50	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig00745	188	535	-1.638	1.94E-46	SGD|S000028422 - symbol:TAR1 "Mitochondrial protein potentially involved in respiratory metabolism" species:4932 "Saccharomyces cerevisiae" [GO:0003674 "molecular_function" evidence=ND] [GO:0043457 "regulation of cellular respiration" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IEA;IMP] SGD:S000028422 GO:GO:0005739 EMBL:BK006945 EMBL:U53879 GO:GO:0043457 EMBL:Z73326 EMBL:AF479964 RefSeq:NP_690845.1 ProteinModelPortal:Q8TGM6 STRING:Q8TGM6 EnsemblFungi:YLR154W-C GeneID:1466405 KEGG:sce:YLR154W-C CYGD:YLR154w-c eggNOG:NOG79861 OMA:SCSKEHR OrthoDB:EOG466ZX8 NextBio:967146 Genevestigator:Q8TGM6 GermOnline:YLR154W-C Uniprot:Q8TGM6
Root	Isotig00746	113	273	-1.402	8.19E-20	No hit
Root	Isotig00747	4	53	-3.857	5.31E-13	TAIR|locus:2152160 - symbol:BGLU13 "beta glucosidase 13" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=IEA;ISS] [GO:0005975 "carbohydrate metabolic process" evidence=IEA] [GO:0043169 "cation binding" evidence=IEA] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR001360 InterPro:IPR013781 InterPro:IPR018120 Pfam:PF00232 PRINTS:PR00131 PROSITE:PS00572 PROSITE:PS00653 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0043169 InterPro:IPR017853 Gene3D:G3DSA:3.20.20.80 SUPFAM:SSF51445 GO:GO:0005975 GO:GO:0008422 CAZy:GH1 eggNOG:COG2723 HOGENOM:HBG316462 PANTHER:PTHR10353 EMBL:AB024024 HSSP:P26205 KO:K01188 ProtClustDB:CLSN2683204 EMBL:BT033043 IPI:IPI00536489 RefSeq:NP_199277.1 UniGene:At.50504 UniGene:At.75350 ProteinModelPortal:Q9LU02 SMR:Q9LU02 STRING:Q9LU02 PRIDE:Q9LU02 EnsemblPlants:AT5G44640.1 GeneID:834493

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						KEGG:ath:AT5G44640 TAIR:At5g44640 InParanoid:Q9LU02 OMA:EVIAKKH PhylomeDB:Q9LU02 Genevestigator:Q9LU02 Uniprot:Q9LU02
Root	Isotig00748	4	53	-3.857	5.31E-13	TAIR|locus:2152160 - symbol:BGLU13 "beta glucosidase 13" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=IEA;ISS] [GO:0005975 "carbohydrate metabolic process" evidence=IEA] [GO:0043169 "cation binding" evidence=IEA] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR001360 InterPro:IPR013781 InterPro:IPR018120 Pfam:PF00232 PRINTS:PR00131 PROSITE:PS00572 PROSITE:PS00653 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0043169 InterPro:IPR017853 Gene3D:G3DSA:3.20.20.80 SUPFAM:SSF51445 GO:GO:0005975 GO:GO:0008422 CAZy:GH1 eggNOG:COG2723 HOGENOM:HBG316462 PANTHER:PTHR10353 EMBL:AB024024 HSSP:P26205 KO:K01188 ProtClustDB:CLSN2683204 EMBL:BT033043 IPI:IPI00536489 RefSeq:NP_199277.1 UniGene:At.50504 UniGene:At.75350 ProteinModelPortal:Q9LU02 SMR:Q9LU02 STRING:Q9LU02 PRIDE:Q9LU02 EnsemblPlants:AT5G44640.1 GeneID:834493 KEGG:ath:AT5G44640 TAIR:At5g44640 InParanoid:Q9LU02 OMA:EVIAKKH PhylomeDB:Q9LU02 Genevestigator:Q9LU02 Uniprot:Q9LU02
Root	Isotig00749	4	44	-3.588	1.46E-10	TAIR|locus:2197960 - symbol:BGLU40 "beta glucosidase 40" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=IEA;ISS] [GO:0005975 "carbohydrate metabolic process" evidence=IEA] [GO:0043169 "cation binding" evidence=IEA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] InterPro:IPR001360 InterPro:IPR013781 InterPro:IPR018120 Pfam:PF00232 PRINTS:PR00131 PROSITE:PS00572 PROSITE:PS00653 EMBL:CP002684 GenomeReviews:CT485782_GR EMBL:AC013427 GO:GO:0048046 GO:GO:0009507 GO:GO:0043169 InterPro:IPR017853 Gene3D:G3DSA:3.20.20.80 SUPFAM:SSF51445 GO:GO:0005975 GO:GO:0008422 CAZy:GH1 eggNOG:COG2723 PANTHER:PTHR10353 HSSP:P26205 KO:K01188 EMBL:AY045927 EMBL:AY142610 EMBL:AY085043 EMBL:AK221011 IPI:IPI00537698 PIR:F86392 RefSeq:NP_173978.1 UniGene:At.15959 ProteinModelPortal:Q9FZE0 SMR:Q9FZE0 STRING:Q9FZE0 PRIDE:Q9FZE0 EnsemblPlants:AT1G26560.1 GeneID:839196 KEGG:ath:AT1G26560 TAIR:At1g26560 InParanoid:Q9FZE0 OMA:NDFAAYA PhylomeDB:Q9FZE0 ProtClustDB:CLSN2682658 ArrayExpress:Q9FZE0 Uniprot:Q9FZE0
Root	Isotig00750	4	44	-3.588	1.46E-10	TAIR|locus:2197960 - symbol:BGLU40 "beta glucosidase 40" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=IEA;ISS] [GO:0005975 "carbohydrate metabolic process" evidence=IEA] [GO:0043169 "cation binding" evidence=IEA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] InterPro:IPR001360 InterPro:IPR013781 InterPro:IPR018120 Pfam:PF00232 PRINTS:PR00131 PROSITE:PS00572 PROSITE:PS00653 EMBL:CP002684 GenomeReviews:CT485782_GR EMBL:AC013427 GO:GO:0048046 GO:GO:0009507 GO:GO:0043169 InterPro:IPR017853 Gene3D:G3DSA:3.20.20.80 SUPFAM:SSF51445 GO:GO:0005975 GO:GO:0008422 CAZy:GH1 eggNOG:COG2723 PANTHER:PTHR10353 HSSP:P26205 KO:K01188 EMBL:AY045927 EMBL:AY142610 EMBL:AY085043 EMBL:AK221011 IPI:IPI00537698 PIR:F86392 RefSeq:NP_173978.1 UniGene:At.15959 ProteinModelPortal:Q9FZE0 SMR:Q9FZE0 STRING:Q9FZE0 PRIDE:Q9FZE0 EnsemblPlants:AT1G26560.1 GeneID:839196 KEGG:ath:AT1G26560 TAIR:At1g26560 InParanoid:Q9FZE0 OMA:NDFAAYA PhylomeDB:Q9FZE0 ProtClustDB:CLSN2682658 ArrayExpress:Q9FZE0 Uniprot:Q9FZE0
Root	Isotig00751	1	43	-5.555	3.04E-12	TAIR|locus:2152160 - symbol:BGLU13 "beta glucosidase 13" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=IEA;ISS] [GO:0005975 "carbohydrate metabolic process" evidence=IEA] [GO:0043169 "cation binding" evidence=IEA] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR001360 InterPro:IPR013781 InterPro:IPR018120 Pfam:PF00232 PRINTS:PR00131 PROSITE:PS00572 PROSITE:PS00653 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0043169 InterPro:IPR017853 Gene3D:G3DSA:3.20.20.80 SUPFAM:SSF51445 GO:GO:0005975 GO:GO:0008422 CAZy:GH1 eggNOG:COG2723 HOGENOM:HBG316462 PANTHER:PTHR10353 EMBL:AB024024 HSSP:P26205 KO:K01188 ProtClustDB:CLSN2683204 EMBL:BT033043 IPI:IPI00536489 RefSeq:NP_199277.1 UniGene:At.50504 UniGene:At.75350 ProteinModelPortal:Q9LU02 SMR:Q9LU02 STRING:Q9LU02 PRIDE:Q9LU02 EnsemblPlants:AT5G44640.1 GeneID:834493 KEGG:ath:AT5G44640 TAIR:At5g44640 InParanoid:Q9LU02 OMA:EVIAKKH PhylomeDB:Q9LU02 Genevestigator:Q9LU02 Uniprot:Q9LU02

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig00752	1	43	-5.555	3.04E-12	TAIR|locus:2152160 - symbol:BGLU13 "beta glucosidase 13" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=IEA;ISS] [GO:0005975 "carbohydrate metabolic process" evidence=IEA] [GO:0043169 "cation binding" evidence=IEA] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR001360 InterPro:IPR013781 InterPro:IPR018120 Pfam:PF00232 PRINTS:PR00131 PROSITE:PS00572 PROSITE:PS00653 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0043169 InterPro:IPR017853 Gene3D:G3DSA:3.20.20.80 SUPFAM:SSF51445 GO:GO:0005975 GO:GO:0008422 CAZy:GH1 eggNOG:COG2723 HOGENOM:HBG316462 PANTHER:PTHR10353 EMBL:AB024024 HSSP:P26205 KO:K01188 ProtClustDB:CLSN2683204 EMBL:BT033043 IPI:IPI00536489 RefSeq:NP_199277.1 UniGene:At.50504 UniGene:At.75350 ProteinModelPortal:Q9LU02 SMR:Q9LU02 STRING:Q9LU02 PRIDE:Q9LU02 EnsemblPlants:AT5G44640.1 GeneID:834493 KEGG:ath:AT5G44640 TAIR:At5g44640 InParanoid:Q9LU02 OMA:EVIAKKH PhylomeDB:Q9LU02 Genevestigator:Q9LU02 Uniprot:Q9LU02
Root	Isotig00753	1	44	-5.588	1.69E-12	TAIR|locus:2152160 - symbol:BGLU13 "beta glucosidase 13" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=IEA;ISS] [GO:0005975 "carbohydrate metabolic process" evidence=IEA] [GO:0043169 "cation binding" evidence=IEA] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR001360 InterPro:IPR013781 InterPro:IPR018120 Pfam:PF00232 PRINTS:PR00131 PROSITE:PS00572 PROSITE:PS00653 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0043169 InterPro:IPR017853 Gene3D:G3DSA:3.20.20.80 SUPFAM:SSF51445 GO:GO:0005975 GO:GO:0008422 CAZy:GH1 eggNOG:COG2723 HOGENOM:HBG316462 PANTHER:PTHR10353 EMBL:AB024024 HSSP:P26205 KO:K01188 ProtClustDB:CLSN2683204 EMBL:BT033043 IPI:IPI00536489 RefSeq:NP_199277.1 UniGene:At.50504 UniGene:At.75350 ProteinModelPortal:Q9LU02 SMR:Q9LU02 STRING:Q9LU02 PRIDE:Q9LU02 EnsemblPlants:AT5G44640.1 GeneID:834493 KEGG:ath:AT5G44640 TAIR:At5g44640 InParanoid:Q9LU02 OMA:EVIAKKH PhylomeDB:Q9LU02 Genevestigator:Q9LU02 Uniprot:Q9LU02
Root	Isotig00754	1	44	-5.588	1.69E-12	TAIR|locus:2152160 - symbol:BGLU13 "beta glucosidase 13" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=IEA;ISS] [GO:0005975 "carbohydrate metabolic process" evidence=IEA] [GO:0043169 "cation binding" evidence=IEA] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR001360 InterPro:IPR013781 InterPro:IPR018120 Pfam:PF00232 PRINTS:PR00131 PROSITE:PS00572 PROSITE:PS00653 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0043169 InterPro:IPR017853 Gene3D:G3DSA:3.20.20.80 SUPFAM:SSF51445 GO:GO:0005975 GO:GO:0008422 CAZy:GH1 eggNOG:COG2723 HOGENOM:HBG316462 PANTHER:PTHR10353 EMBL:AB024024 HSSP:P26205 KO:K01188 ProtClustDB:CLSN2683204 EMBL:BT033043 IPI:IPI00536489 RefSeq:NP_199277.1 UniGene:At.50504 UniGene:At.75350 ProteinModelPortal:Q9LU02 SMR:Q9LU02 STRING:Q9LU02 PRIDE:Q9LU02 EnsemblPlants:AT5G44640.1 GeneID:834493 KEGG:ath:AT5G44640 TAIR:At5g44640 InParanoid:Q9LU02 OMA:EVIAKKH PhylomeDB:Q9LU02 Genevestigator:Q9LU02 Uniprot:Q9LU02
Root	Isotig00755	1	34	-5.216	6.54E-10	TAIR|locus:2197960 - symbol:BGLU40 "beta glucosidase 40" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=IEA;ISS] [GO:0005975 "carbohydrate metabolic process" evidence=IEA] [GO:0043169 "cation binding" evidence=IEA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] InterPro:IPR001360 InterPro:IPR013781 InterPro:IPR018120 Pfam:PF00232 PRINTS:PR00131 PROSITE:PS00572 PROSITE:PS00653 EMBL:CP002684 GenomeReviews:CT485782_GR EMBL:AC013427 GO:GO:0048046 GO:GO:0009507 GO:GO:0043169 InterPro:IPR017853 Gene3D:G3DSA:3.20.20.80 SUPFAM:SSF51445 GO:GO:0005975 GO:GO:0008422 CAZy:GH1 eggNOG:COG2723 PANTHER:PTHR10353 HSSP:P26205 KO:K01188 EMBL:AY045927 EMBL:AY142610 EMBL:AY085043 EMBL:AK221011 IPI:IPI00537698 PIR:F86392 RefSeq:NP_173978.1 UniGene:At.15959 ProteinModelPortal:Q9FZE0 SMR:Q9FZE0 STRING:Q9FZE0 PRIDE:Q9FZE0 EnsemblPlants:AT1G26560.1 GeneID:839196 KEGG:ath:AT1G26560 TAIR:At1g26560 InParanoid:Q9FZE0 OMA:NDFAAYA PhylomeDB:Q9FZE0 ProtClustDB:CLSN2682658 ArrayExpress:Q9FZE0 Uniprot:Q9FZE0
Root	Isotig00756	1	34	-5.216	6.54E-10	TAIR|locus:2197960 - symbol:BGLU40 "beta glucosidase 40" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=IEA;ISS] [GO:0005975 "carbohydrate metabolic process" evidence=IEA] [GO:0043169 "cation binding"

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						evidence=IEA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] InterPro:IPR001360 InterPro:IPR013781 InterPro:IPR018120 Pfam:PF00232 PRINTS:PR00131 PROSITE:PS00572 PROSITE:PS00653 EMBL:CP002684 GenomeReviews:CT485782_GR EMBL:AC013427 GO:GO:0048046 GO:GO:0009507 GO:GO:0043169 InterPro:IPR017853 Gene3D:G3DSA:3.20.20.80 SUPFAM:SSF51445 GO:GO:0005975 GO:GO:0008422 CAZy:GH1 eggNOG:COG2723 PANTHER:PTHR10353 HSSP:P26205 KO:K01188 EMBL:AY045927 EMBL:AY142610 EMBL:AY085043 EMBL:AK221011 IPI:IPI00537698 PIR:F86392 RefSeq:NP_173978.1 UniGene:At.15959 ProteinModelPortal:Q9FZE0 SMR:Q9FZE0 STRING:Q9FZE0 PRIDE:Q9FZE0 EnsemblPlants:AT1G26560.1 GeneID:839196 KEGG:ath:AT1G26560 TAIR:At1g26560 InParanoid:Q9FZE0 OMA:NDFAAYA PhylomeDB:Q9FZE0 ProtClustDB:CLSN2682658 ArrayExpress:Q9FZE0 Uniprot:Q9FZE0
Root	Isotig00757	1	35	-5.258	3.57E-10	TAIR|locus:2197960 - symbol:BGLU40 "beta glucosidase 40" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=IEA;ISS] [GO:0005975 "carbohydrate metabolic process" evidence=IEA] [GO:0043169 "cation binding" evidence=IEA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] InterPro:IPR001360 InterPro:IPR013781 InterPro:IPR018120 Pfam:PF00232 PRINTS:PR00131 PROSITE:PS00572 PROSITE:PS00653 EMBL:CP002684 GenomeReviews:CT485782_GR EMBL:AC013427 GO:GO:0048046 GO:GO:0009507 GO:GO:0043169 InterPro:IPR017853 Gene3D:G3DSA:3.20.20.80 SUPFAM:SSF51445 GO:GO:0005975 GO:GO:0008422 CAZy:GH1 eggNOG:COG2723 PANTHER:PTHR10353 HSSP:P26205 KO:K01188 EMBL:AY045927 EMBL:AY142610 EMBL:AY085043 EMBL:AK221011 IPI:IPI00537698 PIR:F86392 RefSeq:NP_173978.1 UniGene:At.15959 ProteinModelPortal:Q9FZE0 SMR:Q9FZE0 STRING:Q9FZE0 PRIDE:Q9FZE0 EnsemblPlants:AT1G26560.1 GeneID:839196 KEGG:ath:AT1G26560 TAIR:At1g26560 InParanoid:Q9FZE0 OMA:NDFAAYA PhylomeDB:Q9FZE0 ProtClustDB:CLSN2682658 ArrayExpress:Q9FZE0 Uniprot:Q9FZE0
Root	Isotig00759	1	35	-5.258	3.57E-10	TAIR|locus:2197960 - symbol:BGLU40 "beta glucosidase 40" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=IEA;ISS] [GO:0005975 "carbohydrate metabolic process" evidence=IEA] [GO:0043169 "cation binding" evidence=IEA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] InterPro:IPR001360 InterPro:IPR013781 InterPro:IPR018120 Pfam:PF00232 PRINTS:PR00131 PROSITE:PS00572 PROSITE:PS00653 EMBL:CP002684 GenomeReviews:CT485782_GR EMBL:AC013427 GO:GO:0048046 GO:GO:0009507 GO:GO:0043169 InterPro:IPR017853 Gene3D:G3DSA:3.20.20.80 SUPFAM:SSF51445 GO:GO:0005975 GO:GO:0008422 CAZy:GH1 eggNOG:COG2723 PANTHER:PTHR10353 HSSP:P26205 KO:K01188 EMBL:AY045927 EMBL:AY142610 EMBL:AY085043 EMBL:AK221011 IPI:IPI00537698 PIR:F86392 RefSeq:NP_173978.1 UniGene:At.15959 ProteinModelPortal:Q9FZE0 SMR:Q9FZE0 STRING:Q9FZE0 PRIDE:Q9FZE0 EnsemblPlants:AT1G26560.1 GeneID:839196 KEGG:ath:AT1G26560 TAIR:At1g26560 InParanoid:Q9FZE0 OMA:NDFAAYA PhylomeDB:Q9FZE0 ProtClustDB:CLSN2682658 ArrayExpress:Q9FZE0 Uniprot:Q9FZE0
Root	Isotig00773	15	58	-2.080	3.03E-08	TAIR|locus:2151581 - symbol:AT5G61510 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0008270 "zinc ion binding" evidence=IEA] [GO:0016491 "oxidoreductase activity" evidence=IEA] [GO:0009644 "response to high light intensity" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA] [GO:0030154 "cell differentiation" evidence=IEP] InterPro:IPR002085 InterPro:IPR013149 InterPro:IPR013154 InterPro:IPR016040 Pfam:PF00107 Pfam:PF08240 GO:GO:0005829 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 GO:GO:0008270 GO:GO:0016491 HOGENOM:HBG753318 InterPro:IPR011032 PANTHER:PTHR11695 SUPFAM:SSF50129 GO:GO:0009644 eggNOG:COG0604 KO:K00344 EMBL:BT029771 IPI:IPI00528545 RefSeq:NP_200959.2 UniGene:At.29101 ProteinModelPortal:A1L4Y4 SMR:A1L4Y4 PRIDE:A1L4Y4 EnsemblPlants:AT5G61510.1 GeneID:836272 KEGG:ath:AT5G61510 TAIR:At5g61510 InParanoid:A1L4Y4 OMA:AEEQILP PhylomeDB:A1L4Y4 ProtClustDB:CLSN2681116 Genevestigator:A1L4Y4 Uniprot:A1L4Y4
Root	Isotig00774	15	57	-2.055	5.06E-08	TAIR|locus:2151581 - symbol:AT5G61510 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0008270 "zinc ion binding" evidence=IEA] [GO:0016491 "oxidoreductase activity" evidence=IEA] [GO:0009644 "response to high light intensity" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA] [GO:0030154 "cell differentiation" evidence=IEP] InterPro:IPR002085 InterPro:IPR013149 InterPro:IPR013154 InterPro:IPR016040 Pfam:PF00107 Pfam:PF08240 GO:GO:0005829 EMBL:CP002688

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GenomeReviews:BA000015_GR GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 GO:GO:0008270 GO:GO:0016491 HOGENOM:HBG753318 InterPro:IPR011032 PANTHER:PTHR11695 SUPFAM:SSF50129 GO:GO:0009644 eggNOG:COG0604 KO:K00344 EMBL:BT029771 IPI:IPI00528545 RefSeq:NP_200959.2 UniGene:At.29101 ProteinModelPortal:A1L4Y4 SMR:A1L4Y4 PRIDE:A1L4Y4 EnsemblPlants:AT5G61510.1 GeneID:836272 KEGG:ath:AT5G61510 TAIR:At5g61510 InParanoid:A1L4Y4 OMA:AEEQILP PhylomeDB:A1L4Y4 ProtClustDB:CLSN2681116 Genevestigator:A1L4Y4 Uniprot:A1L4Y4
Root	Isotig00775	15	57	-2.055	5.06E-08	TAIR|locus:2151581 - symbol:AT5G61510 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0008270 "zinc ion binding" evidence=IEA] [GO:0016491 "oxidoreductase activity" evidence=IEA] [GO:0009644 "response to high light intensity" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA] [GO:0030154 "cell differentiation" evidence=IEP] InterPro:IPR002085 InterPro:IPR013149 InterPro:IPR013154 InterPro:IPR016040 Pfam:PF00107 Pfam:PF08240 GO:GO:0005829 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 GO:GO:0008270 GO:GO:0016491 HOGENOM:HBG753318 InterPro:IPR011032 PANTHER:PTHR11695 SUPFAM:SSF50129 GO:GO:0009644 eggNOG:COG0604 KO:K00344 EMBL:BT029771 IPI:IPI00528545 RefSeq:NP_200959.2 UniGene:At.29101 ProteinModelPortal:A1L4Y4 SMR:A1L4Y4 PRIDE:A1L4Y4 EnsemblPlants:AT5G61510.1 GeneID:836272 KEGG:ath:AT5G61510 TAIR:At5g61510 InParanoid:A1L4Y4 OMA:AEEQILP PhylomeDB:A1L4Y4 ProtClustDB:CLSN2681116 Genevestigator:A1L4Y4 Uniprot:A1L4Y4
Root	Isotig00776	15	56	-2.029	8.42E-08	TAIR|locus:2151581 - symbol:AT5G61510 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0008270 "zinc ion binding" evidence=IEA] [GO:0016491 "oxidoreductase activity" evidence=IEA] [GO:0009644 "response to high light intensity" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA] [GO:0030154 "cell differentiation" evidence=IEP] InterPro:IPR002085 InterPro:IPR013149 InterPro:IPR013154 InterPro:IPR016040 Pfam:PF00107 Pfam:PF08240 GO:GO:0005829 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 GO:GO:0008270 GO:GO:0016491 HOGENOM:HBG753318 InterPro:IPR011032 PANTHER:PTHR11695 SUPFAM:SSF50129 GO:GO:0009644 eggNOG:COG0604 KO:K00344 EMBL:BT029771 IPI:IPI00528545 RefSeq:NP_200959.2 UniGene:At.29101 ProteinModelPortal:A1L4Y4 SMR:A1L4Y4 PRIDE:A1L4Y4 EnsemblPlants:AT5G61510.1 GeneID:836272 KEGG:ath:AT5G61510 TAIR:At5g61510 InParanoid:A1L4Y4 OMA:AEEQILP PhylomeDB:A1L4Y4 ProtClustDB:CLSN2681116 Genevestigator:A1L4Y4 Uniprot:A1L4Y4
Root	Isotig00777	0	48	-6.714	3.16E-13	TAIR|locus:2089428 - symbol:LBO1 "AT3G21420" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0008152 "metabolic process" evidence=ISS] [GO:0016491 "oxidoreductase activity" evidence=IEA;ISS] InterPro:IPR005123 Pfam:PF03171 PROSITE:PS51471 EMBL:CP002686 GenomeReviews:BA000014_GR eggNOG:COG3491 HOGENOM:HBG749762 GO:GO:0016706 HSSP:Q96323 EMBL:AP001305 EMBL:AY084795 EMBL:BT005988 EMBL:AK227427 IPI:IPI00545861 RefSeq:NP_566685.1 UniGene:At.38063 ProteinModelPortal:Q9LIF4 SMR:Q9LIF4 PRIDE:Q9LIF4 EnsemblPlants:AT3G21420.1 GeneID:821696 KEGG:ath:AT3G21420 TAIR:At3g21420 InParanoid:Q9LIF4 OMA:FIREEYE PhylomeDB:Q9LIF4 ProtClustDB:PLN02758 Genevestigator:Q9LIF4 Uniprot:Q9LIF4
Root	Isotig00778	0	47	-6.684	5.35E-13	TAIR|locus:2089428 - symbol:LBO1 "AT3G21420" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0008152 "metabolic process" evidence=ISS] [GO:0016491 "oxidoreductase activity" evidence=IEA;ISS] InterPro:IPR005123 Pfam:PF03171 PROSITE:PS51471 EMBL:CP002686 GenomeReviews:BA000014_GR eggNOG:COG3491 HOGENOM:HBG749762 GO:GO:0016706 HSSP:Q96323 EMBL:AP001305 EMBL:AY084795 EMBL:BT005988 EMBL:AK227427 IPI:IPI00545861 RefSeq:NP_566685.1 UniGene:At.38063 ProteinModelPortal:Q9LIF4 SMR:Q9LIF4 PRIDE:Q9LIF4 EnsemblPlants:AT3G21420.1 GeneID:821696 KEGG:ath:AT3G21420 TAIR:At3g21420 InParanoid:Q9LIF4 OMA:FIREEYE PhylomeDB:Q9LIF4 ProtClustDB:PLN02758 Genevestigator:Q9LIF4 Uniprot:Q9LIF4
Root	Isotig00779	0	47	-6.684	5.35E-13	TAIR|locus:2089428 - symbol:LBO1 "AT3G21420" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0008152 "metabolic process" evidence=ISS] [GO:0016491 "oxidoreductase activity" evidence=IEA;ISS] InterPro:IPR005123 Pfam:PF03171 PROSITE:PS51471 EMBL:CP002686 GenomeReviews:BA000014_GR eggNOG:COG3491 HOGENOM:HBG749762 GO:GO:0016706 HSSP:Q96323 EMBL:AP001305 EMBL:AY084795 EMBL:BT005988 EMBL:AK227427 IPI:IPI00545861 RefSeq:NP_566685.1 UniGene:At.38063 ProteinModelPortal:Q9LIF4 SMR:Q9LIF4 PRIDE:Q9LIF4 EnsemblPlants:AT3G21420.1 GeneID:821696 KEGG:ath:AT3G21420 TAIR:At3g21420 InParanoid:Q9LIF4 OMA:FIREEYE PhylomeDB:Q9LIF4 ProtClustDB:PLN02758 Genevestigator:Q9LIF4 Uniprot:Q9LIF4

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig00780	0	46	-6.653	9.06E-13	TAIR|locus:2089428 - symbol:LBO1 "AT3G21420" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0008152 "metabolic process" evidence=ISS] [GO:0016491 "oxidoreductase activity" evidence=IEA;ISS] InterPro:IPR005123 Pfam:PF03171 PROSITE:PS51471 EMBL:CP002686 GenomeReviews:BA000014_GR eggNOG:COG3491 HOGENOM:HBG749762 GO:GO:0016706 HSSP:Q96323 EMBL:AP001305 EMBL:AY084795 EMBL:BT005988 EMBL:AK227427 IPI:IPI00545861 RefSeq:NP_566685.1 UniGene:At.38063 ProteinModelPortal:Q9LIF4 SMR:Q9LIF4 PRIDE:Q9LIF4 EnsemblPlants:AT3G21420.1 GeneID:821696 KEGG:ath:AT3G21420 TAIR:At3g21420 InParanoid:Q9LIF4 OMA:FIREEYE PhylomeDB:Q9LIF4 ProtClustDB:PLN02758 Genevestigator:Q9LIF4 Uniprot:Q9LIF4
Root	Isotig00781	0	47	-6.684	5.35E-13	TAIR|locus:2089428 - symbol:LBO1 "AT3G21420" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0008152 "metabolic process" evidence=ISS] [GO:0016491 "oxidoreductase activity" evidence=IEA;ISS] InterPro:IPR005123 Pfam:PF03171 PROSITE:PS51471 EMBL:CP002686 GenomeReviews:BA000014_GR eggNOG:COG3491 HOGENOM:HBG749762 GO:GO:0016706 HSSP:Q96323 EMBL:AP001305 EMBL:AY084795 EMBL:BT005988 EMBL:AK227427 IPI:IPI00545861 RefSeq:NP_566685.1 UniGene:At.38063 ProteinModelPortal:Q9LIF4 SMR:Q9LIF4 PRIDE:Q9LIF4 EnsemblPlants:AT3G21420.1 GeneID:821696 KEGG:ath:AT3G21420 TAIR:At3g21420 InParanoid:Q9LIF4 OMA:FIREEYE PhylomeDB:Q9LIF4 ProtClustDB:PLN02758 Genevestigator:Q9LIF4 Uniprot:Q9LIF4
Root	Isotig00782	0	46	-6.653	9.06E-13	TAIR|locus:2089428 - symbol:LBO1 "AT3G21420" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0008152 "metabolic process" evidence=ISS] [GO:0016491 "oxidoreductase activity" evidence=IEA;ISS] InterPro:IPR005123 Pfam:PF03171 PROSITE:PS51471 EMBL:CP002686 GenomeReviews:BA000014_GR eggNOG:COG3491 HOGENOM:HBG749762 GO:GO:0016706 HSSP:Q96323 EMBL:AP001305 EMBL:AY084795 EMBL:BT005988 EMBL:AK227427 IPI:IPI00545861 RefSeq:NP_566685.1 UniGene:At.38063 ProteinModelPortal:Q9LIF4 SMR:Q9LIF4 PRIDE:Q9LIF4 EnsemblPlants:AT3G21420.1 GeneID:821696 KEGG:ath:AT3G21420 TAIR:At3g21420 InParanoid:Q9LIF4 OMA:FIREEYE PhylomeDB:Q9LIF4 ProtClustDB:PLN02758 Genevestigator:Q9LIF4 Uniprot:Q9LIF4
Root	Isotig00783	0	46	-6.653	9.06E-13	TAIR|locus:2089428 - symbol:LBO1 "AT3G21420" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0008152 "metabolic process" evidence=ISS] [GO:0016491 "oxidoreductase activity" evidence=IEA;ISS] InterPro:IPR005123 Pfam:PF03171 PROSITE:PS51471 EMBL:CP002686 GenomeReviews:BA000014_GR eggNOG:COG3491 HOGENOM:HBG749762 GO:GO:0016706 HSSP:Q96323 EMBL:AP001305 EMBL:AY084795 EMBL:BT005988 EMBL:AK227427 IPI:IPI00545861 RefSeq:NP_566685.1 UniGene:At.38063 ProteinModelPortal:Q9LIF4 SMR:Q9LIF4 PRIDE:Q9LIF4 EnsemblPlants:AT3G21420.1 GeneID:821696 KEGG:ath:AT3G21420 TAIR:At3g21420 InParanoid:Q9LIF4 OMA:FIREEYE PhylomeDB:Q9LIF4 ProtClustDB:PLN02758 Genevestigator:Q9LIF4 Uniprot:Q9LIF4
Root	Isotig00784	0	45	-6.621	1.54E-12	TAIR|locus:2089428 - symbol:LBO1 "AT3G21420" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0008152 "metabolic process" evidence=ISS] [GO:0016491 "oxidoreductase activity" evidence=IEA;ISS] InterPro:IPR005123 Pfam:PF03171 PROSITE:PS51471 EMBL:CP002686 GenomeReviews:BA000014_GR eggNOG:COG3491 HOGENOM:HBG749762 GO:GO:0016706 HSSP:Q96323 EMBL:AP001305 EMBL:AY084795 EMBL:BT005988 EMBL:AK227427 IPI:IPI00545861 RefSeq:NP_566685.1 UniGene:At.38063 ProteinModelPortal:Q9LIF4 SMR:Q9LIF4 PRIDE:Q9LIF4 EnsemblPlants:AT3G21420.1 GeneID:821696 KEGG:ath:AT3G21420 TAIR:At3g21420 InParanoid:Q9LIF4 OMA:FIREEYE PhylomeDB:Q9LIF4 ProtClustDB:PLN02758 Genevestigator:Q9LIF4 Uniprot:Q9LIF4
Root	Isotig00786	131	270	-1.172	3.12E-15	ZFIN|ZDB-GENE-070410-9 - symbol:zgc:158463 "zgc:158463" species:7955 "Danio rerio" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] ZFIN:ZDB-GENE-070410-9 EMBL:BX296557 EMBL:BX537263 EMBL:BC129240 IPI:IPI00837201 RefSeq:NP_001091866.1 RefSeq:XP_003200836.1 UniGene:Dr.155369 Ensembl:ENSDART00000102863 Ensembl:ENSDART00000126982 GeneID:100037361 GeneID:100151188 KEGG:dre:100037361 KEGG:dre:100151188 eggNOG:NOG298153 GeneTree:ENSGT00390000016898 InParanoid:A2VD29 OMA:ACHQHAL OrthoDB:EOG4FJ8BF Bgee:A2VD29 Uniprot:A2VD29
Root	Isotig00787	131	269	-1.167	4.41E-15	ZFIN|ZDB-GENE-070410-9 - symbol:zgc:158463 "zgc:158463" species:7955 "Danio rerio" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] ZFIN:ZDB-GENE-070410-9 EMBL:BX296557 EMBL:BX537263 EMBL:BC129240 IPI:IPI00837201 RefSeq:NP_001091866.1 RefSeq:XP_003200836.1 UniGene:Dr.155369 Ensembl:ENSDART00000102863 Ensembl:ENSDART00000126982 GeneID:100037361 GeneID:100151188

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						KEGG:dre:100037361 KEGG:dre:100151188 eggNOG:NOG298153 GeneTree:ENSGT00390000016898 InParanoid:A2VD29 OMA:ACHQHAL OrthoDB:EOG4FJ8BF Bgee:A2VD29 Uniprot:A2VD29
Root	Isotig00788	218	456	-1.194	2.53E-25	ZFIN|ZDB-GENE-070410-9 - symbol:zgc:158463 "zgc:158463" species:7955 "Danio rerio" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] ZFIN:ZDB-GENE-070410-9 EMBL:BX296557 EMBL:BX537263 EMBL:BC129240 IPI:IPI00837201 RefSeq:NP_001091866.1 RefSeq:XP_003200836.1 UniGene:Dr.155369 Ensembl:ENSDART00000102863 Ensembl:ENSDART00000126982 GeneID:100037361 GeneID:100151188 KEGG:dre:100037361 KEGG:dre:100151188 eggNOG:NOG298153 GeneTree:ENSGT00390000016898 InParanoid:A2VD29 OMA:ACHQHAL OrthoDB:EOG4FJ8BF Bgee:A2VD29 Uniprot:A2VD29
Root	Isotig00789	218	455	-1.191	3.59E-25	ZFIN|ZDB-GENE-070410-9 - symbol:zgc:158463 "zgc:158463" species:7955 "Danio rerio" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] ZFIN:ZDB-GENE-070410-9 EMBL:BX296557 EMBL:BX537263 EMBL:BC129240 IPI:IPI00837201 RefSeq:NP_001091866.1 RefSeq:XP_003200836.1 UniGene:Dr.155369 Ensembl:ENSDART00000102863 Ensembl:ENSDART00000126982 GeneID:100037361 GeneID:100151188 KEGG:dre:100037361 KEGG:dre:100151188 eggNOG:NOG298153 GeneTree:ENSGT00390000016898 InParanoid:A2VD29 OMA:ACHQHAL OrthoDB:EOG4FJ8BF Bgee:A2VD29 Uniprot:A2VD29
Root	Isotig00790	130	270	-1.183	1.94E-15	ZFIN|ZDB-GENE-070410-9 - symbol:zgc:158463 "zgc:158463" species:7955 "Danio rerio" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] ZFIN:ZDB-GENE-070410-9 EMBL:BX296557 EMBL:BX537263 EMBL:BC129240 IPI:IPI00837201 RefSeq:NP_001091866.1 RefSeq:XP_003200836.1 UniGene:Dr.155369 Ensembl:ENSDART00000102863 Ensembl:ENSDART00000126982 GeneID:100037361 GeneID:100151188 KEGG:dre:100037361 KEGG:dre:100151188 eggNOG:NOG298153 GeneTree:ENSGT00390000016898 InParanoid:A2VD29 OMA:ACHQHAL OrthoDB:EOG4FJ8BF Bgee:A2VD29 Uniprot:A2VD29
Root	Isotig00791	130	269	-1.178	2.75E-15	ZFIN|ZDB-GENE-070410-9 - symbol:zgc:158463 "zgc:158463" species:7955 "Danio rerio" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] ZFIN:ZDB-GENE-070410-9 EMBL:BX296557 EMBL:BX537263 EMBL:BC129240 IPI:IPI00837201 RefSeq:NP_001091866.1 RefSeq:XP_003200836.1 UniGene:Dr.155369 Ensembl:ENSDART00000102863 Ensembl:ENSDART00000126982 GeneID:100037361 GeneID:100151188 KEGG:dre:100037361 KEGG:dre:100151188 eggNOG:NOG298153 GeneTree:ENSGT00390000016898 InParanoid:A2VD29 OMA:ACHQHAL OrthoDB:EOG4FJ8BF Bgee:A2VD29 Uniprot:A2VD29
Root	Isotig00792	217	456	-1.200	1.56E-25	ZFIN|ZDB-GENE-070410-9 - symbol:zgc:158463 "zgc:158463" species:7955 "Danio rerio" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] ZFIN:ZDB-GENE-070410-9 EMBL:BX296557 EMBL:BX537263 EMBL:BC129240 IPI:IPI00837201 RefSeq:NP_001091866.1 RefSeq:XP_003200836.1 UniGene:Dr.155369 Ensembl:ENSDART00000102863 Ensembl:ENSDART00000126982 GeneID:100037361 GeneID:100151188 KEGG:dre:100037361 KEGG:dre:100151188 eggNOG:NOG298153 GeneTree:ENSGT00390000016898 InParanoid:A2VD29 OMA:ACHQHAL OrthoDB:EOG4FJ8BF Bgee:A2VD29 Uniprot:A2VD29
Root	Isotig00793	217	455	-1.197	2.22E-25	ZFIN|ZDB-GENE-070410-9 - symbol:zgc:158463 "zgc:158463" species:7955 "Danio rerio" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] ZFIN:ZDB-GENE-070410-9 EMBL:BX296557 EMBL:BX537263 EMBL:BC129240 IPI:IPI00837201 RefSeq:NP_001091866.1 RefSeq:XP_003200836.1 UniGene:Dr.155369 Ensembl:ENSDART00000102863 Ensembl:ENSDART00000126982 GeneID:100037361 GeneID:100151188 KEGG:dre:100037361 KEGG:dre:100151188 eggNOG:NOG298153 GeneTree:ENSGT00390000016898 InParanoid:A2VD29 OMA:ACHQHAL OrthoDB:EOG4FJ8BF Bgee:A2VD29 Uniprot:A2VD29
Root	Isotig00794	100	206	-1.172	5.81E-12	ZFIN|ZDB-GENE-070410-9 - symbol:zgc:158463 "zgc:158463" species:7955 "Danio rerio" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] ZFIN:ZDB-GENE-070410-9 EMBL:BX296557 EMBL:BX537263 EMBL:BC129240 IPI:IPI00837201 RefSeq:NP_001091866.1 RefSeq:XP_003200836.1 UniGene:Dr.155369 Ensembl:ENSDART00000102863 Ensembl:ENSDART00000126982 GeneID:100037361 GeneID:100151188 KEGG:dre:100037361 KEGG:dre:100151188 eggNOG:NOG298153 GeneTree:ENSGT00390000016898 InParanoid:A2VD29 OMA:ACHQHAL OrthoDB:EOG4FJ8BF Bgee:A2VD29 Uniprot:A2VD29

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig00795	100	205	-1.165	8.21E-12	ZFIN|ZDB-GENE-070410-9 - symbol:zgc:158463 "zgc:158463" species:7955 "Danio rerio" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] ZFIN:ZDB-GENE-070410-9 EMBL:BX296557 EMBL:BX537263 EMBL:BC129240 IPI:IPI00837201 RefSeq:NP_001091866.1 RefSeq:XP_003200836.1 UniGene:Dr.155369 Ensembl:ENSDART00000102863 Ensembl:ENSDART00000126982 GeneID:100037361 GeneID:100151188 KEGG:dre:100037361 KEGG:dre:100151188 eggNOG:NOG298153 GeneTree:ENSGT00390000016898 InParanoid:A2VD29 OMA:ACHQHAL OrthoDB:EOG4FJ8BF Bgee:A2VD29 Uniprot:A2VD29
Root	Isotig00796	132	268	-1.151	9.91E-15	No hit
Root	Isotig00797	99	206	-1.186	3.60E-12	ZFIN|ZDB-GENE-070410-9 - symbol:zgc:158463 "zgc:158463" species:7955 "Danio rerio" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] ZFIN:ZDB-GENE-070410-9 EMBL:BX296557 EMBL:BX537263 EMBL:BC129240 IPI:IPI00837201 RefSeq:NP_001091866.1 RefSeq:XP_003200836.1 UniGene:Dr.155369 Ensembl:ENSDART00000102863 Ensembl:ENSDART00000126982 GeneID:100037361 GeneID:100151188 KEGG:dre:100037361 KEGG:dre:100151188 eggNOG:NOG298153 GeneTree:ENSGT00390000016898 InParanoid:A2VD29 OMA:ACHQHAL OrthoDB:EOG4FJ8BF Bgee:A2VD29 Uniprot:A2VD29
Root	Isotig00798	99	205	-1.179	5.11E-12	ZFIN|ZDB-GENE-070410-9 - symbol:zgc:158463 "zgc:158463" species:7955 "Danio rerio" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] ZFIN:ZDB-GENE-070410-9 EMBL:BX296557 EMBL:BX537263 EMBL:BC129240 IPI:IPI00837201 RefSeq:NP_001091866.1 RefSeq:XP_003200836.1 UniGene:Dr.155369 Ensembl:ENSDART00000102863 Ensembl:ENSDART00000126982 GeneID:100037361 GeneID:100151188 KEGG:dre:100037361 KEGG:dre:100151188 eggNOG:NOG298153 GeneTree:ENSGT00390000016898 InParanoid:A2VD29 OMA:ACHQHAL OrthoDB:EOG4FJ8BF Bgee:A2VD29 Uniprot:A2VD29
Root	Isotig00799	1	22	-4.588	1.10E-06	TAIR|locus:2097993 - symbol:AT3G62160 "AT3G62160" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0016740 "transferase activity" evidence=ISS] [GO:0016747 "transferase activity, transferring acyl groups other than amino-acyl groups" evidence=IEA] InterPro:IPR003480 Pfam:PF02458 EMBL:CP002686 GenomeReviews:BA000014_GR InterPro:IPR023213 Gene3D:G3DSA:3.30.559.10 GO:GO:0016747 EMBL:AL138651 HOGENOM:HBG599319 EMBL:BT020224 EMBL:BT020438 IPI:IPI00527765 PIR:T48008 RefSeq:NP_191775.1 UniGene:At.34171 ProteinModelPortal:Q9M1Q8 PRIDE:Q9M1Q8 EnsemblPlants:AT3G62160.1 GeneID:825389 KEGG:ath:AT3G62160 TAIR:At3g62160 eggNOG:NOG284877 InParanoid:Q9M1Q8 OMA:GFVMGLR PhylomeDB:Q9M1Q8 ProtClustDB:CLSN2684119 Genevestigator:Q9M1Q8 Uniprot:Q9M1Q8
Root	Isotig00800	1	22	-4.588	1.10E-06	TAIR|locus:2097993 - symbol:AT3G62160 "AT3G62160" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0016740 "transferase activity" evidence=ISS] [GO:0016747 "transferase activity, transferring acyl groups other than amino-acyl groups" evidence=IEA] InterPro:IPR003480 Pfam:PF02458 EMBL:CP002686 GenomeReviews:BA000014_GR InterPro:IPR023213 Gene3D:G3DSA:3.30.559.10 GO:GO:0016747 EMBL:AL138651 HOGENOM:HBG599319 EMBL:BT020224 EMBL:BT020438 IPI:IPI00527765 PIR:T48008 RefSeq:NP_191775.1 UniGene:At.34171 ProteinModelPortal:Q9M1Q8 PRIDE:Q9M1Q8 EnsemblPlants:AT3G62160.1 GeneID:825389 KEGG:ath:AT3G62160 TAIR:At3g62160 eggNOG:NOG284877 InParanoid:Q9M1Q8 OMA:GFVMGLR PhylomeDB:Q9M1Q8 ProtClustDB:CLSN2684119 Genevestigator:Q9M1Q8 Uniprot:Q9M1Q8
Root	Isotig00801	0	23	-5.653	3.32E-07	TAIR|locus:2097993 - symbol:AT3G62160 "AT3G62160" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0016740 "transferase activity" evidence=ISS] [GO:0016747 "transferase activity, transferring acyl groups other than amino-acyl groups" evidence=IEA] InterPro:IPR003480 Pfam:PF02458 EMBL:CP002686 GenomeReviews:BA000014_GR InterPro:IPR023213 Gene3D:G3DSA:3.30.559.10 GO:GO:0016747 EMBL:AL138651 HOGENOM:HBG599319 EMBL:BT020224 EMBL:BT020438 IPI:IPI00527765 PIR:T48008 RefSeq:NP_191775.1 UniGene:At.34171 ProteinModelPortal:Q9M1Q8 PRIDE:Q9M1Q8 EnsemblPlants:AT3G62160.1 GeneID:825389 KEGG:ath:AT3G62160 TAIR:At3g62160 eggNOG:NOG284877 InParanoid:Q9M1Q8 OMA:GFVMGLR PhylomeDB:Q9M1Q8 ProtClustDB:CLSN2684119 Genevestigator:Q9M1Q8 Uniprot:Q9M1Q8
Root	Isotig00802	0	23	-5.653	3.32E-07	TAIR|locus:2097993 - symbol:AT3G62160 "AT3G62160" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0016740 "transferase activity" evidence=ISS] [GO:0016747 "transferase activity, transferring acyl groups other than amino-acyl groups"

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						evidence=IEA] InterPro:IPR003480 Pfam:PF02458 EMBL:CP002686 GenomeReviews:BA000014_GR InterPro:IPR023213 Gene3D:G3DSA:3.30.559.10 GO:GO:0016747 EMBL:AL138651 HOGENOM:HBG599319 EMBL:BT020224 EMBL:BT020438 IPI:IPI00527765 PIR:T48008 RefSeq:NP_191775.1 UniGene:At.34171 ProteinModelPortal:Q9M1Q8 PRIDE:Q9M1Q8 EnsemblPlants:AT3G62160.1 GeneID:825389 KEGG:ath:AT3G62160 TAIR:At3g62160 eggNOG:NOG284877 InParanoid:Q9M1Q8 OMA:GFVMGLR PhylomeDB:Q9M1Q8 ProtClustDB:CLSN2684119 Genevestigator:Q9M1Q8 Uniprot:Q9M1Q8
Root	Isotig00803	0	21	-5.521	1.09E-06	TAIR|locus:2097993 - symbol:AT3G62160 "AT3G62160" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0016740 "transferase activity" evidence=ISS] [GO:0016747 "transferase activity, transferring acyl groups other than amino-acyl groups" evidence=IEA] InterPro:IPR003480 Pfam:PF02458 EMBL:CP002686 GenomeReviews:BA000014_GR InterPro:IPR023213 Gene3D:G3DSA:3.30.559.10 GO:GO:0016747 EMBL:AL138651 HOGENOM:HBG599319 EMBL:BT020224 EMBL:BT020438 IPI:IPI00527765 PIR:T48008 RefSeq:NP_191775.1 UniGene:At.34171 ProteinModelPortal:Q9M1Q8 PRIDE:Q9M1Q8 EnsemblPlants:AT3G62160.1 GeneID:825389 KEGG:ath:AT3G62160 TAIR:At3g62160 eggNOG:NOG284877 InParanoid:Q9M1Q8 OMA:GFVMGLR PhylomeDB:Q9M1Q8 ProtClustDB:CLSN2684119 Genevestigator:Q9M1Q8 Uniprot:Q9M1Q8
Root	Isotig00804	0	21	-5.521	1.09E-06	TAIR|locus:2097993 - symbol:AT3G62160 "AT3G62160" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0016740 "transferase activity" evidence=ISS] [GO:0016747 "transferase activity, transferring acyl groups other than amino-acyl groups" evidence=IEA] InterPro:IPR003480 Pfam:PF02458 EMBL:CP002686 GenomeReviews:BA000014_GR InterPro:IPR023213 Gene3D:G3DSA:3.30.559.10 GO:GO:0016747 EMBL:AL138651 HOGENOM:HBG599319 EMBL:BT020224 EMBL:BT020438 IPI:IPI00527765 PIR:T48008 RefSeq:NP_191775.1 UniGene:At.34171 ProteinModelPortal:Q9M1Q8 PRIDE:Q9M1Q8 EnsemblPlants:AT3G62160.1 GeneID:825389 KEGG:ath:AT3G62160 TAIR:At3g62160 eggNOG:NOG284877 InParanoid:Q9M1Q8 OMA:GFVMGLR PhylomeDB:Q9M1Q8 ProtClustDB:CLSN2684119 Genevestigator:Q9M1Q8 Uniprot:Q9M1Q8
Root	Isotig00805	0	22	-5.588	6.01E-07	TAIR|locus:2097993 - symbol:AT3G62160 "AT3G62160" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0016740 "transferase activity" evidence=ISS] [GO:0016747 "transferase activity, transferring acyl groups other than amino-acyl groups" evidence=IEA] InterPro:IPR003480 Pfam:PF02458 EMBL:CP002686 GenomeReviews:BA000014_GR InterPro:IPR023213 Gene3D:G3DSA:3.30.559.10 GO:GO:0016747 EMBL:AL138651 HOGENOM:HBG599319 EMBL:BT020224 EMBL:BT020438 IPI:IPI00527765 PIR:T48008 RefSeq:NP_191775.1 UniGene:At.34171 ProteinModelPortal:Q9M1Q8 PRIDE:Q9M1Q8 EnsemblPlants:AT3G62160.1 GeneID:825389 KEGG:ath:AT3G62160 TAIR:At3g62160 eggNOG:NOG284877 InParanoid:Q9M1Q8 OMA:GFVMGLR PhylomeDB:Q9M1Q8 ProtClustDB:CLSN2684119 Genevestigator:Q9M1Q8 Uniprot:Q9M1Q8
Root	Isotig00806	0	22	-5.588	6.01E-07	TAIR|locus:2097993 - symbol:AT3G62160 "AT3G62160" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0016740 "transferase activity" evidence=ISS] [GO:0016747 "transferase activity, transferring acyl groups other than amino-acyl groups" evidence=IEA] InterPro:IPR003480 Pfam:PF02458 EMBL:CP002686 GenomeReviews:BA000014_GR InterPro:IPR023213 Gene3D:G3DSA:3.30.559.10 GO:GO:0016747 EMBL:AL138651 HOGENOM:HBG599319 EMBL:BT020224 EMBL:BT020438 IPI:IPI00527765 PIR:T48008 RefSeq:NP_191775.1 UniGene:At.34171 ProteinModelPortal:Q9M1Q8 PRIDE:Q9M1Q8 EnsemblPlants:AT3G62160.1 GeneID:825389 KEGG:ath:AT3G62160 TAIR:At3g62160 eggNOG:NOG284877 InParanoid:Q9M1Q8 OMA:GFVMGLR PhylomeDB:Q9M1Q8 ProtClustDB:CLSN2684119 Genevestigator:Q9M1Q8 Uniprot:Q9M1Q8
Root	Isotig00808	0	11	-4.588	0.000569522	TAIR|locus:2097993 - symbol:AT3G62160 "AT3G62160" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0016740 "transferase activity" evidence=ISS] [GO:0016747 "transferase activity, transferring acyl groups other than amino-acyl groups" evidence=IEA] InterPro:IPR003480 Pfam:PF02458 EMBL:CP002686 GenomeReviews:BA000014_GR InterPro:IPR023213 Gene3D:G3DSA:3.30.559.10 GO:GO:0016747 EMBL:AL138651 HOGENOM:HBG599319 EMBL:BT020224 EMBL:BT020438 IPI:IPI00527765 PIR:T48008 RefSeq:NP_191775.1 UniGene:At.34171 ProteinModelPortal:Q9M1Q8 PRIDE:Q9M1Q8 EnsemblPlants:AT3G62160.1 GeneID:825389 KEGG:ath:AT3G62160 TAIR:At3g62160 eggNOG:NOG284877 InParanoid:Q9M1Q8 OMA:GFVMGLR PhylomeDB:Q9M1Q8 ProtClustDB:CLSN2684119 Genevestigator:Q9M1Q8 Uniprot:Q9M1Q8

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig00811	15	72	-2.392	1.76E-11	TAIR|locus:2057589 - symbol:PHO2 "AT2G33770" species:3702 "Arabidopsis thaliana" [GO:0004842 "ubiquitin-protein ligase activity" evidence=ISS] [GO:0005575 "cellular_component" evidence=ND] [GO:0016036 "cellular response to phosphate starvation" evidence=IMP] [GO:0055062 "phosphate ion homeostasis" evidence=IMP] [GO:0006817 "phosphate ion transport" evidence=IMP] InterPro:IPR000608 Pfam:PF00179 PROSITE:PS50127 GO:GO:0005524 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0016036 GO:GO:0004842 InterPro:IPR016135 Gene3D:G3DSA:3.10.110.10 SUPFAM:SSF54495 GO:GO:0055062 EMBL:U78721 PROSITE:PS00183 GO:GO:0006817 HOGENOM:HBG319025 EMBL:DQ027037 EMBL:AY074292 EMBL:AY091326 EMBL:AK229934 EMBL:AK230162 IPI:IPI00518927 IPI:IPI00900502 PIR:D84749 RefSeq:NP_850218.1 UniGene:At.14693 ProteinModelPortal:Q8VY10 SMR:Q8VY10 STRING:Q8VY10 PRIDE:Q8VY10 EnsemblPlants:AT2G33770.1 GeneID:817943 KEGG:ath:AT2G33770 TAIR:At2g33770 eggNOG:NOG315712 InParanoid:Q8VY10 OMA:RVYEERM PhylomeDB:Q8VY10 ProtClustDB:CLSN2918162 Genevestigator:Q8VY10 Uniprot:Q8VY10
Root	Isotig00812	15	69	-2.331	9.01E-11	TAIR|locus:2057589 - symbol:PHO2 "AT2G33770" species:3702 "Arabidopsis thaliana" [GO:0004842 "ubiquitin-protein ligase activity" evidence=ISS] [GO:0005575 "cellular_component" evidence=ND] [GO:0016036 "cellular response to phosphate starvation" evidence=IMP] [GO:0055062 "phosphate ion homeostasis" evidence=IMP] [GO:0006817 "phosphate ion transport" evidence=IMP] InterPro:IPR000608 Pfam:PF00179 PROSITE:PS50127 GO:GO:0005524 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0016036 GO:GO:0004842 InterPro:IPR016135 Gene3D:G3DSA:3.10.110.10 SUPFAM:SSF54495 GO:GO:0055062 EMBL:U78721 PROSITE:PS00183 GO:GO:0006817 HOGENOM:HBG319025 EMBL:DQ027037 EMBL:AY074292 EMBL:AY091326 EMBL:AK229934 EMBL:AK230162 IPI:IPI00518927 IPI:IPI00900502 PIR:D84749 RefSeq:NP_850218.1 UniGene:At.14693 ProteinModelPortal:Q8VY10 SMR:Q8VY10 STRING:Q8VY10 PRIDE:Q8VY10 EnsemblPlants:AT2G33770.1 GeneID:817943 KEGG:ath:AT2G33770 TAIR:At2g33770 eggNOG:NOG315712 InParanoid:Q8VY10 OMA:RVYEERM PhylomeDB:Q8VY10 ProtClustDB:CLSN2918162 Genevestigator:Q8VY10 Uniprot:Q8VY10
Root	Isotig00813	15	72	-2.392	1.76E-11	TAIR|locus:2057589 - symbol:PHO2 "AT2G33770" species:3702 "Arabidopsis thaliana" [GO:0004842 "ubiquitin-protein ligase activity" evidence=ISS] [GO:0005575 "cellular_component" evidence=ND] [GO:0016036 "cellular response to phosphate starvation" evidence=IMP] [GO:0055062 "phosphate ion homeostasis" evidence=IMP] [GO:0006817 "phosphate ion transport" evidence=IMP] InterPro:IPR000608 Pfam:PF00179 PROSITE:PS50127 GO:GO:0005524 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0016036 GO:GO:0004842 InterPro:IPR016135 Gene3D:G3DSA:3.10.110.10 SUPFAM:SSF54495 GO:GO:0055062 EMBL:U78721 PROSITE:PS00183 GO:GO:0006817 HOGENOM:HBG319025 EMBL:DQ027037 EMBL:AY074292 EMBL:AY091326 EMBL:AK229934 EMBL:AK230162 IPI:IPI00518927 IPI:IPI00900502 PIR:D84749 RefSeq:NP_850218.1 UniGene:At.14693 ProteinModelPortal:Q8VY10 SMR:Q8VY10 STRING:Q8VY10 PRIDE:Q8VY10 EnsemblPlants:AT2G33770.1 GeneID:817943 KEGG:ath:AT2G33770 TAIR:At2g33770 eggNOG:NOG315712 InParanoid:Q8VY10 OMA:RVYEERM PhylomeDB:Q8VY10 ProtClustDB:CLSN2918162 Genevestigator:Q8VY10 Uniprot:Q8VY10
Root	Isotig00814	15	69	-2.331	9.01E-11	TAIR|locus:2057589 - symbol:PHO2 "AT2G33770" species:3702 "Arabidopsis thaliana" [GO:0004842 "ubiquitin-protein ligase activity" evidence=ISS] [GO:0005575 "cellular_component" evidence=ND] [GO:0016036 "cellular response to phosphate starvation" evidence=IMP] [GO:0055062 "phosphate ion homeostasis" evidence=IMP] [GO:0006817 "phosphate ion transport" evidence=IMP] InterPro:IPR000608 Pfam:PF00179 PROSITE:PS50127 GO:GO:0005524 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0016036 GO:GO:0004842 InterPro:IPR016135 Gene3D:G3DSA:3.10.110.10 SUPFAM:SSF54495 GO:GO:0055062 EMBL:U78721 PROSITE:PS00183 GO:GO:0006817 HOGENOM:HBG319025 EMBL:DQ027037 EMBL:AY074292 EMBL:AY091326 EMBL:AK229934 EMBL:AK230162 IPI:IPI00518927 IPI:IPI00900502 PIR:D84749 RefSeq:NP_850218.1 UniGene:At.14693 ProteinModelPortal:Q8VY10 SMR:Q8VY10 STRING:Q8VY10 PRIDE:Q8VY10 EnsemblPlants:AT2G33770.1 GeneID:817943 KEGG:ath:AT2G33770 TAIR:At2g33770 eggNOG:NOG315712 InParanoid:Q8VY10 OMA:RVYEERM PhylomeDB:Q8VY10 ProtClustDB:CLSN2918162 Genevestigator:Q8VY10 Uniprot:Q8VY10
Root	Isotig00815	16	72	-2.299	5.10E-11	TAIR|locus:2057589 - symbol:PHO2 "AT2G33770" species:3702 "Arabidopsis thaliana" [GO:0004842 "ubiquitin-protein ligase activity" evidence=ISS] [GO:0005575 "cellular_component" evidence=ND] [GO:0016036 "cellular response to phosphate starvation" evidence=IMP] [GO:0055062 "phosphate ion homeostasis" evidence=IMP] [GO:0006817 "phosphate ion transport" evidence=IMP] InterPro:IPR000608 Pfam:PF00179 PROSITE:PS50127

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0005524 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0016036 GO:GO:0004842 InterPro:IPR016135 Gene3D:G3DSA:3.10.110.10 SUPFAM:SSF54495 GO:GO:0055062 EMBL:U78721 PROSITE:PS00183 GO:GO:0006817 HOGENOM:HBG319025 EMBL:DQ027037 EMBL:AY074292 EMBL:AY091326 EMBL:AK229934 EMBL:AK230162 IPI:IPI00518927 IPI:IPI00900502 PIR:D84749 RefSeq:NP_850218.1 UniGene:At.14693 ProteinModelPortal:Q8VY10 SMR:Q8VY10 STRING:Q8VY10 PRIDE:Q8VY10 EnsemblPlants:AT2G33770.1 GeneID:817943 KEGG:ath:AT2G33770 TAIR:At2g33770 eggNOG:NOG315712 InParanoid:Q8VY10 OMA:RVYEERM PhylomeDB:Q8VY10 ProtClustDB:CLSN2918162 Genevestigator:Q8VY10 Uniprot:Q8VY10
Root	Isotig00816	16	69	-2.237	2.53E-10	TAIR|locus:2057589 - symbol:PHO2 "AT2G33770" species:3702 "Arabidopsis thaliana" [GO:0004842 "ubiquitin-protein ligase activity" evidence=ISS] [GO:0005575 "cellular_component" evidence=ND] [GO:0016036 "cellular response to phosphate starvation" evidence=IMP] [GO:0055062 "phosphate ion homeostasis" evidence=IMP] [GO:0006817 "phosphate ion transport" evidence=IMP] InterPro:IPR000608 Pfam:PF00179 PROSITE:PS50127 GO:GO:0005524 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0016036 GO:GO:0004842 InterPro:IPR016135 Gene3D:G3DSA:3.10.110.10 SUPFAM:SSF54495 GO:GO:0055062 EMBL:U78721 PROSITE:PS00183 GO:GO:0006817 HOGENOM:HBG319025 EMBL:DQ027037 EMBL:AY074292 EMBL:AY091326 EMBL:AK229934 EMBL:AK230162 IPI:IPI00518927 IPI:IPI00900502 PIR:D84749 RefSeq:NP_850218.1 UniGene:At.14693 ProteinModelPortal:Q8VY10 SMR:Q8VY10 STRING:Q8VY10 PRIDE:Q8VY10 EnsemblPlants:AT2G33770.1 GeneID:817943 KEGG:ath:AT2G33770 TAIR:At2g33770 eggNOG:NOG315712 InParanoid:Q8VY10 OMA:RVYEERM PhylomeDB:Q8VY10 ProtClustDB:CLSN2918162 Genevestigator:Q8VY10 Uniprot:Q8VY10
Root	Isotig00817	16	72	-2.299	5.10E-11	TAIR|locus:2057589 - symbol:PHO2 "AT2G33770" species:3702 "Arabidopsis thaliana" [GO:0004842 "ubiquitin-protein ligase activity" evidence=ISS] [GO:0005575 "cellular_component" evidence=ND] [GO:0016036 "cellular response to phosphate starvation" evidence=IMP] [GO:0055062 "phosphate ion homeostasis" evidence=IMP] [GO:0006817 "phosphate ion transport" evidence=IMP] InterPro:IPR000608 Pfam:PF00179 PROSITE:PS50127 GO:GO:0005524 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0016036 GO:GO:0004842 InterPro:IPR016135 Gene3D:G3DSA:3.10.110.10 SUPFAM:SSF54495 GO:GO:0055062 EMBL:U78721 PROSITE:PS00183 GO:GO:0006817 HOGENOM:HBG319025 EMBL:DQ027037 EMBL:AY074292 EMBL:AY091326 EMBL:AK229934 EMBL:AK230162 IPI:IPI00518927 IPI:IPI00900502 PIR:D84749 RefSeq:NP_850218.1 UniGene:At.14693 ProteinModelPortal:Q8VY10 SMR:Q8VY10 STRING:Q8VY10 PRIDE:Q8VY10 EnsemblPlants:AT2G33770.1 GeneID:817943 KEGG:ath:AT2G33770 TAIR:At2g33770 eggNOG:NOG315712 InParanoid:Q8VY10 OMA:RVYEERM PhylomeDB:Q8VY10 ProtClustDB:CLSN2918162 Genevestigator:Q8VY10 Uniprot:Q8VY10
Root	Isotig00818	16	69	-2.237	2.53E-10	TAIR|locus:2057589 - symbol:PHO2 "AT2G33770" species:3702 "Arabidopsis thaliana" [GO:0004842 "ubiquitin-protein ligase activity" evidence=ISS] [GO:0005575 "cellular_component" evidence=ND] [GO:0016036 "cellular response to phosphate starvation" evidence=IMP] [GO:0055062 "phosphate ion homeostasis" evidence=IMP] [GO:0006817 "phosphate ion transport" evidence=IMP] InterPro:IPR000608 Pfam:PF00179 PROSITE:PS50127 GO:GO:0005524 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0016036 GO:GO:0004842 InterPro:IPR016135 Gene3D:G3DSA:3.10.110.10 SUPFAM:SSF54495 GO:GO:0055062 EMBL:U78721 PROSITE:PS00183 GO:GO:0006817 HOGENOM:HBG319025 EMBL:DQ027037 EMBL:AY074292 EMBL:AY091326 EMBL:AK229934 EMBL:AK230162 IPI:IPI00518927 IPI:IPI00900502 PIR:D84749 RefSeq:NP_850218.1 UniGene:At.14693 ProteinModelPortal:Q8VY10 SMR:Q8VY10 STRING:Q8VY10 PRIDE:Q8VY10 EnsemblPlants:AT2G33770.1 GeneID:817943 KEGG:ath:AT2G33770 TAIR:At2g33770 eggNOG:NOG315712 InParanoid:Q8VY10 OMA:RVYEERM PhylomeDB:Q8VY10 ProtClustDB:CLSN2918162 Genevestigator:Q8VY10 Uniprot:Q8VY10
Root	Isotig00819	11	57	-2.502	8.21E-10	TAIR|locus:2057589 - symbol:PHO2 "AT2G33770" species:3702 "Arabidopsis thaliana" [GO:0004842 "ubiquitin-protein ligase activity" evidence=ISS] [GO:0005575 "cellular_component" evidence=ND] [GO:0016036 "cellular response to phosphate starvation" evidence=IMP] [GO:0055062 "phosphate ion homeostasis" evidence=IMP] [GO:0006817 "phosphate ion transport" evidence=IMP] InterPro:IPR000608 Pfam:PF00179 PROSITE:PS50127 GO:GO:0005524 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0016036 GO:GO:0004842 InterPro:IPR016135 Gene3D:G3DSA:3.10.110.10 SUPFAM:SSF54495 GO:GO:0055062 EMBL:U78721 PROSITE:PS00183 GO:GO:0006817 HOGENOM:HBG319025 EMBL:DQ027037 EMBL:AY074292 EMBL:AY091326 EMBL:AK229934 EMBL:AK230162 IPI:IPI00518927 IPI:IPI00900502 PIR:D84749

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						RefSeq:NP_850218.1 UniGene:At.14693 ProteinModelPortal:Q8VY10 SMR:Q8VY10 STRING:Q8VY10 PRIDE:Q8VY10 EnsemblPlants:AT2G33770.1 GeneID:817943 KEGG:ath:AT2G33770 TAIR:At2g33770 eggNOG:NOG315712 InParanoid:Q8VY10 OMA:RVYEERM PhylomeDB:Q8VY10 ProtClustDB:CLSN2918162 Genevestigator:Q8VY10 Uniprot:Q8VY10
Root	Isotig00820	11	57	-2.502	8.21E-10	TAIR|locus:2057589 - symbol:PHO2 "AT2G33770" species:3702 "Arabidopsis thaliana" [GO:0004842 "ubiquitin-protein ligase activity" evidence=ISS] [GO:0005575 "cellular_component" evidence=ND] [GO:0016036 "cellular response to phosphate starvation" evidence=IMP] [GO:0055062 "phosphate ion homeostasis" evidence=IMP] [GO:0006817 "phosphate ion transport" evidence=IMP] InterPro:IPR000608 Pfam:PF00179 PROSITE:PS50127 GO:GO:0005524 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0016036 GO:GO:0004842 InterPro:IPR016135 Gene3D:G3DSA:3.10.110.10 SUPFAM:SSF54495 GO:GO:0055062 EMBL:U78721 PROSITE:PS00183 GO:GO:0006817 HOGENOM:HBG319025 EMBL:DQ027037 EMBL:AY074292 EMBL:AY091326 EMBL:AK229934 EMBL:AK230162 IPI:IPI00518927 IPI:IPI00900502 PIR:D84749 RefSeq:NP_850218.1 UniGene:At.14693 ProteinModelPortal:Q8VY10 SMR:Q8VY10 STRING:Q8VY10 PRIDE:Q8VY10 EnsemblPlants:AT2G33770.1 GeneID:817943 KEGG:ath:AT2G33770 TAIR:At2g33770 eggNOG:NOG315712 InParanoid:Q8VY10 OMA:RVYEERM PhylomeDB:Q8VY10 ProtClustDB:CLSN2918162 Genevestigator:Q8VY10 Uniprot:Q8VY10
Root	Isotig00821	12	57	-2.377	2.51E-09	TAIR|locus:2057589 - symbol:PHO2 "AT2G33770" species:3702 "Arabidopsis thaliana" [GO:0004842 "ubiquitin-protein ligase activity" evidence=ISS] [GO:0005575 "cellular_component" evidence=ND] [GO:0016036 "cellular response to phosphate starvation" evidence=IMP] [GO:0055062 "phosphate ion homeostasis" evidence=IMP] [GO:0006817 "phosphate ion transport" evidence=IMP] InterPro:IPR000608 Pfam:PF00179 PROSITE:PS50127 GO:GO:0005524 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0016036 GO:GO:0004842 InterPro:IPR016135 Gene3D:G3DSA:3.10.110.10 SUPFAM:SSF54495 GO:GO:0055062 EMBL:U78721 PROSITE:PS00183 GO:GO:0006817 HOGENOM:HBG319025 EMBL:DQ027037 EMBL:AY074292 EMBL:AY091326 EMBL:AK229934 EMBL:AK230162 IPI:IPI00518927 IPI:IPI00900502 PIR:D84749 RefSeq:NP_850218.1 UniGene:At.14693 ProteinModelPortal:Q8VY10 SMR:Q8VY10 STRING:Q8VY10 PRIDE:Q8VY10 EnsemblPlants:AT2G33770.1 GeneID:817943 KEGG:ath:AT2G33770 TAIR:At2g33770 eggNOG:NOG315712 InParanoid:Q8VY10 OMA:RVYEERM PhylomeDB:Q8VY10 ProtClustDB:CLSN2918162 Genevestigator:Q8VY10 Uniprot:Q8VY10
Root	Isotig00822	12	57	-2.377	2.51E-09	TAIR|locus:2057589 - symbol:PHO2 "AT2G33770" species:3702 "Arabidopsis thaliana" [GO:0004842 "ubiquitin-protein ligase activity" evidence=ISS] [GO:0005575 "cellular_component" evidence=ND] [GO:0016036 "cellular response to phosphate starvation" evidence=IMP] [GO:0055062 "phosphate ion homeostasis" evidence=IMP] [GO:0006817 "phosphate ion transport" evidence=IMP] InterPro:IPR000608 Pfam:PF00179 PROSITE:PS50127 GO:GO:0005524 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0016036 GO:GO:0004842 InterPro:IPR016135 Gene3D:G3DSA:3.10.110.10 SUPFAM:SSF54495 GO:GO:0055062 EMBL:U78721 PROSITE:PS00183 GO:GO:0006817 HOGENOM:HBG319025 EMBL:DQ027037 EMBL:AY074292 EMBL:AY091326 EMBL:AK229934 EMBL:AK230162 IPI:IPI00518927 IPI:IPI00900502 PIR:D84749 RefSeq:NP_850218.1 UniGene:At.14693 ProteinModelPortal:Q8VY10 SMR:Q8VY10 STRING:Q8VY10 PRIDE:Q8VY10 EnsemblPlants:AT2G33770.1 GeneID:817943 KEGG:ath:AT2G33770 TAIR:At2g33770 eggNOG:NOG315712 InParanoid:Q8VY10 OMA:RVYEERM PhylomeDB:Q8VY10 ProtClustDB:CLSN2918162 Genevestigator:Q8VY10 Uniprot:Q8VY10
Root	Isotig00823	18	0	5.041	1.86E-05	UNIPROTKB|Q93RX7 - symbol:SCO6295 "Putative ABC transporter ATP-binding protein" species:1902 "Streptomyces coelicolor" [GO:0016021 "integral to membrane" evidence=IBA] [GO:0042626 "ATPase activity, coupled to transmembrane movement of substances" evidence=IBA] [GO:0055085 "transmembrane transport" evidence=IBA] InterPro:IPR001140 InterPro:IPR003439 InterPro:IPR003593 InterPro:IPR011527 InterPro:IPR017871 Pfam:PF00005 Pfam:PF00664 PROSITE:PS00211 PROSITE:PS50893 SMART:SM00382 GO:GO:0016021 GO:GO:0005524 HOGENOM:HBG758042 GO:GO:0042626 InterPro:IPR017940 SUPFAM:SSF90123 PROSITE:PS50929 HSSP:P08716 GenomeReviews:AL645882_GR KO:K06147 EMBL:AL939127 RefSeq:NP_630393.1 ProteinModelPortal:Q93RX7 GeneID:1101736 KEGG:sco:SCO6295 PATRIC:23742526 OMA:AHVTEFA PhylomeDB:Q93RX7 ProtClustDB:CLSK2519402 Uniprot:Q93RX7
Root	Isotig00824	18	0	5.041	1.86E-05	No hit
Root	Isotig00825	16	0	4.871	5.89E-05	UNIPROTKB|Q93RX7 - symbol:SCO6295 "Putative ABC transporter ATP-binding protein" species:1902 "Streptomyces coelicolor" [GO:0016021 "integral to membrane" evidence=IBA] [GO:0042626 "ATPase activity,

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						coupled to transmembrane movement of substances" evidence=IBA] [GO:0055085 "transmembrane transport" evidence=IBA] InterPro:IPR001140 InterPro:IPR003439 InterPro:IPR003593 InterPro:IPR011527 InterPro:IPR017871 Pfam:PF00005 Pfam:PF00664 PROSITE:PS00211 PROSITE:PS50893 SMART:SM00382 GO:GO:0016021 GO:GO:0005524 HOGENOM:HBG758042 GO:GO:0042626 InterPro:IPR017940 SUPFAM:SSF90123 PROSITE:PS50929 HSSP:P08716 GenomeReviews:AL645882_GR KO:K06147 EMBL:AL939127 RefSeq:NP_630393.1 ProteinModelPortal:Q93RX7 GeneID:1101736 KEGG:sco:SCO6295 PATRIC:23742526 OMA:AHVTEFA PhylomeDB:Q93RX7 ProtClustDB:CLSK2519402 Uniprot:Q93RX7
Root	Isotig00826	16	0	4.871	5.89E-05	No hit
Root	Isotig00854	42	121	-1.656	7.13E-12	TAIR|locus:2103085 - symbol:GAPC1 "AT3G04120" species:3702 "Arabidopsis thaliana" [GO:0006096 "glycolysis" evidence=ISS;IDA;TAS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0006979 "response to oxidative stress" evidence=IEP;IDA] [GO:0005740 "mitochondrial envelope" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA;TAS] [GO:0006094 "gluconeogenesis" evidence=TAS] [GO:0042542 "response to hydrogen peroxide" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0008886 "glyceraldehyde-3-phosphate dehydrogenase (NADP+) (non-phosphorylating) activity" evidence=IDA] [GO:0010154 "fruit development" evidence=IMP] [GO:0048316 "seed development" evidence=IMP] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] [GO:0004365 "glyceraldehyde-3-phosphate dehydrogenase (NAD+) (phosphorylating) activity" evidence=TAS] [GO:0006950 "response to stress" evidence=IEP] [GO:0009408 "response to heat" evidence=IEP] [GO:0009744 "response to sucrose stimulus" evidence=IEP] InterPro:IPR006424 InterPro:IPR016040 InterPro:IPR020828 InterPro:IPR020829 InterPro:IPR020830 InterPro:IPR020831 Pfam:PF00044 Pfam:PF02800 PIRSF:PIRSF000149 PRINTS:PR00078 PROSITE:PS00071 SMART:SM00846 GO:GO:0005829 GO:GO:0005886 GO:GO:0048046 GO:GO:0005634 GO:GO:0046686 GO:GO:0005774 GO:GO:0009507 EMBL:CP002686 GenomeReviews:BA000014_GR Gene3D:G3DSA:3.40.50.720 GO:GO:0051287 GO:GO:0050661 GO:GO:0005507 GO:GO:0006094 GO:GO:0009651 GO:GO:0009408 GO:GO:0005740 GO:GO:0009744 GO:GO:0048316 GO:GO:0042542 GO:GO:0006096 EMBL:AC016829 eggNOG:COG0057 HOGENOM:HBG571736 PANTHER:PTHR10836 GO:GO:0004365 KO:K00134 TIGRFAMs:TIGR01534 OMA:CESTGVF EMBL:M64116 EMBL:M64119 EMBL:AY052267 EMBL:AY060521 EMBL:AY140084 EMBL:F20074 IPI:IPI00527494 PIR:JQ1287 RefSeq:NP_187062.1 UniGene:At.22963 UniGene:At.24406 UniGene:At.71328 ProteinModelPortal:P25858 SMR:P25858 STRING:P25858 PRIDE:P25858 EnsemblPlants:AT3G04120.1 GeneID:819567 KEGG:ath:AT3G04120 TAIR:At3g04120 InParanoid:P25858 PhylomeDB:P25858 ProtClustDB:PLN02358 ArrayExpress:P25858 Genevestigator:P25858 GermOnline:AT3G04120 GO:GO:0008886 Uniprot:P25858
Root	Isotig00855	38	102	-1.553	1.84E-09	TAIR|locus:2103085 - symbol:GAPC1 "AT3G04120" species:3702 "Arabidopsis thaliana" [GO:0006096 "glycolysis" evidence=ISS;IDA;TAS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0006979 "response to oxidative stress" evidence=IEP;IDA] [GO:0005740 "mitochondrial envelope" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA;TAS] [GO:0006094 "gluconeogenesis" evidence=TAS] [GO:0042542 "response to hydrogen peroxide" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0008886 "glyceraldehyde-3-phosphate dehydrogenase (NADP+) (non-phosphorylating) activity" evidence=IDA] [GO:0010154 "fruit development" evidence=IMP] [GO:0048316 "seed development" evidence=IMP] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] [GO:0004365 "glyceraldehyde-3-phosphate dehydrogenase (NAD+) (phosphorylating) activity" evidence=TAS] [GO:0006950 "response to stress" evidence=IEP] [GO:0009408 "response to heat" evidence=IEP] [GO:0009744 "response to sucrose stimulus" evidence=IEP] InterPro:IPR006424 InterPro:IPR016040 InterPro:IPR020828 InterPro:IPR020829 InterPro:IPR020830 InterPro:IPR020831 Pfam:PF00044 Pfam:PF02800 PIRSF:PIRSF000149 PRINTS:PR00078 PROSITE:PS00071 SMART:SM00846 GO:GO:0005829 GO:GO:0005886 GO:GO:0048046 GO:GO:0005634 GO:GO:0046686 GO:GO:0005774 GO:GO:0009507 EMBL:CP002686 GenomeReviews:BA000014_GR Gene3D:G3DSA:3.40.50.720 GO:GO:0051287 GO:GO:0050661 GO:GO:0005507 GO:GO:0006094 GO:GO:0009651 GO:GO:0009408 GO:GO:0005740

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0009744 GO:GO:0048316 GO:GO:0042542 GO:GO:0006096 EMBL:AC016829 eggNOG:COG0057 HOGENOM:HBG571736 PANTHER:PTHR10836 GO:GO:0004365 KO:K00134 TIGRFAMs:TIGR01534 OMA:CESTGVF EMBL:M64116 EMBL:M64119 EMBL:AY052267 EMBL:AY060521 EMBL:AY140084 EMBL:F20074 IPI:IPI00527494 PIR:JQ1287 RefSeq:NP_187062.1 UniGene:At.22963 UniGene:At.24406 UniGene:At.71328 ProteinModelPortal:P25858 SMR:P25858 STRING:P25858 PRIDE:P25858 EnsemblPlants:AT3G04120.1 GeneID:819567 KEGG:ath:AT3G04120 TAIR:At3g04120 InParanoid:P25858 PhylomeDB:P25858 ProtClustDB:PLN02358 ArrayExpress:P25858 Genevestigator:P25858 GermOnline:AT3G04120 GO:GO:0008886 Uniprot:P25858
Root	Isotig00856	42	124	-1.691	1.86E-12	TAIR|locus:2103085 - symbol:GAPC1 "AT3G04120" species:3702 "Arabidopsis thaliana" [GO:0006096 "glycolysis" evidence=ISS;IDA;TAS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0006979 "response to oxidative stress" evidence=IEP;IDA] [GO:0005740 "mitochondrial envelope" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA;TAS] [GO:0006094 "gluconeogenesis" evidence=TAS] [GO:0042542 "response to hydrogen peroxide" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0008886 "glyceraldehyde-3-phosphate dehydrogenase (NADP+) (non-phosphorylating) activity" evidence=IDA] [GO:0010154 "fruit development" evidence=IMP] [GO:0048316 "seed development" evidence=IMP] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] [GO:0004365 "glyceraldehyde-3-phosphate dehydrogenase (NAD+) (phosphorylating) activity" evidence=TAS] [GO:0006950 "response to stress" evidence=IEP] [GO:0009408 "response to heat" evidence=IEP] [GO:0009744 "response to sucrose stimulus" evidence=IEP] InterPro:IPR006424 InterPro:IPR016040 InterPro:IPR020828 InterPro:IPR020829 InterPro:IPR020830 InterPro:IPR020831 Pfam:PF00044 Pfam:PF02800 PIRSF:PIRSF000149 PRINTS:PR00078 PROSITE:PS00071 SMART:SM00846 GO:GO:0005829 GO:GO:0005886 GO:GO:0048046 GO:GO:0005634 GO:GO:0046686 GO:GO:0005774 GO:GO:0009507 EMBL:CP002686 GenomeReviews:BA000014_GR Gene3D:G3DSA:3.40.50.720 GO:GO:0051287 GO:GO:0050661 GO:GO:0005507 GO:GO:0006094 GO:GO:0009651 GO:GO:0009408 GO:GO:0005740 GO:GO:0009744 GO:GO:0048316 GO:GO:0042542 GO:GO:0006096 EMBL:AC016829 eggNOG:COG0057 HOGENOM:HBG571736 PANTHER:PTHR10836 GO:GO:0004365 KO:K00134 TIGRFAMs:TIGR01534 OMA:CESTGVF EMBL:M64116 EMBL:M64119 EMBL:AY052267 EMBL:AY060521 EMBL:AY140084 EMBL:F20074 IPI:IPI00527494 PIR:JQ1287 RefSeq:NP_187062.1 UniGene:At.22963 UniGene:At.24406 UniGene:At.71328 ProteinModelPortal:P25858 SMR:P25858 STRING:P25858 PRIDE:P25858 EnsemblPlants:AT3G04120.1 GeneID:819567 KEGG:ath:AT3G04120 TAIR:At3g04120 InParanoid:P25858 PhylomeDB:P25858 ProtClustDB:PLN02358 ArrayExpress:P25858 Genevestigator:P25858 GermOnline:AT3G04120 GO:GO:0008886 Uniprot:P25858
Root	Isotig00858	42	119	-1.631	1.73E-11	TAIR|locus:2103085 - symbol:GAPC1 "AT3G04120" species:3702 "Arabidopsis thaliana" [GO:0006096 "glycolysis" evidence=ISS;IDA;TAS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0006979 "response to oxidative stress" evidence=IEP;IDA] [GO:0005740 "mitochondrial envelope" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA;TAS] [GO:0006094 "gluconeogenesis" evidence=TAS] [GO:0042542 "response to hydrogen peroxide" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0008886 "glyceraldehyde-3-phosphate dehydrogenase (NADP+) (non-phosphorylating) activity" evidence=IDA] [GO:0010154 "fruit development" evidence=IMP] [GO:0048316 "seed development" evidence=IMP] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] [GO:0004365 "glyceraldehyde-3-phosphate dehydrogenase (NAD+) (phosphorylating) activity" evidence=TAS] [GO:0006950 "response to stress" evidence=IEP] [GO:0009408 "response to heat" evidence=IEP] [GO:0009744 "response to sucrose stimulus" evidence=IEP] InterPro:IPR006424 InterPro:IPR016040 InterPro:IPR020828 InterPro:IPR020829 InterPro:IPR020830 InterPro:IPR020831 Pfam:PF00044 Pfam:PF02800 PIRSF:PIRSF000149 PRINTS:PR00078 PROSITE:PS00071 SMART:SM00846 GO:GO:0005829 GO:GO:0005886 GO:GO:0048046 GO:GO:0005634 GO:GO:0046686 GO:GO:0005774 GO:GO:0009507 EMBL:CP002686 GenomeReviews:BA000014_GR Gene3D:G3DSA:3.40.50.720 GO:GO:0051287 GO:GO:0050661 GO:GO:0005507 GO:GO:0006094 GO:GO:0009651 GO:GO:0009408 GO:GO:0005740 GO:GO:0009744 GO:GO:0048316 GO:GO:0042542 GO:GO:0006096 EMBL:AC016829 eggNOG:COG0057

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						HOGENOM:HBG571736 PANTHER:PTHR10836 GO:GO:0004365 KO:K00134 TIGRFAMs:TIGR01534 OMA:CESTGVF EMBL:M64116 EMBL:M64119 EMBL:AY052267 EMBL:AY060521 EMBL:AY140084 EMBL:F20074 IPI:IPI00527494 PIR:JQ1287 RefSeq:NP_187062.1 UniGene:At.22963 UniGene:At.24406 UniGene:At.71328 ProteinModelPortal:P25858 SMR:P25858 STRING:P25858 PRIDE:P25858 EnsemblPlants:AT3G04120.1 GeneID:819567 KEGG:ath:AT3G04120 TAIR:At3g04120 InParanoid:P25858 PhylomeDB:P25858 ProtClustDB:PLN02358 ArrayExpress:P25858 Genevestigator:P25858 GermOnline:AT3G04120 GO:GO:0008886 Uniprot:P25858
Root	Isotig00859	38	100	-1.525	4.32E-09	TAIR|locus:2103085 - symbol:GAPC1 "AT3G04120" species:3702 "Arabidopsis thaliana" [GO:0006096 "glycolysis" evidence=ISS;IDA;TAS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0006979 "response to oxidative stress" evidence=IEP;IDA] [GO:0005740 "mitochondrial envelope" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA;TAS] [GO:0006094 "gluconeogenesis" evidence=TAS] [GO:0042542 "response to hydrogen peroxide" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0008886 "glyceraldehyde-3-phosphate dehydrogenase (NADP+) (non-phosphorylating) activity" evidence=IDA] [GO:0010154 "fruit development" evidence=IMP] [GO:0048316 "seed development" evidence=IMP] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] [GO:0004365 "glyceraldehyde-3-phosphate dehydrogenase (NAD+) (phosphorylating) activity" evidence=TAS] [GO:0006950 "response to stress" evidence=IEP] [GO:0009408 "response to heat" evidence=IEP] [GO:0009744 "response to sucrose stimulus" evidence=IEP] InterPro:IPR006424 InterPro:IPR016040 InterPro:IPR020828 InterPro:IPR020829 InterPro:IPR020830 InterPro:IPR020831 Pfam:PF00044 Pfam:PF02800 PIRSF:PIRSF000149 PRINTS:PR00078 PROSITE:PS00071 SMART:SM00846 GO:GO:0005829 GO:GO:0005886 GO:GO:0048046 GO:GO:0005634 GO:GO:0046686 GO:GO:0005774 GO:GO:0009507 EMBL:CP002686 GenomeReviews:BA000014_GR Gene3D:G3DSA:3.40.50.720 GO:GO:0051287 GO:GO:0050661 GO:GO:0005507 GO:GO:0006094 GO:GO:0009651 GO:GO:0009408 GO:GO:0005740 GO:GO:0009744 GO:GO:0048316 GO:GO:0042542 GO:GO:0006096 EMBL:AC016829 eggNOG:COG0057 HOGENOM:HBG571736 PANTHER:PTHR10836 GO:GO:0004365 KO:K00134 TIGRFAMs:TIGR01534 OMA:CESTGVF EMBL:M64116 EMBL:M64119 EMBL:AY052267 EMBL:AY060521 EMBL:AY140084 EMBL:F20074 IPI:IPI00527494 PIR:JQ1287 RefSeq:NP_187062.1 UniGene:At.22963 UniGene:At.24406 UniGene:At.71328 ProteinModelPortal:P25858 SMR:P25858 STRING:P25858 PRIDE:P25858 EnsemblPlants:AT3G04120.1 GeneID:819567 KEGG:ath:AT3G04120 TAIR:At3g04120 InParanoid:P25858 PhylomeDB:P25858 ProtClustDB:PLN02358 ArrayExpress:P25858 Genevestigator:P25858 GermOnline:AT3G04120 GO:GO:0008886 Uniprot:P25858
Root	Isotig00860	42	122	-1.667	4.57E-12	TAIR|locus:2103085 - symbol:GAPC1 "AT3G04120" species:3702 "Arabidopsis thaliana" [GO:0006096 "glycolysis" evidence=ISS;IDA;TAS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0006979 "response to oxidative stress" evidence=IEP;IDA] [GO:0005740 "mitochondrial envelope" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA;TAS] [GO:0006094 "gluconeogenesis" evidence=TAS] [GO:0042542 "response to hydrogen peroxide" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0008886 "glyceraldehyde-3-phosphate dehydrogenase (NADP+) (non-phosphorylating) activity" evidence=IDA] [GO:0010154 "fruit development" evidence=IMP] [GO:0048316 "seed development" evidence=IMP] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] [GO:0004365 "glyceraldehyde-3-phosphate dehydrogenase (NAD+) (phosphorylating) activity" evidence=TAS] [GO:0006950 "response to stress" evidence=IEP] [GO:0009408 "response to heat" evidence=IEP] [GO:0009744 "response to sucrose stimulus" evidence=IEP] InterPro:IPR006424 InterPro:IPR016040 InterPro:IPR020828 InterPro:IPR020829 InterPro:IPR020830 InterPro:IPR020831 Pfam:PF00044 Pfam:PF02800 PIRSF:PIRSF000149 PRINTS:PR00078 PROSITE:PS00071 SMART:SM00846 GO:GO:0005829 GO:GO:0005886 GO:GO:0048046 GO:GO:0005634 GO:GO:0046686 GO:GO:0005774 GO:GO:0009507 EMBL:CP002686 GenomeReviews:BA000014_GR Gene3D:G3DSA:3.40.50.720 GO:GO:0051287 GO:GO:0050661 GO:GO:0005507 GO:GO:0006094 GO:GO:0009651 GO:GO:0009408 GO:GO:0005740 GO:GO:0009744 GO:GO:0048316 GO:GO:0042542 GO:GO:0006096 EMBL:AC016829 eggNOG:COG0057 HOGENOM:HBG571736 PANTHER:PTHR10836 GO:GO:0004365 KO:K00134 TIGRFAMs:TIGR01534

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						OMA:CESTGVF EMBL:M64116 EMBL:M64119 EMBL:AY052267 EMBL:AY060521 EMBL:AY140084 EMBL:F20074 IPI:IPI00527494 PIR:JQ1287 RefSeq:NP_187062.1 UniGene:At.22963 UniGene:At.24406 UniGene:At.71328 ProteinModelPortal:P25858 SMR:P25858 STRING:P25858 PRIDE:P25858 EnsemblPlants:AT3G04120.1 GeneID:819567 KEGG:ath:AT3G04120 TAIR:At3g04120 InParanoid:P25858 PhylomeDB:P25858 ProtClustDB:PLN02358 ArrayExpress:P25858 Genevestigator:P25858 GermOnline:AT3G04120 GO:GO:0008886 Uniprot:P25858
Root	Isotig00879	9	67	-3.025	1.96E-13	TAIR|locus:2205677 - symbol:FRUCT5 "AT1G55120" species:3702 "Arabidopsis thaliana" [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=ISS] [GO:0005975 "carbohydrate metabolic process" evidence=IEA] [GO:0031219 "levanase activity" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] InterPro:IPR001362 InterPro:IPR018053 PROSITE:PS00609 SMART:SM00640 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0048046 GO:GO:0005773 GO:GO:0005618 InterPro:IPR008985 SUPFAM:SSF49899 InterPro:IPR023296 Gene3D:G3DSA:2.115.10.20 SUPFAM:SSF75005 EMBL:AC073944 CAZy:GH32 eggNOG:COG1621 HOGENOM:HBG317462 InterPro:IPR013189 InterPro:IPR013148 Pfam:PF08244 Pfam:PF00251 EMBL:AB029310 EMBL:AK176675 IPI:IPI00548648 PIR:G96592 RefSeq:NP_564676.1 UniGene:At.458 ProteinModelPortal:Q67XZ3 SMR:Q67XZ3 PRIDE:Q67XZ3 EnsemblPlants:AT1G55120.1 GeneID:841955 KEGG:ath:AT1G55120 TAIR:At1g55120 InParanoid:Q67XZ3 OMA:HSIVESY PhylomeDB:Q67XZ3 ProtClustDB:CLSN2688819 ArrayExpress:Q67XZ3 Genevestigator:Q67XZ3 GO:GO:0051669 Uniprot:Q67XZ3
Root	Isotig00880	13	64	-2.429	1.59E-10	TAIR|locus:2205677 - symbol:FRUCT5 "AT1G55120" species:3702 "Arabidopsis thaliana" [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=ISS] [GO:0005975 "carbohydrate metabolic process" evidence=IEA] [GO:0031219 "levanase activity" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] InterPro:IPR001362 InterPro:IPR018053 PROSITE:PS00609 SMART:SM00640 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0048046 GO:GO:0005773 GO:GO:0005618 InterPro:IPR008985 SUPFAM:SSF49899 InterPro:IPR023296 Gene3D:G3DSA:2.115.10.20 SUPFAM:SSF75005 EMBL:AC073944 CAZy:GH32 eggNOG:COG1621 HOGENOM:HBG317462 InterPro:IPR013189 InterPro:IPR013148 Pfam:PF08244 Pfam:PF00251 EMBL:AB029310 EMBL:AK176675 IPI:IPI00548648 PIR:G96592 RefSeq:NP_564676.1 UniGene:At.458 ProteinModelPortal:Q67XZ3 SMR:Q67XZ3 PRIDE:Q67XZ3 EnsemblPlants:AT1G55120.1 GeneID:841955 KEGG:ath:AT1G55120 TAIR:At1g55120 InParanoid:Q67XZ3 OMA:HSIVESY PhylomeDB:Q67XZ3 ProtClustDB:CLSN2688819 ArrayExpress:Q67XZ3 Genevestigator:Q67XZ3 GO:GO:0051669 Uniprot:Q67XZ3
Root	Isotig00881	8	67	-3.195	4.74E-14	TAIR|locus:2205677 - symbol:FRUCT5 "AT1G55120" species:3702 "Arabidopsis thaliana" [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=ISS] [GO:0005975 "carbohydrate metabolic process" evidence=IEA] [GO:0031219 "levanase activity" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] InterPro:IPR001362 InterPro:IPR018053 PROSITE:PS00609 SMART:SM00640 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0048046 GO:GO:0005773 GO:GO:0005618 InterPro:IPR008985 SUPFAM:SSF49899 InterPro:IPR023296 Gene3D:G3DSA:2.115.10.20 SUPFAM:SSF75005 EMBL:AC073944 CAZy:GH32 eggNOG:COG1621 HOGENOM:HBG317462 InterPro:IPR013189 InterPro:IPR013148 Pfam:PF08244 Pfam:PF00251 EMBL:AB029310 EMBL:AK176675 IPI:IPI00548648 PIR:G96592 RefSeq:NP_564676.1 UniGene:At.458 ProteinModelPortal:Q67XZ3 SMR:Q67XZ3 PRIDE:Q67XZ3 EnsemblPlants:AT1G55120.1 GeneID:841955 KEGG:ath:AT1G55120 TAIR:At1g55120 InParanoid:Q67XZ3 OMA:HSIVESY PhylomeDB:Q67XZ3 ProtClustDB:CLSN2688819 ArrayExpress:Q67XZ3 Genevestigator:Q67XZ3 GO:GO:0051669 Uniprot:Q67XZ3
Root	Isotig00882	12	64	-2.544	5.12E-11	TAIR|locus:2205677 - symbol:FRUCT5 "AT1G55120" species:3702 "Arabidopsis thaliana" [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=ISS] [GO:0005975 "carbohydrate metabolic process" evidence=IEA] [GO:0031219 "levanase activity" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] InterPro:IPR001362 InterPro:IPR018053 PROSITE:PS00609 SMART:SM00640 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0048046 GO:GO:0005773 GO:GO:0005618 InterPro:IPR008985 SUPFAM:SSF49899 InterPro:IPR023296 Gene3D:G3DSA:2.115.10.20 SUPFAM:SSF75005 EMBL:AC073944 CAZy:GH32 eggNOG:COG1621 HOGENOM:HBG317462 InterPro:IPR013189 InterPro:IPR013148 Pfam:PF08244 Pfam:PF00251 EMBL:AB029310 EMBL:AK176675 IPI:IPI00548648 PIR:G96592 RefSeq:NP_564676.1 UniGene:At.458 ProteinModelPortal:Q67XZ3 SMR:Q67XZ3 PRIDE:Q67XZ3 EnsemblPlants:AT1G55120.1 GeneID:841955 KEGG:ath:AT1G55120 TAIR:At1g55120 InParanoid:Q67XZ3 OMA:HSIVESY PhylomeDB:Q67XZ3 ProtClustDB:CLSN2688819 ArrayExpress:Q67XZ3 Genevestigator:Q67XZ3 GO:GO:0051669 Uniprot:Q67XZ3
Root	Isotig00903	4	50	-3.773	3.46E-12	TAIR|locus:2005527 - symbol:ELI3-1 "elicitor-activated gene 3-1" species:3702 "Arabidopsis thaliana" [GO:0008270 "zinc ion binding" evidence=IEA] [GO:0016491 "oxidoreductase activity" evidence=IEA] [GO:0009617 "response to

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						bacterium" evidence=IEP] [GO:0009626 "plant-type hypersensitive response" evidence=IGI] [GO:0045551 "cinnamyl-alcohol dehydrogenase activity" evidence=IDA] [GO:0009809 "lignin biosynthetic process" evidence=IEP] InterPro:IPR002085 InterPro:IPR002328 InterPro:IPR013149 InterPro:IPR013154 InterPro:IPR016040 Pfam:PF00107 Pfam:PF08240 PROSITE:PS00059 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0009617 EMBL:AL161592 GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 GO:GO:0008270 eggNOG:COG1064 HOGENOM:HBG753318 InterPro:IPR011032 PANTHER:PTHR11695 SUPFAM:SSF50129 EMBL:AL035538 GO:GO:0009809 GO:GO:0045551 GO:GO:0052747 EMBL:Y16848 EMBL:X67816 EMBL:AY302079 EMBL:AF360225 EMBL:AY040066 EMBL:AY050407 EMBL:AY050931 EMBL:AY056385 EMBL:BT002729 EMBL:AK317050 IPI:IPI00545521 IPI:IPI00657154 PIR:T05625 RefSeq:NP_001031805.1 RefSeq:NP_195511.1 UniGene:At.24464 ProteinModelPortal:Q02971 SMR:Q02971 PRIDE:Q02971 EnsemblPlants:AT4G37980.1 GeneID:829954 KEGG:ath:AT4G37980 TAIR:At4g37980 InParanoid:Q02971 OMA:WSSLAST PhylomeDB:Q02971 ProtClustDB:CLSN2685373 ArrayExpress:Q02971 Genevestigator:Q02971 Uniprot:Q02971
Root	Isotig00904	4	50	-3.773	3.46E-12	TAIR|locus:2005527 - symbol:ELI3-1 "elicitor-activated gene 3-1" species:3702 "Arabidopsis thaliana" [GO:0008270 "zinc ion binding" evidence=IEA] [GO:0016491 "oxidoreductase activity" evidence=IEA] [GO:0009617 "response to bacterium" evidence=IEP] [GO:0009626 "plant-type hypersensitive response" evidence=IGI] [GO:0045551 "cinnamyl-alcohol dehydrogenase activity" evidence=IDA] [GO:0009809 "lignin biosynthetic process" evidence=IEP] InterPro:IPR002085 InterPro:IPR002328 InterPro:IPR013149 InterPro:IPR013154 InterPro:IPR016040 Pfam:PF00107 Pfam:PF08240 PROSITE:PS00059 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0009617 EMBL:AL161592 GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 GO:GO:0008270 eggNOG:COG1064 HOGENOM:HBG753318 InterPro:IPR011032 PANTHER:PTHR11695 SUPFAM:SSF50129 EMBL:AL035538 GO:GO:0009809 GO:GO:0045551 GO:GO:0052747 EMBL:Y16848 EMBL:X67816 EMBL:AY302079 EMBL:AF360225 EMBL:AY040066 EMBL:AY050407 EMBL:AY050931 EMBL:AY056385 EMBL:BT002729 EMBL:AK317050 IPI:IPI00545521 IPI:IPI00657154 PIR:T05625 RefSeq:NP_001031805.1 RefSeq:NP_195511.1 UniGene:At.24464 ProteinModelPortal:Q02971 SMR:Q02971 PRIDE:Q02971 EnsemblPlants:AT4G37980.1 GeneID:829954 KEGG:ath:AT4G37980 TAIR:At4g37980 InParanoid:Q02971 OMA:WSSLAST PhylomeDB:Q02971 ProtClustDB:CLSN2685373 ArrayExpress:Q02971 Genevestigator:Q02971 Uniprot:Q02971
Root	Isotig00905	2	34	-4.216	2.89E-09	TAIR|locus:2005527 - symbol:ELI3-1 "elicitor-activated gene 3-1" species:3702 "Arabidopsis thaliana" [GO:0008270 "zinc ion binding" evidence=IEA] [GO:0016491 "oxidoreductase activity" evidence=IEA] [GO:0009617 "response to bacterium" evidence=IEP] [GO:0009626 "plant-type hypersensitive response" evidence=IGI] [GO:0045551 "cinnamyl-alcohol dehydrogenase activity" evidence=IDA] [GO:0009809 "lignin biosynthetic process" evidence=IEP] InterPro:IPR002085 InterPro:IPR002328 InterPro:IPR013149 InterPro:IPR013154 InterPro:IPR016040 Pfam:PF00107 Pfam:PF08240 PROSITE:PS00059 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0009617 EMBL:AL161592 GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 GO:GO:0008270 eggNOG:COG1064 HOGENOM:HBG753318 InterPro:IPR011032 PANTHER:PTHR11695 SUPFAM:SSF50129 EMBL:AL035538 GO:GO:0009809 GO:GO:0045551 GO:GO:0052747 EMBL:Y16848 EMBL:X67816 EMBL:AY302079 EMBL:AF360225 EMBL:AY040066 EMBL:AY050407 EMBL:AY050931 EMBL:AY056385 EMBL:BT002729 EMBL:AK317050 IPI:IPI00545521 IPI:IPI00657154 PIR:T05625 RefSeq:NP_001031805.1 RefSeq:NP_195511.1 UniGene:At.24464 ProteinModelPortal:Q02971 SMR:Q02971 PRIDE:Q02971 EnsemblPlants:AT4G37980.1 GeneID:829954 KEGG:ath:AT4G37980 TAIR:At4g37980 InParanoid:Q02971 OMA:WSSLAST PhylomeDB:Q02971 ProtClustDB:CLSN2685373 ArrayExpress:Q02971 Genevestigator:Q02971 Uniprot:Q02971
Root	Isotig00907	2	34	-4.216	2.89E-09	TAIR|locus:2005527 - symbol:ELI3-1 "elicitor-activated gene 3-1" species:3702 "Arabidopsis thaliana" [GO:0008270 "zinc ion binding" evidence=IEA] [GO:0016491 "oxidoreductase activity" evidence=IEA] [GO:0009617 "response to bacterium" evidence=IEP] [GO:0009626 "plant-type hypersensitive response" evidence=IGI] [GO:0045551 "cinnamyl-alcohol dehydrogenase activity" evidence=IDA] [GO:0009809 "lignin biosynthetic process" evidence=IEP] InterPro:IPR002085 InterPro:IPR002328 InterPro:IPR013149 InterPro:IPR013154 InterPro:IPR016040 Pfam:PF00107 Pfam:PF08240 PROSITE:PS00059 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0009617 EMBL:AL161592 GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 GO:GO:0008270 eggNOG:COG1064 HOGENOM:HBG753318 InterPro:IPR011032 PANTHER:PTHR11695 SUPFAM:SSF50129 EMBL:AL035538 GO:GO:0009809 GO:GO:0045551 GO:GO:0052747 EMBL:Y16848 EMBL:X67816

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EMBL:AY302079 EMBL:AF360225 EMBL:AY040066 EMBL:AY050407 EMBL:AY050931 EMBL:AY056385 EMBL:BT002729 EMBL:AK317050 IPI:IPI00545521 IPI:IPI00657154 PIR:T05625 RefSeq:NP_001031805.1 RefSeq:NP_195511.1 UniGene:At.24464 ProteinModelPortal:Q02971 SMR:Q02971 PRIDE:Q02971 EnsemblPlants:AT4G37980.1 GeneID:829954 KEGG:ath:AT4G37980 TAIR:At4g37980 InParanoid:Q02971 OMA:WSSLAST PhylomeDB:Q02971 ProtClustDB:CLSN2685373 ArrayExpress:Q02971 Genevestigator:Q02971 Uniprot:Q02971
Root	Isotig00909	46	8	2.395	2.70E-07	TAIR|locus:2138121 - symbol:UGE2 "AT4G23920" species:3702 "Arabidopsis thaliana" [GO:0003978 "UDP-glucose 4-epimerase activity" evidence=IGI;IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0046983 "protein dimerization activity" evidence=IPI] [GO:0042546 "cell wall biogenesis" evidence=IMP] InterPro:IPR001509 InterPro:IPR005886 InterPro:IPR016040 Pfam:PF01370 GO:GO:0005829 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 HOGENOM:HBG755066 GO:GO:0046983 GO:GO:0050662 eggNOG:COG1087 GO:GO:0003978 GO:GO:0006012 InterPro:IPR025308 PANTHER:PTHR10366:SF39 Pfam:PF13950 TIGRFAMs:TIGR01179 EMBL:AL078468 EMBL:AL161560 KO:K01784 GO:GO:0042546 ProtClustDB:PLN02240 EMBL:BT008539 IPI:IPI00516246 PIR:T08911 RefSeq:NP_194123.1 UniGene:At.3390 ProteinModelPortal:Q9T0A7 SMR:Q9T0A7 IntAct:Q9T0A7 STRING:Q9T0A7 PRIDE:Q9T0A7 EnsemblPlants:AT4G23920.1 GeneID:828492 KEGG:ath:AT4G23920 TAIR:At4g23920 InParanoid:Q9T0A7 OMA:SAINPYG PhylomeDB:Q9T0A7 ArrayExpress:Q9T0A7 Genevestigator:Q9T0A7 GermOnline:AT4G23920 Uniprot:Q9T0A7
Root	Isotig00911	31	3	3.240	8.04E-07	TAIR|locus:2138121 - symbol:UGE2 "AT4G23920" species:3702 "Arabidopsis thaliana" [GO:0003978 "UDP-glucose 4-epimerase activity" evidence=IGI;IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0046983 "protein dimerization activity" evidence=IPI] [GO:0042546 "cell wall biogenesis" evidence=IMP] InterPro:IPR001509 InterPro:IPR005886 InterPro:IPR016040 Pfam:PF01370 GO:GO:0005829 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 HOGENOM:HBG755066 GO:GO:0046983 GO:GO:0050662 eggNOG:COG1087 GO:GO:0003978 GO:GO:0006012 InterPro:IPR025308 PANTHER:PTHR10366:SF39 Pfam:PF13950 TIGRFAMs:TIGR01179 EMBL:AL078468 EMBL:AL161560 KO:K01784 GO:GO:0042546 ProtClustDB:PLN02240 EMBL:BT008539 IPI:IPI00516246 PIR:T08911 RefSeq:NP_194123.1 UniGene:At.3390 ProteinModelPortal:Q9T0A7 SMR:Q9T0A7 IntAct:Q9T0A7 STRING:Q9T0A7 PRIDE:Q9T0A7 EnsemblPlants:AT4G23920.1 GeneID:828492 KEGG:ath:AT4G23920 TAIR:At4g23920 InParanoid:Q9T0A7 OMA:SAINPYG PhylomeDB:Q9T0A7 ArrayExpress:Q9T0A7 Genevestigator:Q9T0A7 GermOnline:AT4G23920 Uniprot:Q9T0A7
Root	Isotig00915	58	95	-0.841	0.000381099	TAIR|locus:2129256 - symbol:HOG1 "AT4G13940" species:3702 "Arabidopsis thaliana" [GO:0004013 "adenosylhomocysteinase activity" evidence=ISS;IMP] [GO:0006730 "one-carbon metabolic process" evidence=ISS] [GO:0009793 "embryo development ending in seed dormancy" evidence=IMP;NAS] [GO:0005773 "vacuole" evidence=IDA] [GO:0006346 "methylation-dependent chromatin silencing" evidence=IMP] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] [GO:0016441 "posttranscriptional gene silencing" evidence=IMP] InterPro:IPR000043 InterPro:IPR020082 Pfam:PF05221 PIRSF:PIRSF001109 PROSITE:PS00738 PROSITE:PS00739 SMART:SM00996 InterPro:IPR015878 Pfam:PF00670 GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005774 EMBL:Z97335 GO:GO:0005507 GO:GO:0009793 GO:GO:0006730 EMBL:AL161537 GO:GO:0006346 GO:GO:0016441 EMBL:AF059581 EMBL:AF325037 EMBL:AY042866 EMBL:AY049279 EMBL:AY081468 EMBL:AY090284 EMBL:BT002404 EMBL:AY085669 EMBL:Z97059 IPI:IPI00527713 PIR:C71400 RefSeq:NP_193130.1 UniGene:At.24056 UniGene:At.24845 UniGene:At.71956 UniGene:At.74987 UniGene:At.74988 ProteinModelPortal:O23255 SMR:O23255 IntAct:O23255 STRING:O23255 PRIDE:O23255 ProMEX:O23255 EnsemblPlants:AT4G13940.1 GeneID:827028 KEGG:ath:AT4G13940 TAIR:At4g13940 eggNOG:COG0499 HOGENOM:HBG352029 InParanoid:O23255 KO:K01251 OMA:ELFTKTE PhylomeDB:O23255 ProtClustDB:PLN02494 ArrayExpress:O23255 Genevestigator:O23255 GO:GO:0004013 PANTHER:PTHR23420 SMART:SM00997 TIGRFAMs:TIGR00936 Uniprot:O23255
Root	Isotig00916	68	111	-0.836	0.000132787	TAIR|locus:2129256 - symbol:HOG1 "AT4G13940" species:3702 "Arabidopsis thaliana" [GO:0004013 "adenosylhomocysteinase activity" evidence=ISS;IMP] [GO:0006730 "one-carbon metabolic process" evidence=ISS]

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						[GO:0009793 "embryo development ending in seed dormancy" evidence=IMP;NAS] [GO:0005773 "vacuole" evidence=IDA] [GO:0006346 "methylation-dependent chromatin silencing" evidence=IMP] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] [GO:0016441 "posttranscriptional gene silencing" evidence=IMP] InterPro:IPR000043 InterPro:IPR020082 Pfam:PF05221 PIRSF:PIRSF001109 PROSITE:PS00738 PROSITE:PS00739 SMART:SM00996 InterPro:IPR015878 Pfam:PF00670 GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005774 EMBL:Z97335 GO:GO:0005507 GO:GO:0009793 GO:GO:0006730 EMBL:AL161537 GO:GO:0006346 GO:GO:0016441 EMBL:AF059581 EMBL:AF325037 EMBL:AY042866 EMBL:AY049279 EMBL:AY081468 EMBL:AY090284 EMBL:BT002404 EMBL:AY085669 EMBL:Z97059 IPI:IPI00527713 PIR:C71400 RefSeq:NP_193130.1 UniGene:At.24056 UniGene:At.24845 UniGene:At.71956 UniGene:At.74987 UniGene:At.74988 ProteinModelPortal:O23255 SMR:O23255 IntAct:O23255 STRING:O23255 PRIDE:O23255 ProMEX:O23255 EnsemblPlants:AT4G13940.1 GeneID:827028 KEGG:ath:AT4G13940 TAIR:At4g13940 eggNOG:COG0499 HOGENOM:HBG352029 InParanoid:O23255 KO:K01251 OMA:ELFTKTE PhylomeDB:O23255 ProtClustDB:PLN02494 ArrayExpress:O23255 Genevestigator:O23255 GO:GO:0004013 PANTHER:PTHR23420 SMART:SM00997 TIGRFAMs:TIGR00936 Uniprot:O23255
Root	Isotig00917	61	110	-0.980	1.37E-05	TAIR|locus:2129256 - symbol:HOG1 "AT4G13940" species:3702 "Arabidopsis thaliana" [GO:0004013 "adenosylhomocysteinase activity" evidence=ISS;IMP] [GO:0006730 "one-carbon metabolic process" evidence=ISS] [GO:0009793 "embryo development ending in seed dormancy" evidence=IMP;NAS] [GO:0005773 "vacuole" evidence=IDA] [GO:0006346 "methylation-dependent chromatin silencing" evidence=IMP] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] [GO:0016441 "posttranscriptional gene silencing" evidence=IMP] InterPro:IPR000043 InterPro:IPR020082 Pfam:PF05221 PIRSF:PIRSF001109 PROSITE:PS00738 PROSITE:PS00739 SMART:SM00996 InterPro:IPR015878 Pfam:PF00670 GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005774 EMBL:Z97335 GO:GO:0005507 GO:GO:0009793 GO:GO:0006730 EMBL:AL161537 GO:GO:0006346 GO:GO:0016441 EMBL:AF059581 EMBL:AF325037 EMBL:AY042866 EMBL:AY049279 EMBL:AY081468 EMBL:AY090284 EMBL:BT002404 EMBL:AY085669 EMBL:Z97059 IPI:IPI00527713 PIR:C71400 RefSeq:NP_193130.1 UniGene:At.24056 UniGene:At.24845 UniGene:At.71956 UniGene:At.74987 UniGene:At.74988 ProteinModelPortal:O23255 SMR:O23255 IntAct:O23255 STRING:O23255 PRIDE:O23255 ProMEX:O23255 EnsemblPlants:AT4G13940.1 GeneID:827028 KEGG:ath:AT4G13940 TAIR:At4g13940 eggNOG:COG0499 HOGENOM:HBG352029 InParanoid:O23255 KO:K01251 OMA:ELFTKTE PhylomeDB:O23255 ProtClustDB:PLN02494 ArrayExpress:O23255 Genevestigator:O23255 GO:GO:0004013 PANTHER:PTHR23420 SMART:SM00997 TIGRFAMs:TIGR00936 Uniprot:O23255
Root	Isotig00919	53	87	-0.844	0.000647735	TAIR|locus:2129256 - symbol:HOG1 "AT4G13940" species:3702 "Arabidopsis thaliana" [GO:0004013 "adenosylhomocysteinase activity" evidence=ISS;IMP] [GO:0006730 "one-carbon metabolic process" evidence=ISS] [GO:0009793 "embryo development ending in seed dormancy" evidence=IMP;NAS] [GO:0005773 "vacuole" evidence=IDA] [GO:0006346 "methylation-dependent chromatin silencing" evidence=IMP] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] [GO:0016441 "posttranscriptional gene silencing" evidence=IMP] InterPro:IPR000043 InterPro:IPR020082 Pfam:PF05221 PIRSF:PIRSF001109 PROSITE:PS00738 PROSITE:PS00739 SMART:SM00996 InterPro:IPR015878 Pfam:PF00670 GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005774 EMBL:Z97335 GO:GO:0005507 GO:GO:0009793 GO:GO:0006730 EMBL:AL161537 GO:GO:0006346 GO:GO:0016441 EMBL:AF059581 EMBL:AF325037 EMBL:AY042866 EMBL:AY049279 EMBL:AY081468 EMBL:AY090284 EMBL:BT002404 EMBL:AY085669 EMBL:Z97059 IPI:IPI00527713 PIR:C71400 RefSeq:NP_193130.1 UniGene:At.24056 UniGene:At.24845 UniGene:At.71956 UniGene:At.74987 UniGene:At.74988 ProteinModelPortal:O23255 SMR:O23255 IntAct:O23255

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						STRING:O23255 PRIDE:O23255 ProMEX:O23255 EnsemblPlants:AT4G13940.1 GeneID:827028 KEGG:ath:AT4G13940 TAIR:At4g13940 eggNOG:COG0499 HOGENOM:HBG352029 InParanoid:O23255 KO:K01251 OMA:ELFTKTE PhylomeDB:O23255 ProtClustDB:PLN02494 ArrayExpress:O23255 Genevestigator:O23255 GO:GO:0004013 PANTHER:PTHR23420 SMART:SM00997 TIGRFAMs:TIGR00936 Uniprot:O23255
Root	Isotig00927	26	62	-1.383	1.73E-05	TAIR|locus:2054027 - symbol:TPS11 "trehalose phosphatase/synthase 11" species:3702 "Arabidopsis thaliana" [GO:0005992 "trehalose biosynthetic process" evidence=IEA] [GO:0008152 "metabolic process" evidence=IEA] [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0003825 "alpha,alpha-trehalose-phosphate synthase (UDP-forming) activity" evidence=IMP] [GO:0004805 "trehalose-phosphatase activity" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001830 InterPro:IPR003337 InterPro:IPR006379 Pfam:PF00982 Pfam:PF02358 GO:GO:0005829 GO:GO:0005739 EMBL:CP002685 GenomeReviews:CT485783_GR InterPro:IPR023214 Gene3D:G3DSA:3.40.50.1000 SUPFAM:SSF56784 EMBL:AC005724 GO:GO:0005992 TIGRFAMs:TIGR01484 CAZy:GT20 eggNOG:COG0380 HOGENOM:HBG559076 GO:GO:0003825 HSSP:P31677 TIGRFAMs:TIGR00685 EMBL:AV822913 EMBL:AY042865 EMBL:AY081537 IPI:IPI00538425 IPI:IPI00889354 PIR:E84567 RefSeq:NP_179460.1 UniGene:At.25317 ProteinModelPortal:Q9ZV48 STRING:Q9ZV48 PRIDE:Q9ZV48 EnsemblPlants:AT2G18700.1 GeneID:816385 KEGG:ath:AT2G18700 TAIR:At2g18700 InParanoid:Q9ZV48 OMA:LQRACKD PhylomeDB:Q9ZV48 ProtClustDB:CLSN2912887 Genevestigator:Q9ZV48 Uniprot:Q9ZV48
Root	Isotig00930	25	60	-1.392	2.15E-05	TAIR|locus:2054027 - symbol:TPS11 "trehalose phosphatase/synthase 11" species:3702 "Arabidopsis thaliana" [GO:0005992 "trehalose biosynthetic process" evidence=IEA] [GO:0008152 "metabolic process" evidence=IEA] [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0003825 "alpha,alpha-trehalose-phosphate synthase (UDP-forming) activity" evidence=IMP] [GO:0004805 "trehalose-phosphatase activity" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001830 InterPro:IPR003337 InterPro:IPR006379 Pfam:PF00982 Pfam:PF02358 GO:GO:0005829 GO:GO:0005739 EMBL:CP002685 GenomeReviews:CT485783_GR InterPro:IPR023214 Gene3D:G3DSA:3.40.50.1000 SUPFAM:SSF56784 EMBL:AC005724 GO:GO:0005992 TIGRFAMs:TIGR01484 CAZy:GT20 eggNOG:COG0380 HOGENOM:HBG559076 GO:GO:0003825 HSSP:P31677 TIGRFAMs:TIGR00685 EMBL:AV822913 EMBL:AY042865 EMBL:AY081537 IPI:IPI00538425 IPI:IPI00889354 PIR:E84567 RefSeq:NP_179460.1 UniGene:At.25317 ProteinModelPortal:Q9ZV48 STRING:Q9ZV48 PRIDE:Q9ZV48 EnsemblPlants:AT2G18700.1 GeneID:816385 KEGG:ath:AT2G18700 TAIR:At2g18700 InParanoid:Q9ZV48 OMA:LQRACKD PhylomeDB:Q9ZV48 ProtClustDB:CLSN2912887 Genevestigator:Q9ZV48 Uniprot:Q9ZV48
Root	Isotig00931	26	62	-1.383	1.73E-05	TAIR|locus:2054027 - symbol:TPS11 "trehalose phosphatase/synthase 11" species:3702 "Arabidopsis thaliana" [GO:0005992 "trehalose biosynthetic process" evidence=IEA] [GO:0008152 "metabolic process" evidence=IEA] [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0003825 "alpha,alpha-trehalose-phosphate synthase (UDP-forming) activity" evidence=IMP] [GO:0004805 "trehalose-phosphatase activity" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001830 InterPro:IPR003337 InterPro:IPR006379 Pfam:PF00982 Pfam:PF02358 GO:GO:0005829 GO:GO:0005739 EMBL:CP002685 GenomeReviews:CT485783_GR InterPro:IPR023214 Gene3D:G3DSA:3.40.50.1000 SUPFAM:SSF56784 EMBL:AC005724 GO:GO:0005992 TIGRFAMs:TIGR01484 CAZy:GT20 eggNOG:COG0380 HOGENOM:HBG559076 GO:GO:0003825 HSSP:P31677 TIGRFAMs:TIGR00685 EMBL:AV822913 EMBL:AY042865 EMBL:AY081537 IPI:IPI00538425 IPI:IPI00889354 PIR:E84567 RefSeq:NP_179460.1 UniGene:At.25317 ProteinModelPortal:Q9ZV48 STRING:Q9ZV48 PRIDE:Q9ZV48 EnsemblPlants:AT2G18700.1 GeneID:816385 KEGG:ath:AT2G18700 TAIR:At2g18700 InParanoid:Q9ZV48 OMA:LQRACKD PhylomeDB:Q9ZV48 ProtClustDB:CLSN2912887 Genevestigator:Q9ZV48 Uniprot:Q9ZV48
Root	Isotig00932	17	52	-1.742	3.19E-06	TAIR|locus:2054027 - symbol:TPS11 "trehalose phosphatase/synthase 11" species:3702 "Arabidopsis thaliana" [GO:0005992 "trehalose biosynthetic process" evidence=IEA] [GO:0008152 "metabolic process" evidence=IEA] [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0003825 "alpha,alpha-trehalose-phosphate synthase (UDP-forming) activity" evidence=IMP] [GO:0004805 "trehalose-phosphatase activity" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001830 InterPro:IPR003337 InterPro:IPR006379 Pfam:PF00982 Pfam:PF02358 GO:GO:0005829 GO:GO:0005739 EMBL:CP002685 GenomeReviews:CT485783_GR InterPro:IPR023214 Gene3D:G3DSA:3.40.50.1000 SUPFAM:SSF56784 EMBL:AC005724 GO:GO:0005992 TIGRFAMs:TIGR01484

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						CAZy:GT20 eggNOG:COG0380 HOGENOM:HBG559076 GO:GO:0003825 HSSP:P31677 TIGRFAMs:TIGR00685 EMBL:AV822913 EMBL:AY042865 EMBL:AY081537 IPI:IPI00538425 IPI:IPI00889354 PIR:E84567 RefSeq:NP_179460.1 UniGene:At.25317 ProteinModelPortal:Q9ZV48 STRING:Q9ZV48 PRIDE:Q9ZV48 EnsemblPlants:AT2G18700.1 GeneID:816385 KEGG:ath:AT2G18700 TAIR:At2g18700 InParanoid:Q9ZV48 OMA:LQRACKD PhylomeDB:Q9ZV48 ProtClustDB:CLSN2912887 Genevestigator:Q9ZV48 Uniprot:Q9ZV48
Root	Isotig00933	17	42	-1.434	0.000278343	TAIR|locus:2054027 - symbol:TPS11 "trehalose phosphatase/synthase 11" species:3702 "Arabidopsis thaliana" [GO:0005992 "trehalose biosynthetic process" evidence=IEA] [GO:0008152 "metabolic process" evidence=IEA] [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0003825 "alpha,alpha-trehalose-phosphate synthase (UDP-forming) activity" evidence=IMP] [GO:0004805 "trehalose-phosphatase activity" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001830 InterPro:IPR003337 InterPro:IPR006379 Pfam:PF00982 Pfam:PF02358 GO:GO:0005829 GO:GO:0005739 EMBL:CP002685 GenomeReviews:CT485783_GR InterPro:IPR023214 Gene3D:G3DSA:3.40.50.1000 SUPFAM:SSF56784 EMBL:AC005724 GO:GO:0005992 TIGRFAMs:TIGR01484 CAZy:GT20 eggNOG:COG0380 HOGENOM:HBG559076 GO:GO:0003825 HSSP:P31677 TIGRFAMs:TIGR00685 EMBL:AV822913 EMBL:AY042865 EMBL:AY081537 IPI:IPI00538425 IPI:IPI00889354 PIR:E84567 RefSeq:NP_179460.1 UniGene:At.25317 ProteinModelPortal:Q9ZV48 STRING:Q9ZV48 PRIDE:Q9ZV48 EnsemblPlants:AT2G18700.1 GeneID:816385 KEGG:ath:AT2G18700 TAIR:At2g18700 InParanoid:Q9ZV48 OMA:LQRACKD PhylomeDB:Q9ZV48 ProtClustDB:CLSN2912887 Genevestigator:Q9ZV48 Uniprot:Q9ZV48
Root	Isotig00934	25	60	-1.392	2.15E-05	TAIR|locus:2054027 - symbol:TPS11 "trehalose phosphatase/synthase 11" species:3702 "Arabidopsis thaliana" [GO:0005992 "trehalose biosynthetic process" evidence=IEA] [GO:0008152 "metabolic process" evidence=IEA] [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0003825 "alpha,alpha-trehalose-phosphate synthase (UDP-forming) activity" evidence=IMP] [GO:0004805 "trehalose-phosphatase activity" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001830 InterPro:IPR003337 InterPro:IPR006379 Pfam:PF00982 Pfam:PF02358 GO:GO:0005829 GO:GO:0005739 EMBL:CP002685 GenomeReviews:CT485783_GR InterPro:IPR023214 Gene3D:G3DSA:3.40.50.1000 SUPFAM:SSF56784 EMBL:AC005724 GO:GO:0005992 TIGRFAMs:TIGR01484 CAZy:GT20 eggNOG:COG0380 HOGENOM:HBG559076 GO:GO:0003825 HSSP:P31677 TIGRFAMs:TIGR00685 EMBL:AV822913 EMBL:AY042865 EMBL:AY081537 IPI:IPI00538425 IPI:IPI00889354 PIR:E84567 RefSeq:NP_179460.1 UniGene:At.25317 ProteinModelPortal:Q9ZV48 STRING:Q9ZV48 PRIDE:Q9ZV48 EnsemblPlants:AT2G18700.1 GeneID:816385 KEGG:ath:AT2G18700 TAIR:At2g18700 InParanoid:Q9ZV48 OMA:LQRACKD PhylomeDB:Q9ZV48 ProtClustDB:CLSN2912887 Genevestigator:Q9ZV48 Uniprot:Q9ZV48
Root	Isotig00935	16	66	-2.173	1.23E-09	TAIR|locus:2054027 - symbol:TPS11 "trehalose phosphatase/synthase 11" species:3702 "Arabidopsis thaliana" [GO:0005992 "trehalose biosynthetic process" evidence=IEA] [GO:0008152 "metabolic process" evidence=IEA] [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0003825 "alpha,alpha-trehalose-phosphate synthase (UDP-forming) activity" evidence=IMP] [GO:0004805 "trehalose-phosphatase activity" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001830 InterPro:IPR003337 InterPro:IPR006379 Pfam:PF00982 Pfam:PF02358 GO:GO:0005829 GO:GO:0005739 EMBL:CP002685 GenomeReviews:CT485783_GR InterPro:IPR023214 Gene3D:G3DSA:3.40.50.1000 SUPFAM:SSF56784 EMBL:AC005724 GO:GO:0005992 TIGRFAMs:TIGR01484 CAZy:GT20 eggNOG:COG0380 HOGENOM:HBG559076 GO:GO:0003825 HSSP:P31677 TIGRFAMs:TIGR00685 EMBL:AV822913 EMBL:AY042865 EMBL:AY081537 IPI:IPI00538425 IPI:IPI00889354 PIR:E84567 RefSeq:NP_179460.1 UniGene:At.25317 ProteinModelPortal:Q9ZV48 STRING:Q9ZV48 PRIDE:Q9ZV48 EnsemblPlants:AT2G18700.1 GeneID:816385 KEGG:ath:AT2G18700 TAIR:At2g18700 InParanoid:Q9ZV48 OMA:LQRACKD PhylomeDB:Q9ZV48 ProtClustDB:CLSN2912887 Genevestigator:Q9ZV48 Uniprot:Q9ZV48
Root	Isotig00936	15	64	-2.222	1.31E-09	TAIR|locus:2054027 - symbol:TPS11 "trehalose phosphatase/synthase 11" species:3702 "Arabidopsis thaliana" [GO:0005992 "trehalose biosynthetic process" evidence=IEA] [GO:0008152 "metabolic process" evidence=IEA] [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0003825 "alpha,alpha-trehalose-phosphate synthase (UDP-forming) activity" evidence=IMP] [GO:0004805 "trehalose-phosphatase activity" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001830 InterPro:IPR003337 InterPro:IPR006379 Pfam:PF00982 Pfam:PF02358 GO:GO:0005829 GO:GO:0005739 EMBL:CP002685 GenomeReviews:CT485783_GR InterPro:IPR023214 Gene3D:G3DSA:3.40.50.1000 SUPFAM:SSF56784 EMBL:AC005724 GO:GO:0005992 TIGRFAMs:TIGR01484

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						CAZy:GT20 eggNOG:COG0380 HOGENOM:HBG559076 GO:GO:0003825 HSSP:P31677 TIGRFAMs:TIGR00685 EMBL:AV822913 EMBL:AY042865 EMBL:AY081537 IPI:IPI00538425 IPI:IPI00889354 PIR:E84567 RefSeq:NP_179460.1 UniGene:At.25317 ProteinModelPortal:Q9ZV48 STRING:Q9ZV48 PRIDE:Q9ZV48 EnsemblPlants:AT2G18700.1 GeneID:816385 KEGG:ath:AT2G18700 TAIR:At2g18700 InParanoid:Q9ZV48 OMA:LQRACKD PhylomeDB:Q9ZV48 ProtClustDB:CLSN2912887 Genevestigator:Q9ZV48 Uniprot:Q9ZV48
Root	Isotig00947	7	39	-2.607	2.03E-07	TAIR|locus:2164391 - symbol:NAC103 "AT5G64060" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0007275 "multicellular organismal development" evidence=ISS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] InterPro:IPR003441 Pfam:PF02365 PROSITE:PS51005 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0006355 GO:GO:0003677 HSSP:Q9C932 SUPFAM:SSF101941 EMBL:AB008266 IPI:IPI00520409 RefSeq:NP_201211.1 UniGene:At.50553 ProteinModelPortal:Q9FMJ1 SMR:Q9FMJ1 DNASU:836527 EnsemblPlants:AT5G64060.1 GeneID:836527 KEGG:ath:AT5G64060 TAIR:At5g64060 eggNOG:NOG122520 HOGENOM:HBG317258 InParanoid:Q9FMJ1 OMA:ANRSTEC PhylomeDB:Q9FMJ1 ProtClustDB:CLSN2686235 Genevestigator:Q9FMJ1 Uniprot:Q9FMJ1
Root	Isotig00948	8	38	-2.377	1.13E-06	TAIR|locus:2164391 - symbol:NAC103 "AT5G64060" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0007275 "multicellular organismal development" evidence=ISS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] InterPro:IPR003441 Pfam:PF02365 PROSITE:PS51005 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0006355 GO:GO:0003677 HSSP:Q9C932 SUPFAM:SSF101941 EMBL:AB008266 IPI:IPI00520409 RefSeq:NP_201211.1 UniGene:At.50553 ProteinModelPortal:Q9FMJ1 SMR:Q9FMJ1 DNASU:836527 EnsemblPlants:AT5G64060.1 GeneID:836527 KEGG:ath:AT5G64060 TAIR:At5g64060 eggNOG:NOG122520 HOGENOM:HBG317258 InParanoid:Q9FMJ1 OMA:ANRSTEC PhylomeDB:Q9FMJ1 ProtClustDB:CLSN2686235 Genevestigator:Q9FMJ1 Uniprot:Q9FMJ1
Root	Isotig00949	7	39	-2.607	2.03E-07	TAIR|locus:2164391 - symbol:NAC103 "AT5G64060" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0007275 "multicellular organismal development" evidence=ISS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] InterPro:IPR003441 Pfam:PF02365 PROSITE:PS51005 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0006355 GO:GO:0003677 HSSP:Q9C932 SUPFAM:SSF101941 EMBL:AB008266 IPI:IPI00520409 RefSeq:NP_201211.1 UniGene:At.50553 ProteinModelPortal:Q9FMJ1 SMR:Q9FMJ1 DNASU:836527 EnsemblPlants:AT5G64060.1 GeneID:836527 KEGG:ath:AT5G64060 TAIR:At5g64060 eggNOG:NOG122520 HOGENOM:HBG317258 InParanoid:Q9FMJ1 OMA:ANRSTEC PhylomeDB:Q9FMJ1 ProtClustDB:CLSN2686235 Genevestigator:Q9FMJ1 Uniprot:Q9FMJ1
Root	Isotig00950	8	36	-2.299	3.42E-06	TAIR|locus:2184742 - symbol:NAC082 "AT5G09330" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0007275 "multicellular organismal development" evidence=ISS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] InterPro:IPR003441 Pfam:PF02365 PROSITE:PS51005 EMBL:CP002688 GO:GO:0006355 GO:GO:0003677 EMBL:AL391712 HSSP:Q9C932 SUPFAM:SSF101941 ProtClustDB:CLSN2686235 EMBL:BT020263 EMBL:AK317217 IPI:IPI00527439 RefSeq:NP_001078551.1 RefSeq:NP_001078552.1 RefSeq:NP_196495.1 UniGene:At.48014 UniGene:At.67761 ProteinModelPortal:Q9FY82 SMR:Q9FY82 IntAct:Q9FY82 STRING:Q9FY82 PRIDE:Q9FY82 EnsemblPlants:AT5G09330.1 EnsemblPlants:AT5G09330.2 EnsemblPlants:AT5G09330.3 EnsemblPlants:AT5G09330.4 GeneID:830792 KEGG:ath:AT5G09330 TAIR:At5g09330 InParanoid:Q9FY82 OMA:QDLTAPL PhylomeDB:Q9FY82 Genevestigator:Q9FY82 Uniprot:Q9FY82
Root	Isotig00951	8	38	-2.377	1.13E-06	TAIR|locus:2164391 - symbol:NAC103 "AT5G64060" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0007275 "multicellular organismal development" evidence=ISS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] InterPro:IPR003441 Pfam:PF02365 PROSITE:PS51005 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0006355 GO:GO:0003677 HSSP:Q9C932 SUPFAM:SSF101941 EMBL:AB008266 IPI:IPI00520409 RefSeq:NP_201211.1 UniGene:At.50553 ProteinModelPortal:Q9FMJ1 SMR:Q9FMJ1 DNASU:836527 EnsemblPlants:AT5G64060.1 GeneID:836527 KEGG:ath:AT5G64060 TAIR:At5g64060 eggNOG:NOG122520 HOGENOM:HBG317258 InParanoid:Q9FMJ1 OMA:ANRSTEC PhylomeDB:Q9FMJ1 ProtClustDB:CLSN2686235 Genevestigator:Q9FMJ1 Uniprot:Q9FMJ1

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig00952	9	35	-2.088	1.60E-05	TAIR|locus:2184742 - symbol:NAC082 "AT5G09330" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0007275 "multicellular organismal development" evidence=ISS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] InterPro:IPR003441 Pfam:PF02365 PROSITE:PS51005 EMBL:CP002688 GO:GO:0006355 GO:GO:0003677 EMBL:AL391712 HSSP:Q9C932 SUPFAM:SSF101941 ProtClustDB:CLSN2686235 EMBL:BT020263 EMBL:AK317217 IPI:IPI00527439 RefSeq:NP_001078551.1 RefSeq:NP_001078552.1 RefSeq:NP_196495.1 UniGene:At.48014 UniGene:At.67761 ProteinModelPortal:Q9FY82 SMR:Q9FY82 IntAct:Q9FY82 STRING:Q9FY82 PRIDE:Q9FY82 EnsemblPlants:AT5G09330.1 EnsemblPlants:AT5G09330.2 EnsemblPlants:AT5G09330.3 EnsemblPlants:AT5G09330.4 GeneID:830792 KEGG:ath:AT5G09330 TAIR:At5g09330 InParanoid:Q9FY82 OMA:QDLTAPL PhylomeDB:Q9FY82 Genevestigator:Q9FY82 Uniprot:Q9FY82
Root	Isotig00953	8	36	-2.299	3.42E-06	TAIR|locus:2184742 - symbol:NAC082 "AT5G09330" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0007275 "multicellular organismal development" evidence=ISS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] InterPro:IPR003441 Pfam:PF02365 PROSITE:PS51005 EMBL:CP002688 GO:GO:0006355 GO:GO:0003677 EMBL:AL391712 HSSP:Q9C932 SUPFAM:SSF101941 ProtClustDB:CLSN2686235 EMBL:BT020263 EMBL:AK317217 IPI:IPI00527439 RefSeq:NP_001078551.1 RefSeq:NP_001078552.1 RefSeq:NP_196495.1 UniGene:At.48014 UniGene:At.67761 ProteinModelPortal:Q9FY82 SMR:Q9FY82 IntAct:Q9FY82 STRING:Q9FY82 PRIDE:Q9FY82 EnsemblPlants:AT5G09330.1 EnsemblPlants:AT5G09330.2 EnsemblPlants:AT5G09330.3 EnsemblPlants:AT5G09330.4 GeneID:830792 KEGG:ath:AT5G09330 TAIR:At5g09330 InParanoid:Q9FY82 OMA:QDLTAPL PhylomeDB:Q9FY82 Genevestigator:Q9FY82 Uniprot:Q9FY82
Root	Isotig00954	9	35	-2.088	1.60E-05	TAIR|locus:2184742 - symbol:NAC082 "AT5G09330" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0007275 "multicellular organismal development" evidence=ISS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] InterPro:IPR003441 Pfam:PF02365 PROSITE:PS51005 EMBL:CP002688 GO:GO:0006355 GO:GO:0003677 EMBL:AL391712 HSSP:Q9C932 SUPFAM:SSF101941 ProtClustDB:CLSN2686235 EMBL:BT020263 EMBL:AK317217 IPI:IPI00527439 RefSeq:NP_001078551.1 RefSeq:NP_001078552.1 RefSeq:NP_196495.1 UniGene:At.48014 UniGene:At.67761 ProteinModelPortal:Q9FY82 SMR:Q9FY82 IntAct:Q9FY82 STRING:Q9FY82 PRIDE:Q9FY82 EnsemblPlants:AT5G09330.1 EnsemblPlants:AT5G09330.2 EnsemblPlants:AT5G09330.3 EnsemblPlants:AT5G09330.4 GeneID:830792 KEGG:ath:AT5G09330 TAIR:At5g09330 InParanoid:Q9FY82 OMA:QDLTAPL PhylomeDB:Q9FY82 Genevestigator:Q9FY82 Uniprot:Q9FY82
Root	Isotig00955	5	23	-2.331	0.000182103	TAIR|locus:2164391 - symbol:NAC103 "AT5G64060" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0007275 "multicellular organismal development" evidence=ISS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] InterPro:IPR003441 Pfam:PF02365 PROSITE:PS51005 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0006355 GO:GO:0003677 HSSP:Q9C932 SUPFAM:SSF101941 EMBL:AB008266 IPI:IPI00520409 RefSeq:NP_201211.1 UniGene:At.50553 ProteinModelPortal:Q9FMJ1 SMR:Q9FMJ1 DNASU:836527 EnsemblPlants:AT5G64060.1 GeneID:836527 KEGG:ath:AT5G64060 TAIR:At5g64060 eggNOG:NOG122520 HOGENOM:HBG317258 InParanoid:Q9FMJ1 OMA:ANRSTEC PhylomeDB:Q9FMJ1 ProtClustDB:CLSN2686235 Genevestigator:Q9FMJ1 Uniprot:Q9FMJ1
Root	Isotig00956	5	23	-2.331	0.000182103	TAIR|locus:2164391 - symbol:NAC103 "AT5G64060" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0007275 "multicellular organismal development" evidence=ISS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] InterPro:IPR003441 Pfam:PF02365 PROSITE:PS51005 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0006355 GO:GO:0003677 HSSP:Q9C932 SUPFAM:SSF101941 EMBL:AB008266 IPI:IPI00520409 RefSeq:NP_201211.1 UniGene:At.50553 ProteinModelPortal:Q9FMJ1 SMR:Q9FMJ1 DNASU:836527 EnsemblPlants:AT5G64060.1 GeneID:836527 KEGG:ath:AT5G64060 TAIR:At5g64060 eggNOG:NOG122520 HOGENOM:HBG317258 InParanoid:Q9FMJ1 OMA:ANRSTEC PhylomeDB:Q9FMJ1 ProtClustDB:CLSN2686235 Genevestigator:Q9FMJ1 Uniprot:Q9FMJ1

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig00967	40	2	4.193	7.78E-10	SGD|S000028422 - symbol:TAR1 "Mitochondrial protein potentially involved in respiratory metabolism" species:4932 "Saccharomyces cerevisiae" [GO:0003674 "molecular_function" evidence=ND] [GO:0043457 "regulation of cellular respiration" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IEA;IMP] SGD:S000028422 GO:GO:0005739 EMBL:BK006945 EMBL:U53879 GO:GO:0043457 EMBL:Z73326 EMBL:AF479964 RefSeq:NP_690845.1 ProteinModelPortal:Q8TGM6 STRING:Q8TGM6 EnsemblFungi:YLR154W-C GeneID:1466405 KEGG:sce:YLR154W-C CYGD:YLR154w-c eggNOG:NOG79861 OMA:SCSKEHR OrthoDB:EOG466ZX8 NextBio:967146 Genevestigator:Q8TGM6 GermOnline:YLR154W-C Uniprot:Q8TGM6
Root	Isotig00968	40	2	4.193	7.78E-10	SGD|S000028422 - symbol:TAR1 "Mitochondrial protein potentially involved in respiratory metabolism" species:4932 "Saccharomyces cerevisiae" [GO:0003674 "molecular_function" evidence=ND] [GO:0043457 "regulation of cellular respiration" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IEA;IMP] SGD:S000028422 GO:GO:0005739 EMBL:BK006945 EMBL:U53879 GO:GO:0043457 EMBL:Z73326 EMBL:AF479964 RefSeq:NP_690845.1 ProteinModelPortal:Q8TGM6 STRING:Q8TGM6 EnsemblFungi:YLR154W-C GeneID:1466405 KEGG:sce:YLR154W-C CYGD:YLR154w-c eggNOG:NOG79861 OMA:SCSKEHR OrthoDB:EOG466ZX8 NextBio:967146 Genevestigator:Q8TGM6 GermOnline:YLR154W-C Uniprot:Q8TGM6
Root	Isotig00969	40	2	4.193	7.78E-10	SGD|S000028422 - symbol:TAR1 "Mitochondrial protein potentially involved in respiratory metabolism" species:4932 "Saccharomyces cerevisiae" [GO:0003674 "molecular_function" evidence=ND] [GO:0043457 "regulation of cellular respiration" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IEA;IMP] SGD:S000028422 GO:GO:0005739 EMBL:BK006945 EMBL:U53879 GO:GO:0043457 EMBL:Z73326 EMBL:AF479964 RefSeq:NP_690845.1 ProteinModelPortal:Q8TGM6 STRING:Q8TGM6 EnsemblFungi:YLR154W-C GeneID:1466405 KEGG:sce:YLR154W-C CYGD:YLR154w-c eggNOG:NOG79861 OMA:SCSKEHR OrthoDB:EOG466ZX8 NextBio:967146 Genevestigator:Q8TGM6 GermOnline:YLR154W-C Uniprot:Q8TGM6
Root	Isotig00970	22	0	5.330	1.93E-06	SGD|S000028422 - symbol:TAR1 "Mitochondrial protein potentially involved in respiratory metabolism" species:4932 "Saccharomyces cerevisiae" [GO:0003674 "molecular_function" evidence=ND] [GO:0043457 "regulation of cellular respiration" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IEA;IMP] SGD:S000028422 GO:GO:0005739 EMBL:BK006945 EMBL:U53879 GO:GO:0043457 EMBL:Z73326 EMBL:AF479964 RefSeq:NP_690845.1 ProteinModelPortal:Q8TGM6 STRING:Q8TGM6 EnsemblFungi:YLR154W-C GeneID:1466405 KEGG:sce:YLR154W-C CYGD:YLR154w-c eggNOG:NOG79861 OMA:SCSKEHR OrthoDB:EOG466ZX8 NextBio:967146 Genevestigator:Q8TGM6 GermOnline:YLR154W-C Uniprot:Q8TGM6
Root	Isotig00971	26	1	4.571	4.15E-07	RGD|727924 - symbol:LOC257642 "rRNA promoter binding protein" species:10116 "Rattus norvegicus" [GO:0003690 "double-stranded DNA binding" evidence=IDA] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=IDA] [GO:0008134 "transcription factor binding" evidence=IDA] [GO:0008283 "cell proliferation" evidence=IDA] [GO:0009303 "rRNA transcription" evidence=IDA] RGD:727924 GO:GO:0008134 GO:GO:0008283 GO:GO:0003700 GO:GO:0003690 GO:GO:0009303 EMBL:U77931 IPI:IPI00195015 RefSeq:NP_671477.1 GeneID:257642 KEGG:rno:257642 NextBio:624170 Genevestigator:Q99JC0 Uniprot:Q99JC0
Root	Isotig00972	26	1	4.571	4.15E-07	RGD|727924 - symbol:LOC257642 "rRNA promoter binding protein" species:10116 "Rattus norvegicus" [GO:0003690 "double-stranded DNA binding" evidence=IDA] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=IDA] [GO:0008134 "transcription factor binding" evidence=IDA] [GO:0008283 "cell proliferation" evidence=IDA] [GO:0009303 "rRNA transcription" evidence=IDA] RGD:727924 GO:GO:0008134 GO:GO:0008283 GO:GO:0003700 GO:GO:0003690 GO:GO:0009303 EMBL:U77931 IPI:IPI00195015 RefSeq:NP_671477.1 GeneID:257642 KEGG:rno:257642 NextBio:624170 Genevestigator:Q99JC0 Uniprot:Q99JC0
Root	Isotig00973	26	1	4.571	4.15E-07	RGD|727924 - symbol:LOC257642 "rRNA promoter binding protein" species:10116 "Rattus norvegicus" [GO:0003690 "double-stranded DNA binding" evidence=IDA] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=IDA] [GO:0008134 "transcription factor binding" evidence=IDA] [GO:0008283 "cell proliferation" evidence=IDA] [GO:0009303 "rRNA transcription" evidence=IDA] RGD:727924 GO:GO:0008134 GO:GO:0008283 GO:GO:0003700 GO:GO:0003690 GO:GO:0009303 EMBL:U77931 IPI:IPI00195015 RefSeq:NP_671477.1 GeneID:257642 KEGG:rno:257642 NextBio:624170 Genevestigator:Q99JC0 Uniprot:Q99JC0
Root	Isotig00974	26	1	4.571	4.15E-07	RGD|727924 - symbol:LOC257642 "rRNA promoter binding protein" species:10116 "Rattus norvegicus" [GO:0003690 "double-stranded DNA binding" evidence=IDA] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=IDA] [GO:0008134 "transcription factor binding" evidence=IDA] [GO:0008283 "cell proliferation" evidence=IDA] [GO:0009303 "rRNA transcription" evidence=IDA] RGD:727924 GO:GO:0008134 GO:GO:0008283 GO:GO:0003700 GO:GO:0003690 GO:GO:0009303 EMBL:U77931 IPI:IPI00195015 RefSeq:NP_671477.1 GeneID:257642 KEGG:rno:257642 NextBio:624170 Genevestigator:Q99JC0 Uniprot:Q99JC0

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig00975	26	1	4.571	4.15E-07	RGD|727924 - symbol:LOC257642 "rRNA promoter binding protein" species:10116 "Rattus norvegicus" [GO:0003690 "double-stranded DNA binding" evidence=IDA] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=IDA] [GO:0008134 "transcription factor binding" evidence=IDA] [GO:0008283 "cell proliferation" evidence=IDA] [GO:0009303 "rRNA transcription" evidence=IDA] RGD:727924 GO:GO:0008134 GO:GO:0008283 GO:GO:0003700 GO:GO:0003690 GO:GO:0009303 EMBL:U77931 IPI:IPI00195015 RefSeq:NP_671477.1 GeneID:257642 KEGG:rno:257642 NextBio:624170 Genevestigator:Q99JC0 Uniprot:Q99JC0
Root	Isotig00976	26	1	4.571	4.15E-07	RGD|727924 - symbol:LOC257642 "rRNA promoter binding protein" species:10116 "Rattus norvegicus" [GO:0003690 "double-stranded DNA binding" evidence=IDA] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=IDA] [GO:0008134 "transcription factor binding" evidence=IDA] [GO:0008283 "cell proliferation" evidence=IDA] [GO:0009303 "rRNA transcription" evidence=IDA] RGD:727924 GO:GO:0008134 GO:GO:0008283 GO:GO:0003700 GO:GO:0003690 GO:GO:0009303 EMBL:U77931 IPI:IPI00195015 RefSeq:NP_671477.1 GeneID:257642 KEGG:rno:257642 NextBio:624170 Genevestigator:Q99JC0 Uniprot:Q99JC0
Root	Isotig00977	27	59	-1.257	9.88E-05	TAIR|locus:2041434 - symbol:ABCB4 "AT2G47000" species:3702 "Arabidopsis thaliana" [GO:0042626 "ATPase activity, coupled to transmembrane movement of substances" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0008559 "xenobiotic-transporting ATPase activity" evidence=IDA] [GO:0009733 "response to auxin stimulus" evidence=IEP] [GO:0009735 "response to cytokinin stimulus" evidence=IEP] [GO:0009926 "auxin polar transport" evidence=TAS] [GO:0016020 "membrane" evidence=IDA] [GO:0009630 "gravitropism" evidence=IMP] [GO:0010540 "basipetal auxin transport" evidence=IMP] [GO:0010315 "auxin efflux" evidence=IMP] [GO:0048767 "root hair elongation" evidence=IMP] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR001140 InterPro:IPR003439 InterPro:IPR003593 InterPro:IPR011527 InterPro:IPR017871 Pfam:PF00005 Pfam:PF00664 PROSITE:PS00211 PROSITE:PS50893 SMART:SM00382 GO:GO:0016021 GO:GO:0005886 GO:GO:0009506 GO:GO:0005524 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009735 eggNOG:COG1132 HOGENOM:HBG758042 KO:K05658 InterPro:IPR017940 SUPFAM:SSF90123 PROSITE:PS50929 GO:GO:0008559 GO:GO:0010540 ProtClustDB:CLSN2683573 EMBL:AC004411 IPI:IPI00538726 PIR:T02187 RefSeq:NP_182223.1 UniGene:At.43921 UniGene:At.67170 ProteinModelPortal:O80725 SMR:O80725 STRING:O80725 TCDB:3.A.1.201.7 PRIDE:O80725 ProMEX:O80725 EnsemblPlants:AT2G47000.1 GeneID:819314 KEGG:ath:AT2G47000 TAIR:At2g47000 InParanoid:O80725 OMA:IMDRESK PhylomeDB:O80725 ArrayExpress:O80725 Genevestigator:O80725 GermOnline:AT2G47000 GO:GO:0010315 GO:GO:0009630 GO:GO:0048767 Uniprot:O80725
Root	Isotig00978	27	60	-1.281	6.74E-05	TAIR|locus:2097978 - symbol:ABCB21 "ATP-binding cassette B21" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=IEA] [GO:0042626 "ATPase activity, coupled to transmembrane movement of substances" evidence=ISS] [GO:0055085 "transmembrane transport" evidence=IEA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] InterPro:IPR001140 InterPro:IPR003439 InterPro:IPR003593 InterPro:IPR011527 InterPro:IPR017871 Pfam:PF00005 Pfam:PF00664 PROSITE:PS00211 PROSITE:PS50893 SMART:SM00382 GO:GO:0016021 GO:GO:0005886 GO:GO:0005524 GO:GO:0005774 EMBL:CP002686 GenomeReviews:BA000014_GR eggNOG:COG1132 HOGENOM:HBG758042 GO:GO:0042626 InterPro:IPR017940 SUPFAM:SSF90123 PROSITE:PS50929 EMBL:AL138651 IPI:IPI00546798 PIR:T48007 RefSeq:NP_191774.2 UniGene:At.34174 ProteinModelPortal:Q9M1Q9 STRING:Q9M1Q9 PRIDE:Q9M1Q9 GeneID:825388 KEGG:ath:AT3G62150 TAIR:At3g62150 InParanoid:Q9M1Q9 OMA:PFHKLFA PhylomeDB:Q9M1Q9 ProtClustDB:CLSN2683573 Genevestigator:Q9M1Q9 GermOnline:AT3G62150 Uniprot:Q9M1Q9
Root	Isotig00979	27	58	-1.232	0.000144193	TAIR|locus:2041434 - symbol:ABCB4 "AT2G47000" species:3702 "Arabidopsis thaliana" [GO:0042626 "ATPase activity, coupled to transmembrane movement of substances" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0008559 "xenobiotic-transporting ATPase activity" evidence=IDA] [GO:0009733 "response to auxin stimulus" evidence=IEP] [GO:0009735 "response to cytokinin stimulus" evidence=IEP] [GO:0009926 "auxin polar transport" evidence=TAS] [GO:0016020 "membrane" evidence=IDA] [GO:0009630 "gravitropism" evidence=IMP] [GO:0010540 "basipetal auxin transport" evidence=IMP] [GO:0010315 "auxin efflux" evidence=IMP] [GO:0048767 "root hair elongation" evidence=IMP] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR001140 InterPro:IPR003439 InterPro:IPR003593 InterPro:IPR011527 InterPro:IPR017871 Pfam:PF00005 Pfam:PF00664 PROSITE:PS00211 PROSITE:PS50893 SMART:SM00382 GO:GO:0016021 GO:GO:0005886 GO:GO:0009506 GO:GO:0005524 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009735 eggNOG:COG1132 HOGENOM:HBG758042 KO:K05658 InterPro:IPR017940

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						SUPFAM:SSF90123 PROSITE:PS50929 GO:GO:0008559 GO:GO:0010540 ProtClustDB:CLSN2683573 EMBL:AC004411 IPI:IPI00538726 PIR:T02187 RefSeq:NP_182223.1 UniGene:At.43921 UniGene:At.67170 ProteinModelPortal:O80725 SMR:O80725 STRING:O80725 TCDB:3.A.1.201.7 PRIDE:O80725 ProMEX:O80725 EnsemblPlants:AT2G47000.1 GeneID:819314 KEGG:ath:AT2G47000 TAIR:At2g47000 InParanoid:O80725 OMA:IMDRESK PhylomeDB:O80725 ArrayExpress:O80725 Genevestigator:O80725 GermOnline:AT2G47000 GO:GO:0010315 GO:GO:0009630 GO:GO:0048767 Uniprot:O80725
Root	Isotig00980	27	59	-1.257	9.88E-05	TAIR|locus:2097978 - symbol:ABCB21 "ATP-binding cassette B21" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=IEA] [GO:0042626 "ATPase activity, coupled to transmembrane movement of substances" evidence=ISS] [GO:0055085 "transmembrane transport" evidence=IEA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] InterPro:IPR001140 InterPro:IPR003439 InterPro:IPR003593 InterPro:IPR011527 InterPro:IPR017871 Pfam:PF00005 Pfam:PF00664 PROSITE:PS00211 PROSITE:PS50893 SMART:SM00382 GO:GO:0016021 GO:GO:0005886 GO:GO:0005524 GO:GO:0005774 EMBL:CP002686 GenomeReviews:BA000014_GR eggNOG:COG1132 HOGENOM:HBG758042 GO:GO:0042626 InterPro:IPR017940 SUPFAM:SSF90123 PROSITE:PS50929 EMBL:AL138651 IPI:IPI00546798 PIR:T48007 RefSeq:NP_191774.2 UniGene:At.34174 ProteinModelPortal:Q9M1Q9 STRING:Q9M1Q9 PRIDE:Q9M1Q9 GeneID:825388 KEGG:ath:AT3G62150 TAIR:At3g62150 InParanoid:Q9M1Q9 OMA:PFHKLFA PhylomeDB:Q9M1Q9 ProtClustDB:CLSN2683573 Genevestigator:Q9M1Q9 GermOnline:AT3G62150 Uniprot:Q9M1Q9
Root	Isotig00981	27	59	-1.257	9.88E-05	TAIR|locus:2097978 - symbol:ABCB21 "ATP-binding cassette B21" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=IEA] [GO:0042626 "ATPase activity, coupled to transmembrane movement of substances" evidence=ISS] [GO:0055085 "transmembrane transport" evidence=IEA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] InterPro:IPR001140 InterPro:IPR003439 InterPro:IPR003593 InterPro:IPR011527 InterPro:IPR017871 Pfam:PF00005 Pfam:PF00664 PROSITE:PS00211 PROSITE:PS50893 SMART:SM00382 GO:GO:0016021 GO:GO:0005886 GO:GO:0005524 GO:GO:0005774 EMBL:CP002686 GenomeReviews:BA000014_GR eggNOG:COG1132 HOGENOM:HBG758042 GO:GO:0042626 InterPro:IPR017940 SUPFAM:SSF90123 PROSITE:PS50929 EMBL:AL138651 IPI:IPI00546798 PIR:T48007 RefSeq:NP_191774.2 UniGene:At.34174 ProteinModelPortal:Q9M1Q9 STRING:Q9M1Q9 PRIDE:Q9M1Q9 GeneID:825388 KEGG:ath:AT3G62150 TAIR:At3g62150 InParanoid:Q9M1Q9 OMA:PFHKLFA PhylomeDB:Q9M1Q9 ProtClustDB:CLSN2683573 Genevestigator:Q9M1Q9 GermOnline:AT3G62150 Uniprot:Q9M1Q9
Root	Isotig00984	27	58	-1.232	0.000144193	TAIR|locus:2097978 - symbol:ABCB21 "ATP-binding cassette B21" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=IEA] [GO:0042626 "ATPase activity, coupled to transmembrane movement of substances" evidence=ISS] [GO:0055085 "transmembrane transport" evidence=IEA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] InterPro:IPR001140 InterPro:IPR003439 InterPro:IPR003593 InterPro:IPR011527 InterPro:IPR017871 Pfam:PF00005 Pfam:PF00664 PROSITE:PS00211 PROSITE:PS50893 SMART:SM00382 GO:GO:0016021 GO:GO:0005886 GO:GO:0005524 GO:GO:0005774 EMBL:CP002686 GenomeReviews:BA000014_GR eggNOG:COG1132 HOGENOM:HBG758042 GO:GO:0042626 InterPro:IPR017940 SUPFAM:SSF90123 PROSITE:PS50929 EMBL:AL138651 IPI:IPI00546798 PIR:T48007 RefSeq:NP_191774.2 UniGene:At.34174 ProteinModelPortal:Q9M1Q9 STRING:Q9M1Q9 PRIDE:Q9M1Q9 GeneID:825388 KEGG:ath:AT3G62150 TAIR:At3g62150 InParanoid:Q9M1Q9 OMA:PFHKLFA PhylomeDB:Q9M1Q9 ProtClustDB:CLSN2683573 Genevestigator:Q9M1Q9 GermOnline:AT3G62150 Uniprot:Q9M1Q9
Root	Isotig00996	7	24	-1.907	0.000762598	TAIR|locus:2034310 - symbol:ACC1 "AT1G36160" species:3702 "Arabidopsis thaliana" [GO:0003989 "acetyl-CoA carboxylase activity" evidence=ISS] [GO:0010072 "primary shoot apical meristem specification" evidence=IMP] [GO:0030497 "fatty acid elongation" evidence=IMP] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009793 "embryo development ending in seed dormancy" evidence=IMP] [GO:0009933 "meristem structural organization" evidence=IMP] [GO:0009735 "response to cytokinin stimulus" evidence=IMP] [GO:0048364 "root development" evidence=IMP] [GO:0048367 "shoot development" evidence=IMP] InterPro:IPR000022 InterPro:IPR005479 InterPro:IPR005481 InterPro:IPR005482 InterPro:IPR011761 InterPro:IPR011762 InterPro:IPR011763 InterPro:IPR011764 InterPro:IPR013537 InterPro:IPR013815 InterPro:IPR013816 Pfam:PF00289 Pfam:PF01039 Pfam:PF02785 Pfam:PF02786 Pfam:PF08326 PROSITE:PS00866 PROSITE:PS00867 PROSITE:PS50975 PROSITE:PS50979 PROSITE:PS50980 PROSITE:PS50989 SMART:SM00878 InterPro:IPR013817

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						InterPro:IPR016185 InterPro:IPR001882 InterPro:IPR000089 Pfam:PF00364 EMBL:CP002684 GO:GO:0005829 GO:GO:0005886 GO:GO:0005524 GO:GO:0009735 GO:GO:0046872 GO:GO:0030497 GO:GO:0048364 eggNOG:COG0511 KO:K11262 GO:GO:0003989 GO:GO:0004075 InterPro:IPR011054 InterPro:IPR011053 Gene3D:G3DSA:3.30.1490.20 Gene3D:G3DSA:3.30.470.20 Gene3D:G3DSA:3.40.50.20 SUPFAM:SSF51230 SUPFAM:SSF52440 SUPFAM:SSF51246 PROSITE:PS00188 PROSITE:PS50968 OMA:DGLREYK HSSP:Q00955 EMBL:L27074 EMBL:D34630 EMBL:AF062308 EMBL:AC006228 EMBL:AC025781 EMBL:AK229488 IPI:IPI00543409 PIR:D86483 RefSeq:NP_001185143.1 RefSeq:NP_174849.2 UniGene:At.39402 ProteinModelPortal:Q38970 SMR:Q38970 IntAct:Q38970 STRING:Q38970 PRIDE:Q38971 EnsemblPlants:AT1G36160.1 EnsemblPlants:AT1G36160.2 GeneID:840521 KEGG:ath:AT1G36160 TAIR:At1g36160 InParanoid:Q38970 PhylomeDB:Q38970 ProtClustDB:CLSN2681517 Genevestigator:Q38970 GO:GO:0010072 Uniprot:Q38970
Root	Isotig01021	204	22	3.084	3.38E-35	SGD|S000028422 - symbol:TAR1 "Mitochondrial protein potentially involved in respiratory metabolism" species:4932 "Saccharomyces cerevisiae" [GO:0003674 "molecular_function" evidence=ND] [GO:0043457 "regulation of cellular respiration" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IEA;IMP] SGD:S000028422 GO:GO:0005739 EMBL:BK006945 EMBL:U53879 GO:GO:0043457 EMBL:Z73326 EMBL:AF479964 RefSeq:NP_690845.1 ProteinModelPortal:Q8TGM6 STRING:Q8TGM6 EnsemblFungi:YLR154W-C GeneID:1466405 KEGG:sce:YLR154W-C CYGD:YLR154w-c eggNOG:NOG79861 OMA:SCSKEHR OrthoDB:EOG466ZX8 NextBio:967146 Genevestigator:Q8TGM6 GermOnline:YLR154W-C Uniprot:Q8TGM6
Root	Isotig01022	181	15	3.464	1.44E-34	SGD|S000028422 - symbol:TAR1 "Mitochondrial protein potentially involved in respiratory metabolism" species:4932 "Saccharomyces cerevisiae" [GO:0003674 "molecular_function" evidence=ND] [GO:0043457 "regulation of cellular respiration" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IEA;IMP] SGD:S000028422 GO:GO:0005739 EMBL:BK006945 EMBL:U53879 GO:GO:0043457 EMBL:Z73326 EMBL:AF479964 RefSeq:NP_690845.1 ProteinModelPortal:Q8TGM6 STRING:Q8TGM6 EnsemblFungi:YLR154W-C GeneID:1466405 KEGG:sce:YLR154W-C CYGD:YLR154w-c eggNOG:NOG79861 OMA:SCSKEHR OrthoDB:EOG466ZX8 NextBio:967146 Genevestigator:Q8TGM6 GermOnline:YLR154W-C Uniprot:Q8TGM6
Root	Isotig01023	198	21	3.108	1.90E-34	SGD|S000028422 - symbol:TAR1 "Mitochondrial protein potentially involved in respiratory metabolism" species:4932 "Saccharomyces cerevisiae" [GO:0003674 "molecular_function" evidence=ND] [GO:0043457 "regulation of cellular respiration" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IEA;IMP] SGD:S000028422 GO:GO:0005739 EMBL:BK006945 EMBL:U53879 GO:GO:0043457 EMBL:Z73326 EMBL:AF479964 RefSeq:NP_690845.1 ProteinModelPortal:Q8TGM6 STRING:Q8TGM6 EnsemblFungi:YLR154W-C GeneID:1466405 KEGG:sce:YLR154W-C CYGD:YLR154w-c eggNOG:NOG79861 OMA:SCSKEHR OrthoDB:EOG466ZX8 NextBio:967146 Genevestigator:Q8TGM6 GermOnline:YLR154W-C Uniprot:Q8TGM6
Root	Isotig01024	88	7	3.523	7.49E-18	SGD|S000028422 - symbol:TAR1 "Mitochondrial protein potentially involved in respiratory metabolism" species:4932 "Saccharomyces cerevisiae" [GO:0003674 "molecular_function" evidence=ND] [GO:0043457 "regulation of cellular respiration" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IEA;IMP] SGD:S000028422 GO:GO:0005739 EMBL:BK006945 EMBL:U53879 GO:GO:0043457 EMBL:Z73326 EMBL:AF479964 RefSeq:NP_690845.1 ProteinModelPortal:Q8TGM6 STRING:Q8TGM6 EnsemblFungi:YLR154W-C GeneID:1466405 KEGG:sce:YLR154W-C CYGD:YLR154w-c eggNOG:NOG79861 OMA:SCSKEHR OrthoDB:EOG466ZX8 NextBio:967146 Genevestigator:Q8TGM6 GermOnline:YLR154W-C Uniprot:Q8TGM6
Root	Isotig01025	200	22	3.055	2.96E-34	SGD|S000028422 - symbol:TAR1 "Mitochondrial protein potentially involved in respiratory metabolism" species:4932 "Saccharomyces cerevisiae" [GO:0003674 "molecular_function" evidence=ND] [GO:0043457 "regulation of cellular respiration" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IEA;IMP] SGD:S000028422 GO:GO:0005739 EMBL:BK006945 EMBL:U53879 GO:GO:0043457 EMBL:Z73326 EMBL:AF479964 RefSeq:NP_690845.1 ProteinModelPortal:Q8TGM6 STRING:Q8TGM6 EnsemblFungi:YLR154W-C GeneID:1466405 KEGG:sce:YLR154W-C CYGD:YLR154w-c eggNOG:NOG79861 OMA:SCSKEHR OrthoDB:EOG466ZX8 NextBio:967146 Genevestigator:Q8TGM6 GermOnline:YLR154W-C Uniprot:Q8TGM6
Root	Isotig01026	177	15	3.432	1.34E-33	SGD|S000028422 - symbol:TAR1 "Mitochondrial protein potentially involved in respiratory metabolism" species:4932 "Saccharomyces cerevisiae" [GO:0003674 "molecular_function" evidence=ND] [GO:0043457 "regulation of cellular respiration" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IEA;IMP] SGD:S000028422 GO:GO:0005739 EMBL:BK006945 EMBL:U53879 GO:GO:0043457 EMBL:Z73326 EMBL:AF479964 RefSeq:NP_690845.1 ProteinModelPortal:Q8TGM6 STRING:Q8TGM6 EnsemblFungi:YLR154W-

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						C GeneID:1466405 KEGG:sce:YLR154W-C CYGD:YLR154w-c eggNOG:NOG79861 OMA:SCSKEHR OrthoDB:EOG466ZX8 NextBio:967146 Genevestigator:Q8TGM6 GermOnline:YLR154W-C Uniprot:Q8TGM6
Root	Isotig01027	194	21	3.079	1.67E-33	SGD|S000028422 - symbol:TAR1 "Mitochondrial protein potentially involved in respiratory metabolism" species:4932 "Saccharomyces cerevisiae" [GO:0003674 "molecular_function" evidence=ND] [GO:0043457 "regulation of cellular respiration" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IEA;IMP] SGD:S000028422 GO:GO:0005739 EMBL:BK006945 EMBL:U53879 GO:GO:0043457 EMBL:Z73326 EMBL:AF479964 RefSeq:NP_690845.1 ProteinModelPortal:Q8TGM6 STRING:Q8TGM6 EnsemblFungi:YLR154W-C GeneID:1466405 KEGG:sce:YLR154W-C CYGD:YLR154w-c eggNOG:NOG79861 OMA:SCSKEHR OrthoDB:EOG466ZX8 NextBio:967146 Genevestigator:Q8TGM6 GermOnline:YLR154W-C Uniprot:Q8TGM6
Root	Isotig01028	84	7	3.456	7.08E-17	SGD|S000028422 - symbol:TAR1 "Mitochondrial protein potentially involved in respiratory metabolism" species:4932 "Saccharomyces cerevisiae" [GO:0003674 "molecular_function" evidence=ND] [GO:0043457 "regulation of cellular respiration" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IEA;IMP] SGD:S000028422 GO:GO:0005739 EMBL:BK006945 EMBL:U53879 GO:GO:0043457 EMBL:Z73326 EMBL:AF479964 RefSeq:NP_690845.1 ProteinModelPortal:Q8TGM6 STRING:Q8TGM6 EnsemblFungi:YLR154W-C GeneID:1466405 KEGG:sce:YLR154W-C CYGD:YLR154w-c eggNOG:NOG79861 OMA:SCSKEHR OrthoDB:EOG466ZX8 NextBio:967146 Genevestigator:Q8TGM6 GermOnline:YLR154W-C Uniprot:Q8TGM6
Root	Isotig01041	19	50	-1.525	3.30E-05	TAIR|locus:2205235 - symbol:LOS1 "AT1G56070" species:3702 "Arabidopsis thaliana" [GO:0003746 "translation elongation factor activity" evidence=ISS] [GO:0008135 "translation factor activity, nucleic acid binding" evidence=ISS] [GO:0009409 "response to cold" evidence=IMP] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR000640 InterPro:IPR000795 InterPro:IPR004161 InterPro:IPR005225 InterPro:IPR005517 Pfam:PF00009 Pfam:PF00679 Pfam:PF03144 Pfam:PF03764 PRINTS:PR00315 PROSITE:PS00301 SMART:SM00838 SMART:SM00889 GO:GO:0005525 TIGRFAMs:TIGR00231 EMBL:CP002684 GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 GO:GO:0005774 GO:GO:0009507 GO:GO:0005730 GO:GO:0003924 GO:GO:0005507 GO:GO:0009409 GO:GO:0003746 InterPro:IPR020568 InterPro:IPR014721 Gene3D:G3DSA:3.30.230.10 SUPFAM:SSF54211 InterPro:IPR009000 SUPFAM:SSF50447 InterPro:IPR009022 Gene3D:G3DSA:3.30.70.240 SUPFAM:SSF54980 KO:K03234 OMA:GVMTQTE HSSP:P32324 EMBL:AF367331 EMBL:AY054461 EMBL:BT000661 EMBL:BT000722 EMBL:BT002714 IPI:IPI00517335 RefSeq:NP_849818.1 UniGene:At.47544 ProteinModelPortal:Q9ASR1 SMR:Q9ASR1 STRING:Q9ASR1 PRIDE:Q9ASR1 ProMEX:Q9ASR1 EnsemblPlants:AT1G56070.1 GeneID:842058 KEGG:ath:AT1G56070 TAIR:At1g56070 InParanoid:Q9ASR1 PhylomeDB:Q9ASR1 ProtClustDB:PLN00116 Genevestigator:Q9ASR1 Uniprot:Q9ASR1
Root	Isotig01100	9	53	-2.687	7.37E-10	TAIR|locus:2025327 - symbol:TLP1 "AT1G76900" species:3702 "Arabidopsis thaliana" [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0008081 "phosphoric diester hydrolase activity" evidence=ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=TAS] InterPro:IPR001810 Pfam:PF00646 PROSITE:PS50181 INTERPRO:IPR000007 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0006355 EMBL:AC002291 EMBL:AC079283 SUPFAM:SSF54518 HSSP:O00294 eggNOG:NOG286778 HOGENOM:HBG607533 InterPro:IPR018066 Gene3D:G3DSA:3.20.90.10 Pfam:PF01167 PRINTS:PR01573 PROSITE:PS01200 PROSITE:PS01201 EMBL:AF487267 EMBL:AY139758 EMBL:BT003039 IPI:IPI00531897 PIR:H96797 RefSeq:NP_177816.1 RefSeq:NP_849894.1 UniGene:At.17482 ProteinModelPortal:Q9ZP59 SMR:Q9ZP59 IntAct:Q9ZP59 PRIDE:Q9ZP59 EnsemblPlants:AT1G76900.1 EnsemblPlants:AT1G76900.2 GeneID:844025 KEGG:ath:AT1G76900 TAIR:At1g76900 InParanoid:Q9ZP59 OMA:QDSHEEQ PhylomeDB:Q9ZP59 ProtClustDB:CLSN2682949 Genevestigator:Q9ZP59 Uniprot:Q9ZP59
Root	Isotig01101	9	52	-2.659	1.31E-09	TAIR|locus:2025327 - symbol:TLP1 "AT1G76900" species:3702 "Arabidopsis thaliana" [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0008081 "phosphoric diester hydrolase activity" evidence=ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=TAS] InterPro:IPR001810 Pfam:PF00646 PROSITE:PS50181 INTERPRO:IPR000007 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0006355 EMBL:AC002291 EMBL:AC079283 SUPFAM:SSF54518 HSSP:O00294 eggNOG:NOG286778 HOGENOM:HBG607533 InterPro:IPR018066 Gene3D:G3DSA:3.20.90.10 Pfam:PF01167 PRINTS:PR01573 PROSITE:PS01200 PROSITE:PS01201 EMBL:AF487267 EMBL:AY139758 EMBL:BT003039 IPI:IPI00531897

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						PIR:H96797 RefSeq:NP_177816.1 RefSeq:NP_849894.1 UniGene:At.17482 ProteinModelPortal:Q9ZP59 SMR:Q9ZP59 IntAct:Q9ZP59 PRIDE:Q9ZP59 EnsemblPlants:AT1G76900.1 EnsemblPlants:AT1G76900.2 GeneID:844025 KEGG:ath:AT1G76900 TAIR:At1g76900 InParanoid:Q9ZP59 OMA:QDSHEEQ PhylomeDB:Q9ZP59 ProtClustDB:CLSN2682949 Genevestigator:Q9ZP59 Uniprot:Q9ZP59
Root	Isotig01102	9	53	-2.687	7.37E-10	TAIR|locus:2025327 - symbol:TLP1 "AT1G76900" species:3702 "Arabidopsis thaliana" [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0008081 "phosphoric diester hydrolase activity" evidence=ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=TAS] InterPro:IPR001810 Pfam:PF00646 PROSITE:PS50181 INTERPRO:IPR000007 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0006355 EMBL:AC002291 EMBL:AC079283 SUPFAM:SSF54518 HSSP:O00294 eggNOG:NOG286778 HOGENOM:HBG607533 InterPro:IPR018066 Gene3D:G3DSA:3.20.90.10 Pfam:PF01167 PRINTS:PR01573 PROSITE:PS01200 PROSITE:PS01201 EMBL:AF487267 EMBL:AY139758 EMBL:BT003039 IPI:IPI00531897 PIR:H96797 RefSeq:NP_177816.1 RefSeq:NP_849894.1 UniGene:At.17482 ProteinModelPortal:Q9ZP59 SMR:Q9ZP59 IntAct:Q9ZP59 PRIDE:Q9ZP59 EnsemblPlants:AT1G76900.1 EnsemblPlants:AT1G76900.2 GeneID:844025 KEGG:ath:AT1G76900 TAIR:At1g76900 InParanoid:Q9ZP59 OMA:QDSHEEQ PhylomeDB:Q9ZP59 ProtClustDB:CLSN2682949 Genevestigator:Q9ZP59 Uniprot:Q9ZP59
Root	Isotig01103	9	52	-2.659	1.31E-09	TAIR|locus:2025327 - symbol:TLP1 "AT1G76900" species:3702 "Arabidopsis thaliana" [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0008081 "phosphoric diester hydrolase activity" evidence=ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=TAS] InterPro:IPR001810 Pfam:PF00646 PROSITE:PS50181 INTERPRO:IPR000007 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0006355 EMBL:AC002291 EMBL:AC079283 SUPFAM:SSF54518 HSSP:O00294 eggNOG:NOG286778 HOGENOM:HBG607533 InterPro:IPR018066 Gene3D:G3DSA:3.20.90.10 Pfam:PF01167 PRINTS:PR01573 PROSITE:PS01200 PROSITE:PS01201 EMBL:AF487267 EMBL:AY139758 EMBL:BT003039 IPI:IPI00531897 PIR:H96797 RefSeq:NP_177816.1 RefSeq:NP_849894.1 UniGene:At.17482 ProteinModelPortal:Q9ZP59 SMR:Q9ZP59 IntAct:Q9ZP59 PRIDE:Q9ZP59 EnsemblPlants:AT1G76900.1 EnsemblPlants:AT1G76900.2 GeneID:844025 KEGG:ath:AT1G76900 TAIR:At1g76900 InParanoid:Q9ZP59 OMA:QDSHEEQ PhylomeDB:Q9ZP59 ProtClustDB:CLSN2682949 Genevestigator:Q9ZP59 Uniprot:Q9ZP59
Root	Isotig01104	9	52	-2.659	1.31E-09	TAIR|locus:2025327 - symbol:TLP1 "AT1G76900" species:3702 "Arabidopsis thaliana" [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0008081 "phosphoric diester hydrolase activity" evidence=ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=TAS] InterPro:IPR001810 Pfam:PF00646 PROSITE:PS50181 INTERPRO:IPR000007 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0006355 EMBL:AC002291 EMBL:AC079283 SUPFAM:SSF54518 HSSP:O00294 eggNOG:NOG286778 HOGENOM:HBG607533 InterPro:IPR018066 Gene3D:G3DSA:3.20.90.10 Pfam:PF01167 PRINTS:PR01573 PROSITE:PS01200 PROSITE:PS01201 EMBL:AF487267 EMBL:AY139758 EMBL:BT003039 IPI:IPI00531897 PIR:H96797 RefSeq:NP_177816.1 RefSeq:NP_849894.1 UniGene:At.17482 ProteinModelPortal:Q9ZP59 SMR:Q9ZP59 IntAct:Q9ZP59 PRIDE:Q9ZP59 EnsemblPlants:AT1G76900.1 EnsemblPlants:AT1G76900.2 GeneID:844025 KEGG:ath:AT1G76900 TAIR:At1g76900 InParanoid:Q9ZP59 OMA:QDSHEEQ PhylomeDB:Q9ZP59 ProtClustDB:CLSN2682949 Genevestigator:Q9ZP59 Uniprot:Q9ZP59
Root	Isotig01105	9	52	-2.659	1.31E-09	TAIR|locus:2025327 - symbol:TLP1 "AT1G76900" species:3702 "Arabidopsis thaliana" [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0008081 "phosphoric diester hydrolase activity" evidence=ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=TAS] InterPro:IPR001810 Pfam:PF00646 PROSITE:PS50181 INTERPRO:IPR000007 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0006355 EMBL:AC002291 EMBL:AC079283 SUPFAM:SSF54518 HSSP:O00294 eggNOG:NOG286778 HOGENOM:HBG607533 InterPro:IPR018066 Gene3D:G3DSA:3.20.90.10 Pfam:PF01167 PRINTS:PR01573 PROSITE:PS01200 PROSITE:PS01201 EMBL:AF487267 EMBL:AY139758 EMBL:BT003039 IPI:IPI00531897 PIR:H96797 RefSeq:NP_177816.1 RefSeq:NP_849894.1 UniGene:At.17482 ProteinModelPortal:Q9ZP59 SMR:Q9ZP59 IntAct:Q9ZP59 PRIDE:Q9ZP59 EnsemblPlants:AT1G76900.1 EnsemblPlants:AT1G76900.2 GeneID:844025 KEGG:ath:AT1G76900 TAIR:At1g76900 InParanoid:Q9ZP59 OMA:QDSHEEQ PhylomeDB:Q9ZP59 ProtClustDB:CLSN2682949 Genevestigator:Q9ZP59 Uniprot:Q9ZP59
Root	Isotig01106	9	52	-2.659	1.31E-09	TAIR|locus:2032950 - symbol:TLP10 "AT1G25280" species:3702 "Arabidopsis thaliana" [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0008081 "phosphoric diester hydrolase activity" evidence=ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=TAS] [GO:0005886 "plasma membrane" evidence=IDA] InterPro:IPR001810 Pfam:PF00646 PROSITE:PS50181 INTERPRO:IPR000007

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005886 GO:GO:0005634 GO:GO:0006355 EMBL:AC079374 SUPFAM:SSF54518 EMBL:AF487271 EMBL:AY140459 EMBL:AY140460 EMBL:AY140461 EMBL:AY140462 EMBL:AY140463 EMBL:AY140464 EMBL:AY140465 EMBL:AY140466 EMBL:AY140467 EMBL:AY140468 EMBL:AY140469 EMBL:AK317199 EMBL:BT001997 EMBL:BT006290 IPI:IPI00539910 PIR:E86382 RefSeq:NP_001117353.1 RefSeq:NP_173899.1 RefSeq:NP_973909.1 UniGene:At.23717 HSSP:O00294 ProteinModelPortal:Q9FRH7 SMR:Q9FRH7 IntAct:Q9FRH7 STRING:Q9FRH7 PRIDE:Q9FRH7 EnsemblPlants:AT1G25280.1 GeneID:839112 KEGG:ath:AT1G25280 TAIR:At1g25280 eggNOG:NOG286778 HOGENOM:HBG607533 InParanoid:Q9FRH7 OMA:HSSACEL PhylomeDB:Q9FRH7 ProtClustDB:CLSN2681282 ArrayExpress:Q8H0W5 Genevestigator:Q9FRH7 InterPro:IPR018066 Gene3D:G3DSA:3.20.90.10 Pfam:PF01167 PRINTS:PR01573 PROSITE:PS01200 PROSITE:PS01201 Uniprot:Q9FRH7
Root	Isotig01107	9	51	-2.631	2.33E-09	TAIR|locus:2032950 - symbol:TLP10 "AT1G25280" species:3702 "Arabidopsis thaliana" [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0008081 "phosphoric diester hydrolase activity" evidence=ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=TAS] [GO:0005886 "plasma membrane" evidence=IDA] InterPro:IPR001810 Pfam:PF00646 PROSITE:PS50181 INTERPRO:IPR000007 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005886 GO:GO:0005634 GO:GO:0006355 EMBL:AC079374 SUPFAM:SSF54518 EMBL:AF487271 EMBL:AY140459 EMBL:AY140460 EMBL:AY140461 EMBL:AY140462 EMBL:AY140463 EMBL:AY140464 EMBL:AY140465 EMBL:AY140466 EMBL:AY140467 EMBL:AY140468 EMBL:AY140469 EMBL:AK317199 EMBL:BT001997 EMBL:BT006290 IPI:IPI00539910 PIR:E86382 RefSeq:NP_001117353.1 RefSeq:NP_173899.1 RefSeq:NP_973909.1 UniGene:At.23717 HSSP:O00294 ProteinModelPortal:Q9FRH7 SMR:Q9FRH7 IntAct:Q9FRH7 STRING:Q9FRH7 PRIDE:Q9FRH7 EnsemblPlants:AT1G25280.1 GeneID:839112 KEGG:ath:AT1G25280 TAIR:At1g25280 eggNOG:NOG286778 HOGENOM:HBG607533 InParanoid:Q9FRH7 OMA:HSSACEL PhylomeDB:Q9FRH7 ProtClustDB:CLSN2681282 ArrayExpress:Q8H0W5 Genevestigator:Q9FRH7 InterPro:IPR018066 Gene3D:G3DSA:3.20.90.10 Pfam:PF01167 PRINTS:PR01573 PROSITE:PS01200 PROSITE:PS01201 Uniprot:Q9FRH7
Root	Isotig01108	9	52	-2.659	1.31E-09	TAIR|locus:2032950 - symbol:TLP10 "AT1G25280" species:3702 "Arabidopsis thaliana" [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0008081 "phosphoric diester hydrolase activity" evidence=ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=TAS] [GO:0005886 "plasma membrane" evidence=IDA] InterPro:IPR001810 Pfam:PF00646 PROSITE:PS50181 INTERPRO:IPR000007 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005886 GO:GO:0005634 GO:GO:0006355 EMBL:AC079374 SUPFAM:SSF54518 EMBL:AF487271 EMBL:AY140459 EMBL:AY140460 EMBL:AY140461 EMBL:AY140462 EMBL:AY140463 EMBL:AY140464 EMBL:AY140465 EMBL:AY140466 EMBL:AY140467 EMBL:AY140468 EMBL:AY140469 EMBL:AK317199 EMBL:BT001997 EMBL:BT006290 IPI:IPI00539910 PIR:E86382 RefSeq:NP_001117353.1 RefSeq:NP_173899.1 RefSeq:NP_973909.1 UniGene:At.23717 HSSP:O00294 ProteinModelPortal:Q9FRH7 SMR:Q9FRH7 IntAct:Q9FRH7 STRING:Q9FRH7 PRIDE:Q9FRH7 EnsemblPlants:AT1G25280.1 GeneID:839112 KEGG:ath:AT1G25280 TAIR:At1g25280 eggNOG:NOG286778 HOGENOM:HBG607533 InParanoid:Q9FRH7 OMA:HSSACEL PhylomeDB:Q9FRH7 ProtClustDB:CLSN2681282 ArrayExpress:Q8H0W5 Genevestigator:Q9FRH7 InterPro:IPR018066 Gene3D:G3DSA:3.20.90.10 Pfam:PF01167 PRINTS:PR01573 PROSITE:PS01200 PROSITE:PS01201 Uniprot:Q9FRH7
Root	Isotig01109	9	51	-2.631	2.33E-09	TAIR|locus:2032950 - symbol:TLP10 "AT1G25280" species:3702 "Arabidopsis thaliana" [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0008081 "phosphoric diester hydrolase activity" evidence=ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=TAS] [GO:0005886 "plasma membrane" evidence=IDA] InterPro:IPR001810 Pfam:PF00646 PROSITE:PS50181 INTERPRO:IPR000007 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005886 GO:GO:0005634 GO:GO:0006355 EMBL:AC079374 SUPFAM:SSF54518 EMBL:AF487271 EMBL:AY140459 EMBL:AY140460 EMBL:AY140461 EMBL:AY140462 EMBL:AY140463 EMBL:AY140464 EMBL:AY140465 EMBL:AY140466 EMBL:AY140467 EMBL:AY140468 EMBL:AY140469 EMBL:AK317199 EMBL:BT001997 EMBL:BT006290 IPI:IPI00539910 PIR:E86382 RefSeq:NP_001117353.1 RefSeq:NP_173899.1 RefSeq:NP_973909.1 UniGene:At.23717 HSSP:O00294 ProteinModelPortal:Q9FRH7 SMR:Q9FRH7 IntAct:Q9FRH7 STRING:Q9FRH7 PRIDE:Q9FRH7 EnsemblPlants:AT1G25280.1 GeneID:839112 KEGG:ath:AT1G25280 TAIR:At1g25280 eggNOG:NOG286778 HOGENOM:HBG607533 InParanoid:Q9FRH7 OMA:HSSACEL PhylomeDB:Q9FRH7 ProtClustDB:CLSN2681282 ArrayExpress:Q8H0W5 Genevestigator:Q9FRH7 InterPro:IPR018066 Gene3D:G3DSA:3.20.90.10 Pfam:PF01167 PRINTS:PR01573 PROSITE:PS01200 PROSITE:PS01201 Uniprot:Q9FRH7

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig01110	9	51	-2.631	2.33E-09	TAIR|locus:2032950 - symbol:TLP10 "AT1G25280" species:3702 "Arabidopsis thaliana" [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0008081 "phosphoric diester hydrolase activity" evidence=ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=TAS] [GO:0005886 "plasma membrane" evidence=IDA] InterPro:IPR001810 Pfam:PF00646 PROSITE:PS50181 INTERPRO:IPR000007 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005886 GO:GO:0005634 GO:GO:0006355 EMBL:AC079374 SUPFAM:SSF54518 EMBL:AF487271 EMBL:AY140459 EMBL:AY140460 EMBL:AY140461 EMBL:AY140462 EMBL:AY140463 EMBL:AY140464 EMBL:AY140465 EMBL:AY140466 EMBL:AY140467 EMBL:AY140468 EMBL:AY140469 EMBL:AK317199 EMBL:BT001997 EMBL:BT006290 IPI:IPI00539910 PIR:E86382 RefSeq:NP_001117353.1 RefSeq:NP_173899.1 RefSeq:NP_973909.1 UniGene:At.23717 HSSP:O00294 ProteinModelPortal:Q9FRH7 SMR:Q9FRH7 IntAct:Q9FRH7 STRING:Q9FRH7 PRIDE:Q9FRH7 EnsemblPlants:AT1G25280.1 GeneID:839112 KEGG:ath:AT1G25280 TAIR:At1g25280 eggNOG:NOG286778 HOGENOM:HBG607533 InParanoid:Q9FRH7 OMA:HSSACEL PhylomeDB:Q9FRH7 ProtClustDB:CLSN2681282 ArrayExpress:Q8H0W5 Genevestigator:Q9FRH7 InterPro:IPR018066 Gene3D:G3DSA:3.20.90.10 Pfam:PF01167 PRINTS:PR01573 PROSITE:PS01200 PROSITE:PS01201 Uniprot:Q9FRH7
Root	Isotig01111	9	51	-2.631	2.33E-09	TAIR|locus:2032950 - symbol:TLP10 "AT1G25280" species:3702 "Arabidopsis thaliana" [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0008081 "phosphoric diester hydrolase activity" evidence=ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=TAS] [GO:0005886 "plasma membrane" evidence=IDA] InterPro:IPR001810 Pfam:PF00646 PROSITE:PS50181 INTERPRO:IPR000007 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005886 GO:GO:0005634 GO:GO:0006355 EMBL:AC079374 SUPFAM:SSF54518 EMBL:AF487271 EMBL:AY140459 EMBL:AY140460 EMBL:AY140461 EMBL:AY140462 EMBL:AY140463 EMBL:AY140464 EMBL:AY140465 EMBL:AY140466 EMBL:AY140467 EMBL:AY140468 EMBL:AY140469 EMBL:AK317199 EMBL:BT001997 EMBL:BT006290 IPI:IPI00539910 PIR:E86382 RefSeq:NP_001117353.1 RefSeq:NP_173899.1 RefSeq:NP_973909.1 UniGene:At.23717 HSSP:O00294 ProteinModelPortal:Q9FRH7 SMR:Q9FRH7 IntAct:Q9FRH7 STRING:Q9FRH7 PRIDE:Q9FRH7 EnsemblPlants:AT1G25280.1 GeneID:839112 KEGG:ath:AT1G25280 TAIR:At1g25280 eggNOG:NOG286778 HOGENOM:HBG607533 InParanoid:Q9FRH7 OMA:HSSACEL PhylomeDB:Q9FRH7 ProtClustDB:CLSN2681282 ArrayExpress:Q8H0W5 Genevestigator:Q9FRH7 InterPro:IPR018066 Gene3D:G3DSA:3.20.90.10 Pfam:PF01167 PRINTS:PR01573 PROSITE:PS01200 PROSITE:PS01201 Uniprot:Q9FRH7
Root	Isotig01112	6	25	-2.188	0.000173532	No hit
Root	Isotig01114	5	21	-2.199	0.000555521	No hit
Root	Isotig01116	5	21	-2.199	0.000555521	No hit
Root	Isotig01118	5	22	-2.266	0.000318925	No hit
Root	Isotig01140	77	10	2.816	3.49E-13	TAIR|locus:2202175 - symbol:DA1 "AT1G19270" species:3702 "Arabidopsis thaliana" [GO:0043130 "ubiquitin binding" evidence=IDA;IPI] [GO:0046621 "negative regulation of organ growth" evidence=IMP] [GO:0048317 "seed morphogenesis" evidence=IMP] [GO:0048482 "ovule morphogenesis" evidence=IMP] Pfam:PF00412 InterPro:IPR001781 PROSITE:PS00142 PROSITE:PS00478 PROSITE:PS50023 SMART:SM00132 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0008270 Gene3D:G3DSA:2.10.110.10 InterPro:IPR003903 SMART:SM00726 PROSITE:PS50330 EMBL:AC069143 GO:GO:0043130 GO:GO:0046621 EMBL:BX816571 IPI:IPI00540867 PIR:D86326 RefSeq:NP_173361.1 UniGene:At.21826 ProteinModelPortal:P0C7Q8 SMR:P0C7Q8 STRING:P0C7Q8 PRIDE:P0C7Q8 EnsemblPlants:AT1G19270.1 GeneID:838510 KEGG:ath:AT1G19270 TAIR:At1g19270 eggNOG:NOG312886 HOGENOM:HBG318792 OMA:YHPKCDV PhylomeDB:P0C7Q8 ProtClustDB:CLSN2914207 Genevestigator:P0C7Q8 GO:GO:0048482 GO:GO:0048317 InterPro:IPR022087 Pfam:PF12315 Uniprot:P0C7Q8
Root	Isotig01141	71	7	3.213	1.00E-13	No hit
Root	Isotig01142	70	7	3.193	1.75E-13	No hit
Root	Isotig01144	48	4	3.456	2.82E-10	TAIR|locus:2056799 - symbol:PI4K GAMMA 7 "AT2G03890" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0004430 "1-phosphatidylinositol 4-kinase activity" evidence=IDA] [GO:0046854 "phosphatidylinositol phosphorylation" evidence=IDA] InterPro:IPR000403 Pfam:PF00454 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0004430 HOGENOM:HBG603679 EMBL:AC007196 ProtClustDB:CLSN2687794 EMBL:AY056101 EMBL:BT002696 IPI:IPI00523971 PIR:D84453 RefSeq:NP_565307.1 UniGene:At.24594 ProteinModelPortal:Q9SI52 STRING:Q9SI52 PRIDE:Q9SI52 EnsemblPlants:AT2G03890.1

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GeneID:814915 KEGG:ath:AT2G03890 TAIR:At2g03890 InParanoid:Q9SI52 OMA:MAVAVFK PhylomeDB:Q9SI52 ArrayExpress:Q9SI52 Genevestigator:Q9SI52 Uniprot:Q9SI52
Root	Isotig01145	48	4	3.456	2.82E-10	TAIR|locus:2056799 - symbol:PI4K GAMMA 7 "AT2G03890" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0004430 "1-phosphatidylinositol 4-kinase activity" evidence=IDA] [GO:0046854 "phosphatidylinositol phosphorylation" evidence=IDA] InterPro:IPR000403 Pfam:PF00454 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0004430 HOGENOM:HBG603679 EMBL:AC007196 ProtClustDB:CLSN2687794 EMBL:AY056101 EMBL:BT002696 IPI:IPI00523971 PIR:D84453 RefSeq:NP_565307.1 UniGene:At.24594 ProteinModelPortal:Q9SI52 STRING:Q9SI52 PRIDE:Q9SI52 EnsemblPlants:AT2G03890.1 GeneID:814915 KEGG:ath:AT2G03890 TAIR:At2g03890 InParanoid:Q9SI52 OMA:MAVAVFK PhylomeDB:Q9SI52 ArrayExpress:Q9SI52 Genevestigator:Q9SI52 Uniprot:Q9SI52
Root	Isotig01146	59	13	2.053	1.17E-07	TAIR|locus:2056799 - symbol:PI4K GAMMA 7 "AT2G03890" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0004430 "1-phosphatidylinositol 4-kinase activity" evidence=IDA] [GO:0046854 "phosphatidylinositol phosphorylation" evidence=IDA] InterPro:IPR000403 Pfam:PF00454 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0004430 HOGENOM:HBG603679 EMBL:AC007196 ProtClustDB:CLSN2687794 EMBL:AY056101 EMBL:BT002696 IPI:IPI00523971 PIR:D84453 RefSeq:NP_565307.1 UniGene:At.24594 ProteinModelPortal:Q9SI52 STRING:Q9SI52 PRIDE:Q9SI52 EnsemblPlants:AT2G03890.1 GeneID:814915 KEGG:ath:AT2G03890 TAIR:At2g03890 InParanoid:Q9SI52 OMA:MAVAVFK PhylomeDB:Q9SI52 ArrayExpress:Q9SI52 Genevestigator:Q9SI52 Uniprot:Q9SI52
Root	Isotig01147	54	13	1.925	1.17E-06	TAIR|locus:2056799 - symbol:PI4K GAMMA 7 "AT2G03890" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0004430 "1-phosphatidylinositol 4-kinase activity" evidence=IDA] [GO:0046854 "phosphatidylinositol phosphorylation" evidence=IDA] InterPro:IPR000403 Pfam:PF00454 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0004430 HOGENOM:HBG603679 EMBL:AC007196 ProtClustDB:CLSN2687794 EMBL:AY056101 EMBL:BT002696 IPI:IPI00523971 PIR:D84453 RefSeq:NP_565307.1 UniGene:At.24594 ProteinModelPortal:Q9SI52 STRING:Q9SI52 PRIDE:Q9SI52 EnsemblPlants:AT2G03890.1 GeneID:814915 KEGG:ath:AT2G03890 TAIR:At2g03890 InParanoid:Q9SI52 OMA:MAVAVFK PhylomeDB:Q9SI52 ArrayExpress:Q9SI52 Genevestigator:Q9SI52 Uniprot:Q9SI52
Root	Isotig01148	59	13	2.053	1.17E-07	TAIR|locus:2056799 - symbol:PI4K GAMMA 7 "AT2G03890" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0004430 "1-phosphatidylinositol 4-kinase activity" evidence=IDA] [GO:0046854 "phosphatidylinositol phosphorylation" evidence=IDA] InterPro:IPR000403 Pfam:PF00454 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0004430 HOGENOM:HBG603679 EMBL:AC007196 ProtClustDB:CLSN2687794 EMBL:AY056101 EMBL:BT002696 IPI:IPI00523971 PIR:D84453 RefSeq:NP_565307.1 UniGene:At.24594 ProteinModelPortal:Q9SI52 STRING:Q9SI52 PRIDE:Q9SI52 EnsemblPlants:AT2G03890.1 GeneID:814915 KEGG:ath:AT2G03890 TAIR:At2g03890 InParanoid:Q9SI52 OMA:MAVAVFK PhylomeDB:Q9SI52 ArrayExpress:Q9SI52 Genevestigator:Q9SI52 Uniprot:Q9SI52
Root	Isotig01149	54	13	1.925	1.17E-06	TAIR|locus:2056799 - symbol:PI4K GAMMA 7 "AT2G03890" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0004430 "1-phosphatidylinositol 4-kinase activity" evidence=IDA] [GO:0046854 "phosphatidylinositol phosphorylation" evidence=IDA] InterPro:IPR000403 Pfam:PF00454 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0004430 HOGENOM:HBG603679 EMBL:AC007196 ProtClustDB:CLSN2687794 EMBL:AY056101 EMBL:BT002696 IPI:IPI00523971 PIR:D84453 RefSeq:NP_565307.1 UniGene:At.24594 ProteinModelPortal:Q9SI52 STRING:Q9SI52 PRIDE:Q9SI52 EnsemblPlants:AT2G03890.1 GeneID:814915 KEGG:ath:AT2G03890 TAIR:At2g03890 InParanoid:Q9SI52 OMA:MAVAVFK PhylomeDB:Q9SI52 ArrayExpress:Q9SI52 Genevestigator:Q9SI52 Uniprot:Q9SI52
Root	Isotig01150	59	13	2.053	1.17E-07	TAIR|locus:2056799 - symbol:PI4K GAMMA 7 "AT2G03890" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0004430 "1-phosphatidylinositol 4-kinase activity" evidence=IDA] [GO:0046854 "phosphatidylinositol phosphorylation" evidence=IDA] InterPro:IPR000403 Pfam:PF00454 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0004430 HOGENOM:HBG603679 EMBL:AC007196 ProtClustDB:CLSN2687794 EMBL:AY056101 EMBL:BT002696 IPI:IPI00523971 PIR:D84453 RefSeq:NP_565307.1 UniGene:At.24594 ProteinModelPortal:Q9SI52 STRING:Q9SI52 PRIDE:Q9SI52 EnsemblPlants:AT2G03890.1 GeneID:814915 KEGG:ath:AT2G03890 TAIR:At2g03890 InParanoid:Q9SI52 OMA:MAVAVFK PhylomeDB:Q9SI52 ArrayExpress:Q9SI52 Genevestigator:Q9SI52 Uniprot:Q9SI52
Root	Isotig01151	54	13	1.925	1.17E-06	TAIR|locus:2056799 - symbol:PI4K GAMMA 7 "AT2G03890" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0004430 "1-phosphatidylinositol 4-kinase activity" evidence=IDA]

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						[GO:0046854 "phosphatidylinositol phosphorylation" evidence=IDA] InterPro:IPR000403 Pfam:PF00454 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0004430 HOGENOM:HBG603679 EMBL:AC007196 ProtClustDB:CLSN2687794 EMBL:AY056101 EMBL:BT002696 IPI:IPI00523971 PIR:D84453 RefSeq:NP_565307.1 UniGene:At.24594 ProteinModelPortal:Q9SI52 STRING:Q9SI52 PRIDE:Q9SI52 EnsemblPlants:AT2G03890.1 GeneID:814915 KEGG:ath:AT2G03890 TAIR:At2g03890 InParanoid:Q9SI52 OMA:MAVAVFK PhylomeDB:Q9SI52 ArrayExpress:Q9SI52 Genevestigator:Q9SI52 Uniprot:Q9SI52
Root	Isotig01152	59	13	2.053	1.17E-07	TAIR|locus:2056799 - symbol:PI4K GAMMA 7 "AT2G03890" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0004430 "1-phosphatidylinositol 4-kinase activity" evidence=IDA] [GO:0046854 "phosphatidylinositol phosphorylation" evidence=IDA] InterPro:IPR000403 Pfam:PF00454 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0004430 HOGENOM:HBG603679 EMBL:AC007196 ProtClustDB:CLSN2687794 EMBL:AY056101 EMBL:BT002696 IPI:IPI00523971 PIR:D84453 RefSeq:NP_565307.1 UniGene:At.24594 ProteinModelPortal:Q9SI52 STRING:Q9SI52 PRIDE:Q9SI52 EnsemblPlants:AT2G03890.1 GeneID:814915 KEGG:ath:AT2G03890 TAIR:At2g03890 InParanoid:Q9SI52 OMA:MAVAVFK PhylomeDB:Q9SI52 ArrayExpress:Q9SI52 Genevestigator:Q9SI52 Uniprot:Q9SI52
Root	Isotig01153	54	13	1.925	1.17E-06	TAIR|locus:2056799 - symbol:PI4K GAMMA 7 "AT2G03890" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0004430 "1-phosphatidylinositol 4-kinase activity" evidence=IDA] [GO:0046854 "phosphatidylinositol phosphorylation" evidence=IDA] InterPro:IPR000403 Pfam:PF00454 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0004430 HOGENOM:HBG603679 EMBL:AC007196 ProtClustDB:CLSN2687794 EMBL:AY056101 EMBL:BT002696 IPI:IPI00523971 PIR:D84453 RefSeq:NP_565307.1 UniGene:At.24594 ProteinModelPortal:Q9SI52 STRING:Q9SI52 PRIDE:Q9SI52 EnsemblPlants:AT2G03890.1 GeneID:814915 KEGG:ath:AT2G03890 TAIR:At2g03890 InParanoid:Q9SI52 OMA:MAVAVFK PhylomeDB:Q9SI52 ArrayExpress:Q9SI52 Genevestigator:Q9SI52 Uniprot:Q9SI52
Root	Isotig01154	44	15	1.424	0.000402568	TAIR|locus:2043560 - symbol:PAPS2 "AT2G25850" species:3702 "Arabidopsis thaliana" [GO:0016779 "nucleotidyltransferase activity" evidence=ISS] [GO:0005515 "protein binding" evidence=IPI] [GO:0005634 "nucleus" evidence=IDA] [GO:0043631 "RNA polyadenylation" evidence=IDA] InterPro:IPR002934 InterPro:IPR007010 InterPro:IPR007012 InterPro:IPR011068 InterPro:IPR014492 Pfam:PF01909 Pfam:PF04926 Pfam:PF04928 PIRSF:PIRSF018425 GO:GO:0005634 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0005515 GO:GO:0006351 GO:GO:0003723 EMBL:AC005395 GO:GO:0004652 GO:GO:0043631 eggNOG:COG5186 KO:K14376 Gene3D:G3DSA:3.30.70.590 SUPFAM:SSF55003 HOGENOM:HBG594063 HSSP:P25500 EMBL:AF255297 EMBL:AY039974 EMBL:AY074533 IPI:IPI00518420 PIR:E84653 RefSeq:NP_565611.1 UniGene:At.14867 ProteinModelPortal:O82312 SMR:O82312 IntAct:O82312 STRING:O82312 PRIDE:O82312 EnsemblPlants:AT2G25850.2 GeneID:817127 KEGG:ath:AT2G25850 TAIR:At2g25850 InParanoid:O82312 OMA:MGSESIN PhylomeDB:O82312 ProtClustDB:CLSN2688428 BRENDA:2.7.7.19 ArrayExpress:O82312 Genevestigator:O82312 Uniprot:O82312
Root	Isotig01155	44	15	1.424	0.000402568	TAIR|locus:2043560 - symbol:PAPS2 "AT2G25850" species:3702 "Arabidopsis thaliana" [GO:0016779 "nucleotidyltransferase activity" evidence=ISS] [GO:0005515 "protein binding" evidence=IPI] [GO:0005634 "nucleus" evidence=IDA] [GO:0043631 "RNA polyadenylation" evidence=IDA] InterPro:IPR002934 InterPro:IPR007010 InterPro:IPR007012 InterPro:IPR011068 InterPro:IPR014492 Pfam:PF01909 Pfam:PF04926 Pfam:PF04928 PIRSF:PIRSF018425 GO:GO:0005634 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0005515 GO:GO:0006351 GO:GO:0003723 EMBL:AC005395 GO:GO:0004652 GO:GO:0043631 eggNOG:COG5186 KO:K14376 Gene3D:G3DSA:3.30.70.590 SUPFAM:SSF55003 HOGENOM:HBG594063 HSSP:P25500 EMBL:AF255297 EMBL:AY039974 EMBL:AY074533 IPI:IPI00518420 PIR:E84653 RefSeq:NP_565611.1 UniGene:At.14867 ProteinModelPortal:O82312 SMR:O82312 IntAct:O82312 STRING:O82312 PRIDE:O82312 EnsemblPlants:AT2G25850.2 GeneID:817127 KEGG:ath:AT2G25850 TAIR:At2g25850 InParanoid:O82312 OMA:MGSESIN PhylomeDB:O82312 ProtClustDB:CLSN2688428 BRENDA:2.7.7.19 ArrayExpress:O82312 Genevestigator:O82312 Uniprot:O82312
Root	Isotig01156	44	15	1.424	0.000402568	TAIR|locus:2043560 - symbol:PAPS2 "AT2G25850" species:3702 "Arabidopsis thaliana" [GO:0016779 "nucleotidyltransferase activity" evidence=ISS] [GO:0005515 "protein binding" evidence=IPI] [GO:0005634 "nucleus" evidence=IDA] [GO:0043631 "RNA polyadenylation" evidence=IDA] InterPro:IPR002934 InterPro:IPR007010 InterPro:IPR007012 InterPro:IPR011068 InterPro:IPR014492 Pfam:PF01909 Pfam:PF04926 Pfam:PF04928 PIRSF:PIRSF018425 GO:GO:0005634 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0005515 GO:GO:0006351 GO:GO:0003723 EMBL:AC005395 GO:GO:0004652 GO:GO:0043631 eggNOG:COG5186

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						KO:K14376 Gene3D:G3DSA:3.30.70.590 SUPFAM:SSF55003 HOGENOM:HBG594063 HSSP:P25500 EMBL:AF255297 EMBL:AY039974 EMBL:AY074533 IPI:IPI00518420 PIR:E84653 RefSeq:NP_565611.1 UniGene:At.14867 ProteinModelPortal:O82312 SMR:O82312 IntAct:O82312 STRING:O82312 PRIDE:O82312 EnsemblPlants:AT2G25850.2 GeneID:817127 KEGG:ath:AT2G25850 TAIR:At2g25850 InParanoid:O82312 OMA:MGSESIN PhylomeDB:O82312 ProtClustDB:CLSN2688428 BRENDA:2.7.7.19 ArrayExpress:O82312 Genevestigator:O82312 Uniprot:O82312
Root	Isotig01157	44	15	1.424	0.000402568	TAIR|locus:2043560 - symbol:PAPS2 "AT2G25850" species:3702 "Arabidopsis thaliana" [GO:0016779 "nucleotidyltransferase activity" evidence=ISS] [GO:0005515 "protein binding" evidence=IPI] [GO:0005634 "nucleus" evidence=IDA] [GO:0043631 "RNA polyadenylation" evidence=IDA] InterPro:IPR002934 InterPro:IPR007010 InterPro:IPR007012 InterPro:IPR011068 InterPro:IPR014492 Pfam:PF01909 Pfam:PF04926 Pfam:PF04928 PIRSF:PIRSF018425 GO:GO:0005634 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0005515 GO:GO:0006351 GO:GO:0003723 EMBL:AC005395 GO:GO:0004652 GO:GO:0043631 eggNOG:COG5186 KO:K14376 Gene3D:G3DSA:3.30.70.590 SUPFAM:SSF55003 HOGENOM:HBG594063 HSSP:P25500 EMBL:AF255297 EMBL:AY039974 EMBL:AY074533 IPI:IPI00518420 PIR:E84653 RefSeq:NP_565611.1 UniGene:At.14867 ProteinModelPortal:O82312 SMR:O82312 IntAct:O82312 STRING:O82312 PRIDE:O82312 EnsemblPlants:AT2G25850.2 GeneID:817127 KEGG:ath:AT2G25850 TAIR:At2g25850 InParanoid:O82312 OMA:MGSESIN PhylomeDB:O82312 ProtClustDB:CLSN2688428 BRENDA:2.7.7.19 ArrayExpress:O82312 Genevestigator:O82312 Uniprot:O82312
Root	Isotig01160	18	2	3.041	0.000259481	TAIR|locus:2030943 - symbol:PAPS1 "AT1G17980" species:3702 "Arabidopsis thaliana" [GO:0016779 "nucleotidyltransferase activity" evidence=ISS] [GO:0005515 "protein binding" evidence=IPI] [GO:0005634 "nucleus" evidence=IDA] [GO:0043631 "RNA polyadenylation" evidence=IDA] InterPro:IPR002934 InterPro:IPR007010 InterPro:IPR007012 InterPro:IPR011068 InterPro:IPR014492 Pfam:PF01909 Pfam:PF04926 Pfam:PF04928 PIRSF:PIRSF018425 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005634 GO:GO:0005515 GO:GO:0006351 EMBL:AC034106 GO:GO:0003723 GO:GO:0004652 GO:GO:0043631 UniGene:At.26787 UniGene:At.73166 eggNOG:COG5186 KO:K14376 Gene3D:G3DSA:3.30.70.590 SUPFAM:SSF55003 HSSP:P25500 BRENDA:2.7.7.19 EMBL:BT005990 EMBL:AY323906 EMBL:AK227446 IPI:IPI00540119 PIR:B86315 RefSeq:NP_173240.2 ProteinModelPortal:Q9LMT2 SMR:Q9LMT2 IntAct:Q9LMT2 STRING:Q9LMT2 PRIDE:Q9LMT2 EnsemblPlants:AT1G17980.1 GeneID:838378 KEGG:ath:AT1G17980 TAIR:At1g17980 InParanoid:Q9LMT2 OMA:WDTLFEP PhylomeDB:Q9LMT2 ProtClustDB:CLSN2680711 Genevestigator:Q9LMT2 Uniprot:Q9LMT2
Root	Isotig01161	18	2	3.041	0.000259481	TAIR|locus:2030943 - symbol:PAPS1 "AT1G17980" species:3702 "Arabidopsis thaliana" [GO:0016779 "nucleotidyltransferase activity" evidence=ISS] [GO:0005515 "protein binding" evidence=IPI] [GO:0005634 "nucleus" evidence=IDA] [GO:0043631 "RNA polyadenylation" evidence=IDA] InterPro:IPR002934 InterPro:IPR007010 InterPro:IPR007012 InterPro:IPR011068 InterPro:IPR014492 Pfam:PF01909 Pfam:PF04926 Pfam:PF04928 PIRSF:PIRSF018425 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005634 GO:GO:0005515 GO:GO:0006351 EMBL:AC034106 GO:GO:0003723 GO:GO:0004652 GO:GO:0043631 UniGene:At.26787 UniGene:At.73166 eggNOG:COG5186 KO:K14376 Gene3D:G3DSA:3.30.70.590 SUPFAM:SSF55003 HSSP:P25500 BRENDA:2.7.7.19 EMBL:BT005990 EMBL:AY323906 EMBL:AK227446 IPI:IPI00540119 PIR:B86315 RefSeq:NP_173240.2 ProteinModelPortal:Q9LMT2 SMR:Q9LMT2 IntAct:Q9LMT2 STRING:Q9LMT2 PRIDE:Q9LMT2 EnsemblPlants:AT1G17980.1 GeneID:838378 KEGG:ath:AT1G17980 TAIR:At1g17980 InParanoid:Q9LMT2 OMA:WDTLFEP PhylomeDB:Q9LMT2 ProtClustDB:CLSN2680711 Genevestigator:Q9LMT2 Uniprot:Q9LMT2
Root	Isotig01172	149	74	0.881	9.59E-06	TAIR|locus:2064965 - symbol:EULS3 "AT2G39050" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0030246 "carbohydrate binding" evidence=IDA] GO:GO:0005634 GO:GO:0005737 EMBL:CP002685 GenomeReviews:CT485783_GR InterPro:IPR000772 SUPFAM:SSF50370 PROSITE:PS50231 GO:GO:0030246 EMBL:AC005770 Pfam:PF14200 EMBL:AF411801 EMBL:AY093795 EMBL:AY087909 IPI:IPI00536641 PIR:E84812 RefSeq:NP_565899.1 UniGene:At.22599 ProteinModelPortal:Q945P1 SMR:Q945P1 PRIDE:Q945P1 EnsemblPlants:AT2G39050.1 GeneID:818491 KEGG:ath:AT2G39050 TAIR:At2g39050 eggNOG:NOG254161 HOGENOM:HBG750017 InParanoid:Q945P1 OMA:GYRTIRM PhylomeDB:Q945P1 ProtClustDB:CLSN2681741 ArrayExpress:Q945P1 Genevestigator:Q945P1 Uniprot:Q945P1

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig01173	150	74	0.890	7.38E-06	TAIR|locus:2064965 - symbol:EULS3 "AT2G39050" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0030246 "carbohydrate binding" evidence=IDA] GO:GO:0005634 GO:GO:0005737 EMBL:CP002685 GenomeReviews:CT485783_GR InterPro:IPR000772 SUPFAM:SSF50370 PROSITE:PS50231 GO:GO:0030246 EMBL:AC005770 Pfam:PF14200 EMBL:AF411801 EMBL:AY093795 EMBL:AY087909 IPI:IPI00536641 PIR:E84812 RefSeq:NP_565899.1 UniGene:At.22599 ProteinModelPortal:Q945P1 SMR:Q945P1 PRIDE:Q945P1 EnsemblPlants:AT2G39050.1 GeneID:818491 KEGG:ath:AT2G39050 TAIR:At2g39050 eggNOG:NOG254161 HOGENOM:HBG750017 InParanoid:Q945P1 OMA:GYRTIRM PhylomeDB:Q945P1 ProtClustDB:CLSN2681741 ArrayExpress:Q945P1 Genevestigator:Q945P1 Uniprot:Q945P1
Root	Isotig01174	145	70	0.922	5.71E-06	TAIR|locus:2064965 - symbol:EULS3 "AT2G39050" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0030246 "carbohydrate binding" evidence=IDA] GO:GO:0005634 GO:GO:0005737 EMBL:CP002685 GenomeReviews:CT485783_GR InterPro:IPR000772 SUPFAM:SSF50370 PROSITE:PS50231 GO:GO:0030246 EMBL:AC005770 Pfam:PF14200 EMBL:AF411801 EMBL:AY093795 EMBL:AY087909 IPI:IPI00536641 PIR:E84812 RefSeq:NP_565899.1 UniGene:At.22599 ProteinModelPortal:Q945P1 SMR:Q945P1 PRIDE:Q945P1 EnsemblPlants:AT2G39050.1 GeneID:818491 KEGG:ath:AT2G39050 TAIR:At2g39050 eggNOG:NOG254161 HOGENOM:HBG750017 InParanoid:Q945P1 OMA:GYRTIRM PhylomeDB:Q945P1 ProtClustDB:CLSN2681741 ArrayExpress:Q945P1 Genevestigator:Q945P1 Uniprot:Q945P1
Root	Isotig01175	149	74	0.881	9.59E-06	TAIR|locus:2064965 - symbol:EULS3 "AT2G39050" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0030246 "carbohydrate binding" evidence=IDA] GO:GO:0005634 GO:GO:0005737 EMBL:CP002685 GenomeReviews:CT485783_GR InterPro:IPR000772 SUPFAM:SSF50370 PROSITE:PS50231 GO:GO:0030246 EMBL:AC005770 Pfam:PF14200 EMBL:AF411801 EMBL:AY093795 EMBL:AY087909 IPI:IPI00536641 PIR:E84812 RefSeq:NP_565899.1 UniGene:At.22599 ProteinModelPortal:Q945P1 SMR:Q945P1 PRIDE:Q945P1 EnsemblPlants:AT2G39050.1 GeneID:818491 KEGG:ath:AT2G39050 TAIR:At2g39050 eggNOG:NOG254161 HOGENOM:HBG750017 InParanoid:Q945P1 OMA:GYRTIRM PhylomeDB:Q945P1 ProtClustDB:CLSN2681741 ArrayExpress:Q945P1 Genevestigator:Q945P1 Uniprot:Q945P1
Root	Isotig01176	146	70	0.932	4.35E-06	TAIR|locus:2064965 - symbol:EULS3 "AT2G39050" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0030246 "carbohydrate binding" evidence=IDA] GO:GO:0005634 GO:GO:0005737 EMBL:CP002685 GenomeReviews:CT485783_GR InterPro:IPR000772 SUPFAM:SSF50370 PROSITE:PS50231 GO:GO:0030246 EMBL:AC005770 Pfam:PF14200 EMBL:AF411801 EMBL:AY093795 EMBL:AY087909 IPI:IPI00536641 PIR:E84812 RefSeq:NP_565899.1 UniGene:At.22599 ProteinModelPortal:Q945P1 SMR:Q945P1 PRIDE:Q945P1 EnsemblPlants:AT2G39050.1 GeneID:818491 KEGG:ath:AT2G39050 TAIR:At2g39050 eggNOG:NOG254161 HOGENOM:HBG750017 InParanoid:Q945P1 OMA:GYRTIRM PhylomeDB:Q945P1 ProtClustDB:CLSN2681741 ArrayExpress:Q945P1 Genevestigator:Q945P1 Uniprot:Q945P1
Root	Isotig01177	145	70	0.922	5.71E-06	TAIR|locus:2064965 - symbol:EULS3 "AT2G39050" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0030246 "carbohydrate binding" evidence=IDA] GO:GO:0005634 GO:GO:0005737 EMBL:CP002685 GenomeReviews:CT485783_GR InterPro:IPR000772 SUPFAM:SSF50370 PROSITE:PS50231 GO:GO:0030246 EMBL:AC005770 Pfam:PF14200 EMBL:AF411801 EMBL:AY093795 EMBL:AY087909 IPI:IPI00536641 PIR:E84812 RefSeq:NP_565899.1 UniGene:At.22599 ProteinModelPortal:Q945P1 SMR:Q945P1 PRIDE:Q945P1 EnsemblPlants:AT2G39050.1 GeneID:818491 KEGG:ath:AT2G39050 TAIR:At2g39050 eggNOG:NOG254161 HOGENOM:HBG750017 InParanoid:Q945P1 OMA:GYRTIRM PhylomeDB:Q945P1 ProtClustDB:CLSN2681741 ArrayExpress:Q945P1 Genevestigator:Q945P1 Uniprot:Q945P1
Root	Isotig01178	137	67	0.903	1.46E-05	TAIR|locus:2064965 - symbol:EULS3 "AT2G39050" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0030246 "carbohydrate binding" evidence=IDA] GO:GO:0005634 GO:GO:0005737 EMBL:CP002685 GenomeReviews:CT485783_GR InterPro:IPR000772 SUPFAM:SSF50370 PROSITE:PS50231 GO:GO:0030246 EMBL:AC005770 Pfam:PF14200 EMBL:AF411801 EMBL:AY093795 EMBL:AY087909 IPI:IPI00536641 PIR:E84812 RefSeq:NP_565899.1 UniGene:At.22599 ProteinModelPortal:Q945P1 SMR:Q945P1 PRIDE:Q945P1 EnsemblPlants:AT2G39050.1 GeneID:818491 KEGG:ath:AT2G39050 TAIR:At2g39050

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						eggNOG:NOG254161 HOGENOM:HBG750017 InParanoid:Q945P1 OMA:GYRTIRM PhylomeDB:Q945P1 ProtClustDB:CLSN2681741 ArrayExpress:Q945P1 Genevestigator:Q945P1 Uniprot:Q945P1
Root	Isotig01179	138	67	0.913	1.12E-05	TAIR|locus:2064965 - symbol:EULS3 "AT2G39050" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0030246 "carbohydrate binding" evidence=IDA] GO:GO:0005634 GO:GO:0005737 EMBL:CP002685 GenomeReviews:CT485783_GR InterPro:IPR000772 SUPFAM:SSF50370 PROSITE:PS50231 GO:GO:0030246 EMBL:AC005770 Pfam:PF14200 EMBL:AF411801 EMBL:AY093795 EMBL:AY087909 IPI:IPI00536641 PIR:E84812 RefSeq:NP_565899.1 UniGene:At.22599 ProteinModelPortal:Q945P1 SMR:Q945P1 PRIDE:Q945P1 EnsemblPlants:AT2G39050.1 GeneID:818491 KEGG:ath:AT2G39050 TAIR:At2g39050 eggNOG:NOG254161 HOGENOM:HBG750017 InParanoid:Q945P1 OMA:GYRTIRM PhylomeDB:Q945P1 ProtClustDB:CLSN2681741 ArrayExpress:Q945P1 Genevestigator:Q945P1 Uniprot:Q945P1
Root	Isotig01180	137	67	0.903	1.46E-05	TAIR|locus:2064965 - symbol:EULS3 "AT2G39050" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0030246 "carbohydrate binding" evidence=IDA] GO:GO:0005634 GO:GO:0005737 EMBL:CP002685 GenomeReviews:CT485783_GR InterPro:IPR000772 SUPFAM:SSF50370 PROSITE:PS50231 GO:GO:0030246 EMBL:AC005770 Pfam:PF14200 EMBL:AF411801 EMBL:AY093795 EMBL:AY087909 IPI:IPI00536641 PIR:E84812 RefSeq:NP_565899.1 UniGene:At.22599 ProteinModelPortal:Q945P1 SMR:Q945P1 PRIDE:Q945P1 EnsemblPlants:AT2G39050.1 GeneID:818491 KEGG:ath:AT2G39050 TAIR:At2g39050 eggNOG:NOG254161 HOGENOM:HBG750017 InParanoid:Q945P1 OMA:GYRTIRM PhylomeDB:Q945P1 ProtClustDB:CLSN2681741 ArrayExpress:Q945P1 Genevestigator:Q945P1 Uniprot:Q945P1
Root	Isotig01189	40	7	2.386	1.71E-06	TAIR|locus:2102787 - symbol:AT3G46920 "AT3G46920" species:3702 "Arabidopsis thaliana" [GO:0004672 "protein kinase activity" evidence=ISS] [GO:0006468 "protein phosphorylation" evidence=IEA;ISS] [GO:0004712 "protein serine/threonine/tyrosine kinase activity" evidence=ISS] InterPro:IPR000270 InterPro:IPR000719 InterPro:IPR001245 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 Pfam:PF00564 Pfam:PF07714 PRINTS:PR00109 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 SMART:SM00666 GO:GO:0005524 EMBL:CP002686 GenomeReviews:BA000014_GR eggNOG:COG0515 SUPFAM:SSF56112 GO:GO:0004674 HSSP:P36897 EMBL:AL096859 IPI:IPI00523356 PIR:T12956 RefSeq:NP_190276.1 UniGene:At.43530 ProteinModelPortal:Q9STG4 SMR:Q9STG4 PRIDE:Q9STG4 EnsemblPlants:AT3G46920.1 GeneID:823845 KEGG:ath:AT3G46920 TAIR:At3g46920 HOGENOM:HBG317897 InParanoid:Q9STG4 OMA:PRPSDGM PhylomeDB:Q9STG4 ProtClustDB:CLSN2915679 Genevestigator:Q9STG4 Uniprot:Q9STG4
Root	Isotig01190	40	7	2.386	1.71E-06	TAIR|locus:2102787 - symbol:AT3G46920 "AT3G46920" species:3702 "Arabidopsis thaliana" [GO:0004672 "protein kinase activity" evidence=ISS] [GO:0006468 "protein phosphorylation" evidence=IEA;ISS] [GO:0004712 "protein serine/threonine/tyrosine kinase activity" evidence=ISS] InterPro:IPR000270 InterPro:IPR000719 InterPro:IPR001245 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 Pfam:PF00564 Pfam:PF07714 PRINTS:PR00109 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 SMART:SM00666 GO:GO:0005524 EMBL:CP002686 GenomeReviews:BA000014_GR eggNOG:COG0515 SUPFAM:SSF56112 GO:GO:0004674 HSSP:P36897 EMBL:AL096859 IPI:IPI00523356 PIR:T12956 RefSeq:NP_190276.1 UniGene:At.43530 ProteinModelPortal:Q9STG4 SMR:Q9STG4 PRIDE:Q9STG4 EnsemblPlants:AT3G46920.1 GeneID:823845 KEGG:ath:AT3G46920 TAIR:At3g46920 HOGENOM:HBG317897 InParanoid:Q9STG4 OMA:PRPSDGM PhylomeDB:Q9STG4 ProtClustDB:CLSN2915679 Genevestigator:Q9STG4 Uniprot:Q9STG4
Root	Isotig01191	33	7	2.108	5.57E-05	TAIR|locus:2102787 - symbol:AT3G46920 "AT3G46920" species:3702 "Arabidopsis thaliana" [GO:0004672 "protein kinase activity" evidence=ISS] [GO:0006468 "protein phosphorylation" evidence=IEA;ISS] [GO:0004712 "protein serine/threonine/tyrosine kinase activity" evidence=ISS] InterPro:IPR000270 InterPro:IPR000719 InterPro:IPR001245 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 Pfam:PF00564 Pfam:PF07714 PRINTS:PR00109 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 SMART:SM00666 GO:GO:0005524 EMBL:CP002686 GenomeReviews:BA000014_GR eggNOG:COG0515 SUPFAM:SSF56112 GO:GO:0004674 HSSP:P36897 EMBL:AL096859 IPI:IPI00523356 PIR:T12956 RefSeq:NP_190276.1 UniGene:At.43530 ProteinModelPortal:Q9STG4 SMR:Q9STG4 PRIDE:Q9STG4 EnsemblPlants:AT3G46920.1 GeneID:823845 KEGG:ath:AT3G46920 TAIR:At3g46920 HOGENOM:HBG317897 InParanoid:Q9STG4 OMA:PRPSDGM PhylomeDB:Q9STG4 ProtClustDB:CLSN2915679 Genevestigator:Q9STG4 Uniprot:Q9STG4
Root	Isotig01192	33	7	2.108	5.57E-05	TAIR|locus:2102787 - symbol:AT3G46920 "AT3G46920" species:3702 "Arabidopsis thaliana" [GO:0004672 "protein kinase activity" evidence=ISS] [GO:0006468 "protein phosphorylation" evidence=IEA;ISS] [GO:0004712 "protein

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						serine/threonine/tyrosine kinase activity" evidence=ISS] InterPro:IPR000270 InterPro:IPR000719 InterPro:IPR001245 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 Pfam:PF00564 Pfam:PF07714 PRINTS:PR00109 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 SMART:SM00666 GO:GO:0005524 EMBL:CP002686 GenomeReviews:BA000014_GR eggNOG:COG0515 SUPFAM:SSF56112 GO:GO:0004674 HSSP:P36897 EMBL:AL096859 IPI:IPI00523356 PIR:T12956 RefSeq:NP_190276.1 UniGene:At.43530 ProteinModelPortal:Q9STG4 SMR:Q9STG4 PRIDE:Q9STG4 EnsemblPlants:AT3G46920.1 GeneID:823845 KEGG:ath:AT3G46920 TAIR:At3g46920 HOGENOM:HBG317897 InParanoid:Q9STG4 OMA:PRPSDGM PhylomeDB:Q9STG4 ProtClustDB:CLSN2915679 Genevestigator:Q9STG4 Uniprot:Q9STG4
Root	Isotig01193	30	6	2.193	8.18E-05	TAIR|locus:2102787 - symbol:AT3G46920 "AT3G46920" species:3702 "Arabidopsis thaliana" [GO:0004672 "protein kinase activity" evidence=ISS] [GO:0006468 "protein phosphorylation" evidence=IEA;ISS] [GO:0004712 "protein serine/threonine/tyrosine kinase activity" evidence=ISS] InterPro:IPR000270 InterPro:IPR000719 InterPro:IPR001245 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 Pfam:PF00564 Pfam:PF07714 PRINTS:PR00109 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 SMART:SM00666 GO:GO:0005524 EMBL:CP002686 GenomeReviews:BA000014_GR eggNOG:COG0515 SUPFAM:SSF56112 GO:GO:0004674 HSSP:P36897 EMBL:AL096859 IPI:IPI00523356 PIR:T12956 RefSeq:NP_190276.1 UniGene:At.43530 ProteinModelPortal:Q9STG4 SMR:Q9STG4 PRIDE:Q9STG4 EnsemblPlants:AT3G46920.1 GeneID:823845 KEGG:ath:AT3G46920 TAIR:At3g46920 HOGENOM:HBG317897 InParanoid:Q9STG4 OMA:PRPSDGM PhylomeDB:Q9STG4 ProtClustDB:CLSN2915679 Genevestigator:Q9STG4 Uniprot:Q9STG4
Root	Isotig01205	3	52	-4.244	1.90E-13	TAIR|locus:2149284 - symbol:DIN10 "AT5G20250" species:3702 "Arabidopsis thaliana" [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=ISS] [GO:0009507 "chloroplast" evidence=IDA] [GO:0006979 "response to oxidative stress" evidence=IEP] [GO:0009409 "response to cold" evidence=IEP] [GO:0080167 "response to karrikin" evidence=IEP] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR013785 GO:GO:0009506 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009507 GO:GO:0006979 Gene3D:G3DSA:3.20.20.70 InterPro:IPR017853 SUPFAM:SSF51445 GO:GO:0005975 GO:GO:0009409 GO:GO:0080167 CAZy:GH36 eggNOG:NOG06986 InterPro:IPR008811 Pfam:PF05691 EMBL:AF296825 KO:K06617 GO:GO:0047274 EMBL:AY090237 EMBL:BT000632 EMBL:AK227214 EMBL:AK221808 EMBL:AK316714 EMBL:AK317307 EMBL:AK318923 IPI:IPI00523317 RefSeq:NP_001031910.1 RefSeq:NP_001190347.1 RefSeq:NP_197525.1 RefSeq:NP_851044.2 UniGene:At.25459 UniGene:At.74986 ProteinModelPortal:Q8RX87 IntAct:Q8RX87 STRING:Q8RX87 PRIDE:Q8RX87 EnsemblPlants:AT5G20250.1 EnsemblPlants:AT5G20250.2 EnsemblPlants:AT5G20250.3 GeneID:832147 KEGG:ath:AT5G20250 TAIR:At5g20250 InParanoid:Q8RX87 OMA:SVAYNSV PhylomeDB:Q8RX87 ProtClustDB:PLN02684 Uniprot:Q8RX87
Root	Isotig01206	3	52	-4.244	1.90E-13	TAIR|locus:2149284 - symbol:DIN10 "AT5G20250" species:3702 "Arabidopsis thaliana" [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=ISS] [GO:0009507 "chloroplast" evidence=IDA] [GO:0006979 "response to oxidative stress" evidence=IEP] [GO:0009409 "response to cold" evidence=IEP] [GO:0080167 "response to karrikin" evidence=IEP] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR013785 GO:GO:0009506 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009507 GO:GO:0006979 Gene3D:G3DSA:3.20.20.70 InterPro:IPR017853 SUPFAM:SSF51445 GO:GO:0005975 GO:GO:0009409 GO:GO:0080167 CAZy:GH36 eggNOG:NOG06986 InterPro:IPR008811 Pfam:PF05691 EMBL:AF296825 KO:K06617 GO:GO:0047274 EMBL:AY090237 EMBL:BT000632 EMBL:AK227214 EMBL:AK221808 EMBL:AK316714 EMBL:AK317307 EMBL:AK318923 IPI:IPI00523317 RefSeq:NP_001031910.1 RefSeq:NP_001190347.1 RefSeq:NP_197525.1 RefSeq:NP_851044.2 UniGene:At.25459 UniGene:At.74986 ProteinModelPortal:Q8RX87 IntAct:Q8RX87 STRING:Q8RX87 PRIDE:Q8RX87 EnsemblPlants:AT5G20250.1 EnsemblPlants:AT5G20250.2 EnsemblPlants:AT5G20250.3 GeneID:832147 KEGG:ath:AT5G20250 TAIR:At5g20250 InParanoid:Q8RX87 OMA:SVAYNSV PhylomeDB:Q8RX87 ProtClustDB:PLN02684 Uniprot:Q8RX87
Root	Isotig01207	3	47	-4.099	4.33E-12	TAIR|locus:2149284 - symbol:DIN10 "AT5G20250" species:3702 "Arabidopsis thaliana" [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=ISS] [GO:0009507 "chloroplast" evidence=IDA] [GO:0006979 "response to oxidative stress" evidence=IEP] [GO:0009409 "response to cold" evidence=IEP] [GO:0080167 "response to karrikin" evidence=IEP] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR013785 GO:GO:0009506 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009507 GO:GO:0006979 Gene3D:G3DSA:3.20.20.70 InterPro:IPR017853 SUPFAM:SSF51445 GO:GO:0005975 GO:GO:0009409

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0080167 CAZy:GH36 eggNOG:NOG06986 InterPro:IPR008811 Pfam:PF05691 EMBL:AF296825 KO:K06617 GO:GO:0047274 EMBL:AY090237 EMBL:BT000632 EMBL:AK227214 EMBL:AK221808 EMBL:AK316714 EMBL:AK317307 EMBL:AK318923 IPI:IPI00523317 RefSeq:NP_001031910.1 RefSeq:NP_001190347.1 RefSeq:NP_197525.1 RefSeq:NP_851044.2 UniGene:At.25459 UniGene:At.74986 ProteinModelPortal:Q8RX87 IntAct:Q8RX87 STRING:Q8RX87 PRIDE:Q8RX87 EnsemblPlants:AT5G20250.1 EnsemblPlants:AT5G20250.2 EnsemblPlants:AT5G20250.3 GeneID:832147 KEGG:ath:AT5G20250 TAIR:At5g20250 InParanoid:Q8RX87 OMA:SVAYNSV PhylomeDB:Q8RX87 ProtClustDB:PLN02684 Uniprot:Q8RX87
Root	Isotig01208	3	47	-4.099	4.33E-12	TAIR|locus:2149284 - symbol:DIN10 "AT5G20250" species:3702 "Arabidopsis thaliana" [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=ISS] [GO:0009507 "chloroplast" evidence=IDA] [GO:0006979 "response to oxidative stress" evidence=IEP] [GO:0009409 "response to cold" evidence=IEP] [GO:0080167 "response to karrikin" evidence=IEP] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR013785 GO:GO:0009506 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009507 GO:GO:0006979 Gene3D:G3DSA:3.20.20.70 InterPro:IPR017853 SUPFAM:SSF51445 GO:GO:0005975 GO:GO:0009409 GO:GO:0080167 CAZy:GH36 eggNOG:NOG06986 InterPro:IPR008811 Pfam:PF05691 EMBL:AF296825 KO:K06617 GO:GO:0047274 EMBL:AY090237 EMBL:BT000632 EMBL:AK227214 EMBL:AK221808 EMBL:AK316714 EMBL:AK317307 EMBL:AK318923 IPI:IPI00523317 RefSeq:NP_001031910.1 RefSeq:NP_001190347.1 RefSeq:NP_197525.1 RefSeq:NP_851044.2 UniGene:At.25459 UniGene:At.74986 ProteinModelPortal:Q8RX87 IntAct:Q8RX87 STRING:Q8RX87 PRIDE:Q8RX87 EnsemblPlants:AT5G20250.1 EnsemblPlants:AT5G20250.2 EnsemblPlants:AT5G20250.3 GeneID:832147 KEGG:ath:AT5G20250 TAIR:At5g20250 InParanoid:Q8RX87 OMA:SVAYNSV PhylomeDB:Q8RX87 ProtClustDB:PLN02684 Uniprot:Q8RX87
Root	Isotig01209	3	50	-4.188	6.62E-13	TAIR|locus:2149284 - symbol:DIN10 "AT5G20250" species:3702 "Arabidopsis thaliana" [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=ISS] [GO:0009507 "chloroplast" evidence=IDA] [GO:0006979 "response to oxidative stress" evidence=IEP] [GO:0009409 "response to cold" evidence=IEP] [GO:0080167 "response to karrikin" evidence=IEP] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR013785 GO:GO:0009506 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009507 GO:GO:0006979 Gene3D:G3DSA:3.20.20.70 InterPro:IPR017853 SUPFAM:SSF51445 GO:GO:0005975 GO:GO:0009409 GO:GO:0080167 CAZy:GH36 eggNOG:NOG06986 InterPro:IPR008811 Pfam:PF05691 EMBL:AF296825 KO:K06617 GO:GO:0047274 EMBL:AY090237 EMBL:BT000632 EMBL:AK227214 EMBL:AK221808 EMBL:AK316714 EMBL:AK317307 EMBL:AK318923 IPI:IPI00523317 RefSeq:NP_001031910.1 RefSeq:NP_001190347.1 RefSeq:NP_197525.1 RefSeq:NP_851044.2 UniGene:At.25459 UniGene:At.74986 ProteinModelPortal:Q8RX87 IntAct:Q8RX87 STRING:Q8RX87 PRIDE:Q8RX87 EnsemblPlants:AT5G20250.1 EnsemblPlants:AT5G20250.2 EnsemblPlants:AT5G20250.3 GeneID:832147 KEGG:ath:AT5G20250 TAIR:At5g20250 InParanoid:Q8RX87 OMA:SVAYNSV PhylomeDB:Q8RX87 ProtClustDB:PLN02684 Uniprot:Q8RX87
Root	Isotig01210	3	50	-4.188	6.62E-13	TAIR|locus:2149284 - symbol:DIN10 "AT5G20250" species:3702 "Arabidopsis thaliana" [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=ISS] [GO:0009507 "chloroplast" evidence=IDA] [GO:0006979 "response to oxidative stress" evidence=IEP] [GO:0009409 "response to cold" evidence=IEP] [GO:0080167 "response to karrikin" evidence=IEP] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR013785 GO:GO:0009506 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009507 GO:GO:0006979 Gene3D:G3DSA:3.20.20.70 InterPro:IPR017853 SUPFAM:SSF51445 GO:GO:0005975 GO:GO:0009409 GO:GO:0080167 CAZy:GH36 eggNOG:NOG06986 InterPro:IPR008811 Pfam:PF05691 EMBL:AF296825 KO:K06617 GO:GO:0047274 EMBL:AY090237 EMBL:BT000632 EMBL:AK227214 EMBL:AK221808 EMBL:AK316714 EMBL:AK317307 EMBL:AK318923 IPI:IPI00523317 RefSeq:NP_001031910.1 RefSeq:NP_001190347.1 RefSeq:NP_197525.1 RefSeq:NP_851044.2 UniGene:At.25459 UniGene:At.74986 ProteinModelPortal:Q8RX87 IntAct:Q8RX87 STRING:Q8RX87 PRIDE:Q8RX87 EnsemblPlants:AT5G20250.1 EnsemblPlants:AT5G20250.2 EnsemblPlants:AT5G20250.3 GeneID:832147 KEGG:ath:AT5G20250 TAIR:At5g20250 InParanoid:Q8RX87 OMA:SVAYNSV PhylomeDB:Q8RX87 ProtClustDB:PLN02684 Uniprot:Q8RX87
Root	Isotig01211	0	19	-5.377	3.67E-06	TAIR|locus:2149284 - symbol:DIN10 "AT5G20250" species:3702 "Arabidopsis thaliana" [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=ISS] [GO:0009507 "chloroplast" evidence=IDA] [GO:0006979

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						"response to oxidative stress" evidence=IEP] [GO:0009409 "response to cold" evidence=IEP] [GO:0080167 "response to karrikin" evidence=IEP] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR013785 GO:GO:0009506 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009507 GO:GO:0006979 Gene3D:G3DSA:3.20.20.70 InterPro:IPR017853 SUPFAM:SSF51445 GO:GO:0005975 GO:GO:0009409 GO:GO:0080167 CAZy:GH36 eggNOG:NOG06986 InterPro:IPR008811 Pfam:PF05691 EMBL:AF296825 KO:K06617 GO:GO:0047274 EMBL:AY090237 EMBL:BT000632 EMBL:AK227214 EMBL:AK221808 EMBL:AK316714 EMBL:AK317307 EMBL:AK318923 IPI:IPI00523317 RefSeq:NP_001031910.1 RefSeq:NP_001190347.1 RefSeq:NP_197525.1 RefSeq:NP_851044.2 UniGene:At.25459 UniGene:At.74986 ProteinModelPortal:Q8RX87 IntAct:Q8RX87 STRING:Q8RX87 PRIDE:Q8RX87 EnsemblPlants:AT5G20250.1 EnsemblPlants:AT5G20250.2 EnsemblPlants:AT5G20250.3 GeneID:832147 KEGG:ath:AT5G20250 TAIR:At5g20250 InParanoid:Q8RX87 OMA:SVAYNSV PhylomeDB:Q8RX87 ProtClustDB:PLN02684 Uniprot:Q8RX87
Root	Isotig01212	0	17	-5.216	1.26E-05	TAIR|locus:2149284 - symbol:DIN10 "AT5G20250" species:3702 "Arabidopsis thaliana" [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=ISS] [GO:0009507 "chloroplast" evidence=IDA] [GO:0006979 "response to oxidative stress" evidence=IEP] [GO:0009409 "response to cold" evidence=IEP] [GO:0080167 "response to karrikin" evidence=IEP] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR013785 GO:GO:0009506 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009507 GO:GO:0006979 Gene3D:G3DSA:3.20.20.70 InterPro:IPR017853 SUPFAM:SSF51445 GO:GO:0005975 GO:GO:0009409 GO:GO:0080167 CAZy:GH36 eggNOG:NOG06986 InterPro:IPR008811 Pfam:PF05691 EMBL:AF296825 KO:K06617 GO:GO:0047274 EMBL:AY090237 EMBL:BT000632 EMBL:AK227214 EMBL:AK221808 EMBL:AK316714 EMBL:AK317307 EMBL:AK318923 IPI:IPI00523317 RefSeq:NP_001031910.1 RefSeq:NP_001190347.1 RefSeq:NP_197525.1 RefSeq:NP_851044.2 UniGene:At.25459 UniGene:At.74986 ProteinModelPortal:Q8RX87 IntAct:Q8RX87 STRING:Q8RX87 PRIDE:Q8RX87 EnsemblPlants:AT5G20250.1 EnsemblPlants:AT5G20250.2 EnsemblPlants:AT5G20250.3 GeneID:832147 KEGG:ath:AT5G20250 TAIR:At5g20250 InParanoid:Q8RX87 OMA:SVAYNSV PhylomeDB:Q8RX87 ProtClustDB:PLN02684 Uniprot:Q8RX87
Root	Isotig01227	15	42	-1.614	7.30E-05	TAIR|locus:2182432 - symbol:AT5G35200 species:3702 "Arabidopsis thaliana" [GO:0005543 "phospholipid binding" evidence=IEA] [GO:0005545 "1-phosphatidylinositol binding" evidence=IEA] [GO:0030276 "clathrin binding" evidence=IEA] [GO:0048268 "clathrin coat assembly" evidence=IEA] [GO:0005886 "plasma membrane" evidence=IDA] InterPro:IPR011417 InterPro:IPR014712 Pfam:PF07651 GO:GO:0005886 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005794 GO:GO:0005545 GO:GO:0005905 GO:GO:0006897 GO:GO:0030136 GO:GO:0030276 HOGENOM:HBG744562 GO:GO:0030118 GO:GO:0048268 InterPro:IPR008942 InterPro:IPR013809 Gene3D:G3DSA:1.25.40.90 Gene3D:G3DSA:1.20.58.150 SMART:SM00273 SUPFAM:SSF48464 PROSITE:PS50942 eggNOG:NOG267212 EMBL:AP002031 EMBL:AF080121 EMBL:AY081284 EMBL:BT000375 IPI:IPI00518637 RefSeq:NP_198370.1 UniGene:At.30612 ProteinModelPortal:Q9LHS0 STRING:Q9LHS0 PRIDE:Q9LHS0 EnsemblPlants:AT5G35200.1 GeneID:833474 KEGG:ath:AT5G35200 TAIR:At5g35200 InParanoid:Q9LHS0 OMA:EMQRNDA PhylomeDB:Q9LHS0 ProtClustDB:CLSN2686467 ArrayExpress:Q9LHS0 Genevestigator:Q9LHS0 GermOnline:AT5G35200 Uniprot:Q9LHS0
Root	Isotig01228	15	43	-1.648	4.63E-05	TAIR|locus:2182432 - symbol:AT5G35200 species:3702 "Arabidopsis thaliana" [GO:0005543 "phospholipid binding" evidence=IEA] [GO:0005545 "1-phosphatidylinositol binding" evidence=IEA] [GO:0030276 "clathrin binding" evidence=IEA] [GO:0048268 "clathrin coat assembly" evidence=IEA] [GO:0005886 "plasma membrane" evidence=IDA] InterPro:IPR011417 InterPro:IPR014712 Pfam:PF07651 GO:GO:0005886 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005794 GO:GO:0005545 GO:GO:0005905 GO:GO:0006897 GO:GO:0030136 GO:GO:0030276 HOGENOM:HBG744562 GO:GO:0030118 GO:GO:0048268 InterPro:IPR008942 InterPro:IPR013809 Gene3D:G3DSA:1.25.40.90 Gene3D:G3DSA:1.20.58.150 SMART:SM00273 SUPFAM:SSF48464 PROSITE:PS50942 eggNOG:NOG267212 EMBL:AP002031 EMBL:AF080121 EMBL:AY081284 EMBL:BT000375 IPI:IPI00518637 RefSeq:NP_198370.1 UniGene:At.30612 ProteinModelPortal:Q9LHS0 STRING:Q9LHS0 PRIDE:Q9LHS0 EnsemblPlants:AT5G35200.1 GeneID:833474 KEGG:ath:AT5G35200 TAIR:At5g35200 InParanoid:Q9LHS0 OMA:EMQRNDA PhylomeDB:Q9LHS0 ProtClustDB:CLSN2686467 ArrayExpress:Q9LHS0 Genevestigator:Q9LHS0 GermOnline:AT5G35200 Uniprot:Q9LHS0

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig01229	10	41	-2.165	1.78E-06	TAIR|locus:2182432 - symbol:AT5G35200 species:3702 "Arabidopsis thaliana" [GO:0005543 "phospholipid binding" evidence=IEA] [GO:0005545 "1-phosphatidylinositol binding" evidence=IEA] [GO:0030276 "clathrin binding" evidence=IEA] [GO:0048268 "clathrin coat assembly" evidence=IEA] [GO:0005886 "plasma membrane" evidence=IDA] InterPro:IPR011417 InterPro:IPR014712 Pfam:PF07651 GO:GO:0005886 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005794 GO:GO:0005545 GO:GO:0005905 GO:GO:0006897 GO:GO:0030136 GO:GO:0030276 HOGENOM:HBG744562 GO:GO:0030118 GO:GO:0048268 InterPro:IPR008942 InterPro:IPR013809 Gene3D:G3DSA:1.25.40.90 Gene3D:G3DSA:1.20.58.150 SMART:SM00273 SUPFAM:SSF48464 PROSITE:PS50942 eggNOG:NOG267212 EMBL:AP002031 EMBL:AF080121 EMBL:AY081284 EMBL:BT000375 IPI:IPI00518637 RefSeq:NP_198370.1 UniGene:At.30612 ProteinModelPortal:Q9LHS0 STRING:Q9LHS0 PRIDE:Q9LHS0 EnsemblPlants:AT5G35200.1 GeneID:833474 KEGG:ath:AT5G35200 TAIR:At5g35200 InParanoid:Q9LHS0 OMA:EMQRNDA PhylomeDB:Q9LHS0 ProtClustDB:CLSN2686467 ArrayExpress:Q9LHS0 Genevestigator:Q9LHS0 GermOnline:AT5G35200 Uniprot:Q9LHS0
Root	Isotig01230	15	43	-1.648	4.63E-05	TAIR|locus:2182432 - symbol:AT5G35200 species:3702 "Arabidopsis thaliana" [GO:0005543 "phospholipid binding" evidence=IEA] [GO:0005545 "1-phosphatidylinositol binding" evidence=IEA] [GO:0030276 "clathrin binding" evidence=IEA] [GO:0048268 "clathrin coat assembly" evidence=IEA] [GO:0005886 "plasma membrane" evidence=IDA] InterPro:IPR011417 InterPro:IPR014712 Pfam:PF07651 GO:GO:0005886 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005794 GO:GO:0005545 GO:GO:0005905 GO:GO:0006897 GO:GO:0030136 GO:GO:0030276 HOGENOM:HBG744562 GO:GO:0030118 GO:GO:0048268 InterPro:IPR008942 InterPro:IPR013809 Gene3D:G3DSA:1.25.40.90 Gene3D:G3DSA:1.20.58.150 SMART:SM00273 SUPFAM:SSF48464 PROSITE:PS50942 eggNOG:NOG267212 EMBL:AP002031 EMBL:AF080121 EMBL:AY081284 EMBL:BT000375 IPI:IPI00518637 RefSeq:NP_198370.1 UniGene:At.30612 ProteinModelPortal:Q9LHS0 STRING:Q9LHS0 PRIDE:Q9LHS0 EnsemblPlants:AT5G35200.1 GeneID:833474 KEGG:ath:AT5G35200 TAIR:At5g35200 InParanoid:Q9LHS0 OMA:EMQRNDA PhylomeDB:Q9LHS0 ProtClustDB:CLSN2686467 ArrayExpress:Q9LHS0 Genevestigator:Q9LHS0 GermOnline:AT5G35200 Uniprot:Q9LHS0
Root	Isotig01231	15	44	-1.682	2.92E-05	TAIR|locus:2182432 - symbol:AT5G35200 species:3702 "Arabidopsis thaliana" [GO:0005543 "phospholipid binding" evidence=IEA] [GO:0005545 "1-phosphatidylinositol binding" evidence=IEA] [GO:0030276 "clathrin binding" evidence=IEA] [GO:0048268 "clathrin coat assembly" evidence=IEA] [GO:0005886 "plasma membrane" evidence=IDA] InterPro:IPR011417 InterPro:IPR014712 Pfam:PF07651 GO:GO:0005886 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005794 GO:GO:0005545 GO:GO:0005905 GO:GO:0006897 GO:GO:0030136 GO:GO:0030276 HOGENOM:HBG744562 GO:GO:0030118 GO:GO:0048268 InterPro:IPR008942 InterPro:IPR013809 Gene3D:G3DSA:1.25.40.90 Gene3D:G3DSA:1.20.58.150 SMART:SM00273 SUPFAM:SSF48464 PROSITE:PS50942 eggNOG:NOG267212 EMBL:AP002031 EMBL:AF080121 EMBL:AY081284 EMBL:BT000375 IPI:IPI00518637 RefSeq:NP_198370.1 UniGene:At.30612 ProteinModelPortal:Q9LHS0 STRING:Q9LHS0 PRIDE:Q9LHS0 EnsemblPlants:AT5G35200.1 GeneID:833474 KEGG:ath:AT5G35200 TAIR:At5g35200 InParanoid:Q9LHS0 OMA:EMQRNDA PhylomeDB:Q9LHS0 ProtClustDB:CLSN2686467 ArrayExpress:Q9LHS0 Genevestigator:Q9LHS0 GermOnline:AT5G35200 Uniprot:Q9LHS0
Root	Isotig01232	10	42	-2.199	1.05E-06	TAIR|locus:2182432 - symbol:AT5G35200 species:3702 "Arabidopsis thaliana" [GO:0005543 "phospholipid binding" evidence=IEA] [GO:0005545 "1-phosphatidylinositol binding" evidence=IEA] [GO:0030276 "clathrin binding" evidence=IEA] [GO:0048268 "clathrin coat assembly" evidence=IEA] [GO:0005886 "plasma membrane" evidence=IDA] InterPro:IPR011417 InterPro:IPR014712 Pfam:PF07651 GO:GO:0005886 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005794 GO:GO:0005545 GO:GO:0005905 GO:GO:0006897 GO:GO:0030136 GO:GO:0030276 HOGENOM:HBG744562 GO:GO:0030118 GO:GO:0048268 InterPro:IPR008942 InterPro:IPR013809 Gene3D:G3DSA:1.25.40.90 Gene3D:G3DSA:1.20.58.150 SMART:SM00273 SUPFAM:SSF48464 PROSITE:PS50942 eggNOG:NOG267212 EMBL:AP002031 EMBL:AF080121 EMBL:AY081284 EMBL:BT000375 IPI:IPI00518637 RefSeq:NP_198370.1 UniGene:At.30612 ProteinModelPortal:Q9LHS0 STRING:Q9LHS0 PRIDE:Q9LHS0 EnsemblPlants:AT5G35200.1 GeneID:833474 KEGG:ath:AT5G35200 TAIR:At5g35200 InParanoid:Q9LHS0 OMA:EMQRNDA PhylomeDB:Q9LHS0 ProtClustDB:CLSN2686467 ArrayExpress:Q9LHS0 Genevestigator:Q9LHS0 GermOnline:AT5G35200 Uniprot:Q9LHS0

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig01241	714	55	3.569	4.00E-134	TIGR_CMR|GSU_1062 - symbol:GSU_1062 "cytochrome c family protein, putative" species:243231 "Geobacter sulfurreducens PCA" [GO:0009055 "electron carrier activity" evidence=ISS] EMBL:AE017180 GenomeReviews:AE017180_GR RefSeq:NP_952115.1 GeneID:2688672 KEGG:gsu:GSU1062 PATRIC:22024890 TIGR:GSU1062 HOGENOM:HBG090252 OMA:RIPELND ProtClustDB:CLSK743107 Uniprot:Q74EA1
Root	Isotig01242	714	55	3.569	4.00E-134	No hit
Root	Isotig01243	723	56	3.562	1.45E-135	No hit
Root	Isotig01244	723	56	3.562	1.45E-135	No hit
Root	Isotig01245	630	50	3.526	1.73E-117	No hit
Root	Isotig01246	38	6	2.534	1.37E-06	No hit
Root	Isotig01247	38	6	2.534	1.37E-06	No hit
Root	Isotig01256	78	31	1.202	3.56E-05	UNIPROTKB|Q02817 - symbol:MUC2 "Mucin-2" species:9606 "Homo sapiens" [GO:0005515 "protein binding" evidence=IPI] [GO:0005796 "Golgi lumen" evidence=TAS] [GO:0016266 "O-glycan processing" evidence=TAS] [GO:0043687 "post-translational protein modification" evidence=TAS] [GO:0044267 "cellular protein metabolic process" evidence=TAS] [GO:0070702 "inner mucus layer" evidence=ISS] [GO:0070703 "outer mucus layer" evidence=ISS] Reactome:REACT_17015 InterPro:IPR001007 PROSITE:PS01208 PROSITE:PS50184 SMART:SM00214 GO:GO:0005515 InterPro:IPR002919 Pfam:PF01826 SUPFAM:SSF57567 GO:GO:0043687 eggNOG:NOG12793 GO:GO:0005796 InterPro:IPR001846 Pfam:PF00094 SMART:SM00216 PROSITE:PS51233 GO:GO:0016266 InterPro:IPR014853 Pfam:PF08742 SMART:SM00832 InterPro:IPR006207 PROSITE:PS01185 PROSITE:PS01225 SMART:SM00041 DrugBank:DB01411 EMBL:L21998 EMBL:M74027 EMBL:M94131 EMBL:M94132 IPI:IPI00027201 PIR:A49963 RefSeq:NP_002448.2 UniGene:Hs.315 ProteinModelPortal:Q02817 SMR:Q02817 DIP:DIP-48824N IntAct:Q02817 STRING:Q02817 GlycoSuiteDB:Q02817 PhosphoSite:Q02817 DMDM:2506877 PRIDE:Q02817 Ensembl:ENST00000359061 GeneID:4583 KEGG:hsa:4583 CTD:4583 GeneCards:GC11P001064 HGNC:HGNC:7512 HPA:CAB005317 HPA:CAB016275 HPA:HPA006197 MIM:158370 neXtProt:NX_Q02817 PharmGKB:PA31316 HOVERGEN:HBG004380 InParanoid:Q02817 KO:K10955 NextBio:17613 ArrayExpress:Q02817 Bgee:Q02817 CleanEx:HS_MUC2 Genevestigator:Q02817 GermOnline:ENSG00000198788 GO:GO:0070702 GO:GO:0070703 InterPro:IPR006552 SMART:SM00215 Uniprot:Q02817
Root	Isotig01258	28	3	3.093	4.38E-06	MGI|MGI:2144837 - symbol:Ptpn23 "protein tyrosine phosphatase, non-receptor type 23" species:10090 "Mus musculus" [GO:0005634 "nucleus" evidence=ISO] [GO:0005737 "cytoplasm" evidence=ISO] [GO:0005768 "endosome" evidence=ISO] [GO:0016311 "dephosphorylation" evidence=IEA] [GO:0016791 "phosphatase activity" evidence=IEA] [GO:0004725 "protein tyrosine phosphatase activity" evidence=IEA] [GO:0005932 "microtubule basal body" evidence=ISO] [GO:0005856 "cytoskeleton" evidence=IEA] [GO:0016787 "hydrolase activity" evidence=IEA] [GO:0030030 "cell projection organization" evidence=IEA] [GO:0004721 "phosphoprotein phosphatase activity" evidence=IEA] [GO:0005929 "cilium" evidence=IEA] [GO:0031410 "cytoplasmic vesicle" evidence=IEA] [GO:0042995 "cell projection" evidence=IEA] [GO:0006470 "protein dephosphorylation" evidence=IEA] [GO:0060271 "cilium morphogenesis" evidence=ISO] InterPro:IPR000242 InterPro:IPR000387 InterPro:IPR016130 InterPro:IPR025304 Pfam:PF00102 Pfam:PF13949 PRINTS:PR00700 PROSITE:PS00383 PROSITE:PS50005 PROSITE:PS50055 PROSITE:PS50056 PROSITE:PS50293 SMART:SM00194 MGI:MGI:2144837 GO:GO:0005634 GO:GO:0005768 GO:GO:0016023 GO:GO:0005929 GO:GO:0005932 InterPro:IPR004328 Gene3D:G3DSA:1.25.40.280 Pfam:PF03097 SMART:SM01041 PROSITE:PS51180 GeneTree:ENSGT00650000093161 GO:GO:0060271 GO:GO:0004725 eggNOG:COG5599 KO:K01104 PDB:2W10 PDBsum:2W10 CTD:25930 HOVERGEN:HBG082231 OMA:GPGPHYL EMBL:BY750106 EMBL:CF734421 EMBL:CB248963 EMBL:BC006582 EMBL:BC022721 EMBL:BC059902 EMBL:AK173178 IPI:IPI00464166 IPI:IPI00606716 RefSeq:NP_001074512.1 UniGene:Mm.335477 ProteinModelPortal:Q6PB44 SMR:Q6PB44 DIP:DIP-48351N IntAct:Q6PB44 STRING:Q6PB44 PhosphoSite:Q6PB44 PRIDE:Q6PB44 Ensembl:ENSMUST00000040021 GeneID:104831 KEGG:mmu:104831 UCSC:uc009rty.1 UCSC:uc012hbi.1 HOGENOM:HBG444522 InParanoid:Q6PB44 OrthoDB:EOG4NCMBX PhylomeDB:Q6PB44 NextBio:357310 ArrayExpress:Q6PB44 Bgee:Q6PB44 Genevestigator:Q6PB44 GermOnline:ENSMUSG00000036057 Uniprot:Q6PB44
Root	Isotig01266	1	13	-3.829	0.000362856	TAIR|locus:2025886 - symbol:AT1G59740 "AT1G59740" species:3702 "Arabidopsis thaliana" [GO:0005215 "transporter activity" evidence=ISS] [GO:0006857 "oligopeptide transport" evidence=ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0009624 "response to nematode" evidence=IEP] [GO:0005886 "plasma membrane"

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						evidence=IDA] InterPro:IPR000109 InterPro:IPR018456 Pfam:PF00854 PROSITE:PS01022 PROSITE:PS01023 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005886 GO:GO:0009624 EMBL:AC007258 GO:GO:0005215 InterPro:IPR016196 SUPFAM:SSF103473 eggNOG:COG3104 OMA:AYMISAI GO:GO:0006857 HOGENOM:HBG605267 ProtClustDB:CLSN2679698 EMBL:AY035037 EMBL:AY051041 IPI:IPI00521525 PIR:C96621 RefSeq:NP_176183.1 UniGene:At.11372 ProteinModelPortal:Q93VV5 PRIDE:Q93VV5 EnsemblPlants:AT1G59740.1 GeneID:842267 KEGG:ath:AT1G59740 TAIR:At1g59740 InParanoid:Q93VV5 PhylomeDB:Q93VV5 ArrayExpress:Q93VV5 Genevestigator:Q93VV5 Uniprot:Q93VV5
Root	Isotig01268	1	13	-3.829	0.000362856	TAIR|locus:2025886 - symbol:AT1G59740 "AT1G59740" species:3702 "Arabidopsis thaliana" [GO:0005215 "transporter activity" evidence=ISS] [GO:0006857 "oligopeptide transport" evidence=ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0009624 "response to nematode" evidence=IEP] [GO:0005886 "plasma membrane" evidence=IDA] InterPro:IPR000109 InterPro:IPR018456 Pfam:PF00854 PROSITE:PS01022 PROSITE:PS01023 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005886 GO:GO:0009624 EMBL:AC007258 GO:GO:0005215 InterPro:IPR016196 SUPFAM:SSF103473 eggNOG:COG3104 OMA:AYMISAI GO:GO:0006857 HOGENOM:HBG605267 ProtClustDB:CLSN2679698 EMBL:AY035037 EMBL:AY051041 IPI:IPI00521525 PIR:C96621 RefSeq:NP_176183.1 UniGene:At.11372 ProteinModelPortal:Q93VV5 PRIDE:Q93VV5 EnsemblPlants:AT1G59740.1 GeneID:842267 KEGG:ath:AT1G59740 TAIR:At1g59740 InParanoid:Q93VV5 PhylomeDB:Q93VV5 ArrayExpress:Q93VV5 Genevestigator:Q93VV5 Uniprot:Q93VV5
Root	Isotig01278	21	2	3.263	4.62E-05	No hit
Root	Isotig01279	20	2	3.193	8.23E-05	No hit
Root	Isotig01280	21	2	3.263	4.62E-05	No hit
Root	Isotig01281	21	2	3.263	4.62E-05	No hit
Root	Isotig01282	20	2	3.193	8.23E-05	No hit
Root	Isotig01283	20	2	3.193	8.23E-05	No hit
Root	Isotig01296	85	27	1.526	2.24E-07	TAIR|locus:2075356 - symbol:AT3G46220 "AT3G46220" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0016874 EMBL:AL355775 UniGene:At.1484 UniGene:At.70182 IPI:IPI00517015 PIR:T49263 RefSeq:NP_566883.4 PRIDE:Q9LX73 EnsemblPlants:AT3G46220.1 GeneID:823767 KEGG:ath:AT3G46220 TAIR:At3g46220 eggNOG:NOG277822 HOGENOM:HBG597219 InParanoid:Q9LX73 PhylomeDB:Q9LX73 ProtClustDB:PLN03083 Genevestigator:Q9LX73 InterPro:IPR018611 Pfam:PF09743 Uniprot:Q9LX73
Root	Isotig01297	85	27	1.526	2.24E-07	TAIR|locus:2075356 - symbol:AT3G46220 "AT3G46220" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0016874 EMBL:AL355775 UniGene:At.1484 UniGene:At.70182 IPI:IPI00517015 PIR:T49263 RefSeq:NP_566883.4 PRIDE:Q9LX73 EnsemblPlants:AT3G46220.1 GeneID:823767 KEGG:ath:AT3G46220 TAIR:At3g46220 eggNOG:NOG277822 HOGENOM:HBG597219 InParanoid:Q9LX73 PhylomeDB:Q9LX73 ProtClustDB:PLN03083 Genevestigator:Q9LX73 InterPro:IPR018611 Pfam:PF09743 Uniprot:Q9LX73
Root	Isotig01298	85	27	1.526	2.24E-07	TAIR|locus:2075356 - symbol:AT3G46220 "AT3G46220" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0016874 EMBL:AL355775 UniGene:At.1484 UniGene:At.70182 IPI:IPI00517015 PIR:T49263 RefSeq:NP_566883.4 PRIDE:Q9LX73 EnsemblPlants:AT3G46220.1 GeneID:823767 KEGG:ath:AT3G46220 TAIR:At3g46220 eggNOG:NOG277822 HOGENOM:HBG597219 InParanoid:Q9LX73 PhylomeDB:Q9LX73 ProtClustDB:PLN03083 Genevestigator:Q9LX73 InterPro:IPR018611 Pfam:PF09743 Uniprot:Q9LX73
Root	Isotig01304	17	40	-1.363	0.000639398	TAIR|locus:2029491 - symbol:RAP2.4 "AT1G78080" species:3702 "Arabidopsis thaliana" [GO:0006355 "regulation of transcription, DNA-dependent" evidence=ISS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS;IDA;TAS] [GO:0005515 "protein binding" evidence=IPI] [GO:0005634 "nucleus" evidence=IC;IDA] [GO:0006970 "response to osmotic stress" evidence=IEP] [GO:0071472 "cellular response to salt stress" evidence=IEP] [GO:0003677 "DNA binding" evidence=IDA;TAS] [GO:0009414 "response to water deprivation" evidence=IEP;IMP] [GO:0009416 "response to light stimulus" evidence=IEP] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0009873 "ethylene mediated signaling pathway" evidence=IMP] [GO:0010017 "red or far-red light signaling pathway" evidence=IGI] [GO:0009611 "response to wounding" evidence=IEP] [GO:0009736 "cytokinin mediated signaling pathway" evidence=IMP] [GO:0045595 "regulation of cell differentiation" evidence=IMP] [GO:0009409 "response to cold" evidence=IEP] [GO:0043565 "sequence-specific DNA binding" evidence=IDA] InterPro:IPR001471 InterPro:IPR016177 Pfam:PF00847 PRINTS:PR00367 PROSITE:PS51032

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						SMART:SM00380 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005634 GO:GO:0005515 GO:GO:0009611 GO:GO:0009873 GO:GO:0045595 GO:GO:0043565 GO:GO:0003700 GO:GO:0006351 GO:GO:0009409 GO:GO:0009414 KO:K09286 Gene3D:G3DSA:3.30.730.10 SUPFAM:SSF54171 HSSP:O80337 GO:GO:0009736 GO:GO:0071472 GO:GO:0010017 EMBL:AC009243 HOGENOM:HBG599504 EMBL:AC012680 UniGene:At.25524 EMBL:AF370152 EMBL:AY150468 EMBL:AF003097 IPI:IPI00519366 RefSeq:NP_177931.1 UniGene:At.71798 ProteinModelPortal:Q8H1E4 SMR:Q8H1E4 MINT:MINT-7262714 STRING:Q8H1E4 PRIDE:Q8H1E4 EnsemblPlants:AT1G78080.1 GeneID:844143 KEGG:ath:AT1G78080 TAIR:At1g78080 eggNOG:NOG306355 InParanoid:Q8H1E4 OMA:KLEAICK PhylomeDB:Q8H1E4 ProtClustDB:CLSN2679481 Genevestigator:Q8H1E4 Uniprot:Q8H1E4
Root	Isotig01311	6	25	-2.188	0.000173532	TAIR|locus:505006369 - symbol:ALDH2C4 "AT3G24503" species:3702 "Arabidopsis thaliana" [GO:0004028 "3-chloroallyl aldehyde dehydrogenase activity" evidence=ISS] [GO:0004029 "aldehyde dehydrogenase (NAD) activity" evidence=ISS] [GO:0009699 "phenylpropanoid biosynthetic process" evidence=IDA] [GO:0050269 "coniferyl-aldehyde dehydrogenase activity" evidence=IDA] InterPro:IPR015590 InterPro:IPR016160 InterPro:IPR016161 InterPro:IPR016162 InterPro:IPR016163 Pfam:PF00171 PROSITE:PS00070 PROSITE:PS00687 GO:GO:0005829 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0009699 eggNOG:COG1012 Gene3D:G3DSA:3.40.309.10 Gene3D:G3DSA:3.40.605.10 SUPFAM:SSF53720 HOGENOM:HBG752218 GO:GO:0004029 HSSP:P05091 EMBL:AF349448 EMBL:AB020746 EMBL:AY056398 EMBL:AK221230 IPI:IPI00543086 RefSeq:NP_566749.1 UniGene:At.22894 ProteinModelPortal:Q56YU0 SMR:Q56YU0 IntAct:Q56YU0 STRING:Q56YU0 PRIDE:Q56YU0 ProMEX:Q56YU0 EnsemblPlants:AT3G24503.1 GeneID:822042 KEGG:ath:AT3G24503 TAIR:At3g24503 InParanoid:Q56YU0 KO:K12355 OMA:EMAMEAG PhylomeDB:Q56YU0 ProtClustDB:PLN02766 Genevestigator:Q56YU0 GO:GO:0050269 Uniprot:Q56YU0
Root	Isotig01313	5	21	-2.199	0.000555521	TAIR|locus:505006369 - symbol:ALDH2C4 "AT3G24503" species:3702 "Arabidopsis thaliana" [GO:0004028 "3-chloroallyl aldehyde dehydrogenase activity" evidence=ISS] [GO:0004029 "aldehyde dehydrogenase (NAD) activity" evidence=ISS] [GO:0009699 "phenylpropanoid biosynthetic process" evidence=IDA] [GO:0050269 "coniferyl-aldehyde dehydrogenase activity" evidence=IDA] InterPro:IPR015590 InterPro:IPR016160 InterPro:IPR016161 InterPro:IPR016162 InterPro:IPR016163 Pfam:PF00171 PROSITE:PS00070 PROSITE:PS00687 GO:GO:0005829 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0009699 eggNOG:COG1012 Gene3D:G3DSA:3.40.309.10 Gene3D:G3DSA:3.40.605.10 SUPFAM:SSF53720 HOGENOM:HBG752218 GO:GO:0004029 HSSP:P05091 EMBL:AF349448 EMBL:AB020746 EMBL:AY056398 EMBL:AK221230 IPI:IPI00543086 RefSeq:NP_566749.1 UniGene:At.22894 ProteinModelPortal:Q56YU0 SMR:Q56YU0 IntAct:Q56YU0 STRING:Q56YU0 PRIDE:Q56YU0 ProMEX:Q56YU0 EnsemblPlants:AT3G24503.1 GeneID:822042 KEGG:ath:AT3G24503 TAIR:At3g24503 InParanoid:Q56YU0 KO:K12355 OMA:EMAMEAG PhylomeDB:Q56YU0 ProtClustDB:PLN02766 Genevestigator:Q56YU0 GO:GO:0050269 Uniprot:Q56YU0
Root	Isotig01336	65	18	1.723	7.69E-07	TAIR|locus:2193874 - symbol:AT1G55530 species:3702 "Arabidopsis thaliana" [GO:0008270 "zinc ion binding" evidence=IEA;ISS] InterPro:IPR001841 PROSITE:PS50089 SMART:SM00184 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0008270 InterPro:IPR013083 Gene3D:G3DSA:3.30.40.10 HSSP:Q9LRB7 EMBL:AC005223 eggNOG:NOG235630 HOGENOM:HBG749479 EMBL:AY039608 EMBL:AF424578 EMBL:BT000502 IPI:IPI00534528 PIR:F96597 RefSeq:NP_564693.1 UniGene:At.19898 ProteinModelPortal:Q9ZVU8 SMR:Q9ZVU8 STRING:Q9ZVU8 EnsemblPlants:AT1G55530.1 GeneID:842000 KEGG:ath:AT1G55530 TAIR:At1g55530 InParanoid:Q9ZVU8 OMA:FVEEMED PhylomeDB:Q9ZVU8 ProtClustDB:CLSN2917296 Genevestigator:Q9ZVU8 Uniprot:Q9ZVU8
Root	Isotig01337	65	18	1.723	7.69E-07	TAIR|locus:2193874 - symbol:AT1G55530 species:3702 "Arabidopsis thaliana" [GO:0008270 "zinc ion binding" evidence=IEA;ISS] InterPro:IPR001841 PROSITE:PS50089 SMART:SM00184 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0008270 InterPro:IPR013083 Gene3D:G3DSA:3.30.40.10 HSSP:Q9LRB7 EMBL:AC005223 eggNOG:NOG235630 HOGENOM:HBG749479 EMBL:AY039608 EMBL:AF424578 EMBL:BT000502 IPI:IPI00534528 PIR:F96597 RefSeq:NP_564693.1 UniGene:At.19898 ProteinModelPortal:Q9ZVU8 SMR:Q9ZVU8 STRING:Q9ZVU8 EnsemblPlants:AT1G55530.1 GeneID:842000 KEGG:ath:AT1G55530 TAIR:At1g55530 InParanoid:Q9ZVU8 OMA:FVEEMED PhylomeDB:Q9ZVU8 ProtClustDB:CLSN2917296 Genevestigator:Q9ZVU8 Uniprot:Q9ZVU8
Root	Isotig01340	63	16	1.848	3.27E-07	TAIR|locus:2193874 - symbol:AT1G55530 species:3702 "Arabidopsis thaliana" [GO:0008270 "zinc ion binding" evidence=IEA;ISS] InterPro:IPR001841 PROSITE:PS50089 SMART:SM00184 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0008270 InterPro:IPR013083 Gene3D:G3DSA:3.30.40.10 HSSP:Q9LRB7

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EMBL:AC005223 eggNOG:NOG235630 HOGENOM:HBG749479 EMBL:AY039608 EMBL:AF424578 EMBL:BT000502 IPI:IPI00534528 PIR:F96597 RefSeq:NP_564693.1 UniGene:At.19898 ProteinModelPortal:Q9ZVU8 SMR:Q9ZVU8 STRING:Q9ZVU8 EnsemblPlants:AT1G55530.1 GeneID:842000 KEGG:ath:AT1G55530 TAIR:At1g55530 InParanoid:Q9ZVU8 OMA:FVEEMED PhylomeDB:Q9ZVU8 ProtClustDB:CLSN2917296 Genevestigator:Q9ZVU8 Uniprot:Q9ZVU8
Root	Isotig01341	63	16	1.848	3.27E-07	TAIR|locus:2193874 - symbol:AT1G55530 species:3702 "Arabidopsis thaliana" [GO:0008270 "zinc ion binding" evidence=IEA;ISS] InterPro:IPR001841 PROSITE:PS50089 SMART:SM00184 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0008270 InterPro:IPR013083 Gene3D:G3DSA:3.30.40.10 HSSP:Q9LRB7 EMBL:AC005223 eggNOG:NOG235630 HOGENOM:HBG749479 EMBL:AY039608 EMBL:AF424578 EMBL:BT000502 IPI:IPI00534528 PIR:F96597 RefSeq:NP_564693.1 UniGene:At.19898 ProteinModelPortal:Q9ZVU8 SMR:Q9ZVU8 STRING:Q9ZVU8 EnsemblPlants:AT1G55530.1 GeneID:842000 KEGG:ath:AT1G55530 TAIR:At1g55530 InParanoid:Q9ZVU8 OMA:FVEEMED PhylomeDB:Q9ZVU8 ProtClustDB:CLSN2917296 Genevestigator:Q9ZVU8 Uniprot:Q9ZVU8
Root	Isotig01345	26	69	-1.537	9.31E-07	TAIR|locus:2178843 - symbol:AT5G58620 "AT5G58620" species:3702 "Arabidopsis thaliana" [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=TAS] InterPro:IPR002110 InterPro:IPR000571 Pfam:PF00642 PROSITE:PS50088 PROSITE:PS50103 SMART:SM00248 SMART:SM00356 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0006355 GO:GO:0003677 GO:GO:0008270 InterPro:IPR020683 Gene3D:G3DSA:1.25.40.20 Pfam:PF12796 SUPFAM:SSF48403 PROSITE:PS50297 EMBL:AB020755 eggNOG:NOG69137 HOGENOM:HBG594924 EMBL:AY054176 EMBL:AY062491 EMBL:AY103314 EMBL:BT002083 IPI:IPI00544490 RefSeq:NP_200670.1 UniGene:At.49189 UniGene:At.68520 ProteinModelPortal:Q9LUZ4 SMR:Q9LUZ4 IntAct:Q9LUZ4 PRIDE:Q9LUZ4 EnsemblPlants:AT5G58620.1 GeneID:835976 KEGG:ath:AT5G58620 TAIR:At5g58620 InParanoid:Q9LUZ4 OMA:RSCGSDG PhylomeDB:Q9LUZ4 ProtClustDB:CLSN2914838 ArrayExpress:Q9LUZ4 Genevestigator:Q9LUZ4 Uniprot:Q9LUZ4
Root	Isotig01346	27	66	-1.418	6.20E-06	TAIR|locus:2178843 - symbol:AT5G58620 "AT5G58620" species:3702 "Arabidopsis thaliana" [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=TAS] InterPro:IPR002110 InterPro:IPR000571 Pfam:PF00642 PROSITE:PS50088 PROSITE:PS50103 SMART:SM00248 SMART:SM00356 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0006355 GO:GO:0003677 GO:GO:0008270 InterPro:IPR020683 Gene3D:G3DSA:1.25.40.20 Pfam:PF12796 SUPFAM:SSF48403 PROSITE:PS50297 EMBL:AB020755 eggNOG:NOG69137 HOGENOM:HBG594924 EMBL:AY054176 EMBL:AY062491 EMBL:AY103314 EMBL:BT002083 IPI:IPI00544490 RefSeq:NP_200670.1 UniGene:At.49189 UniGene:At.68520 ProteinModelPortal:Q9LUZ4 SMR:Q9LUZ4 IntAct:Q9LUZ4 PRIDE:Q9LUZ4 EnsemblPlants:AT5G58620.1 GeneID:835976 KEGG:ath:AT5G58620 TAIR:At5g58620 InParanoid:Q9LUZ4 OMA:RSCGSDG PhylomeDB:Q9LUZ4 ProtClustDB:CLSN2914838 ArrayExpress:Q9LUZ4 Genevestigator:Q9LUZ4 Uniprot:Q9LUZ4
Root	Isotig01347	26	65	-1.451	5.07E-06	TAIR|locus:2178843 - symbol:AT5G58620 "AT5G58620" species:3702 "Arabidopsis thaliana" [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=TAS] InterPro:IPR002110 InterPro:IPR000571 Pfam:PF00642 PROSITE:PS50088 PROSITE:PS50103 SMART:SM00248 SMART:SM00356 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0006355 GO:GO:0003677 GO:GO:0008270 InterPro:IPR020683 Gene3D:G3DSA:1.25.40.20 Pfam:PF12796 SUPFAM:SSF48403 PROSITE:PS50297 EMBL:AB020755 eggNOG:NOG69137 HOGENOM:HBG594924 EMBL:AY054176 EMBL:AY062491 EMBL:AY103314 EMBL:BT002083 IPI:IPI00544490 RefSeq:NP_200670.1 UniGene:At.49189 UniGene:At.68520 ProteinModelPortal:Q9LUZ4 SMR:Q9LUZ4 IntAct:Q9LUZ4 PRIDE:Q9LUZ4 EnsemblPlants:AT5G58620.1 GeneID:835976 KEGG:ath:AT5G58620 TAIR:At5g58620 InParanoid:Q9LUZ4 OMA:RSCGSDG PhylomeDB:Q9LUZ4 ProtClustDB:CLSN2914838 ArrayExpress:Q9LUZ4 Genevestigator:Q9LUZ4 Uniprot:Q9LUZ4
Root	Isotig01348	23	71	-1.755	4.46E-08	TAIR|locus:2178843 - symbol:AT5G58620 "AT5G58620" species:3702 "Arabidopsis thaliana" [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=TAS] InterPro:IPR002110 InterPro:IPR000571 Pfam:PF00642 PROSITE:PS50088 PROSITE:PS50103 SMART:SM00248 SMART:SM00356 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0006355 GO:GO:0003677 GO:GO:0008270 InterPro:IPR020683 Gene3D:G3DSA:1.25.40.20 Pfam:PF12796 SUPFAM:SSF48403 PROSITE:PS50297 EMBL:AB020755 eggNOG:NOG69137

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						HOGENOM:HBG594924 EMBL:AY054176 EMBL:AY062491 EMBL:AY103314 EMBL:BT002083 IPI:IPI00544490 RefSeq:NP_200670.1 UniGene:At.49189 UniGene:At.68520 ProteinModelPortal:Q9LUZ4 SMR:Q9LUZ4 IntAct:Q9LUZ4 PRIDE:Q9LUZ4 EnsemblPlants:AT5G58620.1 GeneID:835976 KEGG:ath:AT5G58620 TAIR:At5g58620 InParanoid:Q9LUZ4 OMA:RSCGSDG PhylomeDB:Q9LUZ4 ProtClustDB:CLSN2914838 ArrayExpress:Q9LUZ4 Genevestigator:Q9LUZ4 Uniprot:Q9LUZ4
Root	Isotig01349	24	68	-1.631	3.67E-07	TAIR|locus:2178843 - symbol:AT5G58620 "AT5G58620" species:3702 "Arabidopsis thaliana" [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=TAS] InterPro:IPR002110 InterPro:IPR000571 Pfam:PF00642 PROSITE:PS50088 PROSITE:PS50103 SMART:SM00248 SMART:SM00356 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0006355 GO:GO:0003677 GO:GO:0008270 InterPro:IPR020683 Gene3D:G3DSA:1.25.40.20 Pfam:PF12796 SUPFAM:SSF48403 PROSITE:PS50297 EMBL:AB020755 eggNOG:NOG69137 HOGENOM:HBG594924 EMBL:AY054176 EMBL:AY062491 EMBL:AY103314 EMBL:BT002083 IPI:IPI00544490 RefSeq:NP_200670.1 UniGene:At.49189 UniGene:At.68520 ProteinModelPortal:Q9LUZ4 SMR:Q9LUZ4 IntAct:Q9LUZ4 PRIDE:Q9LUZ4 EnsemblPlants:AT5G58620.1 GeneID:835976 KEGG:ath:AT5G58620 TAIR:At5g58620 InParanoid:Q9LUZ4 OMA:RSCGSDG PhylomeDB:Q9LUZ4 ProtClustDB:CLSN2914838 ArrayExpress:Q9LUZ4 Genevestigator:Q9LUZ4 Uniprot:Q9LUZ4
Root	Isotig01350	30	67	-1.288	2.34E-05	TAIR|locus:2178843 - symbol:AT5G58620 "AT5G58620" species:3702 "Arabidopsis thaliana" [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=TAS] InterPro:IPR002110 InterPro:IPR000571 Pfam:PF00642 PROSITE:PS50088 PROSITE:PS50103 SMART:SM00248 SMART:SM00356 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0006355 GO:GO:0003677 GO:GO:0008270 InterPro:IPR020683 Gene3D:G3DSA:1.25.40.20 Pfam:PF12796 SUPFAM:SSF48403 PROSITE:PS50297 EMBL:AB020755 eggNOG:NOG69137 HOGENOM:HBG594924 EMBL:AY054176 EMBL:AY062491 EMBL:AY103314 EMBL:BT002083 IPI:IPI00544490 RefSeq:NP_200670.1 UniGene:At.49189 UniGene:At.68520 ProteinModelPortal:Q9LUZ4 SMR:Q9LUZ4 IntAct:Q9LUZ4 PRIDE:Q9LUZ4 EnsemblPlants:AT5G58620.1 GeneID:835976 KEGG:ath:AT5G58620 TAIR:At5g58620 InParanoid:Q9LUZ4 OMA:RSCGSDG PhylomeDB:Q9LUZ4 ProtClustDB:CLSN2914838 ArrayExpress:Q9LUZ4 Genevestigator:Q9LUZ4 Uniprot:Q9LUZ4
Root	Isotig01351	31	64	-1.175	0.000120563	TAIR|locus:2178843 - symbol:AT5G58620 "AT5G58620" species:3702 "Arabidopsis thaliana" [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=TAS] InterPro:IPR002110 InterPro:IPR000571 Pfam:PF00642 PROSITE:PS50088 PROSITE:PS50103 SMART:SM00248 SMART:SM00356 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0006355 GO:GO:0003677 GO:GO:0008270 InterPro:IPR020683 Gene3D:G3DSA:1.25.40.20 Pfam:PF12796 SUPFAM:SSF48403 PROSITE:PS50297 EMBL:AB020755 eggNOG:NOG69137 HOGENOM:HBG594924 EMBL:AY054176 EMBL:AY062491 EMBL:AY103314 EMBL:BT002083 IPI:IPI00544490 RefSeq:NP_200670.1 UniGene:At.49189 UniGene:At.68520 ProteinModelPortal:Q9LUZ4 SMR:Q9LUZ4 IntAct:Q9LUZ4 PRIDE:Q9LUZ4 EnsemblPlants:AT5G58620.1 GeneID:835976 KEGG:ath:AT5G58620 TAIR:At5g58620 InParanoid:Q9LUZ4 OMA:RSCGSDG PhylomeDB:Q9LUZ4 ProtClustDB:CLSN2914838 ArrayExpress:Q9LUZ4 Genevestigator:Q9LUZ4 Uniprot:Q9LUZ4
Root	Isotig01352	23	67	-1.672	2.81E-07	TAIR|locus:2178843 - symbol:AT5G58620 "AT5G58620" species:3702 "Arabidopsis thaliana" [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=TAS] InterPro:IPR002110 InterPro:IPR000571 Pfam:PF00642 PROSITE:PS50088 PROSITE:PS50103 SMART:SM00248 SMART:SM00356 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0006355 GO:GO:0003677 GO:GO:0008270 InterPro:IPR020683 Gene3D:G3DSA:1.25.40.20 Pfam:PF12796 SUPFAM:SSF48403 PROSITE:PS50297 EMBL:AB020755 eggNOG:NOG69137 HOGENOM:HBG594924 EMBL:AY054176 EMBL:AY062491 EMBL:AY103314 EMBL:BT002083 IPI:IPI00544490 RefSeq:NP_200670.1 UniGene:At.49189 UniGene:At.68520 ProteinModelPortal:Q9LUZ4 SMR:Q9LUZ4 IntAct:Q9LUZ4 PRIDE:Q9LUZ4 EnsemblPlants:AT5G58620.1 GeneID:835976 KEGG:ath:AT5G58620 TAIR:At5g58620 InParanoid:Q9LUZ4 OMA:RSCGSDG PhylomeDB:Q9LUZ4 ProtClustDB:CLSN2914838 ArrayExpress:Q9LUZ4 Genevestigator:Q9LUZ4 Uniprot:Q9LUZ4
Root	Isotig01353	30	63	-1.199	0.000105278	TAIR|locus:2178843 - symbol:AT5G58620 "AT5G58620" species:3702 "Arabidopsis thaliana" [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=TAS] InterPro:IPR002110 InterPro:IPR000571 Pfam:PF00642 PROSITE:PS50088

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						PROSITE:PS50103 SMART:SM00248 SMART:SM00356 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0006355 GO:GO:0003677 GO:GO:0008270 InterPro:IPR020683 Gene3D:G3DSA:1.25.40.20 Pfam:PF12796 SUPFAM:SSF48403 PROSITE:PS50297 EMBL:AB020755 eggNOG:NOG69137 HOGENOM:HBG594924 EMBL:AY054176 EMBL:AY062491 EMBL:AY103314 EMBL:BT002083 IPI:IPI00544490 RefSeq:NP_200670.1 UniGene:At.49189 UniGene:At.68520 ProteinModelPortal:Q9LUZ4 SMR:Q9LUZ4 IntAct:Q9LUZ4 PRIDE:Q9LUZ4 EnsemblPlants:AT5G58620.1 GeneID:835976 KEGG:ath:AT5G58620 TAIR:At5g58620 InParanoid:Q9LUZ4 OMA:RSCGSDG PhylomeDB:Q9LUZ4 ProtClustDB:CLSN2914838 ArrayExpress:Q9LUZ4 Genevestigator:Q9LUZ4 Uniprot:Q9LUZ4
Root	Isotig01354	53	20	1.277	0.000352505	TAIR|locus:2052005 - symbol:OZF1 "AT2G19810" species:3702 "Arabidopsis thaliana" [GO:0003676 "nucleic acid binding" evidence=ISS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=TAS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0006979 "response to oxidative stress" evidence=IMP] InterPro:IPR000571 PROSITE:PS50103 SMART:SM00356 GO:GO:0005886 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0006979 GO:GO:0006355 GO:GO:0003677 GO:GO:0008270 EMBL:AC005169 EMBL:AY136395 EMBL:BT002114 EMBL:AY084253 IPI:IPI00535519 PIR:D84581 RefSeq:NP_179571.1 UniGene:At.12895 ProteinModelPortal:O82199 SMR:O82199 PRIDE:O82199 EnsemblPlants:AT2G19810.1 GeneID:816500 KEGG:ath:AT2G19810 TAIR:At2g19810 eggNOG:NOG288631 HOGENOM:HBG744620 InParanoid:O82199 OMA:WENGLEE PhylomeDB:O82199 ProtClustDB:CLSN2691160 ArrayExpress:O82199 Genevestigator:O82199 Uniprot:O82199
Root	Isotig01355	51	20	1.222	0.000710992	TAIR|locus:2052005 - symbol:OZF1 "AT2G19810" species:3702 "Arabidopsis thaliana" [GO:0003676 "nucleic acid binding" evidence=ISS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=TAS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0006979 "response to oxidative stress" evidence=IMP] InterPro:IPR000571 PROSITE:PS50103 SMART:SM00356 GO:GO:0005886 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0006979 GO:GO:0006355 GO:GO:0003677 GO:GO:0008270 EMBL:AC005169 EMBL:AY136395 EMBL:BT002114 EMBL:AY084253 IPI:IPI00535519 PIR:D84581 RefSeq:NP_179571.1 UniGene:At.12895 ProteinModelPortal:O82199 SMR:O82199 PRIDE:O82199 EnsemblPlants:AT2G19810.1 GeneID:816500 KEGG:ath:AT2G19810 TAIR:At2g19810 eggNOG:NOG288631 HOGENOM:HBG744620 InParanoid:O82199 OMA:WENGLEE PhylomeDB:O82199 ProtClustDB:CLSN2691160 ArrayExpress:O82199 Genevestigator:O82199 Uniprot:O82199
Root	Isotig01356	46	17	1.307	0.000699665	TAIR|locus:2052005 - symbol:OZF1 "AT2G19810" species:3702 "Arabidopsis thaliana" [GO:0003676 "nucleic acid binding" evidence=ISS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=TAS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0006979 "response to oxidative stress" evidence=IMP] InterPro:IPR000571 PROSITE:PS50103 SMART:SM00356 GO:GO:0005886 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0006979 GO:GO:0006355 GO:GO:0003677 GO:GO:0008270 EMBL:AC005169 EMBL:AY136395 EMBL:BT002114 EMBL:AY084253 IPI:IPI00535519 PIR:D84581 RefSeq:NP_179571.1 UniGene:At.12895 ProteinModelPortal:O82199 SMR:O82199 PRIDE:O82199 EnsemblPlants:AT2G19810.1 GeneID:816500 KEGG:ath:AT2G19810 TAIR:At2g19810 eggNOG:NOG288631 HOGENOM:HBG744620 InParanoid:O82199 OMA:WENGLEE PhylomeDB:O82199 ProtClustDB:CLSN2691160 ArrayExpress:O82199 Genevestigator:O82199 Uniprot:O82199
Root	Isotig01358	51	20	1.222	0.000710992	TAIR|locus:2052005 - symbol:OZF1 "AT2G19810" species:3702 "Arabidopsis thaliana" [GO:0003676 "nucleic acid binding" evidence=ISS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=TAS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0006979 "response to oxidative stress" evidence=IMP] InterPro:IPR000571 PROSITE:PS50103 SMART:SM00356 GO:GO:0005886 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0006979 GO:GO:0006355 GO:GO:0003677 GO:GO:0008270 EMBL:AC005169 EMBL:AY136395 EMBL:BT002114 EMBL:AY084253 IPI:IPI00535519 PIR:D84581 RefSeq:NP_179571.1 UniGene:At.12895 ProteinModelPortal:O82199 SMR:O82199 PRIDE:O82199 EnsemblPlants:AT2G19810.1 GeneID:816500 KEGG:ath:AT2G19810 TAIR:At2g19810 eggNOG:NOG288631 HOGENOM:HBG744620 InParanoid:O82199 OMA:WENGLEE PhylomeDB:O82199 ProtClustDB:CLSN2691160 ArrayExpress:O82199 Genevestigator:O82199 Uniprot:O82199

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig01360	48	18	1.286	0.000627857	TAIR|locus:2052005 - symbol:OZF1 "AT2G19810" species:3702 "Arabidopsis thaliana" [GO:0003676 "nucleic acid binding" evidence=ISS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=TAS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0006979 "response to oxidative stress" evidence=IMP] InterPro:IPR000571 PROSITE:PS50103 SMART:SM00356 GO:GO:0005886 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0006979 GO:GO:0006355 GO:GO:0003677 GO:GO:0008270 EMBL:AC005169 EMBL:AY136395 EMBL:BT002114 EMBL:AY084253 IPI:IPI00535519 PIR:D84581 RefSeq:NP_179571.1 UniGene:At.12895 ProteinModelPortal:O82199 SMR:O82199 PRIDE:O82199 EnsemblPlants:AT2G19810.1 GeneID:816500 KEGG:ath:AT2G19810 TAIR:At2g19810 eggNOG:NOG288631 HOGENOM:HBG744620 InParanoid:O82199 OMA:WENGLEE PhylomeDB:O82199 ProtClustDB:CLSN2691160 ArrayExpress:O82199 Genevestigator:O82199 Uniprot:O82199
Root	Isotig01368	16	55	-1.910	3.35E-07	TAIR|locus:2170867 - symbol:APS4 "AT5G43780" species:3702 "Arabidopsis thaliana" [GO:0004781 "sulfate adenylyltransferase (ATP) activity" evidence=ISS;IMP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0000103 "sulfate assimilation" evidence=TAS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] InterPro:IPR002650 GO:GO:0005739 GO:GO:0005524 GO:GO:0009570 EMBL:CP002688 EMBL:AB026651 GO:GO:0000103 InterPro:IPR014729 Gene3D:G3DSA:3.40.50.620 KO:K13811 ProtClustDB:CLSN2684174 GO:GO:0004781 InterPro:IPR015947 SUPFAM:SSF88697 TIGRFAMs:TIGR00339 EMBL:AF110407 EMBL:AJ012586 EMBL:AY072193 EMBL:AY117323 EMBL:AK226204 IPI:IPI00531868 PIR:T52659 RefSeq:NP_199191.1 UniGene:At.23710 UniGene:At.66691 ProteinModelPortal:Q9S7D8 SMR:Q9S7D8 STRING:Q9S7D8 PRIDE:Q9S7D8 GeneID:834400 KEGG:ath:AT5G43780 TAIR:At5g43780 InParanoid:Q9S7D8 OMA:GITPMFI PhylomeDB:Q9S7D8 ArrayExpress:Q9S7D8 Genevestigator:Q9S7D8 Uniprot:Q9S7D8
Root	Isotig01370	16	55	-1.910	3.35E-07	TAIR|locus:2170867 - symbol:APS4 "AT5G43780" species:3702 "Arabidopsis thaliana" [GO:0004781 "sulfate adenylyltransferase (ATP) activity" evidence=ISS;IMP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0000103 "sulfate assimilation" evidence=TAS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] InterPro:IPR002650 GO:GO:0005739 GO:GO:0005524 GO:GO:0009570 EMBL:CP002688 EMBL:AB026651 GO:GO:0000103 InterPro:IPR014729 Gene3D:G3DSA:3.40.50.620 KO:K13811 ProtClustDB:CLSN2684174 GO:GO:0004781 InterPro:IPR015947 SUPFAM:SSF88697 TIGRFAMs:TIGR00339 EMBL:AF110407 EMBL:AJ012586 EMBL:AY072193 EMBL:AY117323 EMBL:AK226204 IPI:IPI00531868 PIR:T52659 RefSeq:NP_199191.1 UniGene:At.23710 UniGene:At.66691 ProteinModelPortal:Q9S7D8 SMR:Q9S7D8 STRING:Q9S7D8 PRIDE:Q9S7D8 GeneID:834400 KEGG:ath:AT5G43780 TAIR:At5g43780 InParanoid:Q9S7D8 OMA:GITPMFI PhylomeDB:Q9S7D8 ArrayExpress:Q9S7D8 Genevestigator:Q9S7D8 Uniprot:Q9S7D8
Root	Isotig01371	16	55	-1.910	3.35E-07	TAIR|locus:2170867 - symbol:APS4 "AT5G43780" species:3702 "Arabidopsis thaliana" [GO:0004781 "sulfate adenylyltransferase (ATP) activity" evidence=ISS;IMP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0000103 "sulfate assimilation" evidence=TAS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] InterPro:IPR002650 GO:GO:0005739 GO:GO:0005524 GO:GO:0009570 EMBL:CP002688 EMBL:AB026651 GO:GO:0000103 InterPro:IPR014729 Gene3D:G3DSA:3.40.50.620 KO:K13811 ProtClustDB:CLSN2684174 GO:GO:0004781 InterPro:IPR015947 SUPFAM:SSF88697 TIGRFAMs:TIGR00339 EMBL:AF110407 EMBL:AJ012586 EMBL:AY072193 EMBL:AY117323 EMBL:AK226204 IPI:IPI00531868 PIR:T52659 RefSeq:NP_199191.1 UniGene:At.23710 UniGene:At.66691 ProteinModelPortal:Q9S7D8 SMR:Q9S7D8 STRING:Q9S7D8 PRIDE:Q9S7D8 GeneID:834400 KEGG:ath:AT5G43780 TAIR:At5g43780 InParanoid:Q9S7D8 OMA:GITPMFI PhylomeDB:Q9S7D8 ArrayExpress:Q9S7D8 Genevestigator:Q9S7D8 Uniprot:Q9S7D8
Root	Isotig01372	4	53	-3.857	5.31E-13	TAIR|locus:2179887 - symbol:G6PD2 "AT5G13110" species:3702 "Arabidopsis thaliana" [GO:0004345 "glucose-6-phosphate dehydrogenase activity" evidence=ISS;IDA] [GO:0006006 "glucose metabolic process" evidence=ISS;IDA] [GO:0009051 "pentose-phosphate shunt, oxidative branch" evidence=IDA] [GO:0009507 "chloroplast" evidence=ISS] [GO:0009570 "chloroplast stroma" evidence=IDA] InterPro:IPR001282 InterPro:IPR016040 InterPro:IPR019796 InterPro:IPR022674 InterPro:IPR022675 Pfam:PF00479 Pfam:PF02781 PRINTS:PR00079 PROSITE:PS00069 GO:GO:0009570 EMBL:CP002688 GenomeReviews:BA000015_GR Gene3D:G3DSA:3.40.50.720 GO:GO:0050661 GO:GO:0009051 EMBL:AL391711 eggNOG:COG0364 HOGENOM:HBG322449 KO:K00036 GO:GO:0004345 PANTHER:PTHR23429 TIGRFAMs:TIGR00871

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EMBL:AY065042 EMBL:X84229 IPI:IPI00531306 PIR:S71245 RefSeq:NP_196815.2 UniGene:At.61 ProteinModelPortal:Q9FY99 SMR:Q9FY99 IntAct:Q9FY99 STRING:Q9FY99 PRIDE:Q9FY99 EnsemblPlants:AT5G13110.1 GeneID:831150 KEGG:ath:AT5G13110 TAIR:At5g13110 InParanoid:Q9FY99 OMA:FANQMFE PhylomeDB:Q9FY99 ProtClustDB:PLN02333 ArrayExpress:Q9FY99 Genevestigator:Q9FY99 GermOnline:AT5G13110 Uniprot:Q9FY99
Root	Isotig01373	5	55	-3.588	7.73E-13	TAIR|locus:2179887 - symbol:G6PD2 "AT5G13110" species:3702 "Arabidopsis thaliana" [GO:0004345 "glucose-6-phosphate dehydrogenase activity" evidence=ISS;IDA] [GO:0006006 "glucose metabolic process" evidence=ISS;IDA] [GO:0009051 "pentose-phosphate shunt, oxidative branch" evidence=IDA] [GO:0009507 "chloroplast" evidence=ISS] [GO:0009570 "chloroplast stroma" evidence=IDA] InterPro:IPR001282 InterPro:IPR016040 InterPro:IPR019796 InterPro:IPR022674 InterPro:IPR022675 Pfam:PF00479 Pfam:PF02781 PRINTS:PR00079 PROSITE:PS00069 GO:GO:0009570 EMBL:CP002688 GenomeReviews:BA000015_GR Gene3D:G3DSA:3.40.50.720 GO:GO:0050661 GO:GO:0009051 EMBL:AL391711 eggNOG:COG0364 HOGENOM:HBG322449 KO:K00036 GO:GO:0004345 PANTHER:PTHR23429 TIGRFAMs:TIGR00871 EMBL:AY065042 EMBL:X84229 IPI:IPI00531306 PIR:S71245 RefSeq:NP_196815.2 UniGene:At.61 ProteinModelPortal:Q9FY99 SMR:Q9FY99 IntAct:Q9FY99 STRING:Q9FY99 PRIDE:Q9FY99 EnsemblPlants:AT5G13110.1 GeneID:831150 KEGG:ath:AT5G13110 TAIR:At5g13110 InParanoid:Q9FY99 OMA:FANQMFE PhylomeDB:Q9FY99 ProtClustDB:PLN02333 ArrayExpress:Q9FY99 Genevestigator:Q9FY99 GermOnline:AT5G13110 Uniprot:Q9FY99
Root	Isotig01374	4	54	-3.884	2.85E-13	TAIR|locus:2179887 - symbol:G6PD2 "AT5G13110" species:3702 "Arabidopsis thaliana" [GO:0004345 "glucose-6-phosphate dehydrogenase activity" evidence=ISS;IDA] [GO:0006006 "glucose metabolic process" evidence=ISS;IDA] [GO:0009051 "pentose-phosphate shunt, oxidative branch" evidence=IDA] [GO:0009507 "chloroplast" evidence=ISS] [GO:0009570 "chloroplast stroma" evidence=IDA] InterPro:IPR001282 InterPro:IPR016040 InterPro:IPR019796 InterPro:IPR022674 InterPro:IPR022675 Pfam:PF00479 Pfam:PF02781 PRINTS:PR00079 PROSITE:PS00069 GO:GO:0009570 EMBL:CP002688 GenomeReviews:BA000015_GR Gene3D:G3DSA:3.40.50.720 GO:GO:0050661 GO:GO:0009051 EMBL:AL391711 eggNOG:COG0364 HOGENOM:HBG322449 KO:K00036 GO:GO:0004345 PANTHER:PTHR23429 TIGRFAMs:TIGR00871 EMBL:AY065042 EMBL:X84229 IPI:IPI00531306 PIR:S71245 RefSeq:NP_196815.2 UniGene:At.61 ProteinModelPortal:Q9FY99 SMR:Q9FY99 IntAct:Q9FY99 STRING:Q9FY99 PRIDE:Q9FY99 EnsemblPlants:AT5G13110.1 GeneID:831150 KEGG:ath:AT5G13110 TAIR:At5g13110 InParanoid:Q9FY99 OMA:FANQMFE PhylomeDB:Q9FY99 ProtClustDB:PLN02333 ArrayExpress:Q9FY99 Genevestigator:Q9FY99 GermOnline:AT5G13110 Uniprot:Q9FY99
Root	Isotig01375	5	56	-3.614	4.16E-13	TAIR|locus:2179887 - symbol:G6PD2 "AT5G13110" species:3702 "Arabidopsis thaliana" [GO:0004345 "glucose-6-phosphate dehydrogenase activity" evidence=ISS;IDA] [GO:0006006 "glucose metabolic process" evidence=ISS;IDA] [GO:0009051 "pentose-phosphate shunt, oxidative branch" evidence=IDA] [GO:0009507 "chloroplast" evidence=ISS] [GO:0009570 "chloroplast stroma" evidence=IDA] InterPro:IPR001282 InterPro:IPR016040 InterPro:IPR019796 InterPro:IPR022674 InterPro:IPR022675 Pfam:PF00479 Pfam:PF02781 PRINTS:PR00079 PROSITE:PS00069 GO:GO:0009570 EMBL:CP002688 GenomeReviews:BA000015_GR Gene3D:G3DSA:3.40.50.720 GO:GO:0050661 GO:GO:0009051 EMBL:AL391711 eggNOG:COG0364 HOGENOM:HBG322449 KO:K00036 GO:GO:0004345 PANTHER:PTHR23429 TIGRFAMs:TIGR00871 EMBL:AY065042 EMBL:X84229 IPI:IPI00531306 PIR:S71245 RefSeq:NP_196815.2 UniGene:At.61 ProteinModelPortal:Q9FY99 SMR:Q9FY99 IntAct:Q9FY99 STRING:Q9FY99 PRIDE:Q9FY99 EnsemblPlants:AT5G13110.1 GeneID:831150 KEGG:ath:AT5G13110 TAIR:At5g13110 InParanoid:Q9FY99 OMA:FANQMFE PhylomeDB:Q9FY99 ProtClustDB:PLN02333 ArrayExpress:Q9FY99 Genevestigator:Q9FY99 GermOnline:AT5G13110 Uniprot:Q9FY99
Root	Isotig01376	4	53	-3.857	5.31E-13	TAIR|locus:2179887 - symbol:G6PD2 "AT5G13110" species:3702 "Arabidopsis thaliana" [GO:0004345 "glucose-6-phosphate dehydrogenase activity" evidence=ISS;IDA] [GO:0006006 "glucose metabolic process" evidence=ISS;IDA] [GO:0009051 "pentose-phosphate shunt, oxidative branch" evidence=IDA] [GO:0009507 "chloroplast" evidence=ISS] [GO:0009570 "chloroplast stroma" evidence=IDA] InterPro:IPR001282 InterPro:IPR016040 InterPro:IPR019796 InterPro:IPR022674 InterPro:IPR022675 Pfam:PF00479 Pfam:PF02781 PRINTS:PR00079 PROSITE:PS00069 GO:GO:0009570 EMBL:CP002688 GenomeReviews:BA000015_GR Gene3D:G3DSA:3.40.50.720 GO:GO:0050661 GO:GO:0009051 EMBL:AL391711 eggNOG:COG0364 HOGENOM:HBG322449 KO:K00036 GO:GO:0004345 PANTHER:PTHR23429 TIGRFAMs:TIGR00871

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EMBL:AY065042 EMBL:X84229 IPI:IPI00531306 PIR:S71245 RefSeq:NP_196815.2 UniGene:At.61 ProteinModelPortal:Q9FY99 SMR:Q9FY99 IntAct:Q9FY99 STRING:Q9FY99 PRIDE:Q9FY99 EnsemblPlants:AT5G13110.1 GeneID:831150 KEGG:ath:AT5G13110 TAIR:At5g13110 InParanoid:Q9FY99 OMA:FANQMFE PhylomeDB:Q9FY99 ProtClustDB:PLN02333 ArrayExpress:Q9FY99 Genevestigator:Q9FY99 GermOnline:AT5G13110 Uniprot:Q9FY99
Root	Isotig01377	5	55	-3.588	7.73E-13	TAIR|locus:2179887 - symbol:G6PD2 "AT5G13110" species:3702 "Arabidopsis thaliana" [GO:0004345 "glucose-6-phosphate dehydrogenase activity" evidence=ISS;IDA] [GO:0006006 "glucose metabolic process" evidence=ISS;IDA] [GO:0009051 "pentose-phosphate shunt, oxidative branch" evidence=IDA] [GO:0009507 "chloroplast" evidence=ISS] [GO:0009570 "chloroplast stroma" evidence=IDA] InterPro:IPR001282 InterPro:IPR016040 InterPro:IPR019796 InterPro:IPR022674 InterPro:IPR022675 Pfam:PF00479 Pfam:PF02781 PRINTS:PR00079 PROSITE:PS00069 GO:GO:0009570 EMBL:CP002688 GenomeReviews:BA000015_GR Gene3D:G3DSA:3.40.50.720 GO:GO:0050661 GO:GO:0009051 EMBL:AL391711 eggNOG:COG0364 HOGENOM:HBG322449 KO:K00036 GO:GO:0004345 PANTHER:PTHR23429 TIGRFAMs:TIGR00871 EMBL:AY065042 EMBL:X84229 IPI:IPI00531306 PIR:S71245 RefSeq:NP_196815.2 UniGene:At.61 ProteinModelPortal:Q9FY99 SMR:Q9FY99 IntAct:Q9FY99 STRING:Q9FY99 PRIDE:Q9FY99 EnsemblPlants:AT5G13110.1 GeneID:831150 KEGG:ath:AT5G13110 TAIR:At5g13110 InParanoid:Q9FY99 OMA:FANQMFE PhylomeDB:Q9FY99 ProtClustDB:PLN02333 ArrayExpress:Q9FY99 Genevestigator:Q9FY99 GermOnline:AT5G13110 Uniprot:Q9FY99
Root	Isotig01378	1	26	-4.829	8.91E-08	TAIR|locus:2179887 - symbol:G6PD2 "AT5G13110" species:3702 "Arabidopsis thaliana" [GO:0004345 "glucose-6-phosphate dehydrogenase activity" evidence=ISS;IDA] [GO:0006006 "glucose metabolic process" evidence=ISS;IDA] [GO:0009051 "pentose-phosphate shunt, oxidative branch" evidence=IDA] [GO:0009507 "chloroplast" evidence=ISS] [GO:0009570 "chloroplast stroma" evidence=IDA] InterPro:IPR001282 InterPro:IPR016040 InterPro:IPR019796 InterPro:IPR022674 InterPro:IPR022675 Pfam:PF00479 Pfam:PF02781 PRINTS:PR00079 PROSITE:PS00069 GO:GO:0009570 EMBL:CP002688 GenomeReviews:BA000015_GR Gene3D:G3DSA:3.40.50.720 GO:GO:0050661 GO:GO:0009051 EMBL:AL391711 eggNOG:COG0364 HOGENOM:HBG322449 KO:K00036 GO:GO:0004345 PANTHER:PTHR23429 TIGRFAMs:TIGR00871 EMBL:AY065042 EMBL:X84229 IPI:IPI00531306 PIR:S71245 RefSeq:NP_196815.2 UniGene:At.61 ProteinModelPortal:Q9FY99 SMR:Q9FY99 IntAct:Q9FY99 STRING:Q9FY99 PRIDE:Q9FY99 EnsemblPlants:AT5G13110.1 GeneID:831150 KEGG:ath:AT5G13110 TAIR:At5g13110 InParanoid:Q9FY99 OMA:FANQMFE PhylomeDB:Q9FY99 ProtClustDB:PLN02333 ArrayExpress:Q9FY99 Genevestigator:Q9FY99 GermOnline:AT5G13110 Uniprot:Q9FY99
Root	Isotig01379	2	28	-3.936	1.29E-07	TAIR|locus:2179887 - symbol:G6PD2 "AT5G13110" species:3702 "Arabidopsis thaliana" [GO:0004345 "glucose-6-phosphate dehydrogenase activity" evidence=ISS;IDA] [GO:0006006 "glucose metabolic process" evidence=ISS;IDA] [GO:0009051 "pentose-phosphate shunt, oxidative branch" evidence=IDA] [GO:0009507 "chloroplast" evidence=ISS] [GO:0009570 "chloroplast stroma" evidence=IDA] InterPro:IPR001282 InterPro:IPR016040 InterPro:IPR019796 InterPro:IPR022674 InterPro:IPR022675 Pfam:PF00479 Pfam:PF02781 PRINTS:PR00079 PROSITE:PS00069 GO:GO:0009570 EMBL:CP002688 GenomeReviews:BA000015_GR Gene3D:G3DSA:3.40.50.720 GO:GO:0050661 GO:GO:0009051 EMBL:AL391711 eggNOG:COG0364 HOGENOM:HBG322449 KO:K00036 GO:GO:0004345 PANTHER:PTHR23429 TIGRFAMs:TIGR00871 EMBL:AY065042 EMBL:X84229 IPI:IPI00531306 PIR:S71245 RefSeq:NP_196815.2 UniGene:At.61 ProteinModelPortal:Q9FY99 SMR:Q9FY99 IntAct:Q9FY99 STRING:Q9FY99 PRIDE:Q9FY99 EnsemblPlants:AT5G13110.1 GeneID:831150 KEGG:ath:AT5G13110 TAIR:At5g13110 InParanoid:Q9FY99 OMA:FANQMFE PhylomeDB:Q9FY99 ProtClustDB:PLN02333 ArrayExpress:Q9FY99 Genevestigator:Q9FY99 GermOnline:AT5G13110 Uniprot:Q9FY99
Root	Isotig01384	44	11	1.871	1.68E-05	TAIR|locus:2029416 - symbol:AT1G77840 species:3702 "Arabidopsis thaliana" [GO:0003743 "translation initiation factor activity" evidence=IEA;ISS] [GO:0006413 "translational initiation" evidence=IEA] [GO:0006446 "regulation of translational initiation" evidence=ISS] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] InterPro:IPR002735 InterPro:IPR003307 InterPro:IPR016021 InterPro:IPR016024 InterPro:IPR016189 InterPro:IPR016190 Pfam:PF01873 Pfam:PF02020 PROSITE:PS51363 SMART:SM00515 SMART:SM00653 GO:GO:0005525 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005634 GO:GO:0005737 SUPFAM:SSF48371 GO:GO:0003743 GO:GO:0016070 EMBL:AC009243 EMBL:AC012193 Gene3D:G3DSA:1.25.40.180 eggNOG:COG1601 Gene3D:G3DSA:3.30.30.50 SUPFAM:SSF100966

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						SUPFAM:SSF75689 HOGENOM:HBG559646 KO:K03262 ProtClustDB:CLSN2715102 EMBL:AY062694 EMBL:AY065097 EMBL:AY114664 EMBL:BT002163 IPI:IPI00536490 RefSeq:NP_177907.1 UniGene:At.27261 ProteinModelPortal:Q9S825 SMR:Q9S825 STRING:Q9S825 PRIDE:Q9S825 DNASU:844119 EnsemblPlants:AT1G77840.1 GeneID:844119 KEGG:ath:AT1G77840 TAIR:At1g77840 InParanoid:Q9S825 OMA:WKNVKPF PhylomeDB:Q9S825 ArrayExpress:Q9S825 Genevestigator:Q9S825 GermOnline:AT1G77840 Uniprot:Q9S825
Root	Isotig01385	43	11	1.838	2.63E-05	TAIR|locus:2029416 - symbol:AT1G77840 species:3702 "Arabidopsis thaliana" [GO:0003743 "translation initiation factor activity" evidence=IEA;ISS] [GO:0006413 "translational initiation" evidence=IEA] [GO:0006446 "regulation of translational initiation" evidence=ISS] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] InterPro:IPR002735 InterPro:IPR003307 InterPro:IPR016021 InterPro:IPR016024 InterPro:IPR016189 InterPro:IPR016190 Pfam:PF01873 Pfam:PF02020 PROSITE:PS51363 SMART:SM00515 SMART:SM00653 GO:GO:0005525 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005634 GO:GO:0005737 SUPFAM:SSF48371 GO:GO:0003743 GO:GO:0016070 EMBL:AC009243 EMBL:AC012193 Gene3D:G3DSA:1.25.40.180 eggNOG:COG1601 Gene3D:G3DSA:3.30.30.50 SUPFAM:SSF100966 SUPFAM:SSF75689 HOGENOM:HBG559646 KO:K03262 ProtClustDB:CLSN2715102 EMBL:AY062694 EMBL:AY065097 EMBL:AY114664 EMBL:BT002163 IPI:IPI00536490 RefSeq:NP_177907.1 UniGene:At.27261 ProteinModelPortal:Q9S825 SMR:Q9S825 STRING:Q9S825 PRIDE:Q9S825 DNASU:844119 EnsemblPlants:AT1G77840.1 GeneID:844119 KEGG:ath:AT1G77840 TAIR:At1g77840 InParanoid:Q9S825 OMA:WKNVKPF PhylomeDB:Q9S825 ArrayExpress:Q9S825 Genevestigator:Q9S825 GermOnline:AT1G77840 Uniprot:Q9S825
Root	Isotig01386	33	10	1.593	0.000866735	TAIR|locus:2196376 - symbol:AT1G36730 species:3702 "Arabidopsis thaliana" [GO:0003743 "translation initiation factor activity" evidence=IEA;ISS] [GO:0006413 "translational initiation" evidence=IEA] [GO:0006446 "regulation of translational initiation" evidence=ISS] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR002735 InterPro:IPR003307 InterPro:IPR016021 InterPro:IPR016024 InterPro:IPR016189 InterPro:IPR016190 Pfam:PF01873 Pfam:PF02020 PROSITE:PS51363 SMART:SM00515 SMART:SM00653 GO:GO:0005525 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 SUPFAM:SSF48371 GO:GO:0003743 GO:GO:0016070 Gene3D:G3DSA:1.25.40.180 UniGene:At.3809 eggNOG:COG1601 Gene3D:G3DSA:3.30.30.50 SUPFAM:SSF100966 SUPFAM:SSF75689 EMBL:AC025782 EMBL:AY056208 EMBL:AY064061 EMBL:AY096371 IPI:IPI00524003 PIR:C86487 RefSeq:NP_174877.1 UniGene:At.22980 UniGene:At.67142 ProteinModelPortal:Q9C8F1 SMR:Q9C8F1 PRIDE:Q9C8F1 EnsemblPlants:AT1G36730.1 GeneID:840582 KEGG:ath:AT1G36730 TAIR:At1g36730 HOGENOM:HBG559646 InParanoid:Q9C8F1 KO:K03262 OMA:HENGNSK PhylomeDB:Q9C8F1 ProtClustDB:CLSN2715102 ArrayExpress:Q9C8F1 Genevestigator:Q9C8F1 GermOnline:AT1G36730 Uniprot:Q9C8F1
Root	Isotig01404	0	12	-4.714	0.000297064	TAIR|locus:2066286 - symbol:PLA2A "AT2G26560" species:3702 "Arabidopsis thaliana" [GO:0045735 "nutrient reservoir activity" evidence=ISS] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0006629 "lipid metabolic process" evidence=IDA] [GO:0009626 "plant-type hypersensitive response" evidence=IEP;IMP] [GO:0016020 "membrane" evidence=IDA] [GO:0016298 "lipase activity" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0008219 "cell death" evidence=IGI] [GO:0031408 "oxylipin biosynthetic process" evidence=IMP] [GO:0051607 "defense response to virus" evidence=IMP] [GO:0071456 "cellular response to hypoxia" evidence=IEP] InterPro:IPR002641 InterPro:IPR016035 Pfam:PF01734 GO:GO:0046686 GO:GO:0005737 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0016020 GO:GO:0071456 GO:GO:0051607 GO:GO:0016298 GO:GO:0009626 GO:GO:0031408 EMBL:AC002505 SUPFAM:SSF52151 eggNOG:COG3621 HSSP:Q8LPW4 HOGENOM:HBG581721 EMBL:AY062644 EMBL:AY093305 IPI:IPI00536283 PIR:T00989 RefSeq:NP_180224.1 UniGene:At.12388 ProteinModelPortal:O48723 SMR:O48723 IntAct:O48723 STRING:O48723 PRIDE:O48723 DNASU:817197 EnsemblPlants:AT2G26560.1 GeneID:817197 KEGG:ath:AT2G26560 TAIR:At2g26560 InParanoid:O48723 OMA:NENAYET PhylomeDB:O48723 ProtClustDB:CLSN2913024 ArrayExpress:O48723 Genevestigator:O48723 Uniprot:O48723
Root	Isotig01405	0	12	-4.714	0.000297064	TAIR|locus:2114995 - symbol:PLP1 "AT4G37070" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0045735 "nutrient reservoir activity" evidence=ISS] [GO:0004620 "phospholipase activity" evidence=IDA] [GO:0010311 "lateral root formation" evidence=IMP] InterPro:IPR002641 InterPro:IPR016035 Pfam:PF01734 EMBL:CP002687 GO:GO:0006629 GO:GO:0010311 EMBL:Z99707 EMBL:AL161590 SUPFAM:SSF52151 GO:GO:0004620 EMBL:BT029750 IPI:IPI00528835 PIR:H85437

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						RefSeq:NP_849511.1 UniGene:At.23952 HSSP:Q8LPW4 ProteinModelPortal:O23179 SMR:O23179 PRIDE:O23179 EnsemblPlants:AT4G37070.2 GeneID:829861 KEGG:ath:AT4G37070 TAIR:At4g37070 InParanoid:O23179 OMA:ITMESSR PhylomeDB:O23179 ProtClustDB:CLSN2685599 ArrayExpress:O23179 Genevestigator:O23179 Uniprot:O23179
Root	Isotig01406	0	11	-4.588	0.000569522	TAIR|locus:2066286 - symbol:PLA2A "AT2G26560" species:3702 "Arabidopsis thaliana" [GO:0045735 "nutrient reservoir activity" evidence=ISS] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0006629 "lipid metabolic process" evidence=IDA] [GO:0009626 "plant-type hypersensitive response" evidence=IEP;IMP] [GO:0016020 "membrane" evidence=IDA] [GO:0016298 "lipase activity" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0008219 "cell death" evidence=IGI] [GO:0031408 "oxylipin biosynthetic process" evidence=IMP] [GO:0051607 "defense response to virus" evidence=IMP] [GO:0071456 "cellular response to hypoxia" evidence=IEP] InterPro:IPR002641 InterPro:IPR016035 Pfam:PF01734 GO:GO:0046686 GO:GO:0005737 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0016020 GO:GO:0071456 GO:GO:0051607 GO:GO:0016298 GO:GO:0009626 GO:GO:0031408 EMBL:AC002505 SUPFAM:SSF52151 eggNOG:COG3621 HSSP:Q8LPW4 HOGENOM:HBG581721 EMBL:AY062644 EMBL:AY093305 IPI:IPI00536283 PIR:T00989 RefSeq:NP_180224.1 UniGene:At.12388 ProteinModelPortal:O48723 SMR:O48723 IntAct:O48723 STRING:O48723 PRIDE:O48723 DNASU:817197 EnsemblPlants:AT2G26560.1 GeneID:817197 KEGG:ath:AT2G26560 TAIR:At2g26560 InParanoid:O48723 OMA:NENAYET PhylomeDB:O48723 ProtClustDB:CLSN2913024 ArrayExpress:O48723 Genevestigator:O48723 Uniprot:O48723
Root	Isotig01407	0	12	-4.714	0.000297064	TAIR|locus:2114995 - symbol:PLP1 "AT4G37070" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0045735 "nutrient reservoir activity" evidence=ISS] [GO:0004620 "phospholipase activity" evidence=IDA] [GO:0010311 "lateral root formation" evidence=IMP] InterPro:IPR002641 InterPro:IPR016035 Pfam:PF01734 EMBL:CP002687 GO:GO:0006629 GO:GO:0010311 EMBL:Z99707 EMBL:AL161590 SUPFAM:SSF52151 GO:GO:0004620 EMBL:BT029750 IPI:IPI00528835 PIR:H85437 RefSeq:NP_849511.1 UniGene:At.23952 HSSP:Q8LPW4 ProteinModelPortal:O23179 SMR:O23179 PRIDE:O23179 EnsemblPlants:AT4G37070.2 GeneID:829861 KEGG:ath:AT4G37070 TAIR:At4g37070 InParanoid:O23179 OMA:ITMESSR PhylomeDB:O23179 ProtClustDB:CLSN2685599 ArrayExpress:O23179 Genevestigator:O23179 Uniprot:O23179
Root	Isotig01408	0	11	-4.588	0.000569522	TAIR|locus:2066286 - symbol:PLA2A "AT2G26560" species:3702 "Arabidopsis thaliana" [GO:0045735 "nutrient reservoir activity" evidence=ISS] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0006629 "lipid metabolic process" evidence=IDA] [GO:0009626 "plant-type hypersensitive response" evidence=IEP;IMP] [GO:0016020 "membrane" evidence=IDA] [GO:0016298 "lipase activity" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0008219 "cell death" evidence=IGI] [GO:0031408 "oxylipin biosynthetic process" evidence=IMP] [GO:0051607 "defense response to virus" evidence=IMP] [GO:0071456 "cellular response to hypoxia" evidence=IEP] InterPro:IPR002641 InterPro:IPR016035 Pfam:PF01734 GO:GO:0046686 GO:GO:0005737 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0016020 GO:GO:0071456 GO:GO:0051607 GO:GO:0016298 GO:GO:0009626 GO:GO:0031408 EMBL:AC002505 SUPFAM:SSF52151 eggNOG:COG3621 HSSP:Q8LPW4 HOGENOM:HBG581721 EMBL:AY062644 EMBL:AY093305 IPI:IPI00536283 PIR:T00989 RefSeq:NP_180224.1 UniGene:At.12388 ProteinModelPortal:O48723 SMR:O48723 IntAct:O48723 STRING:O48723 PRIDE:O48723 DNASU:817197 EnsemblPlants:AT2G26560.1 GeneID:817197 KEGG:ath:AT2G26560 TAIR:At2g26560 InParanoid:O48723 OMA:NENAYET PhylomeDB:O48723 ProtClustDB:CLSN2913024 ArrayExpress:O48723 Genevestigator:O48723 Uniprot:O48723
Root	Isotig01409	0	12	-4.714	0.000297064	TAIR|locus:2114995 - symbol:PLP1 "AT4G37070" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0045735 "nutrient reservoir activity" evidence=ISS] [GO:0004620 "phospholipase activity" evidence=IDA] [GO:0010311 "lateral root formation" evidence=IMP] InterPro:IPR002641 InterPro:IPR016035 Pfam:PF01734 EMBL:CP002687 GO:GO:0006629 GO:GO:0010311 EMBL:Z99707 EMBL:AL161590 SUPFAM:SSF52151 GO:GO:0004620 EMBL:BT029750 IPI:IPI00528835 PIR:H85437 RefSeq:NP_849511.1 UniGene:At.23952 HSSP:Q8LPW4 ProteinModelPortal:O23179 SMR:O23179 PRIDE:O23179 EnsemblPlants:AT4G37070.2 GeneID:829861 KEGG:ath:AT4G37070 TAIR:At4g37070 InParanoid:O23179 OMA:ITMESSR PhylomeDB:O23179 ProtClustDB:CLSN2685599 ArrayExpress:O23179 Genevestigator:O23179 Uniprot:O23179
Root	Isotig01410	0	11	-4.588	0.000569522	TAIR|locus:2066286 - symbol:PLA2A "AT2G26560" species:3702 "Arabidopsis thaliana" [GO:0045735 "nutrient reservoir activity" evidence=ISS] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0006629 "lipid metabolic process"

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						evidence=IDA] [GO:0009626 "plant-type hypersensitive response" evidence=IEP;IMP] [GO:0016020 "membrane" evidence=IDA] [GO:0016298 "lipase activity" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0008219 "cell death" evidence=IGI] [GO:0031408 "oxylipin biosynthetic process" evidence=IMP] [GO:0051607 "defense response to virus" evidence=IMP] [GO:0071456 "cellular response to hypoxia" evidence=IEP] InterPro:IPR002641 InterPro:IPR016035 Pfam:PF01734 GO:GO:0046686 GO:GO:0005737 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0016020 GO:GO:0071456 GO:GO:0051607 GO:GO:0016298 GO:GO:0009626 GO:GO:0031408 EMBL:AC002505 SUPFAM:SSF52151 eggNOG:COG3621 HSSP:Q8LPW4 HOGENOM:HBG581721 EMBL:AY062644 EMBL:AY093305 IPI:IPI00536283 PIR:T00989 RefSeq:NP_180224.1 UniGene:At.12388 ProteinModelPortal:O48723 SMR:O48723 IntAct:O48723 STRING:O48723 PRIDE:O48723 DNASU:817197 EnsemblPlants:AT2G26560.1 GeneID:817197 KEGG:ath:AT2G26560 TAIR:At2g26560 InParanoid:O48723 OMA:NENAYET PhylomeDB:O48723 ProtClustDB:CLSN2913024 ArrayExpress:O48723 Genevestigator:O48723 Uniprot:O48723
Root	Isotig01411	0	11	-4.588	0.000569522	TAIR|locus:2066286 - symbol:PLA2A "AT2G26560" species:3702 "Arabidopsis thaliana" [GO:0045735 "nutrient reservoir activity" evidence=ISS] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0006629 "lipid metabolic process" evidence=IDA] [GO:0009626 "plant-type hypersensitive response" evidence=IEP;IMP] [GO:0016020 "membrane" evidence=IDA] [GO:0016298 "lipase activity" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0008219 "cell death" evidence=IGI] [GO:0031408 "oxylipin biosynthetic process" evidence=IMP] [GO:0051607 "defense response to virus" evidence=IMP] [GO:0071456 "cellular response to hypoxia" evidence=IEP] InterPro:IPR002641 InterPro:IPR016035 Pfam:PF01734 GO:GO:0046686 GO:GO:0005737 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0016020 GO:GO:0071456 GO:GO:0051607 GO:GO:0016298 GO:GO:0009626 GO:GO:0031408 EMBL:AC002505 SUPFAM:SSF52151 eggNOG:COG3621 HSSP:Q8LPW4 HOGENOM:HBG581721 EMBL:AY062644 EMBL:AY093305 IPI:IPI00536283 PIR:T00989 RefSeq:NP_180224.1 UniGene:At.12388 ProteinModelPortal:O48723 SMR:O48723 IntAct:O48723 STRING:O48723 PRIDE:O48723 DNASU:817197 EnsemblPlants:AT2G26560.1 GeneID:817197 KEGG:ath:AT2G26560 TAIR:At2g26560 InParanoid:O48723 OMA:NENAYET PhylomeDB:O48723 ProtClustDB:CLSN2913024 ArrayExpress:O48723 Genevestigator:O48723 Uniprot:O48723
Root	Isotig01427	56	19	1.430	6.16E-05	TAIR|locus:2160917 - symbol:RBOHD "AT5G47910" species:3702 "Arabidopsis thaliana" [GO:0006952 "defense response" evidence=IMP] [GO:0072593 "reactive oxygen species metabolic process" evidence=IMP;TAS] [GO:0016174 "NAD(P)H oxidase activity" evidence=IMP;TAS] [GO:0009408 "response to heat" evidence=IMP] [GO:0043069 "negative regulation of programmed cell death" evidence=IGI] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0050832 "defense response to fungus" evidence=IMP] [GO:0009611 "response to wounding" evidence=IEP] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR000778 InterPro:IPR011992 InterPro:IPR013112 InterPro:IPR013121 InterPro:IPR013130 InterPro:IPR013623 InterPro:IPR017927 InterPro:IPR017938 Pfam:PF01794 Pfam:PF08022 Pfam:PF08030 Pfam:PF08414 PRINTS:PR00466 PROSITE:PS51384 Prosite:PS00018 GO:GO:0016021 GO:GO:0005886 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005509 GO:GO:0009611 GO:GO:0050832 GO:GO:0005506 GO:GO:0009055 GO:GO:0050660 InterPro:IPR018247 InterPro:IPR018249 Gene3D:G3DSA:1.10.238.10 PROSITE:PS50222 GO:GO:0009408 GO:GO:0043069 EMBL:AB016886 GO:GO:0072593 GO:GO:0004601 SUPFAM:SSF63380 HOGENOM:HBG591219 GO:GO:0016174 eggNOG:COG4097 KO:K13447 EMBL:AF055357 EMBL:AF424625 EMBL:BT002651 IPI:IPI00522047 PIR:T51804 RefSeq:NP_199602.1 UniGene:At.23270 ProteinModelPortal:Q9FIJ0 SMR:Q9FIJ0 STRING:Q9FIJ0 PeroxiBase:3286 PRIDE:Q9FIJ0 EnsemblPlants:AT5G47910.1 GeneID:834842 KEGG:ath:AT5G47910 TAIR:At5g47910 InParanoid:Q9FIJ0 OMA:FTYKFIQ PhylomeDB:Q9FIJ0 ProtClustDB:CLSN2916327 Genevestigator:Q9FIJ0 Uniprot:Q9FIJ0
Root	Isotig01428	65	16	1.893	1.34E-07	TAIR|locus:2160917 - symbol:RBOHD "AT5G47910" species:3702 "Arabidopsis thaliana" [GO:0006952 "defense response" evidence=IMP] [GO:0072593 "reactive oxygen species metabolic process" evidence=IMP;TAS] [GO:0016174 "NAD(P)H oxidase activity" evidence=IMP;TAS] [GO:0009408 "response to heat" evidence=IMP] [GO:0043069 "negative regulation of programmed cell death" evidence=IGI] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0050832 "defense response to fungus" evidence=IMP] [GO:0009611 "response to wounding" evidence=IEP] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR000778 InterPro:IPR011992 InterPro:IPR013112 InterPro:IPR013121 InterPro:IPR013130 InterPro:IPR013623 InterPro:IPR017927 InterPro:IPR017938 Pfam:PF01794 Pfam:PF08022 Pfam:PF08030 Pfam:PF08414 PRINTS:PR00466 PROSITE:PS51384 Prosite:PS00018 GO:GO:0016021 GO:GO:0005886 EMBL:CP002688

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GenomeReviews:BA000015_GR GO:GO:0005509 GO:GO:0009611 GO:GO:0050832 GO:GO:0005506 GO:GO:0009055 GO:GO:0050660 InterPro:IPR018247 InterPro:IPR018249 Gene3D:G3DSA:1.10.238.10 PROSITE:PS50222 GO:GO:0009408 GO:GO:0043069 EMBL:AB016886 GO:GO:0072593 GO:GO:0004601 SUPFAM:SSF63380 HOGENOM:HBG591219 GO:GO:0016174 eggNOG:COG4097 KO:K13447 EMBL:AF055357 EMBL:AF424625 EMBL:BT002651 IPI:IPI00522047 PIR:T51804 RefSeq:NP_199602.1 UniGene:At.23270 ProteinModelPortal:Q9FIJ0 SMR:Q9FIJ0 STRING:Q9FIJ0 PeroxiBase:3286 PRIDE:Q9FIJ0 EnsemblPlants:AT5G47910.1 GeneID:834842 KEGG:ath:AT5G47910 TAIR:At5g47910 InParanoid:Q9FIJ0 OMA:FTYKFIQ PhylomeDB:Q9FIJ0 ProtClustDB:CLSN2916327 Genevestigator:Q9FIJ0 Uniprot:Q9FIJ0
Root	Isotig01431	55	18	1.482	4.54E-05	TAIR|locus:2036104 - symbol:RBOHB "respiratory burst oxidase homolog B" species:3702 "Arabidopsis thaliana" [GO:0016020 "membrane" evidence=IEA] [GO:0016021 "integral to membrane" evidence=IEA] [GO:0009408 "response to heat" evidence=IMP] [GO:0009845 "seed germination" evidence=IMP] [GO:0016174 "NAD(P)H oxidase activity" evidence=IMP] [GO:0006952 "defense response" evidence=TAS] InterPro:IPR000778 InterPro:IPR002048 InterPro:IPR011992 InterPro:IPR013112 InterPro:IPR013121 InterPro:IPR013130 InterPro:IPR013623 InterPro:IPR017927 InterPro:IPR017938 Pfam:PF01794 Pfam:PF08022 Pfam:PF08030 Pfam:PF08414 PRINTS:PR00466 PROSITE:PS51384 SMART:SM00054 Prosite:PS00018 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005509 GO:GO:0005506 GO:GO:0009055 GO:GO:0050660 InterPro:IPR018249 Gene3D:G3DSA:1.10.238.10 PROSITE:PS50222 GO:GO:0009408 GO:GO:0009845 GO:GO:0004601 SUPFAM:SSF63380 EMBL:AC000106 eggNOG:NOG287712 HOGENOM:HBG591219 GO:GO:0016174 UniGene:At.10379 UniGene:At.42241 EMBL:AF055354 EMBL:BT005716 IPI:IPI00517116 IPI:IPI00520396 PIR:A86223 PIR:B86223 RefSeq:NP_172383.3 RefSeq:NP_973799.1 ProteinModelPortal:Q9SBI0 SMR:Q9SBI0 STRING:Q9SBI0 PeroxiBase:3283 PRIDE:Q9SBI0 EnsemblPlants:AT1G09090.2 GeneID:837430 KEGG:ath:AT1G09090 TAIR:At1g09090 InParanoid:Q9SBI0 OMA:LWISICI PhylomeDB:Q9SBI0 ArrayExpress:Q84TJ9 Genevestigator:Q9SBI0 Uniprot:Q9SBI0
Root	Isotig01432	53	16	1.599	2.32E-05	TAIR|locus:2036104 - symbol:RBOHB "respiratory burst oxidase homolog B" species:3702 "Arabidopsis thaliana" [GO:0016020 "membrane" evidence=IEA] [GO:0016021 "integral to membrane" evidence=IEA] [GO:0009408 "response to heat" evidence=IMP] [GO:0009845 "seed germination" evidence=IMP] [GO:0016174 "NAD(P)H oxidase activity" evidence=IMP] [GO:0006952 "defense response" evidence=TAS] InterPro:IPR000778 InterPro:IPR002048 InterPro:IPR011992 InterPro:IPR013112 InterPro:IPR013121 InterPro:IPR013130 InterPro:IPR013623 InterPro:IPR017927 InterPro:IPR017938 Pfam:PF01794 Pfam:PF08022 Pfam:PF08030 Pfam:PF08414 PRINTS:PR00466 PROSITE:PS51384 SMART:SM00054 Prosite:PS00018 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005509 GO:GO:0005506 GO:GO:0009055 GO:GO:0050660 InterPro:IPR018249 Gene3D:G3DSA:1.10.238.10 PROSITE:PS50222 GO:GO:0009408 GO:GO:0009845 GO:GO:0004601 SUPFAM:SSF63380 EMBL:AC000106 eggNOG:NOG287712 HOGENOM:HBG591219 GO:GO:0016174 UniGene:At.10379 UniGene:At.42241 EMBL:AF055354 EMBL:BT005716 IPI:IPI00517116 IPI:IPI00520396 PIR:A86223 PIR:B86223 RefSeq:NP_172383.3 RefSeq:NP_973799.1 ProteinModelPortal:Q9SBI0 SMR:Q9SBI0 STRING:Q9SBI0 PeroxiBase:3283 PRIDE:Q9SBI0 EnsemblPlants:AT1G09090.2 GeneID:837430 KEGG:ath:AT1G09090 TAIR:At1g09090 InParanoid:Q9SBI0 OMA:LWISICI PhylomeDB:Q9SBI0 ArrayExpress:Q84TJ9 Genevestigator:Q9SBI0 Uniprot:Q9SBI0
Root	Isotig01449	9	28	-1.766	0.000557996	TAIR|locus:2038836 - symbol:PDE331 "AT2G01190" species:3702 "Arabidopsis thaliana" [GO:0005634 "nucleus" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR000270 Pfam:PF00564 SMART:SM00666 GO:GO:0005829 GO:GO:0005634 EMBL:CP002685 EMBL:AC006200 ProtClustDB:CLSN2687650 EMBL:AY070060 EMBL:AY117302 IPI:IPI00548472 PIR:F84421 RefSeq:NP_565256.1 UniGene:At.19855 UniGene:At.72006 UniGene:At.74187 UniGene:At.74214 ProteinModelPortal:Q9ZU48 IntAct:Q9ZU48 PRIDE:Q9ZU48 EnsemblPlants:AT2G01190.1 GeneID:814647 KEGG:ath:AT2G01190 TAIR:At2g01190 InParanoid:Q9ZU48 OMA:YDRTISA PhylomeDB:Q9ZU48 ArrayExpress:Q9ZU48 Genevestigator:Q9ZU48 Uniprot:Q9ZU48
Root	Isotig01455	18	67	-2.025	4.84E-09	TAIR|locus:2195623 - symbol:AT1G60420 species:3702 "Arabidopsis thaliana" [GO:0016209 "antioxidant activity" evidence=IEA] [GO:0016491 "oxidoreductase activity" evidence=IEA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0009860 "pollen tube growth" evidence=IMP] [GO:0010183 "pollen tube guidance" evidence=IMP] [GO:0080092 "regulation of pollen tube growth" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR011424 InterPro:IPR017937 Pfam:PF07649 PROSITE:PS00194 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0046686 GO:GO:0009860 InterPro:IPR012336

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						Gene3D:G3DSA:3.40.30.10 SUPFAM:SSF52833 GO:GO:0045454 PROSITE:PS51352 GO:GO:0080092 GO:GO:0010183 eggNOG:COG0526 GO:GO:0047134 EMBL:AC004473 EMBL:AY065433 EMBL:AY117231 EMBL:AY087396 IPI:IPI00537432 PIR:T02292 RefSeq:NP_564756.1 UniGene:At.10685 UniGene:At.64112 PDB:1V5N PDBsum:1V5N ProteinModelPortal:O80763 SMR:O80763 IntAct:O80763 PRIDE:O80763 EnsemblPlants:AT1G60420.1 GeneID:842337 KEGG:ath:AT1G60420 TAIR:At1g60420 HOGENOM:HBG594354 InParanoid:O80763 OMA:QMPWLAL PhylomeDB:O80763 ProtClustDB:CLSN2917334 ArrayExpress:O80763 Genevestigator:O80763 Uniprot:O80763
Root	Isotig01456	22	75	-1.898	2.97E-09	TAIR|locus:2195623 - symbol:AT1G60420 species:3702 "Arabidopsis thaliana" [GO:0016209 "antioxidant activity" evidence=IEA] [GO:0016491 "oxidoreductase activity" evidence=IEA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0009860 "pollen tube growth" evidence=IMP] [GO:0010183 "pollen tube guidance" evidence=IMP] [GO:0080092 "regulation of pollen tube growth" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR011424 InterPro:IPR017937 Pfam:PF07649 PROSITE:PS00194 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0046686 GO:GO:0009860 InterPro:IPR012336 Gene3D:G3DSA:3.40.30.10 SUPFAM:SSF52833 GO:GO:0045454 PROSITE:PS51352 GO:GO:0080092 GO:GO:0010183 eggNOG:COG0526 GO:GO:0047134 EMBL:AC004473 EMBL:AY065433 EMBL:AY117231 EMBL:AY087396 IPI:IPI00537432 PIR:T02292 RefSeq:NP_564756.1 UniGene:At.10685 UniGene:At.64112 PDB:1V5N PDBsum:1V5N ProteinModelPortal:O80763 SMR:O80763 IntAct:O80763 PRIDE:O80763 EnsemblPlants:AT1G60420.1 GeneID:842337 KEGG:ath:AT1G60420 TAIR:At1g60420 HOGENOM:HBG594354 InParanoid:O80763 OMA:QMPWLAL PhylomeDB:O80763 ProtClustDB:CLSN2917334 ArrayExpress:O80763 Genevestigator:O80763 Uniprot:O80763
Root	Isotig01457	19	71	-2.031	1.58E-09	TAIR|locus:2195623 - symbol:AT1G60420 species:3702 "Arabidopsis thaliana" [GO:0016209 "antioxidant activity" evidence=IEA] [GO:0016491 "oxidoreductase activity" evidence=IEA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0009860 "pollen tube growth" evidence=IMP] [GO:0010183 "pollen tube guidance" evidence=IMP] [GO:0080092 "regulation of pollen tube growth" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR011424 InterPro:IPR017937 Pfam:PF07649 PROSITE:PS00194 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0046686 GO:GO:0009860 InterPro:IPR012336 Gene3D:G3DSA:3.40.30.10 SUPFAM:SSF52833 GO:GO:0045454 PROSITE:PS51352 GO:GO:0080092 GO:GO:0010183 eggNOG:COG0526 GO:GO:0047134 EMBL:AC004473 EMBL:AY065433 EMBL:AY117231 EMBL:AY087396 IPI:IPI00537432 PIR:T02292 RefSeq:NP_564756.1 UniGene:At.10685 UniGene:At.64112 PDB:1V5N PDBsum:1V5N ProteinModelPortal:O80763 SMR:O80763 IntAct:O80763 PRIDE:O80763 EnsemblPlants:AT1G60420.1 GeneID:842337 KEGG:ath:AT1G60420 TAIR:At1g60420 HOGENOM:HBG594354 InParanoid:O80763 OMA:QMPWLAL PhylomeDB:O80763 ProtClustDB:CLSN2917334 ArrayExpress:O80763 Genevestigator:O80763 Uniprot:O80763
Root	Isotig01458	15	66	-2.266	4.53E-10	TAIR|locus:2195623 - symbol:AT1G60420 species:3702 "Arabidopsis thaliana" [GO:0016209 "antioxidant activity" evidence=IEA] [GO:0016491 "oxidoreductase activity" evidence=IEA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0009860 "pollen tube growth" evidence=IMP] [GO:0010183 "pollen tube guidance" evidence=IMP] [GO:0080092 "regulation of pollen tube growth" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR011424 InterPro:IPR017937 Pfam:PF07649 PROSITE:PS00194 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0046686 GO:GO:0009860 InterPro:IPR012336 Gene3D:G3DSA:3.40.30.10 SUPFAM:SSF52833 GO:GO:0045454 PROSITE:PS51352 GO:GO:0080092 GO:GO:0010183 eggNOG:COG0526 GO:GO:0047134 EMBL:AC004473 EMBL:AY065433 EMBL:AY117231 EMBL:AY087396 IPI:IPI00537432 PIR:T02292 RefSeq:NP_564756.1 UniGene:At.10685 UniGene:At.64112 PDB:1V5N PDBsum:1V5N ProteinModelPortal:O80763 SMR:O80763 IntAct:O80763 PRIDE:O80763 EnsemblPlants:AT1G60420.1 GeneID:842337 KEGG:ath:AT1G60420 TAIR:At1g60420 HOGENOM:HBG594354 InParanoid:O80763 OMA:QMPWLAL PhylomeDB:O80763 ProtClustDB:CLSN2917334 ArrayExpress:O80763 Genevestigator:O80763 Uniprot:O80763
Root	Isotig01459	19	74	-2.090	3.44E-10	TAIR|locus:2195623 - symbol:AT1G60420 species:3702 "Arabidopsis thaliana" [GO:0016209 "antioxidant activity" evidence=IEA] [GO:0016491 "oxidoreductase activity" evidence=IEA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0009860 "pollen tube growth" evidence=IMP] [GO:0010183 "pollen tube guidance" evidence=IMP] [GO:0080092 "regulation of pollen tube growth" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR011424 InterPro:IPR017937 Pfam:PF07649 PROSITE:PS00194 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0046686 GO:GO:0009860 InterPro:IPR012336

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						Gene3D:G3DSA:3.40.30.10 SUPFAM:SSF52833 GO:GO:0045454 PROSITE:PS51352 GO:GO:0080092 GO:GO:0010183 eggNOG:COG0526 GO:GO:0047134 EMBL:AC004473 EMBL:AY065433 EMBL:AY117231 EMBL:AY087396 IPI:IPI00537432 PIR:T02292 RefSeq:NP_564756.1 UniGene:At.10685 UniGene:At.64112 PDB:1V5N PDBsum:1V5N ProteinModelPortal:O80763 SMR:O80763 IntAct:O80763 PRIDE:O80763 EnsemblPlants:AT1G60420.1 GeneID:842337 KEGG:ath:AT1G60420 TAIR:At1g60420 HOGENOM:HBG594354 InParanoid:O80763 OMA:QMPWLAL PhylomeDB:O80763 ProtClustDB:CLSN2917334 ArrayExpress:O80763 Genevestigator:O80763 Uniprot:O80763
Root	Isotig01460	16	70	-2.258	1.49E-10	TAIR|locus:2195623 - symbol:AT1G60420 species:3702 "Arabidopsis thaliana" [GO:0016209 "antioxidant activity" evidence=IEA] [GO:0016491 "oxidoreductase activity" evidence=IEA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0009860 "pollen tube growth" evidence=IMP] [GO:0010183 "pollen tube guidance" evidence=IMP] [GO:0080092 "regulation of pollen tube growth" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR011424 InterPro:IPR017937 Pfam:PF07649 PROSITE:PS00194 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0046686 GO:GO:0009860 InterPro:IPR012336 Gene3D:G3DSA:3.40.30.10 SUPFAM:SSF52833 GO:GO:0045454 PROSITE:PS51352 GO:GO:0080092 GO:GO:0010183 eggNOG:COG0526 GO:GO:0047134 EMBL:AC004473 EMBL:AY065433 EMBL:AY117231 EMBL:AY087396 IPI:IPI00537432 PIR:T02292 RefSeq:NP_564756.1 UniGene:At.10685 UniGene:At.64112 PDB:1V5N PDBsum:1V5N ProteinModelPortal:O80763 SMR:O80763 IntAct:O80763 PRIDE:O80763 EnsemblPlants:AT1G60420.1 GeneID:842337 KEGG:ath:AT1G60420 TAIR:At1g60420 HOGENOM:HBG594354 InParanoid:O80763 OMA:QMPWLAL PhylomeDB:O80763 ProtClustDB:CLSN2917334 ArrayExpress:O80763 Genevestigator:O80763 Uniprot:O80763
Root	Isotig01461	0	17	-5.216	1.26E-05	TAIR|locus:2083604 - symbol:LAC7 "laccase 7" species:3702 "Arabidopsis thaliana" [GO:0046274 "lignin catabolic process" evidence=IEA] [GO:0048046 "apoplast" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] InterPro:IPR001117 InterPro:IPR002355 InterPro:IPR011706 InterPro:IPR011707 InterPro:IPR017761 Pfam:PF00394 Pfam:PF07731 Pfam:PF07732 PROSITE:PS00079 PROSITE:PS00080 GO:GO:0048046 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005507 InterPro:IPR008972 Gene3D:G3DSA:2.60.40.420 SUPFAM:SSF49503 EMBL:AC011436 eggNOG:COG2132 HOGENOM:HBG749556 GO:GO:0052716 GO:GO:0046274 PANTHER:PTHR11709:SF9 TIGRFAMs:TIGR03389 HSSP:P37064 EMBL:AK117639 EMBL:BT004971 IPI:IPI00528510 RefSeq:NP_187533.1 UniGene:At.40144 ProteinModelPortal:Q9SR40 SMR:Q9SR40 PRIDE:Q9SR40 EnsemblPlants:AT3G09220.1 GeneID:820078 KEGG:ath:AT3G09220 TAIR:At3g09220 InParanoid:Q9SR40 OMA:WHAHASF PhylomeDB:Q9SR40 ProtClustDB:CLSN2685122 ArrayExpress:Q9SR40 Genevestigator:Q9SR40 Uniprot:Q9SR40
Root	Isotig01469	6	53	-3.272	1.24E-11	TAIR|locus:2204858 - symbol:AT1G02260 "AT1G02260" species:3702 "Arabidopsis thaliana" [GO:0005215 "transporter activity" evidence=ISS] [GO:0015137 "citrate transmembrane transporter activity" evidence=IEA] [GO:0015746 "citrate transport" evidence=IEA] [GO:0016021 "integral to membrane" evidence=IEA;ISS] [GO:0055085 "transmembrane transport" evidence=IEA] InterPro:IPR004680 Pfam:PF03600 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR eggNOG:COG1055 OMA:SANVICA GO:GO:0015137 EMBL:U89959 HOGENOM:HBG727257 EMBL:BT023463 IPI:IPI00519219 RefSeq:NP_171728.2 UniGene:At.48101 STRING:O81915 PRIDE:O81915 EnsemblPlants:AT1G02260.1 GeneID:839344 KEGG:ath:AT1G02260 TAIR:At1g02260 InParanoid:O81915 PhylomeDB:O81915 ProtClustDB:CLSN2918462 Genevestigator:O81915 Uniprot:O81915
Root	Isotig01470	6	59	-3.427	3.13E-13	TAIR|locus:2204858 - symbol:AT1G02260 "AT1G02260" species:3702 "Arabidopsis thaliana" [GO:0005215 "transporter activity" evidence=ISS] [GO:0015137 "citrate transmembrane transporter activity" evidence=IEA] [GO:0015746 "citrate transport" evidence=IEA] [GO:0016021 "integral to membrane" evidence=IEA;ISS] [GO:0055085 "transmembrane transport" evidence=IEA] InterPro:IPR004680 Pfam:PF03600 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR eggNOG:COG1055 OMA:SANVICA GO:GO:0015137 EMBL:U89959 HOGENOM:HBG727257 EMBL:BT023463 IPI:IPI00519219 RefSeq:NP_171728.2 UniGene:At.48101 STRING:O81915 PRIDE:O81915 EnsemblPlants:AT1G02260.1 GeneID:839344 KEGG:ath:AT1G02260 TAIR:At1g02260 InParanoid:O81915 PhylomeDB:O81915 ProtClustDB:CLSN2918462 Genevestigator:O81915 Uniprot:O81915
Root	Isotig01471	6	57	-3.377	1.07E-12	TAIR|locus:2204858 - symbol:AT1G02260 "AT1G02260" species:3702 "Arabidopsis thaliana" [GO:0005215 "transporter activity" evidence=ISS] [GO:0015137 "citrate transmembrane transporter activity" evidence=IEA] [GO:0015746 "citrate transport" evidence=IEA] [GO:0016021 "integral to membrane" evidence=IEA;ISS]

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						[GO:0055085 "transmembrane transport" evidence=IEA] InterPro:IPR004680 Pfam:PF03600 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR eggNOG:COG1055 OMA:SANVICA GO:GO:0015137 EMBL:U89959 HOGENOM:HBG727257 EMBL:BT023463 IPI:IPI00519219 RefSeq:NP_171728.2 UniGene:At.48101 STRING:O81915 PRIDE:O81915 EnsemblPlants:AT1G02260.1 GeneID:839344 KEGG:ath:AT1G02260 TAIR:At1g02260 InParanoid:O81915 PhylomeDB:O81915 ProtClustDB:CLSN2918462 Genevestigator:O81915 Uniprot:O81915
Root	Isotig01472	6	33	-2.588	1.92E-06	TAIR|locus:2204858 - symbol:AT1G02260 "AT1G02260" species:3702 "Arabidopsis thaliana" [GO:0005215 "transporter activity" evidence=ISS] [GO:0015137 "citrate transmembrane transporter activity" evidence=IEA] [GO:0015746 "citrate transport" evidence=IEA] [GO:0016021 "integral to membrane" evidence=IEA;ISS] [GO:0055085 "transmembrane transport" evidence=IEA] InterPro:IPR004680 Pfam:PF03600 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR eggNOG:COG1055 OMA:SANVICA GO:GO:0015137 EMBL:U89959 HOGENOM:HBG727257 EMBL:BT023463 IPI:IPI00519219 RefSeq:NP_171728.2 UniGene:At.48101 STRING:O81915 PRIDE:O81915 EnsemblPlants:AT1G02260.1 GeneID:839344 KEGG:ath:AT1G02260 TAIR:At1g02260 InParanoid:O81915 PhylomeDB:O81915 ProtClustDB:CLSN2918462 Genevestigator:O81915 Uniprot:O81915
Root	Isotig01473	0	22	-5.588	6.01E-07	No hit
Root	Isotig01474	0	28	-5.936	1.79E-08	No hit
Root	Isotig01475	0	26	-5.829	5.70E-08	No hit
Root	Isotig01490	25	70	-1.614	3.05E-07	TAIR|locus:2136308 - symbol:CESA2 "AT4G39350" species:3702 "Arabidopsis thaliana" [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0016759 "cellulose synthase activity" evidence=ISS;IMP] [GO:0005886 "plasma membrane" evidence=IDA;TAS] [GO:0009833 "primary cell wall biogenesis" evidence=TAS] [GO:0030244 "cellulose biosynthetic process" evidence=IMP] InterPro:IPR001841 InterPro:IPR005150 Pfam:PF03552 PROSITE:PS50089 SMART:SM00184 Prosite:PS00518 GO:GO:0016021 GO:GO:0005886 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0008270 InterPro:IPR013083 Gene3D:G3DSA:3.30.40.10 GO:GO:0007047 EMBL:AL161595 CAZy:GT2 eggNOG:COG1215 GO:GO:0016760 GO:GO:0030244 EMBL:AL050351 HOGENOM:HBG744549 KO:K10999 EMBL:AF027173 EMBL:AY059858 EMBL:AY093308 IPI:IPI00521119 PIR:T08583 RefSeq:NP_195645.1 UniGene:At.3315 ProteinModelPortal:O48947 SMR:O48947 STRING:O48947 PRIDE:O48947 EnsemblPlants:AT4G39350.1 GeneID:830090 KEGG:ath:AT4G39350 GeneFarm:5085 TAIR:At4g39350 InParanoid:O48947 OMA:IHALENV PhylomeDB:O48947 ProtClustDB:PLN02436 Genevestigator:O48947 GermOnline:AT4G39350 Uniprot:O48947
Root	Isotig01491	26	70	-1.558	6.04E-07	TAIR|locus:2136308 - symbol:CESA2 "AT4G39350" species:3702 "Arabidopsis thaliana" [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0016759 "cellulose synthase activity" evidence=ISS;IMP] [GO:0005886 "plasma membrane" evidence=IDA;TAS] [GO:0009833 "primary cell wall biogenesis" evidence=TAS] [GO:0030244 "cellulose biosynthetic process" evidence=IMP] InterPro:IPR001841 InterPro:IPR005150 Pfam:PF03552 PROSITE:PS50089 SMART:SM00184 Prosite:PS00518 GO:GO:0016021 GO:GO:0005886 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0008270 InterPro:IPR013083 Gene3D:G3DSA:3.30.40.10 GO:GO:0007047 EMBL:AL161595 CAZy:GT2 eggNOG:COG1215 GO:GO:0016760 GO:GO:0030244 EMBL:AL050351 HOGENOM:HBG744549 KO:K10999 EMBL:AF027173 EMBL:AY059858 EMBL:AY093308 IPI:IPI00521119 PIR:T08583 RefSeq:NP_195645.1 UniGene:At.3315 ProteinModelPortal:O48947 SMR:O48947 STRING:O48947 PRIDE:O48947 EnsemblPlants:AT4G39350.1 GeneID:830090 KEGG:ath:AT4G39350 GeneFarm:5085 TAIR:At4g39350 InParanoid:O48947 OMA:IHALENV PhylomeDB:O48947 ProtClustDB:PLN02436 Genevestigator:O48947 GermOnline:AT4G39350 Uniprot:O48947
Root	Isotig01492	23	66	-1.650	4.42E-07	TAIR|locus:2136308 - symbol:CESA2 "AT4G39350" species:3702 "Arabidopsis thaliana" [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0016759 "cellulose synthase activity" evidence=ISS;IMP] [GO:0005886 "plasma membrane" evidence=IDA;TAS] [GO:0009833 "primary cell wall biogenesis" evidence=TAS] [GO:0030244 "cellulose biosynthetic process" evidence=IMP] InterPro:IPR001841 InterPro:IPR005150 Pfam:PF03552 PROSITE:PS50089 SMART:SM00184 Prosite:PS00518 GO:GO:0016021 GO:GO:0005886 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0008270 InterPro:IPR013083 Gene3D:G3DSA:3.30.40.10 GO:GO:0007047 EMBL:AL161595 CAZy:GT2 eggNOG:COG1215 GO:GO:0016760 GO:GO:0030244 EMBL:AL050351 HOGENOM:HBG744549 KO:K10999 EMBL:AF027173 EMBL:AY059858 EMBL:AY093308 IPI:IPI00521119 PIR:T08583 RefSeq:NP_195645.1 UniGene:At.3315 ProteinModelPortal:O48947 SMR:O48947 STRING:O48947 PRIDE:O48947 EnsemblPlants:AT4G39350.1 GeneID:830090

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						KEGG:ath:AT4G39350 GeneFarm:5085 TAIR:At4g39350 InParanoid:O48947 OMA:IHALENV PhylomeDB:O48947 ProtClustDB:PLN02436 Genevestigator:O48947 GermOnline:AT4G39350 Uniprot:O48947
Root	Isotig01493	25	69	-1.594	4.74E-07	TAIR|locus:2136308 - symbol:CESA2 "AT4G39350" species:3702 "Arabidopsis thaliana" [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0016759 "cellulose synthase activity" evidence=ISS;IMP] [GO:0005886 "plasma membrane" evidence=IDA;TAS] [GO:0009833 "primary cell wall biogenesis" evidence=TAS] [GO:0030244 "cellulose biosynthetic process" evidence=IMP] InterPro:IPR001841 InterPro:IPR005150 Pfam:PF03552 PROSITE:PS50089 SMART:SM00184 Prosite:PS00518 GO:GO:0016021 GO:GO:0005886 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0008270 InterPro:IPR013083 Gene3D:G3DSA:3.30.40.10 GO:GO:0007047 EMBL:AL161595 CAZy:GT2 eggNOG:COG1215 GO:GO:0016760 GO:GO:0030244 EMBL:AL050351 HOGENOM:HBG744549 KO:K10999 EMBL:AF027173 EMBL:AY059858 EMBL:AY093308 IPI:IPI00521119 PIR:T08583 RefSeq:NP_195645.1 UniGene:At.3315 ProteinModelPortal:O48947 SMR:O48947 STRING:O48947 PRIDE:O48947 EnsemblPlants:AT4G39350.1 GeneID:830090 KEGG:ath:AT4G39350 GeneFarm:5085 TAIR:At4g39350 InParanoid:O48947 OMA:IHALENV PhylomeDB:O48947 ProtClustDB:PLN02436 Genevestigator:O48947 GermOnline:AT4G39350 Uniprot:O48947
Root	Isotig01494	26	69	-1.537	9.31E-07	TAIR|locus:2136308 - symbol:CESA2 "AT4G39350" species:3702 "Arabidopsis thaliana" [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0016759 "cellulose synthase activity" evidence=ISS;IMP] [GO:0005886 "plasma membrane" evidence=IDA;TAS] [GO:0009833 "primary cell wall biogenesis" evidence=TAS] [GO:0030244 "cellulose biosynthetic process" evidence=IMP] InterPro:IPR001841 InterPro:IPR005150 Pfam:PF03552 PROSITE:PS50089 SMART:SM00184 Prosite:PS00518 GO:GO:0016021 GO:GO:0005886 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0008270 InterPro:IPR013083 Gene3D:G3DSA:3.30.40.10 GO:GO:0007047 EMBL:AL161595 CAZy:GT2 eggNOG:COG1215 GO:GO:0016760 GO:GO:0030244 EMBL:AL050351 HOGENOM:HBG744549 KO:K10999 EMBL:AF027173 EMBL:AY059858 EMBL:AY093308 IPI:IPI00521119 PIR:T08583 RefSeq:NP_195645.1 UniGene:At.3315 ProteinModelPortal:O48947 SMR:O48947 STRING:O48947 PRIDE:O48947 EnsemblPlants:AT4G39350.1 GeneID:830090 KEGG:ath:AT4G39350 GeneFarm:5085 TAIR:At4g39350 InParanoid:O48947 OMA:IHALENV PhylomeDB:O48947 ProtClustDB:PLN02436 Genevestigator:O48947 GermOnline:AT4G39350 Uniprot:O48947
Root	Isotig01495	23	65	-1.628	6.92E-07	TAIR|locus:2136308 - symbol:CESA2 "AT4G39350" species:3702 "Arabidopsis thaliana" [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0016759 "cellulose synthase activity" evidence=ISS;IMP] [GO:0005886 "plasma membrane" evidence=IDA;TAS] [GO:0009833 "primary cell wall biogenesis" evidence=TAS] [GO:0030244 "cellulose biosynthetic process" evidence=IMP] InterPro:IPR001841 InterPro:IPR005150 Pfam:PF03552 PROSITE:PS50089 SMART:SM00184 Prosite:PS00518 GO:GO:0016021 GO:GO:0005886 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0008270 InterPro:IPR013083 Gene3D:G3DSA:3.30.40.10 GO:GO:0007047 EMBL:AL161595 CAZy:GT2 eggNOG:COG1215 GO:GO:0016760 GO:GO:0030244 EMBL:AL050351 HOGENOM:HBG744549 KO:K10999 EMBL:AF027173 EMBL:AY059858 EMBL:AY093308 IPI:IPI00521119 PIR:T08583 RefSeq:NP_195645.1 UniGene:At.3315 ProteinModelPortal:O48947 SMR:O48947 STRING:O48947 PRIDE:O48947 EnsemblPlants:AT4G39350.1 GeneID:830090 KEGG:ath:AT4G39350 GeneFarm:5085 TAIR:At4g39350 InParanoid:O48947 OMA:IHALENV PhylomeDB:O48947 ProtClustDB:PLN02436 Genevestigator:O48947 GermOnline:AT4G39350 Uniprot:O48947
Root	Isotig01496	13	40	-1.750	4.15E-05	TAIR|locus:2196245 - symbol:CAT2 "cationic amino acid transporter 2" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=IEA;ISS] [GO:0006865 "amino acid transport" evidence=IEA] [GO:0015171 "amino acid transmembrane transporter activity" evidence=IEA] [GO:0016020 "membrane" evidence=ISS] [GO:0055085 "transmembrane transport" evidence=IEA] [GO:0009705 "plant-type vacuole membrane" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] InterPro:IPR002293 PIRSF:PIRSF006060 GO:GO:0016021 EMBL:CP002684 eggNOG:COG0531 PANTHER:PTHR11785 GO:GO:0015171 GO:GO:0009705 InterPro:IPR015606 PANTHER:PTHR11785:SF53 EMBL:AF367304 EMBL:BT000457 EMBL:BT046174 IPI:IPI00542604 RefSeq:NP_849822.1 UniGene:At.43759 ProteinModelPortal:Q9ASS7 PRIDE:Q8H182 EnsemblPlants:AT1G58030.1 GeneID:842170 KEGG:ath:AT1G58030 TAIR:At1g58030 InParanoid:Q9ASS7 OMA:RRIVAGW PhylomeDB:Q9ASS7 ProtClustDB:CLSN2680360 Genevestigator:Q9ASS7 Uniprot:Q9ASS7
Root	Isotig01497	14	40	-1.644	8.83E-05	TAIR|locus:2196245 - symbol:CAT2 "cationic amino acid transporter 2" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=IEA;ISS] [GO:0006865 "amino acid transport" evidence=IEA] [GO:0015171 "amino acid transmembrane transporter activity" evidence=IEA] [GO:0016020 "membrane" evidence=ISS]

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						[GO:0055085 "transmembrane transport" evidence=IEA] [GO:0009705 "plant-type vacuole membrane" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] InterPro:IPR002293 PIRSF:PIRSF006060 GO:GO:0016021 EMBL:CP002684 eggNOG:COG0531 PANTHER:PTHR11785 GO:GO:0015171 GO:GO:0009705 InterPro:IPR015606 PANTHER:PTHR11785:SF53 EMBL:AF367304 EMBL:BT000457 EMBL:BT046174 IPI:IPI00542604 RefSeq:NP_849822.1 UniGene:At.43759 ProteinModelPortal:Q9ASS7 PRIDE:Q8H182 EnsemblPlants:AT1G58030.1 GeneID:842170 KEGG:ath:AT1G58030 TAIR:At1g58030 InParanoid:Q9ASS7 OMA:RRIVAGW PhylomeDB:Q9ASS7 ProtClustDB:CLSN2680360 Genevestigator:Q9ASS7 Uniprot:Q9ASS7
Root	Isotig01498	14	42	-1.714	3.49E-05	TAIR|locus:2196245 - symbol:CAT2 "cationic amino acid transporter 2" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=IEA;ISS] [GO:0006865 "amino acid transport" evidence=IEA] [GO:0015171 "amino acid transmembrane transporter activity" evidence=IEA] [GO:0016020 "membrane" evidence=ISS] [GO:0055085 "transmembrane transport" evidence=IEA] [GO:0009705 "plant-type vacuole membrane" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] InterPro:IPR002293 PIRSF:PIRSF006060 GO:GO:0016021 EMBL:CP002684 eggNOG:COG0531 PANTHER:PTHR11785 GO:GO:0015171 GO:GO:0009705 InterPro:IPR015606 PANTHER:PTHR11785:SF53 EMBL:AF367304 EMBL:BT000457 EMBL:BT046174 IPI:IPI00542604 RefSeq:NP_849822.1 UniGene:At.43759 ProteinModelPortal:Q9ASS7 PRIDE:Q8H182 EnsemblPlants:AT1G58030.1 GeneID:842170 KEGG:ath:AT1G58030 TAIR:At1g58030 InParanoid:Q9ASS7 OMA:RRIVAGW PhylomeDB:Q9ASS7 ProtClustDB:CLSN2680360 Genevestigator:Q9ASS7 Uniprot:Q9ASS7
Root	Isotig01499	14	40	-1.644	8.83E-05	TAIR|locus:2196245 - symbol:CAT2 "cationic amino acid transporter 2" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=IEA;ISS] [GO:0006865 "amino acid transport" evidence=IEA] [GO:0015171 "amino acid transmembrane transporter activity" evidence=IEA] [GO:0016020 "membrane" evidence=ISS] [GO:0055085 "transmembrane transport" evidence=IEA] [GO:0009705 "plant-type vacuole membrane" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] InterPro:IPR002293 PIRSF:PIRSF006060 GO:GO:0016021 EMBL:CP002684 eggNOG:COG0531 PANTHER:PTHR11785 GO:GO:0015171 GO:GO:0009705 InterPro:IPR015606 PANTHER:PTHR11785:SF53 EMBL:AF367304 EMBL:BT000457 EMBL:BT046174 IPI:IPI00542604 RefSeq:NP_849822.1 UniGene:At.43759 ProteinModelPortal:Q9ASS7 PRIDE:Q8H182 EnsemblPlants:AT1G58030.1 GeneID:842170 KEGG:ath:AT1G58030 TAIR:At1g58030 InParanoid:Q9ASS7 OMA:RRIVAGW PhylomeDB:Q9ASS7 ProtClustDB:CLSN2680360 Genevestigator:Q9ASS7 Uniprot:Q9ASS7
Root	Isotig01500	15	42	-1.614	7.30E-05	TAIR|locus:2196245 - symbol:CAT2 "cationic amino acid transporter 2" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=IEA;ISS] [GO:0006865 "amino acid transport" evidence=IEA] [GO:0015171 "amino acid transmembrane transporter activity" evidence=IEA] [GO:0016020 "membrane" evidence=ISS] [GO:0055085 "transmembrane transport" evidence=IEA] [GO:0009705 "plant-type vacuole membrane" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] InterPro:IPR002293 PIRSF:PIRSF006060 GO:GO:0016021 EMBL:CP002684 eggNOG:COG0531 PANTHER:PTHR11785 GO:GO:0015171 GO:GO:0009705 InterPro:IPR015606 PANTHER:PTHR11785:SF53 EMBL:AF367304 EMBL:BT000457 EMBL:BT046174 IPI:IPI00542604 RefSeq:NP_849822.1 UniGene:At.43759 ProteinModelPortal:Q9ASS7 PRIDE:Q8H182 EnsemblPlants:AT1G58030.1 GeneID:842170 KEGG:ath:AT1G58030 TAIR:At1g58030 InParanoid:Q9ASS7 OMA:RRIVAGW PhylomeDB:Q9ASS7 ProtClustDB:CLSN2680360 Genevestigator:Q9ASS7 Uniprot:Q9ASS7
Root	Isotig01501	15	40	-1.544	0.00017868	TAIR|locus:2196245 - symbol:CAT2 "cationic amino acid transporter 2" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=IEA;ISS] [GO:0006865 "amino acid transport" evidence=IEA] [GO:0015171 "amino acid transmembrane transporter activity" evidence=IEA] [GO:0016020 "membrane" evidence=ISS] [GO:0055085 "transmembrane transport" evidence=IEA] [GO:0009705 "plant-type vacuole membrane" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] InterPro:IPR002293 PIRSF:PIRSF006060 GO:GO:0016021 EMBL:CP002684 eggNOG:COG0531 PANTHER:PTHR11785 GO:GO:0015171 GO:GO:0009705 InterPro:IPR015606 PANTHER:PTHR11785:SF53 EMBL:AF367304 EMBL:BT000457 EMBL:BT046174 IPI:IPI00542604 RefSeq:NP_849822.1 UniGene:At.43759 ProteinModelPortal:Q9ASS7 PRIDE:Q8H182 EnsemblPlants:AT1G58030.1 GeneID:842170 KEGG:ath:AT1G58030 TAIR:At1g58030 InParanoid:Q9ASS7 OMA:RRIVAGW PhylomeDB:Q9ASS7 ProtClustDB:CLSN2680360 Genevestigator:Q9ASS7 Uniprot:Q9ASS7

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig01508	38	9	1.949	3.95E-05	TAIR|locus:2016407 - symbol:AT1G19450 "AT1G19450" species:3702 "Arabidopsis thaliana" [GO:0005351 "sugar:hydrogen symporter activity" evidence=ISS] [GO:0006810 "transport" evidence=IEA] [GO:0015144 "carbohydrate transmembrane transporter activity" evidence=ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0055085 "transmembrane transport" evidence=IEA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] InterPro:IPR003663 InterPro:IPR005828 InterPro:IPR005829 Pfam:PF00083 PRINTS:PR00171 PROSITE:PS00216 PROSITE:PS00217 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005774 eggNOG:COG0477 InterPro:IPR016196 SUPFAM:SSF103473 GO:GO:0008643 InterPro:IPR020846 PROSITE:PS50850 HOGENOM:HBG744444 GO:GO:0022891 TIGRFAMs:TIGR00879 EMBL:AC025808 EMBL:AY059848 EMBL:AY093274 IPI:IPI00534617 RefSeq:NP_173377.1 UniGene:At.22941 ProteinModelPortal:Q93YP9 IntAct:Q93YP9 PRIDE:Q93YP9 EnsemblPlants:AT1G19450.1 GeneID:838529 KEGG:ath:AT1G19450 TAIR:At1g19450 InParanoid:Q93YP9 OMA:SIGMTIS PhylomeDB:Q93YP9 ProtClustDB:CLSN2682491 ArrayExpress:Q93YP9 Genevestigator:Q93YP9 GermOnline:AT1G19450 Uniprot:Q93YP9
Root	Isotig01509	38	9	1.949	3.95E-05	TAIR|locus:2016407 - symbol:AT1G19450 "AT1G19450" species:3702 "Arabidopsis thaliana" [GO:0005351 "sugar:hydrogen symporter activity" evidence=ISS] [GO:0006810 "transport" evidence=IEA] [GO:0015144 "carbohydrate transmembrane transporter activity" evidence=ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0055085 "transmembrane transport" evidence=IEA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] InterPro:IPR003663 InterPro:IPR005828 InterPro:IPR005829 Pfam:PF00083 PRINTS:PR00171 PROSITE:PS00216 PROSITE:PS00217 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005774 eggNOG:COG0477 InterPro:IPR016196 SUPFAM:SSF103473 GO:GO:0008643 InterPro:IPR020846 PROSITE:PS50850 HOGENOM:HBG744444 GO:GO:0022891 TIGRFAMs:TIGR00879 EMBL:AC025808 EMBL:AY059848 EMBL:AY093274 IPI:IPI00534617 RefSeq:NP_173377.1 UniGene:At.22941 ProteinModelPortal:Q93YP9 IntAct:Q93YP9 PRIDE:Q93YP9 EnsemblPlants:AT1G19450.1 GeneID:838529 KEGG:ath:AT1G19450 TAIR:At1g19450 InParanoid:Q93YP9 OMA:SIGMTIS PhylomeDB:Q93YP9 ProtClustDB:CLSN2682491 ArrayExpress:Q93YP9 Genevestigator:Q93YP9 GermOnline:AT1G19450 Uniprot:Q93YP9
Root	Isotig01510	37	11	1.621	0.00035625	TAIR|locus:2016407 - symbol:AT1G19450 "AT1G19450" species:3702 "Arabidopsis thaliana" [GO:0005351 "sugar:hydrogen symporter activity" evidence=ISS] [GO:0006810 "transport" evidence=IEA] [GO:0015144 "carbohydrate transmembrane transporter activity" evidence=ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0055085 "transmembrane transport" evidence=IEA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] InterPro:IPR003663 InterPro:IPR005828 InterPro:IPR005829 Pfam:PF00083 PRINTS:PR00171 PROSITE:PS00216 PROSITE:PS00217 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005774 eggNOG:COG0477 InterPro:IPR016196 SUPFAM:SSF103473 GO:GO:0008643 InterPro:IPR020846 PROSITE:PS50850 HOGENOM:HBG744444 GO:GO:0022891 TIGRFAMs:TIGR00879 EMBL:AC025808 EMBL:AY059848 EMBL:AY093274 IPI:IPI00534617 RefSeq:NP_173377.1 UniGene:At.22941 ProteinModelPortal:Q93YP9 IntAct:Q93YP9 PRIDE:Q93YP9 EnsemblPlants:AT1G19450.1 GeneID:838529 KEGG:ath:AT1G19450 TAIR:At1g19450 InParanoid:Q93YP9 OMA:SIGMTIS PhylomeDB:Q93YP9 ProtClustDB:CLSN2682491 ArrayExpress:Q93YP9 Genevestigator:Q93YP9 GermOnline:AT1G19450 Uniprot:Q93YP9
Root	Isotig01511	37	11	1.621	0.00035625	TAIR|locus:2016407 - symbol:AT1G19450 "AT1G19450" species:3702 "Arabidopsis thaliana" [GO:0005351 "sugar:hydrogen symporter activity" evidence=ISS] [GO:0006810 "transport" evidence=IEA] [GO:0015144 "carbohydrate transmembrane transporter activity" evidence=ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0055085 "transmembrane transport" evidence=IEA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] InterPro:IPR003663 InterPro:IPR005828 InterPro:IPR005829 Pfam:PF00083 PRINTS:PR00171 PROSITE:PS00216 PROSITE:PS00217 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005774 eggNOG:COG0477 InterPro:IPR016196 SUPFAM:SSF103473 GO:GO:0008643 InterPro:IPR020846 PROSITE:PS50850 HOGENOM:HBG744444 GO:GO:0022891 TIGRFAMs:TIGR00879 EMBL:AC025808 EMBL:AY059848 EMBL:AY093274 IPI:IPI00534617 RefSeq:NP_173377.1 UniGene:At.22941 ProteinModelPortal:Q93YP9 IntAct:Q93YP9 PRIDE:Q93YP9 EnsemblPlants:AT1G19450.1 GeneID:838529 KEGG:ath:AT1G19450 TAIR:At1g19450 InParanoid:Q93YP9 OMA:SIGMTIS PhylomeDB:Q93YP9 ProtClustDB:CLSN2682491 ArrayExpress:Q93YP9 Genevestigator:Q93YP9 GermOnline:AT1G19450 Uniprot:Q93YP9

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig01512	36	10	1.719	0.000240715	TAIR|locus:2025132 - symbol:ERDL6 "AT1G75220" species:3702 "Arabidopsis thaliana" [GO:0005351 "sugar:hydrogen symporter activity" evidence=ISS] [GO:0006810 "transport" evidence=IEA] [GO:0015144 "carbohydrate transmembrane transporter activity" evidence=ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0055085 "transmembrane transport" evidence=IEA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR003663 InterPro:IPR005828 InterPro:IPR005829 Pfam:PF00083 PRINTS:PR00171 PROSITE:PS00216 PROSITE:PS00217 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005774 eggNOG:COG0477 InterPro:IPR016196 SUPFAM:SSF103473 GO:GO:0008643 InterPro:IPR020846 PROSITE:PS50850 HOGENOM:HBG744444 GO:GO:0022891 TIGRFAMs:TIGR00879 EMBL:AC025814 ProtClustDB:CLSN2682491 EMBL:AF412060 EMBL:AY124845 IPI:IPI00528914 PIR:E96782 RefSeq:NP_177658.1 UniGene:At.22004 ProteinModelPortal:Q9FRL3 IntAct:Q9FRL3 PRIDE:Q9FRL3 ProMEX:Q9FRL3 EnsemblPlants:AT1G75220.1 GeneID:843859 KEGG:ath:AT1G75220 TAIR:At1g75220 InParanoid:Q9FRL3 OMA:CISFAKD PhylomeDB:Q9FRL3 Genevestigator:Q9FRL3 GermOnline:AT1G75220 Uniprot:Q9FRL3
Root	Isotig01513	36	10	1.719	0.000240715	TAIR|locus:2025132 - symbol:ERDL6 "AT1G75220" species:3702 "Arabidopsis thaliana" [GO:0005351 "sugar:hydrogen symporter activity" evidence=ISS] [GO:0006810 "transport" evidence=IEA] [GO:0015144 "carbohydrate transmembrane transporter activity" evidence=ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0055085 "transmembrane transport" evidence=IEA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR003663 InterPro:IPR005828 InterPro:IPR005829 Pfam:PF00083 PRINTS:PR00171 PROSITE:PS00216 PROSITE:PS00217 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005774 eggNOG:COG0477 InterPro:IPR016196 SUPFAM:SSF103473 GO:GO:0008643 InterPro:IPR020846 PROSITE:PS50850 HOGENOM:HBG744444 GO:GO:0022891 TIGRFAMs:TIGR00879 EMBL:AC025814 ProtClustDB:CLSN2682491 EMBL:AF412060 EMBL:AY124845 IPI:IPI00528914 PIR:E96782 RefSeq:NP_177658.1 UniGene:At.22004 ProteinModelPortal:Q9FRL3 IntAct:Q9FRL3 PRIDE:Q9FRL3 ProMEX:Q9FRL3 EnsemblPlants:AT1G75220.1 GeneID:843859 KEGG:ath:AT1G75220 TAIR:At1g75220 InParanoid:Q9FRL3 OMA:CISFAKD PhylomeDB:Q9FRL3 Genevestigator:Q9FRL3 GermOnline:AT1G75220 Uniprot:Q9FRL3
Root	Isotig01514	9	27	-1.714	0.000905257	TAIR|locus:2040721 - symbol:SLT1 "AT2G37570" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0042538 "hyperosmotic salinity response" evidence=IMP] EMBL:AC004684 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0042538 UniGene:At.12789 EMBL:AF213400 EMBL:AY054667 EMBL:AY081508 IPI:IPI00542332 PIR:T02523 RefSeq:NP_565864.1 UniGene:At.74051 ProteinModelPortal:O80926 SMR:O80926 EnsemblPlants:AT2G37570.1 GeneID:818333 KEGG:ath:AT2G37570 TAIR:At2g37570 eggNOG:NOG282356 HOGENOM:HBG591490 InParanoid:O80926 OMA:SEHCPPG PhylomeDB:O80926 ProtClustDB:CLSN2688307 ArrayExpress:O80926 Genevestigator:O80926 Uniprot:O80926
Root	Isotig01515	9	27	-1.714	0.000905257	TAIR|locus:2040721 - symbol:SLT1 "AT2G37570" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0042538 "hyperosmotic salinity response" evidence=IMP] EMBL:AC004684 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0042538 UniGene:At.12789 EMBL:AF213400 EMBL:AY054667 EMBL:AY081508 IPI:IPI00542332 PIR:T02523 RefSeq:NP_565864.1 UniGene:At.74051 ProteinModelPortal:O80926 SMR:O80926 EnsemblPlants:AT2G37570.1 GeneID:818333 KEGG:ath:AT2G37570 TAIR:At2g37570 eggNOG:NOG282356 HOGENOM:HBG591490 InParanoid:O80926 OMA:SEHCPPG PhylomeDB:O80926 ProtClustDB:CLSN2688307 ArrayExpress:O80926 Genevestigator:O80926 Uniprot:O80926
Root	Isotig01516	9	27	-1.714	0.000905257	TAIR|locus:2040721 - symbol:SLT1 "AT2G37570" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0042538 "hyperosmotic salinity response" evidence=IMP] EMBL:AC004684 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0042538 UniGene:At.12789 EMBL:AF213400 EMBL:AY054667 EMBL:AY081508 IPI:IPI00542332 PIR:T02523 RefSeq:NP_565864.1 UniGene:At.74051 ProteinModelPortal:O80926 SMR:O80926 EnsemblPlants:AT2G37570.1 GeneID:818333 KEGG:ath:AT2G37570 TAIR:At2g37570 eggNOG:NOG282356 HOGENOM:HBG591490 InParanoid:O80926 OMA:SEHCPPG PhylomeDB:O80926 ProtClustDB:CLSN2688307 ArrayExpress:O80926 Genevestigator:O80926 Uniprot:O80926
Root	Isotig01517	9	27	-1.714	0.000905257	TAIR|locus:2040721 - symbol:SLT1 "AT2G37570" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0042538 "hyperosmotic salinity response" evidence=IMP] EMBL:AC004684 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0042538 UniGene:At.12789 EMBL:AF213400 EMBL:AY054667 EMBL:AY081508 IPI:IPI00542332 PIR:T02523 RefSeq:NP_565864.1 UniGene:At.74051 ProteinModelPortal:O80926 SMR:O80926 EnsemblPlants:AT2G37570.1 GeneID:818333 KEGG:ath:AT2G37570

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						TAIR:At2g37570 eggNOG:NOG282356 HOGENOM:HBG591490 InParanoid:O80926 OMA:SEHCPPG PhylomeDB:O80926 ProtClustDB:CLSN2688307 ArrayExpress:O80926 Genevestigator:O80926 Uniprot:O80926
Root	Isotig01518	7	25	-1.965	0.000455586	TAIR|locus:2040721 - symbol:SLT1 "AT2G37570" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0042538 "hyperosmotic salinity response" evidence=IMP] EMBL:AC004684 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0042538 UniGene:At.12789 EMBL:AF213400 EMBL:AY054667 EMBL:AY081508 IPI:IPI00542332 PIR:T02523 RefSeq:NP_565864.1 UniGene:At.74051 ProteinModelPortal:O80926 SMR:O80926 EnsemblPlants:AT2G37570.1 GeneID:818333 KEGG:ath:AT2G37570 TAIR:At2g37570 eggNOG:NOG282356 HOGENOM:HBG591490 InParanoid:O80926 OMA:SEHCPPG PhylomeDB:O80926 ProtClustDB:CLSN2688307 ArrayExpress:O80926 Genevestigator:O80926 Uniprot:O80926
Root	Isotig01519	7	25	-1.965	0.000455586	TAIR|locus:2040721 - symbol:SLT1 "AT2G37570" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0042538 "hyperosmotic salinity response" evidence=IMP] EMBL:AC004684 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0042538 UniGene:At.12789 EMBL:AF213400 EMBL:AY054667 EMBL:AY081508 IPI:IPI00542332 PIR:T02523 RefSeq:NP_565864.1 UniGene:At.74051 ProteinModelPortal:O80926 SMR:O80926 EnsemblPlants:AT2G37570.1 GeneID:818333 KEGG:ath:AT2G37570 TAIR:At2g37570 eggNOG:NOG282356 HOGENOM:HBG591490 InParanoid:O80926 OMA:SEHCPPG PhylomeDB:O80926 ProtClustDB:CLSN2688307 ArrayExpress:O80926 Genevestigator:O80926 Uniprot:O80926
Root	Isotig01520	15	37	-1.432	0.000655976	TAIR|locus:2030170 - symbol:CKL2 "casein kinase 1-like protein 2" species:3702 "Arabidopsis thaliana" [GO:0004672 "protein kinase activity" evidence=IEA] [GO:0004674 "protein serine/threonine kinase activity" evidence=IEA] [GO:0005524 "ATP binding" evidence=IEA] [GO:0016301 "kinase activity" evidence=ISS] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] InterPro:IPR000719 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 Pfam:PF00069 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005886 GO:GO:0005524 GO:GO:0005634 GO:GO:0005737 eggNOG:COG0515 SUPFAM:SSF56112 GO:GO:0004674 HOGENOM:HBG755340 EMBL:AC010926 KO:K02218 OMA:MDLRVGN HSSP:Q06486 EMBL:AY059850 EMBL:BT010328 EMBL:AY943843 IPI:IPI00517772 PIR:H96751 RefSeq:NP_177415.1 UniGene:At.19326 ProteinModelPortal:Q9CAI5 SMR:Q9CAI5 IntAct:Q9CAI5 STRING:Q9CAI5 PRIDE:Q9CAI5 DNASU:843603 EnsemblPlants:AT1G72710.1 GeneID:843603 KEGG:ath:AT1G72710 TAIR:At1g72710 InParanoid:Q9CAI5 PhylomeDB:Q9CAI5 ProtClustDB:CLSN2912728 Genevestigator:Q9CAI5 Uniprot:Q9CAI5
Root	Isotig01523	14	37	-1.531	0.000341051	TAIR|locus:2030170 - symbol:CKL2 "casein kinase 1-like protein 2" species:3702 "Arabidopsis thaliana" [GO:0004672 "protein kinase activity" evidence=IEA] [GO:0004674 "protein serine/threonine kinase activity" evidence=IEA] [GO:0005524 "ATP binding" evidence=IEA] [GO:0016301 "kinase activity" evidence=ISS] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] InterPro:IPR000719 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 Pfam:PF00069 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005886 GO:GO:0005524 GO:GO:0005634 GO:GO:0005737 eggNOG:COG0515 SUPFAM:SSF56112 GO:GO:0004674 HOGENOM:HBG755340 EMBL:AC010926 KO:K02218 OMA:MDLRVGN HSSP:Q06486 EMBL:AY059850 EMBL:BT010328 EMBL:AY943843 IPI:IPI00517772 PIR:H96751 RefSeq:NP_177415.1 UniGene:At.19326 ProteinModelPortal:Q9CAI5 SMR:Q9CAI5 IntAct:Q9CAI5 STRING:Q9CAI5 PRIDE:Q9CAI5 DNASU:843603 EnsemblPlants:AT1G72710.1 GeneID:843603 KEGG:ath:AT1G72710 TAIR:At1g72710 InParanoid:Q9CAI5 PhylomeDB:Q9CAI5 ProtClustDB:CLSN2912728 Genevestigator:Q9CAI5 Uniprot:Q9CAI5
Root	Isotig01524	16	38	-1.377	0.000799708	TAIR|locus:2030170 - symbol:CKL2 "casein kinase 1-like protein 2" species:3702 "Arabidopsis thaliana" [GO:0004672 "protein kinase activity" evidence=IEA] [GO:0004674 "protein serine/threonine kinase activity" evidence=IEA] [GO:0005524 "ATP binding" evidence=IEA] [GO:0016301 "kinase activity" evidence=ISS] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] InterPro:IPR000719 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 Pfam:PF00069 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005886 GO:GO:0005524 GO:GO:0005634 GO:GO:0005737 eggNOG:COG0515 SUPFAM:SSF56112 GO:GO:0004674 HOGENOM:HBG755340 EMBL:AC010926 KO:K02218 OMA:MDLRVGN HSSP:Q06486 EMBL:AY059850 EMBL:BT010328 EMBL:AY943843 IPI:IPI00517772 PIR:H96751 RefSeq:NP_177415.1 UniGene:At.19326 ProteinModelPortal:Q9CAI5 SMR:Q9CAI5 IntAct:Q9CAI5 STRING:Q9CAI5 PRIDE:Q9CAI5 DNASU:843603 EnsemblPlants:AT1G72710.1 GeneID:843603 KEGG:ath:AT1G72710 TAIR:At1g72710 InParanoid:Q9CAI5 PhylomeDB:Q9CAI5 ProtClustDB:CLSN2912728 Genevestigator:Q9CAI5 Uniprot:Q9CAI5

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig01525	16	38	-1.377	0.000799708	TAIR|locus:2030170 - symbol:CKL2 "casein kinase 1-like protein 2" species:3702 "Arabidopsis thaliana" [GO:0004672 "protein kinase activity" evidence=IEA] [GO:0004674 "protein serine/threonine kinase activity" evidence=IEA] [GO:0005524 "ATP binding" evidence=IEA] [GO:0016301 "kinase activity" evidence=ISS] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] InterPro:IPR000719 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 Pfam:PF00069 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005886 GO:GO:0005524 GO:GO:0005634 GO:GO:0005737 eggNOG:COG0515 SUPFAM:SSF56112 GO:GO:0004674 HOGENOM:HBG755340 EMBL:AC010926 KO:K02218 OMA:MDLRVGN HSSP:Q06486 EMBL:AY059850 EMBL:BT010328 EMBL:AY943843 IPI:IPI00517772 PIR:H96751 RefSeq:NP_177415.1 UniGene:At.19326 ProteinModelPortal:Q9CAI5 SMR:Q9CAI5 IntAct:Q9CAI5 STRING:Q9CAI5 PRIDE:Q9CAI5 DNASU:843603 EnsemblPlants:AT1G72710.1 GeneID:843603 KEGG:ath:AT1G72710 TAIR:At1g72710 InParanoid:Q9CAI5 PhylomeDB:Q9CAI5 ProtClustDB:CLSN2912728 Genevestigator:Q9CAI5 Uniprot:Q9CAI5
Root	Isotig01532	7	55	-3.103	1.58E-11	TAIR|locus:2198035 - symbol:PMEAMT "AT1G48600" species:3702 "Arabidopsis thaliana" [GO:0000234 "phosphoethanolamine N-methyltransferase activity" evidence=ISS] [GO:0006656 "phosphatidylcholine biosynthetic process" evidence=IGI;IDA] [GO:0052667 "phosphomethylethanolamine N-methyltransferase activity" evidence=IDA] EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005737 EMBL:AC020889 eggNOG:COG0500 GO:GO:0006656 HOGENOM:HBG320513 ProtClustDB:PLN02336 GO:GO:0000234 EMBL:AF428454 EMBL:AY063866 EMBL:AY133811 IPI:IPI00539739 PIR:F96525 RefSeq:NP_175293.1 UniGene:At.22426 ProteinModelPortal:Q944H0 SMR:Q944H0 PRIDE:Q944H0 EnsemblPlants:AT1G48600.1 GeneID:841281 KEGG:ath:AT1G48600 TAIR:At1g48600 InParanoid:Q944H0 PhylomeDB:Q944H0 ArrayExpress:Q944H0 Genevestigator:Q944H0 GO:GO:0052667 Uniprot:Q944H0
Root	Isotig01533	6	53	-3.272	1.24E-11	TAIR|locus:2198035 - symbol:PMEAMT "AT1G48600" species:3702 "Arabidopsis thaliana" [GO:0000234 "phosphoethanolamine N-methyltransferase activity" evidence=ISS] [GO:0006656 "phosphatidylcholine biosynthetic process" evidence=IGI;IDA] [GO:0052667 "phosphomethylethanolamine N-methyltransferase activity" evidence=IDA] EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005737 EMBL:AC020889 eggNOG:COG0500 GO:GO:0006656 HOGENOM:HBG320513 ProtClustDB:PLN02336 GO:GO:0000234 EMBL:AF428454 EMBL:AY063866 EMBL:AY133811 IPI:IPI00539739 PIR:F96525 RefSeq:NP_175293.1 UniGene:At.22426 ProteinModelPortal:Q944H0 SMR:Q944H0 PRIDE:Q944H0 EnsemblPlants:AT1G48600.1 GeneID:841281 KEGG:ath:AT1G48600 TAIR:At1g48600 InParanoid:Q944H0 PhylomeDB:Q944H0 ArrayExpress:Q944H0 Genevestigator:Q944H0 GO:GO:0052667 Uniprot:Q944H0
Root	Isotig01534	7	55	-3.103	1.58E-11	TAIR|locus:2088535 - symbol:XPL1 "AT3G18000" species:3702 "Arabidopsis thaliana" [GO:0000234 "phosphoethanolamine N-methyltransferase activity" evidence=IGI;ISS] [GO:0005737 "cytoplasm" evidence=ISS] [GO:0006656 "phosphatidylcholine biosynthetic process" evidence=IGI] [GO:0008168 "methyltransferase activity" evidence=ISS] [GO:0009555 "pollen development" evidence=IMP] [GO:0009826 "unidimensional cell growth" evidence=IMP] [GO:0042425 "choline biosynthetic process" evidence=IMP] [GO:0048528 "post-embryonic root development" evidence=IMP] [GO:0009860 "pollen tube growth" evidence=IMP] [GO:0010183 "pollen tube guidance" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR013216 Pfam:PF08241 GO:GO:0005829 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0009555 GO:GO:0009860 eggNOG:COG0500 GO:GO:0006656 GO:GO:0010183 EMBL:AB019230 GO:GO:0048528 EMBL:AF197940 EMBL:AF367299 EMBL:AY058175 EMBL:AY091683 EMBL:AY093093 IPI:IPI00542357 RefSeq:NP_188427.2 UniGene:At.21159 ProteinModelPortal:Q9FR44 SMR:Q9FR44 STRING:Q9FR44 PRIDE:Q9FR44 EnsemblPlants:AT3G18000.1 GeneID:821324 KEGG:ath:AT3G18000 TAIR:At3g18000 HOGENOM:HBG320513 InParanoid:Q9FR44 KO:K05929 OMA:DQRWGLF PhylomeDB:Q9FR44 ProtClustDB:PLN02336 Genevestigator:Q9FR44 GermOnline:AT3G18000 GO:GO:0000234 GO:GO:0042425 Uniprot:Q9FR44
Root	Isotig01535	6	53	-3.272	1.24E-11	TAIR|locus:2088535 - symbol:XPL1 "AT3G18000" species:3702 "Arabidopsis thaliana" [GO:0000234 "phosphoethanolamine N-methyltransferase activity" evidence=IGI;ISS] [GO:0005737 "cytoplasm" evidence=ISS] [GO:0006656 "phosphatidylcholine biosynthetic process" evidence=IGI] [GO:0008168 "methyltransferase activity" evidence=ISS] [GO:0009555 "pollen development" evidence=IMP] [GO:0009826 "unidimensional cell growth" evidence=IMP] [GO:0042425 "choline biosynthetic process" evidence=IMP] [GO:0048528 "post-embryonic root development" evidence=IMP] [GO:0009860 "pollen tube growth" evidence=IMP] [GO:0010183 "pollen tube guidance" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR013216 Pfam:PF08241 GO:GO:0005829 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0009555 GO:GO:0009860

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						eggNOG:COG0500 GO:GO:0006656 GO:GO:0010183 EMBL:AB019230 GO:GO:0048528 EMBL:AF197940 EMBL:AF367299 EMBL:AY058175 EMBL:AY091683 EMBL:AY093093 IPI:IPI00542357 RefSeq:NP_188427.2 UniGene:At.21159 ProteinModelPortal:Q9FR44 SMR:Q9FR44 STRING:Q9FR44 PRIDE:Q9FR44 EnsemblPlants:AT3G18000.1 GeneID:821324 KEGG:ath:AT3G18000 TAIR:At3g18000 HOGENOM:HBG320513 InParanoid:Q9FR44 KO:K05929 OMA:DQRWGLF PhylomeDB:Q9FR44 ProtClustDB:PLN02336 Genevestigator:Q9FR44 GermOnline:AT3G18000 GO:GO:0000234 GO:GO:0042425 Uniprot:Q9FR44
Root	Isotig01536	6	52	-3.244	2.28E-11	TAIR|locus:2198035 - symbol:PMEAMT "AT1G48600" species:3702 "Arabidopsis thaliana" [GO:0000234 "phosphoethanolamine N-methyltransferase activity" evidence=ISS] [GO:0006656 "phosphatidylcholine biosynthetic process" evidence=IGI;IDA] [GO:0052667 "phosphomethylethanolamine N-methyltransferase activity" evidence=IDA] EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005737 EMBL:AC020889 eggNOG:COG0500 GO:GO:0006656 HOGENOM:HBG320513 ProtClustDB:PLN02336 GO:GO:0000234 EMBL:AF428454 EMBL:AY063866 EMBL:AY133811 IPI:IPI00539739 PIR:F96525 RefSeq:NP_175293.1 UniGene:At.22426 ProteinModelPortal:Q944H0 SMR:Q944H0 PRIDE:Q944H0 EnsemblPlants:AT1G48600.1 GeneID:841281 KEGG:ath:AT1G48600 TAIR:At1g48600 InParanoid:Q944H0 PhylomeDB:Q944H0 ArrayExpress:Q944H0 Genevestigator:Q944H0 GO:GO:0052667 Uniprot:Q944H0
Root	Isotig01537	6	52	-3.244	2.28E-11	TAIR|locus:2088535 - symbol:XPL1 "AT3G18000" species:3702 "Arabidopsis thaliana" [GO:0000234 "phosphoethanolamine N-methyltransferase activity" evidence=IGI;ISS] [GO:0005737 "cytoplasm" evidence=ISS] [GO:0006656 "phosphatidylcholine biosynthetic process" evidence=IGI] [GO:0008168 "methyltransferase activity" evidence=ISS] [GO:0009555 "pollen development" evidence=IMP] [GO:0009826 "unidimensional cell growth" evidence=IMP] [GO:0042425 "choline biosynthetic process" evidence=IMP] [GO:0048528 "post-embryonic root development" evidence=IMP] [GO:0009860 "pollen tube growth" evidence=IMP] [GO:0010183 "pollen tube guidance" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR013216 Pfam:PF08241 GO:GO:0005829 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0009555 GO:GO:0009860 eggNOG:COG0500 GO:GO:0006656 GO:GO:0010183 EMBL:AB019230 GO:GO:0048528 EMBL:AF197940 EMBL:AF367299 EMBL:AY058175 EMBL:AY091683 EMBL:AY093093 IPI:IPI00542357 RefSeq:NP_188427.2 UniGene:At.21159 ProteinModelPortal:Q9FR44 SMR:Q9FR44 STRING:Q9FR44 PRIDE:Q9FR44 EnsemblPlants:AT3G18000.1 GeneID:821324 KEGG:ath:AT3G18000 TAIR:At3g18000 HOGENOM:HBG320513 InParanoid:Q9FR44 KO:K05929 OMA:DQRWGLF PhylomeDB:Q9FR44 ProtClustDB:PLN02336 Genevestigator:Q9FR44 GermOnline:AT3G18000 GO:GO:0000234 GO:GO:0042425 Uniprot:Q9FR44
Root	Isotig01538	42	2	4.263	2.46E-10	No hit
Root	Isotig01539	51	3	3.958	8.66E-12	No hit
Root	Isotig01540	31	3	3.240	8.04E-07	No hit
Root	Isotig01541	40	4	3.193	2.57E-08	No hit
Root	Isotig01543	0	11	-4.588	0.000569522	No hit
Root	Isotig01549	0	13	-4.829	0.000155955	TAIR|locus:2089784 - symbol:AT3G17770 species:3702 "Arabidopsis thaliana" [GO:0004371 "glycerone kinase activity" evidence=IEA;ISS] [GO:0005524 "ATP binding" evidence=IEA] [GO:0006071 "glycerol metabolic process" evidence=IEA;ISS] InterPro:IPR004006 InterPro:IPR004007 InterPro:IPR012734 Pfam:PF02733 Pfam:PF02734 PROSITE:PS51480 PROSITE:PS51481 GO:GO:0005524 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0006071 eggNOG:COG2376 HOGENOM:HBG473357 GO:GO:0004371 SUPFAM:SSF101473 TIGRFAMs:TIGR02361 OMA:GFVGPGL EMBL:BT023733 IPI:IPI00529007 RefSeq:NP_188404.1 UniGene:At.38659 UniGene:At.67784 ProteinModelPortal:Q494P3 SMR:Q494P3 PRIDE:Q494P3 EnsemblPlants:AT3G17770.1 GeneID:821045 KEGG:ath:AT3G17770 TAIR:At3g17770 InParanoid:Q494P3 PhylomeDB:Q494P3 ProtClustDB:CLSN2684338 Genevestigator:Q494P3 Uniprot:Q494P3
Root	Isotig01574	0	28	-5.936	1.79E-08	TAIR|locus:2010718 - symbol:NAS4 "AT1G56430" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0030410 "nicotianamine synthase activity" evidence=IGI] [GO:0030418 "nicotianamine biosynthetic process" evidence=IGI] InterPro:IPR004298 Pfam:PF03059 PROSITE:PS51142 EMBL:CP002684 GenomeReviews:CT485782_GR EMBL:AC058785 HOGENOM:HBG594037 KO:K05953 ProtClustDB:PLN03075 GO:GO:0030410 GO:GO:0030418 EMBL:AY099758 EMBL:AY128890 IPI:IPI00540066 PIR:B96606 RefSeq:NP_176038.1 UniGene:At.66920 ProteinModelPortal:Q9C7X5 SMR:Q9C7X5 IntAct:Q9C7X5 STRING:Q9C7X5 PRIDE:Q9C7X5 DNASU:842096 EnsemblPlants:AT1G56430.1 GeneID:842096 KEGG:ath:AT1G56430 TAIR:At1g56430 eggNOG:NOG305103 InParanoid:Q9C7X5 OMA:SENIQEM PhylomeDB:Q9C7X5 ArrayExpress:Q9C7X5 Genevestigator:Q9C7X5 GermOnline:AT1G56430 Uniprot:Q9C7X5

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig01575	0	23	-5.653	3.32E-07	TAIR|locus:2010718 - symbol:NAS4 "AT1G56430" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0030410 "nicotianamine synthase activity" evidence=IGI] [GO:0030418 "nicotianamine biosynthetic process" evidence=IGI] InterPro:IPR004298 Pfam:PF03059 PROSITE:PS51142 EMBL:CP002684 GenomeReviews:CT485782_GR EMBL:AC058785 HOGENOM:HBG594037 KO:K05953 ProtClustDB:PLN03075 GO:GO:0030410 GO:GO:0030418 EMBL:AY099758 EMBL:AY128890 IPI:IPI00540066 PIR:B96606 RefSeq:NP_176038.1 UniGene:At.66920 ProteinModelPortal:Q9C7X5 SMR:Q9C7X5 IntAct:Q9C7X5 STRING:Q9C7X5 PRIDE:Q9C7X5 DNASU:842096 EnsemblPlants:AT1G56430.1 GeneID:842096 KEGG:ath:AT1G56430 TAIR:At1g56430 eggNOG:NOG305103 InParanoid:Q9C7X5 OMA:SENIQEM PhylomeDB:Q9C7X5 ArrayExpress:Q9C7X5 Genevestigator:Q9C7X5 GermOnline:AT1G56430 Uniprot:Q9C7X5
Root	Isotig01576	0	29	-5.987	1.01E-08	TAIR|locus:2010718 - symbol:NAS4 "AT1G56430" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0030410 "nicotianamine synthase activity" evidence=IGI] [GO:0030418 "nicotianamine biosynthetic process" evidence=IGI] InterPro:IPR004298 Pfam:PF03059 PROSITE:PS51142 EMBL:CP002684 GenomeReviews:CT485782_GR EMBL:AC058785 HOGENOM:HBG594037 KO:K05953 ProtClustDB:PLN03075 GO:GO:0030410 GO:GO:0030418 EMBL:AY099758 EMBL:AY128890 IPI:IPI00540066 PIR:B96606 RefSeq:NP_176038.1 UniGene:At.66920 ProteinModelPortal:Q9C7X5 SMR:Q9C7X5 IntAct:Q9C7X5 STRING:Q9C7X5 PRIDE:Q9C7X5 DNASU:842096 EnsemblPlants:AT1G56430.1 GeneID:842096 KEGG:ath:AT1G56430 TAIR:At1g56430 eggNOG:NOG305103 InParanoid:Q9C7X5 OMA:SENIQEM PhylomeDB:Q9C7X5 ArrayExpress:Q9C7X5 Genevestigator:Q9C7X5 GermOnline:AT1G56430 Uniprot:Q9C7X5
Root	Isotig01577	0	23	-5.653	3.32E-07	TAIR|locus:2010718 - symbol:NAS4 "AT1G56430" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0030410 "nicotianamine synthase activity" evidence=IGI] [GO:0030418 "nicotianamine biosynthetic process" evidence=IGI] InterPro:IPR004298 Pfam:PF03059 PROSITE:PS51142 EMBL:CP002684 GenomeReviews:CT485782_GR EMBL:AC058785 HOGENOM:HBG594037 KO:K05953 ProtClustDB:PLN03075 GO:GO:0030410 GO:GO:0030418 EMBL:AY099758 EMBL:AY128890 IPI:IPI00540066 PIR:B96606 RefSeq:NP_176038.1 UniGene:At.66920 ProteinModelPortal:Q9C7X5 SMR:Q9C7X5 IntAct:Q9C7X5 STRING:Q9C7X5 PRIDE:Q9C7X5 DNASU:842096 EnsemblPlants:AT1G56430.1 GeneID:842096 KEGG:ath:AT1G56430 TAIR:At1g56430 eggNOG:NOG305103 InParanoid:Q9C7X5 OMA:SENIQEM PhylomeDB:Q9C7X5 ArrayExpress:Q9C7X5 Genevestigator:Q9C7X5 GermOnline:AT1G56430 Uniprot:Q9C7X5
Root	Isotig01578	0	18	-5.299	6.77E-06	TAIR|locus:2010718 - symbol:NAS4 "AT1G56430" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0030410 "nicotianamine synthase activity" evidence=IGI] [GO:0030418 "nicotianamine biosynthetic process" evidence=IGI] InterPro:IPR004298 Pfam:PF03059 PROSITE:PS51142 EMBL:CP002684 GenomeReviews:CT485782_GR EMBL:AC058785 HOGENOM:HBG594037 KO:K05953 ProtClustDB:PLN03075 GO:GO:0030410 GO:GO:0030418 EMBL:AY099758 EMBL:AY128890 IPI:IPI00540066 PIR:B96606 RefSeq:NP_176038.1 UniGene:At.66920 ProteinModelPortal:Q9C7X5 SMR:Q9C7X5 IntAct:Q9C7X5 STRING:Q9C7X5 PRIDE:Q9C7X5 DNASU:842096 EnsemblPlants:AT1G56430.1 GeneID:842096 KEGG:ath:AT1G56430 TAIR:At1g56430 eggNOG:NOG305103 InParanoid:Q9C7X5 OMA:SENIQEM PhylomeDB:Q9C7X5 ArrayExpress:Q9C7X5 Genevestigator:Q9C7X5 GermOnline:AT1G56430 Uniprot:Q9C7X5
Root	Isotig01579	0	19	-5.377	3.67E-06	TAIR|locus:2010718 - symbol:NAS4 "AT1G56430" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0030410 "nicotianamine synthase activity" evidence=IGI] [GO:0030418 "nicotianamine biosynthetic process" evidence=IGI] InterPro:IPR004298 Pfam:PF03059 PROSITE:PS51142 EMBL:CP002684 GenomeReviews:CT485782_GR EMBL:AC058785 HOGENOM:HBG594037 KO:K05953 ProtClustDB:PLN03075 GO:GO:0030410 GO:GO:0030418 EMBL:AY099758 EMBL:AY128890 IPI:IPI00540066 PIR:B96606 RefSeq:NP_176038.1 UniGene:At.66920 ProteinModelPortal:Q9C7X5 SMR:Q9C7X5 IntAct:Q9C7X5 STRING:Q9C7X5 PRIDE:Q9C7X5 DNASU:842096 EnsemblPlants:AT1G56430.1 GeneID:842096 KEGG:ath:AT1G56430 TAIR:At1g56430 eggNOG:NOG305103 InParanoid:Q9C7X5 OMA:SENIQEM PhylomeDB:Q9C7X5 ArrayExpress:Q9C7X5 Genevestigator:Q9C7X5 GermOnline:AT1G56430 Uniprot:Q9C7X5
Root	Isotig01580	68	7	3.151	5.28E-13	No hit
Root	Isotig01585	26	3	2.987	1.35E-05	No hit
Root	Isotig01598	37	103	-1.606	6.08E-10	TAIR|locus:2170318 - symbol:ATMS1 "AT5G17920" species:3702 "Arabidopsis thaliana" [GO:0003871 "5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase activity" evidence=ISS] [GO:0005829 "cytosol" evidence=ISS;IDA] [GO:0009086 "methionine biosynthetic process" evidence=ISS] [GO:0008705 "methionine synthase activity" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0005886 "plasma

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0005777 "peroxisome" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0010043 "response to zinc ion" evidence=IEP] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR002629 InterPro:IPR006276 InterPro:IPR013215 Pfam:PF01717 Pfam:PF08267 PIRSF:PIRSF000382 GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 GO:GO:0048046 GO:GO:0009570 GO:GO:0046686 GO:GO:0005774 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005777 GO:GO:0010043 GO:GO:0008270 GO:GO:0005507 GO:GO:0009651 EMBL:AB011480 UniGene:At.24550 EMBL:U97200 EMBL:AF370522 EMBL:AY048201 EMBL:AY056098 EMBL:AY057499 EMBL:AY069876 EMBL:AY070771 EMBL:AY091692 IPI:IPI00522440 RefSeq:NP_001078599.1 RefSeq:NP_197294.1 UniGene:At.22340 UniGene:At.71028 PDB:1U1H PDB:1U1J PDB:1U1U PDB:1U22 PDBsum:1U1H PDBsum:1U1J PDBsum:1U1U PDBsum:1U22 ProteinModelPortal:O50008 SMR:O50008 IntAct:O50008 STRING:O50008 SWISS-2DPAGE:O50008 PRIDE:O50008 ProMEX:O50008 EnsemblPlants:AT5G17920.1 EnsemblPlants:AT5G17920.2 GeneID:831660 KEGG:ath:AT5G17920 TAIR:At5g17920 eggNOG:COG0620 HOGENOM:HBG287495 InParanoid:O50008 KO:K00549 OMA:NIWANDF PhylomeDB:O50008 ProtClustDB:PLN02475 BRENDA:2.1.1.14 Genevestigator:O50008 GermOnline:AT5G17920 GO:GO:0003871 GO:GO:0008705 TIGRFAMs:TIGR01371 Uniprot:O50008
Root	Isotig01599	48	112	-1.351	1.39E-08	TAIR|locus:2170318 - symbol:ATMS1 "AT5G17920" species:3702 "Arabidopsis thaliana" [GO:0003871 "5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase activity" evidence=ISS] [GO:0005829 "cytosol" evidence=ISS;IDA] [GO:0009086 "methionine biosynthetic process" evidence=ISS] [GO:0008705 "methionine synthase activity" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0005777 "peroxisome" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0010043 "response to zinc ion" evidence=IEP] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR002629 InterPro:IPR006276 InterPro:IPR013215 Pfam:PF01717 Pfam:PF08267 PIRSF:PIRSF000382 GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 GO:GO:0048046 GO:GO:0009570 GO:GO:0046686 GO:GO:0005774 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005777 GO:GO:0010043 GO:GO:0008270 GO:GO:0005507 GO:GO:0009651 EMBL:AB011480 UniGene:At.24550 EMBL:U97200 EMBL:AF370522 EMBL:AY048201 EMBL:AY056098 EMBL:AY057499 EMBL:AY069876 EMBL:AY070771 EMBL:AY091692 IPI:IPI00522440 RefSeq:NP_001078599.1 RefSeq:NP_197294.1 UniGene:At.22340 UniGene:At.71028 PDB:1U1H PDB:1U1J PDB:1U1U PDB:1U22 PDBsum:1U1H PDBsum:1U1J PDBsum:1U1U PDBsum:1U22 ProteinModelPortal:O50008 SMR:O50008 IntAct:O50008 STRING:O50008 SWISS-2DPAGE:O50008 PRIDE:O50008 ProMEX:O50008 EnsemblPlants:AT5G17920.1 EnsemblPlants:AT5G17920.2 GeneID:831660 KEGG:ath:AT5G17920 TAIR:At5g17920 eggNOG:COG0620 HOGENOM:HBG287495 InParanoid:O50008 KO:K00549 OMA:NIWANDF PhylomeDB:O50008 ProtClustDB:PLN02475 BRENDA:2.1.1.14 Genevestigator:O50008 GermOnline:AT5G17920 GO:GO:0003871 GO:GO:0008705 TIGRFAMs:TIGR01371 Uniprot:O50008
Root	Isotig01600	43	96	-1.288	4.15E-07	TAIR|locus:2170318 - symbol:ATMS1 "AT5G17920" species:3702 "Arabidopsis thaliana" [GO:0003871 "5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase activity" evidence=ISS] [GO:0005829 "cytosol" evidence=ISS;IDA] [GO:0009086 "methionine biosynthetic process" evidence=ISS] [GO:0008705 "methionine synthase activity" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0005777 "peroxisome" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0010043 "response to zinc ion" evidence=IEP] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR002629 InterPro:IPR006276 InterPro:IPR013215 Pfam:PF01717 Pfam:PF08267 PIRSF:PIRSF000382 GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 GO:GO:0048046 GO:GO:0009570 GO:GO:0046686 GO:GO:0005774 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005777 GO:GO:0010043 GO:GO:0008270 GO:GO:0005507 GO:GO:0009651 EMBL:AB011480 UniGene:At.24550 EMBL:U97200 EMBL:AF370522 EMBL:AY048201 EMBL:AY056098 EMBL:AY057499 EMBL:AY069876 EMBL:AY070771

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EMBL:AY091692 IPI:IPI00522440 RefSeq:NP_001078599.1 RefSeq:NP_197294.1 UniGene:At.22340 UniGene:At.71028 PDB:1U1H PDB:1U1J PDB:1U1U PDB:1U22 PDBsum:1U1H PDBsum:1U1J PDBsum:1U1U PDBsum:1U22 ProteinModelPortal:O50008 SMR:O50008 IntAct:O50008 STRING:O50008 SWISS-2DPAGE:O50008 PRIDE:O50008 ProMEX:O50008 EnsemblPlants:AT5G17920.1 EnsemblPlants:AT5G17920.2 GeneID:831660 KEGG:ath:AT5G17920 TAIR:At5g17920 eggNOG:COG0620 HOGENOM:HBG287495 InParanoid:O50008 KO:K00549 OMA:NIWANDF PhylomeDB:O50008 ProtClustDB:PLN02475 BRENDA:2.1.1.14 Genevestigator:O50008 GermOnline:AT5G17920 GO:GO:0003871 GO:GO:0008705 TIGRFAMs:TIGR01371 Uniprot:O50008
Root	Isotig01610	74	31	1.126	0.000132088	TAIR|locus:2036451 - symbol:AT1G50920 "AT1G50920" species:3702 "Arabidopsis thaliana" [GO:0000166 "nucleotide binding" evidence=ISS] [GO:0005525 "GTP binding" evidence=IEA] [GO:0016020 "membrane" evidence=IDA] InterPro:IPR006073 InterPro:IPR010674 InterPro:IPR024926 Pfam:PF06858 PIRSF:PIRSF038919 PRINTS:PR00326 GO:GO:0005525 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005730 GO:GO:0016020 GO:GO:0042254 EMBL:AC079284 EMBL:AY096652 IPI:IPI00535306 PIR:C96546 RefSeq:NP_175505.1 UniGene:At.25047 UniGene:At.27911 ProteinModelPortal:Q9C6I8 SMR:Q9C6I8 STRING:Q9C6I8 PRIDE:Q9C6I8 EnsemblPlants:AT1G50920.1 GeneID:841514 KEGG:ath:AT1G50920 TAIR:At1g50920 eggNOG:COG1084 HOGENOM:HBG628350 InParanoid:Q9C6I8 KO:K06943 OMA:FHSIRPL PhylomeDB:Q9C6I8 ProtClustDB:CLSN2718068 ArrayExpress:Q9C6I8 Genevestigator:Q9C6I8 GermOnline:AT1G50920 InterPro:IPR012973 Pfam:PF08155 Uniprot:Q9C6I8
Root	Isotig01612	63	28	1.041	0.000938592	TAIR|locus:2036451 - symbol:AT1G50920 "AT1G50920" species:3702 "Arabidopsis thaliana" [GO:0000166 "nucleotide binding" evidence=ISS] [GO:0005525 "GTP binding" evidence=IEA] [GO:0016020 "membrane" evidence=IDA] InterPro:IPR006073 InterPro:IPR010674 InterPro:IPR024926 Pfam:PF06858 PIRSF:PIRSF038919 PRINTS:PR00326 GO:GO:0005525 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005730 GO:GO:0016020 GO:GO:0042254 EMBL:AC079284 EMBL:AY096652 IPI:IPI00535306 PIR:C96546 RefSeq:NP_175505.1 UniGene:At.25047 UniGene:At.27911 ProteinModelPortal:Q9C6I8 SMR:Q9C6I8 STRING:Q9C6I8 PRIDE:Q9C6I8 EnsemblPlants:AT1G50920.1 GeneID:841514 KEGG:ath:AT1G50920 TAIR:At1g50920 eggNOG:COG1084 HOGENOM:HBG628350 InParanoid:Q9C6I8 KO:K06943 OMA:FHSIRPL PhylomeDB:Q9C6I8 ProtClustDB:CLSN2718068 ArrayExpress:Q9C6I8 Genevestigator:Q9C6I8 GermOnline:AT1G50920 InterPro:IPR012973 Pfam:PF08155 Uniprot:Q9C6I8
Root	Isotig01617	19	47	-1.436	0.000118801	TAIR|locus:2118701 - symbol:AT4G30600 species:3702 "Arabidopsis thaliana" [GO:0000166 "nucleotide binding" evidence=IEA] [GO:0003924 "GTPase activity" evidence=IEA] [GO:0005047 "signal recognition particle binding" evidence=IEA] [GO:0005525 "GTP binding" evidence=IEA;ISS] [GO:0005786 "signal recognition particle, endoplasmic reticulum targeting" evidence=ISS] [GO:0006605 "protein targeting" evidence=ISS] [GO:0006614 "SRP-dependent cotranslational protein targeting to membrane" evidence=IEA] [GO:0006886 "intracellular protein transport" evidence=IEA] [GO:0017111 "nucleoside-triphosphatase activity" evidence=IEA] [GO:0005783 "endoplasmic reticulum" evidence=IDA] InterPro:IPR000897 InterPro:IPR003593 InterPro:IPR007222 InterPro:IPR011012 InterPro:IPR013822 Pfam:PF00448 Pfam:PF02881 Pfam:PF04086 PROSITE:PS00300 SMART:SM00382 SMART:SM00962 GO:GO:0005525 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0004872 GO:GO:0003924 EMBL:AL161577 SUPFAM:SSF64356 eggNOG:COG0552 HOGENOM:HBG562580 GO:GO:0006614 Gene3D:G3DSA:1.20.120.140 SUPFAM:SSF47364 GO:GO:0005785 GO:GO:0005047 KO:K13431 OMA:QGESMMD EMBL:AY065066 EMBL:AY133612 IPI:IPI00534083 PIR:A85358 RefSeq:NP_194789.1 UniGene:At.4581 HSSP:P83749 ProteinModelPortal:Q9M0A0 SMR:Q9M0A0 STRING:Q9M0A0 PRIDE:Q9M0A0 EnsemblPlants:AT4G30600.1 GeneID:829183 KEGG:ath:AT4G30600 TAIR:At4g30600 InParanoid:Q9M0A0 PhylomeDB:Q9M0A0 ProtClustDB:CLSN2685629 ArrayExpress:Q9M0A0 Genevestigator:Q9M0A0 Uniprot:Q9M0A0
Root	Isotig01618	19	43	-1.307	0.000609156	TAIR|locus:2118701 - symbol:AT4G30600 species:3702 "Arabidopsis thaliana" [GO:0000166 "nucleotide binding" evidence=IEA] [GO:0003924 "GTPase activity" evidence=IEA] [GO:0005047 "signal recognition particle binding" evidence=IEA] [GO:0005525 "GTP binding" evidence=IEA;ISS] [GO:0005786 "signal recognition particle, endoplasmic reticulum targeting" evidence=ISS] [GO:0006605 "protein targeting" evidence=ISS] [GO:0006614 "SRP-dependent cotranslational protein targeting to membrane" evidence=IEA] [GO:0006886 "intracellular protein transport" evidence=IEA] [GO:0017111 "nucleoside-triphosphatase activity" evidence=IEA] [GO:0005783 "endoplasmic reticulum" evidence=IDA] InterPro:IPR000897 InterPro:IPR003593 InterPro:IPR007222 InterPro:IPR011012 InterPro:IPR013822 Pfam:PF00448 Pfam:PF02881 Pfam:PF04086 PROSITE:PS00300

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						SMART:SM00382 SMART:SM00962 GO:GO:0005525 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0004872 GO:GO:0003924 EMBL:AL161577 SUPFAM:SSF64356 eggNOG:COG0552 HOGENOM:HBG562580 GO:GO:0006614 Gene3D:G3DSA:1.20.120.140 SUPFAM:SSF47364 GO:GO:0005785 GO:GO:0005047 KO:K13431 OMA:QGESMMD EMBL:AY065066 EMBL:AY133612 IPI:IPI00534083 PIR:A85358 RefSeq:NP_194789.1 UniGene:At.4581 HSSP:P83749 ProteinModelPortal:Q9M0A0 SMR:Q9M0A0 STRING:Q9M0A0 PRIDE:Q9M0A0 EnsemblPlants:AT4G30600.1 GeneID:829183 KEGG:ath:AT4G30600 TAIR:At4g30600 InParanoid:Q9M0A0 PhylomeDB:Q9M0A0 ProtClustDB:CLSN2685629 ArrayExpress:Q9M0A0 Genevestigator:Q9M0A0 Uniprot:Q9M0A0
Root	Isotig01628	14	1	3.678	0.000484579	No hit
Root	Isotig01629	25	0	5.515	3.68E-07	No hit
Root	Isotig01630	30	0	5.778	2.46E-08	No hit
Root	Isotig01632	30	0	5.778	2.46E-08	No hit
Root	Isotig01633	19	0	5.119	1.05E-05	No hit
Root	Isotig01639	105	14	2.778	3.30E-17	No hit
Root	Isotig01640	105	14	2.778	3.30E-17	No hit
Root	Isotig01641	105	14	2.778	3.30E-17	No hit
Root	Isotig01659	53	0	6.599	2.10E-13	TAIR|locus:2179117 - symbol:AT5G01300 "AT5G01300" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0008429 "phosphatidylethanolamine binding" evidence=ISS] Pfam:PF01161 EMBL:CP002688 GenomeReviews:BA000015_GR InterPro:IPR008914 Gene3D:G3DSA:3.90.280.10 SUPFAM:SSF49777 EMBL:AL161746 KO:K06910 HOGENOM:HBG649023 InterPro:IPR005247 TIGRFAMs:TIGR00481 UniGene:At.33912 UniGene:At.48967 EMBL:AY065369 EMBL:AY096477 IPI:IPI00535873 PIR:T48152 RefSeq:NP_195750.1 HSSP:P77368 ProteinModelPortal:Q9M042 SMR:Q9M042 PRIDE:Q9M042 ProMEX:Q9M042 EnsemblPlants:AT5G01300.1 GeneID:830983 KEGG:ath:AT5G01300 TAIR:At5g01300 InParanoid:Q9M042 OMA:LEWYNVP PhylomeDB:Q9M042 ProtClustDB:CLSN2687113 ArrayExpress:Q9M042 Genevestigator:Q9M042 Uniprot:Q9M042
Root	Isotig01660	59	0	6.754	1.18E-14	TAIR|locus:2179117 - symbol:AT5G01300 "AT5G01300" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0008429 "phosphatidylethanolamine binding" evidence=ISS] Pfam:PF01161 EMBL:CP002688 GenomeReviews:BA000015_GR InterPro:IPR008914 Gene3D:G3DSA:3.90.280.10 SUPFAM:SSF49777 EMBL:AL161746 KO:K06910 HOGENOM:HBG649023 InterPro:IPR005247 TIGRFAMs:TIGR00481 UniGene:At.33912 UniGene:At.48967 EMBL:AY065369 EMBL:AY096477 IPI:IPI00535873 PIR:T48152 RefSeq:NP_195750.1 HSSP:P77368 ProteinModelPortal:Q9M042 SMR:Q9M042 PRIDE:Q9M042 ProMEX:Q9M042 EnsemblPlants:AT5G01300.1 GeneID:830983 KEGG:ath:AT5G01300 TAIR:At5g01300 InParanoid:Q9M042 OMA:LEWYNVP PhylomeDB:Q9M042 ProtClustDB:CLSN2687113 ArrayExpress:Q9M042 Genevestigator:Q9M042 Uniprot:Q9M042
Root	Isotig01661	57	8	2.704	8.93E-10	TAIR|locus:2086102 - symbol:AT3G17020 "AT3G17020" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0006950 "response to stress" evidence=ISS] [GO:0009409 "response to cold" evidence=IEP] [GO:0005886 "plasma membrane" evidence=IDA] InterPro:IPR006016 Pfam:PF00582 GO:GO:0005886 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0009409 EMBL:AB026636 InterPro:IPR014729 Gene3D:G3DSA:3.40.50.620 HOGENOM:HBG733992 InterPro:IPR006015 PRINTS:PR01438 EMBL:AF378888 EMBL:AY050480 IPI:IPI00534820 RefSeq:NP_566564.1 UniGene:At.24032 ProteinModelPortal:Q9LSP5 SMR:Q9LSP5 IntAct:Q9LSP5 STRING:Q9LSP5 PRIDE:Q9LSP5 EnsemblPlants:AT3G17020.1 GeneID:820958 KEGG:ath:AT3G17020 TAIR:At3g17020 eggNOG:NOG302561 InParanoid:Q9LSP5 OMA:GEMQLWE PhylomeDB:Q9LSP5 ProtClustDB:CLSN2688467 Genevestigator:Q9LSP5 Uniprot:Q9LSP5
Root	Isotig01662	64	8	2.871	2.12E-11	TAIR|locus:2086102 - symbol:AT3G17020 "AT3G17020" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0006950 "response to stress" evidence=ISS] [GO:0009409 "response to cold" evidence=IEP] [GO:0005886 "plasma membrane" evidence=IDA] InterPro:IPR006016 Pfam:PF00582 GO:GO:0005886 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0009409 EMBL:AB026636 InterPro:IPR014729 Gene3D:G3DSA:3.40.50.620 HOGENOM:HBG733992 InterPro:IPR006015 PRINTS:PR01438 EMBL:AF378888 EMBL:AY050480 IPI:IPI00534820 RefSeq:NP_566564.1 UniGene:At.24032

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						ProteinModelPortal:Q9LSP5 SMR:Q9LSP5 IntAct:Q9LSP5 STRING:Q9LSP5 PRIDE:Q9LSP5 EnsemblPlants:AT3G17020.1 GeneID:820958 KEGG:ath:AT3G17020 TAIR:At3g17020 eggNOG:NOG302561 InParanoid:Q9LSP5 OMA:GEMQLWE PhylomeDB:Q9LSP5 ProtClustDB:CLSN2688467 Genevestigator:Q9LSP5 Uniprot:Q9LSP5
Root	Isotig01663	57	8	2.704	8.93E-10	TAIR|locus:2086102 - symbol:AT3G17020 "AT3G17020" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0006950 "response to stress" evidence=ISS] [GO:0009409 "response to cold" evidence=IEP] [GO:0005886 "plasma membrane" evidence=IDA] InterPro:IPR006016 Pfam:PF00582 GO:GO:0005886 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0009409 EMBL:AB026636 InterPro:IPR014729 Gene3D:G3DSA:3.40.50.620 HOGENOM:HBG733992 InterPro:IPR006015 PRINTS:PR01438 EMBL:AF378888 EMBL:AY050480 IPI:IPI00534820 RefSeq:NP_566564.1 UniGene:At.24032 ProteinModelPortal:Q9LSP5 SMR:Q9LSP5 IntAct:Q9LSP5 STRING:Q9LSP5 PRIDE:Q9LSP5 EnsemblPlants:AT3G17020.1 GeneID:820958 KEGG:ath:AT3G17020 TAIR:At3g17020 eggNOG:NOG302561 InParanoid:Q9LSP5 OMA:GEMQLWE PhylomeDB:Q9LSP5 ProtClustDB:CLSN2688467 Genevestigator:Q9LSP5 Uniprot:Q9LSP5
Root	Isotig01669	12	61	-2.475	2.75E-10	UNIPROTKB|Q43848 - symbol:Q43848 "Transketolase, chloroplastic" species:4113 "Solanum tuberosum" [GO:0004802 "transketolase activity" evidence=ISS] [GO:0009535 "chloroplast thylakoid membrane" evidence=ISS] InterPro:IPR005476 InterPro:IPR005478 InterPro:IPR009014 InterPro:IPR015941 Pfam:PF02780 InterPro:IPR005475 Pfam:PF00456 Pfam:PF02779 InterPro:IPR005474 GO:GO:0046872 GO:GO:0009535 SMART:SM00861 InterPro:IPR020826 Gene3D:G3DSA:3.40.50.920 SUPFAM:SSF52922 PROSITE:PS00801 PROSITE:PS00802 GO:GO:0004802 TIGRFAMs:TIGR00232 EMBL:Z50099 PIR:S58083 ProteinModelPortal:Q43848 SMR:Q43848 PRIDE:Q43848 Uniprot:Q43848
Root	Isotig01670	13	62	-2.383	4.79E-10	TAIR|locus:2101871 - symbol:AT3G60750 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004802 "transketolase activity" evidence=IEA;ISS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0005829 "cytosol" evidence=RCA] InterPro:IPR005476 InterPro:IPR005478 InterPro:IPR009014 InterPro:IPR015941 Pfam:PF02780 InterPro:IPR005475 Pfam:PF00456 Pfam:PF02779 InterPro:IPR005474 GO:GO:0009570 GO:GO:0046686 EMBL:CP002686 GO:GO:0009941 GO:GO:0009651 SMART:SM00861 InterPro:IPR020826 Gene3D:G3DSA:3.40.50.920 SUPFAM:SSF52922 PROSITE:PS00801 PROSITE:PS00802 GO:GO:0004802 KO:K00615 TIGRFAMs:TIGR00232 OMA:LAFNENV EMBL:AY091094 EMBL:AY133860 IPI:IPI00537782 RefSeq:NP_567103.1 UniGene:At.24156 UniGene:At.68080 HSSP:P23254 ProteinModelPortal:Q8RWV0 SMR:Q8RWV0 IntAct:Q8RWV0 STRING:Q8RWV0 PRIDE:Q8RWV0 ProMEX:Q8RWV0 EnsemblPlants:AT3G60750.1 GeneID:825246 KEGG:ath:AT3G60750 TAIR:At3g60750 InParanoid:Q8RWV0 PhylomeDB:Q8RWV0 ProtClustDB:PLN02790 ArrayExpress:Q8RWV0 Genevestigator:Q8RWV0 Uniprot:Q8RWV0
Root	Isotig01671	14	63	-2.299	8.06E-10	UNIPROTKB|Q43848 - symbol:Q43848 "Transketolase, chloroplastic" species:4113 "Solanum tuberosum" [GO:0004802 "transketolase activity" evidence=ISS] [GO:0009535 "chloroplast thylakoid membrane" evidence=ISS] InterPro:IPR005476 InterPro:IPR005478 InterPro:IPR009014 InterPro:IPR015941 Pfam:PF02780 InterPro:IPR005475 Pfam:PF00456 Pfam:PF02779 InterPro:IPR005474 GO:GO:0046872 GO:GO:0009535 SMART:SM00861 InterPro:IPR020826 Gene3D:G3DSA:3.40.50.920 SUPFAM:SSF52922 PROSITE:PS00801 PROSITE:PS00802 GO:GO:0004802 TIGRFAMs:TIGR00232 EMBL:Z50099 PIR:S58083 ProteinModelPortal:Q43848 SMR:Q43848 PRIDE:Q43848 Uniprot:Q43848
Root	Isotig01672	6	31	-2.498	6.06E-06	UNIPROTKB|Q43848 - symbol:Q43848 "Transketolase, chloroplastic" species:4113 "Solanum tuberosum" [GO:0004802 "transketolase activity" evidence=ISS] [GO:0009535 "chloroplast thylakoid membrane" evidence=ISS] InterPro:IPR005476 InterPro:IPR005478 InterPro:IPR009014 InterPro:IPR015941 Pfam:PF02780 InterPro:IPR005475 Pfam:PF00456 Pfam:PF02779 InterPro:IPR005474 GO:GO:0046872 GO:GO:0009535 SMART:SM00861 InterPro:IPR020826 Gene3D:G3DSA:3.40.50.920 SUPFAM:SSF52922 PROSITE:PS00801 PROSITE:PS00802 GO:GO:0004802 TIGRFAMs:TIGR00232 EMBL:Z50099 PIR:S58083 ProteinModelPortal:Q43848 SMR:Q43848 PRIDE:Q43848 Uniprot:Q43848
Root	Isotig01701	0	35	-6.258	3.45E-10	TAIR|locus:2158187 - symbol:ARA12 "AT5G67360" species:3702 "Arabidopsis thaliana" [GO:0006508 "proteolysis" evidence=ISS] [GO:0004252 "serine-type endopeptidase activity" evidence=IDA] [GO:0005576 "extracellular region" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0009505 "plant-type cell wall" evidence=IDA]

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						[GO:0010214 "seed coat development" evidence=IMP] [GO:0048359 "mucilage metabolic process involved seed coat development" evidence=IMP] [GO:0080001 "mucilage extrusion from seed coat" evidence=IMP] [GO:0048046 "apoplast" evidence=IDA] InterPro:IPR000209 InterPro:IPR010259 Pfam:PF00082 Pfam:PF05922 InterPro:IPR003137 Prosite:PS00137 Prosite:PS00138 PANTHER:PTHR10795 Pfam:PF02225 GO:GO:0048046 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0042802 GO:GO:0006508 GO:GO:0004252 GO:GO:0009505 GO:GO:0043086 InterPro:IPR023828 InterPro:IPR015500 Gene3D:G3DSA:3.40.50.200 PRINTS:PR00723 SUPFAM:SSF52743 PROSITE:PS00136 eggNOG:COG1404 EMBL:AB007645 GO:GO:0080001 HOGENOM:HBG591621 EMBL:AF065639 EMBL:AF360285 EMBL:AY091773 EMBL:AY142612 EMBL:BT001082 EMBL:X85974 IPI:IPI00548134 PIR:JC7519 PIR:S52770 RefSeq:NP_569048.1 UniGene:At.23238 UniGene:At.67722 UniGene:At.71531 ProteinModelPortal:O65351 SMR:O65351 STRING:O65351 MEROPS:S08.112 PRIDE:O65351 EnsemblPlants:AT5G67360.1 GeneID:836871 KEGG:ath:AT5G67360 GeneFarm:1964 TAIR:At5g67360 InParanoid:O65351 OMA:TYIVHMA PhylomeDB:O65351 ProtClustDB:CLSN2690100 ArrayExpress:O65351 Genevestigator:O65351 GermOnline:AT5G67360 GO:GO:0048359 Uniprot:O65351
Root	Isotig01702	0	31	-6.083	3.24E-09	TAIR|locus:2158187 - symbol:ARA12 "AT5G67360" species:3702 "Arabidopsis thaliana" [GO:0006508 "proteolysis" evidence=ISS] [GO:0004252 "serine-type endopeptidase activity" evidence=IDA] [GO:0005576 "extracellular region" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0009505 "plant-type cell wall" evidence=IDA] [GO:0010214 "seed coat development" evidence=IMP] [GO:0048359 "mucilage metabolic process involved seed coat development" evidence=IMP] [GO:0080001 "mucilage extrusion from seed coat" evidence=IMP] [GO:0048046 "apoplast" evidence=IDA] InterPro:IPR000209 InterPro:IPR010259 Pfam:PF00082 Pfam:PF05922 InterPro:IPR003137 Prosite:PS00137 Prosite:PS00138 PANTHER:PTHR10795 Pfam:PF02225 GO:GO:0048046 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0042802 GO:GO:0006508 GO:GO:0004252 GO:GO:0009505 GO:GO:0043086 InterPro:IPR023828 InterPro:IPR015500 Gene3D:G3DSA:3.40.50.200 PRINTS:PR00723 SUPFAM:SSF52743 PROSITE:PS00136 eggNOG:COG1404 EMBL:AB007645 GO:GO:0080001 HOGENOM:HBG591621 EMBL:AF065639 EMBL:AF360285 EMBL:AY091773 EMBL:AY142612 EMBL:BT001082 EMBL:X85974 IPI:IPI00548134 PIR:JC7519 PIR:S52770 RefSeq:NP_569048.1 UniGene:At.23238 UniGene:At.67722 UniGene:At.71531 ProteinModelPortal:O65351 SMR:O65351 STRING:O65351 MEROPS:S08.112 PRIDE:O65351 EnsemblPlants:AT5G67360.1 GeneID:836871 KEGG:ath:AT5G67360 GeneFarm:1964 TAIR:At5g67360 InParanoid:O65351 OMA:TYIVHMA PhylomeDB:O65351 ProtClustDB:CLSN2690100 ArrayExpress:O65351 Genevestigator:O65351 GermOnline:AT5G67360 GO:GO:0048359 Uniprot:O65351
Root	Isotig01703	0	37	-6.338	1.15E-10	TAIR|locus:2158187 - symbol:ARA12 "AT5G67360" species:3702 "Arabidopsis thaliana" [GO:0006508 "proteolysis" evidence=ISS] [GO:0004252 "serine-type endopeptidase activity" evidence=IDA] [GO:0005576 "extracellular region" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0009505 "plant-type cell wall" evidence=IDA] [GO:0010214 "seed coat development" evidence=IMP] [GO:0048359 "mucilage metabolic process involved seed coat development" evidence=IMP] [GO:0080001 "mucilage extrusion from seed coat" evidence=IMP] [GO:0048046 "apoplast" evidence=IDA] InterPro:IPR000209 InterPro:IPR010259 Pfam:PF00082 Pfam:PF05922 InterPro:IPR003137 Prosite:PS00137 Prosite:PS00138 PANTHER:PTHR10795 Pfam:PF02225 GO:GO:0048046 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0042802 GO:GO:0006508 GO:GO:0004252 GO:GO:0009505 GO:GO:0043086 InterPro:IPR023828 InterPro:IPR015500 Gene3D:G3DSA:3.40.50.200 PRINTS:PR00723 SUPFAM:SSF52743 PROSITE:PS00136 eggNOG:COG1404 EMBL:AB007645 GO:GO:0080001 HOGENOM:HBG591621 EMBL:AF065639 EMBL:AF360285 EMBL:AY091773 EMBL:AY142612 EMBL:BT001082 EMBL:X85974 IPI:IPI00548134 PIR:JC7519 PIR:S52770 RefSeq:NP_569048.1 UniGene:At.23238 UniGene:At.67722 UniGene:At.71531 ProteinModelPortal:O65351 SMR:O65351 STRING:O65351 MEROPS:S08.112 PRIDE:O65351 EnsemblPlants:AT5G67360.1 GeneID:836871 KEGG:ath:AT5G67360 GeneFarm:1964 TAIR:At5g67360 InParanoid:O65351 OMA:TYIVHMA PhylomeDB:O65351 ProtClustDB:CLSN2690100 ArrayExpress:O65351 Genevestigator:O65351 GermOnline:AT5G67360 GO:GO:0048359 Uniprot:O65351
Root	Isotig01704	0	33	-6.173	1.05E-09	TAIR|locus:2158187 - symbol:ARA12 "AT5G67360" species:3702 "Arabidopsis thaliana" [GO:0006508 "proteolysis" evidence=ISS] [GO:0004252 "serine-type endopeptidase activity" evidence=IDA] [GO:0005576 "extracellular region" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0009505 "plant-type cell wall" evidence=IDA] [GO:0010214 "seed coat development" evidence=IMP] [GO:0048359 "mucilage metabolic process involved seed

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						coat development" evidence=IMP] [GO:0080001 "mucilage extrusion from seed coat" evidence=IMP] [GO:0048046 "apoplast" evidence=IDA] InterPro:IPR000209 InterPro:IPR010259 Pfam:PF00082 Pfam:PF05922 InterPro:IPR003137 Prosite:PS00137 Prosite:PS00138 PANTHER:PTHR10795 Pfam:PF02225 GO:GO:0048046 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0042802 GO:GO:0006508 GO:GO:0004252 GO:GO:0009505 GO:GO:0043086 InterPro:IPR023828 InterPro:IPR015500 Gene3D:G3DSA:3.40.50.200 PRINTS:PR00723 SUPFAM:SSF52743 PROSITE:PS00136 eggNOG:COG1404 EMBL:AB007645 GO:GO:0080001 HOGENOM:HBG591621 EMBL:AF065639 EMBL:AF360285 EMBL:AY091773 EMBL:AY142612 EMBL:BT001082 EMBL:X85974 IPI:IPI00548134 PIR:JC7519 PIR:S52770 RefSeq:NP_569048.1 UniGene:At.23238 UniGene:At.67722 UniGene:At.71531 ProteinModelPortal:O65351 SMR:O65351 STRING:O65351 MEROPS:S08.112 PRIDE:O65351 EnsemblPlants:AT5G67360.1 GeneID:836871 KEGG:ath:AT5G67360 GeneFarm:1964 TAIR:At5g67360 InParanoid:O65351 OMA:TYIVHMA PhylomeDB:O65351 ProtClustDB:CLSN2690100 ArrayExpress:O65351 Genevestigator:O65351 GermOnline:AT5G67360 GO:GO:0048359 Uniprot:O65351
Root	Isotig01705	0	31	-6.083	3.24E-09	TAIR|locus:2158187 - symbol:ARA12 "AT5G67360" species:3702 "Arabidopsis thaliana" [GO:0006508 "proteolysis" evidence=ISS] [GO:0004252 "serine-type endopeptidase activity" evidence=IDA] [GO:0005576 "extracellular region" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0009505 "plant-type cell wall" evidence=IDA] [GO:0010214 "seed coat development" evidence=IMP] [GO:0048359 "mucilage metabolic process involved seed coat development" evidence=IMP] [GO:0080001 "mucilage extrusion from seed coat" evidence=IMP] [GO:0048046 "apoplast" evidence=IDA] InterPro:IPR000209 InterPro:IPR010259 Pfam:PF00082 Pfam:PF05922 InterPro:IPR003137 Prosite:PS00137 Prosite:PS00138 PANTHER:PTHR10795 Pfam:PF02225 GO:GO:0048046 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0042802 GO:GO:0006508 GO:GO:0004252 GO:GO:0009505 GO:GO:0043086 InterPro:IPR023828 InterPro:IPR015500 Gene3D:G3DSA:3.40.50.200 PRINTS:PR00723 SUPFAM:SSF52743 PROSITE:PS00136 eggNOG:COG1404 EMBL:AB007645 GO:GO:0080001 HOGENOM:HBG591621 EMBL:AF065639 EMBL:AF360285 EMBL:AY091773 EMBL:AY142612 EMBL:BT001082 EMBL:X85974 IPI:IPI00548134 PIR:JC7519 PIR:S52770 RefSeq:NP_569048.1 UniGene:At.23238 UniGene:At.67722 UniGene:At.71531 ProteinModelPortal:O65351 SMR:O65351 STRING:O65351 MEROPS:S08.112 PRIDE:O65351 EnsemblPlants:AT5G67360.1 GeneID:836871 KEGG:ath:AT5G67360 GeneFarm:1964 TAIR:At5g67360 InParanoid:O65351 OMA:TYIVHMA PhylomeDB:O65351 ProtClustDB:CLSN2690100 ArrayExpress:O65351 Genevestigator:O65351 GermOnline:AT5G67360 GO:GO:0048359 Uniprot:O65351
Root	Isotig01706	0	33	-6.173	1.05E-09	TAIR|locus:2158187 - symbol:ARA12 "AT5G67360" species:3702 "Arabidopsis thaliana" [GO:0006508 "proteolysis" evidence=ISS] [GO:0004252 "serine-type endopeptidase activity" evidence=IDA] [GO:0005576 "extracellular region" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0009505 "plant-type cell wall" evidence=IDA] [GO:0010214 "seed coat development" evidence=IMP] [GO:0048359 "mucilage metabolic process involved seed coat development" evidence=IMP] [GO:0080001 "mucilage extrusion from seed coat" evidence=IMP] [GO:0048046 "apoplast" evidence=IDA] InterPro:IPR000209 InterPro:IPR010259 Pfam:PF00082 Pfam:PF05922 InterPro:IPR003137 Prosite:PS00137 Prosite:PS00138 PANTHER:PTHR10795 Pfam:PF02225 GO:GO:0048046 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0042802 GO:GO:0006508 GO:GO:0004252 GO:GO:0009505 GO:GO:0043086 InterPro:IPR023828 InterPro:IPR015500 Gene3D:G3DSA:3.40.50.200 PRINTS:PR00723 SUPFAM:SSF52743 PROSITE:PS00136 eggNOG:COG1404 EMBL:AB007645 GO:GO:0080001 HOGENOM:HBG591621 EMBL:AF065639 EMBL:AF360285 EMBL:AY091773 EMBL:AY142612 EMBL:BT001082 EMBL:X85974 IPI:IPI00548134 PIR:JC7519 PIR:S52770 RefSeq:NP_569048.1 UniGene:At.23238 UniGene:At.67722 UniGene:At.71531 ProteinModelPortal:O65351 SMR:O65351 STRING:O65351 MEROPS:S08.112 PRIDE:O65351 EnsemblPlants:AT5G67360.1 GeneID:836871 KEGG:ath:AT5G67360 GeneFarm:1964 TAIR:At5g67360 InParanoid:O65351 OMA:TYIVHMA PhylomeDB:O65351 ProtClustDB:CLSN2690100 ArrayExpress:O65351 Genevestigator:O65351 GermOnline:AT5G67360 GO:GO:0048359 Uniprot:O65351
Root	Isotig01707	0	15	-5.036	4.38E-05	TAIR|locus:2131566 - symbol:SLP2 "AT4G34980" species:3702 "Arabidopsis thaliana" [GO:0004252 "serine-type endopeptidase activity" evidence=IBA] [GO:0005618 "cell wall" evidence=IBA] [GO:0006508 "proteolysis" evidence=ISS] [GO:0008152 "metabolic process" evidence=IBA] [GO:0008236 "serine-type peptidase activity" evidence=ISS] [GO:0009827 "plant-type cell wall modification" evidence=TAS] [GO:0048196 "plant extracellular matrix" evidence=ISS] [GO:0016020 "membrane" evidence=IDA] InterPro:IPR000209 InterPro:IPR010259

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						Pfam:PF00082 Pfam:PF05922 InterPro:IPR003137 Prosite:PS00138 PANTHER:PTHR10795 Pfam:PF02225 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005576 GO:GO:0042802 GO:GO:0016020 GO:GO:0006508 GO:GO:0004252 EMBL:AL022023 EMBL:AL161586 GO:GO:0043086 InterPro:IPR023828 InterPro:IPR015500 InterPro:IPR009020 Gene3D:G3DSA:3.40.50.200 PRINTS:PR00723 SUPFAM:SSF52743 SUPFAM:SSF54897 HSSP:Q99405 eggNOG:COG1404 GO:GO:0009827 HOGENOM:HBG591621 EMBL:AY074375 EMBL:AY096357 IPI:IPI00522734 PIR:T05768 RefSeq:NP_567972.1 UniGene:At.27496 UniGene:At.28167 UniGene:At.69469 ProteinModelPortal:O49607 SMR:O49607 STRING:O49607 MEROPS:S08.A39 PRIDE:O49607 EnsemblPlants:AT4G34980.1 GeneID:829650 KEGG:ath:AT4G34980 TAIR:At4g34980 InParanoid:O49607 OMA:IFPTHYH PhylomeDB:O49607 ProtClustDB:CLSN2689763 Genevestigator:O49607 Uniprot:O49607
Root	Isotig01708	0	17	-5.216	1.26E-05	TAIR|locus:2131566 - symbol:SLP2 "AT4G34980" species:3702 "Arabidopsis thaliana" [GO:0004252 "serine-type endopeptidase activity" evidence=IBA] [GO:0005618 "cell wall" evidence=IBA] [GO:0006508 "proteolysis" evidence=ISS] [GO:0008152 "metabolic process" evidence=IBA] [GO:0008236 "serine-type peptidase activity" evidence=ISS] [GO:0009827 "plant-type cell wall modification" evidence=TAS] [GO:0048196 "plant extracellular matrix" evidence=ISS] [GO:0016020 "membrane" evidence=IDA] InterPro:IPR000209 InterPro:IPR010259 Pfam:PF00082 Pfam:PF05922 InterPro:IPR003137 Prosite:PS00138 PANTHER:PTHR10795 Pfam:PF02225 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005576 GO:GO:0042802 GO:GO:0016020 GO:GO:0006508 GO:GO:0004252 EMBL:AL022023 EMBL:AL161586 GO:GO:0043086 InterPro:IPR023828 InterPro:IPR015500 InterPro:IPR009020 Gene3D:G3DSA:3.40.50.200 PRINTS:PR00723 SUPFAM:SSF52743 SUPFAM:SSF54897 HSSP:Q99405 eggNOG:COG1404 GO:GO:0009827 HOGENOM:HBG591621 EMBL:AY074375 EMBL:AY096357 IPI:IPI00522734 PIR:T05768 RefSeq:NP_567972.1 UniGene:At.27496 UniGene:At.28167 UniGene:At.69469 ProteinModelPortal:O49607 SMR:O49607 STRING:O49607 MEROPS:S08.A39 PRIDE:O49607 EnsemblPlants:AT4G34980.1 GeneID:829650 KEGG:ath:AT4G34980 TAIR:At4g34980 InParanoid:O49607 OMA:IFPTHYH PhylomeDB:O49607 ProtClustDB:CLSN2689763 Genevestigator:O49607 Uniprot:O49607
Root	Isotig01770	0	13	-4.829	0.000155955	TAIR|locus:2180315 - symbol:EMB2775 "EMBRYO DEFECTIVE 2775" species:3702 "Arabidopsis thaliana" [GO:0000166 "nucleotide binding" evidence=IEA] [GO:0003677 "DNA binding" evidence=IEA] [GO:0005524 "ATP binding" evidence=IEA] [GO:0005634 "nucleus" evidence=IEA] [GO:0009793 "embryo development ending in seed dormancy" evidence=IMP] [GO:0017111 "nucleoside-triphosphatase activity" evidence=IEA] InterPro:IPR003593 InterPro:IPR008921 SMART:SM00382 InterPro:IPR013748 GO:GO:0005524 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0006260 eggNOG:COG0470 GO:GO:0003689 SUPFAM:SSF48019 GO:GO:0005663 Pfam:PF08542 KO:K10756 OMA:TRIMCLL HOGENOM:HBG330815 HSSP:Q8U4J3 EMBL:AY074381 EMBL:AY091236 IPI:IPI00528406 RefSeq:NP_198126.1 UniGene:At.19785 ProteinModelPortal:Q8VXX4 SMR:Q8VXX4 STRING:Q8VXX4 PRIDE:Q8VXX4 EnsemblPlants:AT5G27740.1 GeneID:832836 KEGG:ath:AT5G27740 TAIR:At5g27740 InParanoid:Q8VXX4 PhylomeDB:Q8VXX4 ProtClustDB:CLSN2687133 ArrayExpress:Q8VXX4 Genevestigator:Q8VXX4 Uniprot:Q8VXX4
Root	Isotig01771	3	44	-4.003	2.84E-11	UNIPROTKB|Q6VMW0 - symbol:OMT2 "8-hydroxyquercetin 8-O-methyltransferase" species:34256 "Mentha x piperita" [GO:0009812 "flavonoid metabolic process" evidence=IDA] [GO:0030761 "8-hydroxyquercitin 8-O-methyltransferase activity" evidence=IDA] [GO:0032259 "methylation" evidence=IDA] InterPro:IPR001077 InterPro:IPR012967 InterPro:IPR016461 Pfam:PF00891 Pfam:PF08100 PIRSF:PIRSF005739 InterPro:IPR011991 Gene3D:G3DSA:1.10.10.10 GO:GO:0046983 GO:GO:0008171 GO:GO:0009812 EMBL:AY337459 ProteinModelPortal:Q6VMW0 BRENDA:2.1.1.88 GO:GO:0030761 Uniprot:Q6VMW0
Root	Isotig01772	1	34	-5.216	6.54E-10	UNIPROTKB|Q6VMW0 - symbol:OMT2 "8-hydroxyquercetin 8-O-methyltransferase" species:34256 "Mentha x piperita" [GO:0009812 "flavonoid metabolic process" evidence=IDA] [GO:0030761 "8-hydroxyquercitin 8-O-methyltransferase activity" evidence=IDA] [GO:0032259 "methylation" evidence=IDA] InterPro:IPR001077 InterPro:IPR012967 InterPro:IPR016461 Pfam:PF00891 Pfam:PF08100 PIRSF:PIRSF005739 InterPro:IPR011991 Gene3D:G3DSA:1.10.10.10 GO:GO:0046983 GO:GO:0008171 GO:GO:0009812 EMBL:AY337459 ProteinModelPortal:Q6VMW0 BRENDA:2.1.1.88 GO:GO:0030761 Uniprot:Q6VMW0
Root	Isotig01773	3	41	-3.902	1.87E-10	UNIPROTKB|Q6VMW0 - symbol:OMT2 "8-hydroxyquercetin 8-O-methyltransferase" species:34256 "Mentha x piperita" [GO:0009812 "flavonoid metabolic process" evidence=IDA] [GO:0030761 "8-hydroxyquercitin 8-O-methyltransferase activity" evidence=IDA] [GO:0032259 "methylation" evidence=IDA] InterPro:IPR001077 InterPro:IPR012967 InterPro:IPR016461 Pfam:PF00891 Pfam:PF08100 PIRSF:PIRSF005739 InterPro:IPR011991

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						Gene3D:G3DSA:1.10.10.10 GO:GO:0046983 GO:GO:0008171 GO:GO:0009812 EMBL:AY337459 ProteinModelPortal:Q6VMW0 BRENDA:2.1.1.88 GO:GO:0030761 Uniprot:Q6VMW0
Root	Isotig01774	3	44	-4.003	2.84E-11	UNIPROTKB|Q6VMW0 - symbol:OMT2 "8-hydroxyquercetin 8-O-methyltransferase" species:34256 "Mentha x piperita" [GO:0009812 "flavonoid metabolic process" evidence=IDA] [GO:0030761 "8-hydroxyquercitin 8-O-methyltransferase activity" evidence=IDA] [GO:0032259 "methylation" evidence=IDA] InterPro:IPR001077 InterPro:IPR012967 InterPro:IPR016461 Pfam:PF00891 Pfam:PF08100 PIRSF:PIRSF005739 InterPro:IPR011991 Gene3D:G3DSA:1.10.10.10 GO:GO:0046983 GO:GO:0008171 GO:GO:0009812 EMBL:AY337459 ProteinModelPortal:Q6VMW0 BRENDA:2.1.1.88 GO:GO:0030761 Uniprot:Q6VMW0
Root	Isotig01775	2	28	-3.936	1.29E-07	UNIPROTKB|Q6VMW0 - symbol:OMT2 "8-hydroxyquercetin 8-O-methyltransferase" species:34256 "Mentha x piperita" [GO:0009812 "flavonoid metabolic process" evidence=IDA] [GO:0030761 "8-hydroxyquercitin 8-O-methyltransferase activity" evidence=IDA] [GO:0032259 "methylation" evidence=IDA] InterPro:IPR001077 InterPro:IPR012967 InterPro:IPR016461 Pfam:PF00891 Pfam:PF08100 PIRSF:PIRSF005739 InterPro:IPR011991 Gene3D:G3DSA:1.10.10.10 GO:GO:0046983 GO:GO:0008171 GO:GO:0009812 EMBL:AY337459 ProteinModelPortal:Q6VMW0 BRENDA:2.1.1.88 GO:GO:0030761 Uniprot:Q6VMW0
Root	Isotig01776	1	31	-5.083	4.06E-09	UNIPROTKB|Q6VMW0 - symbol:OMT2 "8-hydroxyquercetin 8-O-methyltransferase" species:34256 "Mentha x piperita" [GO:0009812 "flavonoid metabolic process" evidence=IDA] [GO:0030761 "8-hydroxyquercitin 8-O-methyltransferase activity" evidence=IDA] [GO:0032259 "methylation" evidence=IDA] InterPro:IPR001077 InterPro:IPR012967 InterPro:IPR016461 Pfam:PF00891 Pfam:PF08100 PIRSF:PIRSF005739 InterPro:IPR011991 Gene3D:G3DSA:1.10.10.10 GO:GO:0046983 GO:GO:0008171 GO:GO:0009812 EMBL:AY337459 ProteinModelPortal:Q6VMW0 BRENDA:2.1.1.88 GO:GO:0030761 Uniprot:Q6VMW0
Root	Isotig01777	1	34	-5.216	6.54E-10	UNIPROTKB|Q6VMW0 - symbol:OMT2 "8-hydroxyquercetin 8-O-methyltransferase" species:34256 "Mentha x piperita" [GO:0009812 "flavonoid metabolic process" evidence=IDA] [GO:0030761 "8-hydroxyquercitin 8-O-methyltransferase activity" evidence=IDA] [GO:0032259 "methylation" evidence=IDA] InterPro:IPR001077 InterPro:IPR012967 InterPro:IPR016461 Pfam:PF00891 Pfam:PF08100 PIRSF:PIRSF005739 InterPro:IPR011991 Gene3D:G3DSA:1.10.10.10 GO:GO:0046983 GO:GO:0008171 GO:GO:0009812 EMBL:AY337459 ProteinModelPortal:Q6VMW0 BRENDA:2.1.1.88 GO:GO:0030761 Uniprot:Q6VMW0
Root	Isotig01778	18	44	-1.418	0.000224092	TAIR|locus:2185168 - symbol:SIS "AT5G02020" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0009651 "response to salt stress" evidence=IMP] EMBL:CP002688 GO:GO:0009651 EMBL:AL162508 EMBL:AY058150 EMBL:AY094053 IPI:IPI00528966 PIR:T48223 RefSeq:NP_195822.1 UniGene:At.23336 UniGene:At.70618 EnsemblPlants:AT5G02020.1 GeneID:831782 KEGG:ath:AT5G02020 TAIR:At5g02020 eggNOG:NOG285266 InParanoid:Q9LZM9 OMA:GSKESSY PhylomeDB:Q9LZM9 ProtClustDB:CLSN2687303 Genevestigator:Q9LZM9 Uniprot:Q9LZM9
Root	Isotig01779	5	44	-3.266	6.87E-10	TAIR|locus:2185168 - symbol:SIS "AT5G02020" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0009651 "response to salt stress" evidence=IMP] EMBL:CP002688 GO:GO:0009651 EMBL:AL162508 EMBL:AY058150 EMBL:AY094053 IPI:IPI00528966 PIR:T48223 RefSeq:NP_195822.1 UniGene:At.23336 UniGene:At.70618 EnsemblPlants:AT5G02020.1 GeneID:831782 KEGG:ath:AT5G02020 TAIR:At5g02020 eggNOG:NOG285266 InParanoid:Q9LZM9 OMA:GSKESSY PhylomeDB:Q9LZM9 ProtClustDB:CLSN2687303 Genevestigator:Q9LZM9 Uniprot:Q9LZM9
Root	Isotig01780	18	44	-1.418	0.000224092	TAIR|locus:2185168 - symbol:SIS "AT5G02020" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0009651 "response to salt stress" evidence=IMP] EMBL:CP002688 GO:GO:0009651 EMBL:AL162508 EMBL:AY058150 EMBL:AY094053 IPI:IPI00528966 PIR:T48223 RefSeq:NP_195822.1 UniGene:At.23336 UniGene:At.70618 EnsemblPlants:AT5G02020.1 GeneID:831782 KEGG:ath:AT5G02020 TAIR:At5g02020 eggNOG:NOG285266 InParanoid:Q9LZM9 OMA:GSKESSY PhylomeDB:Q9LZM9 ProtClustDB:CLSN2687303 Genevestigator:Q9LZM9 Uniprot:Q9LZM9
Root	Isotig01781	5	44	-3.266	6.87E-10	TAIR|locus:2185168 - symbol:SIS "AT5G02020" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0009651 "response to salt stress" evidence=IMP] EMBL:CP002688 GO:GO:0009651 EMBL:AL162508 EMBL:AY058150 EMBL:AY094053 IPI:IPI00528966 PIR:T48223 RefSeq:NP_195822.1 UniGene:At.23336 UniGene:At.70618 EnsemblPlants:AT5G02020.1 GeneID:831782 KEGG:ath:AT5G02020 TAIR:At5g02020 eggNOG:NOG285266 InParanoid:Q9LZM9 OMA:GSKESSY PhylomeDB:Q9LZM9 ProtClustDB:CLSN2687303 Genevestigator:Q9LZM9 Uniprot:Q9LZM9
Root	Isotig01783	5	35	-2.936	1.63E-07	TAIR|locus:504954988 - symbol:AT5G05965 "AT5G05965" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002688

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GenomeReviews:BA000015_GR EMBL:AY735673 IPI:IPI00516315 RefSeq:NP_680147.1 UniGene:At.43072 UniGene:At.66777 EnsemblPlants:AT5G05965.1 GeneID:830482 KEGG:ath:AT5G05965 TAIR:At5g05965 eggNOG:NOG286329 HOGENOM:HBG317139 OMA:DERSSHE PhylomeDB:Q5XV49 ProtClustDB:CLSN2917816 Genevestigator:Q5XV49 Uniprot:Q5XV49
Root	Isotig01800	39	69	-0.952	0.000771235	TAIR|locus:2135887 - symbol:SHD "SHEPHERD" species:3702 "Arabidopsis thaliana" [GO:0005524 "ATP binding" evidence=IEA;ISS] [GO:0006457 "protein folding" evidence=ISS] [GO:0051082 "unfolded protein binding" evidence=IEA] [GO:0005783 "endoplasmic reticulum" evidence=ISS;IDA] [GO:0009934 "regulation of meristem structural organization" evidence=IMP] [GO:0010075 "regulation of meristem growth" evidence=IMP] [GO:0005634 "nucleus" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0009306 "protein secretion" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009414 "response to water deprivation" evidence=IMP] [GO:0009651 "response to salt stress" evidence=IMP] [GO:0005829 "cytosol" evidence=RCA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR001404 InterPro:IPR003594 InterPro:IPR019805 Pfam:PF00183 PIRSF:PIRSF002583 PROSITE:PS00298 SMART:SM00387 GO:GO:0005739 GO:GO:0005886 GO:GO:0009506 GO:GO:0005524 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005634 GO:GO:0046686 GO:GO:0005774 GO:GO:0009507 GO:GO:0006457 GO:GO:0051082 GO:GO:0009306 GO:GO:0009409 GO:GO:0009651 GO:GO:0009414 GO:GO:0005788 PROSITE:PS00014 EMBL:AL078637 EMBL:AL161561 Gene3D:G3DSA:3.30.565.10 SUPFAM:SSF55874 InterPro:IPR020568 SUPFAM:SSF54211 EMBL:AC002343 GO:GO:0010075 GO:GO:0009934 eggNOG:COG0326 HOGENOM:HBG631012 PANTHER:PTHR11528 EMBL:AB064528 EMBL:AY039895 EMBL:AY072394 EMBL:BT004527 EMBL:AK221485 IPI:IPI00524027 PIR:T09882 RefSeq:NP_194150.1 UniGene:At.24111 ProteinModelPortal:Q9STX5 SMR:Q9STX5 STRING:Q9STX5 PRIDE:Q9STX5 EnsemblPlants:AT4G24190.1 GeneID:828520 KEGG:ath:AT4G24190 TAIR:At4g24190 InParanoid:Q9STX5 PhylomeDB:Q9STX5 ProtClustDB:CLSN2716298 Genevestigator:Q9STX5 InterPro:IPR020575 PRINTS:PR00775 Uniprot:Q9STX5
Root	Isotig01801	40	70	-0.936	0.000837113	TAIR|locus:2135887 - symbol:SHD "SHEPHERD" species:3702 "Arabidopsis thaliana" [GO:0005524 "ATP binding" evidence=IEA;ISS] [GO:0006457 "protein folding" evidence=ISS] [GO:0051082 "unfolded protein binding" evidence=IEA] [GO:0005783 "endoplasmic reticulum" evidence=ISS;IDA] [GO:0009934 "regulation of meristem structural organization" evidence=IMP] [GO:0010075 "regulation of meristem growth" evidence=IMP] [GO:0005634 "nucleus" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0009306 "protein secretion" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009414 "response to water deprivation" evidence=IMP] [GO:0009651 "response to salt stress" evidence=IMP] [GO:0005829 "cytosol" evidence=RCA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR001404 InterPro:IPR003594 InterPro:IPR019805 Pfam:PF00183 PIRSF:PIRSF002583 PROSITE:PS00298 SMART:SM00387 GO:GO:0005739 GO:GO:0005886 GO:GO:0009506 GO:GO:0005524 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005634 GO:GO:0046686 GO:GO:0005774 GO:GO:0009507 GO:GO:0006457 GO:GO:0051082 GO:GO:0009306 GO:GO:0009409 GO:GO:0009651 GO:GO:0009414 GO:GO:0005788 PROSITE:PS00014 EMBL:AL078637 EMBL:AL161561 Gene3D:G3DSA:3.30.565.10 SUPFAM:SSF55874 InterPro:IPR020568 SUPFAM:SSF54211 EMBL:AC002343 GO:GO:0010075 GO:GO:0009934 eggNOG:COG0326 HOGENOM:HBG631012 PANTHER:PTHR11528 EMBL:AB064528 EMBL:AY039895 EMBL:AY072394 EMBL:BT004527 EMBL:AK221485 IPI:IPI00524027 PIR:T09882 RefSeq:NP_194150.1 UniGene:At.24111 ProteinModelPortal:Q9STX5 SMR:Q9STX5 STRING:Q9STX5 PRIDE:Q9STX5 EnsemblPlants:AT4G24190.1 GeneID:828520 KEGG:ath:AT4G24190 TAIR:At4g24190 InParanoid:Q9STX5 PhylomeDB:Q9STX5 ProtClustDB:CLSN2716298 Genevestigator:Q9STX5 InterPro:IPR020575 PRINTS:PR00775 Uniprot:Q9STX5
Root	Isotig01822	4	26	-2.829	9.39E-06	TAIR|locus:2180617 - symbol:AT5G25930 species:3702 "Arabidopsis thaliana" [GO:0006468 "protein phosphorylation" evidence=IEA] [GO:0016301 "kinase activity" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] Pfam:PF00560 InterPro:IPR001611 InterPro:IPR000719 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 Pfam:PF00069 PROSITE:PS00107

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						PROSITE:PS00108 PROSITE:PS50011 GO:GO:0016021 GO:GO:0005886 GO:GO:0005524 EMBL:CP002688 GO:GO:0004872 SUPFAM:SSF56112 GO:GO:0004674 HOGENOM:HBG755340 InterPro:IPR013320 Gene3D:G3DSA:2.60.120.200 KO:K00924 EMBL:AF149413 InterPro:IPR013210 Pfam:PF08263 EMBL:BT004058 EMBL:FJ708783 IPI:IPI00529952 RefSeq:NP_197965.1 UniGene:At.30881 UniGene:At.66768 ProteinModelPortal:Q9XGZ2 SMR:Q9XGZ2 STRING:Q9XGZ2 PRIDE:Q9XGZ2 EnsemblPlants:AT5G25930.1 GeneID:832662 KEGG:ath:AT5G25930 TAIR:At5g25930 InParanoid:Q9XGZ2 OMA:NIREENV PhylomeDB:Q9XGZ2 ProtClustDB:CLSN2916431 ArrayExpress:Q9XGZ2 Genevestigator:Q9XGZ2 Uniprot:Q9XGZ2
Root	Isotig01823	5	26	-2.507	3.30E-05	TAIR|locus:2180617 - symbol:AT5G25930 species:3702 "Arabidopsis thaliana" [GO:0006468 "protein phosphorylation" evidence=IEA] [GO:0016301 "kinase activity" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] Pfam:PF00560 InterPro:IPR001611 InterPro:IPR000719 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 Pfam:PF00069 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 GO:GO:0016021 GO:GO:0005886 GO:GO:0005524 EMBL:CP002688 GO:GO:0004872 SUPFAM:SSF56112 GO:GO:0004674 HOGENOM:HBG755340 InterPro:IPR013320 Gene3D:G3DSA:2.60.120.200 KO:K00924 EMBL:AF149413 InterPro:IPR013210 Pfam:PF08263 EMBL:BT004058 EMBL:FJ708783 IPI:IPI00529952 RefSeq:NP_197965.1 UniGene:At.30881 UniGene:At.66768 ProteinModelPortal:Q9XGZ2 SMR:Q9XGZ2 STRING:Q9XGZ2 PRIDE:Q9XGZ2 EnsemblPlants:AT5G25930.1 GeneID:832662 KEGG:ath:AT5G25930 TAIR:At5g25930 InParanoid:Q9XGZ2 OMA:NIREENV PhylomeDB:Q9XGZ2 ProtClustDB:CLSN2916431 ArrayExpress:Q9XGZ2 Genevestigator:Q9XGZ2 Uniprot:Q9XGZ2
Root	Isotig01824	3	25	-3.188	4.22E-06	TAIR|locus:2180617 - symbol:AT5G25930 species:3702 "Arabidopsis thaliana" [GO:0006468 "protein phosphorylation" evidence=IEA] [GO:0016301 "kinase activity" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] Pfam:PF00560 InterPro:IPR001611 InterPro:IPR000719 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 Pfam:PF00069 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 GO:GO:0016021 GO:GO:0005886 GO:GO:0005524 EMBL:CP002688 GO:GO:0004872 SUPFAM:SSF56112 GO:GO:0004674 HOGENOM:HBG755340 InterPro:IPR013320 Gene3D:G3DSA:2.60.120.200 KO:K00924 EMBL:AF149413 InterPro:IPR013210 Pfam:PF08263 EMBL:BT004058 EMBL:FJ708783 IPI:IPI00529952 RefSeq:NP_197965.1 UniGene:At.30881 UniGene:At.66768 ProteinModelPortal:Q9XGZ2 SMR:Q9XGZ2 STRING:Q9XGZ2 PRIDE:Q9XGZ2 EnsemblPlants:AT5G25930.1 GeneID:832662 KEGG:ath:AT5G25930 TAIR:At5g25930 InParanoid:Q9XGZ2 OMA:NIREENV PhylomeDB:Q9XGZ2 ProtClustDB:CLSN2916431 ArrayExpress:Q9XGZ2 Genevestigator:Q9XGZ2 Uniprot:Q9XGZ2
Root	Isotig01825	4	25	-2.773	1.71E-05	TAIR|locus:2180617 - symbol:AT5G25930 species:3702 "Arabidopsis thaliana" [GO:0006468 "protein phosphorylation" evidence=IEA] [GO:0016301 "kinase activity" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] Pfam:PF00560 InterPro:IPR001611 InterPro:IPR000719 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 Pfam:PF00069 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 GO:GO:0016021 GO:GO:0005886 GO:GO:0005524 EMBL:CP002688 GO:GO:0004872 SUPFAM:SSF56112 GO:GO:0004674 HOGENOM:HBG755340 InterPro:IPR013320 Gene3D:G3DSA:2.60.120.200 KO:K00924 EMBL:AF149413 InterPro:IPR013210 Pfam:PF08263 EMBL:BT004058 EMBL:FJ708783 IPI:IPI00529952 RefSeq:NP_197965.1 UniGene:At.30881 UniGene:At.66768 ProteinModelPortal:Q9XGZ2 SMR:Q9XGZ2 STRING:Q9XGZ2 PRIDE:Q9XGZ2 EnsemblPlants:AT5G25930.1 GeneID:832662 KEGG:ath:AT5G25930 TAIR:At5g25930 InParanoid:Q9XGZ2 OMA:NIREENV PhylomeDB:Q9XGZ2 ProtClustDB:CLSN2916431 ArrayExpress:Q9XGZ2 Genevestigator:Q9XGZ2 Uniprot:Q9XGZ2
Root	Isotig01826	4	25	-2.773	1.71E-05	TAIR|locus:2180617 - symbol:AT5G25930 species:3702 "Arabidopsis thaliana" [GO:0006468 "protein phosphorylation" evidence=IEA] [GO:0016301 "kinase activity" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] Pfam:PF00560 InterPro:IPR001611 InterPro:IPR000719 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 Pfam:PF00069 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 GO:GO:0016021 GO:GO:0005886 GO:GO:0005524 EMBL:CP002688 GO:GO:0004872 SUPFAM:SSF56112 GO:GO:0004674 HOGENOM:HBG755340 InterPro:IPR013320 Gene3D:G3DSA:2.60.120.200 KO:K00924 EMBL:AF149413 InterPro:IPR013210 Pfam:PF08263 EMBL:BT004058 EMBL:FJ708783 IPI:IPI00529952 RefSeq:NP_197965.1 UniGene:At.30881 UniGene:At.66768

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						ProteinModelPortal:Q9XGZ2 SMR:Q9XGZ2 STRING:Q9XGZ2 PRIDE:Q9XGZ2 EnsemblPlants:AT5G25930.1 GeneID:832662 KEGG:ath:AT5G25930 TAIR:At5g25930 InParanoid:Q9XGZ2 OMA:NIREENV PhylomeDB:Q9XGZ2 ProtClustDB:CLSN2916431 ArrayExpress:Q9XGZ2 Genevestigator:Q9XGZ2 Uniprot:Q9XGZ2
Root	Isotig01827	5	25	-2.451	5.85E-05	TAIR|locus:2180617 - symbol:AT5G25930 species:3702 "Arabidopsis thaliana" [GO:0006468 "protein phosphorylation" evidence=IEA] [GO:0016301 "kinase activity" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] Pfam:PF00560 InterPro:IPR001611 InterPro:IPR000719 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 Pfam:PF00069 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 GO:GO:0016021 GO:GO:0005886 GO:GO:0005524 EMBL:CP002688 GO:GO:0004872 SUPFAM:SSF56112 GO:GO:0004674 HOGENOM:HBG755340 InterPro:IPR013320 Gene3D:G3DSA:2.60.120.200 KO:K00924 EMBL:AF149413 InterPro:IPR013210 Pfam:PF08263 EMBL:BT004058 EMBL:FJ708783 IPI:IPI00529952 RefSeq:NP_197965.1 UniGene:At.30881 UniGene:At.66768 ProteinModelPortal:Q9XGZ2 SMR:Q9XGZ2 STRING:Q9XGZ2 PRIDE:Q9XGZ2 EnsemblPlants:AT5G25930.1 GeneID:832662 KEGG:ath:AT5G25930 TAIR:At5g25930 InParanoid:Q9XGZ2 OMA:NIREENV PhylomeDB:Q9XGZ2 ProtClustDB:CLSN2916431 ArrayExpress:Q9XGZ2 Genevestigator:Q9XGZ2 Uniprot:Q9XGZ2
Root	Isotig01846	34	5	2.637	3.03E-06	TAIR|locus:2169985 - symbol:NFS1 "AT5G65720" species:3702 "Arabidopsis thaliana" [GO:0008483 "transaminase activity" evidence=ISS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0031071 "cysteine desulfurase activity" evidence=IDA] [GO:0005524 "ATP binding" evidence=IDA] [GO:0016226 "iron-sulfur cluster assembly" evidence=IDA] [GO:0008270 "zinc ion binding" evidence=IDA] InterPro:IPR000192 InterPro:IPR010240 InterPro:IPR015421 InterPro:IPR015422 Pfam:PF00266 GO:GO:0005739 GO:GO:0005524 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0030170 InterPro:IPR015424 Gene3D:G3DSA:3.40.640.10 Gene3D:G3DSA:3.90.1150.10 SUPFAM:SSF53383 EMBL:AB010075 EMBL:AL021684 GO:GO:0008270 GO:GO:0016226 HOGENOM:HBG635316 GO:GO:0031071 GO:GO:0006534 eggNOG:COG1104 KO:K04487 OMA:CIHHVKR InterPro:IPR016454 PIRSF:PIRSF005572 TIGRFAMs:TIGR02006 EMBL:AJ243393 EMBL:AF229854 EMBL:AY050874 EMBL:AY096358 IPI:IPI00545655 PIR:T05896 RefSeq:NP_201373.1 UniGene:At.696 ProteinModelPortal:O49543 SMR:O49543 STRING:O49543 PRIDE:O49543 EnsemblPlants:AT5G65720.1 GeneID:836701 KEGG:ath:AT5G65720 TAIR:At5g65720 InParanoid:O49543 PhylomeDB:O49543 ProtClustDB:PLN02651 BRENDA:2.8.1.6 ArrayExpress:O49543 Genevestigator:O49543 GermOnline:AT5G65720 Uniprot:O49543
Root	Isotig01847	36	5	2.719	1.04E-06	TAIR|locus:2169985 - symbol:NFS1 "AT5G65720" species:3702 "Arabidopsis thaliana" [GO:0008483 "transaminase activity" evidence=ISS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0031071 "cysteine desulfurase activity" evidence=IDA] [GO:0005524 "ATP binding" evidence=IDA] [GO:0016226 "iron-sulfur cluster assembly" evidence=IDA] [GO:0008270 "zinc ion binding" evidence=IDA] InterPro:IPR000192 InterPro:IPR010240 InterPro:IPR015421 InterPro:IPR015422 Pfam:PF00266 GO:GO:0005739 GO:GO:0005524 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0030170 InterPro:IPR015424 Gene3D:G3DSA:3.40.640.10 Gene3D:G3DSA:3.90.1150.10 SUPFAM:SSF53383 EMBL:AB010075 EMBL:AL021684 GO:GO:0008270 GO:GO:0016226 HOGENOM:HBG635316 GO:GO:0031071 GO:GO:0006534 eggNOG:COG1104 KO:K04487 OMA:CIHHVKR InterPro:IPR016454 PIRSF:PIRSF005572 TIGRFAMs:TIGR02006 EMBL:AJ243393 EMBL:AF229854 EMBL:AY050874 EMBL:AY096358 IPI:IPI00545655 PIR:T05896 RefSeq:NP_201373.1 UniGene:At.696 ProteinModelPortal:O49543 SMR:O49543 STRING:O49543 PRIDE:O49543 EnsemblPlants:AT5G65720.1 GeneID:836701 KEGG:ath:AT5G65720 TAIR:At5g65720 InParanoid:O49543 PhylomeDB:O49543 ProtClustDB:PLN02651 BRENDA:2.8.1.6 ArrayExpress:O49543 Genevestigator:O49543 GermOnline:AT5G65720 Uniprot:O49543
Root	Isotig01848	32	5	2.549	8.76E-06	TAIR|locus:2169985 - symbol:NFS1 "AT5G65720" species:3702 "Arabidopsis thaliana" [GO:0008483 "transaminase activity" evidence=ISS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0031071 "cysteine desulfurase activity" evidence=IDA] [GO:0005524 "ATP binding" evidence=IDA] [GO:0016226 "iron-sulfur cluster assembly" evidence=IDA] [GO:0008270 "zinc ion binding" evidence=IDA] InterPro:IPR000192 InterPro:IPR010240 InterPro:IPR015421 InterPro:IPR015422 Pfam:PF00266 GO:GO:0005739 GO:GO:0005524 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0030170 InterPro:IPR015424 Gene3D:G3DSA:3.40.640.10 Gene3D:G3DSA:3.90.1150.10 SUPFAM:SSF53383 EMBL:AB010075 EMBL:AL021684 GO:GO:0008270 GO:GO:0016226 HOGENOM:HBG635316 GO:GO:0031071 GO:GO:0006534 eggNOG:COG1104 KO:K04487

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						OMA:CIHHVKR InterPro:IPR016454 PIRSF:PIRSF005572 TIGRFAMs:TIGR02006 EMBL:AJ243393 EMBL:AF229854 EMBL:AY050874 EMBL:AY096358 IPI:IPI00545655 PIR:T05896 RefSeq:NP_201373.1 UniGene:At.696 ProteinModelPortal:O49543 SMR:O49543 STRING:O49543 PRIDE:O49543 EnsemblPlants:AT5G65720.1 GeneID:836701 KEGG:ath:AT5G65720 TAIR:At5g65720 InParanoid:O49543 PhylomeDB:O49543 ProtClustDB:PLN02651 BRENDA:2.8.1.6 ArrayExpress:O49543 Genevestigator:O49543 GermOnline:AT5G65720 Uniprot:O49543
Root	Isotig01849	34	5	2.637	3.03E-06	TAIR|locus:2169985 - symbol:NFS1 "AT5G65720" species:3702 "Arabidopsis thaliana" [GO:0008483 "transaminase activity" evidence=ISS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0031071 "cysteine desulfurase activity" evidence=IDA] [GO:0005524 "ATP binding" evidence=IDA] [GO:0016226 "iron-sulfur cluster assembly" evidence=IDA] [GO:0008270 "zinc ion binding" evidence=IDA] InterPro:IPR000192 InterPro:IPR010240 InterPro:IPR015421 InterPro:IPR015422 Pfam:PF00266 GO:GO:0005739 GO:GO:0005524 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0030170 InterPro:IPR015424 Gene3D:G3DSA:3.40.640.10 Gene3D:G3DSA:3.90.1150.10 SUPFAM:SSF53383 EMBL:AB010075 EMBL:AL021684 GO:GO:0008270 GO:GO:0016226 HOGENOM:HBG635316 GO:GO:0031071 GO:GO:0006534 eggNOG:COG1104 KO:K04487 OMA:CIHHVKR InterPro:IPR016454 PIRSF:PIRSF005572 TIGRFAMs:TIGR02006 EMBL:AJ243393 EMBL:AF229854 EMBL:AY050874 EMBL:AY096358 IPI:IPI00545655 PIR:T05896 RefSeq:NP_201373.1 UniGene:At.696 ProteinModelPortal:O49543 SMR:O49543 STRING:O49543 PRIDE:O49543 EnsemblPlants:AT5G65720.1 GeneID:836701 KEGG:ath:AT5G65720 TAIR:At5g65720 InParanoid:O49543 PhylomeDB:O49543 ProtClustDB:PLN02651 BRENDA:2.8.1.6 ArrayExpress:O49543 Genevestigator:O49543 GermOnline:AT5G65720 Uniprot:O49543
Root	Isotig01850	36	5	2.719	1.04E-06	TAIR|locus:2169985 - symbol:NFS1 "AT5G65720" species:3702 "Arabidopsis thaliana" [GO:0008483 "transaminase activity" evidence=ISS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0031071 "cysteine desulfurase activity" evidence=IDA] [GO:0005524 "ATP binding" evidence=IDA] [GO:0016226 "iron-sulfur cluster assembly" evidence=IDA] [GO:0008270 "zinc ion binding" evidence=IDA] InterPro:IPR000192 InterPro:IPR010240 InterPro:IPR015421 InterPro:IPR015422 Pfam:PF00266 GO:GO:0005739 GO:GO:0005524 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0030170 InterPro:IPR015424 Gene3D:G3DSA:3.40.640.10 Gene3D:G3DSA:3.90.1150.10 SUPFAM:SSF53383 EMBL:AB010075 EMBL:AL021684 GO:GO:0008270 GO:GO:0016226 HOGENOM:HBG635316 GO:GO:0031071 GO:GO:0006534 eggNOG:COG1104 KO:K04487 OMA:CIHHVKR InterPro:IPR016454 PIRSF:PIRSF005572 TIGRFAMs:TIGR02006 EMBL:AJ243393 EMBL:AF229854 EMBL:AY050874 EMBL:AY096358 IPI:IPI00545655 PIR:T05896 RefSeq:NP_201373.1 UniGene:At.696 ProteinModelPortal:O49543 SMR:O49543 STRING:O49543 PRIDE:O49543 EnsemblPlants:AT5G65720.1 GeneID:836701 KEGG:ath:AT5G65720 TAIR:At5g65720 InParanoid:O49543 PhylomeDB:O49543 ProtClustDB:PLN02651 BRENDA:2.8.1.6 ArrayExpress:O49543 Genevestigator:O49543 GermOnline:AT5G65720 Uniprot:O49543
Root	Isotig01851	32	5	2.549	8.76E-06	TAIR|locus:2169985 - symbol:NFS1 "AT5G65720" species:3702 "Arabidopsis thaliana" [GO:0008483 "transaminase activity" evidence=ISS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0031071 "cysteine desulfurase activity" evidence=IDA] [GO:0005524 "ATP binding" evidence=IDA] [GO:0016226 "iron-sulfur cluster assembly" evidence=IDA] [GO:0008270 "zinc ion binding" evidence=IDA] InterPro:IPR000192 InterPro:IPR010240 InterPro:IPR015421 InterPro:IPR015422 Pfam:PF00266 GO:GO:0005739 GO:GO:0005524 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0030170 InterPro:IPR015424 Gene3D:G3DSA:3.40.640.10 Gene3D:G3DSA:3.90.1150.10 SUPFAM:SSF53383 EMBL:AB010075 EMBL:AL021684 GO:GO:0008270 GO:GO:0016226 HOGENOM:HBG635316 GO:GO:0031071 GO:GO:0006534 eggNOG:COG1104 KO:K04487 OMA:CIHHVKR InterPro:IPR016454 PIRSF:PIRSF005572 TIGRFAMs:TIGR02006 EMBL:AJ243393 EMBL:AF229854 EMBL:AY050874 EMBL:AY096358 IPI:IPI00545655 PIR:T05896 RefSeq:NP_201373.1 UniGene:At.696 ProteinModelPortal:O49543 SMR:O49543 STRING:O49543 PRIDE:O49543 EnsemblPlants:AT5G65720.1 GeneID:836701 KEGG:ath:AT5G65720 TAIR:At5g65720 InParanoid:O49543 PhylomeDB:O49543 ProtClustDB:PLN02651 BRENDA:2.8.1.6 ArrayExpress:O49543 Genevestigator:O49543 GermOnline:AT5G65720 Uniprot:O49543
Root	Isotig01858	0	14	-4.936	8.24E-05	TAIR|locus:2205190 - symbol:NRT2:1 "AT1G08090" species:3702 "Arabidopsis thaliana" [GO:0015112 "nitrate transmembrane transporter activity" evidence=ISS;TAS] [GO:0015706 "nitrate transport" evidence=IMP] [GO:0016020 "membrane" evidence=ISS] [GO:0048527 "lateral root development" evidence=IMP] [GO:0010167 "response to nitrate" evidence=IEP] InterPro:IPR011701 Pfam:PF07690 GO:GO:0016021 EMBL:CP002684

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GenomeReviews:CT485782_GR GO:GO:0005886 GO:GO:0048527 InterPro:IPR016196 SUPFAM:SSF103473 PROSITE:PS50850 GO:GO:0015112 GO:GO:0042128 GO:GO:0010167 EMBL:AC026875 eggNOG:COG2223 EMBL:Z97058 EMBL:AF019748 EMBL:AF093754 IPI:IPI00522021 PIR:T51836 RefSeq:NP_172288.1 UniGene:At.5407 ProteinModelPortal:O82811 SMR:O82811 IntAct:O82811 STRING:O82811 TCDB:2.A.1.8.12 PRIDE:O82811 ProMEX:O82811 EnsemblPlants:AT1G08090.1 GeneID:837327 KEGG:ath:AT1G08090 TAIR:At1g08090 HOGENOM:HBG617617 InParanoid:O82811 OMA:ANFAIVP PhylomeDB:O82811 ProtClustDB:PLN00028 Genevestigator:O82811 Uniprot:O82811
Root	Isotig01859	0	14	-4.936	8.24E-05	TAIR|locus:2205190 - symbol:NRT2:1 "AT1G08090" species:3702 "Arabidopsis thaliana" [GO:0015112 "nitrate transmembrane transporter activity" evidence=ISS;TAS] [GO:0015706 "nitrate transport" evidence=IMP] [GO:0016020 "membrane" evidence=ISS] [GO:0048527 "lateral root development" evidence=IMP] [GO:0010167 "response to nitrate" evidence=IEP] InterPro:IPR011701 Pfam:PF07690 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005886 GO:GO:0048527 InterPro:IPR016196 SUPFAM:SSF103473 PROSITE:PS50850 GO:GO:0015112 GO:GO:0042128 GO:GO:0010167 EMBL:AC026875 eggNOG:COG2223 EMBL:Z97058 EMBL:AF019748 EMBL:AF093754 IPI:IPI00522021 PIR:T51836 RefSeq:NP_172288.1 UniGene:At.5407 ProteinModelPortal:O82811 SMR:O82811 IntAct:O82811 STRING:O82811 TCDB:2.A.1.8.12 PRIDE:O82811 ProMEX:O82811 EnsemblPlants:AT1G08090.1 GeneID:837327 KEGG:ath:AT1G08090 TAIR:At1g08090 HOGENOM:HBG617617 InParanoid:O82811 OMA:ANFAIVP PhylomeDB:O82811 ProtClustDB:PLN00028 Genevestigator:O82811 Uniprot:O82811
Root	Isotig01860	0	13	-4.829	0.000155955	TAIR|locus:2205190 - symbol:NRT2:1 "AT1G08090" species:3702 "Arabidopsis thaliana" [GO:0015112 "nitrate transmembrane transporter activity" evidence=ISS;TAS] [GO:0015706 "nitrate transport" evidence=IMP] [GO:0016020 "membrane" evidence=ISS] [GO:0048527 "lateral root development" evidence=IMP] [GO:0010167 "response to nitrate" evidence=IEP] InterPro:IPR011701 Pfam:PF07690 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005886 GO:GO:0048527 InterPro:IPR016196 SUPFAM:SSF103473 PROSITE:PS50850 GO:GO:0015112 GO:GO:0042128 GO:GO:0010167 EMBL:AC026875 eggNOG:COG2223 EMBL:Z97058 EMBL:AF019748 EMBL:AF093754 IPI:IPI00522021 PIR:T51836 RefSeq:NP_172288.1 UniGene:At.5407 ProteinModelPortal:O82811 SMR:O82811 IntAct:O82811 STRING:O82811 TCDB:2.A.1.8.12 PRIDE:O82811 ProMEX:O82811 EnsemblPlants:AT1G08090.1 GeneID:837327 KEGG:ath:AT1G08090 TAIR:At1g08090 HOGENOM:HBG617617 InParanoid:O82811 OMA:ANFAIVP PhylomeDB:O82811 ProtClustDB:PLN00028 Genevestigator:O82811 Uniprot:O82811
Root	Isotig01861	0	13	-4.829	0.000155955	TAIR|locus:2205190 - symbol:NRT2:1 "AT1G08090" species:3702 "Arabidopsis thaliana" [GO:0015112 "nitrate transmembrane transporter activity" evidence=ISS;TAS] [GO:0015706 "nitrate transport" evidence=IMP] [GO:0016020 "membrane" evidence=ISS] [GO:0048527 "lateral root development" evidence=IMP] [GO:0010167 "response to nitrate" evidence=IEP] InterPro:IPR011701 Pfam:PF07690 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005886 GO:GO:0048527 InterPro:IPR016196 SUPFAM:SSF103473 PROSITE:PS50850 GO:GO:0015112 GO:GO:0042128 GO:GO:0010167 EMBL:AC026875 eggNOG:COG2223 EMBL:Z97058 EMBL:AF019748 EMBL:AF093754 IPI:IPI00522021 PIR:T51836 RefSeq:NP_172288.1 UniGene:At.5407 ProteinModelPortal:O82811 SMR:O82811 IntAct:O82811 STRING:O82811 TCDB:2.A.1.8.12 PRIDE:O82811 ProMEX:O82811 EnsemblPlants:AT1G08090.1 GeneID:837327 KEGG:ath:AT1G08090 TAIR:At1g08090 HOGENOM:HBG617617 InParanoid:O82811 OMA:ANFAIVP PhylomeDB:O82811 ProtClustDB:PLN00028 Genevestigator:O82811 Uniprot:O82811
Root	Isotig01870	0	11	-4.588	0.000569522	TAIR|locus:2153924 - symbol:DMR6 "AT5G24530" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0009813 "flavonoid biosynthetic process" evidence=ISS] [GO:0016491 "oxidoreductase activity" evidence=IEA] [GO:0016706 "oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors" evidence=ISS] [GO:0009617 "response to bacterium" evidence=IGI] [GO:0009620 "response to fungus" evidence=IEP;IGI] InterPro:IPR005123 Pfam:PF03171 PROSITE:PS51471 EMBL:CP002688 GO:GO:0009617 GO:GO:0016706 HSSP:Q96323 GO:GO:0009620 EMBL:AB010068 EMBL:AF386975 EMBL:AY081455 IPI:IPI00531388 RefSeq:NP_197841.1 UniGene:At.23761 ProteinModelPortal:Q9FLV0 SMR:Q9FLV0 IntAct:Q9FLV0 STRING:Q9FLV0 PRIDE:Q9FLV0 EnsemblPlants:AT5G24530.1 GeneID:832524 KEGG:ath:AT5G24530 TAIR:At5g24530 InParanoid:Q9FLV0 OMA:NPHPDAF PhylomeDB:Q9FLV0 ProtClustDB:PLN02639 ArrayExpress:Q9FLV0 Genevestigator:Q9FLV0 Uniprot:Q9FLV0

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig01871	0	11	-4.588	0.000569522	TAIR|locus:2153924 - symbol:DMR6 "AT5G24530" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0009813 "flavonoid biosynthetic process" evidence=ISS] [GO:0016491 "oxidoreductase activity" evidence=IEA] [GO:0016706 "oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors" evidence=ISS] [GO:0009617 "response to bacterium" evidence=IGI] [GO:0009620 "response to fungus" evidence=IEP;IGI] InterPro:IPR005123 Pfam:PF03171 PROSITE:PS51471 EMBL:CP002688 GO:GO:0009617 GO:GO:0016706 HSSP:Q96323 GO:GO:0009620 EMBL:AB010068 EMBL:AF386975 EMBL:AY081455 IPI:IPI00531388 RefSeq:NP_197841.1 UniGene:At.23761 ProteinModelPortal:Q9FLV0 SMR:Q9FLV0 IntAct:Q9FLV0 STRING:Q9FLV0 PRIDE:Q9FLV0 EnsemblPlants:AT5G24530.1 GeneID:832524 KEGG:ath:AT5G24530 TAIR:At5g24530 InParanoid:Q9FLV0 OMA:NPHPDAF PhylomeDB:Q9FLV0 ProtClustDB:PLN02639 ArrayExpress:Q9FLV0 Genevestigator:Q9FLV0 Uniprot:Q9FLV0
Root	Isotig01872	0	11	-4.588	0.000569522	TAIR|locus:2153924 - symbol:DMR6 "AT5G24530" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0009813 "flavonoid biosynthetic process" evidence=ISS] [GO:0016491 "oxidoreductase activity" evidence=IEA] [GO:0016706 "oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors" evidence=ISS] [GO:0009617 "response to bacterium" evidence=IGI] [GO:0009620 "response to fungus" evidence=IEP;IGI] InterPro:IPR005123 Pfam:PF03171 PROSITE:PS51471 EMBL:CP002688 GO:GO:0009617 GO:GO:0016706 HSSP:Q96323 GO:GO:0009620 EMBL:AB010068 EMBL:AF386975 EMBL:AY081455 IPI:IPI00531388 RefSeq:NP_197841.1 UniGene:At.23761 ProteinModelPortal:Q9FLV0 SMR:Q9FLV0 IntAct:Q9FLV0 STRING:Q9FLV0 PRIDE:Q9FLV0 EnsemblPlants:AT5G24530.1 GeneID:832524 KEGG:ath:AT5G24530 TAIR:At5g24530 InParanoid:Q9FLV0 OMA:NPHPDAF PhylomeDB:Q9FLV0 ProtClustDB:PLN02639 ArrayExpress:Q9FLV0 Genevestigator:Q9FLV0 Uniprot:Q9FLV0
Root	Isotig01873	0	11	-4.588	0.000569522	TAIR|locus:2153924 - symbol:DMR6 "AT5G24530" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0009813 "flavonoid biosynthetic process" evidence=ISS] [GO:0016491 "oxidoreductase activity" evidence=IEA] [GO:0016706 "oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors" evidence=ISS] [GO:0009617 "response to bacterium" evidence=IGI] [GO:0009620 "response to fungus" evidence=IEP;IGI] InterPro:IPR005123 Pfam:PF03171 PROSITE:PS51471 EMBL:CP002688 GO:GO:0009617 GO:GO:0016706 HSSP:Q96323 GO:GO:0009620 EMBL:AB010068 EMBL:AF386975 EMBL:AY081455 IPI:IPI00531388 RefSeq:NP_197841.1 UniGene:At.23761 ProteinModelPortal:Q9FLV0 SMR:Q9FLV0 IntAct:Q9FLV0 STRING:Q9FLV0 PRIDE:Q9FLV0 EnsemblPlants:AT5G24530.1 GeneID:832524 KEGG:ath:AT5G24530 TAIR:At5g24530 InParanoid:Q9FLV0 OMA:NPHPDAF PhylomeDB:Q9FLV0 ProtClustDB:PLN02639 ArrayExpress:Q9FLV0 Genevestigator:Q9FLV0 Uniprot:Q9FLV0
Root	Isotig01882	7	40	-2.644	1.14E-07	TAIR|locus:2180547 - symbol:NADP-ME3 "AT5G25880" species:3702 "Arabidopsis thaliana" [GO:0004470 "malic enzyme activity" evidence=ISS] [GO:0006108 "malate metabolic process" evidence=ISS;IDA] [GO:0016652 "oxidoreductase activity, acting on NADH or NADPH, NAD or NADP as acceptor" evidence=ISS] [GO:0004473 "malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+) activity" evidence=IDA] [GO:0051260 "protein homooligomerization" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001891 InterPro:IPR012301 InterPro:IPR012302 InterPro:IPR015884 InterPro:IPR016040 Pfam:PF00390 Pfam:PF03949 PIRSF:PIRSF000106 PRINTS:PR00072 PROSITE:PS00331 SMART:SM00919 GO:GO:0005829 EMBL:CP002688 GenomeReviews:BA000015_GR Gene3D:G3DSA:3.40.50.720 GO:GO:0051287 GO:GO:0046872 GO:GO:0051260 EMBL:AF149413 GO:GO:0006108 HOGENOM:HBG289821 GO:GO:0016619 Gene3D:G3DSA:3.40.50.10380 KO:K00029 GO:GO:0004473 HSSP:P40927 ProtClustDB:PLN03129 IPI:IPI00535942 RefSeq:NP_197960.1 UniGene:At.43327 ProteinModelPortal:Q9XGZ0 SMR:Q9XGZ0 STRING:Q9XGZ0 PRIDE:Q9XGZ0 EnsemblPlants:AT5G25880.1 GeneID:832657 KEGG:ath:AT5G25880 TAIR:At5g25880 InParanoid:Q9XGZ0 OMA:RERETHY PhylomeDB:Q9XGZ0 Genevestigator:Q9XGZ0 Uniprot:Q9XGZ0
Root	Isotig01883	7	40	-2.644	1.14E-07	TAIR|locus:2180547 - symbol:NADP-ME3 "AT5G25880" species:3702 "Arabidopsis thaliana" [GO:0004470 "malic enzyme activity" evidence=ISS] [GO:0006108 "malate metabolic process" evidence=ISS;IDA] [GO:0016652 "oxidoreductase activity, acting on NADH or NADPH, NAD or NADP as acceptor" evidence=ISS] [GO:0004473 "malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+) activity" evidence=IDA] [GO:0051260 "protein homooligomerization" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001891 InterPro:IPR012301 InterPro:IPR012302 InterPro:IPR015884 InterPro:IPR016040 Pfam:PF00390 Pfam:PF03949

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						PIRSF:PIRSF000106 PRINTS:PR00072 PROSITE:PS00331 SMART:SM00919 GO:GO:0005829 EMBL:CP002688 GenomeReviews:BA000015_GR Gene3D:G3DSA:3.40.50.720 GO:GO:0051287 GO:GO:0046872 GO:GO:0051260 EMBL:AF149413 GO:GO:0006108 HOGENOM:HBG289821 GO:GO:0016619 Gene3D:G3DSA:3.40.50.10380 KO:K00029 GO:GO:0004473 HSSP:P40927 ProtClustDB:PLN03129 IPI:IPI00535942 RefSeq:NP_197960.1 UniGene:At.43327 ProteinModelPortal:Q9XGZ0 SMR:Q9XGZ0 STRING:Q9XGZ0 PRIDE:Q9XGZ0 EnsemblPlants:AT5G25880.1 GeneID:832657 KEGG:ath:AT5G25880 TAIR:At5g25880 InParanoid:Q9XGZ0 OMA:RERETHY PhylomeDB:Q9XGZ0 Genevestigator:Q9XGZ0 Uniprot:Q9XGZ0
Root	Isotig01884	7	40	-2.644	1.14E-07	TAIR|locus:2180547 - symbol:NADP-ME3 "AT5G25880" species:3702 "Arabidopsis thaliana" [GO:0004470 "malic enzyme activity" evidence=ISS] [GO:0006108 "malate metabolic process" evidence=ISS;IDA] [GO:0016652 "oxidoreductase activity, acting on NADH or NADPH, NAD or NADP as acceptor" evidence=ISS] [GO:0004473 "malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+) activity" evidence=IDA] [GO:0051260 "protein homooligomerization" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001891 InterPro:IPR012301 InterPro:IPR012302 InterPro:IPR015884 InterPro:IPR016040 Pfam:PF00390 Pfam:PF03949 PIRSF:PIRSF000106 PRINTS:PR00072 PROSITE:PS00331 SMART:SM00919 GO:GO:0005829 EMBL:CP002688 GenomeReviews:BA000015_GR Gene3D:G3DSA:3.40.50.720 GO:GO:0051287 GO:GO:0046872 GO:GO:0051260 EMBL:AF149413 GO:GO:0006108 HOGENOM:HBG289821 GO:GO:0016619 Gene3D:G3DSA:3.40.50.10380 KO:K00029 GO:GO:0004473 HSSP:P40927 ProtClustDB:PLN03129 IPI:IPI00535942 RefSeq:NP_197960.1 UniGene:At.43327 ProteinModelPortal:Q9XGZ0 SMR:Q9XGZ0 STRING:Q9XGZ0 PRIDE:Q9XGZ0 EnsemblPlants:AT5G25880.1 GeneID:832657 KEGG:ath:AT5G25880 TAIR:At5g25880 InParanoid:Q9XGZ0 OMA:RERETHY PhylomeDB:Q9XGZ0 Genevestigator:Q9XGZ0 Uniprot:Q9XGZ0
Root	Isotig01894	1	26	-4.829	8.91E-08	TAIR|locus:2024046 - symbol:AT1G24620 species:3702 "Arabidopsis thaliana" [GO:0005509 "calcium ion binding" evidence=IEA;ISS] [GO:0005634 "nucleus" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0048767 "root hair elongation" evidence=IMP] InterPro:IPR002048 InterPro:IPR011992 SMART:SM00054 Prosite:PS00018 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005634 GO:GO:0005737 GO:GO:0005509 InterPro:IPR018247 InterPro:IPR018249 Gene3D:G3DSA:1.10.238.10 PROSITE:PS50222 GO:GO:0009409 GO:GO:0048767 EMBL:AC000103 eggNOG:COG5126 HOGENOM:HBG746798 HSSP:P62157 KO:K13448 EMBL:DQ446288 IPI:IPI00543078 PIR:F86379 RefSeq:NP_173866.1 UniGene:At.51279 ProteinModelPortal:Q9FYK2 SMR:Q9FYK2 PRIDE:Q9FYK2 EnsemblPlants:AT1G24620.1 GeneID:839076 KEGG:ath:AT1G24620 TAIR:At1g24620 InParanoid:Q9FYK2 OMA:GDECSIA PhylomeDB:Q9FYK2 ProtClustDB:CLSN2682405 Genevestigator:Q9FYK2 Uniprot:Q9FYK2
Root	Isotig01895	1	26	-4.829	8.91E-08	TAIR|locus:2024046 - symbol:AT1G24620 species:3702 "Arabidopsis thaliana" [GO:0005509 "calcium ion binding" evidence=IEA;ISS] [GO:0005634 "nucleus" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0048767 "root hair elongation" evidence=IMP] InterPro:IPR002048 InterPro:IPR011992 SMART:SM00054 Prosite:PS00018 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005634 GO:GO:0005737 GO:GO:0005509 InterPro:IPR018247 InterPro:IPR018249 Gene3D:G3DSA:1.10.238.10 PROSITE:PS50222 GO:GO:0009409 GO:GO:0048767 EMBL:AC000103 eggNOG:COG5126 HOGENOM:HBG746798 HSSP:P62157 KO:K13448 EMBL:DQ446288 IPI:IPI00543078 PIR:F86379 RefSeq:NP_173866.1 UniGene:At.51279 ProteinModelPortal:Q9FYK2 SMR:Q9FYK2 PRIDE:Q9FYK2 EnsemblPlants:AT1G24620.1 GeneID:839076 KEGG:ath:AT1G24620 TAIR:At1g24620 InParanoid:Q9FYK2 OMA:GDECSIA PhylomeDB:Q9FYK2 ProtClustDB:CLSN2682405 Genevestigator:Q9FYK2 Uniprot:Q9FYK2
Root	Isotig01896	1	26	-4.829	8.91E-08	TAIR|locus:2024046 - symbol:AT1G24620 species:3702 "Arabidopsis thaliana" [GO:0005509 "calcium ion binding" evidence=IEA;ISS] [GO:0005634 "nucleus" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0048767 "root hair elongation" evidence=IMP] InterPro:IPR002048 InterPro:IPR011992 SMART:SM00054 Prosite:PS00018 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005634 GO:GO:0005737 GO:GO:0005509 InterPro:IPR018247 InterPro:IPR018249 Gene3D:G3DSA:1.10.238.10 PROSITE:PS50222 GO:GO:0009409 GO:GO:0048767 EMBL:AC000103 eggNOG:COG5126 HOGENOM:HBG746798 HSSP:P62157 KO:K13448 EMBL:DQ446288 IPI:IPI00543078 PIR:F86379 RefSeq:NP_173866.1 UniGene:At.51279 ProteinModelPortal:Q9FYK2 SMR:Q9FYK2 PRIDE:Q9FYK2 EnsemblPlants:AT1G24620.1 GeneID:839076 KEGG:ath:AT1G24620 TAIR:At1g24620 InParanoid:Q9FYK2 OMA:GDECSIA PhylomeDB:Q9FYK2 ProtClustDB:CLSN2682405 Genevestigator:Q9FYK2 Uniprot:Q9FYK2
Root	Isotig01897	1	26	-4.829	8.91E-08	TAIR|locus:2024046 - symbol:AT1G24620 species:3702 "Arabidopsis thaliana" [GO:0005509 "calcium ion binding" evidence=IEA;ISS] [GO:0005634 "nucleus" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP]

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						[GO:0005737 "cytoplasm" evidence=IDA] [GO:0048767 "root hair elongation" evidence=IMP] InterPro:IPR002048 InterPro:IPR011992 SMART:SM00054 Prosite:PS00018 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005634 GO:GO:0005737 GO:GO:0005509 InterPro:IPR018247 InterPro:IPR018249 Gene3D:G3DSA:1.10.238.10 PROSITE:PS50222 GO:GO:0009409 GO:GO:0048767 EMBL:AC000103 eggNOG:COG5126 HOGENOM:HBG746798 HSSP:P62157 KO:K13448 EMBL:DQ446288 IPI:IPI00543078 PIR:F86379 RefSeq:NP_173866.1 UniGene:At.51279 ProteinModelPortal:Q9FYK2 SMR:Q9FYK2 PRIDE:Q9FYK2 EnsemblPlants:AT1G24620.1 GeneID:839076 KEGG:ath:AT1G24620 TAIR:At1g24620 InParanoid:Q9FYK2 OMA:GDECSIA PhylomeDB:Q9FYK2 ProtClustDB:CLSN2682405 Genevestigator:Q9FYK2 Uniprot:Q9FYK2
Root	Isotig01898	1	26	-4.829	8.91E-08	TAIR|locus:2024046 - symbol:AT1G24620 species:3702 "Arabidopsis thaliana" [GO:0005509 "calcium ion binding" evidence=IEA;ISS] [GO:0005634 "nucleus" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0048767 "root hair elongation" evidence=IMP] InterPro:IPR002048 InterPro:IPR011992 SMART:SM00054 Prosite:PS00018 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005634 GO:GO:0005737 GO:GO:0005509 InterPro:IPR018247 InterPro:IPR018249 Gene3D:G3DSA:1.10.238.10 PROSITE:PS50222 GO:GO:0009409 GO:GO:0048767 EMBL:AC000103 eggNOG:COG5126 HOGENOM:HBG746798 HSSP:P62157 KO:K13448 EMBL:DQ446288 IPI:IPI00543078 PIR:F86379 RefSeq:NP_173866.1 UniGene:At.51279 ProteinModelPortal:Q9FYK2 SMR:Q9FYK2 PRIDE:Q9FYK2 EnsemblPlants:AT1G24620.1 GeneID:839076 KEGG:ath:AT1G24620 TAIR:At1g24620 InParanoid:Q9FYK2 OMA:GDECSIA PhylomeDB:Q9FYK2 ProtClustDB:CLSN2682405 Genevestigator:Q9FYK2 Uniprot:Q9FYK2
Root	Isotig01899	1	26	-4.829	8.91E-08	TAIR|locus:2024046 - symbol:AT1G24620 species:3702 "Arabidopsis thaliana" [GO:0005509 "calcium ion binding" evidence=IEA;ISS] [GO:0005634 "nucleus" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0048767 "root hair elongation" evidence=IMP] InterPro:IPR002048 InterPro:IPR011992 SMART:SM00054 Prosite:PS00018 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005634 GO:GO:0005737 GO:GO:0005509 InterPro:IPR018247 InterPro:IPR018249 Gene3D:G3DSA:1.10.238.10 PROSITE:PS50222 GO:GO:0009409 GO:GO:0048767 EMBL:AC000103 eggNOG:COG5126 HOGENOM:HBG746798 HSSP:P62157 KO:K13448 EMBL:DQ446288 IPI:IPI00543078 PIR:F86379 RefSeq:NP_173866.1 UniGene:At.51279 ProteinModelPortal:Q9FYK2 SMR:Q9FYK2 PRIDE:Q9FYK2 EnsemblPlants:AT1G24620.1 GeneID:839076 KEGG:ath:AT1G24620 TAIR:At1g24620 InParanoid:Q9FYK2 OMA:GDECSIA PhylomeDB:Q9FYK2 ProtClustDB:CLSN2682405 Genevestigator:Q9FYK2 Uniprot:Q9FYK2
Root	Isotig01933	2	21	-3.521	1.10E-05	TAIR|locus:2181072 - symbol:AT5G01740 "AT5G01740" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002688 GenomeReviews:BA000015_GR EMBL:AL162351 HOGENOM:HBG606004 InterPro:IPR009798 Pfam:PF07107 EMBL:AY075604 EMBL:BT014870 IPI:IPI00541380 PIR:T48195 RefSeq:NP_195794.1 UniGene:At.33512 ProteinModelPortal:Q9LZX2 DNASU:831686 EnsemblPlants:AT5G01740.1 GeneID:831686 KEGG:ath:AT5G01740 TAIR:At5g01740 eggNOG:NOG315363 InParanoid:Q9LZX2 OMA:CVIAEGW PhylomeDB:Q9LZX2 ProtClustDB:CLSN2687137 Genevestigator:Q9LZX2 Uniprot:Q9LZX2
Root	Isotig01955	130	72	0.723	0.000483064	TAIR|locus:2159300 - symbol:ABCF1 "AT5G60790" species:3702 "Arabidopsis thaliana" [GO:0005215 "transporter activity" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] InterPro:IPR003439 InterPro:IPR003593 InterPro:IPR017871 Pfam:PF00005 PROSITE:PS00211 PROSITE:PS50893 SMART:SM00382 GO:GO:0005886 GO:GO:0005524 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0006810 GO:GO:0016887 HOGENOM:HBG758042 EMBL:AB015472 EMBL:AY140066 EMBL:BT000946 EMBL:BT008363 EMBL:AK317570 EMBL:AK317690 IPI:IPI00540333 RefSeq:NP_200887.1 UniGene:At.9321 ProteinModelPortal:Q9FJH6 SMR:Q9FJH6 IntAct:Q9FJH6 STRING:Q9FJH6 PRIDE:Q9FJH6 EnsemblPlants:AT5G60790.1 GeneID:836200 KEGG:ath:AT5G60790 TAIR:At5g60790 eggNOG:COG0488 InParanoid:Q9FJH6 KO:K06185 OMA:YHQHLHE PhylomeDB:Q9FJH6 ProtClustDB:CLSN2686703 ArrayExpress:Q9FJH6 Genevestigator:Q9FJH6 Uniprot:Q9FJH6
Root	Isotig01957	130	72	0.723	0.000483064	TAIR|locus:2159300 - symbol:ABCF1 "AT5G60790" species:3702 "Arabidopsis thaliana" [GO:0005215 "transporter activity" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] InterPro:IPR003439 InterPro:IPR003593 InterPro:IPR017871 Pfam:PF00005 PROSITE:PS00211 PROSITE:PS50893 SMART:SM00382 GO:GO:0005886 GO:GO:0005524 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0006810 GO:GO:0016887 HOGENOM:HBG758042 EMBL:AB015472 EMBL:AY140066 EMBL:BT000946 EMBL:BT008363 EMBL:AK317570 EMBL:AK317690 IPI:IPI00540333 RefSeq:NP_200887.1 UniGene:At.9321 ProteinModelPortal:Q9FJH6 SMR:Q9FJH6 IntAct:Q9FJH6 STRING:Q9FJH6 PRIDE:Q9FJH6 EnsemblPlants:AT5G60790.1 GeneID:836200

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						KEGG:ath:AT5G60790 TAIR:At5g60790 eggNOG:COG0488 InParanoid:Q9FJH6 KO:K06185 OMA:YHQHLHE PhylomeDB:Q9FJH6 ProtClustDB:CLSN2686703 ArrayExpress:Q9FJH6 Genevestigator:Q9FJH6 Uniprot:Q9FJH6
Root	Isotig01959	7	32	-2.322	1.06E-05	TAIR|locus:2157022 - symbol:GH9A1 "AT5G49720" species:3702 "Arabidopsis thaliana" [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=ISS] [GO:0009504 "cell plate" evidence=IDA] [GO:0009826 "unidimensional cell growth" evidence=IMP] [GO:0009735 "response to cytokinin stimulus" evidence=IMP] [GO:0048367 "shoot development" evidence=IMP] [GO:0030244 "cellulose biosynthetic process" evidence=IMP;TAS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005769 "early endosome" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] [GO:0042538 "hyperosmotic salinity response" evidence=IMP] [GO:0043622 "cortical microtubule organization" evidence=IMP] [GO:0008810 "cellulase activity" evidence=ISS] InterPro:IPR001701 InterPro:IPR008928 InterPro:IPR012341 InterPro:IPR018221 Pfam:PF00759 PROSITE:PS00592 PROSITE:PS00698 GO:GO:0016021 GO:GO:0005886 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009735 GO:GO:0005794 GO:GO:0030245 GO:GO:0009826 GO:GO:0007047 Gene3D:G3DSA:1.50.10.10 SUPFAM:SSF48208 GO:GO:0048367 GO:GO:0005769 GO:GO:0042538 GO:GO:0043622 UniGene:At.23416 GO:GO:0009504 GO:GO:0030244 GO:GO:0008810 CAZy:GH9 EMBL:AB025613 HSSP:P26221 HOGENOM:HBG746347 ProtClustDB:CLSN2679649 EMBL:U37702 EMBL:AF073875 EMBL:AF074092 EMBL:AF074375 EMBL:AY037218 EMBL:BT002221 EMBL:AY086165 EMBL:AK221941 EMBL:AK222193 IPI:IPI00523242 PIR:S71215 RefSeq:NP_199783.1 UniGene:At.21098 ProteinModelPortal:Q38890 SMR:Q38890 STRING:Q38890 PRIDE:Q38890 EnsemblPlants:AT5G49720.1 GeneID:835035 KEGG:ath:AT5G49720 TAIR:At5g49720 eggNOG:NOG257354 InParanoid:Q38890 OMA:DEFIWGG PhylomeDB:Q38890 Genevestigator:Q38890 GermOnline:AT5G49720 Uniprot:Q38890
Root	Isotig01960	7	31	-2.276	1.84E-05	TAIR|locus:2157022 - symbol:GH9A1 "AT5G49720" species:3702 "Arabidopsis thaliana" [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=ISS] [GO:0009504 "cell plate" evidence=IDA] [GO:0009826 "unidimensional cell growth" evidence=IMP] [GO:0009735 "response to cytokinin stimulus" evidence=IMP] [GO:0048367 "shoot development" evidence=IMP] [GO:0030244 "cellulose biosynthetic process" evidence=IMP;TAS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005769 "early endosome" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] [GO:0042538 "hyperosmotic salinity response" evidence=IMP] [GO:0043622 "cortical microtubule organization" evidence=IMP] [GO:0008810 "cellulase activity" evidence=ISS] InterPro:IPR001701 InterPro:IPR008928 InterPro:IPR012341 InterPro:IPR018221 Pfam:PF00759 PROSITE:PS00592 PROSITE:PS00698 GO:GO:0016021 GO:GO:0005886 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009735 GO:GO:0005794 GO:GO:0030245 GO:GO:0009826 GO:GO:0007047 Gene3D:G3DSA:1.50.10.10 SUPFAM:SSF48208 GO:GO:0048367 GO:GO:0005769 GO:GO:0042538 GO:GO:0043622 UniGene:At.23416 GO:GO:0009504 GO:GO:0030244 GO:GO:0008810 CAZy:GH9 EMBL:AB025613 HSSP:P26221 HOGENOM:HBG746347 ProtClustDB:CLSN2679649 EMBL:U37702 EMBL:AF073875 EMBL:AF074092 EMBL:AF074375 EMBL:AY037218 EMBL:BT002221 EMBL:AY086165 EMBL:AK221941 EMBL:AK222193 IPI:IPI00523242 PIR:S71215 RefSeq:NP_199783.1 UniGene:At.21098 ProteinModelPortal:Q38890 SMR:Q38890 STRING:Q38890 PRIDE:Q38890 EnsemblPlants:AT5G49720.1 GeneID:835035 KEGG:ath:AT5G49720 TAIR:At5g49720 eggNOG:NOG257354 InParanoid:Q38890 OMA:DEFIWGG PhylomeDB:Q38890 Genevestigator:Q38890 GermOnline:AT5G49720 Uniprot:Q38890
Root	Isotig01961	7	31	-2.276	1.84E-05	TAIR|locus:2157022 - symbol:GH9A1 "AT5G49720" species:3702 "Arabidopsis thaliana" [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=ISS] [GO:0009504 "cell plate" evidence=IDA] [GO:0009826 "unidimensional cell growth" evidence=IMP] [GO:0009735 "response to cytokinin stimulus" evidence=IMP] [GO:0048367 "shoot development" evidence=IMP] [GO:0030244 "cellulose biosynthetic process" evidence=IMP;TAS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005769 "early endosome" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] [GO:0042538 "hyperosmotic salinity response" evidence=IMP] [GO:0043622 "cortical microtubule organization" evidence=IMP] [GO:0008810 "cellulase activity" evidence=ISS] InterPro:IPR001701 InterPro:IPR008928 InterPro:IPR012341 InterPro:IPR018221 Pfam:PF00759 PROSITE:PS00592 PROSITE:PS00698 GO:GO:0016021 GO:GO:0005886 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009735 GO:GO:0005794 GO:GO:0030245 GO:GO:0009826 GO:GO:0007047 Gene3D:G3DSA:1.50.10.10 SUPFAM:SSF48208 GO:GO:0048367 GO:GO:0005769 GO:GO:0042538 GO:GO:0043622 UniGene:At.23416 GO:GO:0009504 GO:GO:0030244 GO:GO:0008810 CAZy:GH9 EMBL:AB025613 HSSP:P26221 HOGENOM:HBG746347 ProtClustDB:CLSN2679649 EMBL:U37702 EMBL:AF073875 EMBL:AF074092 EMBL:AF074375 EMBL:AY037218 EMBL:BT002221 EMBL:AY086165

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EMBL:AK221941 EMBL:AK222193 IPI:IPI00523242 PIR:S71215 RefSeq:NP_199783.1 UniGene:At.21098 ProteinModelPortal:Q38890 SMR:Q38890 STRING:Q38890 PRIDE:Q38890 EnsemblPlants:AT5G49720.1 GeneID:835035 KEGG:ath:AT5G49720 TAIR:At5g49720 eggNOG:NOG257354 InParanoid:Q38890 OMA:DEFIWGG PhylomeDB:Q38890 Genevestigator:Q38890 GermOnline:AT5G49720 Uniprot:Q38890
Root	Isotig01962	7	30	-2.229	3.18E-05	TAIR|locus:2157022 - symbol:GH9A1 "AT5G49720" species:3702 "Arabidopsis thaliana" [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=ISS] [GO:0009504 "cell plate" evidence=IDA] [GO:0009826 "unidimensional cell growth" evidence=IMP] [GO:0009735 "response to cytokinin stimulus" evidence=IMP] [GO:0048367 "shoot development" evidence=IMP] [GO:0030244 "cellulose biosynthetic process" evidence=IMP;TAS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005769 "early endosome" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] [GO:0042538 "hyperosmotic salinity response" evidence=IMP] [GO:0043622 "cortical microtubule organization" evidence=IMP] [GO:0008810 "cellulase activity" evidence=ISS] InterPro:IPR001701 InterPro:IPR008928 InterPro:IPR012341 InterPro:IPR018221 Pfam:PF00759 PROSITE:PS00592 PROSITE:PS00698 GO:GO:0016021 GO:GO:0005886 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009735 GO:GO:0005794 GO:GO:0030245 GO:GO:0009826 GO:GO:0007047 Gene3D:G3DSA:1.50.10.10 SUPFAM:SSF48208 GO:GO:0048367 GO:GO:0005769 GO:GO:0042538 GO:GO:0043622 UniGene:At.23416 GO:GO:0009504 GO:GO:0030244 GO:GO:0008810 CAZy:GH9 EMBL:AB025613 HSSP:P26221 HOGENOM:HBG746347 ProtClustDB:CLSN2679649 EMBL:U37702 EMBL:AF073875 EMBL:AF074092 EMBL:AF074375 EMBL:AY037218 EMBL:BT002221 EMBL:AY086165 EMBL:AK221941 EMBL:AK222193 IPI:IPI00523242 PIR:S71215 RefSeq:NP_199783.1 UniGene:At.21098 ProteinModelPortal:Q38890 SMR:Q38890 STRING:Q38890 PRIDE:Q38890 EnsemblPlants:AT5G49720.1 GeneID:835035 KEGG:ath:AT5G49720 TAIR:At5g49720 eggNOG:NOG257354 InParanoid:Q38890 OMA:DEFIWGG PhylomeDB:Q38890 Genevestigator:Q38890 GermOnline:AT5G49720 Uniprot:Q38890
Root	Isotig01964	66	24	1.330	3.85E-05	TAIR|locus:2136849 - symbol:PFK3 "AT4G26270" species:3702 "Arabidopsis thaliana" [GO:0003872 "6-phosphofructokinase activity" evidence=ISS;IDA] [GO:0005945 "6-phosphofructokinase complex" evidence=ISS] [GO:0006096 "glycolysis" evidence=ISS;IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR000023 InterPro:IPR012004 Pfam:PF00365 PIRSF:PIRSF000534 GO:GO:0005524 EMBL:CP002687 GenomeReviews:CT486007_GR EMBL:AL049171 EMBL:AL161564 GO:GO:0006096 HSSP:P00512 eggNOG:COG0205 HOGENOM:HBG316947 KO:K00850 ProtClustDB:PLN02564 GO:GO:0005945 GO:GO:0003872 InterPro:IPR022953 PRINTS:PR00476 SUPFAM:SSF53784 EMBL:AY049245 EMBL:AY090267 IPI:IPI00545493 PIR:T06011 RefSeq:NP_567742.1 UniGene:At.2887 ProteinModelPortal:Q94AA4 SMR:Q94AA4 IntAct:Q94AA4 STRING:Q94AA4 PRIDE:Q94AA4 DNASU:828733 EnsemblPlants:AT4G26270.1 GeneID:828733 KEGG:ath:AT4G26270 TAIR:At4g26270 InParanoid:Q94AA4 OMA:HVEAESI PhylomeDB:Q94AA4 ArrayExpress:Q9STQ7 Genevestigator:Q94AA4 Uniprot:Q94AA4
Root	Isotig01994	25	4	2.515	9.62E-05	TAIR|locus:2028879 - symbol:SRO2 "similar to RCD one 2" species:3702 "Arabidopsis thaliana" [GO:0003950 "NAD+ ADP-ribosyltransferase activity" evidence=IEA] [GO:0008150 "biological_process" evidence=ND] InterPro:IPR012317 PROSITE:PS51059 GO:GO:0007275 EMBL:CP002684 GO:GO:0005634 GO:GO:0006950 EMBL:AC005990 EMBL:AC007945 GO:GO:0003950 InterPro:IPR022003 Pfam:PF12174 EMBL:BT022003 IPI:IPI00547820 PIR:C86369 RefSeq:NP_173769.1 UniGene:At.41541 UniGene:At.49909 ProteinModelPortal:Q9ZUD9 PRIDE:Q9ZUD9 GeneID:838965 KEGG:ath:AT1G23550 TAIR:At1g23550 eggNOG:NOG262161 HOGENOM:HBG320473 InParanoid:Q9ZUD9 OMA:THMNTHI PhylomeDB:Q9ZUD9 ProtClustDB:CLSN2682095 Genevestigator:Q9ZUD9 Uniprot:Q9ZUD9
Root	Isotig01995	22	3	2.745	0.000124336	TAIR|locus:2028879 - symbol:SRO2 "similar to RCD one 2" species:3702 "Arabidopsis thaliana" [GO:0003950 "NAD+ ADP-ribosyltransferase activity" evidence=IEA] [GO:0008150 "biological_process" evidence=ND] InterPro:IPR012317 PROSITE:PS51059 GO:GO:0007275 EMBL:CP002684 GO:GO:0005634 GO:GO:0006950 EMBL:AC005990 EMBL:AC007945 GO:GO:0003950 InterPro:IPR022003 Pfam:PF12174 EMBL:BT022003 IPI:IPI00547820 PIR:C86369 RefSeq:NP_173769.1 UniGene:At.41541 UniGene:At.49909 ProteinModelPortal:Q9ZUD9 PRIDE:Q9ZUD9 GeneID:838965 KEGG:ath:AT1G23550 TAIR:At1g23550 eggNOG:NOG262161 HOGENOM:HBG320473 InParanoid:Q9ZUD9 OMA:THMNTHI PhylomeDB:Q9ZUD9 ProtClustDB:CLSN2682095 Genevestigator:Q9ZUD9 Uniprot:Q9ZUD9
Root	Isotig01996	25	4	2.515	9.62E-05	TAIR|locus:2028879 - symbol:SRO2 "similar to RCD one 2" species:3702 "Arabidopsis thaliana" [GO:0003950 "NAD+ ADP-ribosyltransferase activity" evidence=IEA] [GO:0008150 "biological_process" evidence=ND] InterPro:IPR012317 PROSITE:PS51059 GO:GO:0007275 EMBL:CP002684 GO:GO:0005634 GO:GO:0006950

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EMBL:AC005990 EMBL:AC007945 GO:GO:0003950 InterPro:IPR022003 Pfam:PF12174 EMBL:BT022003 IPI:IPI00547820 PIR:C86369 RefSeq:NP_173769.1 UniGene:At.41541 UniGene:At.49909 ProteinModelPortal:Q9ZUD9 PRIDE:Q9ZUD9 GeneID:838965 KEGG:ath:AT1G23550 TAIR:At1g23550 eggNOG:NOG262161 HOGENOM:HBG320473 InParanoid:Q9ZUD9 OMA:THMNTHI PhylomeDB:Q9ZUD9 ProtClustDB:CLSN2682095 Genevestigator:Q9ZUD9 Uniprot:Q9ZUD9
Root	Isotig01997	22	3	2.745	0.000124336	TAIR|locus:2028879 - symbol:SRO2 "similar to RCD one 2" species:3702 "Arabidopsis thaliana" [GO:0003950 "NAD+ ADP-ribosyltransferase activity" evidence=IEA] [GO:0008150 "biological_process" evidence=ND] InterPro:IPR012317 PROSITE:PS51059 GO:GO:0007275 EMBL:CP002684 GO:GO:0005634 GO:GO:0006950 EMBL:AC005990 EMBL:AC007945 GO:GO:0003950 InterPro:IPR022003 Pfam:PF12174 EMBL:BT022003 IPI:IPI00547820 PIR:C86369 RefSeq:NP_173769.1 UniGene:At.41541 UniGene:At.49909 ProteinModelPortal:Q9ZUD9 PRIDE:Q9ZUD9 GeneID:838965 KEGG:ath:AT1G23550 TAIR:At1g23550 eggNOG:NOG262161 HOGENOM:HBG320473 InParanoid:Q9ZUD9 OMA:THMNTHI PhylomeDB:Q9ZUD9 ProtClustDB:CLSN2682095 Genevestigator:Q9ZUD9 Uniprot:Q9ZUD9
Root	Isotig02003	0	13	-4.829	0.000155955	TAIR|locus:2014912 - symbol:WAK2 "wall-associated kinase 2" species:3702 "Arabidopsis thaliana" [GO:0004672 "protein kinase activity" evidence=IEA] [GO:0004674 "protein serine/threonine kinase activity" evidence=IEA;ISS] [GO:0005509 "calcium ion binding" evidence=IEA] [GO:0005524 "ATP binding" evidence=IEA] [GO:0006468 "protein phosphorylation" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009751 "response to salicylic acid stimulus" evidence=IDA] [GO:0009311 "oligosaccharide metabolic process" evidence=IMP] [GO:0009826 "unidimensional cell growth" evidence=IMP] [GO:0009992 "cellular water homeostasis" evidence=IMP;IDA] InterPro:IPR000719 InterPro:IPR000742 InterPro:IPR001881 InterPro:IPR006210 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR018097 InterPro:IPR025287 Pfam:PF00069 Pfam:PF07645 Pfam:PF13947 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS01187 PROSITE:PS50011 PROSITE:PS50026 SMART:SM00179 SMART:SM00181 InterPro:IPR000152 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005524 GO:GO:0005509 eggNOG:COG0515 SUPFAM:SSF56112 GO:GO:0004674 HOGENOM:HBG755340 GO:GO:0009751 InterPro:IPR013032 PROSITE:PS00022 InterPro:IPR013320 Gene3D:G3DSA:2.60.120.200 GO:GO:0009826 PROSITE:PS01186 GO:GO:0009311 PROSITE:PS00010 GO:GO:0009992 HSSP:P35555 EMBL:AC036104 UniGene:At.23880 ProtClustDB:CLSN2679473 EMBL:AJ012423 EMBL:AF083722 EMBL:AY062531 EMBL:BT010335 IPI:IPI00532952 PIR:T52588 RefSeq:NP_173549.1 UniGene:At.21118 UniGene:At.69963 ProteinModelPortal:Q9LMP1 SMR:Q9LMP1 PRIDE:Q9LMP1 EnsemblPlants:AT1G21270.1 GeneID:838723 KEGG:ath:AT1G21270 GeneFarm:188 TAIR:At1g21270 InParanoid:Q9LMP1 OMA:SCFASAT PhylomeDB:Q9LMP1 Genevestigator:Q9LMP1 GermOnline:AT1G21270 Uniprot:Q9LMP1
Root	Isotig02004	0	21	-5.521	1.09E-06	TAIR|locus:2014952 - symbol:WAK4 "wall associated kinase 4" species:3702 "Arabidopsis thaliana" [GO:0004672 "protein kinase activity" evidence=IEA] [GO:0004674 "protein serine/threonine kinase activity" evidence=IEA;ISS] [GO:0005509 "calcium ion binding" evidence=IEA] [GO:0005524 "ATP binding" evidence=IEA] [GO:0006468 "protein phosphorylation" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009826 "unidimensional cell growth" evidence=IMP] [GO:0048527 "lateral root development" evidence=IMP] InterPro:IPR000719 InterPro:IPR000742 InterPro:IPR001245 InterPro:IPR001881 InterPro:IPR006210 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR018097 InterPro:IPR025287 Pfam:PF07645 Pfam:PF07714 Pfam:PF13947 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS01187 PROSITE:PS50011 PROSITE:PS50026 SMART:SM00179 SMART:SM00181 InterPro:IPR000152 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005524 GO:GO:0005509 eggNOG:COG0515 SUPFAM:SSF56112 GO:GO:0004674 HOGENOM:HBG755340 GO:GO:0048527 PROSITE:PS00022 InterPro:IPR013320 Gene3D:G3DSA:2.60.120.200 GO:GO:0009826 PROSITE:PS01186 PROSITE:PS00010 HSSP:P01130 EMBL:AC036104 ProtClustDB:CLSN2679473 EMBL:AJ009695 IPI:IPI00540619 PIR:D86345 RefSeq:NP_173544.1 UniGene:At.51702 ProteinModelPortal:Q9LMN6 SMR:Q9LMN6 PRIDE:Q9LMN6 EnsemblPlants:AT1G21210.1 GeneID:838716 KEGG:ath:AT1G21210 GeneFarm:177 TAIR:At1g21210 InParanoid:Q9LMN6 OMA:HEANGEC PhylomeDB:Q9LMN6 Genevestigator:Q9LMN6 GermOnline:AT1G21210 Uniprot:Q9LMN6
Root	Isotig02005	1	15	-4.036	9.83E-05	TAIR|locus:2014952 - symbol:WAK4 "wall associated kinase 4" species:3702 "Arabidopsis thaliana" [GO:0004672 "protein kinase activity" evidence=IEA] [GO:0004674 "protein serine/threonine kinase activity" evidence=IEA;ISS] [GO:0005509 "calcium ion binding" evidence=IEA] [GO:0005524 "ATP binding" evidence=IEA] [GO:0006468 "protein phosphorylation" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009826

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						"unidimensional cell growth" evidence=IMP] [GO:0048527 "lateral root development" evidence=IMP] InterPro:IPR000719 InterPro:IPR000742 InterPro:IPR001245 InterPro:IPR001881 InterPro:IPR006210 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR018097 InterPro:IPR025287 Pfam:PF07645 Pfam:PF07714 Pfam:PF13947 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS01187 PROSITE:PS50011 PROSITE:PS50026 SMART:SM00179 SMART:SM00181 InterPro:IPR000152 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005524 GO:GO:0005509 eggNOG:COG0515 SUPFAM:SSF56112 GO:GO:0004674 HOGENOM:HBG755340 GO:GO:0048527 PROSITE:PS00022 InterPro:IPR013320 Gene3D:G3DSA:2.60.120.200 GO:GO:0009826 PROSITE:PS01186 PROSITE:PS00010 HSSP:P01130 EMBL:AC036104 ProtClustDB:CLSN2679473 EMBL:AJ009695 IPI:IPI00540619 PIR:D86345 RefSeq:NP_173544.1 UniGene:At.51702 ProteinModelPortal:Q9LMN6 SMR:Q9LMN6 PRIDE:Q9LMN6 EnsemblPlants:AT1G21210.1 GeneID:838716 KEGG:ath:AT1G21210 GeneFarm:177 TAIR:At1g21210 InParanoid:Q9LMN6 OMA:HEANGEC PhylomeDB:Q9LMN6 Genevestigator:Q9LMN6 GermOnline:AT1G21210 Uniprot:Q9LMN6
Root	Isotig02006	0	11	-4.588	0.000569522	TAIR|locus:2014952 - symbol:WAK4 "wall associated kinase 4" species:3702 "Arabidopsis thaliana" [GO:0004672 "protein kinase activity" evidence=IEA] [GO:0004674 "protein serine/threonine kinase activity" evidence=IEA;ISS] [GO:0005509 "calcium ion binding" evidence=IEA] [GO:0005524 "ATP binding" evidence=IEA] [GO:0006468 "protein phosphorylation" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009826 "unidimensional cell growth" evidence=IMP] [GO:0048527 "lateral root development" evidence=IMP] InterPro:IPR000719 InterPro:IPR000742 InterPro:IPR001245 InterPro:IPR001881 InterPro:IPR006210 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR018097 InterPro:IPR025287 Pfam:PF07645 Pfam:PF07714 Pfam:PF13947 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS01187 PROSITE:PS50011 PROSITE:PS50026 SMART:SM00179 SMART:SM00181 InterPro:IPR000152 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005524 GO:GO:0005509 eggNOG:COG0515 SUPFAM:SSF56112 GO:GO:0004674 HOGENOM:HBG755340 GO:GO:0048527 PROSITE:PS00022 InterPro:IPR013320 Gene3D:G3DSA:2.60.120.200 GO:GO:0009826 PROSITE:PS01186 PROSITE:PS00010 HSSP:P01130 EMBL:AC036104 ProtClustDB:CLSN2679473 EMBL:AJ009695 IPI:IPI00540619 PIR:D86345 RefSeq:NP_173544.1 UniGene:At.51702 ProteinModelPortal:Q9LMN6 SMR:Q9LMN6 PRIDE:Q9LMN6 EnsemblPlants:AT1G21210.1 GeneID:838716 KEGG:ath:AT1G21210 GeneFarm:177 TAIR:At1g21210 InParanoid:Q9LMN6 OMA:HEANGEC PhylomeDB:Q9LMN6 Genevestigator:Q9LMN6 GermOnline:AT1G21210 Uniprot:Q9LMN6
Root	Isotig02007	0	11	-4.588	0.000569522	TAIR|locus:2014952 - symbol:WAK4 "wall associated kinase 4" species:3702 "Arabidopsis thaliana" [GO:0004672 "protein kinase activity" evidence=IEA] [GO:0004674 "protein serine/threonine kinase activity" evidence=IEA;ISS] [GO:0005509 "calcium ion binding" evidence=IEA] [GO:0005524 "ATP binding" evidence=IEA] [GO:0006468 "protein phosphorylation" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009826 "unidimensional cell growth" evidence=IMP] [GO:0048527 "lateral root development" evidence=IMP] InterPro:IPR000719 InterPro:IPR000742 InterPro:IPR001245 InterPro:IPR001881 InterPro:IPR006210 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR018097 InterPro:IPR025287 Pfam:PF07645 Pfam:PF07714 Pfam:PF13947 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS01187 PROSITE:PS50011 PROSITE:PS50026 SMART:SM00179 SMART:SM00181 InterPro:IPR000152 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005524 GO:GO:0005509 eggNOG:COG0515 SUPFAM:SSF56112 GO:GO:0004674 HOGENOM:HBG755340 GO:GO:0048527 PROSITE:PS00022 InterPro:IPR013320 Gene3D:G3DSA:2.60.120.200 GO:GO:0009826 PROSITE:PS01186 PROSITE:PS00010 HSSP:P01130 EMBL:AC036104 ProtClustDB:CLSN2679473 EMBL:AJ009695 IPI:IPI00540619 PIR:D86345 RefSeq:NP_173544.1 UniGene:At.51702 ProteinModelPortal:Q9LMN6 SMR:Q9LMN6 PRIDE:Q9LMN6 EnsemblPlants:AT1G21210.1 GeneID:838716 KEGG:ath:AT1G21210 GeneFarm:177 TAIR:At1g21210 InParanoid:Q9LMN6 OMA:HEANGEC PhylomeDB:Q9LMN6 Genevestigator:Q9LMN6 GermOnline:AT1G21210 Uniprot:Q9LMN6
Root	Isotig02043	8	49	-2.744	2.14E-09	TAIR|locus:2037533 - symbol:AT1G78880 "AT1G78880" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0005886 "plasma membrane" evidence=IDA] EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005886 GO:GO:0006508 EMBL:AC005679 GO:GO:0008233 HOGENOM:HBG318540 ProtClustDB:CLSN2679796 EMBL:AY072176 EMBL:AY096686 EMBL:AY120734 EMBL:BT000364 IPI:IPI00537430 PIR:C96818 RefSeq:NP_178009.1 UniGene:At.21193 PRIDE:Q9ZVA7 EnsemblPlants:AT1G78880.1 GeneID:844225 KEGG:ath:AT1G78880 TAIR:At1g78880 eggNOG:NOG292696 InParanoid:Q9ZVA7 OMA:WNISCER PhylomeDB:Q9ZVA7 ArrayExpress:Q9ZVA7 Genevestigator:Q9ZVA7 Uniprot:Q9ZVA7

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig02045	6	46	-3.068	8.71E-10	No hit
Root	Isotig02078	19	0	5.119	1.05E-05	TAIR|locus:2088404 - symbol:AT3G26840 "AT3G26840" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=ISS] [GO:0008152 "metabolic process" evidence=IEA] [GO:0016746 "transferase activity, transferring acyl groups" evidence=IEA] [GO:0016747 "transferase activity, transferring acyl groups other than amino-acyl groups" evidence=IEA] [GO:0010287 "plastoglobule" evidence=IDA] InterPro:IPR002123 InterPro:IPR007130 Pfam:PF03982 SMART:SM00563 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0016747 EMBL:AB016889 GO:GO:0010287 eggNOG:COG0204 HOGENOM:HBG562431 EMBL:AY056370 EMBL:AF360145 IPI:IPI00541496 RefSeq:NP_566801.1 UniGene:At.6034 UniGene:At.66477 ProteinModelPortal:Q9LW26 SMR:Q9LW26 PRIDE:Q9LW26 EnsemblPlants:AT3G26840.1 GeneID:822299 KEGG:ath:AT3G26840 TAIR:At3g26840 InParanoid:Q9LW26 OMA:DDICEIV PhylomeDB:Q9LW26 ProtClustDB:CLSN2684876 ArrayExpress:Q9LW26 Genevestigator:Q9LW26 Uniprot:Q9LW26
Root	Isotig02079	19	0	5.119	1.05E-05	TAIR|locus:2088404 - symbol:AT3G26840 "AT3G26840" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=ISS] [GO:0008152 "metabolic process" evidence=IEA] [GO:0016746 "transferase activity, transferring acyl groups" evidence=IEA] [GO:0016747 "transferase activity, transferring acyl groups other than amino-acyl groups" evidence=IEA] [GO:0010287 "plastoglobule" evidence=IDA] InterPro:IPR002123 InterPro:IPR007130 Pfam:PF03982 SMART:SM00563 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0016747 EMBL:AB016889 GO:GO:0010287 eggNOG:COG0204 HOGENOM:HBG562431 EMBL:AY056370 EMBL:AF360145 IPI:IPI00541496 RefSeq:NP_566801.1 UniGene:At.6034 UniGene:At.66477 ProteinModelPortal:Q9LW26 SMR:Q9LW26 PRIDE:Q9LW26 EnsemblPlants:AT3G26840.1 GeneID:822299 KEGG:ath:AT3G26840 TAIR:At3g26840 InParanoid:Q9LW26 OMA:DDICEIV PhylomeDB:Q9LW26 ProtClustDB:CLSN2684876 ArrayExpress:Q9LW26 Genevestigator:Q9LW26 Uniprot:Q9LW26
Root	Isotig02082	23	60	-1.512	6.18E-06	TAIR|locus:2102926 - symbol:AT3G30390 "AT3G30390" species:3702 "Arabidopsis thaliana" [GO:0006865 "amino acid transport" evidence=ISS] [GO:0015171 "amino acid transmembrane transporter activity" evidence=ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0005773 "vacuole" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] GO:GO:0016021 GO:GO:0005774 EMBL:CP002686 InterPro:IPR013057 Pfam:PF01490 HOGENOM:HBG601878 EMBL:AY052201 EMBL:AF428287 EMBL:AP001314 IPI:IPI00520585 RefSeq:NP_001030795.1 RefSeq:NP_566854.1 UniGene:At.21575 ProteinModelPortal:Q9LI61 STRING:Q9LI61 PRIDE:Q9LI61 EnsemblPlants:AT3G30390.1 EnsemblPlants:AT3G30390.2 GeneID:822740 KEGG:ath:AT3G30390 TAIR:At3g30390 InParanoid:Q9LI61 OMA:AFICHYN PhylomeDB:Q9LI61 ProtClustDB:CLSN2687270 Genevestigator:Q9LI61 Uniprot:Q9LI61
Root	Isotig02083	23	59	-1.488	9.46E-06	TAIR|locus:2102926 - symbol:AT3G30390 "AT3G30390" species:3702 "Arabidopsis thaliana" [GO:0006865 "amino acid transport" evidence=ISS] [GO:0015171 "amino acid transmembrane transporter activity" evidence=ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0005773 "vacuole" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] GO:GO:0016021 GO:GO:0005774 EMBL:CP002686 InterPro:IPR013057 Pfam:PF01490 HOGENOM:HBG601878 EMBL:AY052201 EMBL:AF428287 EMBL:AP001314 IPI:IPI00520585 RefSeq:NP_001030795.1 RefSeq:NP_566854.1 UniGene:At.21575 ProteinModelPortal:Q9LI61 STRING:Q9LI61 PRIDE:Q9LI61 EnsemblPlants:AT3G30390.1 EnsemblPlants:AT3G30390.2 GeneID:822740 KEGG:ath:AT3G30390 TAIR:At3g30390 InParanoid:Q9LI61 OMA:AFICHYN PhylomeDB:Q9LI61 ProtClustDB:CLSN2687270 Genevestigator:Q9LI61 Uniprot:Q9LI61
Root	Isotig02094	4	29	-2.987	1.53E-06	TAIR|locus:2198928 - symbol:NHO1 "AT1G80460" species:3702 "Arabidopsis thaliana" [GO:0005975 "carbohydrate metabolic process" evidence=ISS] [GO:0019200 "carbohydrate kinase activity" evidence=ISS] [GO:0004370 "glycerol kinase activity" evidence=ISS;IDA] [GO:0009617 "response to bacterium" evidence=IEP] [GO:0019563 "glycerol catabolic process" evidence=IMP] [GO:0002237 "response to molecule of bacterial origin" evidence=IEP] [GO:0010188 "response to microbial phytotoxin" evidence=IEP] [GO:0080167 "response to karrikin" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR000577 InterPro:IPR005999 InterPro:IPR018483 InterPro:IPR018484 InterPro:IPR018485 Pfam:PF00370 Pfam:PF02782 PROSITE:PS00933 EMBL:CP002684 GO:GO:0005829 GO:GO:0080167 GO:GO:0002237 PANTHER:PTHR10196 EMBL:AC018849 GO:GO:0010188 GO:GO:0019563 GO:GO:0006072 KO:K00864 GO:GO:0004370 PANTHER:PTHR10196:SF9 TIGRFAMs:TIGR01311 HSSP:P08859 OMA:DSGVRLE EMBL:AY234854 EMBL:AK316784 IPI:IPI00529626 PIR:D96836 RefSeq:NP_178161.1 UniGene:At.24313 UniGene:At.67688 ProteinModelPortal:Q9M8L4 SMR:Q9M8L4 STRING:Q9M8L4 PRIDE:Q9M8L4 EnsemblPlants:AT1G80460.1 GeneID:844385

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						KEGG:ath:AT1G80460 TAIR:At1g80460 InParanoid:Q9M8L4 PhylomeDB:Q9M8L4 ProtClustDB:PLN02295 Genevestigator:Q9M8L4 Uniprot:Q9M8L4
Root	Isotig02095	4	25	-2.773	1.71E-05	TAIR|locus:2198928 - symbol:NHO1 "AT1G80460" species:3702 "Arabidopsis thaliana" [GO:0005975 "carbohydrate metabolic process" evidence=ISS] [GO:0019200 "carbohydrate kinase activity" evidence=ISS] [GO:0004370 "glycerol kinase activity" evidence=ISS;IDA] [GO:0009617 "response to bacterium" evidence=IEP] [GO:0019563 "glycerol catabolic process" evidence=IMP] [GO:0002237 "response to molecule of bacterial origin" evidence=IEP] [GO:0010188 "response to microbial phytotoxin" evidence=IEP] [GO:0080167 "response to karrikin" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR000577 InterPro:IPR005999 InterPro:IPR018483 InterPro:IPR018484 InterPro:IPR018485 Pfam:PF00370 Pfam:PF02782 PROSITE:PS00933 EMBL:CP002684 GO:GO:0005829 GO:GO:0080167 GO:GO:0002237 PANTHER:PTHR10196 EMBL:AC018849 GO:GO:0010188 GO:GO:0019563 GO:GO:0006072 KO:K00864 GO:GO:0004370 PANTHER:PTHR10196:SF9 TIGRFAMs:TIGR01311 HSSP:P08859 OMA:DSGVRLE EMBL:AY234854 EMBL:AK316784 IPI:IPI00529626 PIR:D96836 RefSeq:NP_178161.1 UniGene:At.24313 UniGene:At.67688 ProteinModelPortal:Q9M8L4 SMR:Q9M8L4 STRING:Q9M8L4 PRIDE:Q9M8L4 EnsemblPlants:AT1G80460.1 GeneID:844385 KEGG:ath:AT1G80460 TAIR:At1g80460 InParanoid:Q9M8L4 PhylomeDB:Q9M8L4 ProtClustDB:PLN02295 Genevestigator:Q9M8L4 Uniprot:Q9M8L4
Root	Isotig02096	3	28	-3.351	6.51E-07	TAIR|locus:2198928 - symbol:NHO1 "AT1G80460" species:3702 "Arabidopsis thaliana" [GO:0005975 "carbohydrate metabolic process" evidence=ISS] [GO:0019200 "carbohydrate kinase activity" evidence=ISS] [GO:0004370 "glycerol kinase activity" evidence=ISS;IDA] [GO:0009617 "response to bacterium" evidence=IEP] [GO:0019563 "glycerol catabolic process" evidence=IMP] [GO:0002237 "response to molecule of bacterial origin" evidence=IEP] [GO:0010188 "response to microbial phytotoxin" evidence=IEP] [GO:0080167 "response to karrikin" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR000577 InterPro:IPR005999 InterPro:IPR018483 InterPro:IPR018484 InterPro:IPR018485 Pfam:PF00370 Pfam:PF02782 PROSITE:PS00933 EMBL:CP002684 GO:GO:0005829 GO:GO:0080167 GO:GO:0002237 PANTHER:PTHR10196 EMBL:AC018849 GO:GO:0010188 GO:GO:0019563 GO:GO:0006072 KO:K00864 GO:GO:0004370 PANTHER:PTHR10196:SF9 TIGRFAMs:TIGR01311 HSSP:P08859 OMA:DSGVRLE EMBL:AY234854 EMBL:AK316784 IPI:IPI00529626 PIR:D96836 RefSeq:NP_178161.1 UniGene:At.24313 UniGene:At.67688 ProteinModelPortal:Q9M8L4 SMR:Q9M8L4 STRING:Q9M8L4 PRIDE:Q9M8L4 EnsemblPlants:AT1G80460.1 GeneID:844385 KEGG:ath:AT1G80460 TAIR:At1g80460 InParanoid:Q9M8L4 PhylomeDB:Q9M8L4 ProtClustDB:PLN02295 Genevestigator:Q9M8L4 Uniprot:Q9M8L4
Root	Isotig02097	3	22	-3.003	2.69E-05	TAIR|locus:2198928 - symbol:NHO1 "AT1G80460" species:3702 "Arabidopsis thaliana" [GO:0005975 "carbohydrate metabolic process" evidence=ISS] [GO:0019200 "carbohydrate kinase activity" evidence=ISS] [GO:0004370 "glycerol kinase activity" evidence=ISS;IDA] [GO:0009617 "response to bacterium" evidence=IEP] [GO:0019563 "glycerol catabolic process" evidence=IMP] [GO:0002237 "response to molecule of bacterial origin" evidence=IEP] [GO:0010188 "response to microbial phytotoxin" evidence=IEP] [GO:0080167 "response to karrikin" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR000577 InterPro:IPR005999 InterPro:IPR018483 InterPro:IPR018484 InterPro:IPR018485 Pfam:PF00370 Pfam:PF02782 PROSITE:PS00933 EMBL:CP002684 GO:GO:0005829 GO:GO:0080167 GO:GO:0002237 PANTHER:PTHR10196 EMBL:AC018849 GO:GO:0010188 GO:GO:0019563 GO:GO:0006072 KO:K00864 GO:GO:0004370 PANTHER:PTHR10196:SF9 TIGRFAMs:TIGR01311 HSSP:P08859 OMA:DSGVRLE EMBL:AY234854 EMBL:AK316784 IPI:IPI00529626 PIR:D96836 RefSeq:NP_178161.1 UniGene:At.24313 UniGene:At.67688 ProteinModelPortal:Q9M8L4 SMR:Q9M8L4 STRING:Q9M8L4 PRIDE:Q9M8L4 EnsemblPlants:AT1G80460.1 GeneID:844385 KEGG:ath:AT1G80460 TAIR:At1g80460 InParanoid:Q9M8L4 PhylomeDB:Q9M8L4 ProtClustDB:PLN02295 Genevestigator:Q9M8L4 Uniprot:Q9M8L4
Root	Isotig02102	1	17	-4.216	2.69E-05	TAIR|locus:2077572 - symbol:RPM1 "AT3G07040" species:3702 "Arabidopsis thaliana" [GO:0006952 "defense response" evidence=ISS;TAS] [GO:0005515 "protein binding" evidence=IPI] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0000166 "nucleotide binding" evidence=ISS] [GO:0009626 "plant-type hypersensitive response" evidence=IDA] Pfam:PF00560 InterPro:IPR001611 InterPro:IPR000767 InterPro:IPR002182 Pfam:PF00931 PRINTS:PR00364 GO:GO:0005886 GO:GO:0005524 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005515 eggNOG:COG4886 GO:GO:0012505 GO:GO:0043531 GO:GO:0009626 EMBL:AC016827 HOGENOM:HBG749068 EMBL:X87851 IPI:IPI00526839 PIR:A57072 RefSeq:NP_187360.1 UniGene:At.40415 ProteinModelPortal:Q39214 SMR:Q39214 STRING:Q39214 PRIDE:Q39214 EnsemblPlants:AT3G07040.1

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GeneID:819889 KEGG:ath:AT3G07040 TAIR:At3g07040 InParanoid:Q39214 KO:K13457 OMA:WREISIA PhylomeDB:Q39214 ProtClustDB:CLSN2915520 ArrayExpress:Q39214 Genevestigator:Q39214 Uniprot:Q39214
Root	Isotig02103	0	17	-5.216	1.26E-05	TAIR|locus:2077572 - symbol:RPM1 "AT3G07040" species:3702 "Arabidopsis thaliana" [GO:0006952 "defense response" evidence=ISS;TAS] [GO:0005515 "protein binding" evidence=IPI] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0000166 "nucleotide binding" evidence=ISS] [GO:0009626 "plant-type hypersensitive response" evidence=IDA] Pfam:PF00560 InterPro:IPR001611 InterPro:IPR000767 InterPro:IPR002182 Pfam:PF00931 PRINTS:PR00364 GO:GO:0005886 GO:GO:0005524 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005515 eggNOG:COG4886 GO:GO:0012505 GO:GO:0043531 GO:GO:0009626 EMBL:AC016827 HOGENOM:HBG749068 EMBL:X87851 IPI:IPI00526839 PIR:A57072 RefSeq:NP_187360.1 UniGene:At.40415 ProteinModelPortal:Q39214 SMR:Q39214 STRING:Q39214 PRIDE:Q39214 EnsemblPlants:AT3G07040.1 GeneID:819889 KEGG:ath:AT3G07040 TAIR:At3g07040 InParanoid:Q39214 KO:K13457 OMA:WREISIA PhylomeDB:Q39214 ProtClustDB:CLSN2915520 ArrayExpress:Q39214 Genevestigator:Q39214 Uniprot:Q39214
Root	Isotig02145	47	0	6.426	3.99E-12	TAIR|locus:2201041 - symbol:AT1G05510 "AT1G05510" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009737 EMBL:AC005106 UniGene:At.20860 InterPro:IPR010686 Pfam:PF06884 eggNOG:NOG05920 HOGENOM:HBG473015 ProtClustDB:CLSN2682017 EMBL:AY070405 EMBL:AY096580 EMBL:AK226452 IPI:IPI00527396 RefSeq:NP_172042.1 UniGene:At.28368 IntAct:Q9ZVY7 PRIDE:Q9ZVY7 ProMEX:Q9ZVY7 DNASU:837053 EnsemblPlants:AT1G05510.1 GeneID:837053 KEGG:ath:AT1G05510 TAIR:At1g05510 InParanoid:Q9ZVY7 OMA:CGHINED PhylomeDB:Q9ZVY7 ArrayExpress:Q9ZVY7 Genevestigator:Q9ZVY7 Uniprot:Q9ZVY7
Root	Isotig02146	47	0	6.426	3.99E-12	TAIR|locus:2201041 - symbol:AT1G05510 "AT1G05510" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009737 EMBL:AC005106 UniGene:At.20860 InterPro:IPR010686 Pfam:PF06884 eggNOG:NOG05920 HOGENOM:HBG473015 ProtClustDB:CLSN2682017 EMBL:AY070405 EMBL:AY096580 EMBL:AK226452 IPI:IPI00527396 RefSeq:NP_172042.1 UniGene:At.28368 IntAct:Q9ZVY7 PRIDE:Q9ZVY7 ProMEX:Q9ZVY7 DNASU:837053 EnsemblPlants:AT1G05510.1 GeneID:837053 KEGG:ath:AT1G05510 TAIR:At1g05510 InParanoid:Q9ZVY7 OMA:CGHINED PhylomeDB:Q9ZVY7 ArrayExpress:Q9ZVY7 Genevestigator:Q9ZVY7 Uniprot:Q9ZVY7
Root	Isotig02147	47	0	6.426	3.99E-12	TAIR|locus:2201041 - symbol:AT1G05510 "AT1G05510" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009737 EMBL:AC005106 UniGene:At.20860 InterPro:IPR010686 Pfam:PF06884 eggNOG:NOG05920 HOGENOM:HBG473015 ProtClustDB:CLSN2682017 EMBL:AY070405 EMBL:AY096580 EMBL:AK226452 IPI:IPI00527396 RefSeq:NP_172042.1 UniGene:At.28368 IntAct:Q9ZVY7 PRIDE:Q9ZVY7 ProMEX:Q9ZVY7 DNASU:837053 EnsemblPlants:AT1G05510.1 GeneID:837053 KEGG:ath:AT1G05510 TAIR:At1g05510 InParanoid:Q9ZVY7 OMA:CGHINED PhylomeDB:Q9ZVY7 ArrayExpress:Q9ZVY7 Genevestigator:Q9ZVY7 Uniprot:Q9ZVY7
Root	Isotig02148	47	0	6.426	3.99E-12	TAIR|locus:2201041 - symbol:AT1G05510 "AT1G05510" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009737 EMBL:AC005106 UniGene:At.20860 InterPro:IPR010686 Pfam:PF06884 eggNOG:NOG05920 HOGENOM:HBG473015 ProtClustDB:CLSN2682017 EMBL:AY070405 EMBL:AY096580 EMBL:AK226452 IPI:IPI00527396 RefSeq:NP_172042.1 UniGene:At.28368 IntAct:Q9ZVY7 PRIDE:Q9ZVY7 ProMEX:Q9ZVY7 DNASU:837053 EnsemblPlants:AT1G05510.1 GeneID:837053 KEGG:ath:AT1G05510 TAIR:At1g05510 InParanoid:Q9ZVY7 OMA:CGHINED PhylomeDB:Q9ZVY7 ArrayExpress:Q9ZVY7 Genevestigator:Q9ZVY7 Uniprot:Q9ZVY7
Root	Isotig02149	47	0	6.426	3.99E-12	TAIR|locus:2201041 - symbol:AT1G05510 "AT1G05510" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009737 EMBL:AC005106 UniGene:At.20860 InterPro:IPR010686 Pfam:PF06884 eggNOG:NOG05920

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						HOGENOM:HBG473015 ProtClustDB:CLSN2682017 EMBL:AY070405 EMBL:AY096580 EMBL:AK226452 IPI:IPI00527396 RefSeq:NP_172042.1 UniGene:At.28368 IntAct:Q9ZVY7 PRIDE:Q9ZVY7 ProMEX:Q9ZVY7 DNASU:837053 EnsemblPlants:AT1G05510.1 GeneID:837053 KEGG:ath:AT1G05510 TAIR:At1g05510 InParanoid:Q9ZVY7 OMA:CGHINED PhylomeDB:Q9ZVY7 ArrayExpress:Q9ZVY7 Genevestigator:Q9ZVY7 Uniprot:Q9ZVY7
Root	Isotig02150	47	0	6.426	3.99E-12	TAIR|locus:2201041 - symbol:AT1G05510 "AT1G05510" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009737 EMBL:AC005106 UniGene:At.20860 InterPro:IPR010686 Pfam:PF06884 eggNOG:NOG05920 HOGENOM:HBG473015 ProtClustDB:CLSN2682017 EMBL:AY070405 EMBL:AY096580 EMBL:AK226452 IPI:IPI00527396 RefSeq:NP_172042.1 UniGene:At.28368 IntAct:Q9ZVY7 PRIDE:Q9ZVY7 ProMEX:Q9ZVY7 DNASU:837053 EnsemblPlants:AT1G05510.1 GeneID:837053 KEGG:ath:AT1G05510 TAIR:At1g05510 InParanoid:Q9ZVY7 OMA:CGHINED PhylomeDB:Q9ZVY7 ArrayExpress:Q9ZVY7 Genevestigator:Q9ZVY7 Uniprot:Q9ZVY7
Root	Isotig02151	47	0	6.426	3.99E-12	TAIR|locus:2201041 - symbol:AT1G05510 "AT1G05510" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009737 EMBL:AC005106 UniGene:At.20860 InterPro:IPR010686 Pfam:PF06884 eggNOG:NOG05920 HOGENOM:HBG473015 ProtClustDB:CLSN2682017 EMBL:AY070405 EMBL:AY096580 EMBL:AK226452 IPI:IPI00527396 RefSeq:NP_172042.1 UniGene:At.28368 IntAct:Q9ZVY7 PRIDE:Q9ZVY7 ProMEX:Q9ZVY7 DNASU:837053 EnsemblPlants:AT1G05510.1 GeneID:837053 KEGG:ath:AT1G05510 TAIR:At1g05510 InParanoid:Q9ZVY7 OMA:CGHINED PhylomeDB:Q9ZVY7 ArrayExpress:Q9ZVY7 Genevestigator:Q9ZVY7 Uniprot:Q9ZVY7
Root	Isotig02152	47	0	6.426	3.99E-12	TAIR|locus:2201041 - symbol:AT1G05510 "AT1G05510" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009737 EMBL:AC005106 UniGene:At.20860 InterPro:IPR010686 Pfam:PF06884 eggNOG:NOG05920 HOGENOM:HBG473015 ProtClustDB:CLSN2682017 EMBL:AY070405 EMBL:AY096580 EMBL:AK226452 IPI:IPI00527396 RefSeq:NP_172042.1 UniGene:At.28368 IntAct:Q9ZVY7 PRIDE:Q9ZVY7 ProMEX:Q9ZVY7 DNASU:837053 EnsemblPlants:AT1G05510.1 GeneID:837053 KEGG:ath:AT1G05510 TAIR:At1g05510 InParanoid:Q9ZVY7 OMA:CGHINED PhylomeDB:Q9ZVY7 ArrayExpress:Q9ZVY7 Genevestigator:Q9ZVY7 Uniprot:Q9ZVY7
Root	Isotig02153	37	104	-1.620	3.92E-10	TAIR|locus:2009600 - symbol:PPC1 "AT1G53310" species:3702 "Arabidopsis thaliana" [GO:0006099 "tricarboxylic acid cycle" evidence=ISS] [GO:0008964 "phosphoenolpyruvate carboxylase activity" evidence=ISS] [GO:0005829 "cytosol" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0016036 "cellular response to phosphate starvation" evidence=IDA] [GO:0051262 "protein tetramerization" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] InterPro:IPR015813 InterPro:IPR018129 InterPro:IPR021135 InterPro:IPR022805 Pfam:PF00311 PRINTS:PR00150 PROSITE:PS00393 PROSITE:PS00781 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0048046 GO:GO:0005515 GO:GO:0051262 EMBL:AC008007 GO:GO:0006099 SUPFAM:SSF51621 GO:GO:0016036 GO:GO:0015979 EMBL:AJ532901 EMBL:AY057507 EMBL:BT000647 IPI:IPI00541694 PIR:D96573 RefSeq:NP_001031178.1 RefSeq:NP_001031179.1 RefSeq:NP_175738.1 UniGene:At.23221 ProteinModelPortal:Q9MAH0 SMR:Q9MAH0 IntAct:Q9MAH0 STRING:Q9MAH0 PRIDE:Q9MAH0 ProMEX:Q9MAH0 EnsemblPlants:AT1G53310.1 EnsemblPlants:AT1G53310.2 EnsemblPlants:AT1G53310.3 GeneID:841765 KEGG:ath:AT1G53310 GeneFarm:5060 TAIR:At1g53310 eggNOG:COG2352 HOGENOM:HBG351035 InParanoid:Q9MAH0 KO:K01595 OMA:HISKEIA PhylomeDB:Q9MAH0 ProtClustDB:CLSN2679806 BRENDA:4.1.1.31 ArrayExpress:Q9MAH0 Genevestigator:Q9MAH0 GermOnline:AT1G53310 GO:GO:0008964 GO:GO:0015977 Uniprot:Q9MAH0
Root	Isotig02154	34	102	-1.714	1.12E-10	TAIR|locus:2009600 - symbol:PPC1 "AT1G53310" species:3702 "Arabidopsis thaliana" [GO:0006099 "tricarboxylic acid cycle" evidence=ISS] [GO:0008964 "phosphoenolpyruvate carboxylase activity" evidence=ISS] [GO:0005829 "cytosol" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0016036 "cellular response to phosphate starvation" evidence=IDA] [GO:0051262 "protein tetramerization" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] InterPro:IPR015813 InterPro:IPR018129 InterPro:IPR021135 InterPro:IPR022805 Pfam:PF00311

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						PRINTS:PR00150 PROSITE:PS00393 PROSITE:PS00781 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0048046 GO:GO:0005515 GO:GO:0051262 EMBL:AC008007 GO:GO:0006099 SUPFAM:SSF51621 GO:GO:0016036 GO:GO:0015979 EMBL:AJ532901 EMBL:AY057507 EMBL:BT000647 IPI:IPI00541694 PIR:D96573 RefSeq:NP_001031178.1 RefSeq:NP_001031179.1 RefSeq:NP_175738.1 UniGene:At.23221 ProteinModelPortal:Q9MAH0 SMR:Q9MAH0 IntAct:Q9MAH0 STRING:Q9MAH0 PRIDE:Q9MAH0 ProMEX:Q9MAH0 EnsemblPlants:AT1G53310.1 EnsemblPlants:AT1G53310.2 EnsemblPlants:AT1G53310.3 GeneID:841765 KEGG:ath:AT1G53310 GeneFarm:5060 TAIR:At1g53310 eggNOG:COG2352 HOGENOM:HBG351035 InParanoid:Q9MAH0 KO:K01595 OMA:HISKEIA PhylomeDB:Q9MAH0 ProtClustDB:CLSN2679806 BRENDA:4.1.1.31 ArrayExpress:Q9MAH0 Genevestigator:Q9MAH0 GermOnline:AT1G53310 GO:GO:0008964 GO:GO:0015977 Uniprot:Q9MAH0
Root	Isotig02155	34	102	-1.714	1.12E-10	TAIR|locus:2009600 - symbol:PPC1 "AT1G53310" species:3702 "Arabidopsis thaliana" [GO:0006099 "tricarboxylic acid cycle" evidence=ISS] [GO:0008964 "phosphoenolpyruvate carboxylase activity" evidence=ISS] [GO:0005829 "cytosol" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0016036 "cellular response to phosphate starvation" evidence=IDA] [GO:0051262 "protein tetramerization" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] InterPro:IPR015813 InterPro:IPR018129 InterPro:IPR021135 InterPro:IPR022805 Pfam:PF00311 PRINTS:PR00150 PROSITE:PS00393 PROSITE:PS00781 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0048046 GO:GO:0005515 GO:GO:0051262 EMBL:AC008007 GO:GO:0006099 SUPFAM:SSF51621 GO:GO:0016036 GO:GO:0015979 EMBL:AJ532901 EMBL:AY057507 EMBL:BT000647 IPI:IPI00541694 PIR:D96573 RefSeq:NP_001031178.1 RefSeq:NP_001031179.1 RefSeq:NP_175738.1 UniGene:At.23221 ProteinModelPortal:Q9MAH0 SMR:Q9MAH0 IntAct:Q9MAH0 STRING:Q9MAH0 PRIDE:Q9MAH0 ProMEX:Q9MAH0 EnsemblPlants:AT1G53310.1 EnsemblPlants:AT1G53310.2 EnsemblPlants:AT1G53310.3 GeneID:841765 KEGG:ath:AT1G53310 GeneFarm:5060 TAIR:At1g53310 eggNOG:COG2352 HOGENOM:HBG351035 InParanoid:Q9MAH0 KO:K01595 OMA:HISKEIA PhylomeDB:Q9MAH0 ProtClustDB:CLSN2679806 BRENDA:4.1.1.31 ArrayExpress:Q9MAH0 Genevestigator:Q9MAH0 GermOnline:AT1G53310 GO:GO:0008964 GO:GO:0015977 Uniprot:Q9MAH0
Root	Isotig02156	37	103	-1.606	6.08E-10	TAIR|locus:2009600 - symbol:PPC1 "AT1G53310" species:3702 "Arabidopsis thaliana" [GO:0006099 "tricarboxylic acid cycle" evidence=ISS] [GO:0008964 "phosphoenolpyruvate carboxylase activity" evidence=ISS] [GO:0005829 "cytosol" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0016036 "cellular response to phosphate starvation" evidence=IDA] [GO:0051262 "protein tetramerization" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] InterPro:IPR015813 InterPro:IPR018129 InterPro:IPR021135 InterPro:IPR022805 Pfam:PF00311 PRINTS:PR00150 PROSITE:PS00393 PROSITE:PS00781 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0048046 GO:GO:0005515 GO:GO:0051262 EMBL:AC008007 GO:GO:0006099 SUPFAM:SSF51621 GO:GO:0016036 GO:GO:0015979 EMBL:AJ532901 EMBL:AY057507 EMBL:BT000647 IPI:IPI00541694 PIR:D96573 RefSeq:NP_001031178.1 RefSeq:NP_001031179.1 RefSeq:NP_175738.1 UniGene:At.23221 ProteinModelPortal:Q9MAH0 SMR:Q9MAH0 IntAct:Q9MAH0 STRING:Q9MAH0 PRIDE:Q9MAH0 ProMEX:Q9MAH0 EnsemblPlants:AT1G53310.1 EnsemblPlants:AT1G53310.2 EnsemblPlants:AT1G53310.3 GeneID:841765 KEGG:ath:AT1G53310 GeneFarm:5060 TAIR:At1g53310 eggNOG:COG2352 HOGENOM:HBG351035 InParanoid:Q9MAH0 KO:K01595 OMA:HISKEIA PhylomeDB:Q9MAH0 ProtClustDB:CLSN2679806 BRENDA:4.1.1.31 ArrayExpress:Q9MAH0 Genevestigator:Q9MAH0 GermOnline:AT1G53310 GO:GO:0008964 GO:GO:0015977 Uniprot:Q9MAH0
Root	Isotig02157	34	101	-1.700	1.76E-10	TAIR|locus:2009600 - symbol:PPC1 "AT1G53310" species:3702 "Arabidopsis thaliana" [GO:0006099 "tricarboxylic acid cycle" evidence=ISS] [GO:0008964 "phosphoenolpyruvate carboxylase activity" evidence=ISS] [GO:0005829 "cytosol" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0016036 "cellular response to phosphate starvation" evidence=IDA] [GO:0051262 "protein tetramerization" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] InterPro:IPR015813 InterPro:IPR018129 InterPro:IPR021135 InterPro:IPR022805 Pfam:PF00311 PRINTS:PR00150 PROSITE:PS00393 PROSITE:PS00781 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0048046 GO:GO:0005515 GO:GO:0051262 EMBL:AC008007 GO:GO:0006099 SUPFAM:SSF51621 GO:GO:0016036 GO:GO:0015979 EMBL:AJ532901 EMBL:AY057507 EMBL:BT000647 IPI:IPI00541694 PIR:D96573 RefSeq:NP_001031178.1 RefSeq:NP_001031179.1 RefSeq:NP_175738.1 UniGene:At.23221 ProteinModelPortal:Q9MAH0 SMR:Q9MAH0 IntAct:Q9MAH0 STRING:Q9MAH0 PRIDE:Q9MAH0 ProMEX:Q9MAH0 EnsemblPlants:AT1G53310.1 EnsemblPlants:AT1G53310.2 EnsemblPlants:AT1G53310.3 GeneID:841765 KEGG:ath:AT1G53310 GeneFarm:5060 TAIR:At1g53310

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						eggNOG:COG2352 HOGENOM:HBG351035 InParanoid:Q9MAH0 KO:K01595 OMA:HISKEIA PhylomeDB:Q9MAH0 ProtClustDB:CLSN2679806 BRENDA:4.1.1.31 ArrayExpress:Q9MAH0 Genevestigator:Q9MAH0 GermOnline:AT1G53310 GO:GO:0008964 GO:GO:0015977 Uniprot:Q9MAH0
Root	Isotig02158	34	101	-1.700	1.76E-10	TAIR|locus:2009600 - symbol:PPC1 "AT1G53310" species:3702 "Arabidopsis thaliana" [GO:0006099 "tricarboxylic acid cycle" evidence=ISS] [GO:0008964 "phosphoenolpyruvate carboxylase activity" evidence=ISS] [GO:0005829 "cytosol" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0016036 "cellular response to phosphate starvation" evidence=IDA] [GO:0051262 "protein tetramerization" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] InterPro:IPR015813 InterPro:IPR018129 InterPro:IPR021135 InterPro:IPR022805 Pfam:PF00311 PRINTS:PR00150 PROSITE:PS00393 PROSITE:PS00781 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0048046 GO:GO:0005515 GO:GO:0051262 EMBL:AC008007 GO:GO:0006099 SUPFAM:SSF51621 GO:GO:0016036 GO:GO:0015979 EMBL:AJ532901 EMBL:AY057507 EMBL:BT000647 IPI:IPI00541694 PIR:D96573 RefSeq:NP_001031178.1 RefSeq:NP_001031179.1 RefSeq:NP_175738.1 UniGene:At.23221 ProteinModelPortal:Q9MAH0 SMR:Q9MAH0 IntAct:Q9MAH0 STRING:Q9MAH0 PRIDE:Q9MAH0 ProMEX:Q9MAH0 EnsemblPlants:AT1G53310.1 EnsemblPlants:AT1G53310.2 EnsemblPlants:AT1G53310.3 GeneID:841765 KEGG:ath:AT1G53310 GeneFarm:5060 TAIR:At1g53310 eggNOG:COG2352 HOGENOM:HBG351035 InParanoid:Q9MAH0 KO:K01595 OMA:HISKEIA PhylomeDB:Q9MAH0 ProtClustDB:CLSN2679806 BRENDA:4.1.1.31 ArrayExpress:Q9MAH0 Genevestigator:Q9MAH0 GermOnline:AT1G53310 GO:GO:0008964 GO:GO:0015977 Uniprot:Q9MAH0
Root	Isotig02171	2	62	-5.083	8.94E-17	TAIR|locus:2172244 - symbol:HA11 "H(+)-ATPase 11" species:3702 "Arabidopsis thaliana" [GO:0006754 "ATP biosynthetic process" evidence=IEA] [GO:0006812 "cation transport" evidence=IEA] [GO:0008152 "metabolic process" evidence=IEA] [GO:0016887 "ATPase activity" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] InterPro:IPR000695 InterPro:IPR001757 InterPro:IPR005834 InterPro:IPR006534 InterPro:IPR008250 Pfam:PF00122 Pfam:PF00702 PRINTS:PR00119 PRINTS:PR00120 InterPro:IPR018303 InterPro:IPR004014 Pfam:PF00690 Prosite:PS00154 GO:GO:0016021 GO:GO:0005886 GO:GO:0005524 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0046872 InterPro:IPR023214 SUPFAM:SSF56784 GO:GO:0006754 eggNOG:COG0474 InterPro:IPR023300 InterPro:IPR023299 InterPro:IPR023298 Gene3D:G3DSA:2.70.150.10 Gene3D:G3DSA:3.40.1110.10 Gene3D:G3DSA:1.20.1110.10 SMART:SM00831 TIGRFAMs:TIGR01494 GO:GO:0008553 EMBL:AB020751 HOGENOM:HBG706356 KO:K01535 PANTHER:PTHR24093:SF61 TIGRFAMs:TIGR01647 EMBL:AY125493 IPI:IPI00531044 RefSeq:NP_201073.1 UniGene:At.28239 UniGene:At.68527 ProteinModelPortal:Q9LV11 SMR:Q9LV11 STRING:Q9LV11 PRIDE:Q9LV11 EnsemblPlants:AT5G62670.1 GeneID:836388 KEGG:ath:AT5G62670 TAIR:At5g62670 InParanoid:Q9LV11 OMA:SHFQRAV PhylomeDB:Q9LV11 ProtClustDB:CLSN2687353 ArrayExpress:Q9LV11 Genevestigator:Q9LV11 GermOnline:AT5G62670 Uniprot:Q9LV11
Root	Isotig02172	2	57	-4.962	1.85E-15	TAIR|locus:2172244 - symbol:HA11 "H(+)-ATPase 11" species:3702 "Arabidopsis thaliana" [GO:0006754 "ATP biosynthetic process" evidence=IEA] [GO:0006812 "cation transport" evidence=IEA] [GO:0008152 "metabolic process" evidence=IEA] [GO:0016887 "ATPase activity" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] InterPro:IPR000695 InterPro:IPR001757 InterPro:IPR005834 InterPro:IPR006534 InterPro:IPR008250 Pfam:PF00122 Pfam:PF00702 PRINTS:PR00119 PRINTS:PR00120 InterPro:IPR018303 InterPro:IPR004014 Pfam:PF00690 Prosite:PS00154 GO:GO:0016021 GO:GO:0005886 GO:GO:0005524 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0046872 InterPro:IPR023214 SUPFAM:SSF56784 GO:GO:0006754 eggNOG:COG0474 InterPro:IPR023300 InterPro:IPR023299 InterPro:IPR023298 Gene3D:G3DSA:2.70.150.10 Gene3D:G3DSA:3.40.1110.10 Gene3D:G3DSA:1.20.1110.10 SMART:SM00831 TIGRFAMs:TIGR01494 GO:GO:0008553 EMBL:AB020751 HOGENOM:HBG706356 KO:K01535 PANTHER:PTHR24093:SF61 TIGRFAMs:TIGR01647 EMBL:AY125493 IPI:IPI00531044 RefSeq:NP_201073.1 UniGene:At.28239 UniGene:At.68527 ProteinModelPortal:Q9LV11 SMR:Q9LV11 STRING:Q9LV11 PRIDE:Q9LV11 EnsemblPlants:AT5G62670.1 GeneID:836388 KEGG:ath:AT5G62670 TAIR:At5g62670 InParanoid:Q9LV11 OMA:SHFQRAV PhylomeDB:Q9LV11 ProtClustDB:CLSN2687353 ArrayExpress:Q9LV11 Genevestigator:Q9LV11 GermOnline:AT5G62670 Uniprot:Q9LV11
Root	Isotig02173	2	57	-4.962	1.85E-15	TAIR|locus:2172244 - symbol:HA11 "H(+)-ATPase 11" species:3702 "Arabidopsis thaliana" [GO:0006754 "ATP biosynthetic process" evidence=IEA] [GO:0006812 "cation transport" evidence=IEA] [GO:0008152 "metabolic

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						process" evidence=IEA] [GO:0016887 "ATPase activity" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] InterPro:IPR000695 InterPro:IPR001757 InterPro:IPR005834 InterPro:IPR006534 InterPro:IPR008250 Pfam:PF00122 Pfam:PF00702 PRINTS:PR00119 PRINTS:PR00120 InterPro:IPR018303 InterPro:IPR004014 Pfam:PF00690 Prosite:PS00154 GO:GO:0016021 GO:GO:0005886 GO:GO:0005524 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0046872 InterPro:IPR023214 SUPFAM:SSF56784 GO:GO:0006754 eggNOG:COG0474 InterPro:IPR023300 InterPro:IPR023299 InterPro:IPR023298 Gene3D:G3DSA:2.70.150.10 Gene3D:G3DSA:3.40.1110.10 Gene3D:G3DSA:1.20.1110.10 SMART:SM00831 TIGRFAMs:TIGR01494 GO:GO:0008553 EMBL:AB020751 HOGENOM:HBG706356 KO:K01535 PANTHER:PTHR24093:SF61 TIGRFAMs:TIGR01647 EMBL:AY125493 IPI:IPI00531044 RefSeq:NP_201073.1 UniGene:At.28239 UniGene:At.68527 ProteinModelPortal:Q9LV11 SMR:Q9LV11 STRING:Q9LV11 PRIDE:Q9LV11 EnsemblPlants:AT5G62670.1 GeneID:836388 KEGG:ath:AT5G62670 TAIR:At5g62670 InParanoid:Q9LV11 OMA:SHFQRAV PhylomeDB:Q9LV11 ProtClustDB:CLSN2687353 ArrayExpress:Q9LV11 Genevestigator:Q9LV11 GermOnline:AT5G62670 Uniprot:Q9LV11
Root	Isotig02174	2	52	-4.829	3.94E-14	TAIR|locus:2172244 - symbol:HA11 "H(+)-ATPase 11" species:3702 "Arabidopsis thaliana" [GO:0006754 "ATP biosynthetic process" evidence=IEA] [GO:0006812 "cation transport" evidence=IEA] [GO:0008152 "metabolic process" evidence=IEA] [GO:0016887 "ATPase activity" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] InterPro:IPR000695 InterPro:IPR001757 InterPro:IPR005834 InterPro:IPR006534 InterPro:IPR008250 Pfam:PF00122 Pfam:PF00702 PRINTS:PR00119 PRINTS:PR00120 InterPro:IPR018303 InterPro:IPR004014 Pfam:PF00690 Prosite:PS00154 GO:GO:0016021 GO:GO:0005886 GO:GO:0005524 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0046872 InterPro:IPR023214 SUPFAM:SSF56784 GO:GO:0006754 eggNOG:COG0474 InterPro:IPR023300 InterPro:IPR023299 InterPro:IPR023298 Gene3D:G3DSA:2.70.150.10 Gene3D:G3DSA:3.40.1110.10 Gene3D:G3DSA:1.20.1110.10 SMART:SM00831 TIGRFAMs:TIGR01494 GO:GO:0008553 EMBL:AB020751 HOGENOM:HBG706356 KO:K01535 PANTHER:PTHR24093:SF61 TIGRFAMs:TIGR01647 EMBL:AY125493 IPI:IPI00531044 RefSeq:NP_201073.1 UniGene:At.28239 UniGene:At.68527 ProteinModelPortal:Q9LV11 SMR:Q9LV11 STRING:Q9LV11 PRIDE:Q9LV11 EnsemblPlants:AT5G62670.1 GeneID:836388 KEGG:ath:AT5G62670 TAIR:At5g62670 InParanoid:Q9LV11 OMA:SHFQRAV PhylomeDB:Q9LV11 ProtClustDB:CLSN2687353 ArrayExpress:Q9LV11 Genevestigator:Q9LV11 GermOnline:AT5G62670 Uniprot:Q9LV11
Root	Isotig02175	3	58	-4.402	4.50E-15	TAIR|locus:2172244 - symbol:HA11 "H(+)-ATPase 11" species:3702 "Arabidopsis thaliana" [GO:0006754 "ATP biosynthetic process" evidence=IEA] [GO:0006812 "cation transport" evidence=IEA] [GO:0008152 "metabolic process" evidence=IEA] [GO:0016887 "ATPase activity" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] InterPro:IPR000695 InterPro:IPR001757 InterPro:IPR005834 InterPro:IPR006534 InterPro:IPR008250 Pfam:PF00122 Pfam:PF00702 PRINTS:PR00119 PRINTS:PR00120 InterPro:IPR018303 InterPro:IPR004014 Pfam:PF00690 Prosite:PS00154 GO:GO:0016021 GO:GO:0005886 GO:GO:0005524 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0046872 InterPro:IPR023214 SUPFAM:SSF56784 GO:GO:0006754 eggNOG:COG0474 InterPro:IPR023300 InterPro:IPR023299 InterPro:IPR023298 Gene3D:G3DSA:2.70.150.10 Gene3D:G3DSA:3.40.1110.10 Gene3D:G3DSA:1.20.1110.10 SMART:SM00831 TIGRFAMs:TIGR01494 GO:GO:0008553 EMBL:AB020751 HOGENOM:HBG706356 KO:K01535 PANTHER:PTHR24093:SF61 TIGRFAMs:TIGR01647 EMBL:AY125493 IPI:IPI00531044 RefSeq:NP_201073.1 UniGene:At.28239 UniGene:At.68527 ProteinModelPortal:Q9LV11 SMR:Q9LV11 STRING:Q9LV11 PRIDE:Q9LV11 EnsemblPlants:AT5G62670.1 GeneID:836388 KEGG:ath:AT5G62670 TAIR:At5g62670 InParanoid:Q9LV11 OMA:SHFQRAV PhylomeDB:Q9LV11 ProtClustDB:CLSN2687353 ArrayExpress:Q9LV11 Genevestigator:Q9LV11 GermOnline:AT5G62670 Uniprot:Q9LV11
Root	Isotig02176	3	53	-4.272	1.02E-13	TAIR|locus:2172244 - symbol:HA11 "H(+)-ATPase 11" species:3702 "Arabidopsis thaliana" [GO:0006754 "ATP biosynthetic process" evidence=IEA] [GO:0006812 "cation transport" evidence=IEA] [GO:0008152 "metabolic process" evidence=IEA] [GO:0016887 "ATPase activity" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] InterPro:IPR000695 InterPro:IPR001757 InterPro:IPR005834 InterPro:IPR006534 InterPro:IPR008250 Pfam:PF00122 Pfam:PF00702 PRINTS:PR00119 PRINTS:PR00120 InterPro:IPR018303 InterPro:IPR004014 Pfam:PF00690 Prosite:PS00154 GO:GO:0016021

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0005886 GO:GO:0005524 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0046872 InterPro:IPR023214 SUPFAM:SSF56784 GO:GO:0006754 eggNOG:COG0474 InterPro:IPR023300 InterPro:IPR023299 InterPro:IPR023298 Gene3D:G3DSA:2.70.150.10 Gene3D:G3DSA:3.40.1110.10 Gene3D:G3DSA:1.20.1110.10 SMART:SM00831 TIGRFAMs:TIGR01494 GO:GO:0008553 EMBL:AB020751 HOGENOM:HBG706356 KO:K01535 PANTHER:PTHR24093:SF61 TIGRFAMs:TIGR01647 EMBL:AY125493 IPI:IPI00531044 RefSeq:NP_201073.1 UniGene:At.28239 UniGene:At.68527 ProteinModelPortal:Q9LV11 SMR:Q9LV11 STRING:Q9LV11 PRIDE:Q9LV11 EnsemblPlants:AT5G62670.1 GeneID:836388 KEGG:ath:AT5G62670 TAIR:At5g62670 InParanoid:Q9LV11 OMA:SHFQRAV PhylomeDB:Q9LV11 ProtClustDB:CLSN2687353 ArrayExpress:Q9LV11 Genevestigator:Q9LV11 GermOnline:AT5G62670 Uniprot:Q9LV11
Root	Isotig02201	96	0	7.456	6.34E-22	TAIR|locus:2024522 - symbol:DAA1 "DUO1-activated ATPase 1" species:3702 "Arabidopsis thaliana" [GO:0000166 "nucleotide binding" evidence=IEA] [GO:0005524 "ATP binding" evidence=IEA] [GO:0016887 "ATPase activity" evidence=ISS] [GO:0017111 "nucleoside-triphosphatase activity" evidence=IEA] [GO:0048235 "pollen sperm cell differentiation" evidence=IEP] InterPro:IPR003593 InterPro:IPR003959 InterPro:IPR003960 Pfam:PF00004 PROSITE:PS00674 SMART:SM00382 EMBL:CP002684 GO:GO:0005524 eggNOG:COG0464 GO:GO:0017111 GO:GO:0048235 EMBL:AC007764 IPI:IPI00891776 RefSeq:NP_001117544.1 UniGene:At.16450 ProteinModelPortal:B3H7I9 SMR:B3H7I9 PRIDE:B3H7I9 EnsemblPlants:AT1G64110.3 GeneID:842716 KEGG:ath:AT1G64110 TAIR:At1g64110 PhylomeDB:B3H7I9 ProtClustDB:CLSN2689017 Genevestigator:B3H7I9 Uniprot:B3H7I9
Root	Isotig02202	99	0	7.500	1.74E-22	TAIR|locus:2024522 - symbol:DAA1 "DUO1-activated ATPase 1" species:3702 "Arabidopsis thaliana" [GO:0000166 "nucleotide binding" evidence=IEA] [GO:0005524 "ATP binding" evidence=IEA] [GO:0016887 "ATPase activity" evidence=ISS] [GO:0017111 "nucleoside-triphosphatase activity" evidence=IEA] [GO:0048235 "pollen sperm cell differentiation" evidence=IEP] InterPro:IPR003593 InterPro:IPR003959 InterPro:IPR003960 Pfam:PF00004 PROSITE:PS00674 SMART:SM00382 EMBL:CP002684 GO:GO:0005524 eggNOG:COG0464 GO:GO:0017111 GO:GO:0048235 EMBL:AC007764 IPI:IPI00891776 RefSeq:NP_001117544.1 UniGene:At.16450 ProteinModelPortal:B3H7I9 SMR:B3H7I9 PRIDE:B3H7I9 EnsemblPlants:AT1G64110.3 GeneID:842716 KEGG:ath:AT1G64110 TAIR:At1g64110 PhylomeDB:B3H7I9 ProtClustDB:CLSN2689017 Genevestigator:B3H7I9 Uniprot:B3H7I9
Root	Isotig02203	92	0	7.395	3.60E-21	TAIR|locus:2024522 - symbol:DAA1 "DUO1-activated ATPase 1" species:3702 "Arabidopsis thaliana" [GO:0000166 "nucleotide binding" evidence=IEA] [GO:0005524 "ATP binding" evidence=IEA] [GO:0016887 "ATPase activity" evidence=ISS] [GO:0017111 "nucleoside-triphosphatase activity" evidence=IEA] [GO:0048235 "pollen sperm cell differentiation" evidence=IEP] InterPro:IPR003593 InterPro:IPR003959 InterPro:IPR003960 Pfam:PF00004 PROSITE:PS00674 SMART:SM00382 EMBL:CP002684 GO:GO:0005524 eggNOG:COG0464 GO:GO:0017111 GO:GO:0048235 EMBL:AC007764 IPI:IPI00891776 RefSeq:NP_001117544.1 UniGene:At.16450 ProteinModelPortal:B3H7I9 SMR:B3H7I9 PRIDE:B3H7I9 EnsemblPlants:AT1G64110.3 GeneID:842716 KEGG:ath:AT1G64110 TAIR:At1g64110 PhylomeDB:B3H7I9 ProtClustDB:CLSN2689017 Genevestigator:B3H7I9 Uniprot:B3H7I9
Root	Isotig02204	95	0	7.441	9.78E-22	TAIR|locus:2024522 - symbol:DAA1 "DUO1-activated ATPase 1" species:3702 "Arabidopsis thaliana" [GO:0000166 "nucleotide binding" evidence=IEA] [GO:0005524 "ATP binding" evidence=IEA] [GO:0016887 "ATPase activity" evidence=ISS] [GO:0017111 "nucleoside-triphosphatase activity" evidence=IEA] [GO:0048235 "pollen sperm cell differentiation" evidence=IEP] InterPro:IPR003593 InterPro:IPR003959 InterPro:IPR003960 Pfam:PF00004 PROSITE:PS00674 SMART:SM00382 EMBL:CP002684 GO:GO:0005524 eggNOG:COG0464 GO:GO:0017111 GO:GO:0048235 EMBL:AC007764 IPI:IPI00891776 RefSeq:NP_001117544.1 UniGene:At.16450 ProteinModelPortal:B3H7I9 SMR:B3H7I9 PRIDE:B3H7I9 EnsemblPlants:AT1G64110.3 GeneID:842716 KEGG:ath:AT1G64110 TAIR:At1g64110 PhylomeDB:B3H7I9 ProtClustDB:CLSN2689017 Genevestigator:B3H7I9 Uniprot:B3H7I9
Root	Isotig02205	49	0	6.486	1.48E-12	TAIR|locus:2024522 - symbol:DAA1 "DUO1-activated ATPase 1" species:3702 "Arabidopsis thaliana" [GO:0000166 "nucleotide binding" evidence=IEA] [GO:0005524 "ATP binding" evidence=IEA] [GO:0016887 "ATPase activity" evidence=ISS] [GO:0017111 "nucleoside-triphosphatase activity" evidence=IEA] [GO:0048235 "pollen sperm cell differentiation" evidence=IEP] InterPro:IPR003593 InterPro:IPR003959 InterPro:IPR003960 Pfam:PF00004 PROSITE:PS00674 SMART:SM00382 EMBL:CP002684 GO:GO:0005524 eggNOG:COG0464 GO:GO:0017111 GO:GO:0048235 EMBL:AC007764 IPI:IPI00891776 RefSeq:NP_001117544.1 UniGene:At.16450

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						ProteinModelPortal:B3H7I9 SMR:B3H7I9 PRIDE:B3H7I9 EnsemblPlants:AT1G64110.3 GeneID:842716 KEGG:ath:AT1G64110 TAIR:At1g64110 PhylomeDB:B3H7I9 ProtClustDB:CLSN2689017 Genevestigator:B3H7I9 Uniprot:B3H7I9
Root	Isotig02206	52	0	6.571	3.42E-13	TAIR|locus:2024522 - symbol:DAA1 "DUO1-activated ATPase 1" species:3702 "Arabidopsis thaliana" [GO:0000166 "nucleotide binding" evidence=IEA] [GO:0005524 "ATP binding" evidence=IEA] [GO:0016887 "ATPase activity" evidence=ISS] [GO:0017111 "nucleoside-triphosphatase activity" evidence=IEA] [GO:0048235 "pollen sperm cell differentiation" evidence=IEP] InterPro:IPR003593 InterPro:IPR003959 InterPro:IPR003960 Pfam:PF00004 PROSITE:PS00674 SMART:SM00382 EMBL:CP002684 GO:GO:0005524 eggNOG:COG0464 GO:GO:0017111 GO:GO:0048235 EMBL:AC007764 IPI:IPI00891776 RefSeq:NP_001117544.1 UniGene:At.16450 ProteinModelPortal:B3H7I9 SMR:B3H7I9 PRIDE:B3H7I9 EnsemblPlants:AT1G64110.3 GeneID:842716 KEGG:ath:AT1G64110 TAIR:At1g64110 PhylomeDB:B3H7I9 ProtClustDB:CLSN2689017 Genevestigator:B3H7I9 Uniprot:B3H7I9
Root	Isotig02211	1	17	-4.216	2.69E-05	TAIR|locus:2143443 - symbol:FLA11 "AT5G03170" species:3702 "Arabidopsis thaliana" [GO:0031225 "anchored to membrane" evidence=TAS] [GO:0009834 "secondary cell wall biogenesis" evidence=IMP] [GO:0005886 "plasma membrane" evidence=IDA] Pfam:PF02469 InterPro:IPR000782 GO:GO:0005886 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0031225 EMBL:AB005240 Gene3D:G3DSA:2.30.180.10 SMART:SM00554 SUPFAM:SSF82153 PROSITE:PS50213 GO:GO:0009834 EMBL:AL163002 EMBL:AF360183 EMBL:AY039999 EMBL:AY085388 IPI:IPI00524222 PIR:T48338 RefSeq:NP_195937.1 UniGene:At.27796 UniGene:At.69706 ProteinModelPortal:Q8LEJ6 SMR:Q8LEJ6 STRING:Q8LEJ6 PRIDE:Q8LEJ6 EnsemblPlants:AT5G03170.1 GeneID:831914 KEGG:ath:AT5G03170 GeneFarm:3783 TAIR:At5g03170 eggNOG:NOG311981 HOGENOM:HBG750250 InParanoid:Q8LEJ6 OMA:AVYQVDQ PhylomeDB:Q8LEJ6 ProtClustDB:CLSN2916901 ArrayExpress:Q9LYW8 Genevestigator:Q8LEJ6 GermOnline:AT5G03170 Uniprot:Q8LEJ6
Root	Isotig02212	1	18	-4.299	1.41E-05	TAIR|locus:2143443 - symbol:FLA11 "AT5G03170" species:3702 "Arabidopsis thaliana" [GO:0031225 "anchored to membrane" evidence=TAS] [GO:0009834 "secondary cell wall biogenesis" evidence=IMP] [GO:0005886 "plasma membrane" evidence=IDA] Pfam:PF02469 InterPro:IPR000782 GO:GO:0005886 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0031225 EMBL:AB005240 Gene3D:G3DSA:2.30.180.10 SMART:SM00554 SUPFAM:SSF82153 PROSITE:PS50213 GO:GO:0009834 EMBL:AL163002 EMBL:AF360183 EMBL:AY039999 EMBL:AY085388 IPI:IPI00524222 PIR:T48338 RefSeq:NP_195937.1 UniGene:At.27796 UniGene:At.69706 ProteinModelPortal:Q8LEJ6 SMR:Q8LEJ6 STRING:Q8LEJ6 PRIDE:Q8LEJ6 EnsemblPlants:AT5G03170.1 GeneID:831914 KEGG:ath:AT5G03170 GeneFarm:3783 TAIR:At5g03170 eggNOG:NOG311981 HOGENOM:HBG750250 InParanoid:Q8LEJ6 OMA:AVYQVDQ PhylomeDB:Q8LEJ6 ProtClustDB:CLSN2916901 ArrayExpress:Q9LYW8 Genevestigator:Q8LEJ6 GermOnline:AT5G03170 Uniprot:Q8LEJ6
Root	Isotig02213	2	34	-4.216	2.89E-09	TAIR|locus:2076244 - symbol:PAL4 "phenylalanine ammonia-lyase 4" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0005737 "cytoplasm" evidence=IEA] [GO:0006559 "L-phenylalanine catabolic process" evidence=IEA] [GO:0009058 "biosynthetic process" evidence=IEA] [GO:0016841 "ammonia-lyase activity" evidence=IEA] InterPro:IPR001106 InterPro:IPR005922 InterPro:IPR008948 InterPro:IPR022313 Pfam:PF00221 PROSITE:PS00488 GO:GO:0005737 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0009698 GO:GO:0009058 SUPFAM:SSF48557 GO:GO:0006559 InterPro:IPR024083 Gene3D:G3DSA:1.10.275.10 EMBL:AC009400 eggNOG:COG2986 HOGENOM:HBG318028 KO:K10775 ProtClustDB:PLN02457 BRENDA:4.3.1.24 InterPro:IPR023144 Gene3D:G3DSA:1.10.274.20 TIGRFAMs:TIGR01226 GO:GO:0016841 EMBL:AY303130 EMBL:AY099657 EMBL:BT000252 IPI:IPI00533524 RefSeq:NP_187645.1 UniGene:At.18429 UniGene:At.67148 ProteinModelPortal:Q9SS45 SMR:Q9SS45 IntAct:Q9SS45 STRING:Q9SS45 PRIDE:Q9SS45 EnsemblPlants:AT3G10340.1 GeneID:820196 KEGG:ath:AT3G10340 TAIR:At3g10340 InParanoid:Q9SS45 OMA:GERQATQ PhylomeDB:Q9SS45 ArrayExpress:Q9SS45 Genevestigator:Q9SS45 GermOnline:AT3G10340 Uniprot:Q9SS45
Root	Isotig02214	2	31	-4.083	1.93E-08	TAIR|locus:2101958 - symbol:PAL2 "AT3G53260" species:3702 "Arabidopsis thaliana" [GO:0006979 "response to oxidative stress" evidence=IEP] [GO:0080167 "response to karrikin" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA] [GO:0006952 "defense response" evidence=TAS] [GO:0009611 "response to wounding" evidence=TAS] [GO:0009699 "phenylpropanoid biosynthetic process" evidence=TAS] [GO:0045548 "phenylalanine ammonia-lyase activity" evidence=ISS;TAS] InterPro:IPR001106 InterPro:IPR005922 InterPro:IPR008948

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						InterPro:IPR022313 Pfam:PF00221 PROSITE:PS00488 GO:GO:0005829 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0006979 GO:GO:0009699 GO:GO:0080167 SUPFAM:SSF48557 GO:GO:0006559 InterPro:IPR024083 Gene3D:G3DSA:1.10.275.10 EMBL:AL132958 eggNOG:COG2986 UniGene:At.21614 HOGENOM:HBG318028 KO:K10775 ProtClustDB:PLN02457 BRENDA:4.3.1.24 GO:GO:0045548 InterPro:IPR023144 Gene3D:G3DSA:1.10.274.20 TIGRFAMs:TIGR01226 EMBL:L33678 EMBL:AY303129 EMBL:AF367308 EMBL:AY092957 EMBL:AY133595 EMBL:BT000035 IPI:IPI00525638 PIR:T46172 RefSeq:NP_190894.1 ProteinModelPortal:P45724 SMR:P45724 IntAct:P45724 STRING:P45724 PRIDE:P45724 EnsemblPlants:AT3G53260.1 GeneID:824493 KEGG:ath:AT3G53260 TAIR:At3g53260 InParanoid:P45724 OMA:PLNWGLA PhylomeDB:P45724 Genevestigator:P45724 GermOnline:AT3G53260 Uniprot:P45724
Root	Isotig02215	2	34	-4.216	2.89E-09	TAIR|locus:2076244 - symbol:PAL4 "phenylalanine ammonia-lyase 4" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0005737 "cytoplasm" evidence=IEA] [GO:0006559 "L-phenylalanine catabolic process" evidence=IEA] [GO:0009058 "biosynthetic process" evidence=IEA] [GO:0016841 "ammonia-lyase activity" evidence=IEA] InterPro:IPR001106 InterPro:IPR005922 InterPro:IPR008948 InterPro:IPR022313 Pfam:PF00221 PROSITE:PS00488 GO:GO:0005737 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0009698 GO:GO:0009058 SUPFAM:SSF48557 GO:GO:0006559 InterPro:IPR024083 Gene3D:G3DSA:1.10.275.10 EMBL:AC009400 eggNOG:COG2986 HOGENOM:HBG318028 KO:K10775 ProtClustDB:PLN02457 BRENDA:4.3.1.24 InterPro:IPR023144 Gene3D:G3DSA:1.10.274.20 TIGRFAMs:TIGR01226 GO:GO:0016841 EMBL:AY303130 EMBL:AY099657 EMBL:BT000252 IPI:IPI00533524 RefSeq:NP_187645.1 UniGene:At.18429 UniGene:At.67148 ProteinModelPortal:Q9SS45 SMR:Q9SS45 IntAct:Q9SS45 STRING:Q9SS45 PRIDE:Q9SS45 EnsemblPlants:AT3G10340.1 GeneID:820196 KEGG:ath:AT3G10340 TAIR:At3g10340 InParanoid:Q9SS45 OMA:GERQATQ PhylomeDB:Q9SS45 ArrayExpress:Q9SS45 Genevestigator:Q9SS45 GermOnline:AT3G10340 Uniprot:Q9SS45
Root	Isotig02216	2	34	-4.216	2.89E-09	TAIR|locus:2076244 - symbol:PAL4 "phenylalanine ammonia-lyase 4" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0005737 "cytoplasm" evidence=IEA] [GO:0006559 "L-phenylalanine catabolic process" evidence=IEA] [GO:0009058 "biosynthetic process" evidence=IEA] [GO:0016841 "ammonia-lyase activity" evidence=IEA] InterPro:IPR001106 InterPro:IPR005922 InterPro:IPR008948 InterPro:IPR022313 Pfam:PF00221 PROSITE:PS00488 GO:GO:0005737 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0009698 GO:GO:0009058 SUPFAM:SSF48557 GO:GO:0006559 InterPro:IPR024083 Gene3D:G3DSA:1.10.275.10 EMBL:AC009400 eggNOG:COG2986 HOGENOM:HBG318028 KO:K10775 ProtClustDB:PLN02457 BRENDA:4.3.1.24 InterPro:IPR023144 Gene3D:G3DSA:1.10.274.20 TIGRFAMs:TIGR01226 GO:GO:0016841 EMBL:AY303130 EMBL:AY099657 EMBL:BT000252 IPI:IPI00533524 RefSeq:NP_187645.1 UniGene:At.18429 UniGene:At.67148 ProteinModelPortal:Q9SS45 SMR:Q9SS45 IntAct:Q9SS45 STRING:Q9SS45 PRIDE:Q9SS45 EnsemblPlants:AT3G10340.1 GeneID:820196 KEGG:ath:AT3G10340 TAIR:At3g10340 InParanoid:Q9SS45 OMA:GERQATQ PhylomeDB:Q9SS45 ArrayExpress:Q9SS45 Genevestigator:Q9SS45 GermOnline:AT3G10340 Uniprot:Q9SS45
Root	Isotig02217	2	31	-4.083	1.93E-08	TAIR|locus:2101958 - symbol:PAL2 "AT3G53260" species:3702 "Arabidopsis thaliana" [GO:0006979 "response to oxidative stress" evidence=IEP] [GO:0080167 "response to karrikin" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA] [GO:0006952 "defense response" evidence=TAS] [GO:0009611 "response to wounding" evidence=TAS] [GO:0009699 "phenylpropanoid biosynthetic process" evidence=TAS] [GO:0045548 "phenylalanine ammonia-lyase activity" evidence=ISS;TAS] InterPro:IPR001106 InterPro:IPR005922 InterPro:IPR008948 InterPro:IPR022313 Pfam:PF00221 PROSITE:PS00488 GO:GO:0005829 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0006979 GO:GO:0009699 GO:GO:0080167 SUPFAM:SSF48557 GO:GO:0006559 InterPro:IPR024083 Gene3D:G3DSA:1.10.275.10 EMBL:AL132958 eggNOG:COG2986 UniGene:At.21614 HOGENOM:HBG318028 KO:K10775 ProtClustDB:PLN02457 BRENDA:4.3.1.24 GO:GO:0045548 InterPro:IPR023144 Gene3D:G3DSA:1.10.274.20 TIGRFAMs:TIGR01226 EMBL:L33678 EMBL:AY303129 EMBL:AF367308 EMBL:AY092957 EMBL:AY133595 EMBL:BT000035 IPI:IPI00525638 PIR:T46172 RefSeq:NP_190894.1 ProteinModelPortal:P45724 SMR:P45724 IntAct:P45724 STRING:P45724 PRIDE:P45724 EnsemblPlants:AT3G53260.1 GeneID:824493 KEGG:ath:AT3G53260 TAIR:At3g53260 InParanoid:P45724 OMA:PLNWGLA PhylomeDB:P45724 Genevestigator:P45724 GermOnline:AT3G53260 Uniprot:P45724

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig02218	2	31	-4.083	1.93E-08	TAIR|locus:2076244 - symbol:PAL4 "phenylalanine ammonia-lyase 4" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0005737 "cytoplasm" evidence=IEA] [GO:0006559 "L-phenylalanine catabolic process" evidence=IEA] [GO:0009058 "biosynthetic process" evidence=IEA] [GO:0016841 "ammonia-lyase activity" evidence=IEA] InterPro:IPR001106 InterPro:IPR005922 InterPro:IPR008948 InterPro:IPR022313 Pfam:PF00221 PROSITE:PS00488 GO:GO:0005737 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0009698 GO:GO:0009058 SUPFAM:SSF48557 GO:GO:0006559 InterPro:IPR024083 Gene3D:G3DSA:1.10.275.10 EMBL:AC009400 eggNOG:COG2986 HOGENOM:HBG318028 KO:K10775 ProtClustDB:PLN02457 BRENDA:4.3.1.24 InterPro:IPR023144 Gene3D:G3DSA:1.10.274.20 TIGRFAMs:TIGR01226 GO:GO:0016841 EMBL:AY303130 EMBL:AY099657 EMBL:BT000252 IPI:IPI00533524 RefSeq:NP_187645.1 UniGene:At.18429 UniGene:At.67148 ProteinModelPortal:Q9SS45 SMR:Q9SS45 IntAct:Q9SS45 STRING:Q9SS45 PRIDE:Q9SS45 EnsemblPlants:AT3G10340.1 GeneID:820196 KEGG:ath:AT3G10340 TAIR:At3g10340 InParanoid:Q9SS45 OMA:GERQATQ PhylomeDB:Q9SS45 ArrayExpress:Q9SS45 Genevestigator:Q9SS45 GermOnline:AT3G10340 Uniprot:Q9SS45
Root	Isotig02237	52	16	1.571	3.49E-05	TAIR|locus:2046079 - symbol:AT2G12400 "AT2G12400" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0009506 "plasmodesma" evidence=IDA] GO:GO:0009506 EMBL:CP002685 GenomeReviews:CT485783_GR eggNOG:NOG277729 HOGENOM:HBG319596 EMBL:BT002043 IPI:IPI00530884 RefSeq:NP_178935.2 UniGene:At.14383 PRIDE:Q8H0U2 EnsemblPlants:AT2G12400.1 GeneID:815712 KEGG:ath:AT2G12400 TAIR:At2g12400 InParanoid:Q8H0U2 OMA:MPLLCNP PhylomeDB:Q8H0U2 ProtClustDB:CLSN2690686 Genevestigator:Q8H0U2 Uniprot:Q8H0U2
Root	Isotig02238	52	15	1.665	1.60E-05	TAIR|locus:2046079 - symbol:AT2G12400 "AT2G12400" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0009506 "plasmodesma" evidence=IDA] GO:GO:0009506 EMBL:CP002685 GenomeReviews:CT485783_GR eggNOG:NOG277729 HOGENOM:HBG319596 EMBL:BT002043 IPI:IPI00530884 RefSeq:NP_178935.2 UniGene:At.14383 PRIDE:Q8H0U2 EnsemblPlants:AT2G12400.1 GeneID:815712 KEGG:ath:AT2G12400 TAIR:At2g12400 InParanoid:Q8H0U2 OMA:MPLLCNP PhylomeDB:Q8H0U2 ProtClustDB:CLSN2690686 Genevestigator:Q8H0U2 Uniprot:Q8H0U2
Root	Isotig02239	51	16	1.543	5.22E-05	TAIR|locus:2046079 - symbol:AT2G12400 "AT2G12400" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0009506 "plasmodesma" evidence=IDA] GO:GO:0009506 EMBL:CP002685 GenomeReviews:CT485783_GR eggNOG:NOG277729 HOGENOM:HBG319596 EMBL:BT002043 IPI:IPI00530884 RefSeq:NP_178935.2 UniGene:At.14383 PRIDE:Q8H0U2 EnsemblPlants:AT2G12400.1 GeneID:815712 KEGG:ath:AT2G12400 TAIR:At2g12400 InParanoid:Q8H0U2 OMA:MPLLCNP PhylomeDB:Q8H0U2 ProtClustDB:CLSN2690686 Genevestigator:Q8H0U2 Uniprot:Q8H0U2
Root	Isotig02240	52	15	1.665	1.60E-05	TAIR|locus:2046079 - symbol:AT2G12400 "AT2G12400" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0009506 "plasmodesma" evidence=IDA] GO:GO:0009506 EMBL:CP002685 GenomeReviews:CT485783_GR eggNOG:NOG277729 HOGENOM:HBG319596 EMBL:BT002043 IPI:IPI00530884 RefSeq:NP_178935.2 UniGene:At.14383 PRIDE:Q8H0U2 EnsemblPlants:AT2G12400.1 GeneID:815712 KEGG:ath:AT2G12400 TAIR:At2g12400 InParanoid:Q8H0U2 OMA:MPLLCNP PhylomeDB:Q8H0U2 ProtClustDB:CLSN2690686 Genevestigator:Q8H0U2 Uniprot:Q8H0U2
Root	Isotig02241	51	15	1.637	2.43E-05	TAIR|locus:2046079 - symbol:AT2G12400 "AT2G12400" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0009506 "plasmodesma" evidence=IDA] GO:GO:0009506 EMBL:CP002685 GenomeReviews:CT485783_GR eggNOG:NOG277729 HOGENOM:HBG319596 EMBL:BT002043 IPI:IPI00530884 RefSeq:NP_178935.2 UniGene:At.14383 PRIDE:Q8H0U2 EnsemblPlants:AT2G12400.1 GeneID:815712 KEGG:ath:AT2G12400 TAIR:At2g12400 InParanoid:Q8H0U2 OMA:MPLLCNP PhylomeDB:Q8H0U2 ProtClustDB:CLSN2690686 Genevestigator:Q8H0U2 Uniprot:Q8H0U2
Root	Isotig02242	51	15	1.637	2.43E-05	TAIR|locus:2046079 - symbol:AT2G12400 "AT2G12400" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0009506 "plasmodesma" evidence=IDA] GO:GO:0009506 EMBL:CP002685 GenomeReviews:CT485783_GR eggNOG:NOG277729 HOGENOM:HBG319596 EMBL:BT002043 IPI:IPI00530884 RefSeq:NP_178935.2 UniGene:At.14383

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						PRIDE:Q8H0U2 EnsemblPlants:AT2G12400.1 GeneID:815712 KEGG:ath:AT2G12400 TAIR:At2g12400 InParanoid:Q8H0U2 OMA:MPLLCNP PhylomeDB:Q8H0U2 ProtClustDB:CLSN2690686 Genevestigator:Q8H0U2 Uniprot:Q8H0U2
Root	Isotig02255	7	39	-2.607	2.03E-07	TAIR|locus:2172249 - symbol:AT5G62680 "AT5G62680" species:3702 "Arabidopsis thaliana" [GO:0005215 "transporter activity" evidence=ISS] [GO:0006857 "oligopeptide transport" evidence=ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0080167 "response to karrikin" evidence=IEP] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000109 Pfam:PF00854 PROSITE:PS01022 PROSITE:PS01023 GO:GO:0016021 GO:GO:0005886 GO:GO:0009506 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0080167 GO:GO:0005215 InterPro:IPR016196 SUPFAM:SSF103473 EMBL:AB020751 eggNOG:COG3104 GO:GO:0006857 UniGene:At.28239 UniGene:At.68527 ProtClustDB:CLSN2687358 EMBL:AK316918 IPI:IPI00527254 RefSeq:NP_201074.1 ProteinModelPortal:Q9LV10 STRING:Q9LV10 PRIDE:Q9LV10 EnsemblPlants:AT5G62680.1 GeneID:836389 KEGG:ath:AT5G62680 TAIR:At5g62680 InParanoid:Q9LV10 OMA:IDSFFNW PhylomeDB:Q9LV10 Genevestigator:Q9LV10 Uniprot:Q9LV10
Root	Isotig02256	7	38	-2.570	3.60E-07	TAIR|locus:2172249 - symbol:AT5G62680 "AT5G62680" species:3702 "Arabidopsis thaliana" [GO:0005215 "transporter activity" evidence=ISS] [GO:0006857 "oligopeptide transport" evidence=ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0080167 "response to karrikin" evidence=IEP] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000109 Pfam:PF00854 PROSITE:PS01022 PROSITE:PS01023 GO:GO:0016021 GO:GO:0005886 GO:GO:0009506 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0080167 GO:GO:0005215 InterPro:IPR016196 SUPFAM:SSF103473 EMBL:AB020751 eggNOG:COG3104 GO:GO:0006857 UniGene:At.28239 UniGene:At.68527 ProtClustDB:CLSN2687358 EMBL:AK316918 IPI:IPI00527254 RefSeq:NP_201074.1 ProteinModelPortal:Q9LV10 STRING:Q9LV10 PRIDE:Q9LV10 EnsemblPlants:AT5G62680.1 GeneID:836389 KEGG:ath:AT5G62680 TAIR:At5g62680 InParanoid:Q9LV10 OMA:IDSFFNW PhylomeDB:Q9LV10 Genevestigator:Q9LV10 Uniprot:Q9LV10
Root	Isotig02257	7	39	-2.607	2.03E-07	TAIR|locus:2172249 - symbol:AT5G62680 "AT5G62680" species:3702 "Arabidopsis thaliana" [GO:0005215 "transporter activity" evidence=ISS] [GO:0006857 "oligopeptide transport" evidence=ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0080167 "response to karrikin" evidence=IEP] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000109 Pfam:PF00854 PROSITE:PS01022 PROSITE:PS01023 GO:GO:0016021 GO:GO:0005886 GO:GO:0009506 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0080167 GO:GO:0005215 InterPro:IPR016196 SUPFAM:SSF103473 EMBL:AB020751 eggNOG:COG3104 GO:GO:0006857 UniGene:At.28239 UniGene:At.68527 ProtClustDB:CLSN2687358 EMBL:AK316918 IPI:IPI00527254 RefSeq:NP_201074.1 ProteinModelPortal:Q9LV10 STRING:Q9LV10 PRIDE:Q9LV10 EnsemblPlants:AT5G62680.1 GeneID:836389 KEGG:ath:AT5G62680 TAIR:At5g62680 InParanoid:Q9LV10 OMA:IDSFFNW PhylomeDB:Q9LV10 Genevestigator:Q9LV10 Uniprot:Q9LV10
Root	Isotig02258	7	29	-2.180	5.47E-05	TAIR|locus:2172249 - symbol:AT5G62680 "AT5G62680" species:3702 "Arabidopsis thaliana" [GO:0005215 "transporter activity" evidence=ISS] [GO:0006857 "oligopeptide transport" evidence=ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0080167 "response to karrikin" evidence=IEP] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000109 Pfam:PF00854 PROSITE:PS01022 PROSITE:PS01023 GO:GO:0016021 GO:GO:0005886 GO:GO:0009506 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0080167 GO:GO:0005215 InterPro:IPR016196 SUPFAM:SSF103473 EMBL:AB020751 eggNOG:COG3104 GO:GO:0006857 UniGene:At.28239 UniGene:At.68527 ProtClustDB:CLSN2687358 EMBL:AK316918 IPI:IPI00527254 RefSeq:NP_201074.1 ProteinModelPortal:Q9LV10 STRING:Q9LV10 PRIDE:Q9LV10 EnsemblPlants:AT5G62680.1 GeneID:836389 KEGG:ath:AT5G62680 TAIR:At5g62680 InParanoid:Q9LV10 OMA:IDSFFNW PhylomeDB:Q9LV10 Genevestigator:Q9LV10 Uniprot:Q9LV10
Root	Isotig02259	7	28	-2.129	9.37E-05	TAIR|locus:2172249 - symbol:AT5G62680 "AT5G62680" species:3702 "Arabidopsis thaliana" [GO:0005215 "transporter activity" evidence=ISS] [GO:0006857 "oligopeptide transport" evidence=ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0080167 "response to karrikin" evidence=IEP] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000109 Pfam:PF00854 PROSITE:PS01022 PROSITE:PS01023 GO:GO:0016021 GO:GO:0005886 GO:GO:0009506 EMBL:CP002688

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GenomeReviews:BA000015_GR GO:GO:0080167 GO:GO:0005215 InterPro:IPR016196 SUPFAM:SSF103473 EMBL:AB020751 eggNOG:COG3104 GO:GO:0006857 UniGene:At.28239 UniGene:At.68527 ProtClustDB:CLSN2687358 EMBL:AK316918 IPI:IPI00527254 RefSeq:NP_201074.1 ProteinModelPortal:Q9LV10 STRING:Q9LV10 PRIDE:Q9LV10 EnsemblPlants:AT5G62680.1 GeneID:836389 KEGG:ath:AT5G62680 TAIR:At5g62680 InParanoid:Q9LV10 OMA:IDSFFNW PhylomeDB:Q9LV10 Genevestigator:Q9LV10 Uniprot:Q9LV10
Root	Isotig02260	7	29	-2.180	5.47E-05	TAIR|locus:2172249 - symbol:AT5G62680 "AT5G62680" species:3702 "Arabidopsis thaliana" [GO:0005215 "transporter activity" evidence=ISS] [GO:0006857 "oligopeptide transport" evidence=ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0080167 "response to karrikin" evidence=IEP] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000109 Pfam:PF00854 PROSITE:PS01022 PROSITE:PS01023 GO:GO:0016021 GO:GO:0005886 GO:GO:0009506 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0080167 GO:GO:0005215 InterPro:IPR016196 SUPFAM:SSF103473 EMBL:AB020751 eggNOG:COG3104 GO:GO:0006857 UniGene:At.28239 UniGene:At.68527 ProtClustDB:CLSN2687358 EMBL:AK316918 IPI:IPI00527254 RefSeq:NP_201074.1 ProteinModelPortal:Q9LV10 STRING:Q9LV10 PRIDE:Q9LV10 EnsemblPlants:AT5G62680.1 GeneID:836389 KEGG:ath:AT5G62680 TAIR:At5g62680 InParanoid:Q9LV10 OMA:IDSFFNW PhylomeDB:Q9LV10 Genevestigator:Q9LV10 Uniprot:Q9LV10
Root	Isotig02261	39	11	1.697	0.000152266	TAIR|locus:2167240 - symbol:GAD "AT5G17330" species:3702 "Arabidopsis thaliana" [GO:0005516 "calmodulin binding" evidence=IDA;TAS;IPI] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA] [GO:0004351 "glutamate decarboxylase activity" evidence=IDA] InterPro:IPR002129 InterPro:IPR010107 InterPro:IPR015421 Pfam:PF00282 PROSITE:PS00392 GO:GO:0005829 GO:GO:0046686 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0030170 InterPro:IPR015424 Gene3D:G3DSA:3.40.640.10 SUPFAM:SSF53383 GO:GO:0006536 GO:GO:0005516 EMBL:AB005238 eggNOG:COG0076 PANTHER:PTHR11999 EMBL:U10034 EMBL:AY094464 EMBL:BT001047 IPI:IPI00530557 RefSeq:NP_197235.1 UniGene:At.25228 PDB:3HBX PDBsum:3HBX ProteinModelPortal:Q42521 SMR:Q42521 STRING:Q42521 PRIDE:Q42521 EnsemblPlants:AT5G17330.1 GeneID:831599 KEGG:ath:AT5G17330 TAIR:At5g17330 HOGENOM:HBG365574 InParanoid:Q42521 KO:K01580 OMA:RRWQNKM PhylomeDB:Q42521 ProtClustDB:CLSN2683665 ArrayExpress:Q42521 Genevestigator:Q42521 GermOnline:AT5G17330 GO:GO:0004351 PANTHER:PTHR11999:SF1 TIGRFAMs:TIGR01788 Uniprot:Q42521
Root	Isotig02263	39	11	1.697	0.000152266	TAIR|locus:2167240 - symbol:GAD "AT5G17330" species:3702 "Arabidopsis thaliana" [GO:0005516 "calmodulin binding" evidence=IDA;TAS;IPI] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA] [GO:0004351 "glutamate decarboxylase activity" evidence=IDA] InterPro:IPR002129 InterPro:IPR010107 InterPro:IPR015421 Pfam:PF00282 PROSITE:PS00392 GO:GO:0005829 GO:GO:0046686 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0030170 InterPro:IPR015424 Gene3D:G3DSA:3.40.640.10 SUPFAM:SSF53383 GO:GO:0006536 GO:GO:0005516 EMBL:AB005238 eggNOG:COG0076 PANTHER:PTHR11999 EMBL:U10034 EMBL:AY094464 EMBL:BT001047 IPI:IPI00530557 RefSeq:NP_197235.1 UniGene:At.25228 PDB:3HBX PDBsum:3HBX ProteinModelPortal:Q42521 SMR:Q42521 STRING:Q42521 PRIDE:Q42521 EnsemblPlants:AT5G17330.1 GeneID:831599 KEGG:ath:AT5G17330 TAIR:At5g17330 HOGENOM:HBG365574 InParanoid:Q42521 KO:K01580 OMA:RRWQNKM PhylomeDB:Q42521 ProtClustDB:CLSN2683665 ArrayExpress:Q42521 Genevestigator:Q42521 GermOnline:AT5G17330 GO:GO:0004351 PANTHER:PTHR11999:SF1 TIGRFAMs:TIGR01788 Uniprot:Q42521
Root	Isotig02267	0	91	-7.637	2.33E-22	TAIR|locus:2046432 - symbol:PHT1;5 "AT2G32830" species:3702 "Arabidopsis thaliana" [GO:0005315 "inorganic phosphate transmembrane transporter activity" evidence=ISS] [GO:0015114 "phosphate ion transmembrane transporter activity" evidence=ISS] [GO:0016021 "integral to membrane" evidence=IEA] [GO:0006817 "phosphate ion transport" evidence=IMP] InterPro:IPR004738 InterPro:IPR005828 Pfam:PF00083 PROSITE:PS00216 PROSITE:PS00217 GO:GO:0016021 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0015293 GO:GO:0005315 eggNOG:COG0477 InterPro:IPR016196 SUPFAM:SSF103473 EMBL:AC003033 InterPro:IPR020846 PROSITE:PS50850 EMBL:AC003974 HOGENOM:HBG744844 KO:K08176 TIGRFAMs:TIGR00887 EMBL:AB000093 EMBL:AY075694 EMBL:AK117670 IPI:IPI00543210 PIR:T01124 RefSeq:NP_180842.1 UniGene:At.38016 ProteinModelPortal:Q8GYF4 EnsemblPlants:AT2G32830.1 GeneID:817844 KEGG:ath:AT2G32830 TAIR:At2g32830 InParanoid:Q8GYF4 OMA:NISWRIM

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						PhylomeDB:Q8GYF4 ProtClustDB:CLSN2913065 Genevestigator:Q8GYF4 GermOnline:AT2G32830 Uniprot:Q8GYF4
Root	Isotig02268	0	91	-7.637	2.33E-22	TAIR|locus:2046432 - symbol:PHT1;5 "AT2G32830" species:3702 "Arabidopsis thaliana" [GO:0005315 "inorganic phosphate transmembrane transporter activity" evidence=ISS] [GO:0015114 "phosphate ion transmembrane transporter activity" evidence=ISS] [GO:0016021 "integral to membrane" evidence=IEA] [GO:0006817 "phosphate ion transport" evidence=IMP] InterPro:IPR004738 InterPro:IPR005828 Pfam:PF00083 PROSITE:PS00216 PROSITE:PS00217 GO:GO:0016021 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0015293 GO:GO:0005315 eggNOG:COG0477 InterPro:IPR016196 SUPFAM:SSF103473 EMBL:AC003033 InterPro:IPR020846 PROSITE:PS50850 EMBL:AC003974 HOGENOM:HBG744844 KO:K08176 TIGRFAMs:TIGR00887 EMBL:AB000093 EMBL:AY075694 EMBL:AK117670 IPI:IPI00543210 PIR:T01124 RefSeq:NP_180842.1 UniGene:At.38016 ProteinModelPortal:Q8GYF4 EnsemblPlants:AT2G32830.1 GeneID:817844 KEGG:ath:AT2G32830 TAIR:At2g32830 InParanoid:Q8GYF4 OMA:NISWRIM PhylomeDB:Q8GYF4 ProtClustDB:CLSN2913065 Genevestigator:Q8GYF4 GermOnline:AT2G32830 Uniprot:Q8GYF4
Root	Isotig02269	0	80	-7.451	3.98E-20	TAIR|locus:2046432 - symbol:PHT1;5 "AT2G32830" species:3702 "Arabidopsis thaliana" [GO:0005315 "inorganic phosphate transmembrane transporter activity" evidence=ISS] [GO:0015114 "phosphate ion transmembrane transporter activity" evidence=ISS] [GO:0016021 "integral to membrane" evidence=IEA] [GO:0006817 "phosphate ion transport" evidence=IMP] InterPro:IPR004738 InterPro:IPR005828 Pfam:PF00083 PROSITE:PS00216 PROSITE:PS00217 GO:GO:0016021 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0015293 GO:GO:0005315 eggNOG:COG0477 InterPro:IPR016196 SUPFAM:SSF103473 EMBL:AC003033 InterPro:IPR020846 PROSITE:PS50850 EMBL:AC003974 HOGENOM:HBG744844 KO:K08176 TIGRFAMs:TIGR00887 EMBL:AB000093 EMBL:AY075694 EMBL:AK117670 IPI:IPI00543210 PIR:T01124 RefSeq:NP_180842.1 UniGene:At.38016 ProteinModelPortal:Q8GYF4 EnsemblPlants:AT2G32830.1 GeneID:817844 KEGG:ath:AT2G32830 TAIR:At2g32830 InParanoid:Q8GYF4 OMA:NISWRIM PhylomeDB:Q8GYF4 ProtClustDB:CLSN2913065 Genevestigator:Q8GYF4 GermOnline:AT2G32830 Uniprot:Q8GYF4
Root	Isotig02270	0	80	-7.451	3.98E-20	TAIR|locus:2046432 - symbol:PHT1;5 "AT2G32830" species:3702 "Arabidopsis thaliana" [GO:0005315 "inorganic phosphate transmembrane transporter activity" evidence=ISS] [GO:0015114 "phosphate ion transmembrane transporter activity" evidence=ISS] [GO:0016021 "integral to membrane" evidence=IEA] [GO:0006817 "phosphate ion transport" evidence=IMP] InterPro:IPR004738 InterPro:IPR005828 Pfam:PF00083 PROSITE:PS00216 PROSITE:PS00217 GO:GO:0016021 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0015293 GO:GO:0005315 eggNOG:COG0477 InterPro:IPR016196 SUPFAM:SSF103473 EMBL:AC003033 InterPro:IPR020846 PROSITE:PS50850 EMBL:AC003974 HOGENOM:HBG744844 KO:K08176 TIGRFAMs:TIGR00887 EMBL:AB000093 EMBL:AY075694 EMBL:AK117670 IPI:IPI00543210 PIR:T01124 RefSeq:NP_180842.1 UniGene:At.38016 ProteinModelPortal:Q8GYF4 EnsemblPlants:AT2G32830.1 GeneID:817844 KEGG:ath:AT2G32830 TAIR:At2g32830 InParanoid:Q8GYF4 OMA:NISWRIM PhylomeDB:Q8GYF4 ProtClustDB:CLSN2913065 Genevestigator:Q8GYF4 GermOnline:AT2G32830 Uniprot:Q8GYF4
Root	Isotig02271	0	63	-7.106	1.51E-16	TAIR|locus:2046432 - symbol:PHT1;5 "AT2G32830" species:3702 "Arabidopsis thaliana" [GO:0005315 "inorganic phosphate transmembrane transporter activity" evidence=ISS] [GO:0015114 "phosphate ion transmembrane transporter activity" evidence=ISS] [GO:0016021 "integral to membrane" evidence=IEA] [GO:0006817 "phosphate ion transport" evidence=IMP] InterPro:IPR004738 InterPro:IPR005828 Pfam:PF00083 PROSITE:PS00216 PROSITE:PS00217 GO:GO:0016021 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0015293 GO:GO:0005315 eggNOG:COG0477 InterPro:IPR016196 SUPFAM:SSF103473 EMBL:AC003033 InterPro:IPR020846 PROSITE:PS50850 EMBL:AC003974 HOGENOM:HBG744844 KO:K08176 TIGRFAMs:TIGR00887 EMBL:AB000093 EMBL:AY075694 EMBL:AK117670 IPI:IPI00543210 PIR:T01124 RefSeq:NP_180842.1 UniGene:At.38016 ProteinModelPortal:Q8GYF4 EnsemblPlants:AT2G32830.1 GeneID:817844 KEGG:ath:AT2G32830 TAIR:At2g32830 InParanoid:Q8GYF4 OMA:NISWRIM PhylomeDB:Q8GYF4 ProtClustDB:CLSN2913065 Genevestigator:Q8GYF4 GermOnline:AT2G32830 Uniprot:Q8GYF4
Root	Isotig02272	0	52	-6.829	3.96E-14	TAIR|locus:2046432 - symbol:PHT1;5 "AT2G32830" species:3702 "Arabidopsis thaliana" [GO:0005315 "inorganic phosphate transmembrane transporter activity" evidence=ISS] [GO:0015114 "phosphate ion transmembrane

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						transporter activity" evidence=ISS] [GO:0016021 "integral to membrane" evidence=IEA] [GO:0006817 "phosphate ion transport" evidence=IMP] InterPro:IPR004738 InterPro:IPR005828 Pfam:PF00083 PROSITE:PS00216 PROSITE:PS00217 GO:GO:0016021 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0015293 GO:GO:0005315 eggNOG:COG0477 InterPro:IPR016196 SUPFAM:SSF103473 EMBL:AC003033 InterPro:IPR020846 PROSITE:PS50850 EMBL:AC003974 HOGENOM:HBG744844 KO:K08176 TIGRFAMs:TIGR00887 EMBL:AB000093 EMBL:AY075694 EMBL:AK117670 IPI:IPI00543210 PIR:T01124 RefSeq:NP_180842.1 UniGene:At.38016 ProteinModelPortal:Q8GYF4 EnsemblPlants:AT2G32830.1 GeneID:817844 KEGG:ath:AT2G32830 TAIR:At2g32830 InParanoid:Q8GYF4 OMA:NISWRIM PhylomeDB:Q8GYF4 ProtClustDB:CLSN2913065 Genevestigator:Q8GYF4 GermOnline:AT2G32830 Uniprot:Q8GYF4
Root	Isotig02279	18	1	4.041	4.47E-05	No hit
Root	Isotig02280	18	1	4.041	4.47E-05	No hit
Root	Isotig02281	15	0	4.778	0.000105609	No hit
Root	Isotig02282	15	0	4.778	0.000105609	No hit
Root	Isotig02283	13	0	4.571	0.000344357	No hit
Root	Isotig02284	13	0	4.571	0.000344357	No hit
Root	Isotig02285	17	45	-1.533	7.67E-05	TAIR|locus:2082787 - symbol:AT3G61490 species:3702 "Arabidopsis thaliana" [GO:0004650 "polygalacturonase activity" evidence=IEA;ISS] [GO:0005975 "carbohydrate metabolic process" evidence=IEA;ISS] InterPro:IPR000743 Pfam:PF00295 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005576 EMBL:AL132962 GO:GO:0005975 CAZy:GH28 eggNOG:COG5434 GO:GO:0004650 InterPro:IPR006626 InterPro:IPR012334 InterPro:IPR011050 Gene3D:G3DSA:2.160.20.10 SMART:SM00710 SUPFAM:SSF51126 GO:GO:0007047 HOGENOM:HBG604585 IPI:IPI00527942 PIR:T47941 RefSeq:NP_001190154.1 RefSeq:NP_191708.1 RefSeq:NP_974473.1 UniGene:At.43625 ProteinModelPortal:Q9M318 SMR:Q9M318 PRIDE:Q9M318 EnsemblPlants:AT3G61490.1 EnsemblPlants:AT3G61490.2 EnsemblPlants:AT3G61490.3 GeneID:825322 KEGG:ath:AT3G61490 TAIR:At3g61490 InParanoid:Q9M318 OMA:CISPYSA PhylomeDB:Q9M318 ProtClustDB:CLSN2915754 Genevestigator:Q9M318 Uniprot:Q9M318
Root	Isotig02286	18	46	-1.483	9.61E-05	TAIR|locus:2082787 - symbol:AT3G61490 species:3702 "Arabidopsis thaliana" [GO:0004650 "polygalacturonase activity" evidence=IEA;ISS] [GO:0005975 "carbohydrate metabolic process" evidence=IEA;ISS] InterPro:IPR000743 Pfam:PF00295 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005576 EMBL:AL132962 GO:GO:0005975 CAZy:GH28 eggNOG:COG5434 GO:GO:0004650 InterPro:IPR006626 InterPro:IPR012334 InterPro:IPR011050 Gene3D:G3DSA:2.160.20.10 SMART:SM00710 SUPFAM:SSF51126 GO:GO:0007047 HOGENOM:HBG604585 IPI:IPI00527942 PIR:T47941 RefSeq:NP_001190154.1 RefSeq:NP_191708.1 RefSeq:NP_974473.1 UniGene:At.43625 ProteinModelPortal:Q9M318 SMR:Q9M318 PRIDE:Q9M318 EnsemblPlants:AT3G61490.1 EnsemblPlants:AT3G61490.2 EnsemblPlants:AT3G61490.3 GeneID:825322 KEGG:ath:AT3G61490 TAIR:At3g61490 InParanoid:Q9M318 OMA:CISPYSA PhylomeDB:Q9M318 ProtClustDB:CLSN2915754 Genevestigator:Q9M318 Uniprot:Q9M318
Root	Isotig02287	17	45	-1.533	7.67E-05	TAIR|locus:2082787 - symbol:AT3G61490 species:3702 "Arabidopsis thaliana" [GO:0004650 "polygalacturonase activity" evidence=IEA;ISS] [GO:0005975 "carbohydrate metabolic process" evidence=IEA;ISS] InterPro:IPR000743 Pfam:PF00295 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005576 EMBL:AL132962 GO:GO:0005975 CAZy:GH28 eggNOG:COG5434 GO:GO:0004650 InterPro:IPR006626 InterPro:IPR012334 InterPro:IPR011050 Gene3D:G3DSA:2.160.20.10 SMART:SM00710 SUPFAM:SSF51126 GO:GO:0007047 HOGENOM:HBG604585 IPI:IPI00527942 PIR:T47941 RefSeq:NP_001190154.1 RefSeq:NP_191708.1 RefSeq:NP_974473.1 UniGene:At.43625 ProteinModelPortal:Q9M318 SMR:Q9M318 PRIDE:Q9M318 EnsemblPlants:AT3G61490.1 EnsemblPlants:AT3G61490.2 EnsemblPlants:AT3G61490.3 GeneID:825322 KEGG:ath:AT3G61490 TAIR:At3g61490 InParanoid:Q9M318 OMA:CISPYSA PhylomeDB:Q9M318 ProtClustDB:CLSN2915754 Genevestigator:Q9M318 Uniprot:Q9M318
Root	Isotig02288	17	45	-1.533	7.67E-05	TAIR|locus:2082787 - symbol:AT3G61490 species:3702 "Arabidopsis thaliana" [GO:0004650 "polygalacturonase activity" evidence=IEA;ISS] [GO:0005975 "carbohydrate metabolic process" evidence=IEA;ISS] InterPro:IPR000743 Pfam:PF00295 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005576 EMBL:AL132962 GO:GO:0005975 CAZy:GH28 eggNOG:COG5434 GO:GO:0004650 InterPro:IPR006626 InterPro:IPR012334 InterPro:IPR011050 Gene3D:G3DSA:2.160.20.10 SMART:SM00710 SUPFAM:SSF51126 GO:GO:0007047 HOGENOM:HBG604585 IPI:IPI00527942 PIR:T47941 RefSeq:NP_001190154.1 RefSeq:NP_191708.1

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						RefSeq:NP_974473.1 UniGene:At.43625 ProteinModelPortal:Q9M318 SMR:Q9M318 PRIDE:Q9M318 EnsemblPlants:AT3G61490.1 EnsemblPlants:AT3G61490.2 EnsemblPlants:AT3G61490.3 GeneID:825322 KEGG:ath:AT3G61490 TAIR:At3g61490 InParanoid:Q9M318 OMA:CISPYSA PhylomeDB:Q9M318 ProtClustDB:CLSN2915754 Genevestigator:Q9M318 Uniprot:Q9M318
Root	Isotig02289	18	46	-1.483	9.61E-05	TAIR|locus:2082787 - symbol:AT3G61490 species:3702 "Arabidopsis thaliana" [GO:0004650 "polygalacturonase activity" evidence=IEA;ISS] [GO:0005975 "carbohydrate metabolic process" evidence=IEA;ISS] InterPro:IPR000743 Pfam:PF00295 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005576 EMBL:AL132962 GO:GO:0005975 CAZy:GH28 eggNOG:COG5434 GO:GO:0004650 InterPro:IPR006626 InterPro:IPR012334 InterPro:IPR011050 Gene3D:G3DSA:2.160.20.10 SMART:SM00710 SUPFAM:SSF51126 GO:GO:0007047 HOGENOM:HBG604585 IPI:IPI00527942 PIR:T47941 RefSeq:NP_001190154.1 RefSeq:NP_191708.1 RefSeq:NP_974473.1 UniGene:At.43625 ProteinModelPortal:Q9M318 SMR:Q9M318 PRIDE:Q9M318 EnsemblPlants:AT3G61490.1 EnsemblPlants:AT3G61490.2 EnsemblPlants:AT3G61490.3 GeneID:825322 KEGG:ath:AT3G61490 TAIR:At3g61490 InParanoid:Q9M318 OMA:CISPYSA PhylomeDB:Q9M318 ProtClustDB:CLSN2915754 Genevestigator:Q9M318 Uniprot:Q9M318
Root	Isotig02290	17	45	-1.533	7.67E-05	TAIR|locus:2082787 - symbol:AT3G61490 species:3702 "Arabidopsis thaliana" [GO:0004650 "polygalacturonase activity" evidence=IEA;ISS] [GO:0005975 "carbohydrate metabolic process" evidence=IEA;ISS] InterPro:IPR000743 Pfam:PF00295 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005576 EMBL:AL132962 GO:GO:0005975 CAZy:GH28 eggNOG:COG5434 GO:GO:0004650 InterPro:IPR006626 InterPro:IPR012334 InterPro:IPR011050 Gene3D:G3DSA:2.160.20.10 SMART:SM00710 SUPFAM:SSF51126 GO:GO:0007047 HOGENOM:HBG604585 IPI:IPI00527942 PIR:T47941 RefSeq:NP_001190154.1 RefSeq:NP_191708.1 RefSeq:NP_974473.1 UniGene:At.43625 ProteinModelPortal:Q9M318 SMR:Q9M318 PRIDE:Q9M318 EnsemblPlants:AT3G61490.1 EnsemblPlants:AT3G61490.2 EnsemblPlants:AT3G61490.3 GeneID:825322 KEGG:ath:AT3G61490 TAIR:At3g61490 InParanoid:Q9M318 OMA:CISPYSA PhylomeDB:Q9M318 ProtClustDB:CLSN2915754 Genevestigator:Q9M318 Uniprot:Q9M318
Root	Isotig02291	17	41	-1.399	0.000423111	TAIR|locus:2089668 - symbol:CYP77A5P ""cytochrome P450, family 77, subfamily A, polypeptide 5 pseudogene"" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0008152 "metabolic process" evidence=IEA] [GO:0009507 "chloroplast" evidence=IDA] InterPro:IPR001354 Pfam:PF02746 GO:GO:0009507 GO:GO:0003824 eggNOG:COG4948 InterPro:IPR013342 InterPro:IPR013341 PANTHER:PTHR13794 SMART:SM00922 EMBL:AF370323 EMBL:AY063111 IPI:IPI00548779 RefSeq:NP_566605.1 UniGene:At.22113 UniGene:At.33094 HSSP:O34508 ProteinModelPortal:Q94K39 SMR:Q94K39 STRING:Q94K39 PRIDE:Q94K39 EnsemblPlants:AT3G18270.1 GeneID:821355 KEGG:ath:AT3G18270 TAIR:At3g18270 InParanoid:Q94K39 OMA:LYADANE PhylomeDB:Q94K39 ProtClustDB:CLSN2688525 ArrayExpress:Q94K39 Genevestigator:Q94K39 Uniprot:Q94K39
Root	Isotig02292	17	41	-1.399	0.000423111	TAIR|locus:2089668 - symbol:CYP77A5P ""cytochrome P450, family 77, subfamily A, polypeptide 5 pseudogene"" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0008152 "metabolic process" evidence=IEA] [GO:0009507 "chloroplast" evidence=IDA] InterPro:IPR001354 Pfam:PF02746 GO:GO:0009507 GO:GO:0003824 eggNOG:COG4948 InterPro:IPR013342 InterPro:IPR013341 PANTHER:PTHR13794 SMART:SM00922 EMBL:AF370323 EMBL:AY063111 IPI:IPI00548779 RefSeq:NP_566605.1 UniGene:At.22113 UniGene:At.33094 HSSP:O34508 ProteinModelPortal:Q94K39 SMR:Q94K39 STRING:Q94K39 PRIDE:Q94K39 EnsemblPlants:AT3G18270.1 GeneID:821355 KEGG:ath:AT3G18270 TAIR:At3g18270 InParanoid:Q94K39 OMA:LYADANE PhylomeDB:Q94K39 ProtClustDB:CLSN2688525 ArrayExpress:Q94K39 Genevestigator:Q94K39 Uniprot:Q94K39
Root	Isotig02293	17	41	-1.399	0.000423111	TAIR|locus:2089668 - symbol:CYP77A5P ""cytochrome P450, family 77, subfamily A, polypeptide 5 pseudogene"" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0008152 "metabolic process" evidence=IEA] [GO:0009507 "chloroplast" evidence=IDA] InterPro:IPR001354 Pfam:PF02746 GO:GO:0009507 GO:GO:0003824 eggNOG:COG4948 InterPro:IPR013342 InterPro:IPR013341 PANTHER:PTHR13794 SMART:SM00922 EMBL:AF370323 EMBL:AY063111 IPI:IPI00548779 RefSeq:NP_566605.1 UniGene:At.22113 UniGene:At.33094 HSSP:O34508 ProteinModelPortal:Q94K39 SMR:Q94K39 STRING:Q94K39 PRIDE:Q94K39 EnsemblPlants:AT3G18270.1 GeneID:821355 KEGG:ath:AT3G18270 TAIR:At3g18270 InParanoid:Q94K39 OMA:LYADANE PhylomeDB:Q94K39 ProtClustDB:CLSN2688525 ArrayExpress:Q94K39 Genevestigator:Q94K39 Uniprot:Q94K39

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig02294	16	41	-1.487	0.000224899	TAIR|locus:2089668 - symbol:CYP77A5P ""cytochrome P450, family 77, subfamily A, polypeptide 5 pseudogene"" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0008152 "metabolic process" evidence=IEA] [GO:0009507 "chloroplast" evidence=IDA] InterPro:IPR001354 Pfam:PF02746 GO:GO:0009507 GO:GO:0003824 eggNOG:COG4948 InterPro:IPR013342 InterPro:IPR013341 PANTHER:PTHR13794 SMART:SM00922 EMBL:AF370323 EMBL:AY063111 IPI:IPI00548779 RefSeq:NP_566605.1 UniGene:At.22113 UniGene:At.33094 HSSP:O34508 ProteinModelPortal:Q94K39 SMR:Q94K39 STRING:Q94K39 PRIDE:Q94K39 EnsemblPlants:AT3G18270.1 GeneID:821355 KEGG:ath:AT3G18270 TAIR:At3g18270 InParanoid:Q94K39 OMA:LYADANE PhylomeDB:Q94K39 ProtClustDB:CLSN2688525 ArrayExpress:Q94K39 Genevestigator:Q94K39 Uniprot:Q94K39
Root	Isotig02295	17	41	-1.399	0.000423111	TAIR|locus:2089668 - symbol:CYP77A5P ""cytochrome P450, family 77, subfamily A, polypeptide 5 pseudogene"" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0008152 "metabolic process" evidence=IEA] [GO:0009507 "chloroplast" evidence=IDA] InterPro:IPR001354 Pfam:PF02746 GO:GO:0009507 GO:GO:0003824 eggNOG:COG4948 InterPro:IPR013342 InterPro:IPR013341 PANTHER:PTHR13794 SMART:SM00922 EMBL:AF370323 EMBL:AY063111 IPI:IPI00548779 RefSeq:NP_566605.1 UniGene:At.22113 UniGene:At.33094 HSSP:O34508 ProteinModelPortal:Q94K39 SMR:Q94K39 STRING:Q94K39 PRIDE:Q94K39 EnsemblPlants:AT3G18270.1 GeneID:821355 KEGG:ath:AT3G18270 TAIR:At3g18270 InParanoid:Q94K39 OMA:LYADANE PhylomeDB:Q94K39 ProtClustDB:CLSN2688525 ArrayExpress:Q94K39 Genevestigator:Q94K39 Uniprot:Q94K39
Root	Isotig02296	16	41	-1.487	0.000224899	TAIR|locus:2089668 - symbol:CYP77A5P ""cytochrome P450, family 77, subfamily A, polypeptide 5 pseudogene"" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0008152 "metabolic process" evidence=IEA] [GO:0009507 "chloroplast" evidence=IDA] InterPro:IPR001354 Pfam:PF02746 GO:GO:0009507 GO:GO:0003824 eggNOG:COG4948 InterPro:IPR013342 InterPro:IPR013341 PANTHER:PTHR13794 SMART:SM00922 EMBL:AF370323 EMBL:AY063111 IPI:IPI00548779 RefSeq:NP_566605.1 UniGene:At.22113 UniGene:At.33094 HSSP:O34508 ProteinModelPortal:Q94K39 SMR:Q94K39 STRING:Q94K39 PRIDE:Q94K39 EnsemblPlants:AT3G18270.1 GeneID:821355 KEGG:ath:AT3G18270 TAIR:At3g18270 InParanoid:Q94K39 OMA:LYADANE PhylomeDB:Q94K39 ProtClustDB:CLSN2688525 ArrayExpress:Q94K39 Genevestigator:Q94K39 Uniprot:Q94K39
Root	Isotig02297	10	39	-2.092	5.12E-06	TAIR|locus:2178128 - symbol:ACT7 "AT5G09810" species:3702 "Arabidopsis thaliana" [GO:0007010 "cytoskeleton organization" evidence=TAS] [GO:0009733 "response to auxin stimulus" evidence=IEP] [GO:0009845 "seed germination" evidence=IMP] [GO:0048364 "root development" evidence=IMP] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0010053 "root epidermal cell differentiation" evidence=IMP] [GO:0048767 "root hair elongation" evidence=IMP] [GO:0051301 "cell division" evidence=IMP] [GO:0005515 "protein binding" evidence=IPI] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005200 "structural constituent of cytoskeleton" evidence=ISS] [GO:0005856 "cytoskeleton" evidence=ISS] [GO:0009416 "response to light stimulus" evidence=IEP] [GO:0009611 "response to wounding" evidence=IEP] InterPro:IPR004001 PROSITE:PS00406 PROSITE:PS00432 InterPro:IPR004000 GO:GO:0005829 GO:GO:0005739 GO:GO:0005886 GO:GO:0009506 GO:GO:0005524 GO:GO:0009570 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005618 GO:GO:0005515 GO:GO:0009733 GO:GO:0009611 GO:GO:0005730 GO:GO:0005856 GO:GO:0051301 GO:GO:0009941 EMBL:AB016893 GO:GO:0048767 GO:GO:0009845 GO:GO:0009416 HOGENOM:HBG559892 PANTHER:PTHR11937 Pfam:PF00022 PRINTS:PR00190 SMART:SM00268 KO:K10355 InterPro:IPR020902 PROSITE:PS01132 ProtClustDB:CLSN2682469 UniGene:At.23346 EMBL:U37281 EMBL:U27811 EMBL:AY062702 EMBL:AY063980 EMBL:AY096397 EMBL:AY114679 EMBL:AY120779 IPI:IPI00524611 PIR:S68107 RefSeq:NP_196543.1 UniGene:At.23605 UniGene:At.24396 ProteinModelPortal:P53492 SMR:P53492 IntAct:P53492 STRING:P53492 PRIDE:P53492 ProMEX:P53492 EnsemblPlants:AT5G09810.1 GeneID:830841 KEGG:ath:AT5G09810 TAIR:At5g09810 InParanoid:P53492 OMA:NSICVIL PhylomeDB:P53492 ArrayExpress:P53492 Genevestigator:P53492 GermOnline:AT5G09810 Uniprot:P53492
Root	Isotig02298	13	40	-1.750	4.15E-05	TAIR|locus:2178128 - symbol:ACT7 "AT5G09810" species:3702 "Arabidopsis thaliana" [GO:0007010 "cytoskeleton organization" evidence=TAS] [GO:0009733 "response to auxin stimulus" evidence=IEP] [GO:0009845 "seed germination" evidence=IMP] [GO:0048364 "root development" evidence=IMP] [GO:0005739 "mitochondrion"

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						evidence=IDA] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0010053 "root epidermal cell differentiation" evidence=IMP] [GO:0048767 "root hair elongation" evidence=IMP] [GO:0051301 "cell division" evidence=IMP] [GO:0005515 "protein binding" evidence=IPI] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005200 "structural constituent of cytoskeleton" evidence=ISS] [GO:0005856 "cytoskeleton" evidence=ISS] [GO:0009416 "response to light stimulus" evidence=IEP] [GO:0009611 "response to wounding" evidence=IEP] InterPro:IPR004001 PROSITE:PS00406 PROSITE:PS00432 InterPro:IPR004000 GO:GO:0005829 GO:GO:0005739 GO:GO:0005886 GO:GO:0009506 GO:GO:0005524 GO:GO:0009570 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005618 GO:GO:0005515 GO:GO:0009733 GO:GO:0009611 GO:GO:0005730 GO:GO:0005856 GO:GO:0051301 GO:GO:0009941 EMBL:AB016893 GO:GO:0048767 GO:GO:0009845 GO:GO:0009416 HOGENOM:HBG559892 PANTHER:PTHR11937 Pfam:PF00022 PRINTS:PR00190 SMART:SM00268 KO:K10355 InterPro:IPR020902 PROSITE:PS01132 ProtClustDB:CLSN2682469 UniGene:At.23346 EMBL:U37281 EMBL:U27811 EMBL:AY062702 EMBL:AY063980 EMBL:AY096397 EMBL:AY114679 EMBL:AY120779 IPI:IPI00524611 PIR:S68107 RefSeq:NP_196543.1 UniGene:At.23605 UniGene:At.24396 ProteinModelPortal:P53492 SMR:P53492 IntAct:P53492 STRING:P53492 PRIDE:P53492 ProMEX:P53492 EnsemblPlants:AT5G09810.1 GeneID:830841 KEGG:ath:AT5G09810 TAIR:At5g09810 InParanoid:P53492 OMA:NSICVIL PhylomeDB:P53492 ArrayExpress:P53492 Genevestigator:P53492 GermOnline:AT5G09810 Uniprot:P53492
Root	Isotig02299	10	39	-2.092	5.12E-06	TAIR|locus:2178128 - symbol:ACT7 "AT5G09810" species:3702 "Arabidopsis thaliana" [GO:0007010 "cytoskeleton organization" evidence=TAS] [GO:0009733 "response to auxin stimulus" evidence=IEP] [GO:0009845 "seed germination" evidence=IMP] [GO:0048364 "root development" evidence=IMP] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0010053 "root epidermal cell differentiation" evidence=IMP] [GO:0048767 "root hair elongation" evidence=IMP] [GO:0051301 "cell division" evidence=IMP] [GO:0005515 "protein binding" evidence=IPI] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005200 "structural constituent of cytoskeleton" evidence=ISS] [GO:0005856 "cytoskeleton" evidence=ISS] [GO:0009416 "response to light stimulus" evidence=IEP] [GO:0009611 "response to wounding" evidence=IEP] InterPro:IPR004001 PROSITE:PS00406 PROSITE:PS00432 InterPro:IPR004000 GO:GO:0005829 GO:GO:0005739 GO:GO:0005886 GO:GO:0009506 GO:GO:0005524 GO:GO:0009570 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005618 GO:GO:0005515 GO:GO:0009733 GO:GO:0009611 GO:GO:0005730 GO:GO:0005856 GO:GO:0051301 GO:GO:0009941 EMBL:AB016893 GO:GO:0048767 GO:GO:0009845 GO:GO:0009416 HOGENOM:HBG559892 PANTHER:PTHR11937 Pfam:PF00022 PRINTS:PR00190 SMART:SM00268 KO:K10355 InterPro:IPR020902 PROSITE:PS01132 ProtClustDB:CLSN2682469 UniGene:At.23346 EMBL:U37281 EMBL:U27811 EMBL:AY062702 EMBL:AY063980 EMBL:AY096397 EMBL:AY114679 EMBL:AY120779 IPI:IPI00524611 PIR:S68107 RefSeq:NP_196543.1 UniGene:At.23605 UniGene:At.24396 ProteinModelPortal:P53492 SMR:P53492 IntAct:P53492 STRING:P53492 PRIDE:P53492 ProMEX:P53492 EnsemblPlants:AT5G09810.1 GeneID:830841 KEGG:ath:AT5G09810 TAIR:At5g09810 InParanoid:P53492 OMA:NSICVIL PhylomeDB:P53492 ArrayExpress:P53492 Genevestigator:P53492 GermOnline:AT5G09810 Uniprot:P53492
Root	Isotig02300	13	40	-1.750	4.15E-05	TAIR|locus:2178128 - symbol:ACT7 "AT5G09810" species:3702 "Arabidopsis thaliana" [GO:0007010 "cytoskeleton organization" evidence=TAS] [GO:0009733 "response to auxin stimulus" evidence=IEP] [GO:0009845 "seed germination" evidence=IMP] [GO:0048364 "root development" evidence=IMP] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0010053 "root epidermal cell differentiation" evidence=IMP] [GO:0048767 "root hair elongation" evidence=IMP] [GO:0051301 "cell division" evidence=IMP] [GO:0005515 "protein binding" evidence=IPI] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005200 "structural constituent of cytoskeleton" evidence=ISS] [GO:0005856 "cytoskeleton" evidence=ISS] [GO:0009416 "response to light stimulus" evidence=IEP] [GO:0009611 "response to wounding" evidence=IEP] InterPro:IPR004001 PROSITE:PS00406 PROSITE:PS00432 InterPro:IPR004000 GO:GO:0005829 GO:GO:0005739 GO:GO:0005886 GO:GO:0009506 GO:GO:0005524 GO:GO:0009570 EMBL:CP002688 GenomeReviews:BA000015_GR

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0005618 GO:GO:0005515 GO:GO:0009733 GO:GO:0009611 GO:GO:0005730 GO:GO:0005856 GO:GO:0051301 GO:GO:0009941 EMBL:AB016893 GO:GO:0048767 GO:GO:0009845 GO:GO:0009416 HOGENOM:HBG559892 PANTHER:PTHR11937 Pfam:PF00022 PRINTS:PR00190 SMART:SM00268 KO:K10355 InterPro:IPR020902 PROSITE:PS01132 ProtClustDB:CLSN2682469 UniGene:At.23346 EMBL:U37281 EMBL:U27811 EMBL:AY062702 EMBL:AY063980 EMBL:AY096397 EMBL:AY114679 EMBL:AY120779 IPI:IPI00524611 PIR:S68107 RefSeq:NP_196543.1 UniGene:At.23605 UniGene:At.24396 ProteinModelPortal:P53492 SMR:P53492 IntAct:P53492 STRING:P53492 PRIDE:P53492 ProMEX:P53492 EnsemblPlants:AT5G09810.1 GeneID:830841 KEGG:ath:AT5G09810 TAIR:At5g09810 InParanoid:P53492 OMA:NSICVIL PhylomeDB:P53492 ArrayExpress:P53492 Genevestigator:P53492 GermOnline:AT5G09810 Uniprot:P53492
Root	Isotig02301	9	40	-2.281	1.10E-06	TAIR|locus:2178128 - symbol:ACT7 "AT5G09810" species:3702 "Arabidopsis thaliana" [GO:0007010 "cytoskeleton organization" evidence=TAS] [GO:0009733 "response to auxin stimulus" evidence=IEP] [GO:0009845 "seed germination" evidence=IMP] [GO:0048364 "root development" evidence=IMP] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0010053 "root epidermal cell differentiation" evidence=IMP] [GO:0048767 "root hair elongation" evidence=IMP] [GO:0051301 "cell division" evidence=IMP] [GO:0005515 "protein binding" evidence=IPI] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005200 "structural constituent of cytoskeleton" evidence=ISS] [GO:0005856 "cytoskeleton" evidence=ISS] [GO:0009416 "response to light stimulus" evidence=IEP] [GO:0009611 "response to wounding" evidence=IEP] InterPro:IPR004001 PROSITE:PS00406 PROSITE:PS00432 InterPro:IPR004000 GO:GO:0005829 GO:GO:0005739 GO:GO:0005886 GO:GO:0009506 GO:GO:0005524 GO:GO:0009570 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005618 GO:GO:0005515 GO:GO:0009733 GO:GO:0009611 GO:GO:0005730 GO:GO:0005856 GO:GO:0051301 GO:GO:0009941 EMBL:AB016893 GO:GO:0048767 GO:GO:0009845 GO:GO:0009416 HOGENOM:HBG559892 PANTHER:PTHR11937 Pfam:PF00022 PRINTS:PR00190 SMART:SM00268 KO:K10355 InterPro:IPR020902 PROSITE:PS01132 ProtClustDB:CLSN2682469 UniGene:At.23346 EMBL:U37281 EMBL:U27811 EMBL:AY062702 EMBL:AY063980 EMBL:AY096397 EMBL:AY114679 EMBL:AY120779 IPI:IPI00524611 PIR:S68107 RefSeq:NP_196543.1 UniGene:At.23605 UniGene:At.24396 ProteinModelPortal:P53492 SMR:P53492 IntAct:P53492 STRING:P53492 PRIDE:P53492 ProMEX:P53492 EnsemblPlants:AT5G09810.1 GeneID:830841 KEGG:ath:AT5G09810 TAIR:At5g09810 InParanoid:P53492 OMA:NSICVIL PhylomeDB:P53492 ArrayExpress:P53492 Genevestigator:P53492 GermOnline:AT5G09810 Uniprot:P53492
Root	Isotig02302	9	40	-2.281	1.10E-06	TAIR|locus:2178128 - symbol:ACT7 "AT5G09810" species:3702 "Arabidopsis thaliana" [GO:0007010 "cytoskeleton organization" evidence=TAS] [GO:0009733 "response to auxin stimulus" evidence=IEP] [GO:0009845 "seed germination" evidence=IMP] [GO:0048364 "root development" evidence=IMP] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0010053 "root epidermal cell differentiation" evidence=IMP] [GO:0048767 "root hair elongation" evidence=IMP] [GO:0051301 "cell division" evidence=IMP] [GO:0005515 "protein binding" evidence=IPI] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005200 "structural constituent of cytoskeleton" evidence=ISS] [GO:0005856 "cytoskeleton" evidence=ISS] [GO:0009416 "response to light stimulus" evidence=IEP] [GO:0009611 "response to wounding" evidence=IEP] InterPro:IPR004001 PROSITE:PS00406 PROSITE:PS00432 InterPro:IPR004000 GO:GO:0005829 GO:GO:0005739 GO:GO:0005886 GO:GO:0009506 GO:GO:0005524 GO:GO:0009570 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005618 GO:GO:0005515 GO:GO:0009733 GO:GO:0009611 GO:GO:0005730 GO:GO:0005856 GO:GO:0051301 GO:GO:0009941 EMBL:AB016893 GO:GO:0048767 GO:GO:0009845 GO:GO:0009416 HOGENOM:HBG559892 PANTHER:PTHR11937 Pfam:PF00022 PRINTS:PR00190 SMART:SM00268 KO:K10355 InterPro:IPR020902 PROSITE:PS01132 ProtClustDB:CLSN2682469 UniGene:At.23346 EMBL:U37281 EMBL:U27811 EMBL:AY062702 EMBL:AY063980 EMBL:AY096397 EMBL:AY114679 EMBL:AY120779 IPI:IPI00524611 PIR:S68107 RefSeq:NP_196543.1 UniGene:At.23605 UniGene:At.24396 ProteinModelPortal:P53492 SMR:P53492 IntAct:P53492 STRING:P53492 PRIDE:P53492 ProMEX:P53492 EnsemblPlants:AT5G09810.1 GeneID:830841 KEGG:ath:AT5G09810 TAIR:At5g09810 InParanoid:P53492

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						OMA:NSICVIL PhylomeDB:P53492 ArrayExpress:P53492 Genevestigator:P53492 GermOnline:AT5G09810 Uniprot:P53492
Root	Isotig02357	14	36	-1.492	0.000528966	TAIR|locus:2012572 - symbol:MIOX1 "myo-inositol oxygenase 1" species:3702 "Arabidopsis thaliana" [GO:0005737 "cytoplasm" evidence=IEA] [GO:0016491 "oxidoreductase activity" evidence=ISS] [GO:0050113 "inositol oxygenase activity" evidence=IMP] [GO:0006949 "syncytium formation" evidence=IGI] InterPro:IPR007828 Pfam:PF05153 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005737 GO:GO:0005506 EMBL:AC010657 EMBL:AC012188 GO:GO:0006949 GO:GO:0019853 GO:GO:0019310 EMBL:AY136388 EMBL:BT000187 EMBL:AK118307 EMBL:AK175115 EMBL:AK175818 EMBL:AK175833 EMBL:AK176690 EMBL:AK221931 IPI:IPI00531494 RefSeq:NP_172904.2 UniGene:At.23143 ProteinModelPortal:Q8L799 SMR:Q8L799 PRIDE:Q8L799 EnsemblPlants:AT1G14520.1 GeneID:838014 KEGG:ath:AT1G14520 TAIR:At1g14520 eggNOG:NOG135479 HOGENOM:HBG332059 InParanoid:Q8L799 KO:K00469 OMA:CELLNEF PhylomeDB:Q8L799 ProtClustDB:CLSN2687348 BioCyc:MetaCyc:AT1G14520-MONOMER Genevestigator:Q8L799 GO:GO:0050113 PANTHER:PTHR12588 Uniprot:Q8L799
Root	Isotig02358	14	36	-1.492	0.000528966	TAIR|locus:2012572 - symbol:MIOX1 "myo-inositol oxygenase 1" species:3702 "Arabidopsis thaliana" [GO:0005737 "cytoplasm" evidence=IEA] [GO:0016491 "oxidoreductase activity" evidence=ISS] [GO:0050113 "inositol oxygenase activity" evidence=IMP] [GO:0006949 "syncytium formation" evidence=IGI] InterPro:IPR007828 Pfam:PF05153 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005737 GO:GO:0005506 EMBL:AC010657 EMBL:AC012188 GO:GO:0006949 GO:GO:0019853 GO:GO:0019310 EMBL:AY136388 EMBL:BT000187 EMBL:AK118307 EMBL:AK175115 EMBL:AK175818 EMBL:AK175833 EMBL:AK176690 EMBL:AK221931 IPI:IPI00531494 RefSeq:NP_172904.2 UniGene:At.23143 ProteinModelPortal:Q8L799 SMR:Q8L799 PRIDE:Q8L799 EnsemblPlants:AT1G14520.1 GeneID:838014 KEGG:ath:AT1G14520 TAIR:At1g14520 eggNOG:NOG135479 HOGENOM:HBG332059 InParanoid:Q8L799 KO:K00469 OMA:CELLNEF PhylomeDB:Q8L799 ProtClustDB:CLSN2687348 BioCyc:MetaCyc:AT1G14520-MONOMER Genevestigator:Q8L799 GO:GO:0050113 PANTHER:PTHR12588 Uniprot:Q8L799
Root	Isotig02359	14	37	-1.531	0.000341051	TAIR|locus:2012572 - symbol:MIOX1 "myo-inositol oxygenase 1" species:3702 "Arabidopsis thaliana" [GO:0005737 "cytoplasm" evidence=IEA] [GO:0016491 "oxidoreductase activity" evidence=ISS] [GO:0050113 "inositol oxygenase activity" evidence=IMP] [GO:0006949 "syncytium formation" evidence=IGI] InterPro:IPR007828 Pfam:PF05153 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005737 GO:GO:0005506 EMBL:AC010657 EMBL:AC012188 GO:GO:0006949 GO:GO:0019853 GO:GO:0019310 EMBL:AY136388 EMBL:BT000187 EMBL:AK118307 EMBL:AK175115 EMBL:AK175818 EMBL:AK175833 EMBL:AK176690 EMBL:AK221931 IPI:IPI00531494 RefSeq:NP_172904.2 UniGene:At.23143 ProteinModelPortal:Q8L799 SMR:Q8L799 PRIDE:Q8L799 EnsemblPlants:AT1G14520.1 GeneID:838014 KEGG:ath:AT1G14520 TAIR:At1g14520 eggNOG:NOG135479 HOGENOM:HBG332059 InParanoid:Q8L799 KO:K00469 OMA:CELLNEF PhylomeDB:Q8L799 ProtClustDB:CLSN2687348 BioCyc:MetaCyc:AT1G14520-MONOMER Genevestigator:Q8L799 GO:GO:0050113 PANTHER:PTHR12588 Uniprot:Q8L799
Root	Isotig02360	14	37	-1.531	0.000341051	TAIR|locus:2012572 - symbol:MIOX1 "myo-inositol oxygenase 1" species:3702 "Arabidopsis thaliana" [GO:0005737 "cytoplasm" evidence=IEA] [GO:0016491 "oxidoreductase activity" evidence=ISS] [GO:0050113 "inositol oxygenase activity" evidence=IMP] [GO:0006949 "syncytium formation" evidence=IGI] InterPro:IPR007828 Pfam:PF05153 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005737 GO:GO:0005506 EMBL:AC010657 EMBL:AC012188 GO:GO:0006949 GO:GO:0019853 GO:GO:0019310 EMBL:AY136388 EMBL:BT000187 EMBL:AK118307 EMBL:AK175115 EMBL:AK175818 EMBL:AK175833 EMBL:AK176690 EMBL:AK221931 IPI:IPI00531494 RefSeq:NP_172904.2 UniGene:At.23143 ProteinModelPortal:Q8L799 SMR:Q8L799 PRIDE:Q8L799 EnsemblPlants:AT1G14520.1 GeneID:838014 KEGG:ath:AT1G14520 TAIR:At1g14520 eggNOG:NOG135479 HOGENOM:HBG332059 InParanoid:Q8L799 KO:K00469 OMA:CELLNEF PhylomeDB:Q8L799 ProtClustDB:CLSN2687348 BioCyc:MetaCyc:AT1G14520-MONOMER Genevestigator:Q8L799 GO:GO:0050113 PANTHER:PTHR12588 Uniprot:Q8L799
Root	Isotig02361	14	36	-1.492	0.000528966	TAIR|locus:2012572 - symbol:MIOX1 "myo-inositol oxygenase 1" species:3702 "Arabidopsis thaliana" [GO:0005737 "cytoplasm" evidence=IEA] [GO:0016491 "oxidoreductase activity" evidence=ISS] [GO:0050113 "inositol oxygenase activity" evidence=IMP] [GO:0006949 "syncytium formation" evidence=IGI] InterPro:IPR007828 Pfam:PF05153 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005737 GO:GO:0005506 EMBL:AC010657 EMBL:AC012188 GO:GO:0006949 GO:GO:0019853 GO:GO:0019310 EMBL:AY136388 EMBL:BT000187 EMBL:AK118307 EMBL:AK175115 EMBL:AK175818 EMBL:AK175833 EMBL:AK176690 EMBL:AK221931

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						IPI:IPI00531494 RefSeq:NP_172904.2 UniGene:At.23143 ProteinModelPortal:Q8L799 SMR:Q8L799 PRIDE:Q8L799 EnsemblPlants:AT1G14520.1 GeneID:838014 KEGG:ath:AT1G14520 TAIR:At1g14520 eggNOG:NOG135479 HOGENOM:HBG332059 InParanoid:Q8L799 KO:K00469 OMA:CELLNEF PhylomeDB:Q8L799 ProtClustDB:CLSN2687348 BioCyc:MetaCyc:AT1G14520-MONOMER Genevestigator:Q8L799 GO:GO:0050113 PANTHER:PTHR12588 Uniprot:Q8L799
Root	Isotig02362	14	36	-1.492	0.000528966	TAIR|locus:2012572 - symbol:MIOX1 "myo-inositol oxygenase 1" species:3702 "Arabidopsis thaliana" [GO:0005737 "cytoplasm" evidence=IEA] [GO:0016491 "oxidoreductase activity" evidence=ISS] [GO:0050113 "inositol oxygenase activity" evidence=IMP] [GO:0006949 "syncytium formation" evidence=IGI] InterPro:IPR007828 Pfam:PF05153 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005737 GO:GO:0005506 EMBL:AC010657 EMBL:AC012188 GO:GO:0006949 GO:GO:0019853 GO:GO:0019310 EMBL:AY136388 EMBL:BT000187 EMBL:AK118307 EMBL:AK175115 EMBL:AK175818 EMBL:AK175833 EMBL:AK176690 EMBL:AK221931 IPI:IPI00531494 RefSeq:NP_172904.2 UniGene:At.23143 ProteinModelPortal:Q8L799 SMR:Q8L799 PRIDE:Q8L799 EnsemblPlants:AT1G14520.1 GeneID:838014 KEGG:ath:AT1G14520 TAIR:At1g14520 eggNOG:NOG135479 HOGENOM:HBG332059 InParanoid:Q8L799 KO:K00469 OMA:CELLNEF PhylomeDB:Q8L799 ProtClustDB:CLSN2687348 BioCyc:MetaCyc:AT1G14520-MONOMER Genevestigator:Q8L799 GO:GO:0050113 PANTHER:PTHR12588 Uniprot:Q8L799
Root	Isotig02387	2	20	-3.451	2.08E-05	TAIR|locus:2195341 - symbol:AT1G09200 species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=IEA;ISS] [GO:0006334 "nucleosome assembly" evidence=IEA] [GO:0005515 "protein binding" evidence=IPI] InterPro:IPR000164 InterPro:IPR007125 InterPro:IPR009072 Pfam:PF00125 PRINTS:PR00622 PROSITE:PS00322 PROSITE:PS00959 SMART:SM00428 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005634 EMBL:CP002688 GenomeReviews:BA000015_GR EMBL:AL353995 EMBL:CP002686 GenomeReviews:BA000014_GR EMBL:AB011479 GO:GO:0005515 GO:GO:0003677 Gene3D:G3DSA:1.10.20.10 SUPFAM:SSF47113 GO:GO:0006334 UniGene:At.1824 GO:GO:0000786 EMBL:AC003114 eggNOG:COG2036 PANTHER:PTHR11426 HOGENOM:HBG715487 EMBL:AB024028 UniGene:At.17610 UniGene:At.22540 UniGene:At.32384 UniGene:At.71559 KO:K11253 OMA:DLRFQSQ EMBL:M35387 EMBL:M17131 EMBL:M17130 EMBL:AK117157 EMBL:AF370577 EMBL:AY037250 EMBL:AY039904 EMBL:AY077654 EMBL:AY081741 EMBL:BT003051 EMBL:BT003162 EMBL:BT005805 EMBL:BT006068 EMBL:AY084316 IPI:IPI00517184 PIR:S06250 RefSeq:NP_189372.1 RefSeq:NP_201339.1 RefSeq:NP_563838.1 RefSeq:NP_568227.1 RefSeq:NP_568228.1 UniGene:At.20804 UniGene:At.21310 UniGene:At.21486 UniGene:At.63772 UniGene:At.73076 ProteinModelPortal:P59226 SMR:P59226 DIP:DIP-48531N STRING:P59226 PRIDE:P59226 EnsemblPlants:AT1G09200.1 EnsemblPlants:AT3G27360.1 EnsemblPlants:AT5G10390.1 EnsemblPlants:AT5G10400.1 EnsemblPlants:AT5G65360.1 GeneID:822357 GeneID:830903 GeneID:830904 GeneID:836661 GeneID:837440 KEGG:ath:AT1G09200 KEGG:ath:AT3G27360 KEGG:ath:AT5G10390 KEGG:ath:AT5G10400 KEGG:ath:AT5G65360 TAIR:At1g09200 TAIR:At3g27360 TAIR:At5g10390 TAIR:At5g10400 TAIR:At5g65360 InParanoid:P59226 PhylomeDB:P59226 ProtClustDB:PLN00121 ArrayExpress:P59226 Genevestigator:P59226 GermOnline:AT1G09200 Uniprot:P59226
Root	Isotig02388	2	20	-3.451	2.08E-05	TAIR|locus:2195341 - symbol:AT1G09200 species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=IEA;ISS] [GO:0006334 "nucleosome assembly" evidence=IEA] [GO:0005515 "protein binding" evidence=IPI] InterPro:IPR000164 InterPro:IPR007125 InterPro:IPR009072 Pfam:PF00125 PRINTS:PR00622 PROSITE:PS00322 PROSITE:PS00959 SMART:SM00428 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005634 EMBL:CP002688 GenomeReviews:BA000015_GR EMBL:AL353995 EMBL:CP002686 GenomeReviews:BA000014_GR EMBL:AB011479 GO:GO:0005515 GO:GO:0003677 Gene3D:G3DSA:1.10.20.10 SUPFAM:SSF47113 GO:GO:0006334 UniGene:At.1824 GO:GO:0000786 EMBL:AC003114 eggNOG:COG2036 PANTHER:PTHR11426 HOGENOM:HBG715487 EMBL:AB024028 UniGene:At.17610 UniGene:At.22540 UniGene:At.32384 UniGene:At.71559 KO:K11253 OMA:DLRFQSQ EMBL:M35387 EMBL:M17131 EMBL:M17130 EMBL:AK117157 EMBL:AF370577 EMBL:AY037250 EMBL:AY039904 EMBL:AY077654 EMBL:AY081741 EMBL:BT003051 EMBL:BT003162 EMBL:BT005805 EMBL:BT006068 EMBL:AY084316 IPI:IPI00517184 PIR:S06250 RefSeq:NP_189372.1 RefSeq:NP_201339.1 RefSeq:NP_563838.1 RefSeq:NP_568227.1 RefSeq:NP_568228.1 UniGene:At.20804 UniGene:At.21310 UniGene:At.21486 UniGene:At.63772 UniGene:At.73076 ProteinModelPortal:P59226 SMR:P59226 DIP:DIP-48531N STRING:P59226 PRIDE:P59226 EnsemblPlants:AT1G09200.1 EnsemblPlants:AT3G27360.1 EnsemblPlants:AT5G10390.1 EnsemblPlants:AT5G10400.1 EnsemblPlants:AT5G65360.1 GeneID:822357 GeneID:830903 GeneID:830904

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GeneID:836661 GeneID:837440 KEGG:ath:AT1G09200 KEGG:ath:AT3G27360 KEGG:ath:AT5G10390 KEGG:ath:AT5G10400 KEGG:ath:AT5G65360 TAIR:At1g09200 TAIR:At3g27360 TAIR:At5g10390 TAIR:At5g10400 TAIR:At5g65360 InParanoid:P59226 PhylomeDB:P59226 ProtClustDB:PLN00121 ArrayExpress:P59226 Genevestigator:P59226 GermOnline:AT1G09200 Uniprot:P59226
Root	Isotig02389	1	20	-4.451	3.92E-06	TAIR|locus:2195341 - symbol:AT1G09200 species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=IEA;ISS] [GO:0006334 "nucleosome assembly" evidence=IEA] [GO:0005515 "protein binding" evidence=IPI] InterPro:IPR000164 InterPro:IPR007125 InterPro:IPR009072 Pfam:PF00125 PRINTS:PR00622 PROSITE:PS00322 PROSITE:PS00959 SMART:SM00428 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005634 EMBL:CP002688 GenomeReviews:BA000015_GR EMBL:AL353995 EMBL:CP002686 GenomeReviews:BA000014_GR EMBL:AB011479 GO:GO:0005515 GO:GO:0003677 Gene3D:G3DSA:1.10.20.10 SUPFAM:SSF47113 GO:GO:0006334 UniGene:At.1824 GO:GO:0000786 EMBL:AC003114 eggNOG:COG2036 PANTHER:PTHR11426 HOGENOM:HBG715487 EMBL:AB024028 UniGene:At.17610 UniGene:At.22540 UniGene:At.32384 UniGene:At.71559 KO:K11253 OMA:DLRFQSQ EMBL:M35387 EMBL:M17131 EMBL:M17130 EMBL:AK117157 EMBL:AF370577 EMBL:AY037250 EMBL:AY039904 EMBL:AY077654 EMBL:AY081741 EMBL:BT003051 EMBL:BT003162 EMBL:BT005805 EMBL:BT006068 EMBL:AY084316 IPI:IPI00517184 PIR:S06250 RefSeq:NP_189372.1 RefSeq:NP_201339.1 RefSeq:NP_563838.1 RefSeq:NP_568227.1 RefSeq:NP_568228.1 UniGene:At.20804 UniGene:At.21310 UniGene:At.21486 UniGene:At.63772 UniGene:At.73076 ProteinModelPortal:P59226 SMR:P59226 DIP:DIP-48531N STRING:P59226 PRIDE:P59226 EnsemblPlants:AT1G09200.1 EnsemblPlants:AT3G27360.1 EnsemblPlants:AT5G10390.1 EnsemblPlants:AT5G10400.1 EnsemblPlants:AT5G65360.1 GeneID:822357 GeneID:830903 GeneID:830904 GeneID:836661 GeneID:837440 KEGG:ath:AT1G09200 KEGG:ath:AT3G27360 KEGG:ath:AT5G10390 KEGG:ath:AT5G10400 KEGG:ath:AT5G65360 TAIR:At1g09200 TAIR:At3g27360 TAIR:At5g10390 TAIR:At5g10400 TAIR:At5g65360 InParanoid:P59226 PhylomeDB:P59226 ProtClustDB:PLN00121 ArrayExpress:P59226 Genevestigator:P59226 GermOnline:AT1G09200 Uniprot:P59226
Root	Isotig02390	1	20	-4.451	3.92E-06	TAIR|locus:2195341 - symbol:AT1G09200 species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=IEA;ISS] [GO:0006334 "nucleosome assembly" evidence=IEA] [GO:0005515 "protein binding" evidence=IPI] InterPro:IPR000164 InterPro:IPR007125 InterPro:IPR009072 Pfam:PF00125 PRINTS:PR00622 PROSITE:PS00322 PROSITE:PS00959 SMART:SM00428 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005634 EMBL:CP002688 GenomeReviews:BA000015_GR EMBL:AL353995 EMBL:CP002686 GenomeReviews:BA000014_GR EMBL:AB011479 GO:GO:0005515 GO:GO:0003677 Gene3D:G3DSA:1.10.20.10 SUPFAM:SSF47113 GO:GO:0006334 UniGene:At.1824 GO:GO:0000786 EMBL:AC003114 eggNOG:COG2036 PANTHER:PTHR11426 HOGENOM:HBG715487 EMBL:AB024028 UniGene:At.17610 UniGene:At.22540 UniGene:At.32384 UniGene:At.71559 KO:K11253 OMA:DLRFQSQ EMBL:M35387 EMBL:M17131 EMBL:M17130 EMBL:AK117157 EMBL:AF370577 EMBL:AY037250 EMBL:AY039904 EMBL:AY077654 EMBL:AY081741 EMBL:BT003051 EMBL:BT003162 EMBL:BT005805 EMBL:BT006068 EMBL:AY084316 IPI:IPI00517184 PIR:S06250 RefSeq:NP_189372.1 RefSeq:NP_201339.1 RefSeq:NP_563838.1 RefSeq:NP_568227.1 RefSeq:NP_568228.1 UniGene:At.20804 UniGene:At.21310 UniGene:At.21486 UniGene:At.63772 UniGene:At.73076 ProteinModelPortal:P59226 SMR:P59226 DIP:DIP-48531N STRING:P59226 PRIDE:P59226 EnsemblPlants:AT1G09200.1 EnsemblPlants:AT3G27360.1 EnsemblPlants:AT5G10390.1 EnsemblPlants:AT5G10400.1 EnsemblPlants:AT5G65360.1 GeneID:822357 GeneID:830903 GeneID:830904 GeneID:836661 GeneID:837440 KEGG:ath:AT1G09200 KEGG:ath:AT3G27360 KEGG:ath:AT5G10390 KEGG:ath:AT5G10400 KEGG:ath:AT5G65360 TAIR:At1g09200 TAIR:At3g27360 TAIR:At5g10390 TAIR:At5g10400 TAIR:At5g65360 InParanoid:P59226 PhylomeDB:P59226 ProtClustDB:PLN00121 ArrayExpress:P59226 Genevestigator:P59226 GermOnline:AT1G09200 Uniprot:P59226
Root	Isotig02391	1	20	-4.451	3.92E-06	TAIR|locus:2195341 - symbol:AT1G09200 species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=IEA;ISS] [GO:0006334 "nucleosome assembly" evidence=IEA] [GO:0005515 "protein binding" evidence=IPI] InterPro:IPR000164 InterPro:IPR007125 InterPro:IPR009072 Pfam:PF00125 PRINTS:PR00622 PROSITE:PS00322 PROSITE:PS00959 SMART:SM00428 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005634 EMBL:CP002688 GenomeReviews:BA000015_GR EMBL:AL353995 EMBL:CP002686 GenomeReviews:BA000014_GR EMBL:AB011479 GO:GO:0005515 GO:GO:0003677 Gene3D:G3DSA:1.10.20.10 SUPFAM:SSF47113 GO:GO:0006334 UniGene:At.1824 GO:GO:0000786 EMBL:AC003114 eggNOG:COG2036 PANTHER:PTHR11426 HOGENOM:HBG715487 EMBL:AB024028 UniGene:At.17610 UniGene:At.22540

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						UniGene:At.32384 UniGene:At.71559 KO:K11253 OMA:DLRFQSQ EMBL:M35387 EMBL:M17131 EMBL:M17130 EMBL:AK117157 EMBL:AF370577 EMBL:AY037250 EMBL:AY039904 EMBL:AY077654 EMBL:AY081741 EMBL:BT003051 EMBL:BT003162 EMBL:BT005805 EMBL:BT006068 EMBL:AY084316 IPI:IPI00517184 PIR:S06250 RefSeq:NP_189372.1 RefSeq:NP_201339.1 RefSeq:NP_563838.1 RefSeq:NP_568227.1 RefSeq:NP_568228.1 UniGene:At.20804 UniGene:At.21310 UniGene:At.21486 UniGene:At.63772 UniGene:At.73076 ProteinModelPortal:P59226 SMR:P59226 DIP:DIP-48531N STRING:P59226 PRIDE:P59226 EnsemblPlants:AT1G09200.1 EnsemblPlants:AT3G27360.1 EnsemblPlants:AT5G10390.1 EnsemblPlants:AT5G10400.1 EnsemblPlants:AT5G65360.1 GeneID:822357 GeneID:830903 GeneID:830904 GeneID:836661 GeneID:837440 KEGG:ath:AT1G09200 KEGG:ath:AT3G27360 KEGG:ath:AT5G10390 KEGG:ath:AT5G10400 KEGG:ath:AT5G65360 TAIR:At1g09200 TAIR:At3g27360 TAIR:At5g10390 TAIR:At5g10400 TAIR:At5g65360 InParanoid:P59226 PhylomeDB:P59226 ProtClustDB:PLN00121 ArrayExpress:P59226 Genevestigator:P59226 GermOnline:AT1G09200 Uniprot:P59226
Root	Isotig02392	1	20	-4.451	3.92E-06	TAIR|locus:2195341 - symbol:AT1G09200 species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=IEA;ISS] [GO:0006334 "nucleosome assembly" evidence=IEA] [GO:0005515 "protein binding" evidence=IPI] InterPro:IPR000164 InterPro:IPR007125 InterPro:IPR009072 Pfam:PF00125 PRINTS:PR00622 PROSITE:PS00322 PROSITE:PS00959 SMART:SM00428 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005634 EMBL:CP002688 GenomeReviews:BA000015_GR EMBL:AL353995 EMBL:CP002686 GenomeReviews:BA000014_GR EMBL:AB011479 GO:GO:0005515 GO:GO:0003677 Gene3D:G3DSA:1.10.20.10 SUPFAM:SSF47113 GO:GO:0006334 UniGene:At.1824 GO:GO:0000786 EMBL:AC003114 eggNOG:COG2036 PANTHER:PTHR11426 HOGENOM:HBG715487 EMBL:AB024028 UniGene:At.17610 UniGene:At.22540 UniGene:At.32384 UniGene:At.71559 KO:K11253 OMA:DLRFQSQ EMBL:M35387 EMBL:M17131 EMBL:M17130 EMBL:AK117157 EMBL:AF370577 EMBL:AY037250 EMBL:AY039904 EMBL:AY077654 EMBL:AY081741 EMBL:BT003051 EMBL:BT003162 EMBL:BT005805 EMBL:BT006068 EMBL:AY084316 IPI:IPI00517184 PIR:S06250 RefSeq:NP_189372.1 RefSeq:NP_201339.1 RefSeq:NP_563838.1 RefSeq:NP_568227.1 RefSeq:NP_568228.1 UniGene:At.20804 UniGene:At.21310 UniGene:At.21486 UniGene:At.63772 UniGene:At.73076 ProteinModelPortal:P59226 SMR:P59226 DIP:DIP-48531N STRING:P59226 PRIDE:P59226 EnsemblPlants:AT1G09200.1 EnsemblPlants:AT3G27360.1 EnsemblPlants:AT5G10390.1 EnsemblPlants:AT5G10400.1 EnsemblPlants:AT5G65360.1 GeneID:822357 GeneID:830903 GeneID:830904 GeneID:836661 GeneID:837440 KEGG:ath:AT1G09200 KEGG:ath:AT3G27360 KEGG:ath:AT5G10390 KEGG:ath:AT5G10400 KEGG:ath:AT5G65360 TAIR:At1g09200 TAIR:At3g27360 TAIR:At5g10390 TAIR:At5g10400 TAIR:At5g65360 InParanoid:P59226 PhylomeDB:P59226 ProtClustDB:PLN00121 ArrayExpress:P59226 Genevestigator:P59226 GermOnline:AT1G09200 Uniprot:P59226
Root	Isotig02405	1	20	-4.451	3.92E-06	TAIR|locus:2157737 - symbol:WR3 "AT5G50200" species:3702 "Arabidopsis thaliana" [GO:0010167 "response to nitrate" evidence=IEP] [GO:0015112 "nitrate transmembrane transporter activity" evidence=IMP] [GO:0015706 "nitrate transport" evidence=IMP] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009611 "response to wounding" evidence=IEP] GO:GO:0016021 GO:GO:0005886 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009611 GO:GO:0015112 GO:GO:0042128 EMBL:AB024031 GO:GO:0010167 EMBL:AJ310933 EMBL:AJ311926 EMBL:AY085586 IPI:IPI00528407 RefSeq:NP_199831.1 RefSeq:NP_851159.1 RefSeq:NP_851160.1 UniGene:At.21028 IntAct:Q9FGS5 STRING:Q9FGS5 TCDB:8.A.20.1.1 PRIDE:Q9FGS5 EnsemblPlants:AT5G50200.1 EnsemblPlants:AT5G50200.2 EnsemblPlants:AT5G50200.3 GeneID:835085 KEGG:ath:AT5G50200 TAIR:At5g50200 eggNOG:NOG312409 InParanoid:Q9FGS5 OMA:VKVKLCY PhylomeDB:Q9FGS5 ProtClustDB:CLSN2687019 Genevestigator:Q9FGS5 InterPro:IPR016605 PIRSF:PIRSF012939 Uniprot:Q9FGS5
Root	Isotig02406	1	20	-4.451	3.92E-06	TAIR|locus:2157737 - symbol:WR3 "AT5G50200" species:3702 "Arabidopsis thaliana" [GO:0010167 "response to nitrate" evidence=IEP] [GO:0015112 "nitrate transmembrane transporter activity" evidence=IMP] [GO:0015706 "nitrate transport" evidence=IMP] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009611 "response to wounding" evidence=IEP] GO:GO:0016021 GO:GO:0005886 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009611 GO:GO:0015112 GO:GO:0042128 EMBL:AB024031 GO:GO:0010167 EMBL:AJ310933 EMBL:AJ311926 EMBL:AY085586 IPI:IPI00528407 RefSeq:NP_199831.1 RefSeq:NP_851159.1 RefSeq:NP_851160.1 UniGene:At.21028 IntAct:Q9FGS5 STRING:Q9FGS5 TCDB:8.A.20.1.1 PRIDE:Q9FGS5 EnsemblPlants:AT5G50200.1 EnsemblPlants:AT5G50200.2 EnsemblPlants:AT5G50200.3 GeneID:835085 KEGG:ath:AT5G50200 TAIR:At5g50200 eggNOG:NOG312409 InParanoid:Q9FGS5 OMA:VKVKLCY

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						PhylomeDB:Q9FGS5 ProtClustDB:CLSN2687019 Genevestigator:Q9FGS5 InterPro:IPR016605 PIRSF:PIRSF012939 Uniprot:Q9FGS5
Root	Isotig02407	1	20	-4.451	3.92E-06	TAIR|locus:2157737 - symbol:WR3 "AT5G50200" species:3702 "Arabidopsis thaliana" [GO:0010167 "response to nitrate" evidence=IEP] [GO:0015112 "nitrate transmembrane transporter activity" evidence=IMP] [GO:0015706 "nitrate transport" evidence=IMP] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009611 "response to wounding" evidence=IEP] GO:GO:0016021 GO:GO:0005886 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009611 GO:GO:0015112 GO:GO:0042128 EMBL:AB024031 GO:GO:0010167 EMBL:AJ310933 EMBL:AJ311926 EMBL:AY085586 IPI:IPI00528407 RefSeq:NP_199831.1 RefSeq:NP_851159.1 RefSeq:NP_851160.1 UniGene:At.21028 IntAct:Q9FGS5 STRING:Q9FGS5 TCDB:8.A.20.1.1 PRIDE:Q9FGS5 EnsemblPlants:AT5G50200.1 EnsemblPlants:AT5G50200.2 EnsemblPlants:AT5G50200.3 GeneID:835085 KEGG:ath:AT5G50200 TAIR:At5g50200 eggNOG:NOG312409 InParanoid:Q9FGS5 OMA:VKVKLCY PhylomeDB:Q9FGS5 ProtClustDB:CLSN2687019 Genevestigator:Q9FGS5 InterPro:IPR016605 PIRSF:PIRSF012939 Uniprot:Q9FGS5
Root	Isotig02408	1	20	-4.451	3.92E-06	TAIR|locus:2157737 - symbol:WR3 "AT5G50200" species:3702 "Arabidopsis thaliana" [GO:0010167 "response to nitrate" evidence=IEP] [GO:0015112 "nitrate transmembrane transporter activity" evidence=IMP] [GO:0015706 "nitrate transport" evidence=IMP] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009611 "response to wounding" evidence=IEP] GO:GO:0016021 GO:GO:0005886 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009611 GO:GO:0015112 GO:GO:0042128 EMBL:AB024031 GO:GO:0010167 EMBL:AJ310933 EMBL:AJ311926 EMBL:AY085586 IPI:IPI00528407 RefSeq:NP_199831.1 RefSeq:NP_851159.1 RefSeq:NP_851160.1 UniGene:At.21028 IntAct:Q9FGS5 STRING:Q9FGS5 TCDB:8.A.20.1.1 PRIDE:Q9FGS5 EnsemblPlants:AT5G50200.1 EnsemblPlants:AT5G50200.2 EnsemblPlants:AT5G50200.3 GeneID:835085 KEGG:ath:AT5G50200 TAIR:At5g50200 eggNOG:NOG312409 InParanoid:Q9FGS5 OMA:VKVKLCY PhylomeDB:Q9FGS5 ProtClustDB:CLSN2687019 Genevestigator:Q9FGS5 InterPro:IPR016605 PIRSF:PIRSF012939 Uniprot:Q9FGS5
Root	Isotig02409	1	20	-4.451	3.92E-06	TAIR|locus:2157737 - symbol:WR3 "AT5G50200" species:3702 "Arabidopsis thaliana" [GO:0010167 "response to nitrate" evidence=IEP] [GO:0015112 "nitrate transmembrane transporter activity" evidence=IMP] [GO:0015706 "nitrate transport" evidence=IMP] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009611 "response to wounding" evidence=IEP] GO:GO:0016021 GO:GO:0005886 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009611 GO:GO:0015112 GO:GO:0042128 EMBL:AB024031 GO:GO:0010167 EMBL:AJ310933 EMBL:AJ311926 EMBL:AY085586 IPI:IPI00528407 RefSeq:NP_199831.1 RefSeq:NP_851159.1 RefSeq:NP_851160.1 UniGene:At.21028 IntAct:Q9FGS5 STRING:Q9FGS5 TCDB:8.A.20.1.1 PRIDE:Q9FGS5 EnsemblPlants:AT5G50200.1 EnsemblPlants:AT5G50200.2 EnsemblPlants:AT5G50200.3 GeneID:835085 KEGG:ath:AT5G50200 TAIR:At5g50200 eggNOG:NOG312409 InParanoid:Q9FGS5 OMA:VKVKLCY PhylomeDB:Q9FGS5 ProtClustDB:CLSN2687019 Genevestigator:Q9FGS5 InterPro:IPR016605 PIRSF:PIRSF012939 Uniprot:Q9FGS5
Root	Isotig02410	1	20	-4.451	3.92E-06	TAIR|locus:2157737 - symbol:WR3 "AT5G50200" species:3702 "Arabidopsis thaliana" [GO:0010167 "response to nitrate" evidence=IEP] [GO:0015112 "nitrate transmembrane transporter activity" evidence=IMP] [GO:0015706 "nitrate transport" evidence=IMP] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009611 "response to wounding" evidence=IEP] GO:GO:0016021 GO:GO:0005886 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009611 GO:GO:0015112 GO:GO:0042128 EMBL:AB024031 GO:GO:0010167 EMBL:AJ310933 EMBL:AJ311926 EMBL:AY085586 IPI:IPI00528407 RefSeq:NP_199831.1 RefSeq:NP_851159.1 RefSeq:NP_851160.1 UniGene:At.21028 IntAct:Q9FGS5 STRING:Q9FGS5 TCDB:8.A.20.1.1 PRIDE:Q9FGS5 EnsemblPlants:AT5G50200.1 EnsemblPlants:AT5G50200.2 EnsemblPlants:AT5G50200.3 GeneID:835085 KEGG:ath:AT5G50200 TAIR:At5g50200 eggNOG:NOG312409 InParanoid:Q9FGS5 OMA:VKVKLCY PhylomeDB:Q9FGS5 ProtClustDB:CLSN2687019 Genevestigator:Q9FGS5 InterPro:IPR016605 PIRSF:PIRSF012939 Uniprot:Q9FGS5
Root	Isotig02417	0	26	-5.829	5.70E-08	UNIPROTKB|B6TYV8 - symbol:CNR2 "Cell number regulator 2" species:4577 "Zea mays" [GO:0008285 "negative regulation of cell proliferation" evidence=IMP] GO:GO:0016021 GO:GO:0008285 InterPro:IPR006461 Pfam:PF04749 TIGRFAMs:TIGR01571 EMBL:HM008654 EMBL:EU970173 EMBL:BT068908 RefSeq:NP_001144684.1 UniGene:Zm.7882 EnsemblPlants:GRMZM2G151230_T01 GeneID:100277715 KEGG:zma:100277715 PhylomeDB:B6TYV8 Uniprot:B6TYV8

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig02418	0	26	-5.829	5.70E-08	UNIPROTKB|B6TYV8 - symbol:CNR2 "Cell number regulator 2" species:4577 "Zea mays" [GO:0008285 "negative regulation of cell proliferation" evidence=IMP] GO:GO:0016021 GO:GO:0008285 InterPro:IPR006461 Pfam:PF04749 TIGRFAMs:TIGR01571 EMBL:HM008654 EMBL:EU970173 EMBL:BT068908 RefSeq:NP_001144684.1 UniGene:Zm.7882 EnsemblPlants:GRMZM2G151230_T01 GeneID:100277715 KEGG:zma:100277715 PhylomeDB:B6TYV8 Uniprot:B6TYV8
Root	Isotig02419	0	26	-5.829	5.70E-08	UNIPROTKB|B6TYV8 - symbol:CNR2 "Cell number regulator 2" species:4577 "Zea mays" [GO:0008285 "negative regulation of cell proliferation" evidence=IMP] GO:GO:0016021 GO:GO:0008285 InterPro:IPR006461 Pfam:PF04749 TIGRFAMs:TIGR01571 EMBL:HM008654 EMBL:EU970173 EMBL:BT068908 RefSeq:NP_001144684.1 UniGene:Zm.7882 EnsemblPlants:GRMZM2G151230_T01 GeneID:100277715 KEGG:zma:100277715 PhylomeDB:B6TYV8 Uniprot:B6TYV8
Root	Isotig02420	0	26	-5.829	5.70E-08	UNIPROTKB|B6TYV8 - symbol:CNR2 "Cell number regulator 2" species:4577 "Zea mays" [GO:0008285 "negative regulation of cell proliferation" evidence=IMP] GO:GO:0016021 GO:GO:0008285 InterPro:IPR006461 Pfam:PF04749 TIGRFAMs:TIGR01571 EMBL:HM008654 EMBL:EU970173 EMBL:BT068908 RefSeq:NP_001144684.1 UniGene:Zm.7882 EnsemblPlants:GRMZM2G151230_T01 GeneID:100277715 KEGG:zma:100277715 PhylomeDB:B6TYV8 Uniprot:B6TYV8
Root	Isotig02421	0	26	-5.829	5.70E-08	UNIPROTKB|B6TYV8 - symbol:CNR2 "Cell number regulator 2" species:4577 "Zea mays" [GO:0008285 "negative regulation of cell proliferation" evidence=IMP] GO:GO:0016021 GO:GO:0008285 InterPro:IPR006461 Pfam:PF04749 TIGRFAMs:TIGR01571 EMBL:HM008654 EMBL:EU970173 EMBL:BT068908 RefSeq:NP_001144684.1 UniGene:Zm.7882 EnsemblPlants:GRMZM2G151230_T01 GeneID:100277715 KEGG:zma:100277715 PhylomeDB:B6TYV8 Uniprot:B6TYV8
Root	Isotig02422	0	26	-5.829	5.70E-08	UNIPROTKB|B6TYV8 - symbol:CNR2 "Cell number regulator 2" species:4577 "Zea mays" [GO:0008285 "negative regulation of cell proliferation" evidence=IMP] GO:GO:0016021 GO:GO:0008285 InterPro:IPR006461 Pfam:PF04749 TIGRFAMs:TIGR01571 EMBL:HM008654 EMBL:EU970173 EMBL:BT068908 RefSeq:NP_001144684.1 UniGene:Zm.7882 EnsemblPlants:GRMZM2G151230_T01 GeneID:100277715 KEGG:zma:100277715 PhylomeDB:B6TYV8 Uniprot:B6TYV8
Root	Isotig02423	37	8	2.080	2.32E-05	TAIR|locus:1005716170 - symbol:CAM6 "AT5G21274" species:3702 "Arabidopsis thaliana" [GO:0005509 "calcium ion binding" evidence=ISS] [GO:0005515 "protein binding" evidence=IPI] [GO:0005829 "cytosol" evidence=RCA] [GO:0019722 "calcium-mediated signaling" evidence=TAS] InterPro:IPR002048 InterPro:IPR011992 SMART:SM00054 Prosite:PS00018 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005509 GO:GO:0005515 GO:GO:0019722 InterPro:IPR018247 InterPro:IPR018249 Gene3D:G3DSA:1.10.238.10 PROSITE:PS50222 EMBL:AC140977 eggNOG:COG5126 HOGENOM:HBG746798 ProtClustDB:CLSN2681765 EMBL:Z12024 EMBL:AY050350 EMBL:AY094037 IPI:IPI00520449 PIR:S35187 RefSeq:NP_850860.1 UniGene:At.21106 ProteinModelPortal:Q03509 SMR:Q03509 IntAct:Q03509 STRING:Q03509 PRIDE:Q03509 EnsemblPlants:AT5G21274.1 GeneID:832245 KEGG:ath:AT5G21274 TAIR:At5g21274 InParanoid:Q03509 OMA:MANKRAK PhylomeDB:Q03509 Genevestigator:Q03509 Uniprot:Q03509
Root	Isotig02424	36	8	2.041	3.74E-05	TAIR|locus:1005716170 - symbol:CAM6 "AT5G21274" species:3702 "Arabidopsis thaliana" [GO:0005509 "calcium ion binding" evidence=ISS] [GO:0005515 "protein binding" evidence=IPI] [GO:0005829 "cytosol" evidence=RCA] [GO:0019722 "calcium-mediated signaling" evidence=TAS] InterPro:IPR002048 InterPro:IPR011992 SMART:SM00054 Prosite:PS00018 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005509 GO:GO:0005515 GO:GO:0019722 InterPro:IPR018247 InterPro:IPR018249 Gene3D:G3DSA:1.10.238.10 PROSITE:PS50222 EMBL:AC140977 eggNOG:COG5126 HOGENOM:HBG746798 ProtClustDB:CLSN2681765 EMBL:Z12024 EMBL:AY050350 EMBL:AY094037 IPI:IPI00520449 PIR:S35187 RefSeq:NP_850860.1 UniGene:At.21106 ProteinModelPortal:Q03509 SMR:Q03509 IntAct:Q03509 STRING:Q03509 PRIDE:Q03509 EnsemblPlants:AT5G21274.1 GeneID:832245 KEGG:ath:AT5G21274 TAIR:At5g21274 InParanoid:Q03509 OMA:MANKRAK PhylomeDB:Q03509 Genevestigator:Q03509 Uniprot:Q03509
Root	Isotig02425	38	8	2.119	1.43E-05	TAIR|locus:1005716170 - symbol:CAM6 "AT5G21274" species:3702 "Arabidopsis thaliana" [GO:0005509 "calcium ion binding" evidence=ISS] [GO:0005515 "protein binding" evidence=IPI] [GO:0005829 "cytosol" evidence=RCA] [GO:0019722 "calcium-mediated signaling" evidence=TAS] InterPro:IPR002048 InterPro:IPR011992 SMART:SM00054 Prosite:PS00018 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005509 GO:GO:0005515 GO:GO:0019722 InterPro:IPR018247 InterPro:IPR018249 Gene3D:G3DSA:1.10.238.10 PROSITE:PS50222 EMBL:AC140977 eggNOG:COG5126 HOGENOM:HBG746798 ProtClustDB:CLSN2681765 EMBL:Z12024 EMBL:AY050350 EMBL:AY094037 IPI:IPI00520449 PIR:S35187 RefSeq:NP_850860.1

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						UniGene:At.21106 ProteinModelPortal:Q03509 SMR:Q03509 IntAct:Q03509 STRING:Q03509 PRIDE:Q03509 EnsemblPlants:AT5G21274.1 GeneID:832245 KEGG:ath:AT5G21274 TAIR:At5g21274 InParanoid:Q03509 OMA:MANKRAK PhylomeDB:Q03509 Genevestigator:Q03509 Uniprot:Q03509
Root	Isotig02426	37	8	2.080	2.32E-05	TAIR|locus:1005716170 - symbol:CAM6 "AT5G21274" species:3702 "Arabidopsis thaliana" [GO:0005509 "calcium ion binding" evidence=ISS] [GO:0005515 "protein binding" evidence=IPI] [GO:0005829 "cytosol" evidence=RCA] [GO:0019722 "calcium-mediated signaling" evidence=TAS] InterPro:IPR002048 InterPro:IPR011992 SMART:SM00054 Prosite:PS00018 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005509 GO:GO:0005515 GO:GO:0019722 InterPro:IPR018247 InterPro:IPR018249 Gene3D:G3DSA:1.10.238.10 PROSITE:PS50222 EMBL:AC140977 eggNOG:COG5126 HOGENOM:HBG746798 ProtClustDB:CLSN2681765 EMBL:Z12024 EMBL:AY050350 EMBL:AY094037 IPI:IPI00520449 PIR:S35187 RefSeq:NP_850860.1 UniGene:At.21106 ProteinModelPortal:Q03509 SMR:Q03509 IntAct:Q03509 STRING:Q03509 PRIDE:Q03509 EnsemblPlants:AT5G21274.1 GeneID:832245 KEGG:ath:AT5G21274 TAIR:At5g21274 InParanoid:Q03509 OMA:MANKRAK PhylomeDB:Q03509 Genevestigator:Q03509 Uniprot:Q03509
Root	Isotig02427	37	8	2.080	2.32E-05	TAIR|locus:1005716170 - symbol:CAM6 "AT5G21274" species:3702 "Arabidopsis thaliana" [GO:0005509 "calcium ion binding" evidence=ISS] [GO:0005515 "protein binding" evidence=IPI] [GO:0005829 "cytosol" evidence=RCA] [GO:0019722 "calcium-mediated signaling" evidence=TAS] InterPro:IPR002048 InterPro:IPR011992 SMART:SM00054 Prosite:PS00018 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005509 GO:GO:0005515 GO:GO:0019722 InterPro:IPR018247 InterPro:IPR018249 Gene3D:G3DSA:1.10.238.10 PROSITE:PS50222 EMBL:AC140977 eggNOG:COG5126 HOGENOM:HBG746798 ProtClustDB:CLSN2681765 EMBL:Z12024 EMBL:AY050350 EMBL:AY094037 IPI:IPI00520449 PIR:S35187 RefSeq:NP_850860.1 UniGene:At.21106 ProteinModelPortal:Q03509 SMR:Q03509 IntAct:Q03509 STRING:Q03509 PRIDE:Q03509 EnsemblPlants:AT5G21274.1 GeneID:832245 KEGG:ath:AT5G21274 TAIR:At5g21274 InParanoid:Q03509 OMA:MANKRAK PhylomeDB:Q03509 Genevestigator:Q03509 Uniprot:Q03509
Root	Isotig02428	36	8	2.041	3.74E-05	TAIR|locus:1005716170 - symbol:CAM6 "AT5G21274" species:3702 "Arabidopsis thaliana" [GO:0005509 "calcium ion binding" evidence=ISS] [GO:0005515 "protein binding" evidence=IPI] [GO:0005829 "cytosol" evidence=RCA] [GO:0019722 "calcium-mediated signaling" evidence=TAS] InterPro:IPR002048 InterPro:IPR011992 SMART:SM00054 Prosite:PS00018 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005509 GO:GO:0005515 GO:GO:0019722 InterPro:IPR018247 InterPro:IPR018249 Gene3D:G3DSA:1.10.238.10 PROSITE:PS50222 EMBL:AC140977 eggNOG:COG5126 HOGENOM:HBG746798 ProtClustDB:CLSN2681765 EMBL:Z12024 EMBL:AY050350 EMBL:AY094037 IPI:IPI00520449 PIR:S35187 RefSeq:NP_850860.1 UniGene:At.21106 ProteinModelPortal:Q03509 SMR:Q03509 IntAct:Q03509 STRING:Q03509 PRIDE:Q03509 EnsemblPlants:AT5G21274.1 GeneID:832245 KEGG:ath:AT5G21274 TAIR:At5g21274 InParanoid:Q03509 OMA:MANKRAK PhylomeDB:Q03509 Genevestigator:Q03509 Uniprot:Q03509
Root	Isotig02435	0	19	-5.377	3.67E-06	TAIR|locus:2035074 - symbol:AT1G52720 "AT1G52720" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002684 GenomeReviews:CT485782_GR EMBL:AC008016 HOGENOM:HBG597979 ProtClustDB:CLSN2688413 EMBL:AY085970 EMBL:BT004752 EMBL:AK228288 IPI:IPI00543215 RefSeq:NP_564614.1 UniGene:At.11637 PRIDE:Q9SSS6 EnsemblPlants:AT1G52720.1 GeneID:841705 KEGG:ath:AT1G52720 TAIR:At1g52720 eggNOG:NOG251124 InParanoid:Q9SSS6 OMA:TWWAPLF PhylomeDB:Q9SSS6 Genevestigator:Q9SSS6 Uniprot:Q9SSS6
Root	Isotig02436	0	18	-5.299	6.77E-06	TAIR|locus:2093247 - symbol:AT3G15630 "AT3G15630" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002686 GenomeReviews:BA000014_GR EMBL:AB017071 EMBL:AY052241 EMBL:AY060508 IPI:IPI00533188 RefSeq:NP_566521.1 UniGene:At.20536 STRING:Q9LW16 EnsemblPlants:AT3G15630.1 GeneID:820805 KEGG:ath:AT3G15630 TAIR:At3g15630 eggNOG:NOG293987 HOGENOM:HBG597979 InParanoid:Q9LW16 OMA:TIISCSA PhylomeDB:Q9LW16 ProtClustDB:CLSN2688413 Genevestigator:Q9LW16 Uniprot:Q9LW16
Root	Isotig02437	0	18	-5.299	6.77E-06	TAIR|locus:2093247 - symbol:AT3G15630 "AT3G15630" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002686 GenomeReviews:BA000014_GR EMBL:AB017071 EMBL:AY052241 EMBL:AY060508 IPI:IPI00533188 RefSeq:NP_566521.1 UniGene:At.20536 STRING:Q9LW16 EnsemblPlants:AT3G15630.1 GeneID:820805 KEGG:ath:AT3G15630 TAIR:At3g15630 eggNOG:NOG293987 HOGENOM:HBG597979 InParanoid:Q9LW16 OMA:TIISCSA PhylomeDB:Q9LW16 ProtClustDB:CLSN2688413 Genevestigator:Q9LW16 Uniprot:Q9LW16

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig02438	0	19	-5.377	3.67E-06	TAIR|locus:2035074 - symbol:AT1G52720 "AT1G52720" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002684 GenomeReviews:CT485782_GR EMBL:AC008016 HOGENOM:HBG597979 ProtClustDB:CLSN2688413 EMBL:AY085970 EMBL:BT004752 EMBL:AK228288 IPI:IPI00543215 RefSeq:NP_564614.1 UniGene:At.11637 PRIDE:Q9SSS6 EnsemblPlants:AT1G52720.1 GeneID:841705 KEGG:ath:AT1G52720 TAIR:At1g52720 eggNOG:NOG251124 InParanoid:Q9SSS6 OMA:TWWAPLF PhylomeDB:Q9SSS6 Genevestigator:Q9SSS6 Uniprot:Q9SSS6
Root	Isotig02439	0	18	-5.299	6.77E-06	TAIR|locus:2093247 - symbol:AT3G15630 "AT3G15630" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002686 GenomeReviews:BA000014_GR EMBL:AB017071 EMBL:AY052241 EMBL:AY060508 IPI:IPI00533188 RefSeq:NP_566521.1 UniGene:At.20536 STRING:Q9LW16 EnsemblPlants:AT3G15630.1 GeneID:820805 KEGG:ath:AT3G15630 TAIR:At3g15630 eggNOG:NOG293987 HOGENOM:HBG597979 InParanoid:Q9LW16 OMA:TIISCSA PhylomeDB:Q9LW16 ProtClustDB:CLSN2688413 Genevestigator:Q9LW16 Uniprot:Q9LW16
Root	Isotig02440	0	18	-5.299	6.77E-06	TAIR|locus:2093247 - symbol:AT3G15630 "AT3G15630" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002686 GenomeReviews:BA000014_GR EMBL:AB017071 EMBL:AY052241 EMBL:AY060508 IPI:IPI00533188 RefSeq:NP_566521.1 UniGene:At.20536 STRING:Q9LW16 EnsemblPlants:AT3G15630.1 GeneID:820805 KEGG:ath:AT3G15630 TAIR:At3g15630 eggNOG:NOG293987 HOGENOM:HBG597979 InParanoid:Q9LW16 OMA:TIISCSA PhylomeDB:Q9LW16 ProtClustDB:CLSN2688413 Genevestigator:Q9LW16 Uniprot:Q9LW16
Root	Isotig02450	1	25	-4.773	1.66E-07	TAIR|locus:2036873 - symbol:BGLU46 "beta glucosidase 46" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=IEA;ISS] [GO:0043169 "cation binding" evidence=IEA] [GO:0008422 "beta-glucosidase activity" evidence=IDA] [GO:0009809 "lignin biosynthetic process" evidence=IMP] [GO:0047782 "coniferin beta-glucosidase activity" evidence=IDA] InterPro:IPR001360 InterPro:IPR013781 InterPro:IPR018120 Pfam:PF00232 PRINTS:PR00131 PROSITE:PS00572 PROSITE:PS00653 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0043169 InterPro:IPR017853 Gene3D:G3DSA:3.20.20.80 SUPFAM:SSF51445 GO:GO:0005975 CAZy:GH1 eggNOG:COG2723 HOGENOM:HBG316462 PANTHER:PTHR10353 EMBL:AC004392 KO:K05350 HSSP:P11546 ProtClustDB:CLSN2682045 GO:GO:0047782 GO:GO:0009809 EMBL:BX816529 EMBL:BT015331 EMBL:BT015708 IPI:IPI00518755 PIR:T02128 RefSeq:NP_850968.1 UniGene:At.27913 ProteinModelPortal:O80690 SMR:O80690 STRING:O80690 PRIDE:O80690 EnsemblPlants:AT1G61820.1 GeneID:842479 KEGG:ath:AT1G61820 TAIR:At1g61820 InParanoid:O80690 OMA:RYMEDIQ PhylomeDB:O80690 Uniprot:O80690
Root	Isotig02461	11	36	-1.839	5.72E-05	TAIR|locus:2174403 - symbol:UBP23 "ubiquitin-specific protease 23" species:3702 "Arabidopsis thaliana" [GO:0004221 "ubiquitin thiolesterase activity" evidence=IEA] [GO:0004843 "ubiquitin-specific protease activity" evidence=ISS] [GO:0006511 "ubiquitin-dependent protein catabolic process" evidence=IEA] InterPro:IPR001394 InterPro:IPR018200 Pfam:PF00443 PROSITE:PS00972 PROSITE:PS00973 PROSITE:PS50235 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0006511 EMBL:AB013396 GO:GO:0008234 GO:GO:0004221 eggNOG:COG5077 HSSP:P54578 KO:K11855 EMBL:AF302671 IPI:IPI00532960 RefSeq:NP_568873.1 UniGene:At.22531 ProteinModelPortal:Q9FPS4 SMR:Q9FPS4 STRING:Q9FPS4 MEROPS:C19.A12 PRIDE:Q9FPS4 EnsemblPlants:AT5G57990.1 GeneID:835910 KEGG:ath:AT5G57990 GeneFarm:1994 TAIR:At5g57990 HOGENOM:HBG317149 InParanoid:Q9FPS4 OMA:MEVATSS PhylomeDB:Q9FPS4 ProtClustDB:CLSN2716507 Genevestigator:Q9FPS4 Uniprot:Q9FPS4
Root	Isotig02462	11	36	-1.839	5.72E-05	TAIR|locus:2174403 - symbol:UBP23 "ubiquitin-specific protease 23" species:3702 "Arabidopsis thaliana" [GO:0004221 "ubiquitin thiolesterase activity" evidence=IEA] [GO:0004843 "ubiquitin-specific protease activity" evidence=ISS] [GO:0006511 "ubiquitin-dependent protein catabolic process" evidence=IEA] InterPro:IPR001394 InterPro:IPR018200 Pfam:PF00443 PROSITE:PS00972 PROSITE:PS00973 PROSITE:PS50235 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0006511 EMBL:AB013396 GO:GO:0008234 GO:GO:0004221 eggNOG:COG5077 HSSP:P54578 KO:K11855 EMBL:AF302671 IPI:IPI00532960 RefSeq:NP_568873.1 UniGene:At.22531 ProteinModelPortal:Q9FPS4 SMR:Q9FPS4 STRING:Q9FPS4 MEROPS:C19.A12 PRIDE:Q9FPS4 EnsemblPlants:AT5G57990.1 GeneID:835910 KEGG:ath:AT5G57990 GeneFarm:1994 TAIR:At5g57990 HOGENOM:HBG317149 InParanoid:Q9FPS4 OMA:MEVATSS PhylomeDB:Q9FPS4 ProtClustDB:CLSN2716507 Genevestigator:Q9FPS4 Uniprot:Q9FPS4

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig02464	3	17	-2.631	0.00056383	TAIR|locus:2199297 - symbol:ENDO 2 "AT1G68290" species:3702 "Arabidopsis thaliana" [GO:0003676 "nucleic acid binding" evidence=ISS] [GO:0004519 "endonuclease activity" evidence=ISS] [GO:0006308 "DNA catabolic process" evidence=IEA;ISS] [GO:0000014 "single-stranded DNA specific endodeoxyribonuclease activity" evidence=IDA] [GO:0043765 "T/G mismatch-specific endonuclease activity" evidence=IDA] InterPro:IPR003154 InterPro:IPR008947 Pfam:PF02265 EMBL:CP002684 GO:GO:0003676 EMBL:AC016447 GO:GO:0004519 GO:GO:0006308 Gene3D:G3DSA:1.10.575.10 SUPFAM:SSF48537 HSSP:P24289 ProtClustDB:CLSN2681945 IPI:IPI00543025 PIR:E96706 RefSeq:NP_176996.1 UniGene:At.35544 UniGene:At.43330 ProteinModelPortal:Q9C9G4 SMR:Q9C9G4 PRIDE:Q9C9G4 EnsemblPlants:AT1G68290.1 GeneID:843158 KEGG:ath:AT1G68290 TAIR:At1g68290 InParanoid:Q9C9G4 OMA:AACDWAY PhylomeDB:Q9C9G4 Genevestigator:Q9C9G4 Uniprot:Q9C9G4
Root	Isotig02465	3	17	-2.631	0.00056383	TAIR|locus:2199297 - symbol:ENDO 2 "AT1G68290" species:3702 "Arabidopsis thaliana" [GO:0003676 "nucleic acid binding" evidence=ISS] [GO:0004519 "endonuclease activity" evidence=ISS] [GO:0006308 "DNA catabolic process" evidence=IEA;ISS] [GO:0000014 "single-stranded DNA specific endodeoxyribonuclease activity" evidence=IDA] [GO:0043765 "T/G mismatch-specific endonuclease activity" evidence=IDA] InterPro:IPR003154 InterPro:IPR008947 Pfam:PF02265 EMBL:CP002684 GO:GO:0003676 EMBL:AC016447 GO:GO:0004519 GO:GO:0006308 Gene3D:G3DSA:1.10.575.10 SUPFAM:SSF48537 HSSP:P24289 ProtClustDB:CLSN2681945 IPI:IPI00543025 PIR:E96706 RefSeq:NP_176996.1 UniGene:At.35544 UniGene:At.43330 ProteinModelPortal:Q9C9G4 SMR:Q9C9G4 PRIDE:Q9C9G4 EnsemblPlants:AT1G68290.1 GeneID:843158 KEGG:ath:AT1G68290 TAIR:At1g68290 InParanoid:Q9C9G4 OMA:AACDWAY PhylomeDB:Q9C9G4 Genevestigator:Q9C9G4 Uniprot:Q9C9G4
Root	Isotig02471	67	20	1.615	1.65E-06	TAIR|locus:2167903 - symbol:PRH75 "AT5G62190" species:3702 "Arabidopsis thaliana" [GO:0008026 "ATP-dependent helicase activity" evidence=ISS] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0016070 "RNA metabolic process" evidence=TAS] [GO:0017151 "DEAD/H-box RNA helicase binding" evidence=ISS] InterPro:IPR000629 InterPro:IPR001650 InterPro:IPR011545 InterPro:IPR012562 Pfam:PF00270 Pfam:PF00271 Pfam:PF08152 PROSITE:PS00039 PROSITE:PS51194 SMART:SM00490 InterPro:IPR014001 GO:GO:0005524 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005730 GO:GO:0003723 GO:GO:0016070 SMART:SM00487 PROSITE:PS51192 EMBL:AB019235 GO:GO:0008026 eggNOG:COG0513 HOGENOM:HBG737336 InterPro:IPR014014 PROSITE:PS51195 EMBL:X99938 EMBL:AY039576 EMBL:AY056137 EMBL:BT008581 IPI:IPI00520493 RefSeq:NP_201025.1 UniGene:At.22598 ProteinModelPortal:Q39189 SMR:Q39189 IntAct:Q39189 STRING:Q39189 PRIDE:Q39189 EnsemblPlants:AT5G62190.1 GeneID:836340 KEGG:ath:AT5G62190 GeneFarm:918 TAIR:At5g62190 InParanoid:Q39189 OMA:PIQATTF PhylomeDB:Q39189 ProtClustDB:CLSN2687322 ArrayExpress:Q9LVB7 Genevestigator:Q39189 GermOnline:AT5G62190 Uniprot:Q39189
Root	Isotig02472	63	19	1.600	3.91E-06	TAIR|locus:2167903 - symbol:PRH75 "AT5G62190" species:3702 "Arabidopsis thaliana" [GO:0008026 "ATP-dependent helicase activity" evidence=ISS] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0016070 "RNA metabolic process" evidence=TAS] [GO:0017151 "DEAD/H-box RNA helicase binding" evidence=ISS] InterPro:IPR000629 InterPro:IPR001650 InterPro:IPR011545 InterPro:IPR012562 Pfam:PF00270 Pfam:PF00271 Pfam:PF08152 PROSITE:PS00039 PROSITE:PS51194 SMART:SM00490 InterPro:IPR014001 GO:GO:0005524 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005730 GO:GO:0003723 GO:GO:0016070 SMART:SM00487 PROSITE:PS51192 EMBL:AB019235 GO:GO:0008026 eggNOG:COG0513 HOGENOM:HBG737336 InterPro:IPR014014 PROSITE:PS51195 EMBL:X99938 EMBL:AY039576 EMBL:AY056137 EMBL:BT008581 IPI:IPI00520493 RefSeq:NP_201025.1 UniGene:At.22598 ProteinModelPortal:Q39189 SMR:Q39189 IntAct:Q39189 STRING:Q39189 PRIDE:Q39189 EnsemblPlants:AT5G62190.1 GeneID:836340 KEGG:ath:AT5G62190 GeneFarm:918 TAIR:At5g62190 InParanoid:Q39189 OMA:PIQATTF PhylomeDB:Q39189 ProtClustDB:CLSN2687322 ArrayExpress:Q9LVB7 Genevestigator:Q39189 GermOnline:AT5G62190 Uniprot:Q39189
Root	Isotig02473	58	14	1.922	4.89E-07	TAIR|locus:2167903 - symbol:PRH75 "AT5G62190" species:3702 "Arabidopsis thaliana" [GO:0008026 "ATP-dependent helicase activity" evidence=ISS] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0016070 "RNA metabolic process" evidence=TAS] [GO:0017151 "DEAD/H-box RNA helicase binding" evidence=ISS] InterPro:IPR000629 InterPro:IPR001650 InterPro:IPR011545 InterPro:IPR012562 Pfam:PF00270 Pfam:PF00271 Pfam:PF08152 PROSITE:PS00039 PROSITE:PS51194 SMART:SM00490 InterPro:IPR014001 GO:GO:0005524 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005730

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0003723 GO:GO:0016070 SMART:SM00487 PROSITE:PS51192 EMBL:AB019235 GO:GO:0008026 eggNOG:COG0513 HOGENOM:HBG737336 InterPro:IPR014014 PROSITE:PS51195 EMBL:X99938 EMBL:AY039576 EMBL:AY056137 EMBL:BT008581 IPI:IPI00520493 RefSeq:NP_201025.1 UniGene:At.22598 ProteinModelPortal:Q39189 SMR:Q39189 IntAct:Q39189 STRING:Q39189 PRIDE:Q39189 EnsemblPlants:AT5G62190.1 GeneID:836340 KEGG:ath:AT5G62190 GeneFarm:918 TAIR:At5g62190 InParanoid:Q39189 OMA:PIQATTF PhylomeDB:Q39189 ProtClustDB:CLSN2687322 ArrayExpress:Q9LVB7 Genevestigator:Q39189 GermOnline:AT5G62190 Uniprot:Q39189
Root	Isotig02474	53	6	3.014	4.34E-10	TAIR|locus:2167903 - symbol:PRH75 "AT5G62190" species:3702 "Arabidopsis thaliana" [GO:0008026 "ATP-dependent helicase activity" evidence=ISS] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0016070 "RNA metabolic process" evidence=TAS] [GO:0017151 "DEAD/H-box RNA helicase binding" evidence=ISS] InterPro:IPR000629 InterPro:IPR001650 InterPro:IPR011545 InterPro:IPR012562 Pfam:PF00270 Pfam:PF00271 Pfam:PF08152 PROSITE:PS00039 PROSITE:PS51194 SMART:SM00490 InterPro:IPR014001 GO:GO:0005524 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005730 GO:GO:0003723 GO:GO:0016070 SMART:SM00487 PROSITE:PS51192 EMBL:AB019235 GO:GO:0008026 eggNOG:COG0513 HOGENOM:HBG737336 InterPro:IPR014014 PROSITE:PS51195 EMBL:X99938 EMBL:AY039576 EMBL:AY056137 EMBL:BT008581 IPI:IPI00520493 RefSeq:NP_201025.1 UniGene:At.22598 ProteinModelPortal:Q39189 SMR:Q39189 IntAct:Q39189 STRING:Q39189 PRIDE:Q39189 EnsemblPlants:AT5G62190.1 GeneID:836340 KEGG:ath:AT5G62190 GeneFarm:918 TAIR:At5g62190 InParanoid:Q39189 OMA:PIQATTF PhylomeDB:Q39189 ProtClustDB:CLSN2687322 ArrayExpress:Q9LVB7 Genevestigator:Q39189 GermOnline:AT5G62190 Uniprot:Q39189
Root	Isotig02475	54	13	1.925	1.17E-06	TAIR|locus:2167903 - symbol:PRH75 "AT5G62190" species:3702 "Arabidopsis thaliana" [GO:0008026 "ATP-dependent helicase activity" evidence=ISS] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0016070 "RNA metabolic process" evidence=TAS] [GO:0017151 "DEAD/H-box RNA helicase binding" evidence=ISS] InterPro:IPR000629 InterPro:IPR001650 InterPro:IPR011545 InterPro:IPR012562 Pfam:PF00270 Pfam:PF00271 Pfam:PF08152 PROSITE:PS00039 PROSITE:PS51194 SMART:SM00490 InterPro:IPR014001 GO:GO:0005524 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005730 GO:GO:0003723 GO:GO:0016070 SMART:SM00487 PROSITE:PS51192 EMBL:AB019235 GO:GO:0008026 eggNOG:COG0513 HOGENOM:HBG737336 InterPro:IPR014014 PROSITE:PS51195 EMBL:X99938 EMBL:AY039576 EMBL:AY056137 EMBL:BT008581 IPI:IPI00520493 RefSeq:NP_201025.1 UniGene:At.22598 ProteinModelPortal:Q39189 SMR:Q39189 IntAct:Q39189 STRING:Q39189 PRIDE:Q39189 EnsemblPlants:AT5G62190.1 GeneID:836340 KEGG:ath:AT5G62190 GeneFarm:918 TAIR:At5g62190 InParanoid:Q39189 OMA:PIQATTF PhylomeDB:Q39189 ProtClustDB:CLSN2687322 ArrayExpress:Q9LVB7 Genevestigator:Q39189 GermOnline:AT5G62190 Uniprot:Q39189
Root	Isotig02486	107	162	-0.727	4.25E-05	UNIPROTKB|B9RXH6 - symbol:RCOM_0903730 "Aspartic proteinase, putative" species:3988 "Ricinus communis" [GO:0005783 "endoplasmic reticulum" evidence=IDA] InterPro:IPR001461 InterPro:IPR001969 InterPro:IPR007856 InterPro:IPR009007 Pfam:PF00026 Pfam:PF05184 PRINTS:PR00792 PROSITE:PS00141 GO:GO:0005783 GO:GO:0006508 GO:GO:0006629 InterPro:IPR008138 InterPro:IPR011001 InterPro:IPR008139 Gene3D:G3DSA:1.10.225.10 Pfam:PF03489 SMART:SM00741 SUPFAM:SSF47862 PROSITE:PS50015 GO:GO:0004190 InterPro:IPR021109 SUPFAM:SSF50630 Gene3D:G3DSA:2.40.70.10 PANTHER:PTHR13683 EMBL:EQ973828 RefSeq:XP_002518445.1 GeneID:8277993 KEGG:rcu:RCOM_0903730 KO:K08245 PhylomeDB:B9RXH6 ProtClustDB:CLSN2926707 Uniprot:B9RXH6
Root	Isotig02487	104	164	-0.786	1.05E-05	UNIPROTKB|B9RXH6 - symbol:RCOM_0903730 "Aspartic proteinase, putative" species:3988 "Ricinus communis" [GO:0005783 "endoplasmic reticulum" evidence=IDA] InterPro:IPR001461 InterPro:IPR001969 InterPro:IPR007856 InterPro:IPR009007 Pfam:PF00026 Pfam:PF05184 PRINTS:PR00792 PROSITE:PS00141 GO:GO:0005783 GO:GO:0006508 GO:GO:0006629 InterPro:IPR008138 InterPro:IPR011001 InterPro:IPR008139 Gene3D:G3DSA:1.10.225.10 Pfam:PF03489 SMART:SM00741 SUPFAM:SSF47862 PROSITE:PS50015 GO:GO:0004190 InterPro:IPR021109 SUPFAM:SSF50630 Gene3D:G3DSA:2.40.70.10 PANTHER:PTHR13683 EMBL:EQ973828 RefSeq:XP_002518445.1 GeneID:8277993 KEGG:rcu:RCOM_0903730 KO:K08245 PhylomeDB:B9RXH6 ProtClustDB:CLSN2926707 Uniprot:B9RXH6
Root	Isotig02488	99	149	-0.719	0.000102289	UNIPROTKB|B9RXH6 - symbol:RCOM_0903730 "Aspartic proteinase, putative" species:3988 "Ricinus communis" [GO:0005783 "endoplasmic reticulum" evidence=IDA] InterPro:IPR001461 InterPro:IPR001969 InterPro:IPR007856 InterPro:IPR009007 Pfam:PF00026 Pfam:PF05184 PRINTS:PR00792 PROSITE:PS00141 GO:GO:0005783

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0006508 GO:GO:0006629 InterPro:IPR008138 InterPro:IPR011001 InterPro:IPR008139 Gene3D:G3DSA:1.10.225.10 Pfam:PF03489 SMART:SM00741 SUPFAM:SSF47862 PROSITE:PS50015 GO:GO:0004190 InterPro:IPR021109 SUPFAM:SSF50630 Gene3D:G3DSA:2.40.70.10 PANTHER:PTHR13683 EMBL:EQ973828 RefSeq:XP_002518445.1 GeneID:8277993 KEGG:rcu:RCOM_0903730 KO:K08245 PhylomeDB:B9RXH6 ProtClustDB:CLSN2926707 Uniprot:B9RXH6
Root	Isotig02489	96	151	-0.782	2.55E-05	UNIPROTKB|B9RXH6 - symbol:RCOM_0903730 "Aspartic proteinase, putative" species:3988 "Ricinus communis" [GO:0005783 "endoplasmic reticulum" evidence=IDA] InterPro:IPR001461 InterPro:IPR001969 InterPro:IPR007856 InterPro:IPR009007 Pfam:PF00026 Pfam:PF05184 PRINTS:PR00792 PROSITE:PS00141 GO:GO:0005783 GO:GO:0006508 GO:GO:0006629 InterPro:IPR008138 InterPro:IPR011001 InterPro:IPR008139 Gene3D:G3DSA:1.10.225.10 Pfam:PF03489 SMART:SM00741 SUPFAM:SSF47862 PROSITE:PS50015 GO:GO:0004190 InterPro:IPR021109 SUPFAM:SSF50630 Gene3D:G3DSA:2.40.70.10 PANTHER:PTHR13683 EMBL:EQ973828 RefSeq:XP_002518445.1 GeneID:8277993 KEGG:rcu:RCOM_0903730 KO:K08245 PhylomeDB:B9RXH6 ProtClustDB:CLSN2926707 Uniprot:B9RXH6
Root	Isotig02493	3	26	-3.244	2.27E-06	TAIR|locus:2083053 - symbol:AT3G49930 "AT3G49930" species:3702 "Arabidopsis thaliana" [GO:0003676 "nucleic acid binding" evidence=ISS] [GO:0005622 "intracellular" evidence=IEA] [GO:0008270 "zinc ion binding" evidence=ISS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=TAS] InterPro:IPR007087 InterPro:IPR013087 InterPro:IPR015880 PROSITE:PS00028 PROSITE:PS50157 SMART:SM00355 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0006355 GO:GO:0008270 GO:GO:0003676 Gene3D:G3DSA:3.30.160.60 GO:GO:0005622 EMBL:AL132978 HSSP:Q38895 HOGENOM:HBG600018 EMBL:BT029377 IPI:IPI00542862 PIR:T45846 RefSeq:NP_190562.1 UniGene:At.35551 ProteinModelPortal:Q9SN24 SMR:Q9SN24 EnsemblPlants:AT3G49930.1 GeneID:824155 KEGG:ath:AT3G49930 TAIR:At3g49930 eggNOG:NOG248161 InParanoid:Q9SN24 OMA:THNCSIC PhylomeDB:Q9SN24 ProtClustDB:CLSN2684382 Genevestigator:Q9SN24 Uniprot:Q9SN24
Root	Isotig02495	3	26	-3.244	2.27E-06	TAIR|locus:2199246 - symbol:STZ "AT1G27730" species:3702 "Arabidopsis thaliana" [GO:0003676 "nucleic acid binding" evidence=ISS] [GO:0008270 "zinc ion binding" evidence=ISS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0005634 "nucleus" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0009414 "response to water deprivation" evidence=IEP;IMP] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] [GO:0035264 "multicellular organism growth" evidence=IMP] [GO:0043565 "sequence-specific DNA binding" evidence=IDA] [GO:0045892 "negative regulation of transcription, DNA-dependent" evidence=IDA] [GO:0010200 "response to chitin" evidence=IEP] [GO:0009611 "response to wounding" evidence=IEP] [GO:0006979 "response to oxidative stress" evidence=IMP] [GO:0009644 "response to high light intensity" evidence=IEP] [GO:0010117 "photoprotection" evidence=IMP] [GO:0015979 "photosynthesis" evidence=IMP] [GO:0009651 "response to salt stress" evidence=IGI;IEP] InterPro:IPR007087 InterPro:IPR013087 InterPro:IPR015880 PROSITE:PS00028 PROSITE:PS50157 SMART:SM00355 EMBL:CP002684 GO:GO:0005634 GO:GO:0006355 GO:GO:0008270 GO:GO:0006351 GO:GO:0003676 EMBL:AC012375 Gene3D:G3DSA:3.30.160.60 EMBL:X95573 EMBL:X98670 EMBL:X98671 EMBL:AF250336 EMBL:AY034998 EMBL:AY063006 IPI:IPI00536591 RefSeq:NP_174094.1 UniGene:At.24624 ProteinModelPortal:Q96289 SMR:Q96289 STRING:Q96289 GeneID:839666 KEGG:ath:AT1G27730 TAIR:At1g27730 eggNOG:NOG276050 InParanoid:Q9SFY6 OMA:HVSSSHR ProtClustDB:CLSN2679322 ArrayExpress:Q96289 Genevestigator:Q96289 Uniprot:Q96289
Root	Isotig02506	13	75	-2.657	3.29E-13	TAIR|locus:2177003 - symbol:TUB6 "AT5G12250" species:3702 "Arabidopsis thaliana" [GO:0009409 "response to cold" evidence=IEP] [GO:0005200 "structural constituent of cytoskeleton" evidence=ISS] [GO:0007017 "microtubule-based process" evidence=ISS] [GO:0015630 "microtubule cytoskeleton" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] InterPro:IPR000217 InterPro:IPR002453 InterPro:IPR003008 InterPro:IPR008280 InterPro:IPR017975 InterPro:IPR018316 Pfam:PF00091 Pfam:PF03953 PRINTS:PR01161 PRINTS:PR01163 PROSITE:PS00227 SMART:SM00864 SMART:SM00865 GO:GO:0005525 GO:GO:0005886 GO:GO:0005737 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005198 GO:GO:0003924 GO:GO:0009409 GO:GO:0009651 GO:GO:0005874 GO:GO:0051258 Gene3D:G3DSA:3.40.50.1440 SUPFAM:SSF52490 GO:GO:0007018 EMBL:AB007727 Gene3D:G3DSA:3.30.1330.20 SUPFAM:SSF55307 HOGENOM:HBG750007 InterPro:IPR023123 Gene3D:G3DSA:1.10.287.600 PANTHER:PTHR11588 InterPro:IPR013838 KO:K07375 ProtClustDB:PLN00220

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						PROSITE:PS00228 OMA:EVINDEH EMBL:M84703 EMBL:AF360260 EMBL:AY040074 IPI:IPI00545934 PIR:JQ1590 RefSeq:NP_196786.1 UniGene:At.23425 UniGene:At.72672 UniGene:At.74848 ProteinModelPortal:P29514 SMR:P29514 STRING:P29514 PRIDE:P29514 EnsemblPlants:AT5G12250.1 GeneID:831100 KEGG:ath:AT5G12250 TAIR:At5g12250 InParanoid:P29514 PhylomeDB:P29514 ArrayExpress:P29514 Genevestigator:P29514 GermOnline:AT5G12250 Uniprot:P29514
Root	Isotig02507	8	60	-3.036	3.21E-12	TAIR|locus:2177003 - symbol:TUB6 "AT5G12250" species:3702 "Arabidopsis thaliana" [GO:0009409 "response to cold" evidence=IEP] [GO:0005200 "structural constituent of cytoskeleton" evidence=ISS] [GO:0007017 "microtubule-based process" evidence=ISS] [GO:0015630 "microtubule cytoskeleton" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] InterPro:IPR000217 InterPro:IPR002453 InterPro:IPR003008 InterPro:IPR008280 InterPro:IPR017975 InterPro:IPR018316 Pfam:PF00091 Pfam:PF03953 PRINTS:PR01161 PRINTS:PR01163 PROSITE:PS00227 SMART:SM00864 SMART:SM00865 GO:GO:0005525 GO:GO:0005886 GO:GO:0005737 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005198 GO:GO:0003924 GO:GO:0009409 GO:GO:0009651 GO:GO:0005874 GO:GO:0051258 Gene3D:G3DSA:3.40.50.1440 SUPFAM:SSF52490 GO:GO:0007018 EMBL:AB007727 Gene3D:G3DSA:3.30.1330.20 SUPFAM:SSF55307 HOGENOM:HBG750007 InterPro:IPR023123 Gene3D:G3DSA:1.10.287.600 PANTHER:PTHR11588 InterPro:IPR013838 KO:K07375 ProtClustDB:PLN00220 PROSITE:PS00228 OMA:EVINDEH EMBL:M84703 EMBL:AF360260 EMBL:AY040074 IPI:IPI00545934 PIR:JQ1590 RefSeq:NP_196786.1 UniGene:At.23425 UniGene:At.72672 UniGene:At.74848 ProteinModelPortal:P29514 SMR:P29514 STRING:P29514 PRIDE:P29514 EnsemblPlants:AT5G12250.1 GeneID:831100 KEGG:ath:AT5G12250 TAIR:At5g12250 InParanoid:P29514 PhylomeDB:P29514 ArrayExpress:P29514 Genevestigator:P29514 GermOnline:AT5G12250 Uniprot:P29514
Root	Isotig02508	15	39	-1.507	0.000277271	TAIR|locus:2177003 - symbol:TUB6 "AT5G12250" species:3702 "Arabidopsis thaliana" [GO:0009409 "response to cold" evidence=IEP] [GO:0005200 "structural constituent of cytoskeleton" evidence=ISS] [GO:0007017 "microtubule-based process" evidence=ISS] [GO:0015630 "microtubule cytoskeleton" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] InterPro:IPR000217 InterPro:IPR002453 InterPro:IPR003008 InterPro:IPR008280 InterPro:IPR017975 InterPro:IPR018316 Pfam:PF00091 Pfam:PF03953 PRINTS:PR01161 PRINTS:PR01163 PROSITE:PS00227 SMART:SM00864 SMART:SM00865 GO:GO:0005525 GO:GO:0005886 GO:GO:0005737 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005198 GO:GO:0003924 GO:GO:0009409 GO:GO:0009651 GO:GO:0005874 GO:GO:0051258 Gene3D:G3DSA:3.40.50.1440 SUPFAM:SSF52490 GO:GO:0007018 EMBL:AB007727 Gene3D:G3DSA:3.30.1330.20 SUPFAM:SSF55307 HOGENOM:HBG750007 InterPro:IPR023123 Gene3D:G3DSA:1.10.287.600 PANTHER:PTHR11588 InterPro:IPR013838 KO:K07375 ProtClustDB:PLN00220 PROSITE:PS00228 OMA:EVINDEH EMBL:M84703 EMBL:AF360260 EMBL:AY040074 IPI:IPI00545934 PIR:JQ1590 RefSeq:NP_196786.1 UniGene:At.23425 UniGene:At.72672 UniGene:At.74848 ProteinModelPortal:P29514 SMR:P29514 STRING:P29514 PRIDE:P29514 EnsemblPlants:AT5G12250.1 GeneID:831100 KEGG:ath:AT5G12250 TAIR:At5g12250 InParanoid:P29514 PhylomeDB:P29514 ArrayExpress:P29514 Genevestigator:P29514 GermOnline:AT5G12250 Uniprot:P29514
Root	Isotig02509	13	76	-2.676	1.86E-13	TAIR|locus:2177003 - symbol:TUB6 "AT5G12250" species:3702 "Arabidopsis thaliana" [GO:0009409 "response to cold" evidence=IEP] [GO:0005200 "structural constituent of cytoskeleton" evidence=ISS] [GO:0007017 "microtubule-based process" evidence=ISS] [GO:0015630 "microtubule cytoskeleton" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] InterPro:IPR000217 InterPro:IPR002453 InterPro:IPR003008 InterPro:IPR008280 InterPro:IPR017975 InterPro:IPR018316 Pfam:PF00091 Pfam:PF03953 PRINTS:PR01161 PRINTS:PR01163 PROSITE:PS00227 SMART:SM00864 SMART:SM00865 GO:GO:0005525 GO:GO:0005886 GO:GO:0005737 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005198 GO:GO:0003924 GO:GO:0009409 GO:GO:0009651 GO:GO:0005874 GO:GO:0051258 Gene3D:G3DSA:3.40.50.1440 SUPFAM:SSF52490 GO:GO:0007018 EMBL:AB007727 Gene3D:G3DSA:3.30.1330.20 SUPFAM:SSF55307 HOGENOM:HBG750007 InterPro:IPR023123 Gene3D:G3DSA:1.10.287.600 PANTHER:PTHR11588 InterPro:IPR013838 KO:K07375 ProtClustDB:PLN00220 PROSITE:PS00228 OMA:EVINDEH EMBL:M84703 EMBL:AF360260 EMBL:AY040074 IPI:IPI00545934 PIR:JQ1590 RefSeq:NP_196786.1 UniGene:At.23425 UniGene:At.72672 UniGene:At.74848 ProteinModelPortal:P29514 SMR:P29514 STRING:P29514 PRIDE:P29514 EnsemblPlants:AT5G12250.1

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GeneID:831100 KEGG:ath:AT5G12250 TAIR:At5g12250 InParanoid:P29514 PhylomeDB:P29514 ArrayExpress:P29514 Genevestigator:P29514 GermOnline:AT5G12250 Uniprot:P29514
Root	Isotig02510	8	61	-3.060	1.76E-12	TAIR|locus:2177003 - symbol:TUB6 "AT5G12250" species:3702 "Arabidopsis thaliana" [GO:0009409 "response to cold" evidence=IEP] [GO:0005200 "structural constituent of cytoskeleton" evidence=ISS] [GO:0007017 "microtubule-based process" evidence=ISS] [GO:0015630 "microtubule cytoskeleton" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] InterPro:IPR000217 InterPro:IPR002453 InterPro:IPR003008 InterPro:IPR008280 InterPro:IPR017975 InterPro:IPR018316 Pfam:PF00091 Pfam:PF03953 PRINTS:PR01161 PRINTS:PR01163 PROSITE:PS00227 SMART:SM00864 SMART:SM00865 GO:GO:0005525 GO:GO:0005886 GO:GO:0005737 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005198 GO:GO:0003924 GO:GO:0009409 GO:GO:0009651 GO:GO:0005874 GO:GO:0051258 Gene3D:G3DSA:3.40.50.1440 SUPFAM:SSF52490 GO:GO:0007018 EMBL:AB007727 Gene3D:G3DSA:3.30.1330.20 SUPFAM:SSF55307 HOGENOM:HBG750007 InterPro:IPR023123 Gene3D:G3DSA:1.10.287.600 PANTHER:PTHR11588 InterPro:IPR013838 KO:K07375 ProtClustDB:PLN00220 PROSITE:PS00228 OMA:EVINDEH EMBL:M84703 EMBL:AF360260 EMBL:AY040074 IPI:IPI00545934 PIR:JQ1590 RefSeq:NP_196786.1 UniGene:At.23425 UniGene:At.72672 UniGene:At.74848 ProteinModelPortal:P29514 SMR:P29514 STRING:P29514 PRIDE:P29514 EnsemblPlants:AT5G12250.1 GeneID:831100 KEGG:ath:AT5G12250 TAIR:At5g12250 InParanoid:P29514 PhylomeDB:P29514 ArrayExpress:P29514 Genevestigator:P29514 GermOnline:AT5G12250 Uniprot:P29514
Root	Isotig02516	10	34	-1.895	6.62E-05	TAIR|locus:2095913 - symbol:AT3G03990 "AT3G03990" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=ISS] EMBL:CP002686 GO:GO:0016787 EMBL:AC011698 ProtClustDB:CLSN2684507 EMBL:AY064145 EMBL:AY097402 IPI:IPI00546981 RefSeq:NP_566220.1 UniGene:At.27069 ProteinModelPortal:Q9SQR3 SMR:Q9SQR3 MEROPS:S33.A18 PRIDE:Q9SQR3 EnsemblPlants:AT3G03990.1 GeneID:819554 KEGG:ath:AT3G03990 TAIR:At3g03990 InParanoid:Q9SQR3 OMA:CAYVGHS PhylomeDB:Q9SQR3 Genevestigator:Q9SQR3 Uniprot:Q9SQR3
Root	Isotig02517	14	38	-1.570	0.000218579	TAIR|locus:2095913 - symbol:AT3G03990 "AT3G03990" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=ISS] EMBL:CP002686 GO:GO:0016787 EMBL:AC011698 ProtClustDB:CLSN2684507 EMBL:AY064145 EMBL:AY097402 IPI:IPI00546981 RefSeq:NP_566220.1 UniGene:At.27069 ProteinModelPortal:Q9SQR3 SMR:Q9SQR3 MEROPS:S33.A18 PRIDE:Q9SQR3 EnsemblPlants:AT3G03990.1 GeneID:819554 KEGG:ath:AT3G03990 TAIR:At3g03990 InParanoid:Q9SQR3 OMA:CAYVGHS PhylomeDB:Q9SQR3 Genevestigator:Q9SQR3 Uniprot:Q9SQR3
Root	Isotig02519	14	38	-1.570	0.000218579	TAIR|locus:2095913 - symbol:AT3G03990 "AT3G03990" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=ISS] EMBL:CP002686 GO:GO:0016787 EMBL:AC011698 ProtClustDB:CLSN2684507 EMBL:AY064145 EMBL:AY097402 IPI:IPI00546981 RefSeq:NP_566220.1 UniGene:At.27069 ProteinModelPortal:Q9SQR3 SMR:Q9SQR3 MEROPS:S33.A18 PRIDE:Q9SQR3 EnsemblPlants:AT3G03990.1 GeneID:819554 KEGG:ath:AT3G03990 TAIR:At3g03990 InParanoid:Q9SQR3 OMA:CAYVGHS PhylomeDB:Q9SQR3 Genevestigator:Q9SQR3 Uniprot:Q9SQR3
Root	Isotig02536	3	23	-3.068	1.45E-05	TAIR|locus:2119246 - symbol:AT4G33500 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004721 "phosphoprotein phosphatase activity" evidence=IEA] [GO:0004722 "protein serine/threonine phosphatase activity" evidence=ISS] [GO:0009507 "chloroplast" evidence=IDA] InterPro:IPR001932 Pfam:PF07228 PROSITE:PS01032 SMART:SM00331 SMART:SM00332 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0009507 GO:GO:0046872 EMBL:AL161583 EMBL:AL035678 GO:GO:0004721 eggNOG:COG0631 Gene3D:G3DSA:3.60.40.10 SUPFAM:SSF81606 EMBL:AY035047 EMBL:AY051052 IPI:IPI00523794 PIR:T06001 RefSeq:NP_567923.1 UniGene:At.382 ProteinModelPortal:Q93V88 STRING:Q93V88 PRIDE:Q93V88 EnsemblPlants:AT4G33500.1 GeneID:829488 KEGG:ath:AT4G33500 TAIR:At4g33500 InParanoid:Q93V88 OMA:IAQKPVI PhylomeDB:Q93V88 ProtClustDB:CLSN2722376 Genevestigator:Q93V88 Uniprot:Q93V88
Root	Isotig02537	3	23	-3.068	1.45E-05	TAIR|locus:2119246 - symbol:AT4G33500 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004721 "phosphoprotein phosphatase activity" evidence=IEA] [GO:0004722 "protein serine/threonine phosphatase activity" evidence=ISS] [GO:0009507 "chloroplast" evidence=IDA] InterPro:IPR001932 Pfam:PF07228 PROSITE:PS01032 SMART:SM00331 SMART:SM00332 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0009507 GO:GO:0046872 EMBL:AL161583 EMBL:AL035678 GO:GO:0004721 eggNOG:COG0631 Gene3D:G3DSA:3.60.40.10 SUPFAM:SSF81606 EMBL:AY035047

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EMBL:AY051052 IPI:IPI00523794 PIR:T06001 RefSeq:NP_567923.1 UniGene:At.382 ProteinModelPortal:Q93V88 STRING:Q93V88 PRIDE:Q93V88 EnsemblPlants:AT4G33500.1 GeneID:829488 KEGG:ath:AT4G33500 TAIR:At4g33500 InParanoid:Q93V88 OMA:IAQKPVI PhylomeDB:Q93V88 ProtClustDB:CLSN2722376 Genevestigator:Q93V88 Uniprot:Q93V88
Root	Isotig02538	3	17	-2.631	0.00056383	TAIR|locus:2119246 - symbol:AT4G33500 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004721 "phosphoprotein phosphatase activity" evidence=IEA] [GO:0004722 "protein serine/threonine phosphatase activity" evidence=ISS] [GO:0009507 "chloroplast" evidence=IDA] InterPro:IPR001932 Pfam:PF07228 PROSITE:PS01032 SMART:SM00331 SMART:SM00332 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0009507 GO:GO:0046872 EMBL:AL161583 EMBL:AL035678 GO:GO:0004721 eggNOG:COG0631 Gene3D:G3DSA:3.60.40.10 SUPFAM:SSF81606 EMBL:AY035047 EMBL:AY051052 IPI:IPI00523794 PIR:T06001 RefSeq:NP_567923.1 UniGene:At.382 ProteinModelPortal:Q93V88 STRING:Q93V88 PRIDE:Q93V88 EnsemblPlants:AT4G33500.1 GeneID:829488 KEGG:ath:AT4G33500 TAIR:At4g33500 InParanoid:Q93V88 OMA:IAQKPVI PhylomeDB:Q93V88 ProtClustDB:CLSN2722376 Genevestigator:Q93V88 Uniprot:Q93V88
Root	Isotig02561	16	1	3.871	0.000146741	TAIR|locus:2119886 - symbol:AT4G29090 species:3702 "Arabidopsis thaliana" [GO:0003676 "nucleic acid binding" evidence=IEA] [GO:0003723 "RNA binding" evidence=ISS] [GO:0003964 "RNA-directed DNA polymerase activity" evidence=ISS] [GO:0006278 "RNA-dependent DNA replication" evidence=ISS] InterPro:IPR012337 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0003676 SUPFAM:SSF53098 GO:GO:0003964 EMBL:AL078470 EMBL:AL161574 ProtClustDB:CLSN2683532 EMBL:DQ056660 IPI:IPI00548066 PIR:T08964 RefSeq:NP_194638.1 UniGene:At.54541 ProteinModelPortal:Q9SZD8 PRIDE:Q9SZD8 EnsemblPlants:AT4G29090.1 GeneID:829030 KEGG:ath:AT4G29090 TAIR:At4g29090 eggNOG:NOG253635 InParanoid:Q9SZD8 OMA:KESACIR PhylomeDB:Q9SZD8 ArrayExpress:Q9SZD8 Genevestigator:Q9SZD8 Uniprot:Q9SZD8
Root	Isotig02562	16	1	3.871	0.000146741	TAIR|locus:2119886 - symbol:AT4G29090 species:3702 "Arabidopsis thaliana" [GO:0003676 "nucleic acid binding" evidence=IEA] [GO:0003723 "RNA binding" evidence=ISS] [GO:0003964 "RNA-directed DNA polymerase activity" evidence=ISS] [GO:0006278 "RNA-dependent DNA replication" evidence=ISS] InterPro:IPR012337 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0003676 SUPFAM:SSF53098 GO:GO:0003964 EMBL:AL078470 EMBL:AL161574 ProtClustDB:CLSN2683532 EMBL:DQ056660 IPI:IPI00548066 PIR:T08964 RefSeq:NP_194638.1 UniGene:At.54541 ProteinModelPortal:Q9SZD8 PRIDE:Q9SZD8 EnsemblPlants:AT4G29090.1 GeneID:829030 KEGG:ath:AT4G29090 TAIR:At4g29090 eggNOG:NOG253635 InParanoid:Q9SZD8 OMA:KESACIR PhylomeDB:Q9SZD8 ArrayExpress:Q9SZD8 Genevestigator:Q9SZD8 Uniprot:Q9SZD8
Root	Isotig02586	0	19	-5.377	3.67E-06	No hit
Root	Isotig02587	0	19	-5.377	3.67E-06	No hit
Root	Isotig02620	13	1	3.571	0.000882483	TAIR|locus:2142908 - symbol:AT5G35930 species:3702 "Arabidopsis thaliana" [GO:0000036 "acyl carrier activity" evidence=IEA] [GO:0003824 "catalytic activity" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008152 "metabolic process" evidence=IEA] [GO:0016208 "AMP binding" evidence=ISS] [GO:0031177 "phosphopantetheine binding" evidence=IEA] [GO:0048037 "cofactor binding" evidence=IEA] InterPro:IPR000873 InterPro:IPR006162 Pfam:PF00501 PROSITE:PS00012 InterPro:IPR006163 InterPro:IPR009081 Pfam:PF00550 Prosite:PS00455 EMBL:CP002688 InterPro:IPR020845 GO:GO:0016874 GO:GO:0003824 GO:GO:0000036 GO:GO:0048037 GO:GO:0031177 Gene3D:G3DSA:1.10.1200.10 SUPFAM:SSF47336 PROSITE:PS50075 eggNOG:COG1520 KO:K00142 InterPro:IPR018391 InterPro:IPR011047 Gene3D:G3DSA:2.140.10.10 SMART:SM00564 SUPFAM:SSF50998 EMBL:AB025602 EMBL:AY099772 IPI:IPI00520530 RefSeq:NP_198442.2 UniGene:At.30571 SMR:F4K1G2 PRIDE:Q9LTK8 EnsemblPlants:AT5G35930.1 GeneID:833582 KEGG:ath:AT5G35930 TAIR:At5g35930 Uniprot:F4K1G2
Root	Isotig02621	13	1	3.571	0.000882483	TAIR|locus:2142908 - symbol:AT5G35930 species:3702 "Arabidopsis thaliana" [GO:0000036 "acyl carrier activity" evidence=IEA] [GO:0003824 "catalytic activity" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008152 "metabolic process" evidence=IEA] [GO:0016208 "AMP binding" evidence=ISS] [GO:0031177 "phosphopantetheine binding" evidence=IEA] [GO:0048037 "cofactor binding" evidence=IEA] InterPro:IPR000873 InterPro:IPR006162 Pfam:PF00501 PROSITE:PS00012 InterPro:IPR006163 InterPro:IPR009081 Pfam:PF00550 Prosite:PS00455 EMBL:CP002688 InterPro:IPR020845 GO:GO:0016874 GO:GO:0003824 GO:GO:0000036 GO:GO:0048037 GO:GO:0031177 Gene3D:G3DSA:1.10.1200.10 SUPFAM:SSF47336 PROSITE:PS50075

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						eggNOG:COG1520 KO:K00142 InterPro:IPR018391 InterPro:IPR011047 Gene3D:G3DSA:2.140.10.10 SMART:SM00564 SUPFAM:SSF50998 EMBL:AB025602 EMBL:AY099772 IPI:IPI00520530 RefSeq:NP_198442.2 UniGene:At.30571 SMR:F4K1G2 PRIDE:Q9LTK8 EnsemblPlants:AT5G35930.1 GeneID:833582 KEGG:ath:AT5G35930 TAIR:At5g35930 Uniprot:F4K1G2
Root	Isotig02622	13	1	3.571	0.000882483	TAIR|locus:2142908 - symbol:AT5G35930 species:3702 "Arabidopsis thaliana" [GO:0000036 "acyl carrier activity" evidence=IEA] [GO:0003824 "catalytic activity" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008152 "metabolic process" evidence=IEA] [GO:0016208 "AMP binding" evidence=ISS] [GO:0031177 "phosphopantetheine binding" evidence=IEA] [GO:0048037 "cofactor binding" evidence=IEA] InterPro:IPR000873 InterPro:IPR006162 Pfam:PF00501 PROSITE:PS00012 InterPro:IPR006163 InterPro:IPR009081 Pfam:PF00550 Prosite:PS00455 EMBL:CP002688 InterPro:IPR020845 GO:GO:0016874 GO:GO:0003824 GO:GO:0000036 GO:GO:0048037 GO:GO:0031177 Gene3D:G3DSA:1.10.1200.10 SUPFAM:SSF47336 PROSITE:PS50075 eggNOG:COG1520 KO:K00142 InterPro:IPR018391 InterPro:IPR011047 Gene3D:G3DSA:2.140.10.10 SMART:SM00564 SUPFAM:SSF50998 EMBL:AB025602 EMBL:AY099772 IPI:IPI00520530 RefSeq:NP_198442.2 UniGene:At.30571 SMR:F4K1G2 PRIDE:Q9LTK8 EnsemblPlants:AT5G35930.1 GeneID:833582 KEGG:ath:AT5G35930 TAIR:At5g35930 Uniprot:F4K1G2
Root	Isotig02623	13	1	3.571	0.000882483	TAIR|locus:2142908 - symbol:AT5G35930 species:3702 "Arabidopsis thaliana" [GO:0000036 "acyl carrier activity" evidence=IEA] [GO:0003824 "catalytic activity" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008152 "metabolic process" evidence=IEA] [GO:0016208 "AMP binding" evidence=ISS] [GO:0031177 "phosphopantetheine binding" evidence=IEA] [GO:0048037 "cofactor binding" evidence=IEA] InterPro:IPR000873 InterPro:IPR006162 Pfam:PF00501 PROSITE:PS00012 InterPro:IPR006163 InterPro:IPR009081 Pfam:PF00550 Prosite:PS00455 EMBL:CP002688 InterPro:IPR020845 GO:GO:0016874 GO:GO:0003824 GO:GO:0000036 GO:GO:0048037 GO:GO:0031177 Gene3D:G3DSA:1.10.1200.10 SUPFAM:SSF47336 PROSITE:PS50075 eggNOG:COG1520 KO:K00142 InterPro:IPR018391 InterPro:IPR011047 Gene3D:G3DSA:2.140.10.10 SMART:SM00564 SUPFAM:SSF50998 EMBL:AB025602 EMBL:AY099772 IPI:IPI00520530 RefSeq:NP_198442.2 UniGene:At.30571 SMR:F4K1G2 PRIDE:Q9LTK8 EnsemblPlants:AT5G35930.1 GeneID:833582 KEGG:ath:AT5G35930 TAIR:At5g35930 Uniprot:F4K1G2
Root	Isotig02640	19	50	-1.525	3.30E-05	TAIR|locus:2135237 - symbol:AGT2 "AT4G39660" species:3702 "Arabidopsis thaliana" [GO:0008453 "alanine-glyoxylate transaminase activity" evidence=ISS;IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0019544 "arginine catabolic process to glutamate" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0008270 "zinc ion binding" evidence=IDA] InterPro:IPR005814 InterPro:IPR015421 InterPro:IPR015422 Pfam:PF00202 PROSITE:PS00600 GO:GO:0005739 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0046686 GO:GO:0005774 GO:GO:0030170 InterPro:IPR015424 Gene3D:G3DSA:3.40.640.10 Gene3D:G3DSA:3.90.1150.10 SUPFAM:SSF53383 GO:GO:0008270 EMBL:AF166351 EMBL:AL022605 EMBL:AL161595 EMBL:AY054264 EMBL:BT002306 IPI:IPI00519673 PIR:T05003 RefSeq:NP_568064.1 UniGene:At.22488 ProteinModelPortal:Q940M2 SMR:Q940M2 STRING:Q940M2 PRIDE:Q940M2 EnsemblPlants:AT4G39660.1 GeneID:830120 KEGG:ath:AT4G39660 GeneFarm:5077 TAIR:At4g39660 eggNOG:COG0160 HOGENOM:HBG725944 InParanoid:Q940M2 KO:K00827 OMA:GIVTVSC PhylomeDB:Q940M2 ProtClustDB:CLSN2683116 ArrayExpress:Q9SU41 Genevestigator:Q940M2 GermOnline:AT4G39660 GO:GO:0008453 GO:GO:0019544 GO:GO:0009853 PANTHER:PTHR11986 Uniprot:Q940M2
Root	Isotig02641	19	45	-1.373	0.000271992	TAIR|locus:2135237 - symbol:AGT2 "AT4G39660" species:3702 "Arabidopsis thaliana" [GO:0008453 "alanine-glyoxylate transaminase activity" evidence=ISS;IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0019544 "arginine catabolic process to glutamate" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0008270 "zinc ion binding" evidence=IDA] InterPro:IPR005814 InterPro:IPR015421 InterPro:IPR015422 Pfam:PF00202 PROSITE:PS00600 GO:GO:0005739 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0046686 GO:GO:0005774 GO:GO:0030170 InterPro:IPR015424 Gene3D:G3DSA:3.40.640.10 Gene3D:G3DSA:3.90.1150.10 SUPFAM:SSF53383 GO:GO:0008270 EMBL:AF166351 EMBL:AL022605 EMBL:AL161595 EMBL:AY054264 EMBL:BT002306 IPI:IPI00519673 PIR:T05003 RefSeq:NP_568064.1 UniGene:At.22488 ProteinModelPortal:Q940M2 SMR:Q940M2 STRING:Q940M2 PRIDE:Q940M2 EnsemblPlants:AT4G39660.1 GeneID:830120 KEGG:ath:AT4G39660 GeneFarm:5077 TAIR:At4g39660 eggNOG:COG0160 HOGENOM:HBG725944 InParanoid:Q940M2 KO:K00827 OMA:GIVTVSC PhylomeDB:Q940M2

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						ProtClustDB:CLSN2683116 ArrayExpress:Q9SU41 Genevestigator:Q940M2 GermOnline:AT4G39660 GO:GO:0008453 GO:GO:0019544 GO:GO:0009853 PANTHER:PTHR11986 Uniprot:Q940M2
Root	Isotig02644	1	20	-4.451	3.92E-06	TAIR|locus:2008855 - symbol:NRT1.1 "AT1G12110" species:3702 "Arabidopsis thaliana" [GO:0005215 "transporter activity" evidence=ISS] [GO:0009414 "response to water deprivation" evidence=IMP] [GO:0010167 "response to nitrate" evidence=IMP] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0015112 "nitrate transmembrane transporter activity" evidence=IMP] [GO:0015706 "nitrate transport" evidence=IMP] InterPro:IPR000109 InterPro:IPR018456 Pfam:PF00854 PROSITE:PS01022 PROSITE:PS01023 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005886 GO:GO:0005515 GO:GO:0009734 GO:GO:0009635 GO:GO:0015293 GO:GO:0009414 InterPro:IPR016196 SUPFAM:SSF103473 EMBL:AC002131 GO:GO:0015112 GO:GO:0042128 GO:GO:0010167 eggNOG:COG3104 GO:GO:0006857 HOGENOM:HBG605267 EMBL:L10357 EMBL:BT002016 EMBL:BT008783 EMBL:AK317498 IPI:IPI00534102 PIR:A45772 RefSeq:NP_563899.1 UniGene:At.19624 ProteinModelPortal:Q05085 IntAct:Q05085 STRING:Q05085 TCDB:2.A.17.3.1 PRIDE:Q05085 EnsemblPlants:AT1G12110.1 GeneID:837763 KEGG:ath:AT1G12110 TAIR:At1g12110 InParanoid:Q05085 OMA:ICAFAIV PhylomeDB:Q05085 ProtClustDB:CLSN2916999 ArrayExpress:Q05085 Genevestigator:Q05085 GermOnline:AT1G12110 Uniprot:Q05085
Root	Isotig02645	1	20	-4.451	3.92E-06	TAIR|locus:2008855 - symbol:NRT1.1 "AT1G12110" species:3702 "Arabidopsis thaliana" [GO:0005215 "transporter activity" evidence=ISS] [GO:0009414 "response to water deprivation" evidence=IMP] [GO:0010167 "response to nitrate" evidence=IMP] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0015112 "nitrate transmembrane transporter activity" evidence=IMP] [GO:0015706 "nitrate transport" evidence=IMP] InterPro:IPR000109 InterPro:IPR018456 Pfam:PF00854 PROSITE:PS01022 PROSITE:PS01023 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005886 GO:GO:0005515 GO:GO:0009734 GO:GO:0009635 GO:GO:0015293 GO:GO:0009414 InterPro:IPR016196 SUPFAM:SSF103473 EMBL:AC002131 GO:GO:0015112 GO:GO:0042128 GO:GO:0010167 eggNOG:COG3104 GO:GO:0006857 HOGENOM:HBG605267 EMBL:L10357 EMBL:BT002016 EMBL:BT008783 EMBL:AK317498 IPI:IPI00534102 PIR:A45772 RefSeq:NP_563899.1 UniGene:At.19624 ProteinModelPortal:Q05085 IntAct:Q05085 STRING:Q05085 TCDB:2.A.17.3.1 PRIDE:Q05085 EnsemblPlants:AT1G12110.1 GeneID:837763 KEGG:ath:AT1G12110 TAIR:At1g12110 InParanoid:Q05085 OMA:ICAFAIV PhylomeDB:Q05085 ProtClustDB:CLSN2916999 ArrayExpress:Q05085 Genevestigator:Q05085 GermOnline:AT1G12110 Uniprot:Q05085
Root	Isotig02646	1	20	-4.451	3.92E-06	TAIR|locus:2008855 - symbol:NRT1.1 "AT1G12110" species:3702 "Arabidopsis thaliana" [GO:0005215 "transporter activity" evidence=ISS] [GO:0009414 "response to water deprivation" evidence=IMP] [GO:0010167 "response to nitrate" evidence=IMP] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0015112 "nitrate transmembrane transporter activity" evidence=IMP] [GO:0015706 "nitrate transport" evidence=IMP] InterPro:IPR000109 InterPro:IPR018456 Pfam:PF00854 PROSITE:PS01022 PROSITE:PS01023 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005886 GO:GO:0005515 GO:GO:0009734 GO:GO:0009635 GO:GO:0015293 GO:GO:0009414 InterPro:IPR016196 SUPFAM:SSF103473 EMBL:AC002131 GO:GO:0015112 GO:GO:0042128 GO:GO:0010167 eggNOG:COG3104 GO:GO:0006857 HOGENOM:HBG605267 EMBL:L10357 EMBL:BT002016 EMBL:BT008783 EMBL:AK317498 IPI:IPI00534102 PIR:A45772 RefSeq:NP_563899.1 UniGene:At.19624 ProteinModelPortal:Q05085 IntAct:Q05085 STRING:Q05085 TCDB:2.A.17.3.1 PRIDE:Q05085 EnsemblPlants:AT1G12110.1 GeneID:837763 KEGG:ath:AT1G12110 TAIR:At1g12110 InParanoid:Q05085 OMA:ICAFAIV PhylomeDB:Q05085 ProtClustDB:CLSN2916999 ArrayExpress:Q05085 Genevestigator:Q05085 GermOnline:AT1G12110 Uniprot:Q05085
Root	Isotig02656	10	50	-2.451	1.32E-08	TAIR|locus:2127776 - symbol:CESA1 "AT4G32410" species:3702 "Arabidopsis thaliana" [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0016759 "cellulose synthase activity" evidence=ISS] [GO:0009832 "plant-type cell wall biogenesis" evidence=TAS] [GO:0030244 "cellulose biosynthetic process" evidence=IMP;TAS] [GO:0009833 "primary cell wall biogenesis" evidence=IMP] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] [GO:0042538 "hyperosmotic salinity response" evidence=IMP] InterPro:IPR001841 InterPro:IPR005150 Pfam:PF03552 PROSITE:PS50089 SMART:SM00184 Prosite:PS00518 GO:GO:0016021 GO:GO:0005886 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005794 GO:GO:0008270 InterPro:IPR013083 Gene3D:G3DSA:3.30.40.10 GO:GO:0007047

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EMBL:AL161581 EMBL:AL034567 CAZy:GT2 GO:GO:0042538 eggNOG:COG1215 GO:GO:0016760 GO:GO:0030244 EMBL:AF027172 EMBL:BT008654 EMBL:AK222115 EMBL:AK226243 IPI:IPI00536785 PIR:T05351 RefSeq:NP_194967.1 UniGene:At.21246 ProteinModelPortal:O48946 SMR:O48946 DIP:DIP-59354N STRING:O48946 PRIDE:O48946 EnsemblPlants:AT4G32410.1 GeneID:829376 KEGG:ath:AT4G32410 GeneFarm:5084 TAIR:At4g32410 HOGENOM:HBG744549 InParanoid:O48946 KO:K10999 OMA:DIENEFN PhylomeDB:O48946 ProtClustDB:PLN02400 Genevestigator:O48946 GermOnline:AT4G32410 GO:GO:0009833 Uniprot:O48946
Root	Isotig02657	10	49	-2.422	2.30E-08	TAIR|locus:2127776 - symbol:CESA1 "AT4G32410" species:3702 "Arabidopsis thaliana" [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0016759 "cellulose synthase activity" evidence=ISS] [GO:0009832 "plant-type cell wall biogenesis" evidence=TAS] [GO:0030244 "cellulose biosynthetic process" evidence=IMP;TAS] [GO:0009833 "primary cell wall biogenesis" evidence=IMP] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] [GO:0042538 "hyperosmotic salinity response" evidence=IMP] InterPro:IPR001841 InterPro:IPR005150 Pfam:PF03552 PROSITE:PS50089 SMART:SM00184 Prosite:PS00518 GO:GO:0016021 GO:GO:0005886 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005794 GO:GO:0008270 InterPro:IPR013083 Gene3D:G3DSA:3.30.40.10 GO:GO:0007047 EMBL:AL161581 EMBL:AL034567 CAZy:GT2 GO:GO:0042538 eggNOG:COG1215 GO:GO:0016760 GO:GO:0030244 EMBL:AF027172 EMBL:BT008654 EMBL:AK222115 EMBL:AK226243 IPI:IPI00536785 PIR:T05351 RefSeq:NP_194967.1 UniGene:At.21246 ProteinModelPortal:O48946 SMR:O48946 DIP:DIP-59354N STRING:O48946 PRIDE:O48946 EnsemblPlants:AT4G32410.1 GeneID:829376 KEGG:ath:AT4G32410 GeneFarm:5084 TAIR:At4g32410 HOGENOM:HBG744549 InParanoid:O48946 KO:K10999 OMA:DIENEFN PhylomeDB:O48946 ProtClustDB:PLN02400 Genevestigator:O48946 GermOnline:AT4G32410 GO:GO:0009833 Uniprot:O48946
Root	Isotig02658	11	50	-2.313	3.93E-08	TAIR|locus:2127776 - symbol:CESA1 "AT4G32410" species:3702 "Arabidopsis thaliana" [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0016759 "cellulose synthase activity" evidence=ISS] [GO:0009832 "plant-type cell wall biogenesis" evidence=TAS] [GO:0030244 "cellulose biosynthetic process" evidence=IMP;TAS] [GO:0009833 "primary cell wall biogenesis" evidence=IMP] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] [GO:0042538 "hyperosmotic salinity response" evidence=IMP] InterPro:IPR001841 InterPro:IPR005150 Pfam:PF03552 PROSITE:PS50089 SMART:SM00184 Prosite:PS00518 GO:GO:0016021 GO:GO:0005886 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005794 GO:GO:0008270 InterPro:IPR013083 Gene3D:G3DSA:3.30.40.10 GO:GO:0007047 EMBL:AL161581 EMBL:AL034567 CAZy:GT2 GO:GO:0042538 eggNOG:COG1215 GO:GO:0016760 GO:GO:0030244 EMBL:AF027172 EMBL:BT008654 EMBL:AK222115 EMBL:AK226243 IPI:IPI00536785 PIR:T05351 RefSeq:NP_194967.1 UniGene:At.21246 ProteinModelPortal:O48946 SMR:O48946 DIP:DIP-59354N STRING:O48946 PRIDE:O48946 EnsemblPlants:AT4G32410.1 GeneID:829376 KEGG:ath:AT4G32410 GeneFarm:5084 TAIR:At4g32410 HOGENOM:HBG744549 InParanoid:O48946 KO:K10999 OMA:DIENEFN PhylomeDB:O48946 ProtClustDB:PLN02400 Genevestigator:O48946 GermOnline:AT4G32410 GO:GO:0009833 Uniprot:O48946
Root	Isotig02659	10	37	-2.016	1.44E-05	TAIR|locus:2127776 - symbol:CESA1 "AT4G32410" species:3702 "Arabidopsis thaliana" [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0016759 "cellulose synthase activity" evidence=ISS] [GO:0009832 "plant-type cell wall biogenesis" evidence=TAS] [GO:0030244 "cellulose biosynthetic process" evidence=IMP;TAS] [GO:0009833 "primary cell wall biogenesis" evidence=IMP] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] [GO:0042538 "hyperosmotic salinity response" evidence=IMP] InterPro:IPR001841 InterPro:IPR005150 Pfam:PF03552 PROSITE:PS50089 SMART:SM00184 Prosite:PS00518 GO:GO:0016021 GO:GO:0005886 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005794 GO:GO:0008270 InterPro:IPR013083 Gene3D:G3DSA:3.30.40.10 GO:GO:0007047 EMBL:AL161581 EMBL:AL034567 CAZy:GT2 GO:GO:0042538 eggNOG:COG1215 GO:GO:0016760 GO:GO:0030244 EMBL:AF027172 EMBL:BT008654 EMBL:AK222115 EMBL:AK226243 IPI:IPI00536785 PIR:T05351 RefSeq:NP_194967.1 UniGene:At.21246 ProteinModelPortal:O48946 SMR:O48946 DIP:DIP-59354N STRING:O48946 PRIDE:O48946 EnsemblPlants:AT4G32410.1 GeneID:829376 KEGG:ath:AT4G32410 GeneFarm:5084 TAIR:At4g32410 HOGENOM:HBG744549 InParanoid:O48946 KO:K10999 OMA:DIENEFN PhylomeDB:O48946 ProtClustDB:PLN02400 Genevestigator:O48946 GermOnline:AT4G32410 GO:GO:0009833 Uniprot:O48946

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig02672	20	0	5.193	5.94E-06	TAIR|locus:2036029 - symbol:AMI1 "AT1G08980" species:3702 "Arabidopsis thaliana" [GO:0004040 "amidase activity" evidence=ISS;IDA] [GO:0009684 "indoleacetic acid biosynthetic process" evidence=IDA] [GO:0016810 "hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds" evidence=IDA] [GO:0043864 "indoleacetamide hydrolase activity" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR000120 Pfam:PF01425 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0004040 GO:GO:0016884 eggNOG:COG0154 InterPro:IPR020556 InterPro:IPR023631 Gene3D:G3DSA:3.90.1300.10 PANTHER:PTHR11895 SUPFAM:SSF75304 PROSITE:PS00571 EMBL:AF202077 EMBL:AC000106 EMBL:AY037198 EMBL:BT004554 IPI:IPI00537072 IPI:IPI00548661 PIR:F86221 RefSeq:NP_563831.1 UniGene:At.21299 HSSP:Q8RJN5 ProteinModelPortal:Q9FR37 SMR:Q9FR37 STRING:Q9FR37 PRIDE:Q9FR37 EnsemblPlants:AT1G08980.1 GeneID:837418 KEGG:ath:AT1G08980 TAIR:At1g08980 HOGENOM:HBG481888 InParanoid:Q9FR37 OMA:IQGAEAW PhylomeDB:Q9FR37 ProtClustDB:PLN02722 Genevestigator:Q9FR37 GO:GO:0043864 GO:GO:0009684 Uniprot:Q9FR37
Root	Isotig02673	21	0	5.263	3.38E-06	TAIR|locus:2036029 - symbol:AMI1 "AT1G08980" species:3702 "Arabidopsis thaliana" [GO:0004040 "amidase activity" evidence=ISS;IDA] [GO:0009684 "indoleacetic acid biosynthetic process" evidence=IDA] [GO:0016810 "hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds" evidence=IDA] [GO:0043864 "indoleacetamide hydrolase activity" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR000120 Pfam:PF01425 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0004040 GO:GO:0016884 eggNOG:COG0154 InterPro:IPR020556 InterPro:IPR023631 Gene3D:G3DSA:3.90.1300.10 PANTHER:PTHR11895 SUPFAM:SSF75304 PROSITE:PS00571 EMBL:AF202077 EMBL:AC000106 EMBL:AY037198 EMBL:BT004554 IPI:IPI00537072 IPI:IPI00548661 PIR:F86221 RefSeq:NP_563831.1 UniGene:At.21299 HSSP:Q8RJN5 ProteinModelPortal:Q9FR37 SMR:Q9FR37 STRING:Q9FR37 PRIDE:Q9FR37 EnsemblPlants:AT1G08980.1 GeneID:837418 KEGG:ath:AT1G08980 TAIR:At1g08980 HOGENOM:HBG481888 InParanoid:Q9FR37 OMA:IQGAEAW PhylomeDB:Q9FR37 ProtClustDB:PLN02722 Genevestigator:Q9FR37 GO:GO:0043864 GO:GO:0009684 Uniprot:Q9FR37
Root	Isotig02674	20	0	5.193	5.94E-06	TAIR|locus:2036029 - symbol:AMI1 "AT1G08980" species:3702 "Arabidopsis thaliana" [GO:0004040 "amidase activity" evidence=ISS;IDA] [GO:0009684 "indoleacetic acid biosynthetic process" evidence=IDA] [GO:0016810 "hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds" evidence=IDA] [GO:0043864 "indoleacetamide hydrolase activity" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR000120 Pfam:PF01425 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0004040 GO:GO:0016884 eggNOG:COG0154 InterPro:IPR020556 InterPro:IPR023631 Gene3D:G3DSA:3.90.1300.10 PANTHER:PTHR11895 SUPFAM:SSF75304 PROSITE:PS00571 EMBL:AF202077 EMBL:AC000106 EMBL:AY037198 EMBL:BT004554 IPI:IPI00537072 IPI:IPI00548661 PIR:F86221 RefSeq:NP_563831.1 UniGene:At.21299 HSSP:Q8RJN5 ProteinModelPortal:Q9FR37 SMR:Q9FR37 STRING:Q9FR37 PRIDE:Q9FR37 EnsemblPlants:AT1G08980.1 GeneID:837418 KEGG:ath:AT1G08980 TAIR:At1g08980 HOGENOM:HBG481888 InParanoid:Q9FR37 OMA:IQGAEAW PhylomeDB:Q9FR37 ProtClustDB:PLN02722 Genevestigator:Q9FR37 GO:GO:0043864 GO:GO:0009684 Uniprot:Q9FR37
Root	Isotig02675	21	0	5.263	3.38E-06	TAIR|locus:2036029 - symbol:AMI1 "AT1G08980" species:3702 "Arabidopsis thaliana" [GO:0004040 "amidase activity" evidence=ISS;IDA] [GO:0009684 "indoleacetic acid biosynthetic process" evidence=IDA] [GO:0016810 "hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds" evidence=IDA] [GO:0043864 "indoleacetamide hydrolase activity" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR000120 Pfam:PF01425 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0004040 GO:GO:0016884 eggNOG:COG0154 InterPro:IPR020556 InterPro:IPR023631 Gene3D:G3DSA:3.90.1300.10 PANTHER:PTHR11895 SUPFAM:SSF75304 PROSITE:PS00571 EMBL:AF202077 EMBL:AC000106 EMBL:AY037198 EMBL:BT004554 IPI:IPI00537072 IPI:IPI00548661 PIR:F86221 RefSeq:NP_563831.1 UniGene:At.21299 HSSP:Q8RJN5 ProteinModelPortal:Q9FR37 SMR:Q9FR37 STRING:Q9FR37 PRIDE:Q9FR37 EnsemblPlants:AT1G08980.1 GeneID:837418 KEGG:ath:AT1G08980 TAIR:At1g08980 HOGENOM:HBG481888 InParanoid:Q9FR37 OMA:IQGAEAW PhylomeDB:Q9FR37 ProtClustDB:PLN02722 Genevestigator:Q9FR37 GO:GO:0043864 GO:GO:0009684 Uniprot:Q9FR37
Root	Isotig02680	97	4	4.471	2.23E-22	TAIR|locus:2017899 - symbol:SGB1 "AT1G79820" species:3702 "Arabidopsis thaliana" [GO:0005351 "sugar:hydrogen symporter activity" evidence=ISS] [GO:0006810 "transport" evidence=IEA] [GO:0015144 "carbohydrate transmembrane transporter activity" evidence=ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0055085 "transmembrane transport" evidence=IEA] [GO:0005794 "Golgi apparatus" evidence=IDA]

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						InterPro:IPR003663 InterPro:IPR005828 InterPro:IPR005829 Pfam:PF00083 PRINTS:PR00171 PROSITE:PS00216 PROSITE:PS00217 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0031969 eggNOG:COG0477 InterPro:IPR016196 SUPFAM:SSF103473 GO:GO:0008643 InterPro:IPR020846 PROSITE:PS50850 EMBL:AC010793 EMBL:AC011717 HOGENOM:HBG744444 GO:GO:0022891 TIGRFAMs:TIGR00879 UniGene:At.14743 UniGene:At.48399 EMBL:AY080624 EMBL:BT008550 EMBL:BT008693 IPI:IPI00536398 IPI:IPI00657574 IPI:IPI00810560 IPI:IPI00810565 PIR:B96829 RefSeq:NP_001031303.1 RefSeq:NP_178100.3 RefSeq:NP_850983.1 ProteinModelPortal:Q2V4B9 PRIDE:Q2V4B9 EnsemblPlants:AT1G79820.1 EnsemblPlants:AT1G79820.2 GeneID:844321 KEGG:ath:AT1G79820 TAIR:At1g79820 InParanoid:Q2V4B9 OMA:MELCVES PhylomeDB:Q2V4B9 ProtClustDB:CLSN2680669 Genevestigator:Q2V4B9 GermOnline:AT1G79820 Uniprot:Q2V4B9
Root	Isotig02681	93	4	4.410	2.14E-21	TAIR|locus:2019554 - symbol:AT1G67300 "AT1G67300" species:3702 "Arabidopsis thaliana" [GO:0005351 "sugar:hydrogen symporter activity" evidence=ISS] [GO:0006810 "transport" evidence=IEA] [GO:0015144 "carbohydrate transmembrane transporter activity" evidence=ISS] [GO:0016020 "membrane" evidence=IEA;ISS] [GO:0016021 "integral to membrane" evidence=IEA] [GO:0055085 "transmembrane transport" evidence=IEA] InterPro:IPR003663 InterPro:IPR005828 InterPro:IPR005829 Pfam:PF00083 PRINTS:PR00171 PROSITE:PS00216 PROSITE:PS00217 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0031969 eggNOG:COG0477 InterPro:IPR016196 SUPFAM:SSF103473 GO:GO:0008643 InterPro:IPR020846 PROSITE:PS50850 HOGENOM:HBG744444 GO:GO:0022891 TIGRFAMs:TIGR00879 EMBL:AC002130 EMBL:AK226899 IPI:IPI00539133 PIR:F96696 RefSeq:NP_176898.1 UniGene:At.21607 UniGene:At.67017 ProteinModelPortal:Q9FYG3 EnsemblPlants:AT1G67300.1 GeneID:843050 KEGG:ath:AT1G67300 TAIR:At1g67300 InParanoid:Q9FYG3 PhylomeDB:Q9FYG3 ProtClustDB:CLSN2681973 Genevestigator:Q9FYG3 Uniprot:Q9FYG3
Root	Isotig02682	84	6	3.678	1.27E-17	TAIR|locus:2019554 - symbol:AT1G67300 "AT1G67300" species:3702 "Arabidopsis thaliana" [GO:0005351 "sugar:hydrogen symporter activity" evidence=ISS] [GO:0006810 "transport" evidence=IEA] [GO:0015144 "carbohydrate transmembrane transporter activity" evidence=ISS] [GO:0016020 "membrane" evidence=IEA;ISS] [GO:0016021 "integral to membrane" evidence=IEA] [GO:0055085 "transmembrane transport" evidence=IEA] InterPro:IPR003663 InterPro:IPR005828 InterPro:IPR005829 Pfam:PF00083 PRINTS:PR00171 PROSITE:PS00216 PROSITE:PS00217 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0031969 eggNOG:COG0477 InterPro:IPR016196 SUPFAM:SSF103473 GO:GO:0008643 InterPro:IPR020846 PROSITE:PS50850 HOGENOM:HBG744444 GO:GO:0022891 TIGRFAMs:TIGR00879 EMBL:AC002130 EMBL:AK226899 IPI:IPI00539133 PIR:F96696 RefSeq:NP_176898.1 UniGene:At.21607 UniGene:At.67017 ProteinModelPortal:Q9FYG3 EnsemblPlants:AT1G67300.1 GeneID:843050 KEGG:ath:AT1G67300 TAIR:At1g67300 InParanoid:Q9FYG3 PhylomeDB:Q9FYG3 ProtClustDB:CLSN2681973 Genevestigator:Q9FYG3 Uniprot:Q9FYG3
Root	Isotig02683	97	4	4.471	2.23E-22	TAIR|locus:2019554 - symbol:AT1G67300 "AT1G67300" species:3702 "Arabidopsis thaliana" [GO:0005351 "sugar:hydrogen symporter activity" evidence=ISS] [GO:0006810 "transport" evidence=IEA] [GO:0015144 "carbohydrate transmembrane transporter activity" evidence=ISS] [GO:0016020 "membrane" evidence=IEA;ISS] [GO:0016021 "integral to membrane" evidence=IEA] [GO:0055085 "transmembrane transport" evidence=IEA] InterPro:IPR003663 InterPro:IPR005828 InterPro:IPR005829 Pfam:PF00083 PRINTS:PR00171 PROSITE:PS00216 PROSITE:PS00217 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0031969 eggNOG:COG0477 InterPro:IPR016196 SUPFAM:SSF103473 GO:GO:0008643 InterPro:IPR020846 PROSITE:PS50850 HOGENOM:HBG744444 GO:GO:0022891 TIGRFAMs:TIGR00879 EMBL:AC002130 EMBL:AK226899 IPI:IPI00539133 PIR:F96696 RefSeq:NP_176898.1 UniGene:At.21607 UniGene:At.67017 ProteinModelPortal:Q9FYG3 EnsemblPlants:AT1G67300.1 GeneID:843050 KEGG:ath:AT1G67300 TAIR:At1g67300 InParanoid:Q9FYG3 PhylomeDB:Q9FYG3 ProtClustDB:CLSN2681973 Genevestigator:Q9FYG3 Uniprot:Q9FYG3
Root	Isotig02688	109	30	1.732	1.32E-10	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig02689	109	30	1.732	1.32E-10	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig02690	109	30	1.732	1.32E-10	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig02705	6	29	-2.402	1.89E-05	TAIR|locus:2006742 - symbol:PAP3 "AT1G14700" species:3702 "Arabidopsis thaliana" [GO:0004722 "protein serine/threonine phosphatase activity" evidence=ISS] [GO:0005773 "vacuole" evidence=IDA] [GO:0003993 "acid phosphatase activity" evidence=ISS] InterPro:IPR004843 InterPro:IPR024927 Pfam:PF00149 PIRSF:PIRSF000898 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005773 GO:GO:0005576 GO:GO:0046872 GO:GO:0003993 eggNOG:COG1409 EMBL:AC006917 KO:K01078 ProtClustDB:CLSN2688499 EMBL:AY686599 EMBL:AY070051 EMBL:BT000877 IPI:IPI00522072 IPI:IPI00846554 PIR:D86281 RefSeq:NP_001077538.1 RefSeq:NP_172923.3 UniGene:At.28419 ProteinModelPortal:Q8H129 SMR:Q8H129 STRING:Q8H129 EnsemblPlants:AT1G14700.1 GeneID:838035 KEGG:ath:AT1G14700 TAIR:At1g14700 HOGENOM:HBG560703 InParanoid:Q8H129 OMA:MRSFIVN PhylomeDB:Q8H129 Genevestigator:Q8H129 Uniprot:Q8H129
Root	Isotig02707	6	130	-4.566	2.60E-32	TAIR|locus:2126026 - symbol:PIP1;4 "AT4G00430" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=ISS] [GO:0015250 "water channel activity" evidence=ISS] [GO:0016020 "membrane" evidence=ISS;IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009414 "response to water deprivation" evidence=IEP] InterPro:IPR000425 InterPro:IPR012269 InterPro:IPR022357 Pfam:PF00230 PRINTS:PR00783 PROSITE:PS00221 GO:GO:0016021 GO:GO:0005886 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0055085 GO:GO:0009414 GO:GO:0005215 GO:GO:0006833 EMBL:AF013293 EMBL:AF195115 EMBL:AL161471 InterPro:IPR023271 Gene3D:G3DSA:1.20.1080.10 SUPFAM:SSF81338 eggNOG:COG0580 HOGENOM:HBG705794 PANTHER:PTHR19139 TIGRFAMs:TIGR00861 OMA:ITHNFKD KO:K09872 ProtClustDB:CLSN2682869 UniGene:At.20518 UniGene:At.20892 EMBL:D26609 EMBL:D85192 EMBL:AY099825 EMBL:AY120785 EMBL:BT000330 EMBL:BT006313 IPI:IPI00521990 PIR:T01528 RefSeq:NP_567178.1 ProteinModelPortal:Q39196 SMR:Q39196 IntAct:Q39196 STRING:Q39196 PRIDE:Q39196 EnsemblPlants:AT4G00430.1 GeneID:827956 KEGG:ath:AT4G00430 GeneFarm:2265 TAIR:At4g00430 InParanoid:Q39196 PhylomeDB:Q39196 ArrayExpress:Q39196 Genevestigator:Q39196 Uniprot:Q39196
Root	Isotig02708	2	122	-6.060	7.53E-32	TAIR|locus:2126026 - symbol:PIP1;4 "AT4G00430" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=ISS] [GO:0015250 "water channel activity" evidence=ISS] [GO:0016020 "membrane" evidence=ISS;IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009414 "response to water deprivation" evidence=IEP] InterPro:IPR000425 InterPro:IPR012269 InterPro:IPR022357 Pfam:PF00230 PRINTS:PR00783 PROSITE:PS00221 GO:GO:0016021 GO:GO:0005886 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0055085 GO:GO:0009414 GO:GO:0005215 GO:GO:0006833 EMBL:AF013293 EMBL:AF195115 EMBL:AL161471 InterPro:IPR023271 Gene3D:G3DSA:1.20.1080.10 SUPFAM:SSF81338 eggNOG:COG0580 HOGENOM:HBG705794 PANTHER:PTHR19139 TIGRFAMs:TIGR00861 OMA:ITHNFKD KO:K09872 ProtClustDB:CLSN2682869 UniGene:At.20518 UniGene:At.20892 EMBL:D26609 EMBL:D85192 EMBL:AY099825 EMBL:AY120785 EMBL:BT000330 EMBL:BT006313 IPI:IPI00521990 PIR:T01528 RefSeq:NP_567178.1 ProteinModelPortal:Q39196 SMR:Q39196 IntAct:Q39196 STRING:Q39196 PRIDE:Q39196

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EnsemblPlants:AT4G00430.1 GeneID:827956 KEGG:ath:AT4G00430 GeneFarm:2265 TAIR:At4g00430 InParanoid:Q39196 PhylomeDB:Q39196 ArrayExpress:Q39196 Genevestigator:Q39196 Uniprot:Q39196
Root	Isotig02709	2	122	-6.060	7.53E-32	TAIR|locus:2126026 - symbol:PIP1;4 "AT4G00430" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=ISS] [GO:0015250 "water channel activity" evidence=ISS] [GO:0016020 "membrane" evidence=ISS;IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009414 "response to water deprivation" evidence=IEP] InterPro:IPR000425 InterPro:IPR012269 InterPro:IPR022357 Pfam:PF00230 PRINTS:PR00783 PROSITE:PS00221 GO:GO:0016021 GO:GO:0005886 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0055085 GO:GO:0009414 GO:GO:0005215 GO:GO:0006833 EMBL:AF013293 EMBL:AF195115 EMBL:AL161471 InterPro:IPR023271 Gene3D:G3DSA:1.20.1080.10 SUPFAM:SSF81338 eggNOG:COG0580 HOGENOM:HBG705794 PANTHER:PTHR19139 TIGRFAMs:TIGR00861 OMA:ITHNFKD KO:K09872 ProtClustDB:CLSN2682869 UniGene:At.20518 UniGene:At.20892 EMBL:D26609 EMBL:D85192 EMBL:AY099825 EMBL:AY120785 EMBL:BT000330 EMBL:BT006313 IPI:IPI00521990 PIR:T01528 RefSeq:NP_567178.1 ProteinModelPortal:Q39196 SMR:Q39196 IntAct:Q39196 STRING:Q39196 PRIDE:Q39196 EnsemblPlants:AT4G00430.1 GeneID:827956 KEGG:ath:AT4G00430 GeneFarm:2265 TAIR:At4g00430 InParanoid:Q39196 PhylomeDB:Q39196 ArrayExpress:Q39196 Genevestigator:Q39196 Uniprot:Q39196
Root	Isotig02743	0	28	-5.936	1.79E-08	TAIR|locus:2030407 - symbol:AAE1 "acyl activating enzyme 1" species:3702 "Arabidopsis thaliana" [GO:0008152 "metabolic process" evidence=IEA] [GO:0016208 "AMP binding" evidence=ISS] [GO:0005777 "peroxisome" evidence=IDA] InterPro:IPR000873 Pfam:PF00501 Prosite:PS00455 EMBL:CP002684 GO:GO:0005777 InterPro:IPR020845 InterPro:IPR025110 Pfam:PF13193 EMBL:AC027665 GO:GO:0003824 EMBL:AC069251 EMBL:AF372942 EMBL:AY078039 EMBL:AF503760 IPI:IPI01019567 PIR:G86338 RefSeq:NP_564116.1 UniGene:At.20481 SMR:F4HUK6 PRIDE:Q9LMW3 EnsemblPlants:AT1G20560.1 GeneID:838644 KEGG:ath:AT1G20560 TAIR:At1g20560 Uniprot:F4HUK6
Root	Isotig02744	0	22	-5.588	6.01E-07	TAIR|locus:2057249 - symbol:AT2G17650 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0008152 "metabolic process" evidence=IEA] InterPro:IPR000873 Pfam:PF00501 Prosite:PS00455 EMBL:CP002685 GenomeReviews:CT485783_GR eggNOG:COG0318 HOGENOM:HBG547964 InterPro:IPR020845 InterPro:IPR025110 Pfam:PF13193 HSSP:P08659 GO:GO:0003824 EMBL:AF503761 EMBL:AC007509 EMBL:AK118689 EMBL:BT005926 IPI:IPI00521948 PIR:G84554 PIR:T08866 RefSeq:NP_179356.1 UniGene:At.40116 ProteinModelPortal:Q9SEY5 SMR:Q9SEY5 PRIDE:Q9SEY5 EnsemblPlants:AT2G17650.1 GeneID:816272 KEGG:ath:AT2G17650 TAIR:At2g17650 InParanoid:Q9SEY5 OMA:LHPVHVY PhylomeDB:Q9SEY5 ProtClustDB:CLSN2913309 ArrayExpress:Q9SEY5 Genevestigator:Q9SEY5 Uniprot:Q9SEY5
Root	Isotig02745	0	22	-5.588	6.01E-07	TAIR|locus:2030407 - symbol:AAE1 "acyl activating enzyme 1" species:3702 "Arabidopsis thaliana" [GO:0008152 "metabolic process" evidence=IEA] [GO:0016208 "AMP binding" evidence=ISS] [GO:0005777 "peroxisome" evidence=IDA] InterPro:IPR000873 Pfam:PF00501 Prosite:PS00455 EMBL:CP002684 GO:GO:0005777 InterPro:IPR020845 InterPro:IPR025110 Pfam:PF13193 EMBL:AC027665 GO:GO:0003824 EMBL:AC069251 EMBL:AF372942 EMBL:AY078039 EMBL:AF503760 IPI:IPI01019567 PIR:G86338 RefSeq:NP_564116.1 UniGene:At.20481 SMR:F4HUK6 PRIDE:Q9LMW3 EnsemblPlants:AT1G20560.1 GeneID:838644 KEGG:ath:AT1G20560 TAIR:At1g20560 Uniprot:F4HUK6
Root	Isotig02759	2	73	-5.319	1.23E-19	TAIR|locus:2084031 - symbol:PIP2A "AT3G53420" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=ISS] [GO:0015250 "water channel activity" evidence=ISS;IDA] [GO:0016020 "membrane" evidence=ISS;IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA;TAS] [GO:0005773 "vacuole" evidence=IDA] [GO:0009414 "response to water deprivation" evidence=IEP] [GO:0080170 "hydrogen peroxide transmembrane transport" evidence=IDA] [GO:0031625 "ubiquitin protein ligase binding" evidence=IPI] [GO:0009737 "response to abscisic acid stimulus" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0006833 "water transport" evidence=IDA] InterPro:IPR000425 InterPro:IPR012269 InterPro:IPR022357 Pfam:PF00230 PRINTS:PR00783 PROSITE:PS00221 GO:GO:0016021 GO:GO:0005886 GO:GO:0009506 GO:GO:0009737 GO:GO:0005773 GO:GO:0009507 EMBL:CP002686 GenomeReviews:BA000014_GR EMBL:AL132966 GO:GO:0009414 GO:GO:0031625 InterPro:IPR023271 Gene3D:G3DSA:1.20.1080.10 SUPFAM:SSF81338 eggNOG:COG0580 HOGENOM:HBG705794 PANTHER:PTHR19139 TIGRFAMs:TIGR00861 GO:GO:0015250 GO:GO:0080170 KO:K09872 EMBL:X75883 EMBL:AY039579 EMBL:AY044327 EMBL:AY056085 EMBL:AF428426 EMBL:AY072374 EMBL:AY087854 IPI:IPI00532482 PIR:S44084 RefSeq:NP_001030851.1 RefSeq:NP_190910.1 UniGene:At.47609

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						ProteinModelPortal:P43286 SMR:P43286 MINT:MINT-6951259 STRING:P43286 TCDB:1.A.8.11.4 PRIDE:P43286 ProMEX:P43286 EnsemblPlants:AT3G53420.1 EnsemblPlants:AT3G53420.2 GeneID:824510 KEGG:ath:AT3G53420 GeneFarm:4866 TAIR:At3g53420 InParanoid:P43286 OMA:VFMAITI PhylomeDB:P43286 ProtClustDB:CLSN2683965 ArrayExpress:P43286 Genevestigator:P43286 GermOnline:AT3G53420 Uniprot:P43286
Root	Isotig02760	3	83	-4.919	9.50E-22	TAIR|locus:2084031 - symbol:PIP2A "AT3G53420" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=ISS] [GO:0015250 "water channel activity" evidence=ISS;IDA] [GO:0016020 "membrane" evidence=ISS;IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA;TAS] [GO:0005773 "vacuole" evidence=IDA] [GO:0009414 "response to water deprivation" evidence=IEP] [GO:0080170 "hydrogen peroxide transmembrane transport" evidence=IDA] [GO:0031625 "ubiquitin protein ligase binding" evidence=IPI] [GO:0009737 "response to abscisic acid stimulus" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0006833 "water transport" evidence=IDA] InterPro:IPR000425 InterPro:IPR012269 InterPro:IPR022357 Pfam:PF00230 PRINTS:PR00783 PROSITE:PS00221 GO:GO:0016021 GO:GO:0005886 GO:GO:0009506 GO:GO:0009737 GO:GO:0005773 GO:GO:0009507 EMBL:CP002686 GenomeReviews:BA000014_GR EMBL:AL132966 GO:GO:0009414 GO:GO:0031625 InterPro:IPR023271 Gene3D:G3DSA:1.20.1080.10 SUPFAM:SSF81338 eggNOG:COG0580 HOGENOM:HBG705794 PANTHER:PTHR19139 TIGRFAMs:TIGR00861 GO:GO:0015250 GO:GO:0080170 KO:K09872 EMBL:X75883 EMBL:AY039579 EMBL:AY044327 EMBL:AY056085 EMBL:AF428426 EMBL:AY072374 EMBL:AY087854 IPI:IPI00532482 PIR:S44084 RefSeq:NP_001030851.1 RefSeq:NP_190910.1 UniGene:At.47609 ProteinModelPortal:P43286 SMR:P43286 MINT:MINT-6951259 STRING:P43286 TCDB:1.A.8.11.4 PRIDE:P43286 ProMEX:P43286 EnsemblPlants:AT3G53420.1 EnsemblPlants:AT3G53420.2 GeneID:824510 KEGG:ath:AT3G53420 GeneFarm:4866 TAIR:At3g53420 InParanoid:P43286 OMA:VFMAITI PhylomeDB:P43286 ProtClustDB:CLSN2683965 ArrayExpress:P43286 Genevestigator:P43286 GermOnline:AT3G53420 Uniprot:P43286
Root	Isotig02761	2	46	-4.653	1.60E-12	TAIR|locus:2084031 - symbol:PIP2A "AT3G53420" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=ISS] [GO:0015250 "water channel activity" evidence=ISS;IDA] [GO:0016020 "membrane" evidence=ISS;IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA;TAS] [GO:0005773 "vacuole" evidence=IDA] [GO:0009414 "response to water deprivation" evidence=IEP] [GO:0080170 "hydrogen peroxide transmembrane transport" evidence=IDA] [GO:0031625 "ubiquitin protein ligase binding" evidence=IPI] [GO:0009737 "response to abscisic acid stimulus" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0006833 "water transport" evidence=IDA] InterPro:IPR000425 InterPro:IPR012269 InterPro:IPR022357 Pfam:PF00230 PRINTS:PR00783 PROSITE:PS00221 GO:GO:0016021 GO:GO:0005886 GO:GO:0009506 GO:GO:0009737 GO:GO:0005773 GO:GO:0009507 EMBL:CP002686 GenomeReviews:BA000014_GR EMBL:AL132966 GO:GO:0009414 GO:GO:0031625 InterPro:IPR023271 Gene3D:G3DSA:1.20.1080.10 SUPFAM:SSF81338 eggNOG:COG0580 HOGENOM:HBG705794 PANTHER:PTHR19139 TIGRFAMs:TIGR00861 GO:GO:0015250 GO:GO:0080170 KO:K09872 EMBL:X75883 EMBL:AY039579 EMBL:AY044327 EMBL:AY056085 EMBL:AF428426 EMBL:AY072374 EMBL:AY087854 IPI:IPI00532482 PIR:S44084 RefSeq:NP_001030851.1 RefSeq:NP_190910.1 UniGene:At.47609 ProteinModelPortal:P43286 SMR:P43286 MINT:MINT-6951259 STRING:P43286 TCDB:1.A.8.11.4 PRIDE:P43286 ProMEX:P43286 EnsemblPlants:AT3G53420.1 EnsemblPlants:AT3G53420.2 GeneID:824510 KEGG:ath:AT3G53420 GeneFarm:4866 TAIR:At3g53420 InParanoid:P43286 OMA:VFMAITI PhylomeDB:P43286 ProtClustDB:CLSN2683965 ArrayExpress:P43286 Genevestigator:P43286 GermOnline:AT3G53420 Uniprot:P43286
Root	Isotig02762	2	46	-4.653	1.60E-12	TAIR|locus:2084031 - symbol:PIP2A "AT3G53420" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=ISS] [GO:0015250 "water channel activity" evidence=ISS;IDA] [GO:0016020 "membrane" evidence=ISS;IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA;TAS] [GO:0005773 "vacuole" evidence=IDA] [GO:0009414 "response to water deprivation" evidence=IEP] [GO:0080170 "hydrogen peroxide transmembrane transport" evidence=IDA] [GO:0031625 "ubiquitin protein ligase binding" evidence=IPI] [GO:0009737 "response to abscisic acid stimulus" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0006833 "water transport" evidence=IDA] InterPro:IPR000425 InterPro:IPR012269 InterPro:IPR022357 Pfam:PF00230 PRINTS:PR00783 PROSITE:PS00221 GO:GO:0016021 GO:GO:0005886 GO:GO:0009506 GO:GO:0009737 GO:GO:0005773 GO:GO:0009507 EMBL:CP002686

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GenomeReviews:BA000014_GR EMBL:AL132966 GO:GO:0009414 GO:GO:0031625 InterPro:IPR023271 Gene3D:G3DSA:1.20.1080.10 SUPFAM:SSF81338 eggNOG:COG0580 HOGENOM:HBG705794 PANTHER:PTHR19139 TIGRFAMs:TIGR00861 GO:GO:0015250 GO:GO:0080170 KO:K09872 EMBL:X75883 EMBL:AY039579 EMBL:AY044327 EMBL:AY056085 EMBL:AF428426 EMBL:AY072374 EMBL:AY087854 IPI:IPI00532482 PIR:S44084 RefSeq:NP_001030851.1 RefSeq:NP_190910.1 UniGene:At.47609 ProteinModelPortal:P43286 SMR:P43286 MINT:MINT-6951259 STRING:P43286 TCDB:1.A.8.11.4 PRIDE:P43286 ProMEX:P43286 EnsemblPlants:AT3G53420.1 EnsemblPlants:AT3G53420.2 GeneID:824510 KEGG:ath:AT3G53420 GeneFarm:4866 TAIR:At3g53420 InParanoid:P43286 OMA:VFMAITI PhylomeDB:P43286 ProtClustDB:CLSN2683965 ArrayExpress:P43286 Genevestigator:P43286 GermOnline:AT3G53420 Uniprot:P43286
Root	Isotig02765	18	1	4.041	4.47E-05	No hit
Root	Isotig02766	12	0	4.456	0.000626491	No hit
Root	Isotig02779	191	61	1.518	1.05E-14	TAIR|locus:2020088 - symbol:AT1G54290 species:3702 "Arabidopsis thaliana" [GO:0003743 "translation initiation factor activity" evidence=IEA;ISS] [GO:0006412 "translation" evidence=IEA] [GO:0006413 "translational initiation" evidence=IEA;ISS] InterPro:IPR001950 InterPro:IPR005874 Pfam:PF01253 PIRSF:PIRSF004499 PROSITE:PS50296 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0006417 EMBL:AC005287 GO:GO:0003743 eggNOG:COG0023 SUPFAM:SSF55159 HOGENOM:HBG522548 KO:K03113 OMA:QNLKTFD TIGRFAMs:TIGR01160 ProtClustDB:CLSN2682406 EMBL:AF372910 EMBL:BT000649 IPI:IPI00530446 PIR:D96584 RefSeq:NP_175831.1 UniGene:At.20055 ProteinModelPortal:Q94JV4 SMR:Q94JV4 IntAct:Q94JV4 STRING:Q94JV4 PRIDE:Q94JV4 EnsemblPlants:AT1G54290.1 GeneID:841870 KEGG:ath:AT1G54290 TAIR:At1g54290 InParanoid:Q94JV4 PhylomeDB:Q94JV4 ArrayExpress:Q94JV4 Genevestigator:Q94JV4 GermOnline:AT1G54290 Uniprot:Q94JV4
Root	Isotig02780	191	60	1.542	5.18E-15	TAIR|locus:2020088 - symbol:AT1G54290 species:3702 "Arabidopsis thaliana" [GO:0003743 "translation initiation factor activity" evidence=IEA;ISS] [GO:0006412 "translation" evidence=IEA] [GO:0006413 "translational initiation" evidence=IEA;ISS] InterPro:IPR001950 InterPro:IPR005874 Pfam:PF01253 PIRSF:PIRSF004499 PROSITE:PS50296 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0006417 EMBL:AC005287 GO:GO:0003743 eggNOG:COG0023 SUPFAM:SSF55159 HOGENOM:HBG522548 KO:K03113 OMA:QNLKTFD TIGRFAMs:TIGR01160 ProtClustDB:CLSN2682406 EMBL:AF372910 EMBL:BT000649 IPI:IPI00530446 PIR:D96584 RefSeq:NP_175831.1 UniGene:At.20055 ProteinModelPortal:Q94JV4 SMR:Q94JV4 IntAct:Q94JV4 STRING:Q94JV4 PRIDE:Q94JV4 EnsemblPlants:AT1G54290.1 GeneID:841870 KEGG:ath:AT1G54290 TAIR:At1g54290 InParanoid:Q94JV4 PhylomeDB:Q94JV4 ArrayExpress:Q94JV4 Genevestigator:Q94JV4 GermOnline:AT1G54290 Uniprot:Q94JV4
Root	Isotig02781	193	60	1.557	2.39E-15	TAIR|locus:2020088 - symbol:AT1G54290 species:3702 "Arabidopsis thaliana" [GO:0003743 "translation initiation factor activity" evidence=IEA;ISS] [GO:0006412 "translation" evidence=IEA] [GO:0006413 "translational initiation" evidence=IEA;ISS] InterPro:IPR001950 InterPro:IPR005874 Pfam:PF01253 PIRSF:PIRSF004499 PROSITE:PS50296 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0006417 EMBL:AC005287 GO:GO:0003743 eggNOG:COG0023 SUPFAM:SSF55159 HOGENOM:HBG522548 KO:K03113 OMA:QNLKTFD TIGRFAMs:TIGR01160 ProtClustDB:CLSN2682406 EMBL:AF372910 EMBL:BT000649 IPI:IPI00530446 PIR:D96584 RefSeq:NP_175831.1 UniGene:At.20055 ProteinModelPortal:Q94JV4 SMR:Q94JV4 IntAct:Q94JV4 STRING:Q94JV4 PRIDE:Q94JV4 EnsemblPlants:AT1G54290.1 GeneID:841870 KEGG:ath:AT1G54290 TAIR:At1g54290 InParanoid:Q94JV4 PhylomeDB:Q94JV4 ArrayExpress:Q94JV4 Genevestigator:Q94JV4 GermOnline:AT1G54290 Uniprot:Q94JV4
Root	Isotig02782	193	59	1.581	1.16E-15	TAIR|locus:2020088 - symbol:AT1G54290 species:3702 "Arabidopsis thaliana" [GO:0003743 "translation initiation factor activity" evidence=IEA;ISS] [GO:0006412 "translation" evidence=IEA] [GO:0006413 "translational initiation" evidence=IEA;ISS] InterPro:IPR001950 InterPro:IPR005874 Pfam:PF01253 PIRSF:PIRSF004499 PROSITE:PS50296 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0006417 EMBL:AC005287 GO:GO:0003743 eggNOG:COG0023 SUPFAM:SSF55159 HOGENOM:HBG522548 KO:K03113 OMA:QNLKTFD TIGRFAMs:TIGR01160 ProtClustDB:CLSN2682406 EMBL:AF372910 EMBL:BT000649 IPI:IPI00530446 PIR:D96584 RefSeq:NP_175831.1 UniGene:At.20055 ProteinModelPortal:Q94JV4 SMR:Q94JV4 IntAct:Q94JV4 STRING:Q94JV4 PRIDE:Q94JV4 EnsemblPlants:AT1G54290.1 GeneID:841870 KEGG:ath:AT1G54290 TAIR:At1g54290 InParanoid:Q94JV4 PhylomeDB:Q94JV4 ArrayExpress:Q94JV4 Genevestigator:Q94JV4 GermOnline:AT1G54290 Uniprot:Q94JV4

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig02803	5	21	-2.199	0.000555521	TAIR|locus:2046673 - symbol:AT2G24550 "AT2G24550" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002685 GenomeReviews:CT485783_GR EMBL:AF411794 EMBL:AY099874 EMBL:BT000317 IPI:IPI00944291 RefSeq:NP_565573.4 UniGene:At.22389 IntAct:Q945P6 PRIDE:Q945P6 EnsemblPlants:AT2G24550.1 GeneID:816991 KEGG:ath:AT2G24550 TAIR:At2g24550 eggNOG:NOG249819 PhylomeDB:Q945P6 ProtClustDB:CLSN2685860 Genevestigator:Q945P6 Uniprot:Q945P6
Root	Isotig02804	5	21	-2.199	0.000555521	TAIR|locus:2046673 - symbol:AT2G24550 "AT2G24550" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002685 GenomeReviews:CT485783_GR EMBL:AF411794 EMBL:AY099874 EMBL:BT000317 IPI:IPI00944291 RefSeq:NP_565573.4 UniGene:At.22389 IntAct:Q945P6 PRIDE:Q945P6 EnsemblPlants:AT2G24550.1 GeneID:816991 KEGG:ath:AT2G24550 TAIR:At2g24550 eggNOG:NOG249819 PhylomeDB:Q945P6 ProtClustDB:CLSN2685860 Genevestigator:Q945P6 Uniprot:Q945P6
Root	Isotig02805	2	14	-2.936	0.000925454	TAIR|locus:2046673 - symbol:AT2G24550 "AT2G24550" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002685 GenomeReviews:CT485783_GR EMBL:AF411794 EMBL:AY099874 EMBL:BT000317 IPI:IPI00944291 RefSeq:NP_565573.4 UniGene:At.22389 IntAct:Q945P6 PRIDE:Q945P6 EnsemblPlants:AT2G24550.1 GeneID:816991 KEGG:ath:AT2G24550 TAIR:At2g24550 eggNOG:NOG249819 PhylomeDB:Q945P6 ProtClustDB:CLSN2685860 Genevestigator:Q945P6 Uniprot:Q945P6
Root	Isotig02806	4	22	-2.588	0.000101225	TAIR|locus:2046673 - symbol:AT2G24550 "AT2G24550" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002685 GenomeReviews:CT485783_GR EMBL:AF411794 EMBL:AY099874 EMBL:BT000317 IPI:IPI00944291 RefSeq:NP_565573.4 UniGene:At.22389 IntAct:Q945P6 PRIDE:Q945P6 EnsemblPlants:AT2G24550.1 GeneID:816991 KEGG:ath:AT2G24550 TAIR:At2g24550 eggNOG:NOG249819 PhylomeDB:Q945P6 ProtClustDB:CLSN2685860 Genevestigator:Q945P6 Uniprot:Q945P6
Root	Isotig02871	50	19	1.267	0.000561936	TAIR|locus:2017854 - symbol:NADP-ME4 "AT1G79750" species:3702 "Arabidopsis thaliana" [GO:0004470 "malic enzyme activity" evidence=ISS] [GO:0006108 "malate metabolic process" evidence=ISS;IDA;TAS] [GO:0016652 "oxidoreductase activity, acting on NADH or NADPH, NAD or NADP as acceptor" evidence=ISS] [GO:0004473 "malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+) activity" evidence=IDA] [GO:0006633 "fatty acid biosynthetic process" evidence=TAS] [GO:0009507 "chloroplast" evidence=IDA] [GO:0042803 "protein homodimerization activity" evidence=IDA] [GO:0051289 "protein homotetramerization" evidence=IDA] [GO:0008270 "zinc ion binding" evidence=IDA] [GO:0050897 "cobalt ion binding" evidence=IDA] InterPro:IPR001891 InterPro:IPR012301 InterPro:IPR012302 InterPro:IPR015884 InterPro:IPR016040 Pfam:PF00390 Pfam:PF03949 PIRSF:PIRSF000106 PRINTS:PR00072 PROSITE:PS00331 SMART:SM00919 EMBL:CP002684 GO:GO:0009507 GO:GO:0042803 Gene3D:G3DSA:3.40.50.720 GO:GO:0051287 GO:GO:0008270 GO:GO:0006633 GO:GO:0051289 GO:GO:0050897 EMBL:AC011717 GO:GO:0006108 GO:GO:0016619 Gene3D:G3DSA:3.40.50.10380 KO:K00029 GO:GO:0004473 OMA:IQTKVDQ UniGene:At.21634 HSSP:P40927 ProtClustDB:PLN03129 EMBL:AY060584 EMBL:AY142064 IPI:IPI00535518 PIR:E96828 RefSeq:NP_178093.1 ProteinModelPortal:Q9CA83 SMR:Q9CA83 IntAct:Q9CA83 STRING:Q9CA83 PRIDE:Q9CA83 EnsemblPlants:AT1G79750.1 GeneID:844314 KEGG:ath:AT1G79750 TAIR:At1g79750 InParanoid:Q9CA83 PhylomeDB:Q9CA83 Genevestigator:Q9CA83 Uniprot:Q9CA83
Root	Isotig02872	32	60	-1.036	0.000772006	UNIPROTKB|B9RYP6 - symbol:RCOM_1312280 "Heat shock protein, putative" species:3988 "Ricinus communis" [GO:0005783 "endoplasmic reticulum" evidence=IDA] InterPro:IPR001023 PRINTS:PR00301 Pfam:PF00012 Prosite:PS00297 Prosite:PS00329 Prosite:PS01036 GO:GO:0005783 GO:GO:0005524 GO:GO:0006950 KO:K09490 InterPro:IPR018181 InterPro:IPR013126 PANTHER:PTHR19375 ProtClustDB:CLSN2713985 GO:GO:0032440 EMBL:EQ973832 RefSeq:XP_002518865.1 ProteinModelPortal:B9RYP6 GeneID:8286262 KEGG:rcu:RCOM_1312280 PhylomeDB:B9RYP6 Uniprot:B9RYP6
Root	Isotig02893	40	10	1.871	4.07E-05	TAIR|locus:2164855 - symbol:AT5G39570 "AT5G39570" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0005634 "nucleus" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] GO:GO:0005829 GO:GO:0005634 EMBL:CP002688 GenomeReviews:BA000015_GR EMBL:AB012243 EMBL:AF083682 EMBL:BT000496 EMBL:AY058080 IPI:IPI00534812 RefSeq:NP_568565.2 UniGene:At.20492 EnsemblPlants:AT5G39570.1 GeneID:833953 KEGG:ath:AT5G39570 TAIR:At5g39570 PhylomeDB:Q9FKA5 Genevestigator:Q9FKA5 Uniprot:Q9FKA5

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig02895	36	7	2.234	1.28E-05	TAIR|locus:2164855 - symbol:AT5G39570 "AT5G39570" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0005634 "nucleus" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] GO:GO:0005829 GO:GO:0005634 EMBL:CP002688 GenomeReviews:BA000015_GR EMBL:AB012243 EMBL:AF083682 EMBL:BT000496 EMBL:AY058080 IPI:IPI00534812 RefSeq:NP_568565.2 UniGene:At.20492 EnsemblPlants:AT5G39570.1 GeneID:833953 KEGG:ath:AT5G39570 TAIR:At5g39570 PhylomeDB:Q9FKA5 Genevestigator:Q9FKA5 Uniprot:Q9FKA5
Root	Isotig02914	23	55	-1.387	5.00E-05	TAIR|locus:2141385 - symbol:SAM-2 "AT4G01850" species:3702 "Arabidopsis thaliana" [GO:0004478 "methionine adenosyltransferase activity" evidence=ISS] [GO:0006556 "S-adenosylmethionine biosynthetic process" evidence=ISS] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0071281 "cellular response to iron ion" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA;RCA] [GO:0070062 "extracellular vesicular exosome" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR002133 InterPro:IPR022628 InterPro:IPR022629 InterPro:IPR022630 InterPro:IPR022631 InterPro:IPR022636 Pfam:PF00438 Pfam:PF02772 Pfam:PF02773 PIRSF:PIRSF000497 PROSITE:PS00376 PROSITE:PS00377 GO:GO:0005829 GO:GO:0009506 GO:GO:0005524 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005618 GO:GO:0071281 GO:GO:0005730 GO:GO:0005507 EMBL:AC007138 EMBL:AL161493 GO:GO:0070062 GO:GO:0006730 KO:K00789 GO:GO:0006556 UniGene:At.24731 eggNOG:COG0192 HOGENOM:HBG443662 ProtClustDB:PLN02243 GO:GO:0004478 PANTHER:PTHR11964 SUPFAM:SSF55973 TIGRFAMs:TIGR01034 EMBL:M33217 EMBL:AY072327 EMBL:AY094454 EMBL:BT000575 EMBL:Z33778 EMBL:Z29136 IPI:IPI00529348 PIR:JQ0410 RefSeq:NP_001078345.1 RefSeq:NP_192094.1 UniGene:At.24433 UniGene:At.71920 ProteinModelPortal:P17562 SMR:P17562 STRING:P17562 PRIDE:P17562 ProMEX:P17562 EnsemblPlants:AT4G01850.1 EnsemblPlants:AT4G01850.2 GeneID:826987 KEGG:ath:AT4G01850 TAIR:At4g01850 InParanoid:P17562 OMA:ATIDYEK PhylomeDB:P17562 ArrayExpress:P17562 Genevestigator:P17562 GermOnline:AT4G01850 Uniprot:P17562
Root	Isotig02915	23	53	-1.333	0.000111751	TAIR|locus:2141385 - symbol:SAM-2 "AT4G01850" species:3702 "Arabidopsis thaliana" [GO:0004478 "methionine adenosyltransferase activity" evidence=ISS] [GO:0006556 "S-adenosylmethionine biosynthetic process" evidence=ISS] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0071281 "cellular response to iron ion" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA;RCA] [GO:0070062 "extracellular vesicular exosome" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR002133 InterPro:IPR022628 InterPro:IPR022629 InterPro:IPR022630 InterPro:IPR022631 InterPro:IPR022636 Pfam:PF00438 Pfam:PF02772 Pfam:PF02773 PIRSF:PIRSF000497 PROSITE:PS00376 PROSITE:PS00377 GO:GO:0005829 GO:GO:0009506 GO:GO:0005524 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005618 GO:GO:0071281 GO:GO:0005730 GO:GO:0005507 EMBL:AC007138 EMBL:AL161493 GO:GO:0070062 GO:GO:0006730 KO:K00789 GO:GO:0006556 UniGene:At.24731 eggNOG:COG0192 HOGENOM:HBG443662 ProtClustDB:PLN02243 GO:GO:0004478 PANTHER:PTHR11964 SUPFAM:SSF55973 TIGRFAMs:TIGR01034 EMBL:M33217 EMBL:AY072327 EMBL:AY094454 EMBL:BT000575 EMBL:Z33778 EMBL:Z29136 IPI:IPI00529348 PIR:JQ0410 RefSeq:NP_001078345.1 RefSeq:NP_192094.1 UniGene:At.24433 UniGene:At.71920 ProteinModelPortal:P17562 SMR:P17562 STRING:P17562 PRIDE:P17562 ProMEX:P17562 EnsemblPlants:AT4G01850.1 EnsemblPlants:AT4G01850.2 GeneID:826987 KEGG:ath:AT4G01850 TAIR:At4g01850 InParanoid:P17562 OMA:ATIDYEK PhylomeDB:P17562 ArrayExpress:P17562 Genevestigator:P17562 GermOnline:AT4G01850 Uniprot:P17562
Root	Isotig02916	23	54	-1.360	7.49E-05	TAIR|locus:2141385 - symbol:SAM-2 "AT4G01850" species:3702 "Arabidopsis thaliana" [GO:0004478 "methionine adenosyltransferase activity" evidence=ISS] [GO:0006556 "S-adenosylmethionine biosynthetic process" evidence=ISS] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0071281 "cellular response to iron ion" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA;RCA] [GO:0070062 "extracellular vesicular exosome" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR002133 InterPro:IPR022628 InterPro:IPR022629 InterPro:IPR022630 InterPro:IPR022631 InterPro:IPR022636 Pfam:PF00438 Pfam:PF02772 Pfam:PF02773 PIRSF:PIRSF000497 PROSITE:PS00376 PROSITE:PS00377 GO:GO:0005829 GO:GO:0009506 GO:GO:0005524 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005618 GO:GO:0071281 GO:GO:0005730 GO:GO:0005507 EMBL:AC007138 EMBL:AL161493 GO:GO:0070062 GO:GO:0006730 KO:K00789 GO:GO:0006556

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						UniGene:At.24731 eggNOG:COG0192 HOGENOM:HBG443662 ProtClustDB:PLN02243 GO:GO:0004478 PANTHER:PTHR11964 SUPFAM:SSF55973 TIGRFAMs:TIGR01034 EMBL:M33217 EMBL:AY072327 EMBL:AY094454 EMBL:BT000575 EMBL:Z33778 EMBL:Z29136 IPI:IPI00529348 PIR:JQ0410 RefSeq:NP_001078345.1 RefSeq:NP_192094.1 UniGene:At.24433 UniGene:At.71920 ProteinModelPortal:P17562 SMR:P17562 STRING:P17562 PRIDE:P17562 ProMEX:P17562 EnsemblPlants:AT4G01850.1 EnsemblPlants:AT4G01850.2 GeneID:826987 KEGG:ath:AT4G01850 TAIR:At4g01850 InParanoid:P17562 OMA:ATIDYEK PhylomeDB:P17562 ArrayExpress:P17562 Genevestigator:P17562 GermOnline:AT4G01850 Uniprot:P17562
Root	Isotig02917	23	55	-1.387	5.00E-05	TAIR|locus:2141385 - symbol:SAM-2 "AT4G01850" species:3702 "Arabidopsis thaliana" [GO:0004478 "methionine adenosyltransferase activity" evidence=ISS] [GO:0006556 "S-adenosylmethionine biosynthetic process" evidence=ISS] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0071281 "cellular response to iron ion" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA;RCA] [GO:0070062 "extracellular vesicular exosome" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR002133 InterPro:IPR022628 InterPro:IPR022629 InterPro:IPR022630 InterPro:IPR022631 InterPro:IPR022636 Pfam:PF00438 Pfam:PF02772 Pfam:PF02773 PIRSF:PIRSF000497 PROSITE:PS00376 PROSITE:PS00377 GO:GO:0005829 GO:GO:0009506 GO:GO:0005524 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005618 GO:GO:0071281 GO:GO:0005730 GO:GO:0005507 EMBL:AC007138 EMBL:AL161493 GO:GO:0070062 GO:GO:0006730 KO:K00789 GO:GO:0006556 UniGene:At.24731 eggNOG:COG0192 HOGENOM:HBG443662 ProtClustDB:PLN02243 GO:GO:0004478 PANTHER:PTHR11964 SUPFAM:SSF55973 TIGRFAMs:TIGR01034 EMBL:M33217 EMBL:AY072327 EMBL:AY094454 EMBL:BT000575 EMBL:Z33778 EMBL:Z29136 IPI:IPI00529348 PIR:JQ0410 RefSeq:NP_001078345.1 RefSeq:NP_192094.1 UniGene:At.24433 UniGene:At.71920 ProteinModelPortal:P17562 SMR:P17562 STRING:P17562 PRIDE:P17562 ProMEX:P17562 EnsemblPlants:AT4G01850.1 EnsemblPlants:AT4G01850.2 GeneID:826987 KEGG:ath:AT4G01850 TAIR:At4g01850 InParanoid:P17562 OMA:ATIDYEK PhylomeDB:P17562 ArrayExpress:P17562 Genevestigator:P17562 GermOnline:AT4G01850 Uniprot:P17562
Root	Isotig02918	23	52	-1.306	0.000165922	TAIR|locus:2141385 - symbol:SAM-2 "AT4G01850" species:3702 "Arabidopsis thaliana" [GO:0004478 "methionine adenosyltransferase activity" evidence=ISS] [GO:0006556 "S-adenosylmethionine biosynthetic process" evidence=ISS] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0071281 "cellular response to iron ion" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA;RCA] [GO:0070062 "extracellular vesicular exosome" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR002133 InterPro:IPR022628 InterPro:IPR022629 InterPro:IPR022630 InterPro:IPR022631 InterPro:IPR022636 Pfam:PF00438 Pfam:PF02772 Pfam:PF02773 PIRSF:PIRSF000497 PROSITE:PS00376 PROSITE:PS00377 GO:GO:0005829 GO:GO:0009506 GO:GO:0005524 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005618 GO:GO:0071281 GO:GO:0005730 GO:GO:0005507 EMBL:AC007138 EMBL:AL161493 GO:GO:0070062 GO:GO:0006730 KO:K00789 GO:GO:0006556 UniGene:At.24731 eggNOG:COG0192 HOGENOM:HBG443662 ProtClustDB:PLN02243 GO:GO:0004478 PANTHER:PTHR11964 SUPFAM:SSF55973 TIGRFAMs:TIGR01034 EMBL:M33217 EMBL:AY072327 EMBL:AY094454 EMBL:BT000575 EMBL:Z33778 EMBL:Z29136 IPI:IPI00529348 PIR:JQ0410 RefSeq:NP_001078345.1 RefSeq:NP_192094.1 UniGene:At.24433 UniGene:At.71920 ProteinModelPortal:P17562 SMR:P17562 STRING:P17562 PRIDE:P17562 ProMEX:P17562 EnsemblPlants:AT4G01850.1 EnsemblPlants:AT4G01850.2 GeneID:826987 KEGG:ath:AT4G01850 TAIR:At4g01850 InParanoid:P17562 OMA:ATIDYEK PhylomeDB:P17562 ArrayExpress:P17562 Genevestigator:P17562 GermOnline:AT4G01850 Uniprot:P17562
Root	Isotig02919	23	53	-1.333	0.000111751	TAIR|locus:2141385 - symbol:SAM-2 "AT4G01850" species:3702 "Arabidopsis thaliana" [GO:0004478 "methionine adenosyltransferase activity" evidence=ISS] [GO:0006556 "S-adenosylmethionine biosynthetic process" evidence=ISS] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0071281 "cellular response to iron ion" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA;RCA] [GO:0070062 "extracellular vesicular exosome" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR002133 InterPro:IPR022628 InterPro:IPR022629 InterPro:IPR022630 InterPro:IPR022631 InterPro:IPR022636 Pfam:PF00438 Pfam:PF02772 Pfam:PF02773 PIRSF:PIRSF000497 PROSITE:PS00376 PROSITE:PS00377 GO:GO:0005829 GO:GO:0009506 GO:GO:0005524 EMBL:CP002687

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GenomeReviews:CT486007_GR GO:GO:0005618 GO:GO:0071281 GO:GO:0005730 GO:GO:0005507 EMBL:AC007138 EMBL:AL161493 GO:GO:0070062 GO:GO:0006730 KO:K00789 GO:GO:0006556 UniGene:At.24731 eggNOG:COG0192 HOGENOM:HBG443662 ProtClustDB:PLN02243 GO:GO:0004478 PANTHER:PTHR11964 SUPFAM:SSF55973 TIGRFAMs:TIGR01034 EMBL:M33217 EMBL:AY072327 EMBL:AY094454 EMBL:BT000575 EMBL:Z33778 EMBL:Z29136 IPI:IPI00529348 PIR:JQ0410 RefSeq:NP_001078345.1 RefSeq:NP_192094.1 UniGene:At.24433 UniGene:At.71920 ProteinModelPortal:P17562 SMR:P17562 STRING:P17562 PRIDE:P17562 ProMEX:P17562 EnsemblPlants:AT4G01850.1 EnsemblPlants:AT4G01850.2 GeneID:826987 KEGG:ath:AT4G01850 TAIR:At4g01850 InParanoid:P17562 OMA:ATIDYEK PhylomeDB:P17562 ArrayExpress:P17562 Genevestigator:P17562 GermOnline:AT4G01850 Uniprot:P17562
Root	Isotig02920	3	57	-4.377	8.39E-15	TAIR|locus:2064895 - symbol:PHT1;4 "AT2G38940" species:3702 "Arabidopsis thaliana" [GO:0005351 "sugar:hydrogen symporter activity" evidence=ISS] [GO:0015114 "phosphate ion transmembrane transporter activity" evidence=ISS] [GO:0015144 "carbohydrate transmembrane transporter activity" evidence=ISS] [GO:0016020 "membrane" evidence=ISS;IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0009737 "response to abscisic acid stimulus" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] [GO:0005315 "inorganic phosphate transmembrane transporter activity" evidence=ISS] InterPro:IPR004738 InterPro:IPR005828 Pfam:PF00083 PROSITE:PS00216 PROSITE:PS00217 GO:GO:0016021 GO:GO:0005886 GO:GO:0009506 GO:GO:0009737 GO:GO:0005634 GO:GO:0005773 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0015293 GO:GO:0005315 eggNOG:COG0477 InterPro:IPR016196 SUPFAM:SSF103473 InterPro:IPR020846 PROSITE:PS50850 EMBL:AC005770 HOGENOM:HBG744844 KO:K08176 TIGRFAMs:TIGR00887 EMBL:U62331 EMBL:AF022872 EMBL:AB016166 IPI:IPI00537042 PIR:C84811 RefSeq:NP_181428.1 UniGene:At.255 UniGene:At.67089 ProteinModelPortal:Q96303 STRING:Q96303 PRIDE:Q96303 EnsemblPlants:AT2G38940.1 GeneID:818479 KEGG:ath:AT2G38940 GeneFarm:5189 TAIR:At2g38940 InParanoid:Q96303 OMA:CYLLIAG PhylomeDB:Q96303 ProtClustDB:CLSN2683235 ArrayExpress:Q96303 Genevestigator:Q96303 GermOnline:AT2G38940 Uniprot:Q96303
Root	Isotig02921	3	57	-4.377	8.39E-15	TAIR|locus:2064895 - symbol:PHT1;4 "AT2G38940" species:3702 "Arabidopsis thaliana" [GO:0005351 "sugar:hydrogen symporter activity" evidence=ISS] [GO:0015114 "phosphate ion transmembrane transporter activity" evidence=ISS] [GO:0015144 "carbohydrate transmembrane transporter activity" evidence=ISS] [GO:0016020 "membrane" evidence=ISS;IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0009737 "response to abscisic acid stimulus" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] [GO:0005315 "inorganic phosphate transmembrane transporter activity" evidence=ISS] InterPro:IPR004738 InterPro:IPR005828 Pfam:PF00083 PROSITE:PS00216 PROSITE:PS00217 GO:GO:0016021 GO:GO:0005886 GO:GO:0009506 GO:GO:0009737 GO:GO:0005634 GO:GO:0005773 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0015293 GO:GO:0005315 eggNOG:COG0477 InterPro:IPR016196 SUPFAM:SSF103473 InterPro:IPR020846 PROSITE:PS50850 EMBL:AC005770 HOGENOM:HBG744844 KO:K08176 TIGRFAMs:TIGR00887 EMBL:U62331 EMBL:AF022872 EMBL:AB016166 IPI:IPI00537042 PIR:C84811 RefSeq:NP_181428.1 UniGene:At.255 UniGene:At.67089 ProteinModelPortal:Q96303 STRING:Q96303 PRIDE:Q96303 EnsemblPlants:AT2G38940.1 GeneID:818479 KEGG:ath:AT2G38940 GeneFarm:5189 TAIR:At2g38940 InParanoid:Q96303 OMA:CYLLIAG PhylomeDB:Q96303 ProtClustDB:CLSN2683235 ArrayExpress:Q96303 Genevestigator:Q96303 GermOnline:AT2G38940 Uniprot:Q96303
Root	Isotig02922	3	57	-4.377	8.39E-15	TAIR|locus:2064895 - symbol:PHT1;4 "AT2G38940" species:3702 "Arabidopsis thaliana" [GO:0005351 "sugar:hydrogen symporter activity" evidence=ISS] [GO:0015114 "phosphate ion transmembrane transporter activity" evidence=ISS] [GO:0015144 "carbohydrate transmembrane transporter activity" evidence=ISS] [GO:0016020 "membrane" evidence=ISS;IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0009737 "response to abscisic acid stimulus" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] [GO:0005315 "inorganic phosphate transmembrane transporter activity" evidence=ISS] InterPro:IPR004738 InterPro:IPR005828 Pfam:PF00083 PROSITE:PS00216 PROSITE:PS00217 GO:GO:0016021 GO:GO:0005886

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0009506 GO:GO:0009737 GO:GO:0005634 GO:GO:0005773 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0015293 GO:GO:0005315 eggNOG:COG0477 InterPro:IPR016196 SUPFAM:SSF103473 InterPro:IPR020846 PROSITE:PS50850 EMBL:AC005770 HOGENOM:HBG744844 KO:K08176 TIGRFAMs:TIGR00887 EMBL:U62331 EMBL:AF022872 EMBL:AB016166 IPI:IPI00537042 PIR:C84811 RefSeq:NP_181428.1 UniGene:At.255 UniGene:At.67089 ProteinModelPortal:Q96303 STRING:Q96303 PRIDE:Q96303 EnsemblPlants:AT2G38940.1 GeneID:818479 KEGG:ath:AT2G38940 GeneFarm:5189 TAIR:At2g38940 InParanoid:Q96303 OMA:CYLLIAG PhylomeDB:Q96303 ProtClustDB:CLSN2683235 ArrayExpress:Q96303 Genevestigator:Q96303 GermOnline:AT2G38940 Uniprot:Q96303
Root	Isotig02923	3	48	-4.129	2.32E-12	TAIR|locus:2064895 - symbol:PHT1;4 "AT2G38940" species:3702 "Arabidopsis thaliana" [GO:0005351 "sugar:hydrogen symporter activity" evidence=ISS] [GO:0015114 "phosphate ion transmembrane transporter activity" evidence=ISS] [GO:0015144 "carbohydrate transmembrane transporter activity" evidence=ISS] [GO:0016020 "membrane" evidence=ISS;IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0009737 "response to abscisic acid stimulus" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] [GO:0005315 "inorganic phosphate transmembrane transporter activity" evidence=ISS] InterPro:IPR004738 InterPro:IPR005828 Pfam:PF00083 PROSITE:PS00216 PROSITE:PS00217 GO:GO:0016021 GO:GO:0005886 GO:GO:0009506 GO:GO:0009737 GO:GO:0005634 GO:GO:0005773 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0015293 GO:GO:0005315 eggNOG:COG0477 InterPro:IPR016196 SUPFAM:SSF103473 InterPro:IPR020846 PROSITE:PS50850 EMBL:AC005770 HOGENOM:HBG744844 KO:K08176 TIGRFAMs:TIGR00887 EMBL:U62331 EMBL:AF022872 EMBL:AB016166 IPI:IPI00537042 PIR:C84811 RefSeq:NP_181428.1 UniGene:At.255 UniGene:At.67089 ProteinModelPortal:Q96303 STRING:Q96303 PRIDE:Q96303 EnsemblPlants:AT2G38940.1 GeneID:818479 KEGG:ath:AT2G38940 GeneFarm:5189 TAIR:At2g38940 InParanoid:Q96303 OMA:CYLLIAG PhylomeDB:Q96303 ProtClustDB:CLSN2683235 ArrayExpress:Q96303 Genevestigator:Q96303 GermOnline:AT2G38940 Uniprot:Q96303
Root	Isotig02924	3	48	-4.129	2.32E-12	TAIR|locus:2064895 - symbol:PHT1;4 "AT2G38940" species:3702 "Arabidopsis thaliana" [GO:0005351 "sugar:hydrogen symporter activity" evidence=ISS] [GO:0015114 "phosphate ion transmembrane transporter activity" evidence=ISS] [GO:0015144 "carbohydrate transmembrane transporter activity" evidence=ISS] [GO:0016020 "membrane" evidence=ISS;IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0009737 "response to abscisic acid stimulus" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] [GO:0005315 "inorganic phosphate transmembrane transporter activity" evidence=ISS] InterPro:IPR004738 InterPro:IPR005828 Pfam:PF00083 PROSITE:PS00216 PROSITE:PS00217 GO:GO:0016021 GO:GO:0005886 GO:GO:0009506 GO:GO:0009737 GO:GO:0005634 GO:GO:0005773 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0015293 GO:GO:0005315 eggNOG:COG0477 InterPro:IPR016196 SUPFAM:SSF103473 InterPro:IPR020846 PROSITE:PS50850 EMBL:AC005770 HOGENOM:HBG744844 KO:K08176 TIGRFAMs:TIGR00887 EMBL:U62331 EMBL:AF022872 EMBL:AB016166 IPI:IPI00537042 PIR:C84811 RefSeq:NP_181428.1 UniGene:At.255 UniGene:At.67089 ProteinModelPortal:Q96303 STRING:Q96303 PRIDE:Q96303 EnsemblPlants:AT2G38940.1 GeneID:818479 KEGG:ath:AT2G38940 GeneFarm:5189 TAIR:At2g38940 InParanoid:Q96303 OMA:CYLLIAG PhylomeDB:Q96303 ProtClustDB:CLSN2683235 ArrayExpress:Q96303 Genevestigator:Q96303 GermOnline:AT2G38940 Uniprot:Q96303
Root	Isotig02925	3	48	-4.129	2.32E-12	TAIR|locus:2064895 - symbol:PHT1;4 "AT2G38940" species:3702 "Arabidopsis thaliana" [GO:0005351 "sugar:hydrogen symporter activity" evidence=ISS] [GO:0015114 "phosphate ion transmembrane transporter activity" evidence=ISS] [GO:0015144 "carbohydrate transmembrane transporter activity" evidence=ISS] [GO:0016020 "membrane" evidence=ISS;IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0009737 "response to abscisic acid stimulus" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] [GO:0005315 "inorganic phosphate transmembrane transporter activity" evidence=ISS] InterPro:IPR004738 InterPro:IPR005828 Pfam:PF00083 PROSITE:PS00216 PROSITE:PS00217 GO:GO:0016021 GO:GO:0005886 GO:GO:0009506 GO:GO:0009737 GO:GO:0005634 GO:GO:0005773 EMBL:CP002685

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GenomeReviews:CT485783_GR GO:GO:0015293 GO:GO:0005315 eggNOG:COG0477 InterPro:IPR016196 SUPFAM:SSF103473 InterPro:IPR020846 PROSITE:PS50850 EMBL:AC005770 HOGENOM:HBG744844 KO:K08176 TIGRFAMs:TIGR00887 EMBL:U62331 EMBL:AF022872 EMBL:AB016166 IPI:IPI00537042 PIR:C84811 RefSeq:NP_181428.1 UniGene:At.255 UniGene:At.67089 ProteinModelPortal:Q96303 STRING:Q96303 PRIDE:Q96303 EnsemblPlants:AT2G38940.1 GeneID:818479 KEGG:ath:AT2G38940 GeneFarm:5189 TAIR:At2g38940 InParanoid:Q96303 OMA:CYLLIAG PhylomeDB:Q96303 ProtClustDB:CLSN2683235 ArrayExpress:Q96303 Genevestigator:Q96303 GermOnline:AT2G38940 Uniprot:Q96303
Root	Isotig02932	33	8	1.915	0.000152977	TAIR|locus:2009041 - symbol:AT1G33970 species:3702 "Arabidopsis thaliana" [GO:0005525 "GTP binding" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0009617 "response to bacterium" evidence=ISS] InterPro:IPR006703 Pfam:PF04548 GO:GO:0005525 EMBL:AC015446 EMBL:AC079286 EMBL:AY087627 IPI:IPI00519038 PIR:D86463 ProteinModelPortal:Q9FE56 SMR:Q9FE56 STRING:Q9FE56 PRIDE:Q9FE56 TAIR:At1g33970 InParanoid:Q9FE56 PhylomeDB:Q9FE56 Genevestigator:Q9FE56 Uniprot:Q9FE56
Root	Isotig02933	33	8	1.915	0.000152977	TAIR|locus:2009041 - symbol:AT1G33970 species:3702 "Arabidopsis thaliana" [GO:0005525 "GTP binding" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0009617 "response to bacterium" evidence=ISS] InterPro:IPR006703 Pfam:PF04548 GO:GO:0005525 EMBL:AC015446 EMBL:AC079286 EMBL:AY087627 IPI:IPI00519038 PIR:D86463 ProteinModelPortal:Q9FE56 SMR:Q9FE56 STRING:Q9FE56 PRIDE:Q9FE56 TAIR:At1g33970 InParanoid:Q9FE56 PhylomeDB:Q9FE56 Genevestigator:Q9FE56 Uniprot:Q9FE56
Root	Isotig02934	33	8	1.915	0.000152977	TAIR|locus:2009041 - symbol:AT1G33970 species:3702 "Arabidopsis thaliana" [GO:0005525 "GTP binding" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0009617 "response to bacterium" evidence=ISS] InterPro:IPR006703 Pfam:PF04548 GO:GO:0005525 EMBL:AC015446 EMBL:AC079286 EMBL:AY087627 IPI:IPI00519038 PIR:D86463 ProteinModelPortal:Q9FE56 SMR:Q9FE56 STRING:Q9FE56 PRIDE:Q9FE56 TAIR:At1g33970 InParanoid:Q9FE56 PhylomeDB:Q9FE56 Genevestigator:Q9FE56 Uniprot:Q9FE56
Root	Isotig02935	33	8	1.915	0.000152977	TAIR|locus:2009041 - symbol:AT1G33970 species:3702 "Arabidopsis thaliana" [GO:0005525 "GTP binding" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0009617 "response to bacterium" evidence=ISS] InterPro:IPR006703 Pfam:PF04548 GO:GO:0005525 EMBL:AC015446 EMBL:AC079286 EMBL:AY087627 IPI:IPI00519038 PIR:D86463 ProteinModelPortal:Q9FE56 SMR:Q9FE56 STRING:Q9FE56 PRIDE:Q9FE56 TAIR:At1g33970 InParanoid:Q9FE56 PhylomeDB:Q9FE56 Genevestigator:Q9FE56 Uniprot:Q9FE56
Root	Isotig02936	33	8	1.915	0.000152977	TAIR|locus:2009041 - symbol:AT1G33970 species:3702 "Arabidopsis thaliana" [GO:0005525 "GTP binding" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0009617 "response to bacterium" evidence=ISS] InterPro:IPR006703 Pfam:PF04548 GO:GO:0005525 EMBL:AC015446 EMBL:AC079286 EMBL:AY087627 IPI:IPI00519038 PIR:D86463 ProteinModelPortal:Q9FE56 SMR:Q9FE56 STRING:Q9FE56 PRIDE:Q9FE56 TAIR:At1g33970 InParanoid:Q9FE56 PhylomeDB:Q9FE56 Genevestigator:Q9FE56 Uniprot:Q9FE56
Root	Isotig02937	33	8	1.915	0.000152977	TAIR|locus:2009041 - symbol:AT1G33970 species:3702 "Arabidopsis thaliana" [GO:0005525 "GTP binding" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0009617 "response to bacterium" evidence=ISS] InterPro:IPR006703 Pfam:PF04548 GO:GO:0005525 EMBL:AC015446 EMBL:AC079286 EMBL:AY087627 IPI:IPI00519038 PIR:D86463 ProteinModelPortal:Q9FE56 SMR:Q9FE56 STRING:Q9FE56 PRIDE:Q9FE56 TAIR:At1g33970 InParanoid:Q9FE56 PhylomeDB:Q9FE56 Genevestigator:Q9FE56 Uniprot:Q9FE56
Root	Isotig02950	13	47	-1.983	1.33E-06	TAIR|locus:2180872 - symbol:UGD3 "AT5G15490" species:3702 "Arabidopsis thaliana" [GO:0003979 "UDP-glucose 6-dehydrogenase activity" evidence=IGI;ISS] [GO:0005618 "cell wall" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0005975 "carbohydrate metabolic process" evidence=IGI] [GO:0052546 "cell wall pectin metabolic process" evidence=IGI] InterPro:IPR001732 InterPro:IPR008927 InterPro:IPR014026 InterPro:IPR014027 InterPro:IPR016040 InterPro:IPR017476 Pfam:PF00984 Pfam:PF03720 Pfam:PF03721 PIRSF:PIRSF000124 SMART:SM00984 GO:GO:0005829 GO:GO:0005634 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005618 Gene3D:G3DSA:3.40.50.720 GO:GO:0051287 SUPFAM:SSF48179 EMBL:AL391143 InterPro:IPR021157 Gene3D:G3DSA:1.20.5.100

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0052546 GO:GO:0003979 HOGENOM:HBG400967 KO:K00012 SUPFAM:SSF52413 TIGRFAMs:TIGR03026 ProtClustDB:PLN02353 EMBL:AY056200 EMBL:BT015794 IPI:IPI00527538 PIR:T51527 RefSeq:NP_197053.1 UniGene:At.20910 HSSP:P11759 ProteinModelPortal:Q9LF33 SMR:Q9LF33 STRING:Q9LF33 PRIDE:Q9LF33 EnsemblPlants:AT5G15490.1 GeneID:831402 KEGG:ath:AT5G15490 TAIR:At5g15490 InParanoid:Q9LF33 OMA:FQRIFEN PhylomeDB:Q9LF33 ArrayExpress:Q9LF33 Genevestigator:Q9LF33 Uniprot:Q9LF33
Root	Isotig02951	13	46	-1.952	2.20E-06	TAIR|locus:2180872 - symbol:UGD3 "AT5G15490" species:3702 "Arabidopsis thaliana" [GO:0003979 "UDP-glucose 6-dehydrogenase activity" evidence=IGI;ISS] [GO:0005618 "cell wall" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0005975 "carbohydrate metabolic process" evidence=IGI] [GO:0052546 "cell wall pectin metabolic process" evidence=IGI] InterPro:IPR001732 InterPro:IPR008927 InterPro:IPR014026 InterPro:IPR014027 InterPro:IPR016040 InterPro:IPR017476 Pfam:PF00984 Pfam:PF03720 Pfam:PF03721 PIRSF:PIRSF000124 SMART:SM00984 GO:GO:0005829 GO:GO:0005634 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005618 Gene3D:G3DSA:3.40.50.720 GO:GO:0051287 SUPFAM:SSF48179 EMBL:AL391143 InterPro:IPR021157 Gene3D:G3DSA:1.20.5.100 GO:GO:0052546 GO:GO:0003979 HOGENOM:HBG400967 KO:K00012 SUPFAM:SSF52413 TIGRFAMs:TIGR03026 ProtClustDB:PLN02353 EMBL:AY056200 EMBL:BT015794 IPI:IPI00527538 PIR:T51527 RefSeq:NP_197053.1 UniGene:At.20910 HSSP:P11759 ProteinModelPortal:Q9LF33 SMR:Q9LF33 STRING:Q9LF33 PRIDE:Q9LF33 EnsemblPlants:AT5G15490.1 GeneID:831402 KEGG:ath:AT5G15490 TAIR:At5g15490 InParanoid:Q9LF33 OMA:FQRIFEN PhylomeDB:Q9LF33 ArrayExpress:Q9LF33 Genevestigator:Q9LF33 Uniprot:Q9LF33
Root	Isotig02953	9	32	-1.959	7.57E-05	TAIR|locus:2180872 - symbol:UGD3 "AT5G15490" species:3702 "Arabidopsis thaliana" [GO:0003979 "UDP-glucose 6-dehydrogenase activity" evidence=IGI;ISS] [GO:0005618 "cell wall" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0005975 "carbohydrate metabolic process" evidence=IGI] [GO:0052546 "cell wall pectin metabolic process" evidence=IGI] InterPro:IPR001732 InterPro:IPR008927 InterPro:IPR014026 InterPro:IPR014027 InterPro:IPR016040 InterPro:IPR017476 Pfam:PF00984 Pfam:PF03720 Pfam:PF03721 PIRSF:PIRSF000124 SMART:SM00984 GO:GO:0005829 GO:GO:0005634 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005618 Gene3D:G3DSA:3.40.50.720 GO:GO:0051287 SUPFAM:SSF48179 EMBL:AL391143 InterPro:IPR021157 Gene3D:G3DSA:1.20.5.100 GO:GO:0052546 GO:GO:0003979 HOGENOM:HBG400967 KO:K00012 SUPFAM:SSF52413 TIGRFAMs:TIGR03026 ProtClustDB:PLN02353 EMBL:AY056200 EMBL:BT015794 IPI:IPI00527538 PIR:T51527 RefSeq:NP_197053.1 UniGene:At.20910 HSSP:P11759 ProteinModelPortal:Q9LF33 SMR:Q9LF33 STRING:Q9LF33 PRIDE:Q9LF33 EnsemblPlants:AT5G15490.1 GeneID:831402 KEGG:ath:AT5G15490 TAIR:At5g15490 InParanoid:Q9LF33 OMA:FQRIFEN PhylomeDB:Q9LF33 ArrayExpress:Q9LF33 Genevestigator:Q9LF33 Uniprot:Q9LF33
Root	Isotig02954	9	31	-1.913	0.000125821	TAIR|locus:2180872 - symbol:UGD3 "AT5G15490" species:3702 "Arabidopsis thaliana" [GO:0003979 "UDP-glucose 6-dehydrogenase activity" evidence=IGI;ISS] [GO:0005618 "cell wall" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0005975 "carbohydrate metabolic process" evidence=IGI] [GO:0052546 "cell wall pectin metabolic process" evidence=IGI] InterPro:IPR001732 InterPro:IPR008927 InterPro:IPR014026 InterPro:IPR014027 InterPro:IPR016040 InterPro:IPR017476 Pfam:PF00984 Pfam:PF03720 Pfam:PF03721 PIRSF:PIRSF000124 SMART:SM00984 GO:GO:0005829 GO:GO:0005634 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005618 Gene3D:G3DSA:3.40.50.720 GO:GO:0051287 SUPFAM:SSF48179 EMBL:AL391143 InterPro:IPR021157 Gene3D:G3DSA:1.20.5.100 GO:GO:0052546 GO:GO:0003979 HOGENOM:HBG400967 KO:K00012 SUPFAM:SSF52413 TIGRFAMs:TIGR03026 ProtClustDB:PLN02353 EMBL:AY056200 EMBL:BT015794 IPI:IPI00527538 PIR:T51527 RefSeq:NP_197053.1 UniGene:At.20910 HSSP:P11759 ProteinModelPortal:Q9LF33 SMR:Q9LF33 STRING:Q9LF33 PRIDE:Q9LF33 EnsemblPlants:AT5G15490.1 GeneID:831402 KEGG:ath:AT5G15490 TAIR:At5g15490 InParanoid:Q9LF33 OMA:FQRIFEN PhylomeDB:Q9LF33 ArrayExpress:Q9LF33 Genevestigator:Q9LF33 Uniprot:Q9LF33
Root	Isotig02960	30	2	3.778	2.52E-07	TAIR|locus:2183901 - symbol:AT5G13200 "AT5G13200" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] Pfam:PF02893 EMBL:CP002688 GenomeReviews:BA000015_GR EMBL:AL391711 EMBL:AL163491 InterPro:IPR004182 SMART:SM00568 HOGENOM:HBG745499 EMBL:BT010714 EMBL:BT012428 EMBL:AK229276 IPI:IPI00528201

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						PIR:T48567 RefSeq:NP_196824.1 UniGene:At.25214 STRING:Q9LYV6 PRIDE:Q9LYV6 DNASU:831159 EnsemblPlants:AT5G13200.1 GeneID:831159 KEGG:ath:AT5G13200 TAIR:At5g13200 eggNOG:NOG289836 InParanoid:Q9LYV6 OMA:WHNLKTG PhylomeDB:Q9LYV6 ProtClustDB:CLSN2686867 Genevestigator:Q9LYV6 Uniprot:Q9LYV6
Root	Isotig02961	30	2	3.778	2.52E-07	TAIR|locus:2183901 - symbol:AT5G13200 "AT5G13200" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] Pfam:PF02893 EMBL:CP002688 GenomeReviews:BA000015_GR EMBL:AL391711 EMBL:AL163491 InterPro:IPR004182 SMART:SM00568 HOGENOM:HBG745499 EMBL:BT010714 EMBL:BT012428 EMBL:AK229276 IPI:IPI00528201 PIR:T48567 RefSeq:NP_196824.1 UniGene:At.25214 STRING:Q9LYV6 PRIDE:Q9LYV6 DNASU:831159 EnsemblPlants:AT5G13200.1 GeneID:831159 KEGG:ath:AT5G13200 TAIR:At5g13200 eggNOG:NOG289836 InParanoid:Q9LYV6 OMA:WHNLKTG PhylomeDB:Q9LYV6 ProtClustDB:CLSN2686867 Genevestigator:Q9LYV6 Uniprot:Q9LYV6
Root	Isotig02962	24	1	4.456	1.32E-06	TAIR|locus:2183901 - symbol:AT5G13200 "AT5G13200" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] Pfam:PF02893 EMBL:CP002688 GenomeReviews:BA000015_GR EMBL:AL391711 EMBL:AL163491 InterPro:IPR004182 SMART:SM00568 HOGENOM:HBG745499 EMBL:BT010714 EMBL:BT012428 EMBL:AK229276 IPI:IPI00528201 PIR:T48567 RefSeq:NP_196824.1 UniGene:At.25214 STRING:Q9LYV6 PRIDE:Q9LYV6 DNASU:831159 EnsemblPlants:AT5G13200.1 GeneID:831159 KEGG:ath:AT5G13200 TAIR:At5g13200 eggNOG:NOG289836 InParanoid:Q9LYV6 OMA:WHNLKTG PhylomeDB:Q9LYV6 ProtClustDB:CLSN2686867 Genevestigator:Q9LYV6 Uniprot:Q9LYV6
Root	Isotig02963	24	1	4.456	1.32E-06	TAIR|locus:2183901 - symbol:AT5G13200 "AT5G13200" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] Pfam:PF02893 EMBL:CP002688 GenomeReviews:BA000015_GR EMBL:AL391711 EMBL:AL163491 InterPro:IPR004182 SMART:SM00568 HOGENOM:HBG745499 EMBL:BT010714 EMBL:BT012428 EMBL:AK229276 IPI:IPI00528201 PIR:T48567 RefSeq:NP_196824.1 UniGene:At.25214 STRING:Q9LYV6 PRIDE:Q9LYV6 DNASU:831159 EnsemblPlants:AT5G13200.1 GeneID:831159 KEGG:ath:AT5G13200 TAIR:At5g13200 eggNOG:NOG289836 InParanoid:Q9LYV6 OMA:WHNLKTG PhylomeDB:Q9LYV6 ProtClustDB:CLSN2686867 Genevestigator:Q9LYV6 Uniprot:Q9LYV6
Root	Isotig02964	26	2	3.571	2.56E-06	TAIR|locus:2183901 - symbol:AT5G13200 "AT5G13200" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] Pfam:PF02893 EMBL:CP002688 GenomeReviews:BA000015_GR EMBL:AL391711 EMBL:AL163491 InterPro:IPR004182 SMART:SM00568 HOGENOM:HBG745499 EMBL:BT010714 EMBL:BT012428 EMBL:AK229276 IPI:IPI00528201 PIR:T48567 RefSeq:NP_196824.1 UniGene:At.25214 STRING:Q9LYV6 PRIDE:Q9LYV6 DNASU:831159 EnsemblPlants:AT5G13200.1 GeneID:831159 KEGG:ath:AT5G13200 TAIR:At5g13200 eggNOG:NOG289836 InParanoid:Q9LYV6 OMA:WHNLKTG PhylomeDB:Q9LYV6 ProtClustDB:CLSN2686867 Genevestigator:Q9LYV6 Uniprot:Q9LYV6
Root	Isotig02965	72	0	7.041	2.73E-17	TAIR|locus:2115235 - symbol:AT4G36600 "AT4G36600" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0009793 "embryo development ending in seed dormancy" evidence=ISS] Pfam:PF02987 EMBL:BT012603 IPI:IPI00516442 PRIDE:Q6NKU0 TAIR:At4g36600 InParanoid:Q6NKU0 PhylomeDB:Q6NKU0 Genevestigator:Q6NKU0 InterPro:IPR004238 Uniprot:Q6NKU0
Root	Isotig02966	64	0	6.871	1.11E-15	TAIR|locus:2035109 - symbol:LEA7 "AT1G52690" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0009793 "embryo development ending in seed dormancy" evidence=ISS] EMBL:CP002684 EMBL:AC008016 EMBL:AF385732 EMBL:AY093968 EMBL:AY087466 EMBL:BT000737 EMBL:BT000739 EMBL:X91919 IPI:IPI00526817 PIR:H96567 RefSeq:NP_175678.1 RefSeq:NP_974009.1 UniGene:At.21275 STRING:Q96270 PRIDE:Q96270 ProMEX:Q96270 DNASU:841701 EnsemblPlants:AT1G52690.1 EnsemblPlants:AT1G52690.2 GeneID:841701 KEGG:ath:AT1G52690 TAIR:At1g52690 InParanoid:Q96270 OMA:MASHQEQ PhylomeDB:Q96270 ProtClustDB:CLSN2679745 ArrayExpress:Q96270 Genevestigator:Q96270 Uniprot:Q96270
Root	Isotig02967	46	0	6.395	6.55E-12	No hit
Root	Isotig02968	62	0	6.825	2.85E-15	TAIR|locus:2035109 - symbol:LEA7 "AT1G52690" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0009793 "embryo development ending in seed dormancy" evidence=ISS] EMBL:CP002684 EMBL:AC008016 EMBL:AF385732

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EMBL:AY093968 EMBL:AY087466 EMBL:BT000737 EMBL:BT000739 EMBL:X91919 IPI:IPI00526817 PIR:H96567 RefSeq:NP_175678.1 RefSeq:NP_974009.1 UniGene:At.21275 STRING:Q96270 PRIDE:Q96270 ProMEX:Q96270 DNASU:841701 EnsemblPlants:AT1G52690.1 EnsemblPlants:AT1G52690.2 GeneID:841701 KEGG:ath:AT1G52690 TAIR:At1g52690 InParanoid:Q96270 OMA:MASHQEQ PhylomeDB:Q96270 ProtClustDB:CLSN2679745 ArrayExpress:Q96270 Genevestigator:Q96270 Uniprot:Q96270
Root	Isotig02969	44	0	6.330	1.78E-11	No hit
Root	Isotig02980	0	24	-5.714	1.84E-07	TAIR|locus:2153529 - symbol:PRX52 "AT5G05340" species:3702 "Arabidopsis thaliana" [GO:0004601 "peroxidase activity" evidence=ISS] [GO:0006979 "response to oxidative stress" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0005618 "cell wall" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0005829 "cytosol" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR000823 InterPro:IPR002016 InterPro:IPR010255 InterPro:IPR019793 InterPro:IPR019794 Pfam:PF00141 PRINTS:PR00458 PRINTS:PR00461 PROSITE:PS00435 PROSITE:PS00436 PROSITE:PS50873 GO:GO:0005829 GO:GO:0048046 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005618 GO:GO:0005515 GO:GO:0020037 GO:GO:0004601 GO:GO:0042744 HOGENOM:HBG597790 SUPFAM:SSF48113 EMBL:AB010692 KO:K00430 EMBL:AY065270 IPI:IPI00527468 RefSeq:NP_196153.1 UniGene:At.28537 ProteinModelPortal:Q9FLC0 SMR:Q9FLC0 IntAct:Q9FLC0 STRING:Q9FLC0 PeroxiBase:218 PRIDE:Q9FLC0 EnsemblPlants:AT5G05340.1 GeneID:830416 KEGG:ath:AT5G05340 GeneFarm:1905 TAIR:At5g05340 eggNOG:NOG298084 InParanoid:Q9FLC0 OMA:TNFRARI PhylomeDB:Q9FLC0 ProtClustDB:CLSN2916362 ArrayExpress:Q9FLC0 Genevestigator:Q9FLC0 GermOnline:AT5G05340 Uniprot:Q9FLC0
Root	Isotig02981	0	28	-5.936	1.79E-08	TAIR|locus:2153529 - symbol:PRX52 "AT5G05340" species:3702 "Arabidopsis thaliana" [GO:0004601 "peroxidase activity" evidence=ISS] [GO:0006979 "response to oxidative stress" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0005618 "cell wall" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0005829 "cytosol" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR000823 InterPro:IPR002016 InterPro:IPR010255 InterPro:IPR019793 InterPro:IPR019794 Pfam:PF00141 PRINTS:PR00458 PRINTS:PR00461 PROSITE:PS00435 PROSITE:PS00436 PROSITE:PS50873 GO:GO:0005829 GO:GO:0048046 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005618 GO:GO:0005515 GO:GO:0020037 GO:GO:0004601 GO:GO:0042744 HOGENOM:HBG597790 SUPFAM:SSF48113 EMBL:AB010692 KO:K00430 EMBL:AY065270 IPI:IPI00527468 RefSeq:NP_196153.1 UniGene:At.28537 ProteinModelPortal:Q9FLC0 SMR:Q9FLC0 IntAct:Q9FLC0 STRING:Q9FLC0 PeroxiBase:218 PRIDE:Q9FLC0 EnsemblPlants:AT5G05340.1 GeneID:830416 KEGG:ath:AT5G05340 GeneFarm:1905 TAIR:At5g05340 eggNOG:NOG298084 InParanoid:Q9FLC0 OMA:TNFRARI PhylomeDB:Q9FLC0 ProtClustDB:CLSN2916362 ArrayExpress:Q9FLC0 Genevestigator:Q9FLC0 GermOnline:AT5G05340 Uniprot:Q9FLC0
Root	Isotig02982	0	24	-5.714	1.84E-07	TAIR|locus:2153529 - symbol:PRX52 "AT5G05340" species:3702 "Arabidopsis thaliana" [GO:0004601 "peroxidase activity" evidence=ISS] [GO:0006979 "response to oxidative stress" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0005618 "cell wall" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0005829 "cytosol" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR000823 InterPro:IPR002016 InterPro:IPR010255 InterPro:IPR019793 InterPro:IPR019794 Pfam:PF00141 PRINTS:PR00458 PRINTS:PR00461 PROSITE:PS00435 PROSITE:PS00436 PROSITE:PS50873 GO:GO:0005829 GO:GO:0048046 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005618 GO:GO:0005515 GO:GO:0020037 GO:GO:0004601 GO:GO:0042744 HOGENOM:HBG597790 SUPFAM:SSF48113 EMBL:AB010692 KO:K00430 EMBL:AY065270 IPI:IPI00527468 RefSeq:NP_196153.1 UniGene:At.28537 ProteinModelPortal:Q9FLC0 SMR:Q9FLC0 IntAct:Q9FLC0 STRING:Q9FLC0 PeroxiBase:218 PRIDE:Q9FLC0 EnsemblPlants:AT5G05340.1 GeneID:830416 KEGG:ath:AT5G05340 GeneFarm:1905 TAIR:At5g05340 eggNOG:NOG298084 InParanoid:Q9FLC0 OMA:TNFRARI PhylomeDB:Q9FLC0 ProtClustDB:CLSN2916362 ArrayExpress:Q9FLC0 Genevestigator:Q9FLC0 GermOnline:AT5G05340 Uniprot:Q9FLC0
Root	Isotig02983	0	28	-5.936	1.79E-08	TAIR|locus:2153529 - symbol:PRX52 "AT5G05340" species:3702 "Arabidopsis thaliana" [GO:0004601 "peroxidase activity" evidence=ISS] [GO:0006979 "response to oxidative stress" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0005618 "cell wall" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0005829 "cytosol" evidence=IDA] [GO:0005794 "Golgi apparatus"

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						evidence=IDA] InterPro:IPR000823 InterPro:IPR002016 InterPro:IPR010255 InterPro:IPR019793 InterPro:IPR019794 Pfam:PF00141 PRINTS:PR00458 PRINTS:PR00461 PROSITE:PS00435 PROSITE:PS00436 PROSITE:PS50873 GO:GO:0005829 GO:GO:0048046 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005618 GO:GO:0005515 GO:GO:0020037 GO:GO:0004601 GO:GO:0042744 HOGENOM:HBG597790 SUPFAM:SSF48113 EMBL:AB010692 KO:K00430 EMBL:AY065270 IPI:IPI00527468 RefSeq:NP_196153.1 UniGene:At.28537 ProteinModelPortal:Q9FLC0 SMR:Q9FLC0 IntAct:Q9FLC0 STRING:Q9FLC0 PeroxiBase:218 PRIDE:Q9FLC0 EnsemblPlants:AT5G05340.1 GeneID:830416 KEGG:ath:AT5G05340 GeneFarm:1905 TAIR:At5g05340 eggNOG:NOG298084 InParanoid:Q9FLC0 OMA:TNFRARI PhylomeDB:Q9FLC0 ProtClustDB:CLSN2916362 ArrayExpress:Q9FLC0 Genevestigator:Q9FLC0 GermOnline:AT5G05340 Uniprot:Q9FLC0
Root	Isotig03000	32	61	-1.060	0.000551724	DICTYBASE|DDB_G0277823 - symbol:alaS "alanyl-tRNA synthetase,alanine-tRNA ligase" species:44689 "Dictyostelium discoideum" [GO:0004813 "alanine-tRNA ligase activity" evidence=ISS] [GO:0005524 "ATP binding" evidence=ISS] [GO:0005737 "cytoplasm" evidence=ISS] [GO:0006419 "alanyl-tRNA aminoacylation" evidence=ISS] InterPro:IPR002318 InterPro:IPR003156 InterPro:IPR012947 InterPro:IPR018162 InterPro:IPR018163 InterPro:IPR018164 InterPro:IPR018165 InterPro:IPR023033 Pfam:PF01411 Pfam:PF02272 Pfam:PF07973 PRINTS:PR00980 PROSITE:PS50860 SMART:SM00863 dictyBase:DDB_G0277823 GO:GO:0005524 GO:GO:0005737 GenomeReviews:CM000152_GR GO:GO:0046872 EMBL:AAFI02000023 GO:GO:0004813 GO:GO:0006419 SUPFAM:SSF55186 GO:GO:0000049 PANTHER:PTHR11777:SF6 eggNOG:COG0013 HOGENOM:HBG354397 KO:K01872 SUPFAM:SSF101353 TIGRFAMs:TIGR00344 EMBL:AF188717 RefSeq:XP_642382.1 HSSP:O67323 ProteinModelPortal:Q54Y20 STRING:Q54Y20 PRIDE:Q54Y20 EnsemblProtists:DDB0214894 GeneID:8621587 KEGG:ddi:DDB_G0277823 OMA:EGSFGTF PhylomeDB:Q54Y20 ProtClustDB:CLSZ2429158 Uniprot:Q54Y20
Root	Isotig03001	32	61	-1.060	0.000551724	TAIR|locus:2011962 - symbol:ALATS "Alanyl-tRNA synthetase" species:3702 "Arabidopsis thaliana" [GO:0000166 "nucleotide binding" evidence=IEA] [GO:0003676 "nucleic acid binding" evidence=IEA] [GO:0004813 "alanine-tRNA ligase activity" evidence=IEA] [GO:0005524 "ATP binding" evidence=IEA] [GO:0006419 "alanyl-tRNA aminoacylation" evidence=ISS] [GO:0016876 "ligase activity, forming aminoacyl-tRNA and related compounds" evidence=IEA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR002318 InterPro:IPR003156 InterPro:IPR012947 InterPro:IPR018162 InterPro:IPR018163 InterPro:IPR018164 InterPro:IPR018165 InterPro:IPR023033 Pfam:PF01411 Pfam:PF02272 Pfam:PF07973 PRINTS:PR00980 PROSITE:PS50860 SMART:SM00863 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0005739 GO:GO:0005524 GO:GO:0046686 GO:GO:0009507 GO:GO:0046872 GO:GO:0004813 GO:GO:0006419 SUPFAM:SSF55186 GO:GO:0000049 EMBL:AC007980 eggNOG:COG0013 HOGENOM:HBG354397 KO:K01872 SUPFAM:SSF101353 TIGRFAMs:TIGR00344 OMA:EGSFGTF EMBL:Z22673 EMBL:BT002526 EMBL:BT008807 EMBL:Y12555 IPI:IPI00537243 IPI:IPI00760312 PIR:D96538 RefSeq:NP_175439.2 UniGene:At.1836 ProteinModelPortal:P36428 SMR:P36428 STRING:P36428 PRIDE:P36428 ProMEX:P36428 EnsemblPlants:AT1G50200.1 GeneID:841442 KEGG:ath:AT1G50200 GeneFarm:2386 TAIR:At1g50200 InParanoid:P36428 PhylomeDB:P36428 ProtClustDB:PLN02900 ArrayExpress:P36428 Genevestigator:P36428 GermOnline:AT1G50200 Uniprot:P36428
Root	Isotig03002	32	61	-1.060	0.000551724	DICTYBASE|DDB_G0277823 - symbol:alaS "alanyl-tRNA synthetase,alanine-tRNA ligase" species:44689 "Dictyostelium discoideum" [GO:0004813 "alanine-tRNA ligase activity" evidence=ISS] [GO:0005524 "ATP binding" evidence=ISS] [GO:0005737 "cytoplasm" evidence=ISS] [GO:0006419 "alanyl-tRNA aminoacylation" evidence=ISS] InterPro:IPR002318 InterPro:IPR003156 InterPro:IPR012947 InterPro:IPR018162 InterPro:IPR018163 InterPro:IPR018164 InterPro:IPR018165 InterPro:IPR023033 Pfam:PF01411 Pfam:PF02272 Pfam:PF07973 PRINTS:PR00980 PROSITE:PS50860 SMART:SM00863 dictyBase:DDB_G0277823 GO:GO:0005524 GO:GO:0005737 GenomeReviews:CM000152_GR GO:GO:0046872 EMBL:AAFI02000023 GO:GO:0004813 GO:GO:0006419 SUPFAM:SSF55186 GO:GO:0000049 PANTHER:PTHR11777:SF6 eggNOG:COG0013 HOGENOM:HBG354397 KO:K01872 SUPFAM:SSF101353 TIGRFAMs:TIGR00344 EMBL:AF188717 RefSeq:XP_642382.1 HSSP:O67323 ProteinModelPortal:Q54Y20 STRING:Q54Y20 PRIDE:Q54Y20 EnsemblProtists:DDB0214894 GeneID:8621587 KEGG:ddi:DDB_G0277823 OMA:EGSFGTF PhylomeDB:Q54Y20 ProtClustDB:CLSZ2429158 Uniprot:Q54Y20

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig03003	32	61	-1.060	0.000551724	TAIR|locus:2011962 - symbol:ALATS "Alanyl-tRNA synthetase" species:3702 "Arabidopsis thaliana" [GO:0000166 "nucleotide binding" evidence=IEA] [GO:0003676 "nucleic acid binding" evidence=IEA] [GO:0004813 "alanine-tRNA ligase activity" evidence=IEA] [GO:0005524 "ATP binding" evidence=IEA] [GO:0006419 "alanyl-tRNA aminoacylation" evidence=ISS] [GO:0016876 "ligase activity, forming aminoacyl-tRNA and related compounds" evidence=IEA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR002318 InterPro:IPR003156 InterPro:IPR012947 InterPro:IPR018162 InterPro:IPR018163 InterPro:IPR018164 InterPro:IPR018165 InterPro:IPR023033 Pfam:PF01411 Pfam:PF02272 Pfam:PF07973 PRINTS:PR00980 PROSITE:PS50860 SMART:SM00863 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0005739 GO:GO:0005524 GO:GO:0046686 GO:GO:0009507 GO:GO:0046872 GO:GO:0004813 GO:GO:0006419 SUPFAM:SSF55186 GO:GO:0000049 EMBL:AC007980 eggNOG:COG0013 HOGENOM:HBG354397 KO:K01872 SUPFAM:SSF101353 TIGRFAMs:TIGR00344 OMA:EGSFGTF EMBL:Z22673 EMBL:BT002526 EMBL:BT008807 EMBL:Y12555 IPI:IPI00537243 IPI:IPI00760312 PIR:D96538 RefSeq:NP_175439.2 UniGene:At.1836 ProteinModelPortal:P36428 SMR:P36428 STRING:P36428 PRIDE:P36428 ProMEX:P36428 EnsemblPlants:AT1G50200.1 GeneID:841442 KEGG:ath:AT1G50200 GeneFarm:2386 TAIR:At1g50200 InParanoid:P36428 PhylomeDB:P36428 ProtClustDB:PLN02900 ArrayExpress:P36428 Genevestigator:P36428 GermOnline:AT1G50200 Uniprot:P36428
Root	Isotig03012	91	294	-1.821	3.25E-30	No hit
Root	Isotig03013	92	293	-1.800	1.12E-29	No hit
Root	Isotig03014	98	275	-1.618	2.83E-24	No hit
Root	Isotig03015	99	274	-1.598	8.59E-24	No hit
Root	Isotig03020	11	67	-2.736	2.75E-12	TAIR|locus:2121013 - symbol:AT4G37900 "AT4G37900" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002687 GenomeReviews:CT486007_GR EMBL:AL161592 EMBL:AL035538 InterPro:IPR009836 Pfam:PF07173 eggNOG:NOG117547 HSSP:P02876 IPI:IPI00547179 PIR:T05617 RefSeq:NP_195503.1 UniGene:At.43494 PRIDE:Q9SZJ2 EnsemblPlants:AT4G37900.1 GeneID:829946 KEGG:ath:AT4G37900 TAIR:At4g37900 HOGENOM:HBG318807 InParanoid:Q9SZJ2 OMA:FMTAVEF PhylomeDB:Q9SZJ2 ProtClustDB:CLSN2681427 ArrayExpress:Q9SZJ2 Genevestigator:Q9SZJ2 Uniprot:Q9SZJ2
Root	Isotig03021	11	69	-2.778	8.64E-13	TAIR|locus:2121013 - symbol:AT4G37900 "AT4G37900" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002687 GenomeReviews:CT486007_GR EMBL:AL161592 EMBL:AL035538 InterPro:IPR009836 Pfam:PF07173 eggNOG:NOG117547 HSSP:P02876 IPI:IPI00547179 PIR:T05617 RefSeq:NP_195503.1 UniGene:At.43494 PRIDE:Q9SZJ2 EnsemblPlants:AT4G37900.1 GeneID:829946 KEGG:ath:AT4G37900 TAIR:At4g37900 HOGENOM:HBG318807 InParanoid:Q9SZJ2 OMA:FMTAVEF PhylomeDB:Q9SZJ2 ProtClustDB:CLSN2681427 ArrayExpress:Q9SZJ2 Genevestigator:Q9SZJ2 Uniprot:Q9SZJ2
Root	Isotig03022	8	71	-3.279	4.18E-15	TAIR|locus:2121013 - symbol:AT4G37900 "AT4G37900" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002687 GenomeReviews:CT486007_GR EMBL:AL161592 EMBL:AL035538 InterPro:IPR009836 Pfam:PF07173 eggNOG:NOG117547 HSSP:P02876 IPI:IPI00547179 PIR:T05617 RefSeq:NP_195503.1 UniGene:At.43494 PRIDE:Q9SZJ2 EnsemblPlants:AT4G37900.1 GeneID:829946 KEGG:ath:AT4G37900 TAIR:At4g37900 HOGENOM:HBG318807 InParanoid:Q9SZJ2 OMA:FMTAVEF PhylomeDB:Q9SZJ2 ProtClustDB:CLSN2681427 ArrayExpress:Q9SZJ2 Genevestigator:Q9SZJ2 Uniprot:Q9SZJ2
Root	Isotig03023	8	73	-3.319	1.24E-15	TAIR|locus:2121013 - symbol:AT4G37900 "AT4G37900" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002687 GenomeReviews:CT486007_GR EMBL:AL161592 EMBL:AL035538 InterPro:IPR009836 Pfam:PF07173 eggNOG:NOG117547 HSSP:P02876 IPI:IPI00547179 PIR:T05617 RefSeq:NP_195503.1 UniGene:At.43494 PRIDE:Q9SZJ2 EnsemblPlants:AT4G37900.1 GeneID:829946 KEGG:ath:AT4G37900 TAIR:At4g37900 HOGENOM:HBG318807 InParanoid:Q9SZJ2 OMA:FMTAVEF PhylomeDB:Q9SZJ2 ProtClustDB:CLSN2681427 ArrayExpress:Q9SZJ2 Genevestigator:Q9SZJ2 Uniprot:Q9SZJ2
Root	Isotig03024	726	13	5.674	1.21E-165	TAIR|locus:2103488 - symbol:SIP2 "AT3G57520" species:3702 "Arabidopsis thaliana" [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=ISS] [GO:0006979 "response to oxidative stress" evidence=IEP] [GO:0080167 "response to karrikin" evidence=IEP] [GO:0034484 "raffinose catabolic process"

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						evidence=IDA] [GO:0047274 "galactinol-sucrose galactosyltransferase activity" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR013785 GO:GO:0009506 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0006979 Gene3D:G3DSA:3.20.20.70 InterPro:IPR017853 SUPFAM:SSF51445 GO:GO:0080167 EMBL:AL133248 CAZy:GH36 eggNOG:NOG06986 InterPro:IPR008811 Pfam:PF05691 GO:GO:0034484 HOGENOM:HBG611539 KO:K06617 GO:GO:0047274 EMBL:AY050772 EMBL:AK226370 IPI:IPI00526258 IPI:IPI00541537 IPI:IPI00544535 PIR:T46188 RefSeq:NP_191311.1 RefSeq:NP_850715.1 UniGene:At.22207 UniGene:At.30900 ProteinModelPortal:Q94A08 STRING:Q94A08 PRIDE:Q94A08 EnsemblPlants:AT3G57520.1 GeneID:824919 KEGG:ath:AT3G57520 TAIR:At3g57520 InParanoid:Q9SCM1 OMA:QFMLLES PhylomeDB:Q94A08 ProtClustDB:PLN02219 BioCyc:MetaCyc:AT3G57520-MONOMER ArrayExpress:Q94A08 Uniprot:Q94A08
Root	Isotig03025	726	13	5.674	1.21E-165	TAIR|locus:2103488 - symbol:SIP2 "AT3G57520" species:3702 "Arabidopsis thaliana" [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=ISS] [GO:0006979 "response to oxidative stress" evidence=IEP] [GO:0080167 "response to karrikin" evidence=IEP] [GO:0034484 "raffinose catabolic process" evidence=IDA] [GO:0047274 "galactinol-sucrose galactosyltransferase activity" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR013785 GO:GO:0009506 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0006979 Gene3D:G3DSA:3.20.20.70 InterPro:IPR017853 SUPFAM:SSF51445 GO:GO:0080167 EMBL:AL133248 CAZy:GH36 eggNOG:NOG06986 InterPro:IPR008811 Pfam:PF05691 GO:GO:0034484 HOGENOM:HBG611539 KO:K06617 GO:GO:0047274 EMBL:AY050772 EMBL:AK226370 IPI:IPI00526258 IPI:IPI00541537 IPI:IPI00544535 PIR:T46188 RefSeq:NP_191311.1 RefSeq:NP_850715.1 UniGene:At.22207 UniGene:At.30900 ProteinModelPortal:Q94A08 STRING:Q94A08 PRIDE:Q94A08 EnsemblPlants:AT3G57520.1 GeneID:824919 KEGG:ath:AT3G57520 TAIR:At3g57520 InParanoid:Q9SCM1 OMA:QFMLLES PhylomeDB:Q94A08 ProtClustDB:PLN02219 BioCyc:MetaCyc:AT3G57520-MONOMER ArrayExpress:Q94A08 Uniprot:Q94A08
Root	Isotig03026	406	5	6.214	5.27E-93	TAIR|locus:2103488 - symbol:SIP2 "AT3G57520" species:3702 "Arabidopsis thaliana" [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=ISS] [GO:0006979 "response to oxidative stress" evidence=IEP] [GO:0080167 "response to karrikin" evidence=IEP] [GO:0034484 "raffinose catabolic process" evidence=IDA] [GO:0047274 "galactinol-sucrose galactosyltransferase activity" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR013785 GO:GO:0009506 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0006979 Gene3D:G3DSA:3.20.20.70 InterPro:IPR017853 SUPFAM:SSF51445 GO:GO:0080167 EMBL:AL133248 CAZy:GH36 eggNOG:NOG06986 InterPro:IPR008811 Pfam:PF05691 GO:GO:0034484 HOGENOM:HBG611539 KO:K06617 GO:GO:0047274 EMBL:AY050772 EMBL:AK226370 IPI:IPI00526258 IPI:IPI00541537 IPI:IPI00544535 PIR:T46188 RefSeq:NP_191311.1 RefSeq:NP_850715.1 UniGene:At.22207 UniGene:At.30900 ProteinModelPortal:Q94A08 STRING:Q94A08 PRIDE:Q94A08 EnsemblPlants:AT3G57520.1 GeneID:824919 KEGG:ath:AT3G57520 TAIR:At3g57520 InParanoid:Q9SCM1 OMA:QFMLLES PhylomeDB:Q94A08 ProtClustDB:PLN02219 BioCyc:MetaCyc:AT3G57520-MONOMER ArrayExpress:Q94A08 Uniprot:Q94A08
Root	Isotig03027	406	5	6.214	5.27E-93	TAIR|locus:2103488 - symbol:SIP2 "AT3G57520" species:3702 "Arabidopsis thaliana" [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=ISS] [GO:0006979 "response to oxidative stress" evidence=IEP] [GO:0080167 "response to karrikin" evidence=IEP] [GO:0034484 "raffinose catabolic process" evidence=IDA] [GO:0047274 "galactinol-sucrose galactosyltransferase activity" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR013785 GO:GO:0009506 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0006979 Gene3D:G3DSA:3.20.20.70 InterPro:IPR017853 SUPFAM:SSF51445 GO:GO:0080167 EMBL:AL133248 CAZy:GH36 eggNOG:NOG06986 InterPro:IPR008811 Pfam:PF05691 GO:GO:0034484 HOGENOM:HBG611539 KO:K06617 GO:GO:0047274 EMBL:AY050772 EMBL:AK226370 IPI:IPI00526258 IPI:IPI00541537 IPI:IPI00544535 PIR:T46188 RefSeq:NP_191311.1 RefSeq:NP_850715.1 UniGene:At.22207 UniGene:At.30900 ProteinModelPortal:Q94A08 STRING:Q94A08 PRIDE:Q94A08 EnsemblPlants:AT3G57520.1 GeneID:824919 KEGG:ath:AT3G57520 TAIR:At3g57520 InParanoid:Q9SCM1 OMA:QFMLLES PhylomeDB:Q94A08 ProtClustDB:PLN02219 BioCyc:MetaCyc:AT3G57520-MONOMER ArrayExpress:Q94A08 Uniprot:Q94A08
Root	Isotig03028	55	20	1.330	0.000171637	TAIR|locus:2036134 - symbol:AVP1 "AT1G15690" species:3702 "Arabidopsis thaliana" [GO:0009414 "response to water deprivation" evidence=IMP] [GO:0009651 "response to salt stress" evidence=IMP] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009678 "hydrogen-translocating pyrophosphatase activity" evidence=IDA]

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						[GO:0009705 "plant-type vacuole membrane" evidence=IDA] [GO:0010248 "establishment or maintenance of transmembrane electrochemical gradient" evidence=TAS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009926 "auxin polar transport" evidence=IGI] [GO:0010008 "endosome membrane" evidence=IDA] [GO:0000325 "plant-type vacuole" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048366 "leaf development" evidence=IMP] [GO:0005829 "cytosol" evidence=RCA] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR004131 Pfam:PF03030 PIRSF:PIRSF001265 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005739 GO:GO:0005886 GO:GO:0009926 GO:GO:0009941 GO:GO:0009651 GO:GO:0009414 GO:GO:0010008 GO:GO:0009705 GO:GO:0048366 GO:GO:0015992 EMBL:AC034256 UniGene:At.21942 UniGene:At.66944 EMBL:M81892 EMBL:AB015138 EMBL:AY065016 EMBL:AY078953 EMBL:BT002481 EMBL:Z17694 EMBL:Z17695 EMBL:AK221989 IPI:IPI00521876 PIR:A38230 RefSeq:NP_173021.1 UniGene:At.67102 UniGene:At.74973 STRING:P31414 TCDB:3.A.10.1.1 PRIDE:P31414 EnsemblPlants:AT1G15690.1 GeneID:838138 KEGG:ath:AT1G15690 GeneFarm:5159 TAIR:At1g15690 eggNOG:COG3808 InParanoid:P31414 KO:K01507 OMA:MAITSIV PhylomeDB:P31414 ProtClustDB:PLN02255 BRENDA:3.6.1.1 ArrayExpress:P31414 Genevestigator:P31414 GermOnline:AT1G15690 GO:GO:0009678 GO:GO:0004427 GO:GO:0010248 TIGRFAMs:TIGR01104 Uniprot:P31414
Root	Isotig03029	55	20	1.330	0.000171637	TAIR|locus:2036134 - symbol:AVP1 "AT1G15690" species:3702 "Arabidopsis thaliana" [GO:0009414 "response to water deprivation" evidence=IMP] [GO:0009651 "response to salt stress" evidence=IMP] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009678 "hydrogen-translocating pyrophosphatase activity" evidence=IDA] [GO:0009705 "plant-type vacuole membrane" evidence=IDA] [GO:0010248 "establishment or maintenance of transmembrane electrochemical gradient" evidence=TAS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009926 "auxin polar transport" evidence=IGI] [GO:0010008 "endosome membrane" evidence=IDA] [GO:0000325 "plant-type vacuole" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048366 "leaf development" evidence=IMP] [GO:0005829 "cytosol" evidence=RCA] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR004131 Pfam:PF03030 PIRSF:PIRSF001265 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005739 GO:GO:0005886 GO:GO:0009926 GO:GO:0009941 GO:GO:0009651 GO:GO:0009414 GO:GO:0010008 GO:GO:0009705 GO:GO:0048366 GO:GO:0015992 EMBL:AC034256 UniGene:At.21942 UniGene:At.66944 EMBL:M81892 EMBL:AB015138 EMBL:AY065016 EMBL:AY078953 EMBL:BT002481 EMBL:Z17694 EMBL:Z17695 EMBL:AK221989 IPI:IPI00521876 PIR:A38230 RefSeq:NP_173021.1 UniGene:At.67102 UniGene:At.74973 STRING:P31414 TCDB:3.A.10.1.1 PRIDE:P31414 EnsemblPlants:AT1G15690.1 GeneID:838138 KEGG:ath:AT1G15690 GeneFarm:5159 TAIR:At1g15690 eggNOG:COG3808 InParanoid:P31414 KO:K01507 OMA:MAITSIV PhylomeDB:P31414 ProtClustDB:PLN02255 BRENDA:3.6.1.1 ArrayExpress:P31414 Genevestigator:P31414 GermOnline:AT1G15690 GO:GO:0009678 GO:GO:0004427 GO:GO:0010248 TIGRFAMs:TIGR01104 Uniprot:P31414
Root	Isotig03044	6	29	-2.402	1.89E-05	TAIR|locus:2143320 - symbol:AT5G27920 "AT5G27920" species:3702 "Arabidopsis thaliana" [GO:0004842 "ubiquitin-protein ligase activity" evidence=ISS] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002688 GenomeReviews:BA000015_GR InterPro:IPR006553 SMART:SM00367 HOGENOM:HBG316674 EMBL:BT005940 EMBL:AK117239 IPI:IPI00538711 RefSeq:NP_568502.1 UniGene:At.30778 ProteinModelPortal:Q8GZ31 SMR:Q8GZ31 PRIDE:Q8GZ31 EnsemblPlants:AT5G27920.1 GeneID:832858 KEGG:ath:AT5G27920 TAIR:At5g27920 InParanoid:Q8GZ31 OMA:GFWALAY PhylomeDB:Q8GZ31 ProtClustDB:CLSN2689880 Genevestigator:Q8GZ31 Uniprot:Q8GZ31
Root	Isotig03045	6	29	-2.402	1.89E-05	TAIR|locus:2143320 - symbol:AT5G27920 "AT5G27920" species:3702 "Arabidopsis thaliana" [GO:0004842 "ubiquitin-protein ligase activity" evidence=ISS] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002688 GenomeReviews:BA000015_GR InterPro:IPR006553 SMART:SM00367 HOGENOM:HBG316674 EMBL:BT005940 EMBL:AK117239 IPI:IPI00538711 RefSeq:NP_568502.1 UniGene:At.30778 ProteinModelPortal:Q8GZ31 SMR:Q8GZ31 PRIDE:Q8GZ31 EnsemblPlants:AT5G27920.1 GeneID:832858 KEGG:ath:AT5G27920 TAIR:At5g27920 InParanoid:Q8GZ31 OMA:GFWALAY PhylomeDB:Q8GZ31 ProtClustDB:CLSN2689880 Genevestigator:Q8GZ31 Uniprot:Q8GZ31

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig03046	6	29	-2.402	1.89E-05	TAIR|locus:2143320 - symbol:AT5G27920 "AT5G27920" species:3702 "Arabidopsis thaliana" [GO:0004842 "ubiquitin-protein ligase activity" evidence=ISS] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002688 GenomeReviews:BA000015_GR InterPro:IPR006553 SMART:SM00367 HOGENOM:HBG316674 EMBL:BT005940 EMBL:AK117239 IPI:IPI00538711 RefSeq:NP_568502.1 UniGene:At.30778 ProteinModelPortal:Q8GZ31 SMR:Q8GZ31 PRIDE:Q8GZ31 EnsemblPlants:AT5G27920.1 GeneID:832858 KEGG:ath:AT5G27920 TAIR:At5g27920 InParanoid:Q8GZ31 OMA:GFWALAY PhylomeDB:Q8GZ31 ProtClustDB:CLSN2689880 Genevestigator:Q8GZ31 Uniprot:Q8GZ31
Root	Isotig03047	6	29	-2.402	1.89E-05	TAIR|locus:2143320 - symbol:AT5G27920 "AT5G27920" species:3702 "Arabidopsis thaliana" [GO:0004842 "ubiquitin-protein ligase activity" evidence=ISS] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002688 GenomeReviews:BA000015_GR InterPro:IPR006553 SMART:SM00367 HOGENOM:HBG316674 EMBL:BT005940 EMBL:AK117239 IPI:IPI00538711 RefSeq:NP_568502.1 UniGene:At.30778 ProteinModelPortal:Q8GZ31 SMR:Q8GZ31 PRIDE:Q8GZ31 EnsemblPlants:AT5G27920.1 GeneID:832858 KEGG:ath:AT5G27920 TAIR:At5g27920 InParanoid:Q8GZ31 OMA:GFWALAY PhylomeDB:Q8GZ31 ProtClustDB:CLSN2689880 Genevestigator:Q8GZ31 Uniprot:Q8GZ31
Root	Isotig03084	2	16	-3.129	0.000262867	TAIR|locus:2125642 - symbol:AT4G32760 "AT4G32760" species:3702 "Arabidopsis thaliana" [GO:0005795 "Golgi stack" evidence=ISS] [GO:0006886 "intracellular protein transport" evidence=IEA;ISS] [GO:0006891 "intra-Golgi vesicle-mediated transport" evidence=ISS] [GO:0008565 "protein transporter activity" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] InterPro:IPR002014 InterPro:IPR004152 Pfam:PF00790 Pfam:PF03127 PROSITE:PS50179 PROSITE:PS50909 GO:GO:0005886 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0006886 GO:GO:0005622 InterPro:IPR008942 Gene3D:G3DSA:1.25.40.90 SUPFAM:SSF48464 InterPro:IPR018205 SMART:SM00288 HSSP:O60784 HOGENOM:HBG597182 EMBL:AY120724 EMBL:BT000033 IPI:IPI00535455 RefSeq:NP_195002.2 UniGene:At.46217 UniGene:At.74836 ProteinModelPortal:Q8L860 SMR:Q8L860 STRING:Q8L860 PRIDE:Q8L860 EnsemblPlants:AT4G32760.1 GeneID:829412 KEGG:ath:AT4G32760 TAIR:At4g32760 InParanoid:Q8L860 OMA:VNNNSPY PhylomeDB:Q8L860 ProtClustDB:CLSN2681621 Genevestigator:Q8L860 Uniprot:Q8L860
Root	Isotig03085	2	16	-3.129	0.000262867	TAIR|locus:2125642 - symbol:AT4G32760 "AT4G32760" species:3702 "Arabidopsis thaliana" [GO:0005795 "Golgi stack" evidence=ISS] [GO:0006886 "intracellular protein transport" evidence=IEA;ISS] [GO:0006891 "intra-Golgi vesicle-mediated transport" evidence=ISS] [GO:0008565 "protein transporter activity" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] InterPro:IPR002014 InterPro:IPR004152 Pfam:PF00790 Pfam:PF03127 PROSITE:PS50179 PROSITE:PS50909 GO:GO:0005886 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0006886 GO:GO:0005622 InterPro:IPR008942 Gene3D:G3DSA:1.25.40.90 SUPFAM:SSF48464 InterPro:IPR018205 SMART:SM00288 HSSP:O60784 HOGENOM:HBG597182 EMBL:AY120724 EMBL:BT000033 IPI:IPI00535455 RefSeq:NP_195002.2 UniGene:At.46217 UniGene:At.74836 ProteinModelPortal:Q8L860 SMR:Q8L860 STRING:Q8L860 PRIDE:Q8L860 EnsemblPlants:AT4G32760.1 GeneID:829412 KEGG:ath:AT4G32760 TAIR:At4g32760 InParanoid:Q8L860 OMA:VNNNSPY PhylomeDB:Q8L860 ProtClustDB:CLSN2681621 Genevestigator:Q8L860 Uniprot:Q8L860
Root	Isotig03086	2	16	-3.129	0.000262867	TAIR|locus:2125642 - symbol:AT4G32760 "AT4G32760" species:3702 "Arabidopsis thaliana" [GO:0005795 "Golgi stack" evidence=ISS] [GO:0006886 "intracellular protein transport" evidence=IEA;ISS] [GO:0006891 "intra-Golgi vesicle-mediated transport" evidence=ISS] [GO:0008565 "protein transporter activity" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] InterPro:IPR002014 InterPro:IPR004152 Pfam:PF00790 Pfam:PF03127 PROSITE:PS50179 PROSITE:PS50909 GO:GO:0005886 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0006886 GO:GO:0005622 InterPro:IPR008942 Gene3D:G3DSA:1.25.40.90 SUPFAM:SSF48464 InterPro:IPR018205 SMART:SM00288 HSSP:O60784 HOGENOM:HBG597182 EMBL:AY120724 EMBL:BT000033 IPI:IPI00535455 RefSeq:NP_195002.2 UniGene:At.46217 UniGene:At.74836 ProteinModelPortal:Q8L860 SMR:Q8L860 STRING:Q8L860 PRIDE:Q8L860 EnsemblPlants:AT4G32760.1 GeneID:829412 KEGG:ath:AT4G32760 TAIR:At4g32760 InParanoid:Q8L860 OMA:VNNNSPY PhylomeDB:Q8L860 ProtClustDB:CLSN2681621 Genevestigator:Q8L860 Uniprot:Q8L860
Root	Isotig03087	2	16	-3.129	0.000262867	TAIR|locus:2125642 - symbol:AT4G32760 "AT4G32760" species:3702 "Arabidopsis thaliana" [GO:0005795 "Golgi stack" evidence=ISS] [GO:0006886 "intracellular protein transport" evidence=IEA;ISS] [GO:0006891 "intra-Golgi vesicle-mediated transport" evidence=ISS] [GO:0008565 "protein transporter activity" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] InterPro:IPR002014 InterPro:IPR004152 Pfam:PF00790 Pfam:PF03127 PROSITE:PS50179 PROSITE:PS50909 GO:GO:0005886

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0006886 GO:GO:0005622 InterPro:IPR008942 Gene3D:G3DSA:1.25.40.90 SUPFAM:SSF48464 InterPro:IPR018205 SMART:SM00288 HSSP:O60784 HOGENOM:HBG597182 EMBL:AY120724 EMBL:BT000033 IPI:IPI00535455 RefSeq:NP_195002.2 UniGene:At.46217 UniGene:At.74836 ProteinModelPortal:Q8L860 SMR:Q8L860 STRING:Q8L860 PRIDE:Q8L860 EnsemblPlants:AT4G32760.1 GeneID:829412 KEGG:ath:AT4G32760 TAIR:At4g32760 InParanoid:Q8L860 OMA:VNNNSPY PhylomeDB:Q8L860 ProtClustDB:CLSN2681621 Genevestigator:Q8L860 Uniprot:Q8L860
Root	Isotig03088	2	19	-3.377	3.93E-05	TAIR|locus:2204858 - symbol:AT1G02260 "AT1G02260" species:3702 "Arabidopsis thaliana" [GO:0005215 "transporter activity" evidence=ISS] [GO:0015137 "citrate transmembrane transporter activity" evidence=IEA] [GO:0015746 "citrate transport" evidence=IEA] [GO:0016021 "integral to membrane" evidence=IEA;ISS] [GO:0055085 "transmembrane transport" evidence=IEA] InterPro:IPR004680 Pfam:PF03600 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR eggNOG:COG1055 OMA:SANVICA GO:GO:0015137 EMBL:U89959 HOGENOM:HBG727257 EMBL:BT023463 IPI:IPI00519219 RefSeq:NP_171728.2 UniGene:At.48101 STRING:O81915 PRIDE:O81915 EnsemblPlants:AT1G02260.1 GeneID:839344 KEGG:ath:AT1G02260 TAIR:At1g02260 InParanoid:O81915 PhylomeDB:O81915 ProtClustDB:CLSN2918462 Genevestigator:O81915 Uniprot:O81915
Root	Isotig03089	2	19	-3.377	3.93E-05	TAIR|locus:2204858 - symbol:AT1G02260 "AT1G02260" species:3702 "Arabidopsis thaliana" [GO:0005215 "transporter activity" evidence=ISS] [GO:0015137 "citrate transmembrane transporter activity" evidence=IEA] [GO:0015746 "citrate transport" evidence=IEA] [GO:0016021 "integral to membrane" evidence=IEA;ISS] [GO:0055085 "transmembrane transport" evidence=IEA] InterPro:IPR004680 Pfam:PF03600 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR eggNOG:COG1055 OMA:SANVICA GO:GO:0015137 EMBL:U89959 HOGENOM:HBG727257 EMBL:BT023463 IPI:IPI00519219 RefSeq:NP_171728.2 UniGene:At.48101 STRING:O81915 PRIDE:O81915 EnsemblPlants:AT1G02260.1 GeneID:839344 KEGG:ath:AT1G02260 TAIR:At1g02260 InParanoid:O81915 PhylomeDB:O81915 ProtClustDB:CLSN2918462 Genevestigator:O81915 Uniprot:O81915
Root	Isotig03090	2	19	-3.377	3.93E-05	TAIR|locus:2204858 - symbol:AT1G02260 "AT1G02260" species:3702 "Arabidopsis thaliana" [GO:0005215 "transporter activity" evidence=ISS] [GO:0015137 "citrate transmembrane transporter activity" evidence=IEA] [GO:0015746 "citrate transport" evidence=IEA] [GO:0016021 "integral to membrane" evidence=IEA;ISS] [GO:0055085 "transmembrane transport" evidence=IEA] InterPro:IPR004680 Pfam:PF03600 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR eggNOG:COG1055 OMA:SANVICA GO:GO:0015137 EMBL:U89959 HOGENOM:HBG727257 EMBL:BT023463 IPI:IPI00519219 RefSeq:NP_171728.2 UniGene:At.48101 STRING:O81915 PRIDE:O81915 EnsemblPlants:AT1G02260.1 GeneID:839344 KEGG:ath:AT1G02260 TAIR:At1g02260 InParanoid:O81915 PhylomeDB:O81915 ProtClustDB:CLSN2918462 Genevestigator:O81915 Uniprot:O81915
Root	Isotig03091	2	19	-3.377	3.93E-05	TAIR|locus:2204858 - symbol:AT1G02260 "AT1G02260" species:3702 "Arabidopsis thaliana" [GO:0005215 "transporter activity" evidence=ISS] [GO:0015137 "citrate transmembrane transporter activity" evidence=IEA] [GO:0015746 "citrate transport" evidence=IEA] [GO:0016021 "integral to membrane" evidence=IEA;ISS] [GO:0055085 "transmembrane transport" evidence=IEA] InterPro:IPR004680 Pfam:PF03600 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR eggNOG:COG1055 OMA:SANVICA GO:GO:0015137 EMBL:U89959 HOGENOM:HBG727257 EMBL:BT023463 IPI:IPI00519219 RefSeq:NP_171728.2 UniGene:At.48101 STRING:O81915 PRIDE:O81915 EnsemblPlants:AT1G02260.1 GeneID:839344 KEGG:ath:AT1G02260 TAIR:At1g02260 InParanoid:O81915 PhylomeDB:O81915 ProtClustDB:CLSN2918462 Genevestigator:O81915 Uniprot:O81915
Root	Isotig03100	2	18	-3.299	7.42E-05	TAIR|locus:2117617 - symbol:PIRL4 "AT4G35470" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0005886 "plasma membrane" evidence=IDA] Pfam:PF00560 InterPro:IPR001611 PROSITE:PS51450 GO:GO:0005886 EMBL:CP002687 GenomeReviews:CT486007_GR eggNOG:COG4886 InterPro:IPR003591 SMART:SM00369 EMBL:AL117188 EMBL:AL161587 HSSP:P07359 ProtClustDB:CLSN2683891 EMBL:AY072324 EMBL:AY128730 EMBL:AY849574 IPI:IPI00541009 PIR:T41744 RefSeq:NP_195272.1 UniGene:At.22486 ProteinModelPortal:Q9SVW8 SMR:Q9SVW8 IntAct:Q9SVW8 STRING:Q9SVW8 PRIDE:Q9SVW8 EnsemblPlants:AT4G35470.1 GeneID:829699 KEGG:ath:AT4G35470 TAIR:At4g35470 HOGENOM:HBG601308 InParanoid:Q9SVW8 OMA:EWLPDSI PhylomeDB:Q9SVW8 Genevestigator:Q9SVW8 Uniprot:Q9SVW8

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig03101	2	18	-3.299	7.42E-05	TAIR|locus:2117617 - symbol:PIRL4 "AT4G35470" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0005886 "plasma membrane" evidence=IDA] Pfam:PF00560 InterPro:IPR001611 PROSITE:PS51450 GO:GO:0005886 EMBL:CP002687 GenomeReviews:CT486007_GR eggNOG:COG4886 InterPro:IPR003591 SMART:SM00369 EMBL:AL117188 EMBL:AL161587 HSSP:P07359 ProtClustDB:CLSN2683891 EMBL:AY072324 EMBL:AY128730 EMBL:AY849574 IPI:IPI00541009 PIR:T41744 RefSeq:NP_195272.1 UniGene:At.22486 ProteinModelPortal:Q9SVW8 SMR:Q9SVW8 IntAct:Q9SVW8 STRING:Q9SVW8 PRIDE:Q9SVW8 EnsemblPlants:AT4G35470.1 GeneID:829699 KEGG:ath:AT4G35470 TAIR:At4g35470 HOGENOM:HBG601308 InParanoid:Q9SVW8 OMA:EWLPDSI PhylomeDB:Q9SVW8 Genevestigator:Q9SVW8 Uniprot:Q9SVW8
Root	Isotig03102	2	18	-3.299	7.42E-05	TAIR|locus:2117617 - symbol:PIRL4 "AT4G35470" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0005886 "plasma membrane" evidence=IDA] Pfam:PF00560 InterPro:IPR001611 PROSITE:PS51450 GO:GO:0005886 EMBL:CP002687 GenomeReviews:CT486007_GR eggNOG:COG4886 InterPro:IPR003591 SMART:SM00369 EMBL:AL117188 EMBL:AL161587 HSSP:P07359 ProtClustDB:CLSN2683891 EMBL:AY072324 EMBL:AY128730 EMBL:AY849574 IPI:IPI00541009 PIR:T41744 RefSeq:NP_195272.1 UniGene:At.22486 ProteinModelPortal:Q9SVW8 SMR:Q9SVW8 IntAct:Q9SVW8 STRING:Q9SVW8 PRIDE:Q9SVW8 EnsemblPlants:AT4G35470.1 GeneID:829699 KEGG:ath:AT4G35470 TAIR:At4g35470 HOGENOM:HBG601308 InParanoid:Q9SVW8 OMA:EWLPDSI PhylomeDB:Q9SVW8 Genevestigator:Q9SVW8 Uniprot:Q9SVW8
Root	Isotig03103	2	18	-3.299	7.42E-05	TAIR|locus:2117617 - symbol:PIRL4 "AT4G35470" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0005886 "plasma membrane" evidence=IDA] Pfam:PF00560 InterPro:IPR001611 PROSITE:PS51450 GO:GO:0005886 EMBL:CP002687 GenomeReviews:CT486007_GR eggNOG:COG4886 InterPro:IPR003591 SMART:SM00369 EMBL:AL117188 EMBL:AL161587 HSSP:P07359 ProtClustDB:CLSN2683891 EMBL:AY072324 EMBL:AY128730 EMBL:AY849574 IPI:IPI00541009 PIR:T41744 RefSeq:NP_195272.1 UniGene:At.22486 ProteinModelPortal:Q9SVW8 SMR:Q9SVW8 IntAct:Q9SVW8 STRING:Q9SVW8 PRIDE:Q9SVW8 EnsemblPlants:AT4G35470.1 GeneID:829699 KEGG:ath:AT4G35470 TAIR:At4g35470 HOGENOM:HBG601308 InParanoid:Q9SVW8 OMA:EWLPDSI PhylomeDB:Q9SVW8 Genevestigator:Q9SVW8 Uniprot:Q9SVW8
Root	Isotig03145	5	36	-2.977	8.93E-08	TAIR|locus:2145944 - symbol:CUE1 "CAB UNDEREXPRESSED 1" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=IEA] [GO:0015297 "antiporter activity" evidence=ISS] [GO:0009528 "plastid inner membrane" evidence=TAS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0015120 "phosphoglycerate transmembrane transporter activity" evidence=IDA] [GO:0015121 "phosphoenolpyruvate:phosphate antiporter activity" evidence=IDA] [GO:0015713 "phosphoglycerate transport" evidence=IDA] [GO:0015714 "phosphoenolpyruvate transport" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009536 "plastid" evidence=IDA] InterPro:IPR000620 InterPro:IPR004696 Pfam:PF00892 Pfam:PF03151 GO:GO:0016021 GO:GO:0005739 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0031969 GO:GO:0008643 EMBL:AC051625 InterPro:IPR004853 eggNOG:NOG312636 KO:K15283 GO:GO:0015120 TIGRFAMs:TIGR00817 EMBL:U66321 EMBL:AF209210 EMBL:AY080788 EMBL:AY133809 EMBL:AY086100 IPI:IPI00534885 RefSeq:NP_198317.1 UniGene:At.14730 STRING:Q8RXN3 PRIDE:Q8RXN3 EnsemblPlants:AT5G33320.1 GeneID:833308 KEGG:ath:AT5G33320 TAIR:At5g33320 InParanoid:Q8RXN3 OMA:HILALCA PhylomeDB:Q8RXN3 ProtClustDB:CLSN2720506 Genevestigator:Q8RXN3 GO:GO:0009528 GO:GO:0015121 Uniprot:Q8RXN3
Root	Isotig03156	7	36	-2.492	1.13E-06	TAIR|locus:2064965 - symbol:EULS3 "AT2G39050" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0030246 "carbohydrate binding" evidence=IDA] GO:GO:0005634 GO:GO:0005737 EMBL:CP002685 GenomeReviews:CT485783_GR InterPro:IPR000772 SUPFAM:SSF50370 PROSITE:PS50231 GO:GO:0030246 EMBL:AC005770 Pfam:PF14200 EMBL:AF411801 EMBL:AY093795 EMBL:AY087909 IPI:IPI00536641 PIR:E84812 RefSeq:NP_565899.1 UniGene:At.22599 ProteinModelPortal:Q945P1 SMR:Q945P1 PRIDE:Q945P1 EnsemblPlants:AT2G39050.1 GeneID:818491 KEGG:ath:AT2G39050 TAIR:At2g39050 eggNOG:NOG254161 HOGENOM:HBG750017 InParanoid:Q945P1 OMA:GYRTIRM PhylomeDB:Q945P1 ProtClustDB:CLSN2681741 ArrayExpress:Q945P1 Genevestigator:Q945P1 Uniprot:Q945P1
Root	Isotig03157	7	36	-2.492	1.13E-06	TAIR|locus:2064965 - symbol:EULS3 "AT2G39050" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm"

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						evidence=IDA] [GO:0030246 "carbohydrate binding" evidence=IDA] GO:GO:0005634 GO:GO:0005737 EMBL:CP002685 GenomeReviews:CT485783_GR InterPro:IPR000772 SUPFAM:SSF50370 PROSITE:PS50231 GO:GO:0030246 EMBL:AC005770 Pfam:PF14200 EMBL:AF411801 EMBL:AY093795 EMBL:AY087909 IPI:IPI00536641 PIR:E84812 RefSeq:NP_565899.1 UniGene:At.22599 ProteinModelPortal:Q945P1 SMR:Q945P1 PRIDE:Q945P1 EnsemblPlants:AT2G39050.1 GeneID:818491 KEGG:ath:AT2G39050 TAIR:At2g39050 eggNOG:NOG254161 HOGENOM:HBG750017 InParanoid:Q945P1 OMA:GYRTIRM PhylomeDB:Q945P1 ProtClustDB:CLSN2681741 ArrayExpress:Q945P1 Genevestigator:Q945P1 Uniprot:Q945P1
Root	Isotig03158	7	36	-2.492	1.13E-06	TAIR|locus:2064965 - symbol:EULS3 "AT2G39050" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0030246 "carbohydrate binding" evidence=IDA] GO:GO:0005634 GO:GO:0005737 EMBL:CP002685 GenomeReviews:CT485783_GR InterPro:IPR000772 SUPFAM:SSF50370 PROSITE:PS50231 GO:GO:0030246 EMBL:AC005770 Pfam:PF14200 EMBL:AF411801 EMBL:AY093795 EMBL:AY087909 IPI:IPI00536641 PIR:E84812 RefSeq:NP_565899.1 UniGene:At.22599 ProteinModelPortal:Q945P1 SMR:Q945P1 PRIDE:Q945P1 EnsemblPlants:AT2G39050.1 GeneID:818491 KEGG:ath:AT2G39050 TAIR:At2g39050 eggNOG:NOG254161 HOGENOM:HBG750017 InParanoid:Q945P1 OMA:GYRTIRM PhylomeDB:Q945P1 ProtClustDB:CLSN2681741 ArrayExpress:Q945P1 Genevestigator:Q945P1 Uniprot:Q945P1
Root	Isotig03159	7	36	-2.492	1.13E-06	TAIR|locus:2064965 - symbol:EULS3 "AT2G39050" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0030246 "carbohydrate binding" evidence=IDA] GO:GO:0005634 GO:GO:0005737 EMBL:CP002685 GenomeReviews:CT485783_GR InterPro:IPR000772 SUPFAM:SSF50370 PROSITE:PS50231 GO:GO:0030246 EMBL:AC005770 Pfam:PF14200 EMBL:AF411801 EMBL:AY093795 EMBL:AY087909 IPI:IPI00536641 PIR:E84812 RefSeq:NP_565899.1 UniGene:At.22599 ProteinModelPortal:Q945P1 SMR:Q945P1 PRIDE:Q945P1 EnsemblPlants:AT2G39050.1 GeneID:818491 KEGG:ath:AT2G39050 TAIR:At2g39050 eggNOG:NOG254161 HOGENOM:HBG750017 InParanoid:Q945P1 OMA:GYRTIRM PhylomeDB:Q945P1 ProtClustDB:CLSN2681741 ArrayExpress:Q945P1 Genevestigator:Q945P1 Uniprot:Q945P1
Root	Isotig03162	14	0	4.678	0.000190242	TAIR|locus:2117607 - symbol:AKR2 "AT4G35450" species:3702 "Arabidopsis thaliana" [GO:0009816 "defense response to bacterium, incompatible interaction" evidence=IMP] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0006457 "protein folding" evidence=IDA] [GO:0031359 "integral to chloroplast outer membrane" evidence=IDA] [GO:0045036 "protein targeting to chloroplast" evidence=IMP;IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0009791 "post-embryonic development" evidence=IMP] [GO:0010228 "vegetative to reproductive phase transition of meristem" evidence=IMP] InterPro:IPR002110 PROSITE:PS50088 SMART:SM00248 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005634 GO:GO:0046686 GO:GO:0006457 eggNOG:COG0666 InterPro:IPR020683 Gene3D:G3DSA:1.25.40.20 Pfam:PF12796 SUPFAM:SSF48403 PROSITE:PS50297 GO:GO:0010228 GO:GO:0009816 EMBL:AF034387 EMBL:U70425 EMBL:AL117188 EMBL:AL161587 EMBL:AF386982 EMBL:AY081477 EMBL:AY087377 IPI:IPI00546461 PIR:T41742 RefSeq:NP_195270.1 RefSeq:NP_849497.1 RefSeq:NP_849498.1 UniGene:At.24072 ProteinModelPortal:Q9SAR5 SMR:Q9SAR5 STRING:Q9SAR5 PRIDE:Q9SAR5 EnsemblPlants:AT4G35450.1 EnsemblPlants:AT4G35450.2 EnsemblPlants:AT4G35450.3 GeneID:829697 KEGG:ath:AT4G35450 GeneFarm:4730 TAIR:At4g35450 HOGENOM:HBG610978 InParanoid:Q9SAR5 OMA:PSIREMA PhylomeDB:Q9SAR5 ProtClustDB:CLSN2683889 ArrayExpress:Q9SAR5 Genevestigator:Q9SAR5 GO:GO:0031359 GO:GO:0045036 Uniprot:Q9SAR5
Root	Isotig03163	14	0	4.678	0.000190242	TAIR|locus:2117607 - symbol:AKR2 "AT4G35450" species:3702 "Arabidopsis thaliana" [GO:0009816 "defense response to bacterium, incompatible interaction" evidence=IMP] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0006457 "protein folding" evidence=IDA] [GO:0031359 "integral to chloroplast outer membrane" evidence=IDA] [GO:0045036 "protein targeting to chloroplast" evidence=IMP;IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0009791 "post-embryonic development" evidence=IMP] [GO:0010228 "vegetative to reproductive phase transition of meristem" evidence=IMP] InterPro:IPR002110 PROSITE:PS50088 SMART:SM00248 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005634 GO:GO:0046686 GO:GO:0006457 eggNOG:COG0666 InterPro:IPR020683 Gene3D:G3DSA:1.25.40.20 Pfam:PF12796 SUPFAM:SSF48403 PROSITE:PS50297 GO:GO:0010228 GO:GO:0009816 EMBL:AF034387 EMBL:U70425 EMBL:AL117188 EMBL:AL161587 EMBL:AF386982 EMBL:AY081477 EMBL:AY087377 IPI:IPI00546461 PIR:T41742 RefSeq:NP_195270.1 RefSeq:NP_849497.1

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						RefSeq:NP_849498.1 UniGene:At.24072 ProteinModelPortal:Q9SAR5 SMR:Q9SAR5 STRING:Q9SAR5 PRIDE:Q9SAR5 EnsemblPlants:AT4G35450.1 EnsemblPlants:AT4G35450.2 EnsemblPlants:AT4G35450.3 GeneID:829697 KEGG:ath:AT4G35450 GeneFarm:4730 TAIR:At4g35450 HOGENOM:HBG610978 InParanoid:Q9SAR5 OMA:PSIREMA PhylomeDB:Q9SAR5 ProtClustDB:CLSN2683889 ArrayExpress:Q9SAR5 Genevestigator:Q9SAR5 GO:GO:0031359 GO:GO:0045036 Uniprot:Q9SAR5
Root	Isotig03188	5	20	-2.129	0.000961902	UNIPROTKB|G4MVS3 - symbol:MGG_01790 "Acyl-CoA desaturase" species:242507 "Magnaporthe oryzae 70-15" [GO:0043581 "mycelium development" evidence=IEP] InterPro:IPR001199 InterPro:IPR001522 InterPro:IPR005804 InterPro:IPR009160 InterPro:IPR015876 InterPro:IPR018506 Pfam:PF00173 Pfam:PF00487 PIRSF:PIRSF000345 PRINTS:PR00075 PROSITE:PS00191 PROSITE:PS00476 PROSITE:PS50255 GO:GO:0005783 GO:GO:0016021 GO:GO:0006633 GO:GO:0020037 KO:K00507 GO:GO:0004768 Gene3D:G3DSA:3.10.120.10 SUPFAM:SSF55856 EMBL:CM001232 RefSeq:XP_363864.1 UniGene:Mgr.16443 GeneID:2679094 Uniprot:G4MVS3
Root	Isotig03189	5	20	-2.129	0.000961902	UNIPROTKB|G4MVS3 - symbol:MGG_01790 "Acyl-CoA desaturase" species:242507 "Magnaporthe oryzae 70-15" [GO:0043581 "mycelium development" evidence=IEP] InterPro:IPR001199 InterPro:IPR001522 InterPro:IPR005804 InterPro:IPR009160 InterPro:IPR015876 InterPro:IPR018506 Pfam:PF00173 Pfam:PF00487 PIRSF:PIRSF000345 PRINTS:PR00075 PROSITE:PS00191 PROSITE:PS00476 PROSITE:PS50255 GO:GO:0005783 GO:GO:0016021 GO:GO:0006633 GO:GO:0020037 KO:K00507 GO:GO:0004768 Gene3D:G3DSA:3.10.120.10 SUPFAM:SSF55856 EMBL:CM001232 RefSeq:XP_363864.1 UniGene:Mgr.16443 GeneID:2679094 Uniprot:G4MVS3
Root	Isotig03200	5	21	-2.199	0.000555521	TAIR|locus:2173108 - symbol:BAG1 "AT5G52060" species:3702 "Arabidopsis thaliana" [GO:0005739 "mitochondrion" evidence=IDA] InterPro:IPR003103 Pfam:PF02179 PROSITE:PS51035 Prosite:PS00299 GO:GO:0005739 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0051087 InterPro:IPR019955 PROSITE:PS50053 EMBL:AB015478 EMBL:AK227095 EMBL:BT030041 IPI:IPI00540126 RefSeq:NP_200019.2 UniGene:At.29642 ProteinModelPortal:Q0WUQ1 SMR:Q0WUQ1 PRIDE:Q9FJ86 EnsemblPlants:AT5G52060.1 GeneID:835281 KEGG:ath:AT5G52060 TAIR:At5g52060 eggNOG:NOG291823 HOGENOM:HBG602117 InParanoid:Q0WUQ1 PhylomeDB:Q0WUQ1 ProtClustDB:CLSN2920552 Genevestigator:Q0WUQ1 Uniprot:Q0WUQ1
Root	Isotig03201	5	21	-2.199	0.000555521	TAIR|locus:2173108 - symbol:BAG1 "AT5G52060" species:3702 "Arabidopsis thaliana" [GO:0005739 "mitochondrion" evidence=IDA] InterPro:IPR003103 Pfam:PF02179 PROSITE:PS51035 Prosite:PS00299 GO:GO:0005739 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0051087 InterPro:IPR019955 PROSITE:PS50053 EMBL:AB015478 EMBL:AK227095 EMBL:BT030041 IPI:IPI00540126 RefSeq:NP_200019.2 UniGene:At.29642 ProteinModelPortal:Q0WUQ1 SMR:Q0WUQ1 PRIDE:Q9FJ86 EnsemblPlants:AT5G52060.1 GeneID:835281 KEGG:ath:AT5G52060 TAIR:At5g52060 eggNOG:NOG291823 HOGENOM:HBG602117 InParanoid:Q0WUQ1 PhylomeDB:Q0WUQ1 ProtClustDB:CLSN2920552 Genevestigator:Q0WUQ1 Uniprot:Q0WUQ1
Root	Isotig03202	4	22	-2.588	0.000101225	TAIR|locus:2173108 - symbol:BAG1 "AT5G52060" species:3702 "Arabidopsis thaliana" [GO:0005739 "mitochondrion" evidence=IDA] InterPro:IPR003103 Pfam:PF02179 PROSITE:PS51035 Prosite:PS00299 GO:GO:0005739 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0051087 InterPro:IPR019955 PROSITE:PS50053 EMBL:AB015478 EMBL:AK227095 EMBL:BT030041 IPI:IPI00540126 RefSeq:NP_200019.2 UniGene:At.29642 ProteinModelPortal:Q0WUQ1 SMR:Q0WUQ1 PRIDE:Q9FJ86 EnsemblPlants:AT5G52060.1 GeneID:835281 KEGG:ath:AT5G52060 TAIR:At5g52060 eggNOG:NOG291823 HOGENOM:HBG602117 InParanoid:Q0WUQ1 PhylomeDB:Q0WUQ1 ProtClustDB:CLSN2920552 Genevestigator:Q0WUQ1 Uniprot:Q0WUQ1
Root	Isotig03203	4	22	-2.588	0.000101225	TAIR|locus:2173108 - symbol:BAG1 "AT5G52060" species:3702 "Arabidopsis thaliana" [GO:0005739 "mitochondrion" evidence=IDA] InterPro:IPR003103 Pfam:PF02179 PROSITE:PS51035 Prosite:PS00299 GO:GO:0005739 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0051087 InterPro:IPR019955 PROSITE:PS50053 EMBL:AB015478 EMBL:AK227095 EMBL:BT030041 IPI:IPI00540126 RefSeq:NP_200019.2 UniGene:At.29642 ProteinModelPortal:Q0WUQ1 SMR:Q0WUQ1 PRIDE:Q9FJ86 EnsemblPlants:AT5G52060.1 GeneID:835281 KEGG:ath:AT5G52060 TAIR:At5g52060 eggNOG:NOG291823 HOGENOM:HBG602117 InParanoid:Q0WUQ1 PhylomeDB:Q0WUQ1 ProtClustDB:CLSN2920552 Genevestigator:Q0WUQ1 Uniprot:Q0WUQ1
Root	Isotig03224	16	38	-1.377	0.000799708	TAIR|locus:2170698 - symbol:HIR1 "HYPERSENSITIVE-INDUCED RESPONSE PROTEIN 1" species:3702 "Arabidopsis thaliana" [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005515 "protein

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						binding" evidence=IPI] [GO:0043424 "protein histidine kinase binding" evidence=IPI] [GO:0005829 "cytosol" evidence=RCA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR001972 InterPro:IPR001107 Pfam:PF01145 GO:GO:0005886 GO:GO:0009506 GO:GO:0005774 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0043424 EMBL:AB009053 eggNOG:COG0330 PANTHER:PTHR10264 SMART:SM00244 EMBL:AY062850 EMBL:AY114572 EMBL:AY086631 IPI:IPI00546529 RefSeq:NP_201080.1 UniGene:At.71021 ProteinModelPortal:Q9FM19 SMR:Q9FM19 IntAct:Q9FM19 PRIDE:Q9FM19 EnsemblPlants:AT5G62740.1 GeneID:836395 KEGG:ath:AT5G62740 TAIR:At5g62740 HOGENOM:HBG519201 InParanoid:Q9FM19 OMA:KANDAYY PhylomeDB:Q9FM19 ProtClustDB:CLSN2682581 ArrayExpress:Q9FM19 Genevestigator:Q9FM19 Uniprot:Q9FM19
Root	Isotig03226	16	38	-1.377	0.000799708	TAIR|locus:2170698 - symbol:HIR1 "HYPERSENSITIVE-INDUCED RESPONSE PROTEIN 1" species:3702 "Arabidopsis thaliana" [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0043424 "protein histidine kinase binding" evidence=IPI] [GO:0005829 "cytosol" evidence=RCA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR001972 InterPro:IPR001107 Pfam:PF01145 GO:GO:0005886 GO:GO:0009506 GO:GO:0005774 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0043424 EMBL:AB009053 eggNOG:COG0330 PANTHER:PTHR10264 SMART:SM00244 EMBL:AY062850 EMBL:AY114572 EMBL:AY086631 IPI:IPI00546529 RefSeq:NP_201080.1 UniGene:At.71021 ProteinModelPortal:Q9FM19 SMR:Q9FM19 IntAct:Q9FM19 PRIDE:Q9FM19 EnsemblPlants:AT5G62740.1 GeneID:836395 KEGG:ath:AT5G62740 TAIR:At5g62740 HOGENOM:HBG519201 InParanoid:Q9FM19 OMA:KANDAYY PhylomeDB:Q9FM19 ProtClustDB:CLSN2682581 ArrayExpress:Q9FM19 Genevestigator:Q9FM19 Uniprot:Q9FM19
Root	Isotig03231	56	23	1.155	0.000692158	TAIR|locus:2064965 - symbol:EULS3 "AT2G39050" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0030246 "carbohydrate binding" evidence=IDA] GO:GO:0005634 GO:GO:0005737 EMBL:CP002685 GenomeReviews:CT485783_GR InterPro:IPR000772 SUPFAM:SSF50370 PROSITE:PS50231 GO:GO:0030246 EMBL:AC005770 Pfam:PF14200 EMBL:AF411801 EMBL:AY093795 EMBL:AY087909 IPI:IPI00536641 PIR:E84812 RefSeq:NP_565899.1 UniGene:At.22599 ProteinModelPortal:Q945P1 SMR:Q945P1 PRIDE:Q945P1 EnsemblPlants:AT2G39050.1 GeneID:818491 KEGG:ath:AT2G39050 TAIR:At2g39050 eggNOG:NOG254161 HOGENOM:HBG750017 InParanoid:Q945P1 OMA:GYRTIRM PhylomeDB:Q945P1 ProtClustDB:CLSN2681741 ArrayExpress:Q945P1 Genevestigator:Q945P1 Uniprot:Q945P1
Root	Isotig03232	50	16	1.515	7.79E-05	TAIR|locus:2064965 - symbol:EULS3 "AT2G39050" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0030246 "carbohydrate binding" evidence=IDA] GO:GO:0005634 GO:GO:0005737 EMBL:CP002685 GenomeReviews:CT485783_GR InterPro:IPR000772 SUPFAM:SSF50370 PROSITE:PS50231 GO:GO:0030246 EMBL:AC005770 Pfam:PF14200 EMBL:AF411801 EMBL:AY093795 EMBL:AY087909 IPI:IPI00536641 PIR:E84812 RefSeq:NP_565899.1 UniGene:At.22599 ProteinModelPortal:Q945P1 SMR:Q945P1 PRIDE:Q945P1 EnsemblPlants:AT2G39050.1 GeneID:818491 KEGG:ath:AT2G39050 TAIR:At2g39050 eggNOG:NOG254161 HOGENOM:HBG750017 InParanoid:Q945P1 OMA:GYRTIRM PhylomeDB:Q945P1 ProtClustDB:CLSN2681741 ArrayExpress:Q945P1 Genevestigator:Q945P1 Uniprot:Q945P1
Root	Isotig03233	56	23	1.155	0.000692158	TAIR|locus:2064965 - symbol:EULS3 "AT2G39050" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0030246 "carbohydrate binding" evidence=IDA] GO:GO:0005634 GO:GO:0005737 EMBL:CP002685 GenomeReviews:CT485783_GR InterPro:IPR000772 SUPFAM:SSF50370 PROSITE:PS50231 GO:GO:0030246 EMBL:AC005770 Pfam:PF14200 EMBL:AF411801 EMBL:AY093795 EMBL:AY087909 IPI:IPI00536641 PIR:E84812 RefSeq:NP_565899.1 UniGene:At.22599 ProteinModelPortal:Q945P1 SMR:Q945P1 PRIDE:Q945P1 EnsemblPlants:AT2G39050.1 GeneID:818491 KEGG:ath:AT2G39050 TAIR:At2g39050 eggNOG:NOG254161 HOGENOM:HBG750017 InParanoid:Q945P1 OMA:GYRTIRM PhylomeDB:Q945P1 ProtClustDB:CLSN2681741 ArrayExpress:Q945P1 Genevestigator:Q945P1 Uniprot:Q945P1
Root	Isotig03234	50	16	1.515	7.79E-05	TAIR|locus:2064965 - symbol:EULS3 "AT2G39050" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0030246 "carbohydrate binding" evidence=IDA] GO:GO:0005634 GO:GO:0005737 EMBL:CP002685 GenomeReviews:CT485783_GR InterPro:IPR000772 SUPFAM:SSF50370 PROSITE:PS50231

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0030246 EMBL:AC005770 Pfam:PF14200 EMBL:AF411801 EMBL:AY093795 EMBL:AY087909 IPI:IPI00536641 PIR:E84812 RefSeq:NP_565899.1 UniGene:At.22599 ProteinModelPortal:Q945P1 SMR:Q945P1 PRIDE:Q945P1 EnsemblPlants:AT2G39050.1 GeneID:818491 KEGG:ath:AT2G39050 TAIR:At2g39050 eggNOG:NOG254161 HOGENOM:HBG750017 InParanoid:Q945P1 OMA:GYRTIRM PhylomeDB:Q945P1 ProtClustDB:CLSN2681741 ArrayExpress:Q945P1 Genevestigator:Q945P1 Uniprot:Q945P1
Root	Isotig03235	23	0	5.395	1.11E-06	TAIR|locus:2087183 - symbol:MYB305 "AT3G24310" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=ISS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=ISS] InterPro:IPR001005 InterPro:IPR009057 Pfam:PF00249 SMART:SM00717 GO:GO:0005634 GO:GO:0006355 GO:GO:0003677 Gene3D:G3DSA:1.10.10.60 SUPFAM:SSF46689 InterPro:IPR017930 PROSITE:PS51294 InterPro:IPR015495 PANTHER:PTHR10641 HSSP:Q03237 EMBL:AY550298 IPI:IPI00525453 ProteinModelPortal:Q6QAD8 PRIDE:Q6QAD8 TAIR:At3g24310 PhylomeDB:Q6QAD8 ArrayExpress:Q6QAD8 Genevestigator:Q6QAD8 Uniprot:Q6QAD8
Root	Isotig03236	23	0	5.395	1.11E-06	TAIR|locus:2087183 - symbol:MYB305 "AT3G24310" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=ISS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=ISS] InterPro:IPR001005 InterPro:IPR009057 Pfam:PF00249 SMART:SM00717 GO:GO:0005634 GO:GO:0006355 GO:GO:0003677 Gene3D:G3DSA:1.10.10.60 SUPFAM:SSF46689 InterPro:IPR017930 PROSITE:PS51294 InterPro:IPR015495 PANTHER:PTHR10641 HSSP:Q03237 EMBL:AY550298 IPI:IPI00525453 ProteinModelPortal:Q6QAD8 PRIDE:Q6QAD8 TAIR:At3g24310 PhylomeDB:Q6QAD8 ArrayExpress:Q6QAD8 Genevestigator:Q6QAD8 Uniprot:Q6QAD8
Root	Isotig03237	23	0	5.395	1.11E-06	TAIR|locus:2087183 - symbol:MYB305 "AT3G24310" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=ISS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=ISS] InterPro:IPR001005 InterPro:IPR009057 Pfam:PF00249 SMART:SM00717 GO:GO:0005634 GO:GO:0006355 GO:GO:0003677 Gene3D:G3DSA:1.10.10.60 SUPFAM:SSF46689 InterPro:IPR017930 PROSITE:PS51294 InterPro:IPR015495 PANTHER:PTHR10641 HSSP:Q03237 EMBL:AY550298 IPI:IPI00525453 ProteinModelPortal:Q6QAD8 PRIDE:Q6QAD8 TAIR:At3g24310 PhylomeDB:Q6QAD8 ArrayExpress:Q6QAD8 Genevestigator:Q6QAD8 Uniprot:Q6QAD8
Root	Isotig03238	23	0	5.395	1.11E-06	TAIR|locus:2087183 - symbol:MYB305 "AT3G24310" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=ISS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=ISS] InterPro:IPR001005 InterPro:IPR009057 Pfam:PF00249 SMART:SM00717 GO:GO:0005634 GO:GO:0006355 GO:GO:0003677 Gene3D:G3DSA:1.10.10.60 SUPFAM:SSF46689 InterPro:IPR017930 PROSITE:PS51294 InterPro:IPR015495 PANTHER:PTHR10641 HSSP:Q03237 EMBL:AY550298 IPI:IPI00525453 ProteinModelPortal:Q6QAD8 PRIDE:Q6QAD8 TAIR:At3g24310 PhylomeDB:Q6QAD8 ArrayExpress:Q6QAD8 Genevestigator:Q6QAD8 Uniprot:Q6QAD8
Root	Isotig03267	81	7	3.404	3.81E-16	No hit
Root	Isotig03268	80	7	3.386	6.66E-16	No hit
Root	Isotig03295	4	41	-3.487	9.45E-10	TAIR|locus:2076904 - symbol:GRF7 "AT3G02520" species:3702 "Arabidopsis thaliana" [GO:0005635 "nuclear envelope" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0045309 "protein phosphorylated amino acid binding" evidence=TAS] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] InterPro:IPR000308 PIRSF:PIRSF000868 PRINTS:PR00305 HOGENOM:HBG611720 GO:GO:0005886 GO:GO:0009506 GO:GO:0019904 InterPro:IPR023409 InterPro:IPR023410 Gene3D:G3DSA:1.20.190.20 PANTHER:PTHR18860 Pfam:PF00244 SMART:SM00101 SUPFAM:SSF48445 PROSITE:PS00796 PROSITE:PS00797 GO:GO:0009507 ProtClustDB:CLSN2688003 EMBL:U60445 EMBL:AF145299 EMBL:AC021640 EMBL:CP002686 EMBL:AY065274 EMBL:AY096526 EMBL:AY087723 IPI:IPI00536399 RefSeq:NP_566174.1 UniGene:At.21863 ProteinModelPortal:Q96300 SMR:Q96300 IntAct:Q96300 STRING:Q96300 PRIDE:Q96300 EnsemblPlants:AT3G02520.1 GeneID:821060 GenomeReviews:BA000014_GR KEGG:ath:AT3G02520 TAIR:At3g02520 InParanoid:Q96300 OMA:KVCQDVL PhylomeDB:Q96300 ArrayExpress:Q96300 Genevestigator:Q96300 GermOnline:AT3G02520 Uniprot:Q96300
Root	Isotig03296	3	43	-3.970	5.33E-11	TAIR|locus:2076904 - symbol:GRF7 "AT3G02520" species:3702 "Arabidopsis thaliana" [GO:0005635 "nuclear envelope" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0045309 "protein phosphorylated amino acid binding" evidence=TAS] [GO:0009507

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						"chloroplast" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] InterPro:IPR000308 PIRSF:PIRSF000868 PRINTS:PR00305 HOGENOM:HBG611720 GO:GO:0005886 GO:GO:0009506 GO:GO:0019904 InterPro:IPR023409 InterPro:IPR023410 Gene3D:G3DSA:1.20.190.20 PANTHER:PTHR18860 Pfam:PF00244 SMART:SM00101 SUPFAM:SSF48445 PROSITE:PS00796 PROSITE:PS00797 GO:GO:0009507 ProtClustDB:CLSN2688003 EMBL:U60445 EMBL:AF145299 EMBL:AC021640 EMBL:CP002686 EMBL:AY065274 EMBL:AY096526 EMBL:AY087723 IPI:IPI00536399 RefSeq:NP_566174.1 UniGene:At.21863 ProteinModelPortal:Q96300 SMR:Q96300 IntAct:Q96300 STRING:Q96300 PRIDE:Q96300 EnsemblPlants:AT3G02520.1 GeneID:821060 GenomeReviews:BA000014_GR KEGG:ath:AT3G02520 TAIR:At3g02520 InParanoid:Q96300 OMA:KVCQDVL PhylomeDB:Q96300 ArrayExpress:Q96300 Genevestigator:Q96300 GermOnline:AT3G02520 Uniprot:Q96300
Root	Isotig03297	4	41	-3.487	9.45E-10	TAIR|locus:2076904 - symbol:GRF7 "AT3G02520" species:3702 "Arabidopsis thaliana" [GO:0005635 "nuclear envelope" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0045309 "protein phosphorylated amino acid binding" evidence=TAS] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] InterPro:IPR000308 PIRSF:PIRSF000868 PRINTS:PR00305 HOGENOM:HBG611720 GO:GO:0005886 GO:GO:0009506 GO:GO:0019904 InterPro:IPR023409 InterPro:IPR023410 Gene3D:G3DSA:1.20.190.20 PANTHER:PTHR18860 Pfam:PF00244 SMART:SM00101 SUPFAM:SSF48445 PROSITE:PS00796 PROSITE:PS00797 GO:GO:0009507 ProtClustDB:CLSN2688003 EMBL:U60445 EMBL:AF145299 EMBL:AC021640 EMBL:CP002686 EMBL:AY065274 EMBL:AY096526 EMBL:AY087723 IPI:IPI00536399 RefSeq:NP_566174.1 UniGene:At.21863 ProteinModelPortal:Q96300 SMR:Q96300 IntAct:Q96300 STRING:Q96300 PRIDE:Q96300 EnsemblPlants:AT3G02520.1 GeneID:821060 GenomeReviews:BA000014_GR KEGG:ath:AT3G02520 TAIR:At3g02520 InParanoid:Q96300 OMA:KVCQDVL PhylomeDB:Q96300 ArrayExpress:Q96300 Genevestigator:Q96300 GermOnline:AT3G02520 Uniprot:Q96300
Root	Isotig03298	3	43	-3.970	5.33E-11	TAIR|locus:2076904 - symbol:GRF7 "AT3G02520" species:3702 "Arabidopsis thaliana" [GO:0005635 "nuclear envelope" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0045309 "protein phosphorylated amino acid binding" evidence=TAS] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] InterPro:IPR000308 PIRSF:PIRSF000868 PRINTS:PR00305 HOGENOM:HBG611720 GO:GO:0005886 GO:GO:0009506 GO:GO:0019904 InterPro:IPR023409 InterPro:IPR023410 Gene3D:G3DSA:1.20.190.20 PANTHER:PTHR18860 Pfam:PF00244 SMART:SM00101 SUPFAM:SSF48445 PROSITE:PS00796 PROSITE:PS00797 GO:GO:0009507 ProtClustDB:CLSN2688003 EMBL:U60445 EMBL:AF145299 EMBL:AC021640 EMBL:CP002686 EMBL:AY065274 EMBL:AY096526 EMBL:AY087723 IPI:IPI00536399 RefSeq:NP_566174.1 UniGene:At.21863 ProteinModelPortal:Q96300 SMR:Q96300 IntAct:Q96300 STRING:Q96300 PRIDE:Q96300 EnsemblPlants:AT3G02520.1 GeneID:821060 GenomeReviews:BA000014_GR KEGG:ath:AT3G02520 TAIR:At3g02520 InParanoid:Q96300 OMA:KVCQDVL PhylomeDB:Q96300 ArrayExpress:Q96300 Genevestigator:Q96300 GermOnline:AT3G02520 Uniprot:Q96300
Root	Isotig03311	1	14	-3.936	0.000188601	TAIR|locus:2117353 - symbol:PAP24 "AT4G24890" species:3702 "Arabidopsis thaliana" [GO:0004722 "protein serine/threonine phosphatase activity" evidence=ISS] [GO:0008150 "biological_process" evidence=ND] [GO:0005618 "cell wall" evidence=IDA] [GO:0003993 "acid phosphatase activity" evidence=ISS] InterPro:IPR004843 InterPro:IPR008963 InterPro:IPR015914 Pfam:PF00149 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005618 GO:GO:0005576 GO:GO:0046872 GO:GO:0003993 eggNOG:COG1409 EMBL:AL161562 EMBL:AL035523 Gene3D:G3DSA:2.60.40.380 SUPFAM:SSF49363 EMBL:AY842025 EMBL:AY142520 IPI:IPI00548773 PIR:T05510 RefSeq:NP_194219.2 UniGene:At.32313 ProteinModelPortal:Q8H1R2 SMR:Q8H1R2 PRIDE:Q8H1R2 EnsemblPlants:AT4G24890.1 GeneID:828591 KEGG:ath:AT4G24890 TAIR:At4g24890 InParanoid:Q8H1R2 OMA:AICEPEN PhylomeDB:Q8H1R2 ProtClustDB:CLSN2918186 Genevestigator:Q8H1R2 Uniprot:Q8H1R2
Root	Isotig03312	1	14	-3.936	0.000188601	TAIR|locus:2117353 - symbol:PAP24 "AT4G24890" species:3702 "Arabidopsis thaliana" [GO:0004722 "protein serine/threonine phosphatase activity" evidence=ISS] [GO:0008150 "biological_process" evidence=ND] [GO:0005618 "cell wall" evidence=IDA] [GO:0003993 "acid phosphatase activity" evidence=ISS] InterPro:IPR004843

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						InterPro:IPR008963 InterPro:IPR015914 Pfam:PF00149 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005618 GO:GO:0005576 GO:GO:0046872 GO:GO:0003993 eggNOG:COG1409 EMBL:AL161562 EMBL:AL035523 Gene3D:G3DSA:2.60.40.380 SUPFAM:SSF49363 EMBL:AY842025 EMBL:AY142520 IPI:IPI00548773 PIR:T05510 RefSeq:NP_194219.2 UniGene:At.32313 ProteinModelPortal:Q8H1R2 SMR:Q8H1R2 PRIDE:Q8H1R2 EnsemblPlants:AT4G24890.1 GeneID:828591 KEGG:ath:AT4G24890 TAIR:At4g24890 InParanoid:Q8H1R2 OMA:AICEPEN PhylomeDB:Q8H1R2 ProtClustDB:CLSN2918186 Genevestigator:Q8H1R2 Uniprot:Q8H1R2
Root	Isotig03313	1	14	-3.936	0.000188601	TAIR|locus:2117353 - symbol:PAP24 "AT4G24890" species:3702 "Arabidopsis thaliana" [GO:0004722 "protein serine/threonine phosphatase activity" evidence=ISS] [GO:0008150 "biological_process" evidence=ND] [GO:0005618 "cell wall" evidence=IDA] [GO:0003993 "acid phosphatase activity" evidence=ISS] InterPro:IPR004843 InterPro:IPR008963 InterPro:IPR015914 Pfam:PF00149 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005618 GO:GO:0005576 GO:GO:0046872 GO:GO:0003993 eggNOG:COG1409 EMBL:AL161562 EMBL:AL035523 Gene3D:G3DSA:2.60.40.380 SUPFAM:SSF49363 EMBL:AY842025 EMBL:AY142520 IPI:IPI00548773 PIR:T05510 RefSeq:NP_194219.2 UniGene:At.32313 ProteinModelPortal:Q8H1R2 SMR:Q8H1R2 PRIDE:Q8H1R2 EnsemblPlants:AT4G24890.1 GeneID:828591 KEGG:ath:AT4G24890 TAIR:At4g24890 InParanoid:Q8H1R2 OMA:AICEPEN PhylomeDB:Q8H1R2 ProtClustDB:CLSN2918186 Genevestigator:Q8H1R2 Uniprot:Q8H1R2
Root	Isotig03314	1	14	-3.936	0.000188601	TAIR|locus:2117353 - symbol:PAP24 "AT4G24890" species:3702 "Arabidopsis thaliana" [GO:0004722 "protein serine/threonine phosphatase activity" evidence=ISS] [GO:0008150 "biological_process" evidence=ND] [GO:0005618 "cell wall" evidence=IDA] [GO:0003993 "acid phosphatase activity" evidence=ISS] InterPro:IPR004843 InterPro:IPR008963 InterPro:IPR015914 Pfam:PF00149 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005618 GO:GO:0005576 GO:GO:0046872 GO:GO:0003993 eggNOG:COG1409 EMBL:AL161562 EMBL:AL035523 Gene3D:G3DSA:2.60.40.380 SUPFAM:SSF49363 EMBL:AY842025 EMBL:AY142520 IPI:IPI00548773 PIR:T05510 RefSeq:NP_194219.2 UniGene:At.32313 ProteinModelPortal:Q8H1R2 SMR:Q8H1R2 PRIDE:Q8H1R2 EnsemblPlants:AT4G24890.1 GeneID:828591 KEGG:ath:AT4G24890 TAIR:At4g24890 InParanoid:Q8H1R2 OMA:AICEPEN PhylomeDB:Q8H1R2 ProtClustDB:CLSN2918186 Genevestigator:Q8H1R2 Uniprot:Q8H1R2
Root	Isotig03381	11	31	-1.624	0.000622299	TAIR|locus:2079924 - symbol:UBQ1 "AT3G52590" species:3702 "Arabidopsis thaliana" [GO:0009793 "embryo development ending in seed dormancy" evidence=NAS] [GO:0003735 "structural constituent of ribosome" evidence=ISS] [GO:0016567 "protein ubiquitination" evidence=TAS] InterPro:IPR000626 Pfam:PF00240 SMART:SM00213 Prosite:PS00299 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005634 GO:GO:0005737 EMBL:AL161503 InterPro:IPR019955 PROSITE:PS50053 UniGene:At.48785 InterPro:IPR019954 eggNOG:COG5272 EMBL:AC012392 InterPro:IPR019956 PRINTS:PR00348 UniGene:At.23108 KO:K08770 EMBL:L05361 EMBL:AY139999 EMBL:BT000701 IPI:IPI00520650 IPI:IPI00895605 RefSeq:NP_001118922.1 RefSeq:NP_849292.1 RefSeq:NP_849299.4 RefSeq:NP_849301.4 RefSeq:NP_974516.4 UniGene:At.24970 UniGene:At.25274 UniGene:At.47590 UniGene:At.74401 ProteinModelPortal:Q8H159 SMR:Q8H159 EnsemblPlants:AT4G05320.2 EnsemblPlants:AT4G05320.4 GeneID:825880 GeneID:828148 KEGG:ath:AT4G02890 KEGG:ath:AT4G05320 TAIR:At4g05320 PhylomeDB:Q8H159 ProtClustDB:CLSN2692469 Uniprot:Q8H159
Root	Isotig03382	9	34	-2.047	2.70E-05	UNIPROTKB|Q5A109 - symbol:UBI3 "Ubiquitin-ribosomal protein fusion S27a" species:237561 "Candida albicans SC5314" [GO:0003735 "structural constituent of ribosome" evidence=IGI] [GO:0005576 "extracellular region" evidence=IDA] [GO:0016567 "protein ubiquitination" evidence=IGI] [GO:0031386 "protein tag" evidence=IGI] [GO:0042254 "ribosome biogenesis" evidence=IGI] InterPro:IPR000626 InterPro:IPR002906 Pfam:PF00240 Pfam:PF01599 SMART:SM00213 CGD:CAL0001506 Prosite:PS00299 GO:GO:0005576 GO:GO:0006412 GO:GO:0016567 GO:GO:0003735 InterPro:IPR019955 PROSITE:PS50053 GO:GO:0005840 GO:GO:0042254 GO:GO:0031386 InterPro:IPR019954 EMBL:AACQ01000086 EMBL:AACQ01000085 InterPro:IPR019956 PRINTS:PR00348 KO:K02977 RefSeq:XP_715397.1 RefSeq:XP_715467.1 ProteinModelPortal:Q5A109 SMR:Q5A109 STRING:Q5A109 GeneID:3642848 GeneID:3642934 KEGG:cal:CaO19.10599 KEGG:cal:CaO19.3087 PhylomeDB:Q5A109 Uniprot:Q5A109
Root	Isotig03455	24	53	-1.272	0.000195269	TAIR|locus:2077793 - symbol:iPGAM2 "AT3G08590" species:3702 "Arabidopsis thaliana" [GO:0046537 "2,3-bisphosphoglycerate-independent phosphoglycerate mutase activity" evidence=IGI;ISS] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA]

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						[GO:0009506 "plasmodesma" evidence=IDA] [GO:0009555 "pollen development" evidence=IGI] [GO:0010118 "stomatal movement" evidence=IGI] InterPro:IPR005995 InterPro:IPR006124 InterPro:IPR011258 InterPro:IPR017849 InterPro:IPR017850 Pfam:PF01676 Pfam:PF06415 PIRSF:PIRSF001492 GO:GO:0005829 GO:GO:0009506 GO:GO:0048046 GO:GO:0046686 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0009555 GO:GO:0010118 GO:GO:0030145 GO:GO:0006096 EMBL:AC012562 Gene3D:G3DSA:3.40.720.10 SUPFAM:SSF53649 eggNOG:COG0696 HOGENOM:HBG613255 KO:K15633 Gene3D:G3DSA:3.40.1450.10 SUPFAM:SSF64158 TIGRFAMs:TIGR01307 ProtClustDB:PLN02538 GO:GO:0046537 EMBL:AY039969 EMBL:AF424615 EMBL:AY113910 IPI:IPI00520882 RefSeq:NP_187471.1 RefSeq:NP_850542.1 UniGene:At.68440 ProteinModelPortal:Q9M9K1 SMR:Q9M9K1 STRING:Q9M9K1 PRIDE:Q9M9K1 EnsemblPlants:AT3G08590.1 EnsemblPlants:AT3G08590.2 GeneID:820006 KEGG:ath:AT3G08590 TAIR:At3g08590 InParanoid:Q9M9K1 OMA:AGRIYAQ PhylomeDB:Q9M9K1 ArrayExpress:Q9M9K1 Genevestigator:Q9M9K1 GermOnline:AT3G08590 Uniprot:Q9M9K1
Root	Isotig03472	5	29	-2.665	5.76E-06	TAIR|locus:2086177 - symbol:LPD1 "AT3G16950" species:3702 "Arabidopsis thaliana" [GO:0004148 "dihydrolipoyl dehydrogenase activity" evidence=ISS] [GO:0006086 "acetyl-CoA biosynthetic process from pyruvate" evidence=TAS] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] InterPro:IPR001327 InterPro:IPR004099 InterPro:IPR006258 InterPro:IPR012999 InterPro:IPR013027 InterPro:IPR016156 InterPro:IPR023753 Pfam:PF00070 Pfam:PF02852 Pfam:PF07992 PRINTS:PR00368 PROSITE:PS00076 GO:GO:0009570 EMBL:CP002686 GO:GO:0005730 GO:GO:0050660 GO:GO:0009941 EMBL:AB026636 GO:GO:0045454 Gene3D:G3DSA:3.30.390.30 SUPFAM:SSF55424 eggNOG:COG1249 KO:K00382 GO:GO:0004148 TIGRFAMs:TIGR01350 GO:GO:0006086 IPI:IPI00846791 RefSeq:NP_001078165.1 UniGene:At.16905 ProteinModelPortal:A8MS68 SMR:A8MS68 STRING:A8MS68 PRIDE:A8MS68 EnsemblPlants:AT3G16950.2 GeneID:820951 KEGG:ath:AT3G16950 TAIR:At3g16950 PhylomeDB:A8MS68 ProtClustDB:CLSN2688461 Genevestigator:A8MS68 Uniprot:A8MS68
Root	Isotig03473	4	24	-2.714	3.10E-05	TAIR|locus:2086177 - symbol:LPD1 "AT3G16950" species:3702 "Arabidopsis thaliana" [GO:0004148 "dihydrolipoyl dehydrogenase activity" evidence=ISS] [GO:0006086 "acetyl-CoA biosynthetic process from pyruvate" evidence=TAS] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] InterPro:IPR001327 InterPro:IPR004099 InterPro:IPR006258 InterPro:IPR012999 InterPro:IPR013027 InterPro:IPR016156 InterPro:IPR023753 Pfam:PF00070 Pfam:PF02852 Pfam:PF07992 PRINTS:PR00368 PROSITE:PS00076 GO:GO:0009570 EMBL:CP002686 GO:GO:0005730 GO:GO:0050660 GO:GO:0009941 EMBL:AB026636 GO:GO:0045454 Gene3D:G3DSA:3.30.390.30 SUPFAM:SSF55424 eggNOG:COG1249 KO:K00382 GO:GO:0004148 TIGRFAMs:TIGR01350 GO:GO:0006086 IPI:IPI00846791 RefSeq:NP_001078165.1 UniGene:At.16905 ProteinModelPortal:A8MS68 SMR:A8MS68 STRING:A8MS68 PRIDE:A8MS68 EnsemblPlants:AT3G16950.2 GeneID:820951 KEGG:ath:AT3G16950 TAIR:At3g16950 PhylomeDB:A8MS68 ProtClustDB:CLSN2688461 Genevestigator:A8MS68 Uniprot:A8MS68
Root	Isotig03478	17	0	4.958	3.30E-05	No hit
Root	Isotig03479	17	0	4.958	3.30E-05	No hit
Root	Isotig03487	0	12	-4.714	0.000297064	TAIR|locus:2122749 - symbol:HKT1 "AT4G10310" species:3702 "Arabidopsis thaliana" [GO:0015081 "sodium ion transmembrane transporter activity" evidence=ISS;IDA] [GO:0006814 "sodium ion transport" evidence=IMP;IDA] [GO:0009651 "response to salt stress" evidence=IGI;IMP] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0006813 "potassium ion transport" evidence=IMP] [GO:0006970 "response to osmotic stress" evidence=IEP] InterPro:IPR003445 InterPro:IPR004773 Pfam:PF02386 GO:GO:0016021 GO:GO:0005886 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0009651 GO:GO:0006814 EMBL:AF096373 EMBL:AL049488 EMBL:AL161517 GO:GO:0015079 EMBL:AF237672 EMBL:AY685182 EMBL:BT005751 IPI:IPI00518872 PIR:T01969 PIR:T04046 RefSeq:NP_567354.1 UniGene:At.2986 ProteinModelPortal:Q84TI7 STRING:Q84TI7 TCDB:2.A.38.3.2 PRIDE:Q84TI7 EnsemblPlants:AT4G10310.1 GeneID:826623 KEGG:ath:AT4G10310 GeneFarm:5166 TAIR:At4g10310 eggNOG:COG0168 HOGENOM:HBG599187 InParanoid:Q84TI7 OMA:VNSRHTG PhylomeDB:Q84TI7 ProtClustDB:CLSN2917526 BioCyc:MetaCyc:MONOMER-14577 Genevestigator:Q84TI7 GermOnline:AT4G10310 TIGRFAMs:TIGR00934 Uniprot:Q84TI7
Root	Isotig03489	0	12	-4.714	0.000297064	TAIR|locus:2122749 - symbol:HKT1 "AT4G10310" species:3702 "Arabidopsis thaliana" [GO:0015081 "sodium ion transmembrane transporter activity" evidence=ISS;IDA] [GO:0006814 "sodium ion transport" evidence=IMP;IDA]

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						[GO:0009651 "response to salt stress" evidence=IGI;IMP] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0006813 "potassium ion transport" evidence=IMP] [GO:0006970 "response to osmotic stress" evidence=IEP] InterPro:IPR003445 InterPro:IPR004773 Pfam:PF02386 GO:GO:0016021 GO:GO:0005886 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0009651 GO:GO:0006814 EMBL:AF096373 EMBL:AL049488 EMBL:AL161517 GO:GO:0015079 EMBL:AF237672 EMBL:AY685182 EMBL:BT005751 IPI:IPI00518872 PIR:T01969 PIR:T04046 RefSeq:NP_567354.1 UniGene:At.2986 ProteinModelPortal:Q84TI7 STRING:Q84TI7 TCDB:2.A.38.3.2 PRIDE:Q84TI7 EnsemblPlants:AT4G10310.1 GeneID:826623 KEGG:ath:AT4G10310 GeneFarm:5166 TAIR:At4g10310 eggNOG:COG0168 HOGENOM:HBG599187 InParanoid:Q84TI7 OMA:VNSRHTG PhylomeDB:Q84TI7 ProtClustDB:CLSN2917526 BioCyc:MetaCyc:MONOMER-14577 Genevestigator:Q84TI7 GermOnline:AT4G10310 TIGRFAMs:TIGR00934 Uniprot:Q84TI7
Root	Isotig03509	19	3	2.534	0.000639389	No hit
Root	Isotig03510	19	3	2.534	0.000639389	No hit
Root	Isotig03512	44	6	2.745	5.73E-08	TAIR|locus:2141060 - symbol:AGD8 "AT4G17890" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=ISS] [GO:0005634 "nucleus" evidence=ISS] [GO:0008060 "ARF GTPase activator activity" evidence=IEA] [GO:0008270 "zinc ion binding" evidence=IEA] [GO:0032312 "regulation of ARF GTPase activity" evidence=IEA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001164 Pfam:PF01412 PRINTS:PR00405 PROSITE:PS50115 SMART:SM00105 GO:GO:0005829 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0008270 EMBL:AL161547 eggNOG:COG5347 GO:GO:0008060 GO:GO:0032312 SUPFAM:SSF57863 HSSP:Q9NP61 HOGENOM:HBG736886 EMBL:AL021889 EMBL:AF360177 EMBL:BT000968 EMBL:AK175252 EMBL:AK176287 EMBL:AK176618 EMBL:AK221239 EMBL:AK221371 EMBL:AK229721 EMBL:AK317033 IPI:IPI00525155 IPI:IPI00657128 PIR:T05075 RefSeq:NP_001031658.1 RefSeq:NP_567543.1 UniGene:At.26724 UniGene:At.66582 ProteinModelPortal:Q8H100 SMR:Q8H100 PRIDE:Q8H100 EnsemblPlants:AT4G17890.1 GeneID:827512 KEGG:ath:AT4G17890 TAIR:At4g17890 InParanoid:Q8H100 OMA:NIGRSAD PhylomeDB:Q8H100 ProtClustDB:CLSN2686195 Genevestigator:Q8H100 Uniprot:Q8H100
Root	Isotig03513	35	5	2.678	1.78E-06	TAIR|locus:2141060 - symbol:AGD8 "AT4G17890" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=ISS] [GO:0005634 "nucleus" evidence=ISS] [GO:0008060 "ARF GTPase activator activity" evidence=IEA] [GO:0008270 "zinc ion binding" evidence=IEA] [GO:0032312 "regulation of ARF GTPase activity" evidence=IEA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001164 Pfam:PF01412 PRINTS:PR00405 PROSITE:PS50115 SMART:SM00105 GO:GO:0005829 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0008270 EMBL:AL161547 eggNOG:COG5347 GO:GO:0008060 GO:GO:0032312 SUPFAM:SSF57863 HSSP:Q9NP61 HOGENOM:HBG736886 EMBL:AL021889 EMBL:AF360177 EMBL:BT000968 EMBL:AK175252 EMBL:AK176287 EMBL:AK176618 EMBL:AK221239 EMBL:AK221371 EMBL:AK229721 EMBL:AK317033 IPI:IPI00525155 IPI:IPI00657128 PIR:T05075 RefSeq:NP_001031658.1 RefSeq:NP_567543.1 UniGene:At.26724 UniGene:At.66582 ProteinModelPortal:Q8H100 SMR:Q8H100 PRIDE:Q8H100 EnsemblPlants:AT4G17890.1 GeneID:827512 KEGG:ath:AT4G17890 TAIR:At4g17890 InParanoid:Q8H100 OMA:NIGRSAD PhylomeDB:Q8H100 ProtClustDB:CLSN2686195 Genevestigator:Q8H100 Uniprot:Q8H100
Root	Isotig03514	41	5	2.907	6.91E-08	TAIR|locus:2141060 - symbol:AGD8 "AT4G17890" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=ISS] [GO:0005634 "nucleus" evidence=ISS] [GO:0008060 "ARF GTPase activator activity" evidence=IEA] [GO:0008270 "zinc ion binding" evidence=IEA] [GO:0032312 "regulation of ARF GTPase activity" evidence=IEA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001164 Pfam:PF01412 PRINTS:PR00405 PROSITE:PS50115 SMART:SM00105 GO:GO:0005829 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0008270 EMBL:AL161547 eggNOG:COG5347 GO:GO:0008060 GO:GO:0032312 SUPFAM:SSF57863 HSSP:Q9NP61 HOGENOM:HBG736886 EMBL:AL021889 EMBL:AF360177 EMBL:BT000968 EMBL:AK175252 EMBL:AK176287 EMBL:AK176618 EMBL:AK221239 EMBL:AK221371 EMBL:AK229721 EMBL:AK317033 IPI:IPI00525155 IPI:IPI00657128 PIR:T05075 RefSeq:NP_001031658.1 RefSeq:NP_567543.1 UniGene:At.26724 UniGene:At.66582 ProteinModelPortal:Q8H100 SMR:Q8H100 PRIDE:Q8H100 EnsemblPlants:AT4G17890.1 GeneID:827512 KEGG:ath:AT4G17890 TAIR:At4g17890 InParanoid:Q8H100 OMA:NIGRSAD PhylomeDB:Q8H100 ProtClustDB:CLSN2686195 Genevestigator:Q8H100 Uniprot:Q8H100
Root	Isotig03521	0	39	-6.414	3.85E-11	UNIPROTKB|A8QW53 - symbol:OMT3 "5-pentadecatrienyl resorcinol O-methyltransferase" species:4558 "Sorghum bicolor" [GO:0008171 "O-methyltransferase activity" evidence=IDA] [GO:0008757 "S-adenosylmethionine-dependent methyltransferase activity" evidence=IDA] [GO:0032259 "methylation" evidence=IDA] InterPro:IPR001077 InterPro:IPR012967 InterPro:IPR016461 Pfam:PF00891 Pfam:PF08100 PIRSF:PIRSF005739

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						InterPro:IPR011991 Gene3D:G3DSA:1.10.10.10 GO:GO:0046983 GO:GO:0008171 GO:GO:0008757 EMBL:EF189708 EMBL:CM000765 RefSeq:XP_002447425.1 UniGene:Sbi.19698 ProteinModelPortal:A8QW53 EnsemblPlants:Sb06g000820.1 GeneID:8080259 KEGG:sbi:SORBI_06g000820 eggNOG:NOG272168 PhylomeDB:A8QW53 ProtClustDB:CLSN2725062 Uniprot:A8QW53
Root	Isotig03522	1	47	-5.684	2.93E-13	UNIPROTKB|A8QW53 - symbol:OMT3 "5-pentadecatrienyl resorcinol O-methyltransferase" species:4558 "Sorghum bicolor" [GO:0008171 "O-methyltransferase activity" evidence=IDA] [GO:0008757 "S-adenosylmethionine-dependent methyltransferase activity" evidence=IDA] [GO:0032259 "methylation" evidence=IDA] InterPro:IPR001077 InterPro:IPR012967 InterPro:IPR016461 Pfam:PF00891 Pfam:PF08100 PIRSF:PIRSF005739 InterPro:IPR011991 Gene3D:G3DSA:1.10.10.10 GO:GO:0046983 GO:GO:0008171 GO:GO:0008757 EMBL:EF189708 EMBL:CM000765 RefSeq:XP_002447425.1 UniGene:Sbi.19698 ProteinModelPortal:A8QW53 EnsemblPlants:Sb06g000820.1 GeneID:8080259 KEGG:sbi:SORBI_06g000820 eggNOG:NOG272168 PhylomeDB:A8QW53 ProtClustDB:CLSN2725062 Uniprot:A8QW53
Root	Isotig03523	1	46	-5.653	5.25E-13	UNIPROTKB|A8QW53 - symbol:OMT3 "5-pentadecatrienyl resorcinol O-methyltransferase" species:4558 "Sorghum bicolor" [GO:0008171 "O-methyltransferase activity" evidence=IDA] [GO:0008757 "S-adenosylmethionine-dependent methyltransferase activity" evidence=IDA] [GO:0032259 "methylation" evidence=IDA] InterPro:IPR001077 InterPro:IPR012967 InterPro:IPR016461 Pfam:PF00891 Pfam:PF08100 PIRSF:PIRSF005739 InterPro:IPR011991 Gene3D:G3DSA:1.10.10.10 GO:GO:0046983 GO:GO:0008171 GO:GO:0008757 EMBL:EF189708 EMBL:CM000765 RefSeq:XP_002447425.1 UniGene:Sbi.19698 ProteinModelPortal:A8QW53 EnsemblPlants:Sb06g000820.1 GeneID:8080259 KEGG:sbi:SORBI_06g000820 eggNOG:NOG272168 PhylomeDB:A8QW53 ProtClustDB:CLSN2725062 Uniprot:A8QW53
Root	Isotig03524	52	106	-1.156	1.02E-06	TAIR|locus:2120222 - symbol:RD19 "AT4G39090" species:3702 "Arabidopsis thaliana" [GO:0006508 "proteolysis" evidence=ISS] [GO:0008234 "cysteine-type peptidase activity" evidence=ISS] [GO:0009269 "response to desiccation" evidence=IEP] [GO:0006970 "response to osmotic stress" evidence=IGI] [GO:0005634 "nucleus" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0042742 "defense response to bacterium" evidence=IMP] [GO:0004197 "cysteine-type endopeptidase activity" evidence=ISS] [GO:0009414 "response to water deprivation" evidence=TAS] [GO:0009651 "response to salt stress" evidence=IEP] InterPro:IPR000668 InterPro:IPR013128 Pfam:PF00112 PRINTS:PR00705 SMART:SM00645 InterPro:IPR000169 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005634 GO:GO:0005773 GO:GO:0042742 eggNOG:COG4870 HOGENOM:HBG746690 ProtClustDB:CLSN2688311 GO:GO:0004197 GO:GO:0006508 InterPro:IPR013201 PANTHER:PTHR12411 Pfam:PF08246 SMART:SM00848 PROSITE:PS00640 PROSITE:PS00139 PROSITE:PS00639 GO:GO:0009651 EMBL:AL035679 EMBL:AL161594 MEROPS:C01.022 EMBL:D13042 EMBL:AY080598 EMBL:AY133844 IPI:IPI00544363 PIR:JN0718 RefSeq:NP_568052.1 UniGene:At.2850 UniGene:At.74924 ProteinModelPortal:P43296 SMR:P43296 STRING:P43296 PRIDE:P43296 EnsemblPlants:AT4G39090.1 GeneID:830064 KEGG:ath:AT4G39090 TAIR:At4g39090 InParanoid:P43296 OMA:EDFDWRD PhylomeDB:P43296 ArrayExpress:P43296 Genevestigator:P43296 GermOnline:AT4G39090 Uniprot:P43296
Root	Isotig03525	45	105	-1.351	3.91E-08	TAIR|locus:2120222 - symbol:RD19 "AT4G39090" species:3702 "Arabidopsis thaliana" [GO:0006508 "proteolysis" evidence=ISS] [GO:0008234 "cysteine-type peptidase activity" evidence=ISS] [GO:0009269 "response to desiccation" evidence=IEP] [GO:0006970 "response to osmotic stress" evidence=IGI] [GO:0005634 "nucleus" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0042742 "defense response to bacterium" evidence=IMP] [GO:0004197 "cysteine-type endopeptidase activity" evidence=ISS] [GO:0009414 "response to water deprivation" evidence=TAS] [GO:0009651 "response to salt stress" evidence=IEP] InterPro:IPR000668 InterPro:IPR013128 Pfam:PF00112 PRINTS:PR00705 SMART:SM00645 InterPro:IPR000169 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005634 GO:GO:0005773 GO:GO:0042742 eggNOG:COG4870 HOGENOM:HBG746690 ProtClustDB:CLSN2688311 GO:GO:0004197 GO:GO:0006508 InterPro:IPR013201 PANTHER:PTHR12411 Pfam:PF08246 SMART:SM00848 PROSITE:PS00640 PROSITE:PS00139 PROSITE:PS00639 GO:GO:0009651 EMBL:AL035679 EMBL:AL161594 MEROPS:C01.022 EMBL:D13042 EMBL:AY080598 EMBL:AY133844 IPI:IPI00544363 PIR:JN0718 RefSeq:NP_568052.1 UniGene:At.2850 UniGene:At.74924 ProteinModelPortal:P43296 SMR:P43296 STRING:P43296 PRIDE:P43296 EnsemblPlants:AT4G39090.1 GeneID:830064 KEGG:ath:AT4G39090 TAIR:At4g39090 InParanoid:P43296 OMA:EDFDWRD PhylomeDB:P43296 ArrayExpress:P43296 Genevestigator:P43296 GermOnline:AT4G39090 Uniprot:P43296

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig03536	35	10	1.678	0.000370903	TAIR|locus:2195077 - symbol:AT1G12760 "AT1G12760" species:3702 "Arabidopsis thaliana" [GO:0008270 "zinc ion binding" evidence=ISS] [GO:0004842 "ubiquitin-protein ligase activity" evidence=IDA] InterPro:IPR001841 PROSITE:PS50089 SMART:SM00184 Prosite:PS00518 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0008270 InterPro:IPR013083 Gene3D:G3DSA:3.30.40.10 HSSP:Q9LRB7 GO:GO:0004842 EMBL:AC025417 eggNOG:NOG277561 HOGENOM:HBG750480 ProtClustDB:CLSN2682050 EMBL:DQ059089 EMBL:AY136370 EMBL:BT000279 IPI:IPI00516637 RefSeq:NP_172736.2 UniGene:At.43884 ProteinModelPortal:Q9LN71 SMR:Q9LN71 PRIDE:Q9LN71 EnsemblPlants:AT1G12760.1 GeneID:837832 KEGG:ath:AT1G12760 TAIR:At1g12760 InParanoid:Q9LN71 OMA:IVWNLAF PhylomeDB:Q9LN71 Genevestigator:Q9LN71 Uniprot:Q9LN71
Root	Isotig03537	38	10	1.797	9.99E-05	TAIR|locus:2195077 - symbol:AT1G12760 "AT1G12760" species:3702 "Arabidopsis thaliana" [GO:0008270 "zinc ion binding" evidence=ISS] [GO:0004842 "ubiquitin-protein ligase activity" evidence=IDA] InterPro:IPR001841 PROSITE:PS50089 SMART:SM00184 Prosite:PS00518 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0008270 InterPro:IPR013083 Gene3D:G3DSA:3.30.40.10 HSSP:Q9LRB7 GO:GO:0004842 EMBL:AC025417 eggNOG:NOG277561 HOGENOM:HBG750480 ProtClustDB:CLSN2682050 EMBL:DQ059089 EMBL:AY136370 EMBL:BT000279 IPI:IPI00516637 RefSeq:NP_172736.2 UniGene:At.43884 ProteinModelPortal:Q9LN71 SMR:Q9LN71 PRIDE:Q9LN71 EnsemblPlants:AT1G12760.1 GeneID:837832 KEGG:ath:AT1G12760 TAIR:At1g12760 InParanoid:Q9LN71 OMA:IVWNLAF PhylomeDB:Q9LN71 Genevestigator:Q9LN71 Uniprot:Q9LN71
Root	Isotig03538	39	10	1.835	6.39E-05	TAIR|locus:2195077 - symbol:AT1G12760 "AT1G12760" species:3702 "Arabidopsis thaliana" [GO:0008270 "zinc ion binding" evidence=ISS] [GO:0004842 "ubiquitin-protein ligase activity" evidence=IDA] InterPro:IPR001841 PROSITE:PS50089 SMART:SM00184 Prosite:PS00518 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0008270 InterPro:IPR013083 Gene3D:G3DSA:3.30.40.10 HSSP:Q9LRB7 GO:GO:0004842 EMBL:AC025417 eggNOG:NOG277561 HOGENOM:HBG750480 ProtClustDB:CLSN2682050 EMBL:DQ059089 EMBL:AY136370 EMBL:BT000279 IPI:IPI00516637 RefSeq:NP_172736.2 UniGene:At.43884 ProteinModelPortal:Q9LN71 SMR:Q9LN71 PRIDE:Q9LN71 EnsemblPlants:AT1G12760.1 GeneID:837832 KEGG:ath:AT1G12760 TAIR:At1g12760 InParanoid:Q9LN71 OMA:IVWNLAF PhylomeDB:Q9LN71 Genevestigator:Q9LN71 Uniprot:Q9LN71
Root	Isotig03542	14	0	4.678	0.000190242	TAIR|locus:2177105 - symbol:ZIFL1 "zinc induced facilitator-like 1" species:3702 "Arabidopsis thaliana" [GO:0015520 "tetracycline:hydrogen antiporter activity" evidence=IEA] [GO:0080167 "response to karrikin" evidence=IEP] InterPro:IPR001958 InterPro:IPR011701 Pfam:PF07690 PRINTS:PR01035 GO:GO:0016021 GO:GO:0005886 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0055085 GO:GO:0080167 GO:GO:0005215 InterPro:IPR016196 SUPFAM:SSF103473 EMBL:AB011484 InterPro:IPR020846 PROSITE:PS50850 eggNOG:NOG309217 EMBL:AY039542 EMBL:AY062867 EMBL:AY102150 EMBL:AK318697 EMBL:AY086758 EMBL:AK221880 IPI:IPI00525646 IPI:IPI00540772 IPI:IPI00657118 IPI:IPI00971349 RefSeq:NP_001031877.1 RefSeq:NP_568290.3 RefSeq:NP_851036.1 UniGene:At.19822 ProteinModelPortal:Q94BZ1 STRING:Q94BZ1 PRIDE:Q94BZ1 EnsemblPlants:AT5G13750.1 GeneID:831220 KEGG:ath:AT5G13750 TAIR:At5g13750 InParanoid:Q94BZ1 OMA:VVFNTLF PhylomeDB:Q94BZ1 ProtClustDB:CLSN2679920 Genevestigator:Q94BZ1 Uniprot:Q94BZ1
Root	Isotig03543	14	0	4.678	0.000190242	TAIR|locus:2177105 - symbol:ZIFL1 "zinc induced facilitator-like 1" species:3702 "Arabidopsis thaliana" [GO:0015520 "tetracycline:hydrogen antiporter activity" evidence=IEA] [GO:0080167 "response to karrikin" evidence=IEP] InterPro:IPR001958 InterPro:IPR011701 Pfam:PF07690 PRINTS:PR01035 GO:GO:0016021 GO:GO:0005886 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0055085 GO:GO:0080167 GO:GO:0005215 InterPro:IPR016196 SUPFAM:SSF103473 EMBL:AB011484 InterPro:IPR020846 PROSITE:PS50850 eggNOG:NOG309217 EMBL:AY039542 EMBL:AY062867 EMBL:AY102150 EMBL:AK318697 EMBL:AY086758 EMBL:AK221880 IPI:IPI00525646 IPI:IPI00540772 IPI:IPI00657118 IPI:IPI00971349 RefSeq:NP_001031877.1 RefSeq:NP_568290.3 RefSeq:NP_851036.1 UniGene:At.19822 ProteinModelPortal:Q94BZ1 STRING:Q94BZ1 PRIDE:Q94BZ1 EnsemblPlants:AT5G13750.1 GeneID:831220 KEGG:ath:AT5G13750 TAIR:At5g13750 InParanoid:Q94BZ1 OMA:VVFNTLF PhylomeDB:Q94BZ1 ProtClustDB:CLSN2679920 Genevestigator:Q94BZ1 Uniprot:Q94BZ1
Root	Isotig03551	1	15	-4.036	9.83E-05	TAIR|locus:2159634 - symbol:AT5G10650 species:3702 "Arabidopsis thaliana" [GO:0008270 "zinc ion binding" evidence=IEA;ISS] InterPro:IPR001841 PROSITE:PS50089 SMART:SM00184 EMBL:CP002688 GO:GO:0008270 InterPro:IPR013083 Gene3D:G3DSA:3.30.40.10 EMBL:BT015918 EMBL:BT020582 IPI:IPI00534438

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						RefSeq:NP_001031869.1 RefSeq:NP_196626.2 UniGene:At.32350 ProteinModelPortal:Q5XEP8 SMR:Q5XEP8 PRIDE:Q5XEP8 EnsemblPlants:AT5G10650.1 EnsemblPlants:AT5G10650.2 GeneID:830929 KEGG:ath:AT5G10650 TAIR:At5g10650 HOGENOM:HBG316343 InParanoid:Q5XEP8 OMA:ISSHGNG PhylomeDB:Q5XEP8 ProtClustDB:CLSN2690147 Genevestigator:Q5XEP8 Uniprot:Q5XEP8
Root	Isotig03552	1	15	-4.036	9.83E-05	TAIR|locus:2159634 - symbol:AT5G10650 species:3702 "Arabidopsis thaliana" [GO:0008270 "zinc ion binding" evidence=IEA;ISS] InterPro:IPR001841 PROSITE:PS50089 SMART:SM00184 EMBL:CP002688 GO:GO:0008270 InterPro:IPR013083 Gene3D:G3DSA:3.30.40.10 EMBL:BT015918 EMBL:BT020582 IPI:IPI00534438 RefSeq:NP_001031869.1 RefSeq:NP_196626.2 UniGene:At.32350 ProteinModelPortal:Q5XEP8 SMR:Q5XEP8 PRIDE:Q5XEP8 EnsemblPlants:AT5G10650.1 EnsemblPlants:AT5G10650.2 GeneID:830929 KEGG:ath:AT5G10650 TAIR:At5g10650 HOGENOM:HBG316343 InParanoid:Q5XEP8 OMA:ISSHGNG PhylomeDB:Q5XEP8 ProtClustDB:CLSN2690147 Genevestigator:Q5XEP8 Uniprot:Q5XEP8
Root	Isotig03553	1	14	-3.936	0.000188601	TAIR|locus:2159634 - symbol:AT5G10650 species:3702 "Arabidopsis thaliana" [GO:0008270 "zinc ion binding" evidence=IEA;ISS] InterPro:IPR001841 PROSITE:PS50089 SMART:SM00184 EMBL:CP002688 GO:GO:0008270 InterPro:IPR013083 Gene3D:G3DSA:3.30.40.10 EMBL:BT015918 EMBL:BT020582 IPI:IPI00534438 RefSeq:NP_001031869.1 RefSeq:NP_196626.2 UniGene:At.32350 ProteinModelPortal:Q5XEP8 SMR:Q5XEP8 PRIDE:Q5XEP8 EnsemblPlants:AT5G10650.1 EnsemblPlants:AT5G10650.2 GeneID:830929 KEGG:ath:AT5G10650 TAIR:At5g10650 HOGENOM:HBG316343 InParanoid:Q5XEP8 OMA:ISSHGNG PhylomeDB:Q5XEP8 ProtClustDB:CLSN2690147 Genevestigator:Q5XEP8 Uniprot:Q5XEP8
Root	Isotig03566	15	44	-1.682	2.92E-05	TAIR|locus:2082642 - symbol:PIP2;5 "plasma membrane intrinsic protein 2;5" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=IEA;ISS] [GO:0015250 "water channel activity" evidence=ISS] [GO:0016020 "membrane" evidence=IEA;ISS] [GO:0016021 "integral to membrane" evidence=IEA] [GO:0055085 "transmembrane transport" evidence=IEA] [GO:0005515 "protein binding" evidence=IPI] InterPro:IPR000425 InterPro:IPR012269 InterPro:IPR022357 Pfam:PF00230 PRINTS:PR00783 PROSITE:PS00221 GO:GO:0016021 GO:GO:0005886 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005515 EMBL:AL049655 GO:GO:0055085 GO:GO:0005215 GO:GO:0006833 InterPro:IPR023271 Gene3D:G3DSA:1.20.1080.10 SUPFAM:SSF81338 eggNOG:COG0580 HOGENOM:HBG705794 PANTHER:PTHR19139 TIGRFAMs:TIGR00861 KO:K09872 EMBL:AF370351 EMBL:AY062981 EMBL:BT000670 EMBL:AY084843 IPI:IPI00520414 PIR:T06738 RefSeq:NP_191042.1 UniGene:At.3117 ProteinModelPortal:Q9SV31 SMR:Q9SV31 IntAct:Q9SV31 PRIDE:Q9SV31 ProMEX:Q9SV31 EnsemblPlants:AT3G54820.1 GeneID:824647 KEGG:ath:AT3G54820 GeneFarm:4870 TAIR:At3g54820 InParanoid:Q9SV31 OMA:FIVHLAT PhylomeDB:Q9SV31 ProtClustDB:CLSN2915746 ArrayExpress:Q9SV31 Genevestigator:Q9SV31 GermOnline:AT3G54820 Uniprot:Q9SV31
Root	Isotig03567	12	34	-1.631	0.000323514	TAIR|locus:2082642 - symbol:PIP2;5 "plasma membrane intrinsic protein 2;5" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=IEA;ISS] [GO:0015250 "water channel activity" evidence=ISS] [GO:0016020 "membrane" evidence=IEA;ISS] [GO:0016021 "integral to membrane" evidence=IEA] [GO:0055085 "transmembrane transport" evidence=IEA] [GO:0005515 "protein binding" evidence=IPI] InterPro:IPR000425 InterPro:IPR012269 InterPro:IPR022357 Pfam:PF00230 PRINTS:PR00783 PROSITE:PS00221 GO:GO:0016021 GO:GO:0005886 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005515 EMBL:AL049655 GO:GO:0055085 GO:GO:0005215 GO:GO:0006833 InterPro:IPR023271 Gene3D:G3DSA:1.20.1080.10 SUPFAM:SSF81338 eggNOG:COG0580 HOGENOM:HBG705794 PANTHER:PTHR19139 TIGRFAMs:TIGR00861 KO:K09872 EMBL:AF370351 EMBL:AY062981 EMBL:BT000670 EMBL:AY084843 IPI:IPI00520414 PIR:T06738 RefSeq:NP_191042.1 UniGene:At.3117 ProteinModelPortal:Q9SV31 SMR:Q9SV31 IntAct:Q9SV31 PRIDE:Q9SV31 ProMEX:Q9SV31 EnsemblPlants:AT3G54820.1 GeneID:824647 KEGG:ath:AT3G54820 GeneFarm:4870 TAIR:At3g54820 InParanoid:Q9SV31 OMA:FIVHLAT PhylomeDB:Q9SV31 ProtClustDB:CLSN2915746 ArrayExpress:Q9SV31 Genevestigator:Q9SV31 GermOnline:AT3G54820 Uniprot:Q9SV31
Root	Isotig03568	9	33	-2.003	4.53E-05	TAIR|locus:2082642 - symbol:PIP2;5 "plasma membrane intrinsic protein 2;5" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=IEA;ISS] [GO:0015250 "water channel activity" evidence=ISS] [GO:0016020 "membrane" evidence=IEA;ISS] [GO:0016021 "integral to membrane" evidence=IEA] [GO:0055085 "transmembrane transport" evidence=IEA] [GO:0005515 "protein binding" evidence=IPI] InterPro:IPR000425 InterPro:IPR012269 InterPro:IPR022357 Pfam:PF00230 PRINTS:PR00783 PROSITE:PS00221 GO:GO:0016021 GO:GO:0005886 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005515 EMBL:AL049655 GO:GO:0055085 GO:GO:0005215 GO:GO:0006833 InterPro:IPR023271 Gene3D:G3DSA:1.20.1080.10 SUPFAM:SSF81338 eggNOG:COG0580 HOGENOM:HBG705794 PANTHER:PTHR19139 TIGRFAMs:TIGR00861 KO:K09872

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EMBL:AF370351 EMBL:AY062981 EMBL:BT000670 EMBL:AY084843 IPI:IPI00520414 PIR:T06738 RefSeq:NP_191042.1 UniGene:At.3117 ProteinModelPortal:Q9SV31 SMR:Q9SV31 IntAct:Q9SV31 PRIDE:Q9SV31 ProMEX:Q9SV31 EnsemblPlants:AT3G54820.1 GeneID:824647 KEGG:ath:AT3G54820 GeneFarm:4870 TAIR:At3g54820 InParanoid:Q9SV31 OMA:FIVHLAT PhylomeDB:Q9SV31 ProtClustDB:CLSN2915746 ArrayExpress:Q9SV31 Genevestigator:Q9SV31 GermOnline:AT3G54820 Uniprot:Q9SV31
Root	Isotig03581	0	18	-5.299	6.77E-06	TAIR|locus:2183730 - symbol:AT5G10770 "AT5G10770" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=ISS] [GO:0004190 "aspartic-type endopeptidase activity" evidence=IEA] [GO:0006508 "proteolysis" evidence=IEA] InterPro:IPR001461 InterPro:IPR009007 Pfam:PF00026 PRINTS:PR00792 EMBL:CP002688 GO:GO:0006508 GO:GO:0004190 InterPro:IPR021109 SUPFAM:SSF50630 Gene3D:G3DSA:2.40.70.10 PANTHER:PTHR13683 HSSP:P00799 EMBL:AY075656 EMBL:BT001004 IPI:IPI00543783 RefSeq:NP_196638.2 UniGene:At.32336 ProteinModelPortal:Q8S9J6 MEROPS:A01.A15 PRIDE:Q8S9J6 EnsemblPlants:AT5G10770.1 GeneID:830944 KEGG:ath:AT5G10770 TAIR:At5g10770 InParanoid:Q8S9J6 OMA:LEVVYDG PhylomeDB:Q8S9J6 ProtClustDB:CLSN2686424 Genevestigator:Q8S9J6 Uniprot:Q8S9J6
Root	Isotig03582	0	18	-5.299	6.77E-06	TAIR|locus:2183730 - symbol:AT5G10770 "AT5G10770" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=ISS] [GO:0004190 "aspartic-type endopeptidase activity" evidence=IEA] [GO:0006508 "proteolysis" evidence=IEA] InterPro:IPR001461 InterPro:IPR009007 Pfam:PF00026 PRINTS:PR00792 EMBL:CP002688 GO:GO:0006508 GO:GO:0004190 InterPro:IPR021109 SUPFAM:SSF50630 Gene3D:G3DSA:2.40.70.10 PANTHER:PTHR13683 HSSP:P00799 EMBL:AY075656 EMBL:BT001004 IPI:IPI00543783 RefSeq:NP_196638.2 UniGene:At.32336 ProteinModelPortal:Q8S9J6 MEROPS:A01.A15 PRIDE:Q8S9J6 EnsemblPlants:AT5G10770.1 GeneID:830944 KEGG:ath:AT5G10770 TAIR:At5g10770 InParanoid:Q8S9J6 OMA:LEVVYDG PhylomeDB:Q8S9J6 ProtClustDB:CLSN2686424 Genevestigator:Q8S9J6 Uniprot:Q8S9J6
Root	Isotig03583	0	15	-5.036	4.38E-05	TAIR|locus:2183730 - symbol:AT5G10770 "AT5G10770" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=ISS] [GO:0004190 "aspartic-type endopeptidase activity" evidence=IEA] [GO:0006508 "proteolysis" evidence=IEA] InterPro:IPR001461 InterPro:IPR009007 Pfam:PF00026 PRINTS:PR00792 EMBL:CP002688 GO:GO:0006508 GO:GO:0004190 InterPro:IPR021109 SUPFAM:SSF50630 Gene3D:G3DSA:2.40.70.10 PANTHER:PTHR13683 HSSP:P00799 EMBL:AY075656 EMBL:BT001004 IPI:IPI00543783 RefSeq:NP_196638.2 UniGene:At.32336 ProteinModelPortal:Q8S9J6 MEROPS:A01.A15 PRIDE:Q8S9J6 EnsemblPlants:AT5G10770.1 GeneID:830944 KEGG:ath:AT5G10770 TAIR:At5g10770 InParanoid:Q8S9J6 OMA:LEVVYDG PhylomeDB:Q8S9J6 ProtClustDB:CLSN2686424 Genevestigator:Q8S9J6 Uniprot:Q8S9J6
Root	Isotig03608	1	21	-4.521	2.07E-06	TAIR|locus:2060984 - symbol:HIS1-3 "histone H1-3" species:3702 "Arabidopsis thaliana" [GO:0000786 "nucleosome" evidence=IEA;ISS] [GO:0003677 "DNA binding" evidence=ISS] [GO:0005634 "nucleus" evidence=IEA] [GO:0006334 "nucleosome assembly" evidence=ISS] [GO:0009414 "response to water deprivation" evidence=IEP] [GO:0031492 "nucleosomal DNA binding" evidence=ISS] InterPro:IPR005818 InterPro:IPR005819 Pfam:PF00538 PRINTS:PR00624 PROSITE:PS51504 SMART:SM00526 GO:GO:0005634 EMBL:CP002685 GO:GO:0003677 InterPro:IPR011991 Gene3D:G3DSA:1.10.10.10 GO:GO:0009414 GO:GO:0006334 GO:GO:0000786 EMBL:AC006201 KO:K11275 EMBL:U72241 EMBL:U73781 EMBL:AY045797 EMBL:AY079414 EMBL:AY084603 IPI:IPI00539258 PIR:F84559 RefSeq:NP_179396.1 UniGene:At.24439 ProteinModelPortal:P94109 SMR:P94109 STRING:P94109 PRIDE:P94109 EnsemblPlants:AT2G18050.1 GeneID:816317 KEGG:ath:AT2G18050 TAIR:At2g18050 eggNOG:NOG258576 InParanoid:P94109 OMA:TKRTRSS PhylomeDB:P94109 ProtClustDB:CLSN2683930 ArrayExpress:P94109 Genevestigator:P94109 Uniprot:P94109
Root	Isotig03609	1	21	-4.521	2.07E-06	TAIR|locus:2060984 - symbol:HIS1-3 "histone H1-3" species:3702 "Arabidopsis thaliana" [GO:0000786 "nucleosome" evidence=IEA;ISS] [GO:0003677 "DNA binding" evidence=ISS] [GO:0005634 "nucleus" evidence=IEA] [GO:0006334 "nucleosome assembly" evidence=ISS] [GO:0009414 "response to water deprivation" evidence=IEP] [GO:0031492 "nucleosomal DNA binding" evidence=ISS] InterPro:IPR005818 InterPro:IPR005819 Pfam:PF00538 PRINTS:PR00624 PROSITE:PS51504 SMART:SM00526 GO:GO:0005634 EMBL:CP002685 GO:GO:0003677 InterPro:IPR011991 Gene3D:G3DSA:1.10.10.10 GO:GO:0009414 GO:GO:0006334 GO:GO:0000786 EMBL:AC006201 KO:K11275 EMBL:U72241 EMBL:U73781 EMBL:AY045797 EMBL:AY079414 EMBL:AY084603 IPI:IPI00539258 PIR:F84559 RefSeq:NP_179396.1 UniGene:At.24439

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						ProteinModelPortal:P94109 SMR:P94109 STRING:P94109 PRIDE:P94109 EnsemblPlants:AT2G18050.1 GeneID:816317 KEGG:ath:AT2G18050 TAIR:At2g18050 eggNOG:NOG258576 InParanoid:P94109 OMA:TKRTRSS PhylomeDB:P94109 ProtClustDB:CLSN2683930 ArrayExpress:P94109 Genevestigator:P94109 Uniprot:P94109
Root	Isotig03610	0	18	-5.299	6.77E-06	TAIR|locus:2064332 - symbol:AT2G30620 "AT2G30620" species:3702 "Arabidopsis thaliana" [GO:0000786 "nucleosome" evidence=ISS] [GO:0003677 "DNA binding" evidence=IEA;ISS] [GO:0005634 "nucleus" evidence=ISS] [GO:0006334 "nucleosome assembly" evidence=IEA;ISS] [GO:0005730 "nucleolus" evidence=IDA] InterPro:IPR005818 InterPro:IPR005819 Pfam:PF00538 PRINTS:PR00624 PROSITE:PS51504 SMART:SM00526 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0005730 GO:GO:0003677 InterPro:IPR011991 Gene3D:G3DSA:1.10.10.10 GO:GO:0006334 GO:GO:0000786 EMBL:U93215 KO:K11275 eggNOG:NOG126832 EMBL:X62459 EMBL:AF360211 EMBL:AY040059 EMBL:AY085789 IPI:IPI00532307 PIR:S19699 RefSeq:NP_180620.1 UniGene:At.20406 ProteinModelPortal:P26569 STRING:P26569 PRIDE:P26569 EnsemblPlants:AT2G30620.1 GeneID:817612 KEGG:ath:AT2G30620 TAIR:At2g30620 HOGENOM:HBG184949 InParanoid:P26569 OMA:HRTPSSH PhylomeDB:P26569 ProtClustDB:CLSN2912930 ArrayExpress:P26569 Genevestigator:P26569 GermOnline:AT2G30620 Uniprot:P26569
Root	Isotig03665	54	0	6.626	1.30E-13	TAIR|locus:2202965 - symbol:MSL6 "AT1G78610" species:3702 "Arabidopsis thaliana" [GO:0016020 "membrane" evidence=ISS] [GO:0055085 "transmembrane transport" evidence=IEA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR006685 Pfam:PF00924 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005886 GO:GO:0009506 GO:GO:0005774 GO:GO:0005216 InterPro:IPR010920 SUPFAM:SSF50182 eggNOG:COG0668 HOGENOM:HBG316372 InterPro:IPR016688 PIRSF:PIRSF017209 ProtClustDB:CLSN2679546 EMBL:AC007260 EMBL:BX813849 IPI:IPI00538543 PIR:G96814 RefSeq:NP_177982.1 UniGene:At.34269 ProteinModelPortal:Q9SYM1 PRIDE:Q9SYM1 EnsemblPlants:AT1G78610.1 GeneID:844197 KEGG:ath:AT1G78610 TAIR:At1g78610 InParanoid:Q9SYM1 OMA:KQRITSY PhylomeDB:Q9SYM1 Genevestigator:Q9SYM1 Uniprot:Q9SYM1
Root	Isotig03666	53	0	6.599	2.10E-13	TAIR|locus:2202965 - symbol:MSL6 "AT1G78610" species:3702 "Arabidopsis thaliana" [GO:0016020 "membrane" evidence=ISS] [GO:0055085 "transmembrane transport" evidence=IEA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR006685 Pfam:PF00924 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005886 GO:GO:0009506 GO:GO:0005774 GO:GO:0005216 InterPro:IPR010920 SUPFAM:SSF50182 eggNOG:COG0668 HOGENOM:HBG316372 InterPro:IPR016688 PIRSF:PIRSF017209 ProtClustDB:CLSN2679546 EMBL:AC007260 EMBL:BX813849 IPI:IPI00538543 PIR:G96814 RefSeq:NP_177982.1 UniGene:At.34269 ProteinModelPortal:Q9SYM1 PRIDE:Q9SYM1 EnsemblPlants:AT1G78610.1 GeneID:844197 KEGG:ath:AT1G78610 TAIR:At1g78610 InParanoid:Q9SYM1 OMA:KQRITSY PhylomeDB:Q9SYM1 Genevestigator:Q9SYM1 Uniprot:Q9SYM1
Root	Isotig03667	46	0	6.395	6.55E-12	TAIR|locus:2202965 - symbol:MSL6 "AT1G78610" species:3702 "Arabidopsis thaliana" [GO:0016020 "membrane" evidence=ISS] [GO:0055085 "transmembrane transport" evidence=IEA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR006685 Pfam:PF00924 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005886 GO:GO:0009506 GO:GO:0005774 GO:GO:0005216 InterPro:IPR010920 SUPFAM:SSF50182 eggNOG:COG0668 HOGENOM:HBG316372 InterPro:IPR016688 PIRSF:PIRSF017209 ProtClustDB:CLSN2679546 EMBL:AC007260 EMBL:BX813849 IPI:IPI00538543 PIR:G96814 RefSeq:NP_177982.1 UniGene:At.34269 ProteinModelPortal:Q9SYM1 PRIDE:Q9SYM1 EnsemblPlants:AT1G78610.1 GeneID:844197 KEGG:ath:AT1G78610 TAIR:At1g78610 InParanoid:Q9SYM1 OMA:KQRITSY PhylomeDB:Q9SYM1 Genevestigator:Q9SYM1 Uniprot:Q9SYM1
Root	Isotig03668	45	0	6.363	1.08E-11	TAIR|locus:2202965 - symbol:MSL6 "AT1G78610" species:3702 "Arabidopsis thaliana" [GO:0016020 "membrane" evidence=ISS] [GO:0055085 "transmembrane transport" evidence=IEA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR006685 Pfam:PF00924 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005886 GO:GO:0009506 GO:GO:0005774 GO:GO:0005216 InterPro:IPR010920 SUPFAM:SSF50182 eggNOG:COG0668 HOGENOM:HBG316372 InterPro:IPR016688 PIRSF:PIRSF017209 ProtClustDB:CLSN2679546 EMBL:AC007260 EMBL:BX813849 IPI:IPI00538543 PIR:G96814 RefSeq:NP_177982.1 UniGene:At.34269

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						ProteinModelPortal:Q9SYM1 PRIDE:Q9SYM1 EnsemblPlants:AT1G78610.1 GeneID:844197 KEGG:ath:AT1G78610 TAIR:At1g78610 InParanoid:Q9SYM1 OMA:KQRITSY PhylomeDB:Q9SYM1 Genevestigator:Q9SYM1 Uniprot:Q9SYM1
Root	Isotig03673	36	105	-1.673	1.24E-10	TAIR|locus:2063354 - symbol:ACO3 "AT2G05710" species:3702 "Arabidopsis thaliana" [GO:0003994 "aconitate hydratase activity" evidence=ISS;IMP] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0006979 "response to oxidative stress" evidence=IMP;IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005829 "cytosol" evidence=RCA;NAS] [GO:0006101 "citrate metabolic process" evidence=IMP] [GO:0006102 "isocitrate metabolic process" evidence=IMP] [GO:0005524 "ATP binding" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR000573 InterPro:IPR001030 InterPro:IPR006249 InterPro:IPR015928 InterPro:IPR015931 InterPro:IPR015932 InterPro:IPR015934 InterPro:IPR015937 Pfam:PF00330 Pfam:PF00694 PRINTS:PR00415 Prosite:PS00450 GO:GO:0005829 GO:GO:0005739 GO:GO:0005524 GO:GO:0009737 GO:GO:0009570 GO:GO:0046686 GO:GO:0005774 GO:GO:0005618 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0006979 GO:GO:0005507 GO:GO:0009651 GO:GO:0051539 GO:GO:0006097 GO:GO:0006099 GO:GO:0006101 eggNOG:COG1048 HOGENOM:HBG289738 KO:K01681 ProtClustDB:PLN00070 GO:GO:0003994 GO:GO:0052632 GO:GO:0052633 GO:GO:0006102 InterPro:IPR018136 Gene3D:G3DSA:3.30.499.10 Gene3D:G3DSA:3.20.19.10 Gene3D:G3DSA:3.40.1060.10 PANTHER:PTHR11670 PANTHER:PTHR11670:SF1 SUPFAM:SSF52016 SUPFAM:SSF53732 TIGRFAMs:TIGR01341 PROSITE:PS01244 EMBL:AC007170 EMBL:AY136414 EMBL:BT008809 IPI:IPI00543590 PIR:B84471 RefSeq:NP_178634.2 UniGene:At.26759 UniGene:At.67769 HSSP:P21399 ProteinModelPortal:Q9SIB9 SMR:Q9SIB9 IntAct:Q9SIB9 STRING:Q9SIB9 ANU-2DPAGE:Q9SIB9 PRIDE:Q9SIB9 EnsemblPlants:AT2G05710.1 GeneID:815120 KEGG:ath:AT2G05710 GeneFarm:4276 TAIR:At2g05710 InParanoid:Q9SIB9 OMA:IKYLVQT PhylomeDB:Q9SIB9 Genevestigator:Q9SIB9 Uniprot:Q9SIB9
Root	Isotig03674	34	102	-1.714	1.12E-10	TAIR|locus:2063354 - symbol:ACO3 "AT2G05710" species:3702 "Arabidopsis thaliana" [GO:0003994 "aconitate hydratase activity" evidence=ISS;IMP] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0006979 "response to oxidative stress" evidence=IMP;IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005829 "cytosol" evidence=RCA;NAS] [GO:0006101 "citrate metabolic process" evidence=IMP] [GO:0006102 "isocitrate metabolic process" evidence=IMP] [GO:0005524 "ATP binding" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR000573 InterPro:IPR001030 InterPro:IPR006249 InterPro:IPR015928 InterPro:IPR015931 InterPro:IPR015932 InterPro:IPR015934 InterPro:IPR015937 Pfam:PF00330 Pfam:PF00694 PRINTS:PR00415 Prosite:PS00450 GO:GO:0005829 GO:GO:0005739 GO:GO:0005524 GO:GO:0009737 GO:GO:0009570 GO:GO:0046686 GO:GO:0005774 GO:GO:0005618 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0006979 GO:GO:0005507 GO:GO:0009651 GO:GO:0051539 GO:GO:0006097 GO:GO:0006099 GO:GO:0006101 eggNOG:COG1048 HOGENOM:HBG289738 KO:K01681 ProtClustDB:PLN00070 GO:GO:0003994 GO:GO:0052632 GO:GO:0052633 GO:GO:0006102 InterPro:IPR018136 Gene3D:G3DSA:3.30.499.10 Gene3D:G3DSA:3.20.19.10 Gene3D:G3DSA:3.40.1060.10 PANTHER:PTHR11670 PANTHER:PTHR11670:SF1 SUPFAM:SSF52016 SUPFAM:SSF53732 TIGRFAMs:TIGR01341 PROSITE:PS01244 EMBL:AC007170 EMBL:AY136414 EMBL:BT008809 IPI:IPI00543590 PIR:B84471 RefSeq:NP_178634.2 UniGene:At.26759 UniGene:At.67769 HSSP:P21399 ProteinModelPortal:Q9SIB9 SMR:Q9SIB9 IntAct:Q9SIB9 STRING:Q9SIB9 ANU-2DPAGE:Q9SIB9 PRIDE:Q9SIB9 EnsemblPlants:AT2G05710.1 GeneID:815120 KEGG:ath:AT2G05710 GeneFarm:4276 TAIR:At2g05710 InParanoid:Q9SIB9 OMA:IKYLVQT PhylomeDB:Q9SIB9 Genevestigator:Q9SIB9 Uniprot:Q9SIB9
Root	Isotig03675	35	101	-1.658	3.63E-10	TAIR|locus:2063354 - symbol:ACO3 "AT2G05710" species:3702 "Arabidopsis thaliana" [GO:0003994 "aconitate hydratase activity" evidence=ISS;IMP] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0006979 "response to oxidative stress" evidence=IMP;IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005829 "cytosol" evidence=RCA;NAS] [GO:0006101 "citrate metabolic process" evidence=IMP] [GO:0006102 "isocitrate metabolic

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						process" evidence=IMP] [GO:0005524 "ATP binding" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR000573 InterPro:IPR001030 InterPro:IPR006249 InterPro:IPR015928 InterPro:IPR015931 InterPro:IPR015932 InterPro:IPR015934 InterPro:IPR015937 Pfam:PF00330 Pfam:PF00694 PRINTS:PR00415 Prosite:PS00450 GO:GO:0005829 GO:GO:0005739 GO:GO:0005524 GO:GO:0009737 GO:GO:0009570 GO:GO:0046686 GO:GO:0005774 GO:GO:0005618 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0006979 GO:GO:0005507 GO:GO:0009651 GO:GO:0051539 GO:GO:0006097 GO:GO:0006099 GO:GO:0006101 eggNOG:COG1048 HOGENOM:HBG289738 KO:K01681 ProtClustDB:PLN00070 GO:GO:0003994 GO:GO:0052632 GO:GO:0052633 GO:GO:0006102 InterPro:IPR018136 Gene3D:G3DSA:3.30.499.10 Gene3D:G3DSA:3.20.19.10 Gene3D:G3DSA:3.40.1060.10 PANTHER:PTHR11670 PANTHER:PTHR11670:SF1 SUPFAM:SSF52016 SUPFAM:SSF53732 TIGRFAMs:TIGR01341 PROSITE:PS01244 EMBL:AC007170 EMBL:AY136414 EMBL:BT008809 IPI:IPI00543590 PIR:B84471 RefSeq:NP_178634.2 UniGene:At.26759 UniGene:At.67769 HSSP:P21399 ProteinModelPortal:Q9SIB9 SMR:Q9SIB9 IntAct:Q9SIB9 STRING:Q9SIB9 ANU-2DPAGE:Q9SIB9 PRIDE:Q9SIB9 EnsemblPlants:AT2G05710.1 GeneID:815120 KEGG:ath:AT2G05710 GeneFarm:4276 TAIR:At2g05710 InParanoid:Q9SIB9 OMA:IKYLVQT PhylomeDB:Q9SIB9 Genevestigator:Q9SIB9 Uniprot:Q9SIB9
Root	Isotig03676	33	98	-1.699	3.29E-10	TAIR|locus:2063354 - symbol:ACO3 "AT2G05710" species:3702 "Arabidopsis thaliana" [GO:0003994 "aconitate hydratase activity" evidence=ISS;IMP] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0006979 "response to oxidative stress" evidence=IMP;IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005829 "cytosol" evidence=RCA;NAS] [GO:0006101 "citrate metabolic process" evidence=IMP] [GO:0006102 "isocitrate metabolic process" evidence=IMP] [GO:0005524 "ATP binding" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR000573 InterPro:IPR001030 InterPro:IPR006249 InterPro:IPR015928 InterPro:IPR015931 InterPro:IPR015932 InterPro:IPR015934 InterPro:IPR015937 Pfam:PF00330 Pfam:PF00694 PRINTS:PR00415 Prosite:PS00450 GO:GO:0005829 GO:GO:0005739 GO:GO:0005524 GO:GO:0009737 GO:GO:0009570 GO:GO:0046686 GO:GO:0005774 GO:GO:0005618 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0006979 GO:GO:0005507 GO:GO:0009651 GO:GO:0051539 GO:GO:0006097 GO:GO:0006099 GO:GO:0006101 eggNOG:COG1048 HOGENOM:HBG289738 KO:K01681 ProtClustDB:PLN00070 GO:GO:0003994 GO:GO:0052632 GO:GO:0052633 GO:GO:0006102 InterPro:IPR018136 Gene3D:G3DSA:3.30.499.10 Gene3D:G3DSA:3.20.19.10 Gene3D:G3DSA:3.40.1060.10 PANTHER:PTHR11670 PANTHER:PTHR11670:SF1 SUPFAM:SSF52016 SUPFAM:SSF53732 TIGRFAMs:TIGR01341 PROSITE:PS01244 EMBL:AC007170 EMBL:AY136414 EMBL:BT008809 IPI:IPI00543590 PIR:B84471 RefSeq:NP_178634.2 UniGene:At.26759 UniGene:At.67769 HSSP:P21399 ProteinModelPortal:Q9SIB9 SMR:Q9SIB9 IntAct:Q9SIB9 STRING:Q9SIB9 ANU-2DPAGE:Q9SIB9 PRIDE:Q9SIB9 EnsemblPlants:AT2G05710.1 GeneID:815120 KEGG:ath:AT2G05710 GeneFarm:4276 TAIR:At2g05710 InParanoid:Q9SIB9 OMA:IKYLVQT PhylomeDB:Q9SIB9 Genevestigator:Q9SIB9 Uniprot:Q9SIB9
Root	Isotig03685	86	35	1.168	2.21E-05	TAIR|locus:2205235 - symbol:LOS1 "AT1G56070" species:3702 "Arabidopsis thaliana" [GO:0003746 "translation elongation factor activity" evidence=ISS] [GO:0008135 "translation factor activity, nucleic acid binding" evidence=ISS] [GO:0009409 "response to cold" evidence=IMP] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR000640 InterPro:IPR000795 InterPro:IPR004161 InterPro:IPR005225 InterPro:IPR005517 Pfam:PF00009 Pfam:PF00679 Pfam:PF03144 Pfam:PF03764 PRINTS:PR00315 PROSITE:PS00301 SMART:SM00838 SMART:SM00889 GO:GO:0005525 TIGRFAMs:TIGR00231 EMBL:CP002684 GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 GO:GO:0005774 GO:GO:0009507 GO:GO:0005730 GO:GO:0003924 GO:GO:0005507 GO:GO:0009409 GO:GO:0003746 InterPro:IPR020568 InterPro:IPR014721 Gene3D:G3DSA:3.30.230.10 SUPFAM:SSF54211 InterPro:IPR009000 SUPFAM:SSF50447 InterPro:IPR009022 Gene3D:G3DSA:3.30.70.240 SUPFAM:SSF54980 KO:K03234 OMA:GVMTQTE HSSP:P32324 EMBL:AF367331 EMBL:AY054461 EMBL:BT000661 EMBL:BT000722 EMBL:BT002714 IPI:IPI00517335

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						RefSeq:NP_849818.1 UniGene:At.47544 ProteinModelPortal:Q9ASR1 SMR:Q9ASR1 STRING:Q9ASR1 PRIDE:Q9ASR1 ProMEX:Q9ASR1 EnsemblPlants:AT1G56070.1 GeneID:842058 KEGG:ath:AT1G56070 TAIR:At1g56070 InParanoid:Q9ASR1 PhylomeDB:Q9ASR1 ProtClustDB:PLN00116 Genevestigator:Q9ASR1 Uniprot:Q9ASR1
Root	Isotig03686	94	37	1.216	4.65E-06	TAIR|locus:2205235 - symbol:LOS1 "AT1G56070" species:3702 "Arabidopsis thaliana" [GO:0003746 "translation elongation factor activity" evidence=ISS] [GO:0008135 "translation factor activity, nucleic acid binding" evidence=ISS] [GO:0009409 "response to cold" evidence=IMP] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR000640 InterPro:IPR000795 InterPro:IPR004161 InterPro:IPR005225 InterPro:IPR005517 Pfam:PF00009 Pfam:PF00679 Pfam:PF03144 Pfam:PF03764 PRINTS:PR00315 PROSITE:PS00301 SMART:SM00838 SMART:SM00889 GO:GO:0005525 TIGRFAMs:TIGR00231 EMBL:CP002684 GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 GO:GO:0005774 GO:GO:0009507 GO:GO:0005730 GO:GO:0003924 GO:GO:0005507 GO:GO:0009409 GO:GO:0003746 InterPro:IPR020568 InterPro:IPR014721 Gene3D:G3DSA:3.30.230.10 SUPFAM:SSF54211 InterPro:IPR009000 SUPFAM:SSF50447 InterPro:IPR009022 Gene3D:G3DSA:3.30.70.240 SUPFAM:SSF54980 KO:K03234 OMA:GVMTQTE HSSP:P32324 EMBL:AF367331 EMBL:AY054461 EMBL:BT000661 EMBL:BT000722 EMBL:BT002714 IPI:IPI00517335 RefSeq:NP_849818.1 UniGene:At.47544 ProteinModelPortal:Q9ASR1 SMR:Q9ASR1 STRING:Q9ASR1 PRIDE:Q9ASR1 ProMEX:Q9ASR1 EnsemblPlants:AT1G56070.1 GeneID:842058 KEGG:ath:AT1G56070 TAIR:At1g56070 InParanoid:Q9ASR1 PhylomeDB:Q9ASR1 ProtClustDB:PLN00116 Genevestigator:Q9ASR1 Uniprot:Q9ASR1
Root	Isotig03693	13	36	-1.598	0.000266476	TAIR|locus:2061838 - symbol:KT2 "AT2G40540" species:3702 "Arabidopsis thaliana" [GO:0015079 "potassium ion transmembrane transporter activity" evidence=ISS;TAS] [GO:0006813 "potassium ion transport" evidence=IC] [GO:0016020 "membrane" evidence=NAS] [GO:0005886 "plasma membrane" evidence=IDA] InterPro:IPR003855 Pfam:PF02705 GO:GO:0016021 GO:GO:0005886 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0015079 EMBL:AC002336 eggNOG:COG3158 KO:K03549 TIGRFAMs:TIGR00794 HOGENOM:HBG606427 EMBL:AF012657 EMBL:BT004049 EMBL:BT005048 IPI:IPI00518306 PIR:G84830 RefSeq:NP_001078032.1 RefSeq:NP_565936.1 UniGene:At.10816 ProteinModelPortal:O22881 PRIDE:O22881 EnsemblPlants:AT2G40540.1 EnsemblPlants:AT2G40540.2 GeneID:818649 KEGG:ath:AT2G40540 GeneFarm:2394 TAIR:At2g40540 InParanoid:O22881 OMA:FKFDIMA PhylomeDB:O22881 ProtClustDB:CLSN2688842 ArrayExpress:O22881 Genevestigator:O22881 GermOnline:AT2G40540 Uniprot:O22881
Root	Isotig03694	13	36	-1.598	0.000266476	TAIR|locus:2061838 - symbol:KT2 "AT2G40540" species:3702 "Arabidopsis thaliana" [GO:0015079 "potassium ion transmembrane transporter activity" evidence=ISS;TAS] [GO:0006813 "potassium ion transport" evidence=IC] [GO:0016020 "membrane" evidence=NAS] [GO:0005886 "plasma membrane" evidence=IDA] InterPro:IPR003855 Pfam:PF02705 GO:GO:0016021 GO:GO:0005886 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0015079 EMBL:AC002336 eggNOG:COG3158 KO:K03549 TIGRFAMs:TIGR00794 HOGENOM:HBG606427 EMBL:AF012657 EMBL:BT004049 EMBL:BT005048 IPI:IPI00518306 PIR:G84830 RefSeq:NP_001078032.1 RefSeq:NP_565936.1 UniGene:At.10816 ProteinModelPortal:O22881 PRIDE:O22881 EnsemblPlants:AT2G40540.1 EnsemblPlants:AT2G40540.2 GeneID:818649 KEGG:ath:AT2G40540 GeneFarm:2394 TAIR:At2g40540 InParanoid:O22881 OMA:FKFDIMA PhylomeDB:O22881 ProtClustDB:CLSN2688842 ArrayExpress:O22881 Genevestigator:O22881 GermOnline:AT2G40540 Uniprot:O22881
Root	Isotig03705	42	0	6.263	4.87E-11	TAIR|locus:2125314 - symbol:PLDDELTA "AT4G35790" species:3702 "Arabidopsis thaliana" [GO:0004630 "phospholipase D activity" evidence=ISS;IMP;IDA] [GO:0046473 "phosphatidic acid metabolic process" evidence=IMP] [GO:0012501 "programmed cell death" evidence=IMP] [GO:0009409 "response to cold" evidence=IEP;IMP] [GO:0005773 "vacuole" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000008 InterPro:IPR001736 InterPro:IPR008973 InterPro:IPR011402 Pfam:PF00168 Pfam:PF00614 PIRSF:PIRSF036470 PROSITE:PS50035 SMART:SM00155 SMART:SM00239 GO:GO:0005886 GO:GO:0009506 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005773 GO:GO:0005509 GO:GO:0046470 GO:GO:0016042

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0009409 InterPro:IPR018029 SUPFAM:SSF49562 PROSITE:PS50004 EMBL:AL031986 EMBL:AL161588 GO:GO:0012501 eggNOG:COG1502 InterPro:IPR015679 PANTHER:PTHR18896 GO:GO:0070290 GO:GO:0004630 GO:GO:0046473 KO:K01115 HOGENOM:HBG748198 InterPro:IPR024632 Pfam:PF12357 EMBL:AF322228 EMBL:AF274239 EMBL:AF306345 EMBL:AB031047 EMBL:AF424632 EMBL:AK227213 IPI:IPI00520107 IPI:IPI00541650 RefSeq:NP_567989.1 RefSeq:NP_849501.1 UniGene:At.22959 ProteinModelPortal:Q9C5Y0 SMR:Q9C5Y0 STRING:Q9C5Y0 PRIDE:Q9C5Y0 EnsemblPlants:AT4G35790.1 GeneID:829733 KEGG:ath:AT4G35790 TAIR:At4g35790 InParanoid:Q9C5Y0 OMA:GRISWIL PhylomeDB:Q9C5Y0 ProtClustDB:PLN03008 ArrayExpress:Q9C5Y0 Genevestigator:Q9C5Y0 Uniprot:Q9C5Y0
Root	Isotig03706	42	0	6.263	4.87E-11	TAIR|locus:2125314 - symbol:PLDDELTA "AT4G35790" species:3702 "Arabidopsis thaliana" [GO:0004630 "phospholipase D activity" evidence=ISS;IMP;IDA] [GO:0046473 "phosphatidic acid metabolic process" evidence=IMP] [GO:0012501 "programmed cell death" evidence=IMP] [GO:0009409 "response to cold" evidence=IEP;IMP] [GO:0005773 "vacuole" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000008 InterPro:IPR001736 InterPro:IPR008973 InterPro:IPR011402 Pfam:PF00168 Pfam:PF00614 PIRSF:PIRSF036470 PROSITE:PS50035 SMART:SM00155 SMART:SM00239 GO:GO:0005886 GO:GO:0009506 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005773 GO:GO:0005509 GO:GO:0046470 GO:GO:0016042 GO:GO:0009409 InterPro:IPR018029 SUPFAM:SSF49562 PROSITE:PS50004 EMBL:AL031986 EMBL:AL161588 GO:GO:0012501 eggNOG:COG1502 InterPro:IPR015679 PANTHER:PTHR18896 GO:GO:0070290 GO:GO:0004630 GO:GO:0046473 KO:K01115 HOGENOM:HBG748198 InterPro:IPR024632 Pfam:PF12357 EMBL:AF322228 EMBL:AF274239 EMBL:AF306345 EMBL:AB031047 EMBL:AF424632 EMBL:AK227213 IPI:IPI00520107 IPI:IPI00541650 RefSeq:NP_567989.1 RefSeq:NP_849501.1 UniGene:At.22959 ProteinModelPortal:Q9C5Y0 SMR:Q9C5Y0 STRING:Q9C5Y0 PRIDE:Q9C5Y0 EnsemblPlants:AT4G35790.1 GeneID:829733 KEGG:ath:AT4G35790 TAIR:At4g35790 InParanoid:Q9C5Y0 OMA:GRISWIL PhylomeDB:Q9C5Y0 ProtClustDB:PLN03008 ArrayExpress:Q9C5Y0 Genevestigator:Q9C5Y0 Uniprot:Q9C5Y0
Root	Isotig03707	42	0	6.263	4.87E-11	TAIR|locus:2125314 - symbol:PLDDELTA "AT4G35790" species:3702 "Arabidopsis thaliana" [GO:0004630 "phospholipase D activity" evidence=ISS;IMP;IDA] [GO:0046473 "phosphatidic acid metabolic process" evidence=IMP] [GO:0012501 "programmed cell death" evidence=IMP] [GO:0009409 "response to cold" evidence=IEP;IMP] [GO:0005773 "vacuole" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000008 InterPro:IPR001736 InterPro:IPR008973 InterPro:IPR011402 Pfam:PF00168 Pfam:PF00614 PIRSF:PIRSF036470 PROSITE:PS50035 SMART:SM00155 SMART:SM00239 GO:GO:0005886 GO:GO:0009506 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005773 GO:GO:0005509 GO:GO:0046470 GO:GO:0016042 GO:GO:0009409 InterPro:IPR018029 SUPFAM:SSF49562 PROSITE:PS50004 EMBL:AL031986 EMBL:AL161588 GO:GO:0012501 eggNOG:COG1502 InterPro:IPR015679 PANTHER:PTHR18896 GO:GO:0070290 GO:GO:0004630 GO:GO:0046473 KO:K01115 HOGENOM:HBG748198 InterPro:IPR024632 Pfam:PF12357 EMBL:AF322228 EMBL:AF274239 EMBL:AF306345 EMBL:AB031047 EMBL:AF424632 EMBL:AK227213 IPI:IPI00520107 IPI:IPI00541650 RefSeq:NP_567989.1 RefSeq:NP_849501.1 UniGene:At.22959 ProteinModelPortal:Q9C5Y0 SMR:Q9C5Y0 STRING:Q9C5Y0 PRIDE:Q9C5Y0 EnsemblPlants:AT4G35790.1 GeneID:829733 KEGG:ath:AT4G35790 TAIR:At4g35790 InParanoid:Q9C5Y0 OMA:GRISWIL PhylomeDB:Q9C5Y0 ProtClustDB:PLN03008 ArrayExpress:Q9C5Y0 Genevestigator:Q9C5Y0 Uniprot:Q9C5Y0
Root	Isotig03708	42	0	6.263	4.87E-11	TAIR|locus:2125314 - symbol:PLDDELTA "AT4G35790" species:3702 "Arabidopsis thaliana" [GO:0004630 "phospholipase D activity" evidence=ISS;IMP;IDA] [GO:0046473 "phosphatidic acid metabolic process" evidence=IMP] [GO:0012501 "programmed cell death" evidence=IMP] [GO:0009409 "response to cold" evidence=IEP;IMP] [GO:0005773 "vacuole" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000008 InterPro:IPR001736 InterPro:IPR008973 InterPro:IPR011402 Pfam:PF00168 Pfam:PF00614 PIRSF:PIRSF036470 PROSITE:PS50035 SMART:SM00155 SMART:SM00239 GO:GO:0005886 GO:GO:0009506 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005773 GO:GO:0005509 GO:GO:0046470 GO:GO:0016042 GO:GO:0009409 InterPro:IPR018029 SUPFAM:SSF49562 PROSITE:PS50004 EMBL:AL031986 EMBL:AL161588 GO:GO:0012501 eggNOG:COG1502 InterPro:IPR015679 PANTHER:PTHR18896 GO:GO:0070290 GO:GO:0004630 GO:GO:0046473 KO:K01115 HOGENOM:HBG748198 InterPro:IPR024632 Pfam:PF12357 EMBL:AF322228 EMBL:AF274239 EMBL:AF306345 EMBL:AB031047 EMBL:AF424632 EMBL:AK227213

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						IPI:IPI00520107 IPI:IPI00541650 RefSeq:NP_567989.1 RefSeq:NP_849501.1 UniGene:At.22959 ProteinModelPortal:Q9C5Y0 SMR:Q9C5Y0 STRING:Q9C5Y0 PRIDE:Q9C5Y0 EnsemblPlants:AT4G35790.1 GeneID:829733 KEGG:ath:AT4G35790 TAIR:At4g35790 InParanoid:Q9C5Y0 OMA:GRISWIL PhylomeDB:Q9C5Y0 ProtClustDB:PLN03008 ArrayExpress:Q9C5Y0 Genevestigator:Q9C5Y0 Uniprot:Q9C5Y0
Root	Isotig03713	0	63	-7.106	1.51E-16	TAIR|locus:2087837 - symbol:LOX5 species:3702 "Arabidopsis thaliana" [GO:0005506 "iron ion binding" evidence=IEA] [GO:0016165 "lipoxygenase activity" evidence=IEA;ISS;IDA] [GO:0016702 "oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen" evidence=IEA] [GO:0046872 "metal ion binding" evidence=IEA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0010386 "lateral root primordium development" evidence=IMP] [GO:0048364 "root development" evidence=IMP] InterPro:IPR000907 InterPro:IPR001024 InterPro:IPR001246 InterPro:IPR013819 InterPro:IPR020833 InterPro:IPR020834 Pfam:PF00305 Pfam:PF01477 PRINTS:PR00087 PRINTS:PR00468 PROSITE:PS00081 PROSITE:PS00711 PROSITE:PS50095 PROSITE:PS51393 SMART:SM00308 GO:GO:0009507 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005506 GO:GO:0031408 EMBL:AB022215 GO:GO:0010386 InterPro:IPR008976 Gene3D:G3DSA:2.60.60.20 SUPFAM:SSF49723 GO:GO:0016165 PANTHER:PTHR11771 SUPFAM:SSF48484 eggNOG:NOG69653 KO:K15718 ProtClustDB:PLN02337 HSSP:P08170 EMBL:AJ302043 IPI:IPI00543707 RefSeq:NP_188879.2 UniGene:At.37889 ProteinModelPortal:Q9LUW0 SMR:Q9LUW0 STRING:Q9LUW0 PRIDE:Q9LUW0 EnsemblPlants:AT3G22400.1 GeneID:821808 KEGG:ath:AT3G22400 TAIR:At3g22400 InParanoid:Q9LUW0 OMA:FDWDESM PhylomeDB:Q9LUW0 Genevestigator:Q9LUW0 Uniprot:Q9LUW0
Root	Isotig03714	0	59	-7.012	1.12E-15	TAIR|locus:2087837 - symbol:LOX5 species:3702 "Arabidopsis thaliana" [GO:0005506 "iron ion binding" evidence=IEA] [GO:0016165 "lipoxygenase activity" evidence=IEA;ISS;IDA] [GO:0016702 "oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen" evidence=IEA] [GO:0046872 "metal ion binding" evidence=IEA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0010386 "lateral root primordium development" evidence=IMP] [GO:0048364 "root development" evidence=IMP] InterPro:IPR000907 InterPro:IPR001024 InterPro:IPR001246 InterPro:IPR013819 InterPro:IPR020833 InterPro:IPR020834 Pfam:PF00305 Pfam:PF01477 PRINTS:PR00087 PRINTS:PR00468 PROSITE:PS00081 PROSITE:PS00711 PROSITE:PS50095 PROSITE:PS51393 SMART:SM00308 GO:GO:0009507 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005506 GO:GO:0031408 EMBL:AB022215 GO:GO:0010386 InterPro:IPR008976 Gene3D:G3DSA:2.60.60.20 SUPFAM:SSF49723 GO:GO:0016165 PANTHER:PTHR11771 SUPFAM:SSF48484 eggNOG:NOG69653 KO:K15718 ProtClustDB:PLN02337 HSSP:P08170 EMBL:AJ302043 IPI:IPI00543707 RefSeq:NP_188879.2 UniGene:At.37889 ProteinModelPortal:Q9LUW0 SMR:Q9LUW0 STRING:Q9LUW0 PRIDE:Q9LUW0 EnsemblPlants:AT3G22400.1 GeneID:821808 KEGG:ath:AT3G22400 TAIR:At3g22400 InParanoid:Q9LUW0 OMA:FDWDESM PhylomeDB:Q9LUW0 Genevestigator:Q9LUW0 Uniprot:Q9LUW0
Root	Isotig03715	0	50	-6.773	1.11E-13	TAIR|locus:2087837 - symbol:LOX5 species:3702 "Arabidopsis thaliana" [GO:0005506 "iron ion binding" evidence=IEA] [GO:0016165 "lipoxygenase activity" evidence=IEA;ISS;IDA] [GO:0016702 "oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen" evidence=IEA] [GO:0046872 "metal ion binding" evidence=IEA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0010386 "lateral root primordium development" evidence=IMP] [GO:0048364 "root development" evidence=IMP] InterPro:IPR000907 InterPro:IPR001024 InterPro:IPR001246 InterPro:IPR013819 InterPro:IPR020833 InterPro:IPR020834 Pfam:PF00305 Pfam:PF01477 PRINTS:PR00087 PRINTS:PR00468 PROSITE:PS00081 PROSITE:PS00711 PROSITE:PS50095 PROSITE:PS51393 SMART:SM00308 GO:GO:0009507 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005506 GO:GO:0031408 EMBL:AB022215 GO:GO:0010386 InterPro:IPR008976 Gene3D:G3DSA:2.60.60.20 SUPFAM:SSF49723 GO:GO:0016165 PANTHER:PTHR11771 SUPFAM:SSF48484 eggNOG:NOG69653 KO:K15718 ProtClustDB:PLN02337 HSSP:P08170 EMBL:AJ302043 IPI:IPI00543707 RefSeq:NP_188879.2 UniGene:At.37889 ProteinModelPortal:Q9LUW0 SMR:Q9LUW0 STRING:Q9LUW0 PRIDE:Q9LUW0 EnsemblPlants:AT3G22400.1 GeneID:821808 KEGG:ath:AT3G22400 TAIR:At3g22400 InParanoid:Q9LUW0 OMA:FDWDESM PhylomeDB:Q9LUW0 Genevestigator:Q9LUW0 Uniprot:Q9LUW0
Root	Isotig03716	0	46	-6.653	9.06E-13	TAIR|locus:2087837 - symbol:LOX5 species:3702 "Arabidopsis thaliana" [GO:0005506 "iron ion binding" evidence=IEA] [GO:0016165 "lipoxygenase activity" evidence=IEA;ISS;IDA] [GO:0016702 "oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen"

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						evidence=IEA] [GO:0046872 "metal ion binding" evidence=IEA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0010386 "lateral root primordium development" evidence=IMP] [GO:0048364 "root development" evidence=IMP] InterPro:IPR000907 InterPro:IPR001024 InterPro:IPR001246 InterPro:IPR013819 InterPro:IPR020833 InterPro:IPR020834 Pfam:PF00305 Pfam:PF01477 PRINTS:PR00087 PRINTS:PR00468 PROSITE:PS00081 PROSITE:PS00711 PROSITE:PS50095 PROSITE:PS51393 SMART:SM00308 GO:GO:0009507 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005506 GO:GO:0031408 EMBL:AB022215 GO:GO:0010386 InterPro:IPR008976 Gene3D:G3DSA:2.60.60.20 SUPFAM:SSF49723 GO:GO:0016165 PANTHER:PTHR11771 SUPFAM:SSF48484 eggNOG:NOG69653 KO:K15718 ProtClustDB:PLN02337 HSSP:P08170 EMBL:AJ302043 IPI:IPI00543707 RefSeq:NP_188879.2 UniGene:At.37889 ProteinModelPortal:Q9LUW0 SMR:Q9LUW0 STRING:Q9LUW0 PRIDE:Q9LUW0 EnsemblPlants:AT3G22400.1 GeneID:821808 KEGG:ath:AT3G22400 TAIR:At3g22400 InParanoid:Q9LUW0 OMA:FDWDESM PhylomeDB:Q9LUW0 Genevestigator:Q9LUW0 Uniprot:Q9LUW0
Root	Isotig03730	35	72	-1.170	4.82E-05	TAIR|locus:2175118 - symbol:AT5G60390 "AT5G60390" species:3702 "Arabidopsis thaliana" [GO:0003746 "translation elongation factor activity" evidence=ISS] [GO:0006414 "translational elongation" evidence=IEA] [GO:0005516 "calmodulin binding" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] PROSITE:PS00301 EMBL:CP002684 EMBL:U63815 EMBL:AC026875 EMBL:X16430 EMBL:AY039583 EMBL:BT000595 IPI:IPI00548618 PIR:S06724 UniGene:At.69737 UniGene:At.74830 EnsemblPlants:AT1G07940.1 EnsemblPlants:AT1G07940.2 TAIR:At1g07940 OMA:FLKAGDA GermOnline:AT1G07940 Uniprot:P0DH99
Root	Isotig03741	5	36	-2.977	8.93E-08	TAIR|locus:2032950 - symbol:TLP10 "AT1G25280" species:3702 "Arabidopsis thaliana" [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0008081 "phosphoric diester hydrolase activity" evidence=ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=TAS] [GO:0005886 "plasma membrane" evidence=IDA] InterPro:IPR001810 Pfam:PF00646 PROSITE:PS50181 INTERPRO:IPR000007 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005886 GO:GO:0005634 GO:GO:0006355 EMBL:AC079374 SUPFAM:SSF54518 EMBL:AF487271 EMBL:AY140459 EMBL:AY140460 EMBL:AY140461 EMBL:AY140462 EMBL:AY140463 EMBL:AY140464 EMBL:AY140465 EMBL:AY140466 EMBL:AY140467 EMBL:AY140468 EMBL:AY140469 EMBL:AK317199 EMBL:BT001997 EMBL:BT006290 IPI:IPI00539910 PIR:E86382 RefSeq:NP_001117353.1 RefSeq:NP_173899.1 RefSeq:NP_973909.1 UniGene:At.23717 HSSP:O00294 ProteinModelPortal:Q9FRH7 SMR:Q9FRH7 IntAct:Q9FRH7 STRING:Q9FRH7 PRIDE:Q9FRH7 EnsemblPlants:AT1G25280.1 GeneID:839112 KEGG:ath:AT1G25280 TAIR:At1g25280 eggNOG:NOG286778 HOGENOM:HBG607533 InParanoid:Q9FRH7 OMA:HSSACEL PhylomeDB:Q9FRH7 ProtClustDB:CLSN2681282 ArrayExpress:Q8H0W5 Genevestigator:Q9FRH7 InterPro:IPR018066 Gene3D:G3DSA:3.20.90.10 Pfam:PF01167 PRINTS:PR01573 PROSITE:PS01200 PROSITE:PS01201 Uniprot:Q9FRH7
Root	Isotig03742	4	37	-3.338	1.13E-08	TAIR|locus:2032950 - symbol:TLP10 "AT1G25280" species:3702 "Arabidopsis thaliana" [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0008081 "phosphoric diester hydrolase activity" evidence=ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=TAS] [GO:0005886 "plasma membrane" evidence=IDA] InterPro:IPR001810 Pfam:PF00646 PROSITE:PS50181 INTERPRO:IPR000007 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005886 GO:GO:0005634 GO:GO:0006355 EMBL:AC079374 SUPFAM:SSF54518 EMBL:AF487271 EMBL:AY140459 EMBL:AY140460 EMBL:AY140461 EMBL:AY140462 EMBL:AY140463 EMBL:AY140464 EMBL:AY140465 EMBL:AY140466 EMBL:AY140467 EMBL:AY140468 EMBL:AY140469 EMBL:AK317199 EMBL:BT001997 EMBL:BT006290 IPI:IPI00539910 PIR:E86382 RefSeq:NP_001117353.1 RefSeq:NP_173899.1 RefSeq:NP_973909.1 UniGene:At.23717 HSSP:O00294 ProteinModelPortal:Q9FRH7 SMR:Q9FRH7 IntAct:Q9FRH7 STRING:Q9FRH7 PRIDE:Q9FRH7 EnsemblPlants:AT1G25280.1 GeneID:839112 KEGG:ath:AT1G25280 TAIR:At1g25280 eggNOG:NOG286778 HOGENOM:HBG607533 InParanoid:Q9FRH7 OMA:HSSACEL PhylomeDB:Q9FRH7 ProtClustDB:CLSN2681282 ArrayExpress:Q8H0W5 Genevestigator:Q9FRH7 InterPro:IPR018066 Gene3D:G3DSA:3.20.90.10 Pfam:PF01167 PRINTS:PR01573 PROSITE:PS01200 PROSITE:PS01201 Uniprot:Q9FRH7
Root	Isotig03743	5	36	-2.977	8.93E-08	TAIR|locus:2032950 - symbol:TLP10 "AT1G25280" species:3702 "Arabidopsis thaliana" [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0008081 "phosphoric diester hydrolase activity" evidence=ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=TAS] [GO:0005886 "plasma

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						membrane" evidence=IDA] InterPro:IPR001810 Pfam:PF00646 PROSITE:PS50181 INTERPRO:IPR000007 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005886 GO:GO:0005634 GO:GO:0006355 EMBL:AC079374 SUPFAM:SSF54518 EMBL:AF487271 EMBL:AY140459 EMBL:AY140460 EMBL:AY140461 EMBL:AY140462 EMBL:AY140463 EMBL:AY140464 EMBL:AY140465 EMBL:AY140466 EMBL:AY140467 EMBL:AY140468 EMBL:AY140469 EMBL:AK317199 EMBL:BT001997 EMBL:BT006290 IPI:IPI00539910 PIR:E86382 RefSeq:NP_001117353.1 RefSeq:NP_173899.1 RefSeq:NP_973909.1 UniGene:At.23717 HSSP:O00294 ProteinModelPortal:Q9FRH7 SMR:Q9FRH7 IntAct:Q9FRH7 STRING:Q9FRH7 PRIDE:Q9FRH7 EnsemblPlants:AT1G25280.1 GeneID:839112 KEGG:ath:AT1G25280 TAIR:At1g25280 eggNOG:NOG286778 HOGENOM:HBG607533 InParanoid:Q9FRH7 OMA:HSSACEL PhylomeDB:Q9FRH7 ProtClustDB:CLSN2681282 ArrayExpress:Q8H0W5 Genevestigator:Q9FRH7 InterPro:IPR018066 Gene3D:G3DSA:3.20.90.10 Pfam:PF01167 PRINTS:PR01573 PROSITE:PS01200 PROSITE:PS01201 Uniprot:Q9FRH7
Root	Isotig03744	4	37	-3.338	1.13E-08	TAIR|locus:2032950 - symbol:TLP10 "AT1G25280" species:3702 "Arabidopsis thaliana" [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0008081 "phosphoric diester hydrolase activity" evidence=ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=TAS] [GO:0005886 "plasma membrane" evidence=IDA] InterPro:IPR001810 Pfam:PF00646 PROSITE:PS50181 INTERPRO:IPR000007 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005886 GO:GO:0005634 GO:GO:0006355 EMBL:AC079374 SUPFAM:SSF54518 EMBL:AF487271 EMBL:AY140459 EMBL:AY140460 EMBL:AY140461 EMBL:AY140462 EMBL:AY140463 EMBL:AY140464 EMBL:AY140465 EMBL:AY140466 EMBL:AY140467 EMBL:AY140468 EMBL:AY140469 EMBL:AK317199 EMBL:BT001997 EMBL:BT006290 IPI:IPI00539910 PIR:E86382 RefSeq:NP_001117353.1 RefSeq:NP_173899.1 RefSeq:NP_973909.1 UniGene:At.23717 HSSP:O00294 ProteinModelPortal:Q9FRH7 SMR:Q9FRH7 IntAct:Q9FRH7 STRING:Q9FRH7 PRIDE:Q9FRH7 EnsemblPlants:AT1G25280.1 GeneID:839112 KEGG:ath:AT1G25280 TAIR:At1g25280 eggNOG:NOG286778 HOGENOM:HBG607533 InParanoid:Q9FRH7 OMA:HSSACEL PhylomeDB:Q9FRH7 ProtClustDB:CLSN2681282 ArrayExpress:Q8H0W5 Genevestigator:Q9FRH7 InterPro:IPR018066 Gene3D:G3DSA:3.20.90.10 Pfam:PF01167 PRINTS:PR01573 PROSITE:PS01200 PROSITE:PS01201 Uniprot:Q9FRH7
Root	Isotig03751	25	6	1.930	0.000926157	TAIR|locus:2044807 - symbol:AT2G35040 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0003937 "IMP cyclohydrolase activity" evidence=IEA;ISS] [GO:0004643 "phosphoribosylaminoimidazolecarboxamide formyltransferase activity" evidence=IEA;ISS] [GO:0006164 "purine nucleotide biosynthetic process" evidence=ISS] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0010319 "stromule" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] HAMAP:MF_00139 InterPro:IPR002695 InterPro:IPR016193 Pfam:PF01808 PIRSF:PIRSF000414 SMART:SM00798 GO:GO:0009570 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0006164 GO:GO:0010319 GO:GO:0009409 SUPFAM:SSF53927 InterPro:IPR011607 Gene3D:G3DSA:3.40.50.1380 Pfam:PF02142 SMART:SM00851 SUPFAM:SSF52335 KO:K00602 GO:GO:0003937 GO:GO:0004643 InterPro:IPR024051 Gene3D:G3DSA:3.40.140.20 PANTHER:PTHR11692 TIGRFAMs:TIGR00355 OMA:FTGTRHF HSSP:P31335 UniGene:At.66385 EMBL:AY091122 EMBL:AY133727 IPI:IPI00542590 RefSeq:NP_850240.1 UniGene:At.43666 ProteinModelPortal:Q8RWT5 SMR:Q8RWT5 STRING:Q8RWT5 PRIDE:Q8RWT5 ProMEX:Q8RWT5 EnsemblPlants:AT2G35040.1 GeneID:818069 KEGG:ath:AT2G35040 TAIR:At2g35040 InParanoid:Q8RWT5 PhylomeDB:Q8RWT5 ProtClustDB:PLN02891 Genevestigator:Q8RWT5 Uniprot:Q8RWT5
Root	Isotig03752	25	6	1.930	0.000926157	TAIR|locus:2044807 - symbol:AT2G35040 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0003937 "IMP cyclohydrolase activity" evidence=IEA;ISS] [GO:0004643 "phosphoribosylaminoimidazolecarboxamide formyltransferase activity" evidence=IEA;ISS] [GO:0006164 "purine nucleotide biosynthetic process" evidence=ISS] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0010319 "stromule" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] HAMAP:MF_00139 InterPro:IPR002695 InterPro:IPR016193 Pfam:PF01808 PIRSF:PIRSF000414 SMART:SM00798 GO:GO:0009570 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0006164 GO:GO:0010319 GO:GO:0009409 SUPFAM:SSF53927 InterPro:IPR011607 Gene3D:G3DSA:3.40.50.1380 Pfam:PF02142 SMART:SM00851 SUPFAM:SSF52335 KO:K00602 GO:GO:0003937 GO:GO:0004643 InterPro:IPR024051 Gene3D:G3DSA:3.40.140.20 PANTHER:PTHR11692 TIGRFAMs:TIGR00355 OMA:FTGTRHF HSSP:P31335 UniGene:At.66385 EMBL:AY091122 EMBL:AY133727 IPI:IPI00542590 RefSeq:NP_850240.1 UniGene:At.43666 ProteinModelPortal:Q8RWT5 SMR:Q8RWT5 STRING:Q8RWT5 PRIDE:Q8RWT5

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						ProMEX:Q8RWT5 EnsemblPlants:AT2G35040.1 GeneID:818069 KEGG:ath:AT2G35040 TAIR:At2g35040 InParanoid:Q8RWT5 PhylomeDB:Q8RWT5 ProtClustDB:PLN02891 Genevestigator:Q8RWT5 Uniprot:Q8RWT5
Root	Isotig03786	4	23	-2.653	5.61E-05	TAIR|locus:2202290 - symbol:TPS7 "AT1G06410" species:3702 "Arabidopsis thaliana" [GO:0004805 "trehalose-phosphatase activity" evidence=IGI;ISS;IMP] [GO:0005992 "trehalose biosynthetic process" evidence=IEA;ISS] [GO:0008152 "metabolic process" evidence=IEA] [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0003825 "alpha,alpha-trehalose-phosphate synthase (UDP-forming) activity" evidence=IGI;IMP] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001830 InterPro:IPR003337 InterPro:IPR006379 Pfam:PF00982 Pfam:PF02358 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 InterPro:IPR023214 Gene3D:G3DSA:3.40.50.1000 SUPFAM:SSF56784 EMBL:AC068143 GO:GO:0005992 TIGRFAMs:TIGR01484 CAZy:GT20 eggNOG:COG0380 HOGENOM:HBG559076 KO:K00697 GO:GO:0003825 HSSP:P31677 KO:K01087 TIGRFAMs:TIGR00685 EMBL:AK228947 IPI:IPI00530498 PIR:A86200 RefSeq:NP_172129.1 UniGene:At.43841 ProteinModelPortal:Q9LMI0 SMR:Q9LMI0 STRING:Q9LMI0 PRIDE:Q9LMI0 EnsemblPlants:AT1G06410.1 GeneID:837152 KEGG:ath:AT1G06410 TAIR:At1g06410 InParanoid:Q9LMI0 OMA:CKDHFRR PhylomeDB:Q9LMI0 ProtClustDB:CLSN2682317 Genevestigator:Q9LMI0 Uniprot:Q9LMI0
Root	Isotig03788	2	16	-3.129	0.000262867	TAIR|locus:2202290 - symbol:TPS7 "AT1G06410" species:3702 "Arabidopsis thaliana" [GO:0004805 "trehalose-phosphatase activity" evidence=IGI;ISS;IMP] [GO:0005992 "trehalose biosynthetic process" evidence=IEA;ISS] [GO:0008152 "metabolic process" evidence=IEA] [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0003825 "alpha,alpha-trehalose-phosphate synthase (UDP-forming) activity" evidence=IGI;IMP] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001830 InterPro:IPR003337 InterPro:IPR006379 Pfam:PF00982 Pfam:PF02358 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 InterPro:IPR023214 Gene3D:G3DSA:3.40.50.1000 SUPFAM:SSF56784 EMBL:AC068143 GO:GO:0005992 TIGRFAMs:TIGR01484 CAZy:GT20 eggNOG:COG0380 HOGENOM:HBG559076 KO:K00697 GO:GO:0003825 HSSP:P31677 KO:K01087 TIGRFAMs:TIGR00685 EMBL:AK228947 IPI:IPI00530498 PIR:A86200 RefSeq:NP_172129.1 UniGene:At.43841 ProteinModelPortal:Q9LMI0 SMR:Q9LMI0 STRING:Q9LMI0 PRIDE:Q9LMI0 EnsemblPlants:AT1G06410.1 GeneID:837152 KEGG:ath:AT1G06410 TAIR:At1g06410 InParanoid:Q9LMI0 OMA:CKDHFRR PhylomeDB:Q9LMI0 ProtClustDB:CLSN2682317 Genevestigator:Q9LMI0 Uniprot:Q9LMI0
Root	Isotig03821	31	5	2.503	1.48E-05	TAIR|locus:2206330 - symbol:GTB1 "global transcription factor group B1" species:3702 "Arabidopsis thaliana" [GO:0003723 "RNA binding" evidence=IEA] [GO:0006333 "chromatin assembly or disassembly" evidence=ISS] [GO:0006352 "transcription initiation, DNA-dependent" evidence=ISS] [GO:0016788 "hydrolase activity, acting on ester bonds" evidence=IEA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000980 InterPro:IPR003029 InterPro:IPR006641 InterPro:IPR017072 PIRSF:PIRSF036947 PROSITE:PS50126 SMART:SM00252 SMART:SM00732 EMBL:CP002684 GO:GO:0005829 GO:GO:0009506 Gene3D:G3DSA:3.30.505.10 GO:GO:0006357 GO:GO:0003746 GO:GO:0016788 InterPro:IPR012340 Gene3D:G3DSA:2.40.50.140 InterPro:IPR016027 SUPFAM:SSF50249 GO:GO:0006139 InterPro:IPR022967 SMART:SM00316 EMBL:AC010795 GO:GO:0032784 eggNOG:COG2183 KO:K11292 InterPro:IPR023323 InterPro:IPR023097 Gene3D:G3DSA:1.10.150.310 Gene3D:G3DSA:1.10.3500.10 PANTHER:PTHR10145 IPI:IPI00846769 RefSeq:NP_176723.3 UniGene:At.20510 ProteinModelPortal:A8MS85 SMR:A8MS85 PRIDE:A8MS85 EnsemblPlants:AT1G65440.1 GeneID:842855 KEGG:ath:AT1G65440 TAIR:At1g65440 InParanoid:A8MS85 OMA:WGSESGG PhylomeDB:A8MS85 ProtClustDB:CLSN2682387 Genevestigator:A8MS85 Uniprot:A8MS85
Root	Isotig03822	33	5	2.593	5.16E-06	TAIR|locus:2206330 - symbol:GTB1 "global transcription factor group B1" species:3702 "Arabidopsis thaliana" [GO:0003723 "RNA binding" evidence=IEA] [GO:0006333 "chromatin assembly or disassembly" evidence=ISS] [GO:0006352 "transcription initiation, DNA-dependent" evidence=ISS] [GO:0016788 "hydrolase activity, acting on ester bonds" evidence=IEA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000980 InterPro:IPR003029 InterPro:IPR006641 InterPro:IPR017072 PIRSF:PIRSF036947 PROSITE:PS50126 SMART:SM00252 SMART:SM00732 EMBL:CP002684 GO:GO:0005829 GO:GO:0009506 Gene3D:G3DSA:3.30.505.10 GO:GO:0006357 GO:GO:0003746 GO:GO:0016788 InterPro:IPR012340 Gene3D:G3DSA:2.40.50.140 InterPro:IPR016027 SUPFAM:SSF50249 GO:GO:0006139 InterPro:IPR022967 SMART:SM00316 EMBL:AC010795 GO:GO:0032784 eggNOG:COG2183 KO:K11292 InterPro:IPR023323 InterPro:IPR023097 Gene3D:G3DSA:1.10.150.310 Gene3D:G3DSA:1.10.3500.10 PANTHER:PTHR10145 IPI:IPI00846769 RefSeq:NP_176723.3 UniGene:At.20510 ProteinModelPortal:A8MS85 SMR:A8MS85 PRIDE:A8MS85 EnsemblPlants:AT1G65440.1 GeneID:842855 KEGG:ath:AT1G65440 TAIR:At1g65440

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						InParanoid:A8MS85 OMA:WGSESGG PhylomeDB:A8MS85 ProtClustDB:CLSN2682387 Genevestigator:A8MS85 Uniprot:A8MS85
Root	Isotig03823	29	5	2.407	4.20E-05	TAIR|locus:2206330 - symbol:GTB1 "global transcription factor group B1" species:3702 "Arabidopsis thaliana" [GO:0003723 "RNA binding" evidence=IEA] [GO:0006333 "chromatin assembly or disassembly" evidence=ISS] [GO:0006352 "transcription initiation, DNA-dependent" evidence=ISS] [GO:0016788 "hydrolase activity, acting on ester bonds" evidence=IEA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000980 InterPro:IPR003029 InterPro:IPR006641 InterPro:IPR017072 PIRSF:PIRSF036947 PROSITE:PS50126 SMART:SM00252 SMART:SM00732 EMBL:CP002684 GO:GO:0005829 GO:GO:0009506 Gene3D:G3DSA:3.30.505.10 GO:GO:0006357 GO:GO:0003746 GO:GO:0016788 InterPro:IPR012340 Gene3D:G3DSA:2.40.50.140 InterPro:IPR016027 SUPFAM:SSF50249 GO:GO:0006139 InterPro:IPR022967 SMART:SM00316 EMBL:AC010795 GO:GO:0032784 eggNOG:COG2183 KO:K11292 InterPro:IPR023323 InterPro:IPR023097 Gene3D:G3DSA:1.10.150.310 Gene3D:G3DSA:1.10.3500.10 PANTHER:PTHR10145 IPI:IPI00846769 RefSeq:NP_176723.3 UniGene:At.20510 ProteinModelPortal:A8MS85 SMR:A8MS85 PRIDE:A8MS85 EnsemblPlants:AT1G65440.1 GeneID:842855 KEGG:ath:AT1G65440 TAIR:At1g65440 InParanoid:A8MS85 OMA:WGSESGG PhylomeDB:A8MS85 ProtClustDB:CLSN2682387 Genevestigator:A8MS85 Uniprot:A8MS85
Root	Isotig03824	31	5	2.503	1.48E-05	TAIR|locus:2206330 - symbol:GTB1 "global transcription factor group B1" species:3702 "Arabidopsis thaliana" [GO:0003723 "RNA binding" evidence=IEA] [GO:0006333 "chromatin assembly or disassembly" evidence=ISS] [GO:0006352 "transcription initiation, DNA-dependent" evidence=ISS] [GO:0016788 "hydrolase activity, acting on ester bonds" evidence=IEA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000980 InterPro:IPR003029 InterPro:IPR006641 InterPro:IPR017072 PIRSF:PIRSF036947 PROSITE:PS50126 SMART:SM00252 SMART:SM00732 EMBL:CP002684 GO:GO:0005829 GO:GO:0009506 Gene3D:G3DSA:3.30.505.10 GO:GO:0006357 GO:GO:0003746 GO:GO:0016788 InterPro:IPR012340 Gene3D:G3DSA:2.40.50.140 InterPro:IPR016027 SUPFAM:SSF50249 GO:GO:0006139 InterPro:IPR022967 SMART:SM00316 EMBL:AC010795 GO:GO:0032784 eggNOG:COG2183 KO:K11292 InterPro:IPR023323 InterPro:IPR023097 Gene3D:G3DSA:1.10.150.310 Gene3D:G3DSA:1.10.3500.10 PANTHER:PTHR10145 IPI:IPI00846769 RefSeq:NP_176723.3 UniGene:At.20510 ProteinModelPortal:A8MS85 SMR:A8MS85 PRIDE:A8MS85 EnsemblPlants:AT1G65440.1 GeneID:842855 KEGG:ath:AT1G65440 TAIR:At1g65440 InParanoid:A8MS85 OMA:WGSESGG PhylomeDB:A8MS85 ProtClustDB:CLSN2682387 Genevestigator:A8MS85 Uniprot:A8MS85
Root	Isotig03829	20	2	3.193	8.23E-05	TAIR|locus:2154905 - symbol:MAN7 "endo-beta-mannase 7" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=IEA;ISS] [GO:0005975 "carbohydrate metabolic process" evidence=IEA] [GO:0043169 "cation binding" evidence=IEA] InterPro:IPR001547 InterPro:IPR013781 Pfam:PF00150 PROSITE:PS00659 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005576 GO:GO:0043169 InterPro:IPR017853 Gene3D:G3DSA:3.20.20.80 SUPFAM:SSF51445 GO:GO:0005975 CAZy:GH5 EMBL:AB013389 eggNOG:COG3934 HOGENOM:HBG316339 GO:GO:0016985 EMBL:BT000452 EMBL:BT008749 IPI:IPI00536325 RefSeq:NP_201447.1 UniGene:At.28865 UniGene:At.67287 ProteinModelPortal:Q9FJZ3 IntAct:Q9FJZ3 PRIDE:Q9FJZ3 EnsemblPlants:AT5G66460.1 GeneID:836778 KEGG:ath:AT5G66460 TAIR:At5g66460 InParanoid:Q9FJZ3 OMA:NRIPGID PhylomeDB:Q9FJZ3 ProtClustDB:CLSN2916497 ArrayExpress:Q9FJZ3 Genevestigator:Q9FJZ3 Uniprot:Q9FJZ3
Root	Isotig03830	20	2	3.193	8.23E-05	TAIR|locus:2154905 - symbol:MAN7 "endo-beta-mannase 7" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=IEA;ISS] [GO:0005975 "carbohydrate metabolic process" evidence=IEA] [GO:0043169 "cation binding" evidence=IEA] InterPro:IPR001547 InterPro:IPR013781 Pfam:PF00150 PROSITE:PS00659 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005576 GO:GO:0043169 InterPro:IPR017853 Gene3D:G3DSA:3.20.20.80 SUPFAM:SSF51445 GO:GO:0005975 CAZy:GH5 EMBL:AB013389 eggNOG:COG3934 HOGENOM:HBG316339 GO:GO:0016985 EMBL:BT000452 EMBL:BT008749 IPI:IPI00536325 RefSeq:NP_201447.1 UniGene:At.28865 UniGene:At.67287 ProteinModelPortal:Q9FJZ3 IntAct:Q9FJZ3 PRIDE:Q9FJZ3 EnsemblPlants:AT5G66460.1 GeneID:836778 KEGG:ath:AT5G66460 TAIR:At5g66460 InParanoid:Q9FJZ3 OMA:NRIPGID PhylomeDB:Q9FJZ3 ProtClustDB:CLSN2916497 ArrayExpress:Q9FJZ3 Genevestigator:Q9FJZ3 Uniprot:Q9FJZ3

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig03831	20	2	3.193	8.23E-05	TAIR|locus:2154905 - symbol:MAN7 "endo-beta-mannase 7" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=IEA;ISS] [GO:0005975 "carbohydrate metabolic process" evidence=IEA] [GO:0043169 "cation binding" evidence=IEA] InterPro:IPR001547 InterPro:IPR013781 Pfam:PF00150 PROSITE:PS00659 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005576 GO:GO:0043169 InterPro:IPR017853 Gene3D:G3DSA:3.20.20.80 SUPFAM:SSF51445 GO:GO:0005975 CAZy:GH5 EMBL:AB013389 eggNOG:COG3934 HOGENOM:HBG316339 GO:GO:0016985 EMBL:BT000452 EMBL:BT008749 IPI:IPI00536325 RefSeq:NP_201447.1 UniGene:At.28865 UniGene:At.67287 ProteinModelPortal:Q9FJZ3 IntAct:Q9FJZ3 PRIDE:Q9FJZ3 EnsemblPlants:AT5G66460.1 GeneID:836778 KEGG:ath:AT5G66460 TAIR:At5g66460 InParanoid:Q9FJZ3 OMA:NRIPGID PhylomeDB:Q9FJZ3 ProtClustDB:CLSN2916497 ArrayExpress:Q9FJZ3 Genevestigator:Q9FJZ3 Uniprot:Q9FJZ3
Root	Isotig03832	20	2	3.193	8.23E-05	TAIR|locus:2154905 - symbol:MAN7 "endo-beta-mannase 7" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=IEA;ISS] [GO:0005975 "carbohydrate metabolic process" evidence=IEA] [GO:0043169 "cation binding" evidence=IEA] InterPro:IPR001547 InterPro:IPR013781 Pfam:PF00150 PROSITE:PS00659 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005576 GO:GO:0043169 InterPro:IPR017853 Gene3D:G3DSA:3.20.20.80 SUPFAM:SSF51445 GO:GO:0005975 CAZy:GH5 EMBL:AB013389 eggNOG:COG3934 HOGENOM:HBG316339 GO:GO:0016985 EMBL:BT000452 EMBL:BT008749 IPI:IPI00536325 RefSeq:NP_201447.1 UniGene:At.28865 UniGene:At.67287 ProteinModelPortal:Q9FJZ3 IntAct:Q9FJZ3 PRIDE:Q9FJZ3 EnsemblPlants:AT5G66460.1 GeneID:836778 KEGG:ath:AT5G66460 TAIR:At5g66460 InParanoid:Q9FJZ3 OMA:NRIPGID PhylomeDB:Q9FJZ3 ProtClustDB:CLSN2916497 ArrayExpress:Q9FJZ3 Genevestigator:Q9FJZ3 Uniprot:Q9FJZ3
Root	Isotig03857	7	79	-3.625	6.61E-18	TAIR|locus:2194864 - symbol:SIAR1 "AT1G44800" species:3702 "Arabidopsis thaliana" [GO:0016020 "membrane" evidence=ISS] [GO:0005515 "protein binding" evidence=IPI] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0006865 "amino acid transport" evidence=IDA] [GO:0015171 "amino acid transmembrane transporter activity" evidence=IDA] [GO:0032973 "amino acid export" evidence=IDA] [GO:0034639 "L-amino acid efflux transmembrane transporter activity" evidence=IDA] [GO:0043090 "amino acid import" evidence=IDA] [GO:0080144 "amino acid homeostasis" evidence=IMP] InterPro:IPR000620 Pfam:PF00892 EMBL:CP002684 GO:GO:0005515 GO:GO:0016020 EMBL:AC020576 ProtClustDB:CLSN2679863 EMBL:AY049306 EMBL:AY149964 IPI:IPI00530851 PIR:A96507 RefSeq:NP_175101.1 UniGene:At.14882 IntAct:Q9LPF1 STRING:Q9LPF1 PRIDE:Q9LPF1 EnsemblPlants:AT1G44800.1 GeneID:841044 KEGG:ath:AT1G44800 TAIR:At1g44800 InParanoid:Q9LPF1 OMA:LIFRLET PhylomeDB:Q9LPF1 Genevestigator:Q9LPF1 Uniprot:Q9LPF1
Root	Isotig03858	7	79	-3.625	6.61E-18	TAIR|locus:2194864 - symbol:SIAR1 "AT1G44800" species:3702 "Arabidopsis thaliana" [GO:0016020 "membrane" evidence=ISS] [GO:0005515 "protein binding" evidence=IPI] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0006865 "amino acid transport" evidence=IDA] [GO:0015171 "amino acid transmembrane transporter activity" evidence=IDA] [GO:0032973 "amino acid export" evidence=IDA] [GO:0034639 "L-amino acid efflux transmembrane transporter activity" evidence=IDA] [GO:0043090 "amino acid import" evidence=IDA] [GO:0080144 "amino acid homeostasis" evidence=IMP] InterPro:IPR000620 Pfam:PF00892 EMBL:CP002684 GO:GO:0005515 GO:GO:0016020 EMBL:AC020576 ProtClustDB:CLSN2679863 EMBL:AY049306 EMBL:AY149964 IPI:IPI00530851 PIR:A96507 RefSeq:NP_175101.1 UniGene:At.14882 IntAct:Q9LPF1 STRING:Q9LPF1 PRIDE:Q9LPF1 EnsemblPlants:AT1G44800.1 GeneID:841044 KEGG:ath:AT1G44800 TAIR:At1g44800 InParanoid:Q9LPF1 OMA:LIFRLET PhylomeDB:Q9LPF1 Genevestigator:Q9LPF1 Uniprot:Q9LPF1
Root	Isotig03859	8	67	-3.195	4.74E-14	TAIR|locus:2194864 - symbol:SIAR1 "AT1G44800" species:3702 "Arabidopsis thaliana" [GO:0016020 "membrane" evidence=ISS] [GO:0005515 "protein binding" evidence=IPI] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0006865 "amino acid transport" evidence=IDA] [GO:0015171 "amino acid transmembrane transporter activity" evidence=IDA] [GO:0032973 "amino acid export" evidence=IDA] [GO:0034639 "L-amino acid efflux transmembrane transporter activity" evidence=IDA] [GO:0043090 "amino acid import" evidence=IDA] [GO:0080144 "amino acid homeostasis" evidence=IMP] InterPro:IPR000620 Pfam:PF00892 EMBL:CP002684 GO:GO:0005515 GO:GO:0016020 EMBL:AC020576 ProtClustDB:CLSN2679863 EMBL:AY049306 EMBL:AY149964 IPI:IPI00530851 PIR:A96507 RefSeq:NP_175101.1 UniGene:At.14882 IntAct:Q9LPF1 STRING:Q9LPF1 PRIDE:Q9LPF1 EnsemblPlants:AT1G44800.1 GeneID:841044 KEGG:ath:AT1G44800 TAIR:At1g44800 InParanoid:Q9LPF1 OMA:LIFRLET PhylomeDB:Q9LPF1 Genevestigator:Q9LPF1 Uniprot:Q9LPF1

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig03860	8	67	-3.195	4.74E-14	TAIR|locus:2194864 - symbol:SIAR1 "AT1G44800" species:3702 "Arabidopsis thaliana" [GO:0016020 "membrane" evidence=ISS] [GO:0005515 "protein binding" evidence=IPI] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0006865 "amino acid transport" evidence=IDA] [GO:0015171 "amino acid transmembrane transporter activity" evidence=IDA] [GO:0032973 "amino acid export" evidence=IDA] [GO:0034639 "L-amino acid efflux transmembrane transporter activity" evidence=IDA] [GO:0043090 "amino acid import" evidence=IDA] [GO:0080144 "amino acid homeostasis" evidence=IMP] InterPro:IPR000620 Pfam:PF00892 EMBL:CP002684 GO:GO:0005515 GO:GO:0016020 EMBL:AC020576 ProtClustDB:CLSN2679863 EMBL:AY049306 EMBL:AY149964 IPI:IPI00530851 PIR:A96507 RefSeq:NP_175101.1 UniGene:At.14882 IntAct:Q9LPF1 STRING:Q9LPF1 PRIDE:Q9LPF1 EnsemblPlants:AT1G44800.1 GeneID:841044 KEGG:ath:AT1G44800 TAIR:At1g44800 InParanoid:Q9LPF1 OMA:LIFRLET PhylomeDB:Q9LPF1 Genevestigator:Q9LPF1 Uniprot:Q9LPF1
Root	Isotig03897	0	35	-6.258	3.45E-10	TAIR|locus:2165041 - symbol:AT5G56790 species:3702 "Arabidopsis thaliana" [GO:0004672 "protein kinase activity" evidence=IEA] [GO:0004713 "protein tyrosine kinase activity" evidence=IEA] [GO:0005524 "ATP binding" evidence=IEA] [GO:0006468 "protein phosphorylation" evidence=IEA] [GO:0016301 "kinase activity" evidence=ISS] InterPro:IPR000719 InterPro:IPR001245 InterPro:IPR008266 InterPro:IPR011009 Pfam:PF07714 PROSITE:PS00109 PROSITE:PS50011 GO:GO:0005524 EMBL:CP002688 eggNOG:COG0515 SUPFAM:SSF56112 GO:GO:0004713 HSSP:P06213 InterPro:IPR014729 Gene3D:G3DSA:3.40.50.620 EMBL:BT000971 IPI:IPI00529362 RefSeq:NP_568843.1 UniGene:At.26344 ProteinModelPortal:Q8H0Z8 SMR:Q8H0Z8 PRIDE:Q8H0Z8 EnsemblPlants:AT5G56790.1 GeneID:835781 KEGG:ath:AT5G56790 TAIR:At5g56790 InParanoid:Q8H0Z8 OMA:DDIHESC PhylomeDB:Q8H0Z8 ProtClustDB:CLSN2684799 Genevestigator:Q8H0Z8 Uniprot:Q8H0Z8
Root	Isotig03898	0	33	-6.173	1.05E-09	TAIR|locus:2165041 - symbol:AT5G56790 species:3702 "Arabidopsis thaliana" [GO:0004672 "protein kinase activity" evidence=IEA] [GO:0004713 "protein tyrosine kinase activity" evidence=IEA] [GO:0005524 "ATP binding" evidence=IEA] [GO:0006468 "protein phosphorylation" evidence=IEA] [GO:0016301 "kinase activity" evidence=ISS] InterPro:IPR000719 InterPro:IPR001245 InterPro:IPR008266 InterPro:IPR011009 Pfam:PF07714 PROSITE:PS00109 PROSITE:PS50011 GO:GO:0005524 EMBL:CP002688 eggNOG:COG0515 SUPFAM:SSF56112 GO:GO:0004713 HSSP:P06213 InterPro:IPR014729 Gene3D:G3DSA:3.40.50.620 EMBL:BT000971 IPI:IPI00529362 RefSeq:NP_568843.1 UniGene:At.26344 ProteinModelPortal:Q8H0Z8 SMR:Q8H0Z8 PRIDE:Q8H0Z8 EnsemblPlants:AT5G56790.1 GeneID:835781 KEGG:ath:AT5G56790 TAIR:At5g56790 InParanoid:Q8H0Z8 OMA:DDIHESC PhylomeDB:Q8H0Z8 ProtClustDB:CLSN2684799 Genevestigator:Q8H0Z8 Uniprot:Q8H0Z8
Root	Isotig03899	0	34	-6.216	6.02E-10	TAIR|locus:2165041 - symbol:AT5G56790 species:3702 "Arabidopsis thaliana" [GO:0004672 "protein kinase activity" evidence=IEA] [GO:0004713 "protein tyrosine kinase activity" evidence=IEA] [GO:0005524 "ATP binding" evidence=IEA] [GO:0006468 "protein phosphorylation" evidence=IEA] [GO:0016301 "kinase activity" evidence=ISS] InterPro:IPR000719 InterPro:IPR001245 InterPro:IPR008266 InterPro:IPR011009 Pfam:PF07714 PROSITE:PS00109 PROSITE:PS50011 GO:GO:0005524 EMBL:CP002688 eggNOG:COG0515 SUPFAM:SSF56112 GO:GO:0004713 HSSP:P06213 InterPro:IPR014729 Gene3D:G3DSA:3.40.50.620 EMBL:BT000971 IPI:IPI00529362 RefSeq:NP_568843.1 UniGene:At.26344 ProteinModelPortal:Q8H0Z8 SMR:Q8H0Z8 PRIDE:Q8H0Z8 EnsemblPlants:AT5G56790.1 GeneID:835781 KEGG:ath:AT5G56790 TAIR:At5g56790 InParanoid:Q8H0Z8 OMA:DDIHESC PhylomeDB:Q8H0Z8 ProtClustDB:CLSN2684799 Genevestigator:Q8H0Z8 Uniprot:Q8H0Z8
Root	Isotig03900	0	32	-6.129	1.84E-09	TAIR|locus:2165041 - symbol:AT5G56790 species:3702 "Arabidopsis thaliana" [GO:0004672 "protein kinase activity" evidence=IEA] [GO:0004713 "protein tyrosine kinase activity" evidence=IEA] [GO:0005524 "ATP binding" evidence=IEA] [GO:0006468 "protein phosphorylation" evidence=IEA] [GO:0016301 "kinase activity" evidence=ISS] InterPro:IPR000719 InterPro:IPR001245 InterPro:IPR008266 InterPro:IPR011009 Pfam:PF07714 PROSITE:PS00109 PROSITE:PS50011 GO:GO:0005524 EMBL:CP002688 eggNOG:COG0515 SUPFAM:SSF56112 GO:GO:0004713 HSSP:P06213 InterPro:IPR014729 Gene3D:G3DSA:3.40.50.620 EMBL:BT000971 IPI:IPI00529362 RefSeq:NP_568843.1 UniGene:At.26344 ProteinModelPortal:Q8H0Z8 SMR:Q8H0Z8 PRIDE:Q8H0Z8 EnsemblPlants:AT5G56790.1 GeneID:835781 KEGG:ath:AT5G56790 TAIR:At5g56790 InParanoid:Q8H0Z8 OMA:DDIHESC PhylomeDB:Q8H0Z8 ProtClustDB:CLSN2684799 Genevestigator:Q8H0Z8 Uniprot:Q8H0Z8
Root	Isotig03901	5	38	-3.055	2.67E-08	UNIPROTKB|P93508 - symbol:P93508 "Calreticulin" species:3988 "Ricinus communis" [GO:0005788 "endoplasmic reticulum lumen" evidence=IDA] InterPro:IPR001580 InterPro:IPR009033 InterPro:IPR009169 InterPro:IPR018124

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						Pfam:PF00262 PIRSF:PIRSF002356 PRINTS:PR00626 PROSITE:PS00803 PROSITE:PS00804 PROSITE:PS00805 GO:GO:0005509 GO:GO:0006457 GO:GO:0005529 GO:GO:0051082 InterPro:IPR008985 InterPro:IPR013320 Gene3D:G3DSA:2.60.120.200 SUPFAM:SSF49899 GO:GO:0005788 PROSITE:PS00014 PANTHER:PTHR11073 SUPFAM:SSF63887 KO:K08057 EMBL:U74631 EMBL:U74630 PIR:T10172 RefSeq:XP_002512501.1 ProteinModelPortal:P93508 SMR:P93508 GeneID:8269812 KEGG:rcu:RCOM_1434770 PhylomeDB:P93508 ProtClustDB:CLSN2719690 Uniprot:P93508
Root	Isotig03902	5	38	-3.055	2.67E-08	UNIPROTKB|P93508 - symbol:P93508 "Calreticulin" species:3988 "Ricinus communis" [GO:0005788 "endoplasmic reticulum lumen" evidence=IDA] InterPro:IPR001580 InterPro:IPR009033 InterPro:IPR009169 InterPro:IPR018124 Pfam:PF00262 PIRSF:PIRSF002356 PRINTS:PR00626 PROSITE:PS00803 PROSITE:PS00804 PROSITE:PS00805 GO:GO:0005509 GO:GO:0006457 GO:GO:0005529 GO:GO:0051082 InterPro:IPR008985 InterPro:IPR013320 Gene3D:G3DSA:2.60.120.200 SUPFAM:SSF49899 GO:GO:0005788 PROSITE:PS00014 PANTHER:PTHR11073 SUPFAM:SSF63887 KO:K08057 EMBL:U74631 EMBL:U74630 PIR:T10172 RefSeq:XP_002512501.1 ProteinModelPortal:P93508 SMR:P93508 GeneID:8269812 KEGG:rcu:RCOM_1434770 PhylomeDB:P93508 ProtClustDB:CLSN2719690 Uniprot:P93508
Root	Isotig03903	5	38	-3.055	2.67E-08	UNIPROTKB|P93508 - symbol:P93508 "Calreticulin" species:3988 "Ricinus communis" [GO:0005788 "endoplasmic reticulum lumen" evidence=IDA] InterPro:IPR001580 InterPro:IPR009033 InterPro:IPR009169 InterPro:IPR018124 Pfam:PF00262 PIRSF:PIRSF002356 PRINTS:PR00626 PROSITE:PS00803 PROSITE:PS00804 PROSITE:PS00805 GO:GO:0005509 GO:GO:0006457 GO:GO:0005529 GO:GO:0051082 InterPro:IPR008985 InterPro:IPR013320 Gene3D:G3DSA:2.60.120.200 SUPFAM:SSF49899 GO:GO:0005788 PROSITE:PS00014 PANTHER:PTHR11073 SUPFAM:SSF63887 KO:K08057 EMBL:U74631 EMBL:U74630 PIR:T10172 RefSeq:XP_002512501.1 ProteinModelPortal:P93508 SMR:P93508 GeneID:8269812 KEGG:rcu:RCOM_1434770 PhylomeDB:P93508 ProtClustDB:CLSN2719690 Uniprot:P93508
Root	Isotig03904	5	38	-3.055	2.67E-08	UNIPROTKB|P93508 - symbol:P93508 "Calreticulin" species:3988 "Ricinus communis" [GO:0005788 "endoplasmic reticulum lumen" evidence=IDA] InterPro:IPR001580 InterPro:IPR009033 InterPro:IPR009169 InterPro:IPR018124 Pfam:PF00262 PIRSF:PIRSF002356 PRINTS:PR00626 PROSITE:PS00803 PROSITE:PS00804 PROSITE:PS00805 GO:GO:0005509 GO:GO:0006457 GO:GO:0005529 GO:GO:0051082 InterPro:IPR008985 InterPro:IPR013320 Gene3D:G3DSA:2.60.120.200 SUPFAM:SSF49899 GO:GO:0005788 PROSITE:PS00014 PANTHER:PTHR11073 SUPFAM:SSF63887 KO:K08057 EMBL:U74631 EMBL:U74630 PIR:T10172 RefSeq:XP_002512501.1 ProteinModelPortal:P93508 SMR:P93508 GeneID:8269812 KEGG:rcu:RCOM_1434770 PhylomeDB:P93508 ProtClustDB:CLSN2719690 Uniprot:P93508
Root	Isotig03915	19	3	2.534	0.000639389	TAIR|locus:2206440 - symbol:AT1G79520 species:3702 "Arabidopsis thaliana" [GO:0006812 "cation transport" evidence=IEA;ISS] [GO:0008324 "cation transmembrane transporter activity" evidence=IEA;ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0055085 "transmembrane transport" evidence=IEA] [GO:0005886 "plasma membrane" evidence=IDA] InterPro:IPR002524 Pfam:PF01545 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005886 GO:GO:0005774 EMBL:AC007202 GO:GO:0008324 PANTHER:PTHR11562 TIGRFAMs:TIGR01297 eggNOG:COG0053 HOGENOM:HBG387227 IPI:IPI00525346 PIR:E96826 RefSeq:NP_178070.2 UniGene:At.43219 ProteinModelPortal:Q9SAJ7 PRIDE:Q9SAJ7 EnsemblPlants:AT1G79520.1 GeneID:844290 KEGG:ath:AT1G79520 TAIR:At1g79520 InParanoid:Q9SAJ7 OMA:YRSIQSL PhylomeDB:Q9SAJ7 Genevestigator:Q9SAJ7 Uniprot:Q9SAJ7
Root	Isotig03989	4	30	-3.036	8.34E-07	TAIR|locus:2058641 - symbol:DEAR3 "AT2G23340" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=ISS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0005634 "nucleus" evidence=ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA;ISS] InterPro:IPR001471 InterPro:IPR016177 Pfam:PF00847 PRINTS:PR00367 PROSITE:PS51032 SMART:SM00380 GO:GO:0005634 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009873 GO:GO:0003677 GO:GO:0003700 GO:GO:0006351 Gene3D:G3DSA:3.30.730.10 SUPFAM:SSF54171 HSSP:O80337 EMBL:AC002391 HOGENOM:HBG749764 EMBL:AK118495 EMBL:BT003741 IPI:IPI00528876 PIR:T00498 RefSeq:NP_179915.1 UniGene:At.43320 ProteinModelPortal:O22174 SMR:O22174 EnsemblPlants:AT2G23340.1 GeneID:816866 KEGG:ath:AT2G23340 TAIR:At2g23340 eggNOG:NOG273209 InParanoid:O22174 OMA:LPDPENS PhylomeDB:O22174 ProtClustDB:CLSN2683886 ArrayExpress:O22174 Genevestigator:O22174 Uniprot:O22174
Root	Isotig03990	4	30	-3.036	8.34E-07	TAIR|locus:2058641 - symbol:DEAR3 "AT2G23340" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=ISS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS]

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						[GO:0005634 "nucleus" evidence=ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA;ISS] InterPro:IPR001471 InterPro:IPR016177 Pfam:PF00847 PRINTS:PR00367 PROSITE:PS51032 SMART:SM00380 GO:GO:0005634 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009873 GO:GO:0003677 GO:GO:0003700 GO:GO:0006351 Gene3D:G3DSA:3.30.730.10 SUPFAM:SSF54171 HSSP:O80337 EMBL:AC002391 HOGENOM:HBG749764 EMBL:AK118495 EMBL:BT003741 IPI:IPI00528876 PIR:T00498 RefSeq:NP_179915.1 UniGene:At.43320 ProteinModelPortal:O22174 SMR:O22174 EnsemblPlants:AT2G23340.1 GeneID:816866 KEGG:ath:AT2G23340 TAIR:At2g23340 eggNOG:NOG273209 InParanoid:O22174 OMA:LPDPENS PhylomeDB:O22174 ProtClustDB:CLSN2683886 ArrayExpress:O22174 Genevestigator:O22174 Uniprot:O22174
Root	Isotig03991	3	27	-3.299	1.22E-06	TAIR|locus:1005716457 - symbol:RAP2.9 "related to AP2 9" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=IEA] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=IEA;ISS] [GO:0005634 "nucleus" evidence=ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA;ISS] InterPro:IPR001471 InterPro:IPR016177 Pfam:PF00847 PRINTS:PR00367 PROSITE:PS51032 SMART:SM00380 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005634 GO:GO:0009873 GO:GO:0003677 GO:GO:0003700 GO:GO:0006351 KO:K09286 Gene3D:G3DSA:3.30.730.10 SUPFAM:SSF54171 HSSP:O80337 HOGENOM:HBG749764 EMBL:AB073166 EMBL:AY560869 EMBL:BT024689 EMBL:AF003102 EMBL:Z37270 IPI:IPI00535753 RefSeq:NP_849340.1 UniGene:At.47204 ProteinModelPortal:Q8W3M3 SMR:Q8W3M3 PRIDE:Q8W3M3 EnsemblPlants:AT4G06746.1 GeneID:826148 KEGG:ath:AT4G06746 TAIR:At4g06746 eggNOG:NOG320996 InParanoid:Q8W3M3 OMA:NKLPEAY PhylomeDB:Q8W3M3 ProtClustDB:CLSN2918026 ArrayExpress:O23111 Genevestigator:Q8W3M3 Uniprot:Q8W3M3
Root	Isotig03992	3	27	-3.299	1.22E-06	TAIR|locus:1005716457 - symbol:RAP2.9 "related to AP2 9" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=IEA] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=IEA;ISS] [GO:0005634 "nucleus" evidence=ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA;ISS] InterPro:IPR001471 InterPro:IPR016177 Pfam:PF00847 PRINTS:PR00367 PROSITE:PS51032 SMART:SM00380 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005634 GO:GO:0009873 GO:GO:0003677 GO:GO:0003700 GO:GO:0006351 KO:K09286 Gene3D:G3DSA:3.30.730.10 SUPFAM:SSF54171 HSSP:O80337 HOGENOM:HBG749764 EMBL:AB073166 EMBL:AY560869 EMBL:BT024689 EMBL:AF003102 EMBL:Z37270 IPI:IPI00535753 RefSeq:NP_849340.1 UniGene:At.47204 ProteinModelPortal:Q8W3M3 SMR:Q8W3M3 PRIDE:Q8W3M3 EnsemblPlants:AT4G06746.1 GeneID:826148 KEGG:ath:AT4G06746 TAIR:At4g06746 eggNOG:NOG320996 InParanoid:Q8W3M3 OMA:NKLPEAY PhylomeDB:Q8W3M3 ProtClustDB:CLSN2918026 ArrayExpress:O23111 Genevestigator:Q8W3M3 Uniprot:Q8W3M3
Root	Isotig04001	26	4	2.571	5.65E-05	TAIR|locus:2149214 - symbol:AT5G20400 "AT5G20400" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0005829 "cytosol" evidence=IDA] [GO:0016706 "oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors" evidence=ISS] InterPro:IPR005123 Pfam:PF03171 PROSITE:PS51471 GO:GO:0005829 EMBL:CP002688 GenomeReviews:BA000015_GR eggNOG:COG3491 HOGENOM:HBG749762 GO:GO:0016706 HSSP:Q96323 GO:GO:0016702 EMBL:BT002900 EMBL:BT005178 IPI:IPI00523248 RefSeq:NP_197540.1 UniGene:At.31186 ProteinModelPortal:Q84K82 SMR:Q84K82 STRING:Q84K82 PRIDE:Q84K82 EnsemblPlants:AT5G20400.1 GeneID:832162 KEGG:ath:AT5G20400 TAIR:At5g20400 InParanoid:Q84K82 OMA:MYGESAT PhylomeDB:Q84K82 ProtClustDB:PLN00417 ArrayExpress:Q84K82 Genevestigator:Q84K82 Uniprot:Q84K82
Root	Isotig04002	26	4	2.571	5.65E-05	TAIR|locus:2149214 - symbol:AT5G20400 "AT5G20400" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0005829 "cytosol" evidence=IDA] [GO:0016706 "oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors" evidence=ISS] InterPro:IPR005123 Pfam:PF03171 PROSITE:PS51471 GO:GO:0005829 EMBL:CP002688 GenomeReviews:BA000015_GR eggNOG:COG3491 HOGENOM:HBG749762 GO:GO:0016706 HSSP:Q96323 GO:GO:0016702 EMBL:BT002900 EMBL:BT005178 IPI:IPI00523248 RefSeq:NP_197540.1 UniGene:At.31186 ProteinModelPortal:Q84K82 SMR:Q84K82 STRING:Q84K82 PRIDE:Q84K82 EnsemblPlants:AT5G20400.1 GeneID:832162 KEGG:ath:AT5G20400

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						TAIR:At5g20400 InParanoid:Q84K82 OMA:MYGESAT PhylomeDB:Q84K82 ProtClustDB:PLN00417 ArrayExpress:Q84K82 Genevestigator:Q84K82 Uniprot:Q84K82
Root	Isotig04003	26	4	2.571	5.65E-05	TAIR|locus:2149214 - symbol:AT5G20400 "AT5G20400" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0005829 "cytosol" evidence=IDA] [GO:0016706 "oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors" evidence=ISS] InterPro:IPR005123 Pfam:PF03171 PROSITE:PS51471 GO:GO:0005829 EMBL:CP002688 GenomeReviews:BA000015_GR eggNOG:COG3491 HOGENOM:HBG749762 GO:GO:0016706 HSSP:Q96323 GO:GO:0016702 EMBL:BT002900 EMBL:BT005178 IPI:IPI00523248 RefSeq:NP_197540.1 UniGene:At.31186 ProteinModelPortal:Q84K82 SMR:Q84K82 STRING:Q84K82 PRIDE:Q84K82 EnsemblPlants:AT5G20400.1 GeneID:832162 KEGG:ath:AT5G20400 TAIR:At5g20400 InParanoid:Q84K82 OMA:MYGESAT PhylomeDB:Q84K82 ProtClustDB:PLN00417 ArrayExpress:Q84K82 Genevestigator:Q84K82 Uniprot:Q84K82
Root	Isotig04004	26	4	2.571	5.65E-05	TAIR|locus:2149214 - symbol:AT5G20400 "AT5G20400" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0005829 "cytosol" evidence=IDA] [GO:0016706 "oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors" evidence=ISS] InterPro:IPR005123 Pfam:PF03171 PROSITE:PS51471 GO:GO:0005829 EMBL:CP002688 GenomeReviews:BA000015_GR eggNOG:COG3491 HOGENOM:HBG749762 GO:GO:0016706 HSSP:Q96323 GO:GO:0016702 EMBL:BT002900 EMBL:BT005178 IPI:IPI00523248 RefSeq:NP_197540.1 UniGene:At.31186 ProteinModelPortal:Q84K82 SMR:Q84K82 STRING:Q84K82 PRIDE:Q84K82 EnsemblPlants:AT5G20400.1 GeneID:832162 KEGG:ath:AT5G20400 TAIR:At5g20400 InParanoid:Q84K82 OMA:MYGESAT PhylomeDB:Q84K82 ProtClustDB:PLN00417 ArrayExpress:Q84K82 Genevestigator:Q84K82 Uniprot:Q84K82
Root	Isotig04025	0	13	-4.829	0.000155955	TAIR|locus:2170101 - symbol:ERF110 "AT5G50080" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=ISS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0005634 "nucleus" evidence=ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA;ISS] InterPro:IPR001471 InterPro:IPR016177 Pfam:PF00847 PRINTS:PR00367 PROSITE:PS51032 SMART:SM00380 GO:GO:0005634 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009873 GO:GO:0003677 GO:GO:0003700 GO:GO:0006351 Gene3D:G3DSA:3.30.730.10 SUPFAM:SSF54171 HSSP:O80337 EMBL:AB026650 EMBL:AJ580378 IPI:IPI00543457 RefSeq:NP_199819.3 UniGene:At.29751 ProteinModelPortal:Q70II3 SMR:Q70II3 STRING:Q70II3 EnsemblPlants:AT5G50080.1 GeneID:835072 KEGG:ath:AT5G50080 TAIR:At5g50080 eggNOG:NOG295694 InParanoid:Q70II3 PhylomeDB:Q70II3 ProtClustDB:CLSN2920550 Genevestigator:Q70II3 Uniprot:Q70II3
Root	Isotig04026	0	13	-4.829	0.000155955	TAIR|locus:2197076 - symbol:RAP2.12 "AT1G53910" species:3702 "Arabidopsis thaliana" [GO:0006355 "regulation of transcription, DNA-dependent" evidence=ISS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS;TAS] [GO:0001666 "response to hypoxia" evidence=IMP] [GO:0005634 "nucleus" evidence=IC;IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0070483 "detection of hypoxia" evidence=IEP] [GO:0003677 "DNA binding" evidence=TAS] InterPro:IPR001471 InterPro:IPR016177 Pfam:PF00847 PRINTS:PR00367 PROSITE:PS51032 SMART:SM00380 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005886 GO:GO:0005634 GO:GO:0009873 GO:GO:0003677 GO:GO:0003700 GO:GO:0006351 KO:K09286 Gene3D:G3DSA:3.30.730.10 SUPFAM:SSF54171 HSSP:O80337 EMBL:AC009324 GO:GO:0070483 HOGENOM:HBG595502 EMBL:AY037260 EMBL:AY057545 EMBL:AY113051 EMBL:AY088204 EMBL:AF003105 IPI:IPI00535772 PIR:D96579 RefSeq:NP_001031185.1 RefSeq:NP_175794.1 UniGene:At.20952 UniGene:At.21295 UniGene:At.68722 ProteinModelPortal:Q9SSA8 SMR:Q9SSA8 IntAct:Q9SSA8 STRING:Q9SSA8 EnsemblPlants:AT1G53910.1 EnsemblPlants:AT1G53910.2 GeneID:841829 KEGG:ath:AT1G53910 TAIR:At1g53910 eggNOG:NOG262386 InParanoid:Q9SSA8 OMA:NEDAVTT PhylomeDB:Q9SSA8 ProtClustDB:CLSN2682146 Genevestigator:Q9SSA8 Uniprot:Q9SSA8
Root	Isotig04027	0	11	-4.588	0.000569522	TAIR|locus:2170101 - symbol:ERF110 "AT5G50080" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=ISS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0005634 "nucleus" evidence=ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA;ISS] InterPro:IPR001471 InterPro:IPR016177 Pfam:PF00847 PRINTS:PR00367 PROSITE:PS51032 SMART:SM00380 GO:GO:0005634 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009873 GO:GO:0003677 GO:GO:0003700 GO:GO:0006351 Gene3D:G3DSA:3.30.730.10 SUPFAM:SSF54171

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						HSSP:O80337 EMBL:AB026650 EMBL:AJ580378 IPI:IPI00543457 RefSeq:NP_199819.3 UniGene:At.29751 ProteinModelPortal:Q70II3 SMR:Q70II3 STRING:Q70II3 EnsemblPlants:AT5G50080.1 GeneID:835072 KEGG:ath:AT5G50080 TAIR:At5g50080 eggNOG:NOG295694 InParanoid:Q70II3 PhylomeDB:Q70II3 ProtClustDB:CLSN2920550 Genevestigator:Q70II3 Uniprot:Q70II3
Root	Isotig04028	0	11	-4.588	0.000569522	TAIR|locus:2197076 - symbol:RAP2.12 "AT1G53910" species:3702 "Arabidopsis thaliana" [GO:0006355 "regulation of transcription, DNA-dependent" evidence=ISS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS;TAS] [GO:0001666 "response to hypoxia" evidence=IMP] [GO:0005634 "nucleus" evidence=IC;IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0070483 "detection of hypoxia" evidence=IEP] [GO:0003677 "DNA binding" evidence=TAS] InterPro:IPR001471 InterPro:IPR016177 Pfam:PF00847 PRINTS:PR00367 PROSITE:PS51032 SMART:SM00380 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005886 GO:GO:0005634 GO:GO:0009873 GO:GO:0003677 GO:GO:0003700 GO:GO:0006351 KO:K09286 Gene3D:G3DSA:3.30.730.10 SUPFAM:SSF54171 HSSP:O80337 EMBL:AC009324 GO:GO:0070483 HOGENOM:HBG595502 EMBL:AY037260 EMBL:AY057545 EMBL:AY113051 EMBL:AY088204 EMBL:AF003105 IPI:IPI00535772 PIR:D96579 RefSeq:NP_001031185.1 RefSeq:NP_175794.1 UniGene:At.20952 UniGene:At.21295 UniGene:At.68722 ProteinModelPortal:Q9SSA8 SMR:Q9SSA8 IntAct:Q9SSA8 STRING:Q9SSA8 EnsemblPlants:AT1G53910.1 EnsemblPlants:AT1G53910.2 GeneID:841829 KEGG:ath:AT1G53910 TAIR:At1g53910 eggNOG:NOG262386 InParanoid:Q9SSA8 OMA:NEDAVTT PhylomeDB:Q9SSA8 ProtClustDB:CLSN2682146 Genevestigator:Q9SSA8 Uniprot:Q9SSA8
Root	Isotig04033	208	17	3.484	1.21E-39	TAIR|locus:2128096 - symbol:AT4G31290 "AT4G31290" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002687 GenomeReviews:CT486007_GR InterPro:IPR013024 Gene3D:G3DSA:3.10.490.10 eggNOG:COG3703 HOGENOM:HBG522249 InterPro:IPR006840 PANTHER:PTHR12192 Pfam:PF04752 UniGene:At.47478 EMBL:BT006411 EMBL:AK227743 IPI:IPI00527527 RefSeq:NP_567871.1 ProteinModelPortal:Q84MC1 STRING:Q84MC1 PRIDE:Q84MC1 EnsemblPlants:AT4G31290.1 GeneID:829256 KEGG:ath:AT4G31290 TAIR:At4g31290 InParanoid:Q84MC1 OMA:WLENDAR PhylomeDB:Q84MC1 ProtClustDB:CLSN2686752 Genevestigator:Q84MC1 Uniprot:Q84MC1
Root	Isotig04034	210	17	3.498	3.98E-40	TAIR|locus:2128096 - symbol:AT4G31290 "AT4G31290" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002687 GenomeReviews:CT486007_GR InterPro:IPR013024 Gene3D:G3DSA:3.10.490.10 eggNOG:COG3703 HOGENOM:HBG522249 InterPro:IPR006840 PANTHER:PTHR12192 Pfam:PF04752 UniGene:At.47478 EMBL:BT006411 EMBL:AK227743 IPI:IPI00527527 RefSeq:NP_567871.1 ProteinModelPortal:Q84MC1 STRING:Q84MC1 PRIDE:Q84MC1 EnsemblPlants:AT4G31290.1 GeneID:829256 KEGG:ath:AT4G31290 TAIR:At4g31290 InParanoid:Q84MC1 OMA:WLENDAR PhylomeDB:Q84MC1 ProtClustDB:CLSN2686752 Genevestigator:Q84MC1 Uniprot:Q84MC1
Root	Isotig04035	165	11	3.778	1.15E-33	TAIR|locus:2128096 - symbol:AT4G31290 "AT4G31290" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002687 GenomeReviews:CT486007_GR InterPro:IPR013024 Gene3D:G3DSA:3.10.490.10 eggNOG:COG3703 HOGENOM:HBG522249 InterPro:IPR006840 PANTHER:PTHR12192 Pfam:PF04752 UniGene:At.47478 EMBL:BT006411 EMBL:AK227743 IPI:IPI00527527 RefSeq:NP_567871.1 ProteinModelPortal:Q84MC1 STRING:Q84MC1 PRIDE:Q84MC1 EnsemblPlants:AT4G31290.1 GeneID:829256 KEGG:ath:AT4G31290 TAIR:At4g31290 InParanoid:Q84MC1 OMA:WLENDAR PhylomeDB:Q84MC1 ProtClustDB:CLSN2686752 Genevestigator:Q84MC1 Uniprot:Q84MC1
Root	Isotig04036	167	11	3.795	3.74E-34	TAIR|locus:2128096 - symbol:AT4G31290 "AT4G31290" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002687 GenomeReviews:CT486007_GR InterPro:IPR013024 Gene3D:G3DSA:3.10.490.10 eggNOG:COG3703 HOGENOM:HBG522249 InterPro:IPR006840 PANTHER:PTHR12192 Pfam:PF04752 UniGene:At.47478 EMBL:BT006411 EMBL:AK227743 IPI:IPI00527527 RefSeq:NP_567871.1 ProteinModelPortal:Q84MC1 STRING:Q84MC1 PRIDE:Q84MC1 EnsemblPlants:AT4G31290.1 GeneID:829256 KEGG:ath:AT4G31290 TAIR:At4g31290 InParanoid:Q84MC1 OMA:WLENDAR PhylomeDB:Q84MC1 ProtClustDB:CLSN2686752 Genevestigator:Q84MC1 Uniprot:Q84MC1
Root	Isotig04049	19	0	5.119	1.05E-05	No hit

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig04050	17	0	4.958	3.30E-05	TAIR|locus:2091353 - symbol:AT3G28040 "AT3G28040" species:3702 "Arabidopsis thaliana" [GO:0004674 "protein serine/threonine kinase activity" evidence=ISS] [GO:0005524 "ATP binding" evidence=ISS] [GO:0006468 "protein phosphorylation" evidence=IEA;ISS] [GO:0007169 "transmembrane receptor protein tyrosine kinase signaling pathway" evidence=ISS] [GO:0016301 "kinase activity" evidence=ISS] Pfam:PF00560 InterPro:IPR001611 InterPro:IPR000719 InterPro:IPR011009 InterPro:IPR017441 Pfam:PF00069 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 PROSITE:PS51450 GO:GO:0016021 GO:GO:0005524 EMBL:CP002686 GenomeReviews:BA000014_GR eggNOG:COG0515 GO:GO:0004872 SUPFAM:SSF56112 HOGENOM:HBG755340 GO:GO:0004672 InterPro:IPR013210 Pfam:PF08263 EMBL:AB028616 EMBL:FJ708729 IPI:IPI00540962 RefSeq:NP_189443.2 UniGene:At.28161 ProteinModelPortal:Q9LRT1 SMR:Q9LRT1 PRIDE:Q9LRT1 EnsemblPlants:AT3G28040.1 GeneID:822428 KEGG:ath:AT3G28040 GeneFarm:2365 TAIR:At3g28040 InParanoid:Q9LRT1 OMA:CTSQIPS PhylomeDB:Q9LRT1 ProtClustDB:CLSN2680201 Uniprot:Q9LRT1
Root	Isotig04065	1	32	-5.129	2.20E-09	TAIR|locus:2013001 - symbol:AT1G71695 species:3702 "Arabidopsis thaliana" [GO:0004601 "peroxidase activity" evidence=IEA;ISS] [GO:0006979 "response to oxidative stress" evidence=IEA] [GO:0020037 "heme binding" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0009505 "plant-type cell wall" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000823 InterPro:IPR002016 InterPro:IPR010255 InterPro:IPR019793 InterPro:IPR019794 Pfam:PF00141 PRINTS:PR00458 PRINTS:PR00461 PROSITE:PS00435 PROSITE:PS00436 PROSITE:PS50873 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009506 GO:GO:0005773 GO:GO:0005576 GO:GO:0016020 GO:GO:0020037 GO:GO:0009505 EMBL:AC012654 EMBL:AC016163 GO:GO:0004601 GO:GO:0042744 HOGENOM:HBG597790 SUPFAM:SSF48113 KO:K00430 EMBL:X98318 EMBL:X98773 EMBL:AF334732 EMBL:BT000715 EMBL:AY087964 IPI:IPI00538176 PIR:A96739 RefSeq:NP_177313.1 UniGene:At.67041 UniGene:At.94 ProteinModelPortal:Q96520 SMR:Q96520 STRING:Q96520 PeroxiBase:93 PRIDE:Q96520 EnsemblPlants:AT1G71695.1 GeneID:843498 KEGG:ath:AT1G71695 GeneFarm:1474 TAIR:At1g71695 eggNOG:NOG252730 InParanoid:Q96520 OMA:NCSARNT PhylomeDB:Q96520 ProtClustDB:CLSN2679267 ArrayExpress:Q96520 Genevestigator:Q96520 GermOnline:AT1G71695 Uniprot:Q96520
Root	Isotig04066	1	32	-5.129	2.20E-09	TAIR|locus:2013001 - symbol:AT1G71695 species:3702 "Arabidopsis thaliana" [GO:0004601 "peroxidase activity" evidence=IEA;ISS] [GO:0006979 "response to oxidative stress" evidence=IEA] [GO:0020037 "heme binding" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0009505 "plant-type cell wall" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000823 InterPro:IPR002016 InterPro:IPR010255 InterPro:IPR019793 InterPro:IPR019794 Pfam:PF00141 PRINTS:PR00458 PRINTS:PR00461 PROSITE:PS00435 PROSITE:PS00436 PROSITE:PS50873 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009506 GO:GO:0005773 GO:GO:0005576 GO:GO:0016020 GO:GO:0020037 GO:GO:0009505 EMBL:AC012654 EMBL:AC016163 GO:GO:0004601 GO:GO:0042744 HOGENOM:HBG597790 SUPFAM:SSF48113 KO:K00430 EMBL:X98318 EMBL:X98773 EMBL:AF334732 EMBL:BT000715 EMBL:AY087964 IPI:IPI00538176 PIR:A96739 RefSeq:NP_177313.1 UniGene:At.67041 UniGene:At.94 ProteinModelPortal:Q96520 SMR:Q96520 STRING:Q96520 PeroxiBase:93 PRIDE:Q96520 EnsemblPlants:AT1G71695.1 GeneID:843498 KEGG:ath:AT1G71695 GeneFarm:1474 TAIR:At1g71695 eggNOG:NOG252730 InParanoid:Q96520 OMA:NCSARNT PhylomeDB:Q96520 ProtClustDB:CLSN2679267 ArrayExpress:Q96520 Genevestigator:Q96520 GermOnline:AT1G71695 Uniprot:Q96520
Root	Isotig04067	1	32	-5.129	2.20E-09	TAIR|locus:2013001 - symbol:AT1G71695 species:3702 "Arabidopsis thaliana" [GO:0004601 "peroxidase activity" evidence=IEA;ISS] [GO:0006979 "response to oxidative stress" evidence=IEA] [GO:0020037 "heme binding" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0009505 "plant-type cell wall" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000823 InterPro:IPR002016 InterPro:IPR010255 InterPro:IPR019793 InterPro:IPR019794 Pfam:PF00141 PRINTS:PR00458 PRINTS:PR00461 PROSITE:PS00435 PROSITE:PS00436 PROSITE:PS50873 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009506 GO:GO:0005773 GO:GO:0005576 GO:GO:0016020 GO:GO:0020037 GO:GO:0009505 EMBL:AC012654 EMBL:AC016163 GO:GO:0004601 GO:GO:0042744 HOGENOM:HBG597790 SUPFAM:SSF48113 KO:K00430 EMBL:X98318 EMBL:X98773 EMBL:AF334732 EMBL:BT000715

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EMBL:AY087964 IPI:IPI00538176 PIR:A96739 RefSeq:NP_177313.1 UniGene:At.67041 UniGene:At.94 ProteinModelPortal:Q96520 SMR:Q96520 STRING:Q96520 PeroxiBase:93 PRIDE:Q96520 EnsemblPlants:AT1G71695.1 GeneID:843498 KEGG:ath:AT1G71695 GeneFarm:1474 TAIR:At1g71695 eggNOG:NOG252730 InParanoid:Q96520 OMA:NCSARNT PhylomeDB:Q96520 ProtClustDB:CLSN2679267 ArrayExpress:Q96520 Genevestigator:Q96520 GermOnline:AT1G71695 Uniprot:Q96520
Root	Isotig04068	1	32	-5.129	2.20E-09	TAIR|locus:2013001 - symbol:AT1G71695 species:3702 "Arabidopsis thaliana" [GO:0004601 "peroxidase activity" evidence=IEA;ISS] [GO:0006979 "response to oxidative stress" evidence=IEA] [GO:0020037 "heme binding" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0009505 "plant-type cell wall" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000823 InterPro:IPR002016 InterPro:IPR010255 InterPro:IPR019793 InterPro:IPR019794 Pfam:PF00141 PRINTS:PR00458 PRINTS:PR00461 PROSITE:PS00435 PROSITE:PS00436 PROSITE:PS50873 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009506 GO:GO:0005773 GO:GO:0005576 GO:GO:0016020 GO:GO:0020037 GO:GO:0009505 EMBL:AC012654 EMBL:AC016163 GO:GO:0004601 GO:GO:0042744 HOGENOM:HBG597790 SUPFAM:SSF48113 KO:K00430 EMBL:X98318 EMBL:X98773 EMBL:AF334732 EMBL:BT000715 EMBL:AY087964 IPI:IPI00538176 PIR:A96739 RefSeq:NP_177313.1 UniGene:At.67041 UniGene:At.94 ProteinModelPortal:Q96520 SMR:Q96520 STRING:Q96520 PeroxiBase:93 PRIDE:Q96520 EnsemblPlants:AT1G71695.1 GeneID:843498 KEGG:ath:AT1G71695 GeneFarm:1474 TAIR:At1g71695 eggNOG:NOG252730 InParanoid:Q96520 OMA:NCSARNT PhylomeDB:Q96520 ProtClustDB:CLSN2679267 ArrayExpress:Q96520 Genevestigator:Q96520 GermOnline:AT1G71695 Uniprot:Q96520
Root	Isotig04089	26	0	5.571	2.13E-07	TAIR|locus:2060984 - symbol:HIS1-3 "histone H1-3" species:3702 "Arabidopsis thaliana" [GO:0000786 "nucleosome" evidence=IEA;ISS] [GO:0003677 "DNA binding" evidence=ISS] [GO:0005634 "nucleus" evidence=IEA] [GO:0006334 "nucleosome assembly" evidence=ISS] [GO:0009414 "response to water deprivation" evidence=IEP] [GO:0031492 "nucleosomal DNA binding" evidence=ISS] InterPro:IPR005818 InterPro:IPR005819 Pfam:PF00538 PRINTS:PR00624 PROSITE:PS51504 SMART:SM00526 GO:GO:0005634 EMBL:CP002685 GO:GO:0003677 InterPro:IPR011991 Gene3D:G3DSA:1.10.10.10 GO:GO:0009414 GO:GO:0006334 GO:GO:0000786 EMBL:AC006201 KO:K11275 EMBL:U72241 EMBL:U73781 EMBL:AY045797 EMBL:AY079414 EMBL:AY084603 IPI:IPI00539258 PIR:F84559 RefSeq:NP_179396.1 UniGene:At.24439 ProteinModelPortal:P94109 SMR:P94109 STRING:P94109 PRIDE:P94109 EnsemblPlants:AT2G18050.1 GeneID:816317 KEGG:ath:AT2G18050 TAIR:At2g18050 eggNOG:NOG258576 InParanoid:P94109 OMA:TKRTRSS PhylomeDB:P94109 ProtClustDB:CLSN2683930 ArrayExpress:P94109 Genevestigator:P94109 Uniprot:P94109
Root	Isotig04090	26	0	5.571	2.13E-07	TAIR|locus:2060984 - symbol:HIS1-3 "histone H1-3" species:3702 "Arabidopsis thaliana" [GO:0000786 "nucleosome" evidence=IEA;ISS] [GO:0003677 "DNA binding" evidence=ISS] [GO:0005634 "nucleus" evidence=IEA] [GO:0006334 "nucleosome assembly" evidence=ISS] [GO:0009414 "response to water deprivation" evidence=IEP] [GO:0031492 "nucleosomal DNA binding" evidence=ISS] InterPro:IPR005818 InterPro:IPR005819 Pfam:PF00538 PRINTS:PR00624 PROSITE:PS51504 SMART:SM00526 GO:GO:0005634 EMBL:CP002685 GO:GO:0003677 InterPro:IPR011991 Gene3D:G3DSA:1.10.10.10 GO:GO:0009414 GO:GO:0006334 GO:GO:0000786 EMBL:AC006201 KO:K11275 EMBL:U72241 EMBL:U73781 EMBL:AY045797 EMBL:AY079414 EMBL:AY084603 IPI:IPI00539258 PIR:F84559 RefSeq:NP_179396.1 UniGene:At.24439 ProteinModelPortal:P94109 SMR:P94109 STRING:P94109 PRIDE:P94109 EnsemblPlants:AT2G18050.1 GeneID:816317 KEGG:ath:AT2G18050 TAIR:At2g18050 eggNOG:NOG258576 InParanoid:P94109 OMA:TKRTRSS PhylomeDB:P94109 ProtClustDB:CLSN2683930 ArrayExpress:P94109 Genevestigator:P94109 Uniprot:P94109
Root	Isotig04091	26	0	5.571	2.13E-07	TAIR|locus:2060984 - symbol:HIS1-3 "histone H1-3" species:3702 "Arabidopsis thaliana" [GO:0000786 "nucleosome" evidence=IEA;ISS] [GO:0003677 "DNA binding" evidence=ISS] [GO:0005634 "nucleus" evidence=IEA] [GO:0006334 "nucleosome assembly" evidence=ISS] [GO:0009414 "response to water deprivation" evidence=IEP] [GO:0031492 "nucleosomal DNA binding" evidence=ISS] InterPro:IPR005818 InterPro:IPR005819 Pfam:PF00538 PRINTS:PR00624 PROSITE:PS51504 SMART:SM00526 GO:GO:0005634 EMBL:CP002685 GO:GO:0003677 InterPro:IPR011991 Gene3D:G3DSA:1.10.10.10 GO:GO:0009414 GO:GO:0006334 GO:GO:0000786 EMBL:AC006201 KO:K11275 EMBL:U72241 EMBL:U73781 EMBL:AY045797 EMBL:AY079414 EMBL:AY084603 IPI:IPI00539258 PIR:F84559 RefSeq:NP_179396.1 UniGene:At.24439

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						ProteinModelPortal:P94109 SMR:P94109 STRING:P94109 PRIDE:P94109 EnsemblPlants:AT2G18050.1 GeneID:816317 KEGG:ath:AT2G18050 TAIR:At2g18050 eggNOG:NOG258576 InParanoid:P94109 OMA:TKRTRSS PhylomeDB:P94109 ProtClustDB:CLSN2683930 ArrayExpress:P94109 Genevestigator:P94109 Uniprot:P94109
Root	Isotig04092	26	0	5.571	2.13E-07	TAIR|locus:2060984 - symbol:HIS1-3 "histone H1-3" species:3702 "Arabidopsis thaliana" [GO:0000786 "nucleosome" evidence=IEA;ISS] [GO:0003677 "DNA binding" evidence=ISS] [GO:0005634 "nucleus" evidence=IEA] [GO:0006334 "nucleosome assembly" evidence=ISS] [GO:0009414 "response to water deprivation" evidence=IEP] [GO:0031492 "nucleosomal DNA binding" evidence=ISS] InterPro:IPR005818 InterPro:IPR005819 Pfam:PF00538 PRINTS:PR00624 PROSITE:PS51504 SMART:SM00526 GO:GO:0005634 EMBL:CP002685 GO:GO:0003677 InterPro:IPR011991 Gene3D:G3DSA:1.10.10.10 GO:GO:0009414 GO:GO:0006334 GO:GO:0000786 EMBL:AC006201 KO:K11275 EMBL:U72241 EMBL:U73781 EMBL:AY045797 EMBL:AY079414 EMBL:AY084603 IPI:IPI00539258 PIR:F84559 RefSeq:NP_179396.1 UniGene:At.24439 ProteinModelPortal:P94109 SMR:P94109 STRING:P94109 PRIDE:P94109 EnsemblPlants:AT2G18050.1 GeneID:816317 KEGG:ath:AT2G18050 TAIR:At2g18050 eggNOG:NOG258576 InParanoid:P94109 OMA:TKRTRSS PhylomeDB:P94109 ProtClustDB:CLSN2683930 ArrayExpress:P94109 Genevestigator:P94109 Uniprot:P94109
Root	Isotig04101	0	15	-5.036	4.38E-05	TAIR|locus:2012607 - symbol:AT1G14550 species:3702 "Arabidopsis thaliana" [GO:0004601 "peroxidase activity" evidence=IEA;ISS] [GO:0020037 "heme binding" evidence=IEA] [GO:0071456 "cellular response to hypoxia" evidence=IEP] InterPro:IPR000823 InterPro:IPR002016 InterPro:IPR010255 InterPro:IPR019793 InterPro:IPR019794 Pfam:PF00141 PRINTS:PR00458 PRINTS:PR00461 PROSITE:PS00435 PROSITE:PS00436 PROSITE:PS50873 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005576 GO:GO:0006979 GO:GO:0071456 GO:GO:0020037 GO:GO:0004601 EMBL:AC010657 EMBL:AC012188 HOGENOM:HBG597790 SUPFAM:SSF48113 KO:K00430 ProtClustDB:CLSN2682957 IPI:IPI00544334 PIR:C86280 RefSeq:NP_172907.1 UniGene:At.51610 ProteinModelPortal:Q9M9Q9 SMR:Q9M9Q9 STRING:Q9M9Q9 PeroxiBase:81 PRIDE:Q9M9Q9 EnsemblPlants:AT1G14550.1 GeneID:838017 KEGG:ath:AT1G14550 GeneFarm:1516 TAIR:At1g14550 eggNOG:NOG274724 InParanoid:Q9M9Q9 OMA:YENSSDI PhylomeDB:Q9M9Q9 ArrayExpress:Q9M9Q9 Genevestigator:Q9M9Q9 GermOnline:AT1G14550 Uniprot:Q9M9Q9
Root	Isotig04102	0	16	-5.129	2.34E-05	TAIR|locus:2012607 - symbol:AT1G14550 species:3702 "Arabidopsis thaliana" [GO:0004601 "peroxidase activity" evidence=IEA;ISS] [GO:0020037 "heme binding" evidence=IEA] [GO:0071456 "cellular response to hypoxia" evidence=IEP] InterPro:IPR000823 InterPro:IPR002016 InterPro:IPR010255 InterPro:IPR019793 InterPro:IPR019794 Pfam:PF00141 PRINTS:PR00458 PRINTS:PR00461 PROSITE:PS00435 PROSITE:PS00436 PROSITE:PS50873 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005576 GO:GO:0006979 GO:GO:0071456 GO:GO:0020037 GO:GO:0004601 EMBL:AC010657 EMBL:AC012188 HOGENOM:HBG597790 SUPFAM:SSF48113 KO:K00430 ProtClustDB:CLSN2682957 IPI:IPI00544334 PIR:C86280 RefSeq:NP_172907.1 UniGene:At.51610 ProteinModelPortal:Q9M9Q9 SMR:Q9M9Q9 STRING:Q9M9Q9 PeroxiBase:81 PRIDE:Q9M9Q9 EnsemblPlants:AT1G14550.1 GeneID:838017 KEGG:ath:AT1G14550 GeneFarm:1516 TAIR:At1g14550 eggNOG:NOG274724 InParanoid:Q9M9Q9 OMA:YENSSDI PhylomeDB:Q9M9Q9 ArrayExpress:Q9M9Q9 Genevestigator:Q9M9Q9 GermOnline:AT1G14550 Uniprot:Q9M9Q9
Root	Isotig04103	0	15	-5.036	4.38E-05	TAIR|locus:2012607 - symbol:AT1G14550 species:3702 "Arabidopsis thaliana" [GO:0004601 "peroxidase activity" evidence=IEA;ISS] [GO:0020037 "heme binding" evidence=IEA] [GO:0071456 "cellular response to hypoxia" evidence=IEP] InterPro:IPR000823 InterPro:IPR002016 InterPro:IPR010255 InterPro:IPR019793 InterPro:IPR019794 Pfam:PF00141 PRINTS:PR00458 PRINTS:PR00461 PROSITE:PS00435 PROSITE:PS00436 PROSITE:PS50873 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005576 GO:GO:0006979 GO:GO:0071456 GO:GO:0020037 GO:GO:0004601 EMBL:AC010657 EMBL:AC012188 HOGENOM:HBG597790 SUPFAM:SSF48113 KO:K00430 ProtClustDB:CLSN2682957 IPI:IPI00544334 PIR:C86280 RefSeq:NP_172907.1 UniGene:At.51610 ProteinModelPortal:Q9M9Q9 SMR:Q9M9Q9 STRING:Q9M9Q9 PeroxiBase:81 PRIDE:Q9M9Q9 EnsemblPlants:AT1G14550.1 GeneID:838017 KEGG:ath:AT1G14550 GeneFarm:1516 TAIR:At1g14550 eggNOG:NOG274724 InParanoid:Q9M9Q9 OMA:YENSSDI PhylomeDB:Q9M9Q9 ArrayExpress:Q9M9Q9 Genevestigator:Q9M9Q9 GermOnline:AT1G14550 Uniprot:Q9M9Q9
Root	Isotig04104	0	16	-5.129	2.34E-05	TAIR|locus:2012607 - symbol:AT1G14550 species:3702 "Arabidopsis thaliana" [GO:0004601 "peroxidase activity" evidence=IEA;ISS] [GO:0020037 "heme binding" evidence=IEA] [GO:0071456 "cellular response to hypoxia" evidence=IEP] InterPro:IPR000823 InterPro:IPR002016 InterPro:IPR010255 InterPro:IPR019793

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						InterPro:IPR019794 Pfam:PF00141 PRINTS:PR00458 PRINTS:PR00461 PROSITE:PS00435 PROSITE:PS00436 PROSITE:PS50873 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005576 GO:GO:0006979 GO:GO:0071456 GO:GO:0020037 GO:GO:0004601 EMBL:AC010657 EMBL:AC012188 HOGENOM:HBG597790 SUPFAM:SSF48113 KO:K00430 ProtClustDB:CLSN2682957 IPI:IPI00544334 PIR:C86280 RefSeq:NP_172907.1 UniGene:At.51610 ProteinModelPortal:Q9M9Q9 SMR:Q9M9Q9 STRING:Q9M9Q9 PeroxiBase:81 PRIDE:Q9M9Q9 EnsemblPlants:AT1G14550.1 GeneID:838017 KEGG:ath:AT1G14550 GeneFarm:1516 TAIR:At1g14550 eggNOG:NOG274724 InParanoid:Q9M9Q9 OMA:YENSSDI PhylomeDB:Q9M9Q9 ArrayExpress:Q9M9Q9 Genevestigator:Q9M9Q9 GermOnline:AT1G14550 Uniprot:Q9M9Q9
Root	Isotig04105	350	0	9.322	4.44E-62	TIGR_CMR|BA_1222 - symbol:BA_1222 "conserved hypothetical protein" species:198094 "Bacillus anthracis str. Ames" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:AE016879 EMBL:AE017334 GenomeReviews:AE016879_GR GenomeReviews:AE017334_GR InterPro:IPR008160 Pfam:PF01391 EMBL:AB281483 EMBL:AJ516936 RefSeq:NP_843695.1 RefSeq:YP_017836.1 PDB:2R6Q PDBsum:2R6Q ProteinModelPortal:Q81JD7 SMR:Q81JD7 IntAct:Q81JD7 EnsemblBacteria:EBBACT00000011819 EnsemblBacteria:EBBACT00000016984 GeneID:1084744 GeneID:2814858 KEGG:ban:BA_1222 KEGG:bar:GBAA_1222 PATRIC:18780046 TIGR:BA_1222 TIGR:GBAA1222 HOGENOM:HBG342646 OMA:SDGLNPD ProtClustDB:CLSK824721 Uniprot:Q81JD7
Root	Isotig04106	292	0	9.061	8.14E-54	UNIPROTKB|G4MN25 - symbol:MGG_05575 "Putative uncharacterized protein" species:242507 "Magnaporthe oryzae 70-15" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CM001231 RefSeq:XP_360201.1 GeneID:2676055 InterPro:IPR021054 Pfam:PF12296 Uniprot:G4MN25
Root	Isotig04107	334	0	9.255	7.77E-60	TIGR_CMR|BA_1222 - symbol:BA_1222 "conserved hypothetical protein" species:198094 "Bacillus anthracis str. Ames" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:AE016879 EMBL:AE017334 GenomeReviews:AE016879_GR GenomeReviews:AE017334_GR InterPro:IPR008160 Pfam:PF01391 EMBL:AB281483 EMBL:AJ516936 RefSeq:NP_843695.1 RefSeq:YP_017836.1 PDB:2R6Q PDBsum:2R6Q ProteinModelPortal:Q81JD7 SMR:Q81JD7 IntAct:Q81JD7 EnsemblBacteria:EBBACT00000011819 EnsemblBacteria:EBBACT00000016984 GeneID:1084744 GeneID:2814858 KEGG:ban:BA_1222 KEGG:bar:GBAA_1222 PATRIC:18780046 TIGR:BA_1222 TIGR:GBAA1222 HOGENOM:HBG342646 OMA:SDGLNPD ProtClustDB:CLSK824721 Uniprot:Q81JD7
Root	Isotig04108	276	0	8.980	1.82E-51	UNIPROTKB|G4MN25 - symbol:MGG_05575 "Putative uncharacterized protein" species:242507 "Magnaporthe oryzae 70-15" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CM001231 RefSeq:XP_360201.1 GeneID:2676055 InterPro:IPR021054 Pfam:PF12296 Uniprot:G4MN25
Root	Isotig04113	0	11	-4.588	0.000569522	UNIPROTKB|Q8L7F6 - symbol:CnB "Calcineurin B-like protein" species:3888 "Pisum sativum" [GO:0005515 "protein binding" evidence=IPI] InterPro:IPR001125 InterPro:IPR002048 InterPro:IPR011992 PRINTS:PR00450 SMART:SM00054 GO:GO:0005509 GO:GO:0005515 InterPro:IPR018249 Gene3D:G3DSA:1.10.238.10 PROSITE:PS50222 EMBL:AY134619 EMBL:AY883569 ProteinModelPortal:Q8L7F6 SMR:Q8L7F6 IntAct:Q8L7F6 Uniprot:Q8L7F6
Root	Isotig04114	0	11	-4.588	0.000569522	UNIPROTKB|Q8L7F6 - symbol:CnB "Calcineurin B-like protein" species:3888 "Pisum sativum" [GO:0005515 "protein binding" evidence=IPI] InterPro:IPR001125 InterPro:IPR002048 InterPro:IPR011992 PRINTS:PR00450 SMART:SM00054 GO:GO:0005509 GO:GO:0005515 InterPro:IPR018249 Gene3D:G3DSA:1.10.238.10 PROSITE:PS50222 EMBL:AY134619 EMBL:AY883569 ProteinModelPortal:Q8L7F6 SMR:Q8L7F6 IntAct:Q8L7F6 Uniprot:Q8L7F6
Root	Isotig04115	0	11	-4.588	0.000569522	UNIPROTKB|Q8L7F6 - symbol:CnB "Calcineurin B-like protein" species:3888 "Pisum sativum" [GO:0005515 "protein binding" evidence=IPI] InterPro:IPR001125 InterPro:IPR002048 InterPro:IPR011992 PRINTS:PR00450 SMART:SM00054 GO:GO:0005509 GO:GO:0005515 InterPro:IPR018249 Gene3D:G3DSA:1.10.238.10 PROSITE:PS50222 EMBL:AY134619 EMBL:AY883569 ProteinModelPortal:Q8L7F6 SMR:Q8L7F6 IntAct:Q8L7F6 Uniprot:Q8L7F6
Root	Isotig04116	0	11	-4.588	0.000569522	UNIPROTKB|Q8L7F6 - symbol:CnB "Calcineurin B-like protein" species:3888 "Pisum sativum" [GO:0005515 "protein binding" evidence=IPI] InterPro:IPR001125 InterPro:IPR002048 InterPro:IPR011992 PRINTS:PR00450 SMART:SM00054 GO:GO:0005509 GO:GO:0005515 InterPro:IPR018249 Gene3D:G3DSA:1.10.238.10

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						PROSITE:PS50222 EMBL:AY134619 EMBL:AY883569 ProteinModelPortal:Q8L7F6 SMR:Q8L7F6 IntAct:Q8L7F6 Uniprot:Q8L7F6
Root	Isotig04117	24	4	2.456	0.000163328	TAIR|locus:2081695 - symbol:ATGSTF13 "AT3G62760" species:3702 "Arabidopsis thaliana" [GO:0004364 "glutathione transferase activity" evidence=ISS] [GO:0005737 "cytoplasm" evidence=NAS] [GO:0009407 "toxin catabolic process" evidence=TAS] InterPro:IPR004045 Pfam:PF02798 PROSITE:PS50404 InterPro:IPR004046 Pfam:PF00043 GO:GO:0005829 EMBL:CP002686 GenomeReviews:BA000014_GR EMBL:AL162651 GO:GO:0009636 InterPro:IPR012336 Gene3D:G3DSA:3.40.30.10 SUPFAM:SSF52833 InterPro:IPR010987 Gene3D:G3DSA:1.20.1050.10 SUPFAM:SSF47616 PROSITE:PS50405 InterPro:IPR017933 GO:GO:0004364 eggNOG:COG0625 HOGENOM:HBG753188 GO:GO:0009407 HSSP:Q9ZP62 IPI:IPI00528803 PIR:T48065 RefSeq:NP_191835.1 UniGene:At.54041 ProteinModelPortal:Q9LZI9 SMR:Q9LZI9 PRIDE:Q9LZI9 EnsemblPlants:AT3G62760.1 GeneID:825451 KEGG:ath:AT3G62760 TAIR:At3g62760 InParanoid:Q9LZI9 OMA:KAWWERL PhylomeDB:Q9LZI9 ProtClustDB:CLSN2684163 Genevestigator:Q9LZI9 Uniprot:Q9LZI9
Root	Isotig04118	24	4	2.456	0.000163328	TAIR|locus:2081695 - symbol:ATGSTF13 "AT3G62760" species:3702 "Arabidopsis thaliana" [GO:0004364 "glutathione transferase activity" evidence=ISS] [GO:0005737 "cytoplasm" evidence=NAS] [GO:0009407 "toxin catabolic process" evidence=TAS] InterPro:IPR004045 Pfam:PF02798 PROSITE:PS50404 InterPro:IPR004046 Pfam:PF00043 GO:GO:0005829 EMBL:CP002686 GenomeReviews:BA000014_GR EMBL:AL162651 GO:GO:0009636 InterPro:IPR012336 Gene3D:G3DSA:3.40.30.10 SUPFAM:SSF52833 InterPro:IPR010987 Gene3D:G3DSA:1.20.1050.10 SUPFAM:SSF47616 PROSITE:PS50405 InterPro:IPR017933 GO:GO:0004364 eggNOG:COG0625 HOGENOM:HBG753188 GO:GO:0009407 HSSP:Q9ZP62 IPI:IPI00528803 PIR:T48065 RefSeq:NP_191835.1 UniGene:At.54041 ProteinModelPortal:Q9LZI9 SMR:Q9LZI9 PRIDE:Q9LZI9 EnsemblPlants:AT3G62760.1 GeneID:825451 KEGG:ath:AT3G62760 TAIR:At3g62760 InParanoid:Q9LZI9 OMA:KAWWERL PhylomeDB:Q9LZI9 ProtClustDB:CLSN2684163 Genevestigator:Q9LZI9 Uniprot:Q9LZI9
Root	Isotig04119	24	4	2.456	0.000163328	TAIR|locus:2081695 - symbol:ATGSTF13 "AT3G62760" species:3702 "Arabidopsis thaliana" [GO:0004364 "glutathione transferase activity" evidence=ISS] [GO:0005737 "cytoplasm" evidence=NAS] [GO:0009407 "toxin catabolic process" evidence=TAS] InterPro:IPR004045 Pfam:PF02798 PROSITE:PS50404 InterPro:IPR004046 Pfam:PF00043 GO:GO:0005829 EMBL:CP002686 GenomeReviews:BA000014_GR EMBL:AL162651 GO:GO:0009636 InterPro:IPR012336 Gene3D:G3DSA:3.40.30.10 SUPFAM:SSF52833 InterPro:IPR010987 Gene3D:G3DSA:1.20.1050.10 SUPFAM:SSF47616 PROSITE:PS50405 InterPro:IPR017933 GO:GO:0004364 eggNOG:COG0625 HOGENOM:HBG753188 GO:GO:0009407 HSSP:Q9ZP62 IPI:IPI00528803 PIR:T48065 RefSeq:NP_191835.1 UniGene:At.54041 ProteinModelPortal:Q9LZI9 SMR:Q9LZI9 PRIDE:Q9LZI9 EnsemblPlants:AT3G62760.1 GeneID:825451 KEGG:ath:AT3G62760 TAIR:At3g62760 InParanoid:Q9LZI9 OMA:KAWWERL PhylomeDB:Q9LZI9 ProtClustDB:CLSN2684163 Genevestigator:Q9LZI9 Uniprot:Q9LZI9
Root	Isotig04120	24	4	2.456	0.000163328	TAIR|locus:2081695 - symbol:ATGSTF13 "AT3G62760" species:3702 "Arabidopsis thaliana" [GO:0004364 "glutathione transferase activity" evidence=ISS] [GO:0005737 "cytoplasm" evidence=NAS] [GO:0009407 "toxin catabolic process" evidence=TAS] InterPro:IPR004045 Pfam:PF02798 PROSITE:PS50404 InterPro:IPR004046 Pfam:PF00043 GO:GO:0005829 EMBL:CP002686 GenomeReviews:BA000014_GR EMBL:AL162651 GO:GO:0009636 InterPro:IPR012336 Gene3D:G3DSA:3.40.30.10 SUPFAM:SSF52833 InterPro:IPR010987 Gene3D:G3DSA:1.20.1050.10 SUPFAM:SSF47616 PROSITE:PS50405 InterPro:IPR017933 GO:GO:0004364 eggNOG:COG0625 HOGENOM:HBG753188 GO:GO:0009407 HSSP:Q9ZP62 IPI:IPI00528803 PIR:T48065 RefSeq:NP_191835.1 UniGene:At.54041 ProteinModelPortal:Q9LZI9 SMR:Q9LZI9 PRIDE:Q9LZI9 EnsemblPlants:AT3G62760.1 GeneID:825451 KEGG:ath:AT3G62760 TAIR:At3g62760 InParanoid:Q9LZI9 OMA:KAWWERL PhylomeDB:Q9LZI9 ProtClustDB:CLSN2684163 Genevestigator:Q9LZI9 Uniprot:Q9LZI9
Root	Isotig04121	14	0	4.678	0.000190242	No hit
Root	Isotig04122	14	0	4.678	0.000190242	No hit
Root	Isotig04159	0	11	-4.588	0.000569522	TAIR|locus:2200281 - symbol:ANN5 "annexin 5" species:3702 "Arabidopsis thaliana" [GO:0005509 "calcium ion binding" evidence=IEA;ISS] [GO:0005544 "calcium-dependent phospholipid binding" evidence=IEA;ISS] [GO:0009408 "response to heat" evidence=IEP] [GO:0009409 "response to cold" evidence=IEP] [GO:0009414 "response to water deprivation" evidence=IEP] [GO:0009639 "response to red or far red light" evidence=IEP] [GO:0009651 "response to salt stress" evidence=IEP] InterPro:IPR001464 InterPro:IPR018252 InterPro:IPR018502 Pfam:PF00191 PRINTS:PR00196 PROSITE:PS00223 SMART:SM00335 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005509 GO:GO:0009409 GO:GO:0009651 EMBL:AC012563 GO:GO:0009414 GO:GO:0009408 GO:GO:0009639 eggNOG:NOG267770 GO:GO:0005544

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						Gene3D:G3DSA:1.10.220.10 PANTHER:PTHR10502 SUPFAM:SSF47874 HOGENOM:HBG745057 InterPro:IPR009118 PANTHER:PTHR10502:SF10 EMBL:AY014797 EMBL:DQ446409 EMBL:DQ652921 IPI:IPI00532119 PIR:B96704 RefSeq:NP_564920.1 UniGene:At.18922 HSSP:P08758 ProteinModelPortal:Q9C9X3 SMR:Q9C9X3 PRIDE:Q9C9X3 EnsemblPlants:AT1G68090.1 GeneID:843137 KEGG:ath:AT1G68090 GeneFarm:1476 TAIR:At1g68090 InParanoid:Q9C9X3 OMA:LYKSMRR PhylomeDB:Q9C9X3 ProtClustDB:CLSN2917400 Genevestigator:Q9C9X3 Uniprot:Q9C9X3
Root	Isotig04160	0	11	-4.588	0.000569522	TAIR|locus:2200281 - symbol:ANN5 "annexin 5" species:3702 "Arabidopsis thaliana" [GO:0005509 "calcium ion binding" evidence=IEA;ISS] [GO:0005544 "calcium-dependent phospholipid binding" evidence=IEA;ISS] [GO:0009408 "response to heat" evidence=IEP] [GO:0009409 "response to cold" evidence=IEP] [GO:0009414 "response to water deprivation" evidence=IEP] [GO:0009639 "response to red or far red light" evidence=IEP] [GO:0009651 "response to salt stress" evidence=IEP] InterPro:IPR001464 InterPro:IPR018252 InterPro:IPR018502 Pfam:PF00191 PRINTS:PR00196 PROSITE:PS00223 SMART:SM00335 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005509 GO:GO:0009409 GO:GO:0009651 EMBL:AC012563 GO:GO:0009414 GO:GO:0009408 GO:GO:0009639 eggNOG:NOG267770 GO:GO:0005544 Gene3D:G3DSA:1.10.220.10 PANTHER:PTHR10502 SUPFAM:SSF47874 HOGENOM:HBG745057 InterPro:IPR009118 PANTHER:PTHR10502:SF10 EMBL:AY014797 EMBL:DQ446409 EMBL:DQ652921 IPI:IPI00532119 PIR:B96704 RefSeq:NP_564920.1 UniGene:At.18922 HSSP:P08758 ProteinModelPortal:Q9C9X3 SMR:Q9C9X3 PRIDE:Q9C9X3 EnsemblPlants:AT1G68090.1 GeneID:843137 KEGG:ath:AT1G68090 GeneFarm:1476 TAIR:At1g68090 InParanoid:Q9C9X3 OMA:LYKSMRR PhylomeDB:Q9C9X3 ProtClustDB:CLSN2917400 Genevestigator:Q9C9X3 Uniprot:Q9C9X3
Root	Isotig04173	1	20	-4.451	3.92E-06	TAIR|locus:2206835 - symbol:NUDT21 "AT1G73540" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0016787 "hydrolase activity" evidence=IEA;ISS] InterPro:IPR000086 InterPro:IPR015797 InterPro:IPR020084 Pfam:PF00293 PROSITE:PS00893 PROSITE:PS51462 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009507 GO:GO:0046872 Gene3D:G3DSA:3.90.79.10 SUPFAM:SSF55811 GO:GO:0016787 HOGENOM:HBG713158 EMBL:AC012396 EMBL:AY072369 EMBL:BT002080 IPI:IPI00544022 PIR:B96762 RefSeq:NP_177495.2 UniGene:At.34983 ProteinModelPortal:Q8VY81 SMR:Q8VY81 STRING:Q8VY81 PRIDE:Q8VY81 EnsemblPlants:AT1G73540.1 GeneID:843688 KEGG:ath:AT1G73540 TAIR:At1g73540 eggNOG:NOG240663 InParanoid:Q8VY81 OMA:RDLQRYN PhylomeDB:Q8VY81 ProtClustDB:CLSN2914542 ArrayExpress:Q8VY81 Genevestigator:Q8VY81 GermOnline:AT1G73540 Uniprot:Q8VY81
Root	Isotig04174	1	20	-4.451	3.92E-06	TAIR|locus:2206835 - symbol:NUDT21 "AT1G73540" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0016787 "hydrolase activity" evidence=IEA;ISS] InterPro:IPR000086 InterPro:IPR015797 InterPro:IPR020084 Pfam:PF00293 PROSITE:PS00893 PROSITE:PS51462 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009507 GO:GO:0046872 Gene3D:G3DSA:3.90.79.10 SUPFAM:SSF55811 GO:GO:0016787 HOGENOM:HBG713158 EMBL:AC012396 EMBL:AY072369 EMBL:BT002080 IPI:IPI00544022 PIR:B96762 RefSeq:NP_177495.2 UniGene:At.34983 ProteinModelPortal:Q8VY81 SMR:Q8VY81 STRING:Q8VY81 PRIDE:Q8VY81 EnsemblPlants:AT1G73540.1 GeneID:843688 KEGG:ath:AT1G73540 TAIR:At1g73540 eggNOG:NOG240663 InParanoid:Q8VY81 OMA:RDLQRYN PhylomeDB:Q8VY81 ProtClustDB:CLSN2914542 ArrayExpress:Q8VY81 Genevestigator:Q8VY81 GermOnline:AT1G73540 Uniprot:Q8VY81
Root	Isotig04175	1	19	-4.377	7.43E-06	TAIR|locus:2206835 - symbol:NUDT21 "AT1G73540" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0016787 "hydrolase activity" evidence=IEA;ISS] InterPro:IPR000086 InterPro:IPR015797 InterPro:IPR020084 Pfam:PF00293 PROSITE:PS00893 PROSITE:PS51462 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009507 GO:GO:0046872 Gene3D:G3DSA:3.90.79.10 SUPFAM:SSF55811 GO:GO:0016787 HOGENOM:HBG713158 EMBL:AC012396 EMBL:AY072369 EMBL:BT002080 IPI:IPI00544022 PIR:B96762 RefSeq:NP_177495.2 UniGene:At.34983 ProteinModelPortal:Q8VY81 SMR:Q8VY81 STRING:Q8VY81 PRIDE:Q8VY81 EnsemblPlants:AT1G73540.1 GeneID:843688 KEGG:ath:AT1G73540 TAIR:At1g73540 eggNOG:NOG240663 InParanoid:Q8VY81 OMA:RDLQRYN PhylomeDB:Q8VY81 ProtClustDB:CLSN2914542 ArrayExpress:Q8VY81 Genevestigator:Q8VY81 GermOnline:AT1G73540 Uniprot:Q8VY81
Root	Isotig04176	1	19	-4.377	7.43E-06	TAIR|locus:2206835 - symbol:NUDT21 "AT1G73540" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0016787 "hydrolase activity" evidence=IEA;ISS] InterPro:IPR000086

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						InterPro:IPR015797 InterPro:IPR020084 Pfam:PF00293 PROSITE:PS00893 PROSITE:PS51462 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009507 GO:GO:0046872 Gene3D:G3DSA:3.90.79.10 SUPFAM:SSF55811 GO:GO:0016787 HOGENOM:HBG713158 EMBL:AC012396 EMBL:AY072369 EMBL:BT002080 IPI:IPI00544022 PIR:B96762 RefSeq:NP_177495.2 UniGene:At.34983 ProteinModelPortal:Q8VY81 SMR:Q8VY81 STRING:Q8VY81 PRIDE:Q8VY81 EnsemblPlants:AT1G73540.1 GeneID:843688 KEGG:ath:AT1G73540 TAIR:At1g73540 eggNOG:NOG240663 InParanoid:Q8VY81 OMA:RDLQRYN PhylomeDB:Q8VY81 ProtClustDB:CLSN2914542 ArrayExpress:Q8VY81 Genevestigator:Q8VY81 GermOnline:AT1G73540 Uniprot:Q8VY81
Root	Isotig04225	14	1	3.678	0.000484579	TAIR|locus:2008445 - symbol:AT1G61260 "AT1G61260" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] InterPro:IPR008480 Pfam:PF05553 EMBL:AK227510 IPI:IPI00518212 TAIR:At1g61260 InParanoid:Q0WTN8 PhylomeDB:Q0WTN8 Genevestigator:Q0WTN8 Uniprot:Q0WTN8
Root	Isotig04226	14	1	3.678	0.000484579	TAIR|locus:2008445 - symbol:AT1G61260 "AT1G61260" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] InterPro:IPR008480 Pfam:PF05553 EMBL:AK227510 IPI:IPI00518212 TAIR:At1g61260 InParanoid:Q0WTN8 PhylomeDB:Q0WTN8 Genevestigator:Q0WTN8 Uniprot:Q0WTN8
Root	Isotig04227	14	1	3.678	0.000484579	TAIR|locus:2008445 - symbol:AT1G61260 "AT1G61260" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] InterPro:IPR008480 Pfam:PF05553 EMBL:AK227510 IPI:IPI00518212 TAIR:At1g61260 InParanoid:Q0WTN8 PhylomeDB:Q0WTN8 Genevestigator:Q0WTN8 Uniprot:Q0WTN8
Root	Isotig04228	14	1	3.678	0.000484579	TAIR|locus:2008445 - symbol:AT1G61260 "AT1G61260" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] InterPro:IPR008480 Pfam:PF05553 EMBL:AK227510 IPI:IPI00518212 TAIR:At1g61260 InParanoid:Q0WTN8 PhylomeDB:Q0WTN8 Genevestigator:Q0WTN8 Uniprot:Q0WTN8
Root	Isotig04233	324	59	2.328	4.19E-41	No hit
Root	Isotig04234	325	59	2.333	2.58E-41	No hit
Root	Isotig04235	324	49	2.596	2.43E-46	No hit
Root	Isotig04236	325	49	2.601	1.46E-46	No hit
Root	Isotig04414	1	118	-7.012	9.07E-30	UNIPROTKB|B2HIN2 - symbol:fadD26 "Long-chain-fatty-acid--AMP ligase FadD26" species:216594 "Mycobacterium marinum M" [GO:0008610 "lipid biosynthetic process" evidence=ISS] InterPro:IPR000873 Pfam:PF00501 eggNOG:COG0318 HOGENOM:HBG547964 GO:GO:0016874 GO:GO:0008610 GO:GO:0006631 KO:K12426 OMA:PARWIQQ ProtClustDB:PRK05850 EMBL:CP000854 RefSeq:YP_001850081.1 ProteinModelPortal:B2HIN2 STRING:B2HIN2 EnsemblBacteria:EBMYCT00000032275 GeneID:6226036 GenomeReviews:CP000854_GR KEGG:mmi:MMAR_1777 PATRIC:18064429 Uniprot:B2HIN2
Root	Isotig04415	1	118	-7.012	9.07E-30	UNIPROTKB|B2HIN2 - symbol:fadD26 "Long-chain-fatty-acid--AMP ligase FadD26" species:216594 "Mycobacterium marinum M" [GO:0008610 "lipid biosynthetic process" evidence=ISS] InterPro:IPR000873 Pfam:PF00501 eggNOG:COG0318 HOGENOM:HBG547964 GO:GO:0016874 GO:GO:0008610 GO:GO:0006631 KO:K12426 OMA:PARWIQQ ProtClustDB:PRK05850 EMBL:CP000854 RefSeq:YP_001850081.1 ProteinModelPortal:B2HIN2 STRING:B2HIN2 EnsemblBacteria:EBMYCT00000032275 GeneID:6226036 GenomeReviews:CP000854_GR KEGG:mmi:MMAR_1777 PATRIC:18064429 Uniprot:B2HIN2
Root	Isotig04416	0	51	-6.801	6.64E-14	UNIPROTKB|B2HIN2 - symbol:fadD26 "Long-chain-fatty-acid--AMP ligase FadD26" species:216594 "Mycobacterium marinum M" [GO:0008610 "lipid biosynthetic process" evidence=ISS] InterPro:IPR000873 Pfam:PF00501 eggNOG:COG0318 HOGENOM:HBG547964 GO:GO:0016874 GO:GO:0008610 GO:GO:0006631 KO:K12426 OMA:PARWIQQ ProtClustDB:PRK05850 EMBL:CP000854 RefSeq:YP_001850081.1 ProteinModelPortal:B2HIN2 STRING:B2HIN2 EnsemblBacteria:EBMYCT00000032275 GeneID:6226036 GenomeReviews:CP000854_GR KEGG:mmi:MMAR_1777 PATRIC:18064429 Uniprot:B2HIN2
Root	Isotig04438	11	98	-3.284	2.74E-20	TAIR|locus:2200216 - symbol:ATTPS6 "AT1G68020" species:3702 "Arabidopsis thaliana" [GO:0004805 "trehalose-phosphatase activity" evidence=IGI;ISS;IMP] [GO:0005992 "trehalose biosynthetic process" evidence=IGI;ISS] [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0003825 "alpha,alpha-trehalose-phosphate synthase (UDP-forming) activity" evidence=IGI;IMP] InterPro:IPR001830 InterPro:IPR003337 InterPro:IPR006379 Pfam:PF00982 Pfam:PF02358 EMBL:CP002684 GenomeReviews:CT485782_GR InterPro:IPR023214 Gene3D:G3DSA:3.40.50.1000 SUPFAM:SSF56784 EMBL:AC012563 GO:GO:0004805

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0005992 TIGRFAMs:TIGR01484 CAZy:GT20 eggNOG:COG0380 HOGENOM:HBG559076 KO:K00697 GO:GO:0003825 HSSP:P31677 TIGRFAMs:TIGR00685 OMA:LMQHPEW EMBL:AY046028 IPI:IPI00516798 IPI:IPI00538850 PIR:C96703 RefSeq:NP_564918.1 RefSeq:NP_974105.1 UniGene:At.19364 ProteinModelPortal:Q94AH8 SMR:Q94AH8 STRING:Q94AH8 PRIDE:Q94AH8 EnsemblPlants:AT1G68020.2 GeneID:843130 KEGG:ath:AT1G68020 TAIR:At1g68020 InParanoid:Q94AH8 PhylomeDB:Q94AH8 ProtClustDB:PLN02205 ArrayExpress:Q94AH8 Genevestigator:Q94AH8 Uniprot:Q94AH8
Root	Isotig04439	9	72	-3.129	9.81E-15	TAIR|locus:2200216 - symbol:ATTPS6 "AT1G68020" species:3702 "Arabidopsis thaliana" [GO:0004805 "trehalose-phosphatase activity" evidence=IGI;ISS;IMP] [GO:0005992 "trehalose biosynthetic process" evidence=IGI;ISS] [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0003825 "alpha,alpha-trehalose-phosphate synthase (UDP-forming) activity" evidence=IGI;IMP] InterPro:IPR001830 InterPro:IPR003337 InterPro:IPR006379 Pfam:PF00982 Pfam:PF02358 EMBL:CP002684 GenomeReviews:CT485782_GR InterPro:IPR023214 Gene3D:G3DSA:3.40.50.1000 SUPFAM:SSF56784 EMBL:AC012563 GO:GO:0004805 GO:GO:0005992 TIGRFAMs:TIGR01484 CAZy:GT20 eggNOG:COG0380 HOGENOM:HBG559076 KO:K00697 GO:GO:0003825 HSSP:P31677 TIGRFAMs:TIGR00685 OMA:LMQHPEW EMBL:AY046028 IPI:IPI00516798 IPI:IPI00538850 PIR:C96703 RefSeq:NP_564918.1 RefSeq:NP_974105.1 UniGene:At.19364 ProteinModelPortal:Q94AH8 SMR:Q94AH8 STRING:Q94AH8 PRIDE:Q94AH8 EnsemblPlants:AT1G68020.2 GeneID:843130 KEGG:ath:AT1G68020 TAIR:At1g68020 InParanoid:Q94AH8 PhylomeDB:Q94AH8 ProtClustDB:PLN02205 ArrayExpress:Q94AH8 Genevestigator:Q94AH8 Uniprot:Q94AH8
Root	Isotig04440	9	92	-3.483	5.13E-20	TAIR|locus:2200216 - symbol:ATTPS6 "AT1G68020" species:3702 "Arabidopsis thaliana" [GO:0004805 "trehalose-phosphatase activity" evidence=IGI;ISS;IMP] [GO:0005992 "trehalose biosynthetic process" evidence=IGI;ISS] [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0003825 "alpha,alpha-trehalose-phosphate synthase (UDP-forming) activity" evidence=IGI;IMP] InterPro:IPR001830 InterPro:IPR003337 InterPro:IPR006379 Pfam:PF00982 Pfam:PF02358 EMBL:CP002684 GenomeReviews:CT485782_GR InterPro:IPR023214 Gene3D:G3DSA:3.40.50.1000 SUPFAM:SSF56784 EMBL:AC012563 GO:GO:0004805 GO:GO:0005992 TIGRFAMs:TIGR01484 CAZy:GT20 eggNOG:COG0380 HOGENOM:HBG559076 KO:K00697 GO:GO:0003825 HSSP:P31677 TIGRFAMs:TIGR00685 OMA:LMQHPEW EMBL:AY046028 IPI:IPI00516798 IPI:IPI00538850 PIR:C96703 RefSeq:NP_564918.1 RefSeq:NP_974105.1 UniGene:At.19364 ProteinModelPortal:Q94AH8 SMR:Q94AH8 STRING:Q94AH8 PRIDE:Q94AH8 EnsemblPlants:AT1G68020.2 GeneID:843130 KEGG:ath:AT1G68020 TAIR:At1g68020 InParanoid:Q94AH8 PhylomeDB:Q94AH8 ProtClustDB:PLN02205 ArrayExpress:Q94AH8 Genevestigator:Q94AH8 Uniprot:Q94AH8
Root	Isotig04456	273	6	5.379	3.36E-63	TAIR|locus:2103488 - symbol:SIP2 "AT3G57520" species:3702 "Arabidopsis thaliana" [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=ISS] [GO:0006979 "response to oxidative stress" evidence=IEP] [GO:0080167 "response to karrikin" evidence=IEP] [GO:0034484 "raffinose catabolic process" evidence=IDA] [GO:0047274 "galactinol-sucrose galactosyltransferase activity" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR013785 GO:GO:0009506 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0006979 Gene3D:G3DSA:3.20.20.70 InterPro:IPR017853 SUPFAM:SSF51445 GO:GO:0080167 EMBL:AL133248 CAZy:GH36 eggNOG:NOG06986 InterPro:IPR008811 Pfam:PF05691 GO:GO:0034484 HOGENOM:HBG611539 KO:K06617 GO:GO:0047274 EMBL:AY050772 EMBL:AK226370 IPI:IPI00526258 IPI:IPI00541537 IPI:IPI00544535 PIR:T46188 RefSeq:NP_191311.1 RefSeq:NP_850715.1 UniGene:At.22207 UniGene:At.30900 ProteinModelPortal:Q94A08 STRING:Q94A08 PRIDE:Q94A08 EnsemblPlants:AT3G57520.1 GeneID:824919 KEGG:ath:AT3G57520 TAIR:At3g57520 InParanoid:Q9SCM1 OMA:QFMLLES PhylomeDB:Q94A08 ProtClustDB:PLN02219 BioCyc:MetaCyc:AT3G57520-MONOMER ArrayExpress:Q94A08 Uniprot:Q94A08
Root	Isotig04459	76	25	1.475	1.79E-06	TAIR|locus:2093227 - symbol:PLDALPHA1 "AT3G15730" species:3702 "Arabidopsis thaliana" [GO:0004630 "phospholipase D activity" evidence=ISS;IDA;IMP] [GO:0005634 "nucleus" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0030136 "clathrin-coated vesicle" evidence=IDA] [GO:0006631 "fatty acid metabolic process" evidence=IMP;TAS] [GO:0005515 "protein binding" evidence=IPI] [GO:0009507 "chloroplast" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0009789 "positive regulation of abscisic acid mediated signaling pathway" evidence=IMP] [GO:0010119 "regulation of stomatal movement" evidence=IMP] [GO:0009845 "seed germination" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005546 "phosphatidylinositol-4,5-bisphosphate binding" evidence=IDA] InterPro:IPR000008

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						InterPro:IPR001736 InterPro:IPR008973 InterPro:IPR011402 Pfam:PF00168 Pfam:PF00614 PIRSF:PIRSF036470 PROSITE:PS50035 SMART:SM00155 SMART:SM00239 GO:GO:0005829 GO:GO:0005739 GO:GO:0005886 GO:GO:0009506 GO:GO:0005634 GO:GO:0005773 GO:GO:0046686 GO:GO:0009507 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005509 GO:GO:0005515 GO:GO:0009738 GO:GO:0009873 GO:GO:0009789 GO:GO:0010119 GO:GO:0046470 GO:GO:0016042 GO:GO:0006631 GO:GO:0030136 GO:GO:0009845 SUPFAM:SSF49562 PROSITE:PS50004 GO:GO:0005546 EMBL:AB017071 eggNOG:COG1502 InterPro:IPR015679 PANTHER:PTHR18896 GO:GO:0070290 GO:GO:0004630 KO:K01115 EMBL:U36381 EMBL:AF428278 IPI:IPI00527854 RefSeq:NP_188194.1 UniGene:At.23882 ProteinModelPortal:Q38882 SMR:Q38882 IntAct:Q38882 STRING:Q38882 PRIDE:Q38882 DNASU:820816 EnsemblPlants:AT3G15730.1 GeneID:820816 KEGG:ath:AT3G15730 TAIR:At3g15730 HOGENOM:HBG748198 InParanoid:Q38882 OMA:KLQYFDV PhylomeDB:Q38882 ProtClustDB:PLN02270 ArrayExpress:Q38882 Genevestigator:Q38882 GermOnline:AT3G15730 InterPro:IPR024632 Pfam:PF12357 Uniprot:Q38882
Root	Isotig04460	55	17	1.565	2.20E-05	TAIR|locus:2093227 - symbol:PLDALPHA1 "AT3G15730" species:3702 "Arabidopsis thaliana" [GO:0004630 "phospholipase D activity" evidence=ISS;IDA;IMP] [GO:0005634 "nucleus" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0030136 "clathrin-coated vesicle" evidence=IDA] [GO:0006631 "fatty acid metabolic process" evidence=IMP;TAS] [GO:0005515 "protein binding" evidence=IPI] [GO:0009507 "chloroplast" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0009789 "positive regulation of abscisic acid mediated signaling pathway" evidence=IMP] [GO:0010119 "regulation of stomatal movement" evidence=IMP] [GO:0009845 "seed germination" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005546 "phosphatidylinositol-4,5-bisphosphate binding" evidence=IDA] InterPro:IPR000008 InterPro:IPR001736 InterPro:IPR008973 InterPro:IPR011402 Pfam:PF00168 Pfam:PF00614 PIRSF:PIRSF036470 PROSITE:PS50035 SMART:SM00155 SMART:SM00239 GO:GO:0005829 GO:GO:0005739 GO:GO:0005886 GO:GO:0009506 GO:GO:0005634 GO:GO:0005773 GO:GO:0046686 GO:GO:0009507 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005509 GO:GO:0005515 GO:GO:0009738 GO:GO:0009873 GO:GO:0009789 GO:GO:0010119 GO:GO:0046470 GO:GO:0016042 GO:GO:0006631 GO:GO:0030136 GO:GO:0009845 SUPFAM:SSF49562 PROSITE:PS50004 GO:GO:0005546 EMBL:AB017071 eggNOG:COG1502 InterPro:IPR015679 PANTHER:PTHR18896 GO:GO:0070290 GO:GO:0004630 KO:K01115 EMBL:U36381 EMBL:AF428278 IPI:IPI00527854 RefSeq:NP_188194.1 UniGene:At.23882 ProteinModelPortal:Q38882 SMR:Q38882 IntAct:Q38882 STRING:Q38882 PRIDE:Q38882 DNASU:820816 EnsemblPlants:AT3G15730.1 GeneID:820816 KEGG:ath:AT3G15730 TAIR:At3g15730 HOGENOM:HBG748198 InParanoid:Q38882 OMA:KLQYFDV PhylomeDB:Q38882 ProtClustDB:PLN02270 ArrayExpress:Q38882 Genevestigator:Q38882 GermOnline:AT3G15730 InterPro:IPR024632 Pfam:PF12357 Uniprot:Q38882
Root	Isotig04461	46	15	1.488	0.000184664	TAIR|locus:2093227 - symbol:PLDALPHA1 "AT3G15730" species:3702 "Arabidopsis thaliana" [GO:0004630 "phospholipase D activity" evidence=ISS;IDA;IMP] [GO:0005634 "nucleus" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0030136 "clathrin-coated vesicle" evidence=IDA] [GO:0006631 "fatty acid metabolic process" evidence=IMP;TAS] [GO:0005515 "protein binding" evidence=IPI] [GO:0009507 "chloroplast" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0009789 "positive regulation of abscisic acid mediated signaling pathway" evidence=IMP] [GO:0010119 "regulation of stomatal movement" evidence=IMP] [GO:0009845 "seed germination" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005546 "phosphatidylinositol-4,5-bisphosphate binding" evidence=IDA] InterPro:IPR000008 InterPro:IPR001736 InterPro:IPR008973 InterPro:IPR011402 Pfam:PF00168 Pfam:PF00614 PIRSF:PIRSF036470 PROSITE:PS50035 SMART:SM00155 SMART:SM00239 GO:GO:0005829 GO:GO:0005739 GO:GO:0005886 GO:GO:0009506 GO:GO:0005634 GO:GO:0005773 GO:GO:0046686 GO:GO:0009507 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005509 GO:GO:0005515 GO:GO:0009738 GO:GO:0009873 GO:GO:0009789 GO:GO:0010119 GO:GO:0046470 GO:GO:0016042 GO:GO:0006631 GO:GO:0030136 GO:GO:0009845 SUPFAM:SSF49562 PROSITE:PS50004 GO:GO:0005546 EMBL:AB017071 eggNOG:COG1502 InterPro:IPR015679 PANTHER:PTHR18896 GO:GO:0070290 GO:GO:0004630 KO:K01115 EMBL:U36381 EMBL:AF428278 IPI:IPI00527854 RefSeq:NP_188194.1 UniGene:At.23882 ProteinModelPortal:Q38882 SMR:Q38882 IntAct:Q38882 STRING:Q38882 PRIDE:Q38882 DNASU:820816 EnsemblPlants:AT3G15730.1 GeneID:820816 KEGG:ath:AT3G15730 TAIR:At3g15730 HOGENOM:HBG748198 InParanoid:Q38882

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						OMA:KLQYFDV PhylomeDB:Q38882 ProtClustDB:PLN02270 ArrayExpress:Q38882 Genevestigator:Q38882 GermOnline:AT3G15730 InterPro:IPR024632 Pfam:PF12357 Uniprot:Q38882
Root	Isotig04483	10	42	-2.199	1.05E-06	TAIR|locus:2152445 - symbol:SAG12 "AT5G45890" species:3702 "Arabidopsis thaliana" [GO:0006508 "proteolysis" evidence=ISS] [GO:0008234 "cysteine-type peptidase activity" evidence=ISS] [GO:0009723 "response to ethylene stimulus" evidence=IEP] [GO:0007568 "aging" evidence=IEP;TAS] [GO:0010150 "leaf senescence" evidence=TAS] [GO:0010282 "senescence-associated vacuole" evidence=IDA] [GO:0009817 "defense response to fungus, incompatible interaction" evidence=IEP] InterPro:IPR000668 InterPro:IPR013128 Pfam:PF00112 PRINTS:PR00705 SMART:SM00645 InterPro:IPR000169 EMBL:CP002688 GO:GO:0004197 GO:GO:0006508 InterPro:IPR013201 PANTHER:PTHR12411 Pfam:PF08246 SMART:SM00848 PROSITE:PS00640 PROSITE:PS00139 PROSITE:PS00639 GO:GO:0010150 GO:GO:0009817 EMBL:AB016870 HSSP:O65039 EMBL:AF370131 EMBL:AY040073 IPI:IPI00544181 RefSeq:NP_568651.1 UniGene:At.75256 UniGene:At.7710 ProteinModelPortal:Q9FJ47 SMR:Q9FJ47 IntAct:Q9FJ47 STRING:Q9FJ47 MEROPS:C01.117 PRIDE:Q9FJ47 EnsemblPlants:AT5G45890.1 GeneID:834629 KEGG:ath:AT5G45890 TAIR:At5g45890 InParanoid:Q9FJ47 OMA:NDEQALM PhylomeDB:Q9FJ47 ProtClustDB:CLSN2917735 ArrayExpress:Q9FJ47 Genevestigator:Q9FJ47 GO:GO:0010282 Uniprot:Q9FJ47
Root	Isotig04485	0	27	-5.884	3.19E-08	TAIR|locus:2152445 - symbol:SAG12 "AT5G45890" species:3702 "Arabidopsis thaliana" [GO:0006508 "proteolysis" evidence=ISS] [GO:0008234 "cysteine-type peptidase activity" evidence=ISS] [GO:0009723 "response to ethylene stimulus" evidence=IEP] [GO:0007568 "aging" evidence=IEP;TAS] [GO:0010150 "leaf senescence" evidence=TAS] [GO:0010282 "senescence-associated vacuole" evidence=IDA] [GO:0009817 "defense response to fungus, incompatible interaction" evidence=IEP] InterPro:IPR000668 InterPro:IPR013128 Pfam:PF00112 PRINTS:PR00705 SMART:SM00645 InterPro:IPR000169 EMBL:CP002688 GO:GO:0004197 GO:GO:0006508 InterPro:IPR013201 PANTHER:PTHR12411 Pfam:PF08246 SMART:SM00848 PROSITE:PS00640 PROSITE:PS00139 PROSITE:PS00639 GO:GO:0010150 GO:GO:0009817 EMBL:AB016870 HSSP:O65039 EMBL:AF370131 EMBL:AY040073 IPI:IPI00544181 RefSeq:NP_568651.1 UniGene:At.75256 UniGene:At.7710 ProteinModelPortal:Q9FJ47 SMR:Q9FJ47 IntAct:Q9FJ47 STRING:Q9FJ47 MEROPS:C01.117 PRIDE:Q9FJ47 EnsemblPlants:AT5G45890.1 GeneID:834629 KEGG:ath:AT5G45890 TAIR:At5g45890 InParanoid:Q9FJ47 OMA:NDEQALM PhylomeDB:Q9FJ47 ProtClustDB:CLSN2917735 ArrayExpress:Q9FJ47 Genevestigator:Q9FJ47 GO:GO:0010282 Uniprot:Q9FJ47
Root	Isotig04489	8	35	-2.258	5.90E-06	TAIR|locus:2088050 - symbol:RFR1 "AT3G23590" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:2000762 "regulation of phenylpropanoid metabolic process" evidence=IMP] EMBL:CP002686 EMBL:AB023036 IPI:IPI00527950 RefSeq:NP_189001.1 UniGene:At.23102 IntAct:Q9LUG9 PRIDE:Q9LUG9 EnsemblPlants:AT3G23590.1 GeneID:821938 KEGG:ath:AT3G23590 TAIR:At3g23590 InParanoid:Q9LUG9 OMA:VNGRINQ PhylomeDB:Q9LUG9 ProtClustDB:CLSN2684326 Genevestigator:Q9LUG9 Uniprot:Q9LUG9
Root	Isotig04498	48	218	-2.312	1.88E-30	TAIR|locus:2057981 - symbol:PAL1 "PHE ammonia lyase 1" species:3702 "Arabidopsis thaliana" [GO:0005737 "cytoplasm" evidence=IEA] [GO:0009699 "phenylpropanoid biosynthetic process" evidence=TAS] [GO:0045548 "phenylalanine ammonia-lyase activity" evidence=ISS;IDA;TAS] [GO:0006979 "response to oxidative stress" evidence=IEP] [GO:0080167 "response to karrikin" evidence=IEP] [GO:0009555 "pollen development" evidence=IMP] [GO:0009819 "drought recovery" evidence=IMP] [GO:0010224 "response to UV-B" evidence=IMP] [GO:0046244 "salicylic acid catabolic process" evidence=IMP] [GO:0046274 "lignin catabolic process" evidence=IMP] [GO:0006952 "defense response" evidence=TAS] [GO:0009611 "response to wounding" evidence=TAS] InterPro:IPR001106 InterPro:IPR005922 InterPro:IPR008948 InterPro:IPR022313 Pfam:PF00221 PROSITE:PS00488 GO:GO:0005737 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0006979 GO:GO:0009058 GO:GO:0080167 EMBL:AC006922 GO:GO:0009555 SUPFAM:SSF48557 GO:GO:0006559 InterPro:IPR024083 Gene3D:G3DSA:1.10.275.10 GO:GO:0010224 eggNOG:COG2986 GO:GO:0046274 EMBL:L33677 EMBL:AY303128 EMBL:AY045919 EMBL:AY079363 EMBL:BT003330 EMBL:X62747 IPI:IPI00519512 PIR:G84787 PIR:S52990 RefSeq:NP_181241.1 UniGene:At.21614 UniGene:At.22705 ProteinModelPortal:P35510 SMR:P35510 IntAct:P35510 STRING:P35510 PRIDE:P35510 EnsemblPlants:AT2G37040.1 GeneID:818280 KEGG:ath:AT2G37040 TAIR:At2g37040 HOGENOM:HBG318028 InParanoid:P35510 KO:K10775 OMA:QRGADFL PhylomeDB:P35510 ProtClustDB:PLN02457 BRENDA:4.3.1.24 Genevestigator:P35510 GermOnline:AT2G37040 GO:GO:0045548 GO:GO:0009819 GO:GO:0046244 InterPro:IPR023144 Gene3D:G3DSA:1.10.274.20 TIGRFAMs:TIGR01226 Uniprot:P35510

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig04499	37	173	-2.354	5.33E-25	TAIR|locus:2057981 - symbol:PAL1 "PHE ammonia lyase 1" species:3702 "Arabidopsis thaliana" [GO:0005737 "cytoplasm" evidence=IEA] [GO:0009699 "phenylpropanoid biosynthetic process" evidence=TAS] [GO:0045548 "phenylalanine ammonia-lyase activity" evidence=ISS;IDA;TAS] [GO:0006979 "response to oxidative stress" evidence=IEP] [GO:0080167 "response to karrikin" evidence=IEP] [GO:0009555 "pollen development" evidence=IMP] [GO:0009819 "drought recovery" evidence=IMP] [GO:0010224 "response to UV-B" evidence=IMP] [GO:0046244 "salicylic acid catabolic process" evidence=IMP] [GO:0046274 "lignin catabolic process" evidence=IMP] [GO:0006952 "defense response" evidence=TAS] [GO:0009611 "response to wounding" evidence=TAS] InterPro:IPR001106 InterPro:IPR005922 InterPro:IPR008948 InterPro:IPR022313 Pfam:PF00221 PROSITE:PS00488 GO:GO:0005737 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0006979 GO:GO:0009058 GO:GO:0080167 EMBL:AC006922 GO:GO:0009555 SUPFAM:SSF48557 GO:GO:0006559 InterPro:IPR024083 Gene3D:G3DSA:1.10.275.10 GO:GO:0010224 eggNOG:COG2986 GO:GO:0046274 EMBL:L33677 EMBL:AY303128 EMBL:AY045919 EMBL:AY079363 EMBL:BT003330 EMBL:X62747 IPI:IPI00519512 PIR:G84787 PIR:S52990 RefSeq:NP_181241.1 UniGene:At.21614 UniGene:At.22705 ProteinModelPortal:P35510 SMR:P35510 IntAct:P35510 STRING:P35510 PRIDE:P35510 EnsemblPlants:AT2G37040.1 GeneID:818280 KEGG:ath:AT2G37040 TAIR:At2g37040 HOGENOM:HBG318028 InParanoid:P35510 KO:K10775 OMA:QRGADFL PhylomeDB:P35510 ProtClustDB:PLN02457 BRENDA:4.3.1.24 Genevestigator:P35510 GermOnline:AT2G37040 GO:GO:0045548 GO:GO:0009819 GO:GO:0046244 InterPro:IPR023144 Gene3D:G3DSA:1.10.274.20 TIGRFAMs:TIGR01226 Uniprot:P35510
Root	Isotig04500	59	190	-1.816	4.94E-20	TAIR|locus:2057981 - symbol:PAL1 "PHE ammonia lyase 1" species:3702 "Arabidopsis thaliana" [GO:0005737 "cytoplasm" evidence=IEA] [GO:0009699 "phenylpropanoid biosynthetic process" evidence=TAS] [GO:0045548 "phenylalanine ammonia-lyase activity" evidence=ISS;IDA;TAS] [GO:0006979 "response to oxidative stress" evidence=IEP] [GO:0080167 "response to karrikin" evidence=IEP] [GO:0009555 "pollen development" evidence=IMP] [GO:0009819 "drought recovery" evidence=IMP] [GO:0010224 "response to UV-B" evidence=IMP] [GO:0046244 "salicylic acid catabolic process" evidence=IMP] [GO:0046274 "lignin catabolic process" evidence=IMP] [GO:0006952 "defense response" evidence=TAS] [GO:0009611 "response to wounding" evidence=TAS] InterPro:IPR001106 InterPro:IPR005922 InterPro:IPR008948 InterPro:IPR022313 Pfam:PF00221 PROSITE:PS00488 GO:GO:0005737 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0006979 GO:GO:0009058 GO:GO:0080167 EMBL:AC006922 GO:GO:0009555 SUPFAM:SSF48557 GO:GO:0006559 InterPro:IPR024083 Gene3D:G3DSA:1.10.275.10 GO:GO:0010224 eggNOG:COG2986 GO:GO:0046274 EMBL:L33677 EMBL:AY303128 EMBL:AY045919 EMBL:AY079363 EMBL:BT003330 EMBL:X62747 IPI:IPI00519512 PIR:G84787 PIR:S52990 RefSeq:NP_181241.1 UniGene:At.21614 UniGene:At.22705 ProteinModelPortal:P35510 SMR:P35510 IntAct:P35510 STRING:P35510 PRIDE:P35510 EnsemblPlants:AT2G37040.1 GeneID:818280 KEGG:ath:AT2G37040 TAIR:At2g37040 HOGENOM:HBG318028 InParanoid:P35510 KO:K10775 OMA:QRGADFL PhylomeDB:P35510 ProtClustDB:PLN02457 BRENDA:4.3.1.24 Genevestigator:P35510 GermOnline:AT2G37040 GO:GO:0045548 GO:GO:0009819 GO:GO:0046244 InterPro:IPR023144 Gene3D:G3DSA:1.10.274.20 TIGRFAMs:TIGR01226 Uniprot:P35510
Root	Isotig04515	119	61	0.835	0.000156576	TAIR|locus:2161815 - symbol:HSP81-2 "AT5G56030" species:3702 "Arabidopsis thaliana" [GO:0005524 "ATP binding" evidence=ISS;IDA] [GO:0006457 "protein folding" evidence=ISS] [GO:0009408 "response to heat" evidence=IEP] [GO:0005515 "protein binding" evidence=IPI] [GO:0006952 "defense response" evidence=IMP] [GO:0009908 "flower development" evidence=IMP] [GO:0048366 "leaf development" evidence=IMP] [GO:0050821 "protein stabilization" evidence=IMP] [GO:0005618 "cell wall" evidence=IDA] [GO:0010286 "heat acclimation" evidence=IEP] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009414 "response to water deprivation" evidence=IMP] [GO:0009651 "response to salt stress" evidence=IMP] [GO:0009816 "defense response to bacterium, incompatible interaction" evidence=IMP] [GO:0016887 "ATPase activity" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0010187 "negative regulation of seed germination" evidence=IMP] [GO:0090332 "stomatal closure" evidence=IMP] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR001404 InterPro:IPR003594 InterPro:IPR019805 Pfam:PF00183 PIRSF:PIRSF002583 PROSITE:PS00298 SMART:SM00387 GO:GO:0005829 GO:GO:0005739 GO:GO:0009506 GO:GO:0005524 GO:GO:0005634 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005618 GO:GO:0006457 GO:GO:0050821 GO:GO:0051082 GO:GO:0016887 GO:GO:0009651 GO:GO:0009414 GO:GO:0010187 GO:GO:0048366 GO:GO:0010286 GO:GO:0009908 GO:GO:0009816 Gene3D:G3DSA:3.30.565.10 SUPFAM:SSF55874 InterPro:IPR020568 SUPFAM:SSF54211 EMBL:AB011476 eggNOG:COG0326 HOGENOM:HBG631012 PANTHER:PTHR11528 InterPro:IPR020575 PRINTS:PR00775

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						KO:K04079 ProtClustDB:CLSN2686109 EMBL:AY062750 EMBL:AY128805 EMBL:BT001944 EMBL:BT002535 IPI:IPI00537112 RefSeq:NP_200414.1 UniGene:At.25243 UniGene:At.27546 UniGene:At.45945 ProteinModelPortal:P55737 SMR:P55737 IntAct:P55737 STRING:P55737 PRIDE:P55737 EnsemblPlants:AT5G56030.1 GeneID:835701 KEGG:ath:AT5G56030 TAIR:At5g56030 InParanoid:P55737 OMA:GFSKNIK PhylomeDB:P55737 Genevestigator:P55737 GermOnline:AT5G56030 GO:GO:0090332 Uniprot:P55737
Root	Isotig04516	14	39	-1.607	0.000139286	TAIR|locus:2036199 - symbol:AT1G15740 "AT1G15740" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] EMBL:CP002684 GenomeReviews:CT485782_GR HSSP:P25147 eggNOG:NOG69615 UniGene:At.48194 UniGene:At.69991 EMBL:AY142631 IPI:IPI00545317 RefSeq:NP_563980.2 ProteinModelPortal:Q8H1Q4 SMR:Q8H1Q4 STRING:Q8H1Q4 PRIDE:Q8H1Q4 EnsemblPlants:AT1G15740.1 GeneID:838143 KEGG:ath:AT1G15740 TAIR:At1g15740 HOGENOM:HBG592941 InParanoid:Q8H1Q4 OMA:GSNGLRH PhylomeDB:Q8H1Q4 ProtClustDB:CLSN2679913 Genevestigator:Q8H1Q4 Uniprot:Q8H1Q4
Root	Isotig04517	15	38	-1.470	0.00042777	TAIR|locus:2036199 - symbol:AT1G15740 "AT1G15740" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] EMBL:CP002684 GenomeReviews:CT485782_GR HSSP:P25147 eggNOG:NOG69615 UniGene:At.48194 UniGene:At.69991 EMBL:AY142631 IPI:IPI00545317 RefSeq:NP_563980.2 ProteinModelPortal:Q8H1Q4 SMR:Q8H1Q4 STRING:Q8H1Q4 PRIDE:Q8H1Q4 EnsemblPlants:AT1G15740.1 GeneID:838143 KEGG:ath:AT1G15740 TAIR:At1g15740 HOGENOM:HBG592941 InParanoid:Q8H1Q4 OMA:GSNGLRH PhylomeDB:Q8H1Q4 ProtClustDB:CLSN2679913 Genevestigator:Q8H1Q4 Uniprot:Q8H1Q4
Root	Isotig04518	15	38	-1.470	0.00042777	TAIR|locus:2036199 - symbol:AT1G15740 "AT1G15740" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] EMBL:CP002684 GenomeReviews:CT485782_GR HSSP:P25147 eggNOG:NOG69615 UniGene:At.48194 UniGene:At.69991 EMBL:AY142631 IPI:IPI00545317 RefSeq:NP_563980.2 ProteinModelPortal:Q8H1Q4 SMR:Q8H1Q4 STRING:Q8H1Q4 PRIDE:Q8H1Q4 EnsemblPlants:AT1G15740.1 GeneID:838143 KEGG:ath:AT1G15740 TAIR:At1g15740 HOGENOM:HBG592941 InParanoid:Q8H1Q4 OMA:GSNGLRH PhylomeDB:Q8H1Q4 ProtClustDB:CLSN2679913 Genevestigator:Q8H1Q4 Uniprot:Q8H1Q4
Root	Isotig04520	34	4	2.958	7.26E-07	TAIR|locus:2159300 - symbol:ABCF1 "AT5G60790" species:3702 "Arabidopsis thaliana" [GO:0005215 "transporter activity" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] InterPro:IPR003439 InterPro:IPR003593 InterPro:IPR017871 Pfam:PF00005 PROSITE:PS00211 PROSITE:PS50893 SMART:SM00382 GO:GO:0005886 GO:GO:0005524 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0006810 GO:GO:0016887 HOGENOM:HBG758042 EMBL:AB015472 EMBL:AY140066 EMBL:BT000946 EMBL:BT008363 EMBL:AK317570 EMBL:AK317690 IPI:IPI00540333 RefSeq:NP_200887.1 UniGene:At.9321 ProteinModelPortal:Q9FJH6 SMR:Q9FJH6 IntAct:Q9FJH6 STRING:Q9FJH6 PRIDE:Q9FJH6 EnsemblPlants:AT5G60790.1 GeneID:836200 KEGG:ath:AT5G60790 TAIR:At5g60790 eggNOG:COG0488 InParanoid:Q9FJH6 KO:K06185 OMA:YHQHLHE PhylomeDB:Q9FJH6 ProtClustDB:CLSN2686703 ArrayExpress:Q9FJH6 Genevestigator:Q9FJH6 Uniprot:Q9FJH6
Root	Isotig04521	35	4	3.000	4.17E-07	TAIR|locus:2159300 - symbol:ABCF1 "AT5G60790" species:3702 "Arabidopsis thaliana" [GO:0005215 "transporter activity" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] InterPro:IPR003439 InterPro:IPR003593 InterPro:IPR017871 Pfam:PF00005 PROSITE:PS00211 PROSITE:PS50893 SMART:SM00382 GO:GO:0005886 GO:GO:0005524 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0006810 GO:GO:0016887 HOGENOM:HBG758042 EMBL:AB015472 EMBL:AY140066 EMBL:BT000946 EMBL:BT008363 EMBL:AK317570 EMBL:AK317690 IPI:IPI00540333 RefSeq:NP_200887.1 UniGene:At.9321 ProteinModelPortal:Q9FJH6 SMR:Q9FJH6 IntAct:Q9FJH6 STRING:Q9FJH6 PRIDE:Q9FJH6 EnsemblPlants:AT5G60790.1 GeneID:836200 KEGG:ath:AT5G60790 TAIR:At5g60790 eggNOG:COG0488 InParanoid:Q9FJH6 KO:K06185 OMA:YHQHLHE PhylomeDB:Q9FJH6 ProtClustDB:CLSN2686703 ArrayExpress:Q9FJH6 Genevestigator:Q9FJH6 Uniprot:Q9FJH6
Root	Isotig04522	64	4	3.871	3.12E-14	TAIR|locus:2181833 - symbol:HSC70-1 "heat shock cognate protein 70-1" species:3702 "Arabidopsis thaliana" [GO:0005524 "ATP binding" evidence=IEA] [GO:0005829 "cytosol" evidence=IDA;RCA;TAS] [GO:0006457 "protein folding" evidence=TAS] [GO:0009408 "response to heat" evidence=IEP;IMP] [GO:0005634 "nucleus" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005730 "nucleolus" evidence=IDA] [GO:0009615 "response to virus" evidence=IEP] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane"

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0042742 "defense response to bacterium" evidence=IMP] [GO:0050832 "defense response to fungus" evidence=IMP] [GO:0048046 "apoplast" evidence=IDA] [GO:0002020 "protease binding" evidence=IPI] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0010187 "negative regulation of seed germination" evidence=IMP] [GO:0090332 "stomatal closure" evidence=IMP] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR001023 PRINTS:PR00301 Pfam:PF00012 Prosite:PS00297 Prosite:PS00329 Prosite:PS01036 GO:GO:0005886 GO:GO:0009506 GO:GO:0005524 GO:GO:0048046 GO:GO:0046686 GO:GO:0005774 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005618 GO:GO:0009507 GO:GO:0042742 GO:GO:0005730 GO:GO:0050832 GO:GO:0002020 GO:GO:0009409 GO:GO:0009408 GO:GO:0009615 GO:GO:0010187 UniGene:At.23663 GO:GO:0022626 eggNOG:COG0443 HOGENOM:HBG334976 InterPro:IPR018181 InterPro:IPR013126 PANTHER:PTHR19375 EMBL:AL162971 KO:K03283 OMA:MAKSTAI GO:GO:0090332 EMBL:X74604 EMBL:AY035123 EMBL:AY057481 EMBL:AY120747 EMBL:BT002754 EMBL:M23108 EMBL:M23105 EMBL:X77199 IPI:IPI00543293 PIR:S46302 PIR:T48271 RefSeq:NP_195870.1 UniGene:At.75212 ProteinModelPortal:P22953 SMR:P22953 IntAct:P22953 STRING:P22953 TCDB:1.A.33.1.1 SWISS-2DPAGE:P22953 World-2DPAGE:0003:P22953 PRIDE:P22953 ProMEX:P22953 EnsemblPlants:AT5G02500.1 GeneID:831020 KEGG:ath:AT5G02500 TAIR:At5g02500 InParanoid:P22953 PhylomeDB:P22953 ProtClustDB:CLSN2916777 Genevestigator:P22953 GermOnline:AT5G02500 Uniprot:P22953
Root	Isotig04523	64	9	2.701	8.63E-11	TAIR|locus:2181833 - symbol:HSC70-1 "heat shock cognate protein 70-1" species:3702 "Arabidopsis thaliana" [GO:0005524 "ATP binding" evidence=IEA] [GO:0005829 "cytosol" evidence=IDA;RCA;TAS] [GO:0006457 "protein folding" evidence=TAS] [GO:0009408 "response to heat" evidence=IEP;IMP] [GO:0005634 "nucleus" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005730 "nucleolus" evidence=IDA] [GO:0009615 "response to virus" evidence=IEP] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0042742 "defense response to bacterium" evidence=IMP] [GO:0050832 "defense response to fungus" evidence=IMP] [GO:0048046 "apoplast" evidence=IDA] [GO:0002020 "protease binding" evidence=IPI] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0010187 "negative regulation of seed germination" evidence=IMP] [GO:0090332 "stomatal closure" evidence=IMP] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR001023 PRINTS:PR00301 Pfam:PF00012 Prosite:PS00297 Prosite:PS00329 Prosite:PS01036 GO:GO:0005886 GO:GO:0009506 GO:GO:0005524 GO:GO:0048046 GO:GO:0046686 GO:GO:0005774 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005618 GO:GO:0009507 GO:GO:0042742 GO:GO:0005730 GO:GO:0050832 GO:GO:0002020 GO:GO:0009409 GO:GO:0009408 GO:GO:0009615 GO:GO:0010187 UniGene:At.23663 GO:GO:0022626 eggNOG:COG0443 HOGENOM:HBG334976 InterPro:IPR018181 InterPro:IPR013126 PANTHER:PTHR19375 EMBL:AL162971 KO:K03283 OMA:MAKSTAI GO:GO:0090332 EMBL:X74604 EMBL:AY035123 EMBL:AY057481 EMBL:AY120747 EMBL:BT002754 EMBL:M23108 EMBL:M23105 EMBL:X77199 IPI:IPI00543293 PIR:S46302 PIR:T48271 RefSeq:NP_195870.1 UniGene:At.75212 ProteinModelPortal:P22953 SMR:P22953 IntAct:P22953 STRING:P22953 TCDB:1.A.33.1.1 SWISS-2DPAGE:P22953 World-2DPAGE:0003:P22953 PRIDE:P22953 ProMEX:P22953 EnsemblPlants:AT5G02500.1 GeneID:831020 KEGG:ath:AT5G02500 TAIR:At5g02500 InParanoid:P22953 PhylomeDB:P22953 ProtClustDB:CLSN2916777 Genevestigator:P22953 GermOnline:AT5G02500 Uniprot:P22953
Root	Isotig04524	61	6	3.217	5.21E-12	TAIR|locus:2181833 - symbol:HSC70-1 "heat shock cognate protein 70-1" species:3702 "Arabidopsis thaliana" [GO:0005524 "ATP binding" evidence=IEA] [GO:0005829 "cytosol" evidence=IDA;RCA;TAS] [GO:0006457 "protein folding" evidence=TAS] [GO:0009408 "response to heat" evidence=IEP;IMP] [GO:0005634 "nucleus" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005730 "nucleolus" evidence=IDA] [GO:0009615 "response to virus" evidence=IEP] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0042742 "defense response to bacterium" evidence=IMP] [GO:0050832 "defense response to fungus" evidence=IMP] [GO:0048046 "apoplast" evidence=IDA] [GO:0002020 "protease binding" evidence=IPI] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0010187 "negative regulation of seed germination" evidence=IMP] [GO:0090332 "stomatal closure" evidence=IMP] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR001023

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						PRINTS:PR00301 Pfam:PF00012 Prosite:PS00297 Prosite:PS00329 Prosite:PS01036 GO:GO:0005886 GO:GO:0009506 GO:GO:0005524 GO:GO:0048046 GO:GO:0046686 GO:GO:0005774 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005618 GO:GO:0009507 GO:GO:0042742 GO:GO:0005730 GO:GO:0050832 GO:GO:0002020 GO:GO:0009409 GO:GO:0009408 GO:GO:0009615 GO:GO:0010187 UniGene:At.23663 GO:GO:0022626 eggNOG:COG0443 HOGENOM:HBG334976 InterPro:IPR018181 InterPro:IPR013126 PANTHER:PTHR19375 EMBL:AL162971 KO:K03283 OMA:MAKSTAI GO:GO:0090332 EMBL:X74604 EMBL:AY035123 EMBL:AY057481 EMBL:AY120747 EMBL:BT002754 EMBL:M23108 EMBL:M23105 EMBL:X77199 IPI:IPI00543293 PIR:S46302 PIR:T48271 RefSeq:NP_195870.1 UniGene:At.75212 ProteinModelPortal:P22953 SMR:P22953 IntAct:P22953 STRING:P22953 TCDB:1.A.33.1.1 SWISS-2DPAGE:P22953 World-2DPAGE:0003:P22953 PRIDE:P22953 ProMEX:P22953 EnsemblPlants:AT5G02500.1 GeneID:831020 KEGG:ath:AT5G02500 TAIR:At5g02500 InParanoid:P22953 PhylomeDB:P22953 ProtClustDB:CLSN2916777 Genevestigator:P22953 GermOnline:AT5G02500 Uniprot:P22953
Root	Isotig04526	17	43	-1.468	0.000182074	TAIR|locus:2179250 - symbol:AT5G25100 "AT5G25100" species:3702 "Arabidopsis thaliana" [GO:0016021 "integral to membrane" evidence=ISS] [GO:0005794 "Golgi apparatus" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR004240 Pfam:PF02990 GO:GO:0016021 GO:GO:0005886 GO:GO:0009506 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005794 eggNOG:NOG315241 HOGENOM:HBG524073 PANTHER:PTHR10766 OMA:VIACSQI EMBL:AF360135 IPI:IPI00521208 RefSeq:NP_568465.1 UniGene:At.19004 UniGene:At.74873 STRING:Q9C5N2 PRIDE:Q9C5N2 EnsemblPlants:AT5G25100.1 GeneID:832581 KEGG:ath:AT5G25100 TAIR:At5g25100 InParanoid:Q9C5N2 PhylomeDB:Q9C5N2 ProtClustDB:CLSN2917711 ArrayExpress:Q9C5N2 Genevestigator:Q9C5N2 Uniprot:Q9C5N2
Root	Isotig04527	16	40	-1.451	0.000345313	TAIR|locus:2179250 - symbol:AT5G25100 "AT5G25100" species:3702 "Arabidopsis thaliana" [GO:0016021 "integral to membrane" evidence=ISS] [GO:0005794 "Golgi apparatus" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR004240 Pfam:PF02990 GO:GO:0016021 GO:GO:0005886 GO:GO:0009506 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005794 eggNOG:NOG315241 HOGENOM:HBG524073 PANTHER:PTHR10766 OMA:VIACSQI EMBL:AF360135 IPI:IPI00521208 RefSeq:NP_568465.1 UniGene:At.19004 UniGene:At.74873 STRING:Q9C5N2 PRIDE:Q9C5N2 EnsemblPlants:AT5G25100.1 GeneID:832581 KEGG:ath:AT5G25100 TAIR:At5g25100 InParanoid:Q9C5N2 PhylomeDB:Q9C5N2 ProtClustDB:CLSN2917711 ArrayExpress:Q9C5N2 Genevestigator:Q9C5N2 Uniprot:Q9C5N2
Root	Isotig04537	11	33	-1.714	0.000243809	TAIR|locus:2026177 - symbol:AT1G62660 species:3702 "Arabidopsis thaliana" [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=IEA;ISS] [GO:0071370 "cellular response to gibberellin stimulus" evidence=IEP] [GO:0000325 "plant-type vacuole" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0009617 "response to bacterium" evidence=IEP] InterPro:IPR001362 InterPro:IPR018053 InterPro:IPR021792 Pfam:PF11837 PROSITE:PS00609 SMART:SM00640 EMBL:CP002684 GO:GO:0005975 InterPro:IPR008985 SUPFAM:SSF49899 InterPro:IPR023296 SUPFAM:SSF75005 CAZy:GH32 KO:K01193 GO:GO:0004575 InterPro:IPR013189 InterPro:IPR013148 Pfam:PF08244 Pfam:PF00251 ProtClustDB:CLSN2687777 EMBL:AY048269 EMBL:AY062481 EMBL:AY063904 EMBL:AY114066 EMBL:X99111 IPI:IPI00517592 PIR:S71268 RefSeq:NP_564798.1 UniGene:At.24113 UniGene:At.67066 ProteinModelPortal:Q43348 SMR:Q43348 STRING:Q43348 PRIDE:Q43348 ProMEX:Q43348 EnsemblPlants:AT1G62660.1 GeneID:842563 KEGG:ath:AT1G62660 TAIR:At1g62660 InParanoid:Q43348 OMA:HSIVEGF PhylomeDB:Q43348 ArrayExpress:Q43348 Genevestigator:Q43348 Uniprot:Q43348
Root	Isotig04538	9	38	-2.207	3.25E-06	TAIR|locus:2026177 - symbol:AT1G62660 species:3702 "Arabidopsis thaliana" [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=IEA;ISS] [GO:0071370 "cellular response to gibberellin stimulus" evidence=IEP] [GO:0000325 "plant-type vacuole" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0009617 "response to bacterium" evidence=IEP] InterPro:IPR001362 InterPro:IPR018053 InterPro:IPR021792 Pfam:PF11837 PROSITE:PS00609 SMART:SM00640 EMBL:CP002684 GO:GO:0005975 InterPro:IPR008985 SUPFAM:SSF49899 InterPro:IPR023296 SUPFAM:SSF75005 CAZy:GH32 KO:K01193 GO:GO:0004575 InterPro:IPR013189 InterPro:IPR013148 Pfam:PF08244 Pfam:PF00251 ProtClustDB:CLSN2687777 EMBL:AY048269 EMBL:AY062481 EMBL:AY063904 EMBL:AY114066 EMBL:X99111 IPI:IPI00517592 PIR:S71268 RefSeq:NP_564798.1 UniGene:At.24113 UniGene:At.67066 ProteinModelPortal:Q43348 SMR:Q43348 STRING:Q43348 PRIDE:Q43348 ProMEX:Q43348 EnsemblPlants:AT1G62660.1 GeneID:842563

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						KEGG:ath:AT1G62660 TAIR:At1g62660 InParanoid:Q43348 OMA:HSIVEGF PhylomeDB:Q43348 ArrayExpress:Q43348 Genevestigator:Q43348 Uniprot:Q43348
Root	Isotig04558	72	0	7.041	2.73E-17	No hit
Root	Isotig04559	40	0	6.193	1.34E-10	No hit
Root	Isotig04560	40	0	6.193	1.34E-10	No hit
Root	Isotig04564	3	39	-3.829	6.57E-10	TAIR|locus:2057981 - symbol:PAL1 "PHE ammonia lyase 1" species:3702 "Arabidopsis thaliana" [GO:0005737 "cytoplasm" evidence=IEA] [GO:0009699 "phenylpropanoid biosynthetic process" evidence=TAS] [GO:0045548 "phenylalanine ammonia-lyase activity" evidence=ISS;IDA;TAS] [GO:0006979 "response to oxidative stress" evidence=IEP] [GO:0080167 "response to karrikin" evidence=IEP] [GO:0009555 "pollen development" evidence=IMP] [GO:0009819 "drought recovery" evidence=IMP] [GO:0010224 "response to UV-B" evidence=IMP] [GO:0046244 "salicylic acid catabolic process" evidence=IMP] [GO:0046274 "lignin catabolic process" evidence=IMP] [GO:0006952 "defense response" evidence=TAS] [GO:0009611 "response to wounding" evidence=TAS] InterPro:IPR001106 InterPro:IPR005922 InterPro:IPR008948 InterPro:IPR022313 Pfam:PF00221 PROSITE:PS00488 GO:GO:0005737 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0006979 GO:GO:0009058 GO:GO:0080167 EMBL:AC006922 GO:GO:0009555 SUPFAM:SSF48557 GO:GO:0006559 InterPro:IPR024083 Gene3D:G3DSA:1.10.275.10 GO:GO:0010224 eggNOG:COG2986 GO:GO:0046274 EMBL:L33677 EMBL:AY303128 EMBL:AY045919 EMBL:AY079363 EMBL:BT003330 EMBL:X62747 IPI:IPI00519512 PIR:G84787 PIR:S52990 RefSeq:NP_181241.1 UniGene:At.21614 UniGene:At.22705 ProteinModelPortal:P35510 SMR:P35510 IntAct:P35510 STRING:P35510 PRIDE:P35510 EnsemblPlants:AT2G37040.1 GeneID:818280 KEGG:ath:AT2G37040 TAIR:At2g37040 HOGENOM:HBG318028 InParanoid:P35510 KO:K10775 OMA:QRGADFL PhylomeDB:P35510 ProtClustDB:PLN02457 BRENDA:4.3.1.24 Genevestigator:P35510 GermOnline:AT2G37040 GO:GO:0045548 GO:GO:0009819 GO:GO:0046244 InterPro:IPR023144 Gene3D:G3DSA:1.10.274.20 TIGRFAMs:TIGR01226 Uniprot:P35510
Root	Isotig04565	3	31	-3.498	9.97E-08	TAIR|locus:2057981 - symbol:PAL1 "PHE ammonia lyase 1" species:3702 "Arabidopsis thaliana" [GO:0005737 "cytoplasm" evidence=IEA] [GO:0009699 "phenylpropanoid biosynthetic process" evidence=TAS] [GO:0045548 "phenylalanine ammonia-lyase activity" evidence=ISS;IDA;TAS] [GO:0006979 "response to oxidative stress" evidence=IEP] [GO:0080167 "response to karrikin" evidence=IEP] [GO:0009555 "pollen development" evidence=IMP] [GO:0009819 "drought recovery" evidence=IMP] [GO:0010224 "response to UV-B" evidence=IMP] [GO:0046244 "salicylic acid catabolic process" evidence=IMP] [GO:0046274 "lignin catabolic process" evidence=IMP] [GO:0006952 "defense response" evidence=TAS] [GO:0009611 "response to wounding" evidence=TAS] InterPro:IPR001106 InterPro:IPR005922 InterPro:IPR008948 InterPro:IPR022313 Pfam:PF00221 PROSITE:PS00488 GO:GO:0005737 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0006979 GO:GO:0009058 GO:GO:0080167 EMBL:AC006922 GO:GO:0009555 SUPFAM:SSF48557 GO:GO:0006559 InterPro:IPR024083 Gene3D:G3DSA:1.10.275.10 GO:GO:0010224 eggNOG:COG2986 GO:GO:0046274 EMBL:L33677 EMBL:AY303128 EMBL:AY045919 EMBL:AY079363 EMBL:BT003330 EMBL:X62747 IPI:IPI00519512 PIR:G84787 PIR:S52990 RefSeq:NP_181241.1 UniGene:At.21614 UniGene:At.22705 ProteinModelPortal:P35510 SMR:P35510 IntAct:P35510 STRING:P35510 PRIDE:P35510 EnsemblPlants:AT2G37040.1 GeneID:818280 KEGG:ath:AT2G37040 TAIR:At2g37040 HOGENOM:HBG318028 InParanoid:P35510 KO:K10775 OMA:QRGADFL PhylomeDB:P35510 ProtClustDB:PLN02457 BRENDA:4.3.1.24 Genevestigator:P35510 GermOnline:AT2G37040 GO:GO:0045548 GO:GO:0009819 GO:GO:0046244 InterPro:IPR023144 Gene3D:G3DSA:1.10.274.20 TIGRFAMs:TIGR01226 Uniprot:P35510
Root	Isotig04566	1	18	-4.299	1.41E-05	TAIR|locus:2057981 - symbol:PAL1 "PHE ammonia lyase 1" species:3702 "Arabidopsis thaliana" [GO:0005737 "cytoplasm" evidence=IEA] [GO:0009699 "phenylpropanoid biosynthetic process" evidence=TAS] [GO:0045548 "phenylalanine ammonia-lyase activity" evidence=ISS;IDA;TAS] [GO:0006979 "response to oxidative stress" evidence=IEP] [GO:0080167 "response to karrikin" evidence=IEP] [GO:0009555 "pollen development" evidence=IMP] [GO:0009819 "drought recovery" evidence=IMP] [GO:0010224 "response to UV-B" evidence=IMP] [GO:0046244 "salicylic acid catabolic process" evidence=IMP] [GO:0046274 "lignin catabolic process" evidence=IMP] [GO:0006952 "defense response" evidence=TAS] [GO:0009611 "response to wounding" evidence=TAS] InterPro:IPR001106 InterPro:IPR005922 InterPro:IPR008948 InterPro:IPR022313 Pfam:PF00221 PROSITE:PS00488 GO:GO:0005737 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0006979 GO:GO:0009058 GO:GO:0080167 EMBL:AC006922 GO:GO:0009555 SUPFAM:SSF48557 GO:GO:0006559 InterPro:IPR024083 Gene3D:G3DSA:1.10.275.10 GO:GO:0010224 eggNOG:COG2986 GO:GO:0046274

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EMBL:L33677 EMBL:AY303128 EMBL:AY045919 EMBL:AY079363 EMBL:BT003330 EMBL:X62747 IPI:IPI00519512 PIR:G84787 PIR:S52990 RefSeq:NP_181241.1 UniGene:At.21614 UniGene:At.22705 ProteinModelPortal:P35510 SMR:P35510 IntAct:P35510 STRING:P35510 PRIDE:P35510 EnsemblPlants:AT2G37040.1 GeneID:818280 KEGG:ath:AT2G37040 TAIR:At2g37040 HOGENOM:HBG318028 InParanoid:P35510 KO:K10775 OMA:QRGADFL PhylomeDB:P35510 ProtClustDB:PLN02457 BRENDA:4.3.1.24 Genevestigator:P35510 GermOnline:AT2G37040 GO:GO:0045548 GO:GO:0009819 GO:GO:0046244 InterPro:IPR023144 Gene3D:G3DSA:1.10.274.20 TIGRFAMs:TIGR01226 Uniprot:P35510
Root	Isotig04594	7	28	-2.129	9.37E-05	TAIR|locus:2153919 - symbol:AT5G24610 "AT5G24610" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002688 GenomeReviews:BA000015_GR EMBL:AB010068 EMBL:AY084888 EMBL:BT025509 EMBL:AK175922 EMBL:AK176057 EMBL:AK176365 IPI:IPI00528071 RefSeq:NP_197849.1 UniGene:At.30951 STRING:Q9FLU3 PRIDE:Q9FLU3 EnsemblPlants:AT5G24610.1 GeneID:832532 KEGG:ath:AT5G24610 TAIR:At5g24610 eggNOG:NOG287708 HOGENOM:HBG587284 InParanoid:Q9FLU3 OMA:FGNMYRC PhylomeDB:Q9FLU3 ProtClustDB:CLSN2684245 ArrayExpress:Q9FLU3 Genevestigator:Q9FLU3 Uniprot:Q9FLU3
Root	Isotig04595	7	28	-2.129	9.37E-05	TAIR|locus:2153919 - symbol:AT5G24610 "AT5G24610" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002688 GenomeReviews:BA000015_GR EMBL:AB010068 EMBL:AY084888 EMBL:BT025509 EMBL:AK175922 EMBL:AK176057 EMBL:AK176365 IPI:IPI00528071 RefSeq:NP_197849.1 UniGene:At.30951 STRING:Q9FLU3 PRIDE:Q9FLU3 EnsemblPlants:AT5G24610.1 GeneID:832532 KEGG:ath:AT5G24610 TAIR:At5g24610 eggNOG:NOG287708 HOGENOM:HBG587284 InParanoid:Q9FLU3 OMA:FGNMYRC PhylomeDB:Q9FLU3 ProtClustDB:CLSN2684245 ArrayExpress:Q9FLU3 Genevestigator:Q9FLU3 Uniprot:Q9FLU3
Root	Isotig04596	7	26	-2.022	0.00027047	TAIR|locus:2114708 - symbol:AT3G49550 "AT3G49550" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002686 GenomeReviews:BA000014_GR EMBL:AL132964 UniGene:At.71999 eggNOG:NOG287708 HOGENOM:HBG587284 ProtClustDB:CLSN2684245 EMBL:BT010506 EMBL:AK176168 IPI:IPI00533036 PIR:T46232 RefSeq:NP_190524.1 UniGene:At.35592 PRIDE:Q9SCK4 EnsemblPlants:AT3G49550.1 GeneID:824117 KEGG:ath:AT3G49550 TAIR:At3g49550 InParanoid:Q9SCK4 OMA:HSSPFER PhylomeDB:Q9SCK4 Genevestigator:Q9SCK4 Uniprot:Q9SCK4
Root	Isotig04606	67	7	3.130	9.17E-13	SGD|S000028422 - symbol:TAR1 "Mitochondrial protein potentially involved in respiratory metabolism" species:4932 "Saccharomyces cerevisiae" [GO:0003674 "molecular_function" evidence=ND] [GO:0043457 "regulation of cellular respiration" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IEA;IMP] SGD:S000028422 GO:GO:0005739 EMBL:BK006945 EMBL:U53879 GO:GO:0043457 EMBL:Z73326 EMBL:AF479964 RefSeq:NP_690845.1 ProteinModelPortal:Q8TGM6 STRING:Q8TGM6 EnsemblFungi:YLR154W-C GeneID:1466405 KEGG:sce:YLR154W-C CYGD:YLR154w-c eggNOG:NOG79861 OMA:SCSKEHR OrthoDB:EOG466ZX8 NextBio:967146 Genevestigator:Q8TGM6 GermOnline:YLR154W-C Uniprot:Q8TGM6
Root	Isotig04607	67	7	3.130	9.17E-13	SGD|S000028422 - symbol:TAR1 "Mitochondrial protein potentially involved in respiratory metabolism" species:4932 "Saccharomyces cerevisiae" [GO:0003674 "molecular_function" evidence=ND] [GO:0043457 "regulation of cellular respiration" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IEA;IMP] SGD:S000028422 GO:GO:0005739 EMBL:BK006945 EMBL:U53879 GO:GO:0043457 EMBL:Z73326 EMBL:AF479964 RefSeq:NP_690845.1 ProteinModelPortal:Q8TGM6 STRING:Q8TGM6 EnsemblFungi:YLR154W-C GeneID:1466405 KEGG:sce:YLR154W-C CYGD:YLR154w-c eggNOG:NOG79861 OMA:SCSKEHR OrthoDB:EOG466ZX8 NextBio:967146 Genevestigator:Q8TGM6 GermOnline:YLR154W-C Uniprot:Q8TGM6
Root	Isotig04608	66	7	3.108	1.59E-12	SGD|S000028422 - symbol:TAR1 "Mitochondrial protein potentially involved in respiratory metabolism" species:4932 "Saccharomyces cerevisiae" [GO:0003674 "molecular_function" evidence=ND] [GO:0043457 "regulation of cellular respiration" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IEA;IMP] SGD:S000028422 GO:GO:0005739 EMBL:BK006945 EMBL:U53879 GO:GO:0043457 EMBL:Z73326 EMBL:AF479964 RefSeq:NP_690845.1 ProteinModelPortal:Q8TGM6 STRING:Q8TGM6 EnsemblFungi:YLR154W-C GeneID:1466405 KEGG:sce:YLR154W-C CYGD:YLR154w-c eggNOG:NOG79861 OMA:SCSKEHR OrthoDB:EOG466ZX8 NextBio:967146 Genevestigator:Q8TGM6 GermOnline:YLR154W-C Uniprot:Q8TGM6

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig04612	9	46	-2.483	3.98E-08	TAIR|locus:2024542 - symbol:AT1G64190 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004616 "phosphogluconate dehydrogenase (decarboxylating) activity" evidence=IEA;ISS] [GO:0016491 "oxidoreductase activity" evidence=IEA] [GO:0050661 "NADP binding" evidence=IEA] [GO:0050662 "coenzyme binding" evidence=IEA] [GO:0016020 "membrane" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR006113 InterPro:IPR006114 InterPro:IPR006115 InterPro:IPR008927 InterPro:IPR012284 InterPro:IPR013328 InterPro:IPR016040 Pfam:PF00393 Pfam:PF03446 PIRSF:PIRSF000109 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0009570 GO:GO:0016020 Gene3D:G3DSA:3.40.50.720 GO:GO:0004616 GO:GO:0006098 Gene3D:G3DSA:1.10.1040.10 SUPFAM:SSF48179 KO:K00033 HOGENOM:HBG286913 GO:GO:0050661 Gene3D:G3DSA:1.20.5.320 TIGRFAMs:TIGR00873 HSSP:P00349 GO:GO:0009651 EMBL:AC007764 UniGene:At.43563 UniGene:At.70356 ProtClustDB:PLN02350 EMBL:BT004568 EMBL:AK227596 IPI:IPI00516481 RefSeq:NP_176601.1 ProteinModelPortal:Q9SH69 SMR:Q9SH69 STRING:Q9SH69 PRIDE:Q9SH69 EnsemblPlants:AT1G64190.1 GeneID:842724 KEGG:ath:AT1G64190 TAIR:At1g64190 InParanoid:Q9SH69 OMA:NTERRIS PhylomeDB:Q9SH69 Genevestigator:Q9SH69 Uniprot:Q9SH69
Root	Isotig04613	8	44	-2.588	3.84E-08	TAIR|locus:2024542 - symbol:AT1G64190 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004616 "phosphogluconate dehydrogenase (decarboxylating) activity" evidence=IEA;ISS] [GO:0016491 "oxidoreductase activity" evidence=IEA] [GO:0050661 "NADP binding" evidence=IEA] [GO:0050662 "coenzyme binding" evidence=IEA] [GO:0016020 "membrane" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR006113 InterPro:IPR006114 InterPro:IPR006115 InterPro:IPR008927 InterPro:IPR012284 InterPro:IPR013328 InterPro:IPR016040 Pfam:PF00393 Pfam:PF03446 PIRSF:PIRSF000109 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0009570 GO:GO:0016020 Gene3D:G3DSA:3.40.50.720 GO:GO:0004616 GO:GO:0006098 Gene3D:G3DSA:1.10.1040.10 SUPFAM:SSF48179 KO:K00033 HOGENOM:HBG286913 GO:GO:0050661 Gene3D:G3DSA:1.20.5.320 TIGRFAMs:TIGR00873 HSSP:P00349 GO:GO:0009651 EMBL:AC007764 UniGene:At.43563 UniGene:At.70356 ProtClustDB:PLN02350 EMBL:BT004568 EMBL:AK227596 IPI:IPI00516481 RefSeq:NP_176601.1 ProteinModelPortal:Q9SH69 SMR:Q9SH69 STRING:Q9SH69 PRIDE:Q9SH69 EnsemblPlants:AT1G64190.1 GeneID:842724 KEGG:ath:AT1G64190 TAIR:At1g64190 InParanoid:Q9SH69 OMA:NTERRIS PhylomeDB:Q9SH69 Genevestigator:Q9SH69 Uniprot:Q9SH69
Root	Isotig04614	3	37	-3.753	2.31E-09	TAIR|locus:2024542 - symbol:AT1G64190 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004616 "phosphogluconate dehydrogenase (decarboxylating) activity" evidence=IEA;ISS] [GO:0016491 "oxidoreductase activity" evidence=IEA] [GO:0050661 "NADP binding" evidence=IEA] [GO:0050662 "coenzyme binding" evidence=IEA] [GO:0016020 "membrane" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR006113 InterPro:IPR006114 InterPro:IPR006115 InterPro:IPR008927 InterPro:IPR012284 InterPro:IPR013328 InterPro:IPR016040 Pfam:PF00393 Pfam:PF03446 PIRSF:PIRSF000109 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0009570 GO:GO:0016020 Gene3D:G3DSA:3.40.50.720 GO:GO:0004616 GO:GO:0006098 Gene3D:G3DSA:1.10.1040.10 SUPFAM:SSF48179 KO:K00033 HOGENOM:HBG286913 GO:GO:0050661 Gene3D:G3DSA:1.20.5.320 TIGRFAMs:TIGR00873 HSSP:P00349 GO:GO:0009651 EMBL:AC007764 UniGene:At.43563 UniGene:At.70356 ProtClustDB:PLN02350 EMBL:BT004568 EMBL:AK227596 IPI:IPI00516481 RefSeq:NP_176601.1 ProteinModelPortal:Q9SH69 SMR:Q9SH69 STRING:Q9SH69 PRIDE:Q9SH69 EnsemblPlants:AT1G64190.1 GeneID:842724 KEGG:ath:AT1G64190 TAIR:At1g64190 InParanoid:Q9SH69 OMA:NTERRIS PhylomeDB:Q9SH69 Genevestigator:Q9SH69 Uniprot:Q9SH69
Root	Isotig04621	102	0	7.543	4.82E-23	TAIR|locus:2010341 - symbol:ERF1-2 "AT1G12920" species:3702 "Arabidopsis thaliana" [GO:0003747 "translation release factor activity" evidence=IGI;ISS] [GO:0006415 "translational termination" evidence=IGI;ISS] [GO:0018444 "translation release factor complex" evidence=TAS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR004403 InterPro:IPR005140 InterPro:IPR005141 InterPro:IPR005142 Pfam:PF03465 Pfam:PF03463 Pfam:PF03464 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0005886 EMBL:AC012187 eggNOG:COG1503 HOGENOM:HBG497188 KO:K03265 ProtClustDB:CLSN2682479 GO:GO:0016149 InterPro:IPR024049 Gene3D:G3DSA:3.30.960.10

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						PANTHER:PTHR10113 SUPFAM:SSF55481 TIGRFAMs:TIGR03676 EMBL:AY034963 EMBL:AY086623 EMBL:X69374 EMBL:U40218 EMBL:Z18188 IPI:IPI00537037 PIR:H86262 PIR:S31445 RefSeq:NP_172752.1 UniGene:At.23958 ProteinModelPortal:Q9LPV8 SMR:Q9LPV8 STRING:Q9LPV8 PRIDE:Q9LPV8 EnsemblPlants:AT1G12920.1 GeneID:837850 KEGG:ath:AT1G12920 TAIR:At1g12920 InParanoid:Q9LPV8 OMA:HETDRNI PhylomeDB:Q9LPV8 ArrayExpress:Q9LPV8 Genevestigator:Q9LPV8 GermOnline:AT1G12920 Uniprot:Q9LPV8
Root	Isotig04622	101	0	7.529	7.39E-23	TAIR|locus:2010341 - symbol:ERF1-2 "AT1G12920" species:3702 "Arabidopsis thaliana" [GO:0003747 "translation release factor activity" evidence=IGI;ISS] [GO:0006415 "translational termination" evidence=IGI;ISS] [GO:0018444 "translation release factor complex" evidence=TAS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR004403 InterPro:IPR005140 InterPro:IPR005141 InterPro:IPR005142 Pfam:PF03465 Pfam:PF03463 Pfam:PF03464 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0005886 EMBL:AC012187 eggNOG:COG1503 HOGENOM:HBG497188 KO:K03265 ProtClustDB:CLSN2682479 GO:GO:0016149 InterPro:IPR024049 Gene3D:G3DSA:3.30.960.10 PANTHER:PTHR10113 SUPFAM:SSF55481 TIGRFAMs:TIGR03676 EMBL:AY034963 EMBL:AY086623 EMBL:X69374 EMBL:U40218 EMBL:Z18188 IPI:IPI00537037 PIR:H86262 PIR:S31445 RefSeq:NP_172752.1 UniGene:At.23958 ProteinModelPortal:Q9LPV8 SMR:Q9LPV8 STRING:Q9LPV8 PRIDE:Q9LPV8 EnsemblPlants:AT1G12920.1 GeneID:837850 KEGG:ath:AT1G12920 TAIR:At1g12920 InParanoid:Q9LPV8 OMA:HETDRNI PhylomeDB:Q9LPV8 ArrayExpress:Q9LPV8 Genevestigator:Q9LPV8 GermOnline:AT1G12920 Uniprot:Q9LPV8
Root	Isotig04623	50	0	6.515	9.09E-13	TAIR|locus:2010341 - symbol:ERF1-2 "AT1G12920" species:3702 "Arabidopsis thaliana" [GO:0003747 "translation release factor activity" evidence=IGI;ISS] [GO:0006415 "translational termination" evidence=IGI;ISS] [GO:0018444 "translation release factor complex" evidence=TAS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR004403 InterPro:IPR005140 InterPro:IPR005141 InterPro:IPR005142 Pfam:PF03465 Pfam:PF03463 Pfam:PF03464 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0005886 EMBL:AC012187 eggNOG:COG1503 HOGENOM:HBG497188 KO:K03265 ProtClustDB:CLSN2682479 GO:GO:0016149 InterPro:IPR024049 Gene3D:G3DSA:3.30.960.10 PANTHER:PTHR10113 SUPFAM:SSF55481 TIGRFAMs:TIGR03676 EMBL:AY034963 EMBL:AY086623 EMBL:X69374 EMBL:U40218 EMBL:Z18188 IPI:IPI00537037 PIR:H86262 PIR:S31445 RefSeq:NP_172752.1 UniGene:At.23958 ProteinModelPortal:Q9LPV8 SMR:Q9LPV8 STRING:Q9LPV8 PRIDE:Q9LPV8 EnsemblPlants:AT1G12920.1 GeneID:837850 KEGG:ath:AT1G12920 TAIR:At1g12920 InParanoid:Q9LPV8 OMA:HETDRNI PhylomeDB:Q9LPV8 ArrayExpress:Q9LPV8 Genevestigator:Q9LPV8 GermOnline:AT1G12920 Uniprot:Q9LPV8
Root	Isotig04659	28	93	-1.861	7.09E-11	TAIR|locus:3439219 - symbol:TUA6 "AT4G14960" species:3702 "Arabidopsis thaliana" [GO:0005874 "microtubule" evidence=IDA] [GO:0045298 "tubulin complex" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005200 "structural constituent of cytoskeleton" evidence=ISS] [GO:0005730 "nucleolus" evidence=IDA] [GO:0000226 "microtubule cytoskeleton organization" evidence=IMP] [GO:0005618 "cell wall" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0071258 "cellular response to gravity" evidence=IMP] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000217 InterPro:IPR002452 InterPro:IPR003008 InterPro:IPR008280 InterPro:IPR017975 InterPro:IPR018316 Pfam:PF00091 Pfam:PF03953 PRINTS:PR01161 PRINTS:PR01162 PROSITE:PS00227 SMART:SM00864 SMART:SM00865 GO:GO:0005525 GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005773 GO:GO:0005618 GO:GO:0005515 GO:GO:0005730 GO:GO:0005198 GO:GO:0003924 GO:GO:0009651 EMBL:AL161540 GO:GO:0000226 GO:GO:0005874 GO:GO:0051258 Gene3D:G3DSA:3.40.50.1440 SUPFAM:SSF52490 GO:GO:0007018 EMBL:Z97337 Gene3D:G3DSA:3.30.1330.20 SUPFAM:SSF55307 GO:GO:0045298 eggNOG:COG5023 GO:GO:0071258 HOGENOM:HBG750007 KO:K07374 InterPro:IPR023123 Gene3D:G3DSA:1.10.287.600 PANTHER:PTHR11588 ProtClustDB:PLN00221 UniGene:At.22368 UniGene:At.48153 EMBL:M84699 EMBL:AY058858 EMBL:AY065347 EMBL:AY079036 EMBL:AY117174 IPI:IPI00520226 PIR:JQ1597 RefSeq:NP_193232.1 ProteinModelPortal:P29511 SMR:P29511 IntAct:P29511 STRING:P29511 PRIDE:P29511 EnsemblPlants:AT4G14960.2 GeneID:827154 KEGG:ath:AT4G14960 TAIR:At4g14960 InParanoid:P29511 OMA:MPSDKAI PhylomeDB:P29511 ArrayExpress:P29511 Genevestigator:P29511 Uniprot:P29511

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig04666	13	37	-1.638	0.000168748	UNIPROTKB|Q84N28 - symbol:OMT1 "Flavone O-methyltransferase 1" species:4565 "Triticum aestivum" [GO:0009611 "response to wounding" evidence=IDA] [GO:0009723 "response to ethylene stimulus" evidence=IDA] [GO:0009751 "response to salicylic acid stimulus" evidence=IDA] [GO:0042542 "response to hydrogen peroxide" evidence=IDA] InterPro:IPR001077 InterPro:IPR012967 InterPro:IPR016461 Pfam:PF00891 Pfam:PF08100 PIRSF:PIRSF005739 GO:GO:0009611 InterPro:IPR011991 Gene3D:G3DSA:1.10.10.10 GO:GO:0009723 GO:GO:0009751 GO:GO:0046983 GO:GO:0042542 GO:GO:0008171 GO:GO:0009813 EMBL:AY226581 UniGene:Ta.336 HSSP:P28002 ProteinModelPortal:Q84N28 SMR:Q84N28 Gramene:Q84N28 Uniprot:Q84N28
Root	Isotig04678	4	19	-2.377	0.000578515	TAIR|locus:2134603 - symbol:CRK41 "cysteine-rich RLK (RECEPTOR-like protein kinase) 41" species:3702 "Arabidopsis thaliana" [GO:0004672 "protein kinase activity" evidence=IEA;ISS] [GO:0004674 "protein serine/threonine kinase activity" evidence=IEA] [GO:0005524 "ATP binding" evidence=IEA] [GO:0006468 "protein phosphorylation" evidence=IEA] InterPro:IPR000719 InterPro:IPR001245 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 Pfam:PF07714 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 GO:GO:0016021 GO:GO:0005524 EMBL:CP002687 GenomeReviews:CT486007_GR eggNOG:COG0515 GO:GO:0004872 SUPFAM:SSF56112 GO:GO:0004674 HOGENOM:HBG755340 EMBL:AF013294 EMBL:AL161491 InterPro:IPR002902 Pfam:PF01657 PROSITE:PS51473 ProtClustDB:CLSN2685554 IPI:IPI00521692 PIR:T01550 RefSeq:NP_567204.3 UniGene:At.34491 ProteinModelPortal:O23081 SMR:O23081 PRIDE:O23081 EnsemblPlants:AT4G00970.1 GeneID:827936 KEGG:ath:AT4G00970 GeneFarm:2566 TAIR:At4g00970 InParanoid:O23081 OMA:VDINSAI PhylomeDB:O23081 ArrayExpress:O23081 Genevestigator:O23081 Uniprot:O23081
Root	Isotig04693	0	43	-6.555	4.45E-12	TAIR|locus:2087368 - symbol:scpl40 "serine carboxypeptidase-like 40" species:3702 "Arabidopsis thaliana" [GO:0004185 "serine-type carboxypeptidase activity" evidence=IEA;ISS] [GO:0006508 "proteolysis" evidence=IEA;ISS] InterPro:IPR001563 InterPro:IPR018202 Pfam:PF00450 PRINTS:PR00724 PROSITE:PS00131 PROSITE:PS00560 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005576 GO:GO:0006508 EMBL:AL163818 GO:GO:0004185 eggNOG:COG2939 PANTHER:PTHR11802 HOGENOM:HBG588032 EMBL:AY087589 EMBL:AK228170 EMBL:BT003126 IPI:IPI00536894 PIR:T49188 RefSeq:NP_191906.1 UniGene:At.33917 UniGene:At.71216 ProteinModelPortal:Q0WRX3 SMR:Q0WRX3 MEROPS:S10.A41 PRIDE:Q0WRX3 EnsemblPlants:AT3G63470.1 GeneID:825522 KEGG:ath:AT3G63470 TAIR:At3g63470 InParanoid:Q0WRX3 OMA:WNNAANV PhylomeDB:Q0WRX3 ProtClustDB:CLSN2914723 Genevestigator:Q0WRX3 Uniprot:Q0WRX3
Root	Isotig04694	0	40	-6.451	2.24E-11	TAIR|locus:2087368 - symbol:scpl40 "serine carboxypeptidase-like 40" species:3702 "Arabidopsis thaliana" [GO:0004185 "serine-type carboxypeptidase activity" evidence=IEA;ISS] [GO:0006508 "proteolysis" evidence=IEA;ISS] InterPro:IPR001563 InterPro:IPR018202 Pfam:PF00450 PRINTS:PR00724 PROSITE:PS00131 PROSITE:PS00560 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005576 GO:GO:0006508 EMBL:AL163818 GO:GO:0004185 eggNOG:COG2939 PANTHER:PTHR11802 HOGENOM:HBG588032 EMBL:AY087589 EMBL:AK228170 EMBL:BT003126 IPI:IPI00536894 PIR:T49188 RefSeq:NP_191906.1 UniGene:At.33917 UniGene:At.71216 ProteinModelPortal:Q0WRX3 SMR:Q0WRX3 MEROPS:S10.A41 PRIDE:Q0WRX3 EnsemblPlants:AT3G63470.1 GeneID:825522 KEGG:ath:AT3G63470 TAIR:At3g63470 InParanoid:Q0WRX3 OMA:WNNAANV PhylomeDB:Q0WRX3 ProtClustDB:CLSN2914723 Genevestigator:Q0WRX3 Uniprot:Q0WRX3
Root	Isotig04695	0	41	-6.487	1.30E-11	TAIR|locus:2087368 - symbol:scpl40 "serine carboxypeptidase-like 40" species:3702 "Arabidopsis thaliana" [GO:0004185 "serine-type carboxypeptidase activity" evidence=IEA;ISS] [GO:0006508 "proteolysis" evidence=IEA;ISS] InterPro:IPR001563 InterPro:IPR018202 Pfam:PF00450 PRINTS:PR00724 PROSITE:PS00131 PROSITE:PS00560 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005576 GO:GO:0006508 EMBL:AL163818 GO:GO:0004185 eggNOG:COG2939 PANTHER:PTHR11802 HOGENOM:HBG588032 EMBL:AY087589 EMBL:AK228170 EMBL:BT003126 IPI:IPI00536894 PIR:T49188 RefSeq:NP_191906.1 UniGene:At.33917 UniGene:At.71216 ProteinModelPortal:Q0WRX3 SMR:Q0WRX3 MEROPS:S10.A41 PRIDE:Q0WRX3 EnsemblPlants:AT3G63470.1 GeneID:825522 KEGG:ath:AT3G63470 TAIR:At3g63470 InParanoid:Q0WRX3 OMA:WNNAANV PhylomeDB:Q0WRX3 ProtClustDB:CLSN2914723 Genevestigator:Q0WRX3 Uniprot:Q0WRX3
Root	Isotig04699	42	14	1.456	0.000438168	TAIR|locus:2142120 - symbol:IIL1 "AT4G13430" species:3702 "Arabidopsis thaliana" [GO:0008152 "metabolic process" evidence=ISS] [GO:0016829 "lyase activity" evidence=ISS] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA]

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						[GO:0019761 "glucosinolate biosynthetic process" evidence=IMP] [GO:0050486 "intramolecular transferase activity, transferring hydroxy groups" evidence=IMP] InterPro:IPR001030 InterPro:IPR006251 InterPro:IPR015931 InterPro:IPR015932 InterPro:IPR015937 Pfam:PF00330 PRINTS:PR00415 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0009570 GO:GO:0046686 GO:GO:0046872 GO:GO:0019761 GO:GO:0051539 Gene3D:G3DSA:3.30.499.10 Gene3D:G3DSA:3.40.1060.10 PANTHER:PTHR11670 SUPFAM:SSF53732 EMBL:AL161536 GO:GO:0009098 EMBL:AL049608 GO:GO:0003861 PANTHER:PTHR11670:SF16 TIGRFAMs:TIGR01343 EMBL:AY045842 EMBL:AY117151 IPI:IPI00543884 PIR:T06300 RefSeq:NP_567405.1 UniGene:At.24538 UniGene:At.67680 ProteinModelPortal:Q94AR8 SMR:Q94AR8 STRING:Q94AR8 PRIDE:Q94AR8 EnsemblPlants:AT4G13430.1 GeneID:826975 KEGG:ath:AT4G13430 TAIR:At4g13430 eggNOG:COG0065 HOGENOM:HBG330745 InParanoid:Q94AR8 KO:K01703 OMA:FTMANMA PhylomeDB:Q94AR8 ProtClustDB:CLSN2689413 BioCyc:ARA:AT4G13430-MONOMER BioCyc:MetaCyc:AT4G13430-MONOMER Genevestigator:Q94AR8 GO:GO:0050486 Uniprot:Q94AR8
Root	Isotig04701	41	13	1.528	0.000317378	TAIR|locus:2142120 - symbol:IIL1 "AT4G13430" species:3702 "Arabidopsis thaliana" [GO:0008152 "metabolic process" evidence=ISS] [GO:0016829 "lyase activity" evidence=ISS] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0019761 "glucosinolate biosynthetic process" evidence=IMP] [GO:0050486 "intramolecular transferase activity, transferring hydroxy groups" evidence=IMP] InterPro:IPR001030 InterPro:IPR006251 InterPro:IPR015931 InterPro:IPR015932 InterPro:IPR015937 Pfam:PF00330 PRINTS:PR00415 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0009570 GO:GO:0046686 GO:GO:0046872 GO:GO:0019761 GO:GO:0051539 Gene3D:G3DSA:3.30.499.10 Gene3D:G3DSA:3.40.1060.10 PANTHER:PTHR11670 SUPFAM:SSF53732 EMBL:AL161536 GO:GO:0009098 EMBL:AL049608 GO:GO:0003861 PANTHER:PTHR11670:SF16 TIGRFAMs:TIGR01343 EMBL:AY045842 EMBL:AY117151 IPI:IPI00543884 PIR:T06300 RefSeq:NP_567405.1 UniGene:At.24538 UniGene:At.67680 ProteinModelPortal:Q94AR8 SMR:Q94AR8 STRING:Q94AR8 PRIDE:Q94AR8 EnsemblPlants:AT4G13430.1 GeneID:826975 KEGG:ath:AT4G13430 TAIR:At4g13430 eggNOG:COG0065 HOGENOM:HBG330745 InParanoid:Q94AR8 KO:K01703 OMA:FTMANMA PhylomeDB:Q94AR8 ProtClustDB:CLSN2689413 BioCyc:ARA:AT4G13430-MONOMER BioCyc:MetaCyc:AT4G13430-MONOMER Genevestigator:Q94AR8 GO:GO:0050486 Uniprot:Q94AR8
Root	Isotig04705	8	45	-2.621	2.17E-08	TAIR|locus:2081988 - symbol:AT3G55840 "AT3G55840" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0005515 "protein binding" evidence=IPI] GO:GO:0005737 EMBL:CP002686 GO:GO:0005515 GO:GO:0006952 EMBL:AL163832 EMBL:DQ132634 EMBL:AY034950 EMBL:AY070026 EMBL:AY085394 IPI:IPI00532415 PIR:T49196 RefSeq:NP_191143.1 UniGene:At.19788 UniGene:At.70251 ProteinModelPortal:Q9LY61 IntAct:Q9LY61 PRIDE:Q9LY61 GeneID:824750 KEGG:ath:AT3G55840 TAIR:At3g55840 eggNOG:NOG286983 InParanoid:Q9LY61 OMA:EANANRT PhylomeDB:Q9LY61 ProtClustDB:CLSN2683387 ArrayExpress:Q9LY61 Genevestigator:Q9LY61 InterPro:IPR009743 InterPro:IPR009869 Pfam:PF07014 Pfam:PF07231 Uniprot:Q9LY61
Root	Isotig04706	6	41	-2.902	1.75E-08	TAIR|locus:2081988 - symbol:AT3G55840 "AT3G55840" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0005515 "protein binding" evidence=IPI] GO:GO:0005737 EMBL:CP002686 GO:GO:0005515 GO:GO:0006952 EMBL:AL163832 EMBL:DQ132634 EMBL:AY034950 EMBL:AY070026 EMBL:AY085394 IPI:IPI00532415 PIR:T49196 RefSeq:NP_191143.1 UniGene:At.19788 UniGene:At.70251 ProteinModelPortal:Q9LY61 IntAct:Q9LY61 PRIDE:Q9LY61 GeneID:824750 KEGG:ath:AT3G55840 TAIR:At3g55840 eggNOG:NOG286983 InParanoid:Q9LY61 OMA:EANANRT PhylomeDB:Q9LY61 ProtClustDB:CLSN2683387 ArrayExpress:Q9LY61 Genevestigator:Q9LY61 InterPro:IPR009743 InterPro:IPR009869 Pfam:PF07014 Pfam:PF07231 Uniprot:Q9LY61
Root	Isotig04707	6	32	-2.544	3.42E-06	TAIR|locus:2081988 - symbol:AT3G55840 "AT3G55840" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0005515 "protein binding" evidence=IPI] GO:GO:0005737 EMBL:CP002686 GO:GO:0005515 GO:GO:0006952 EMBL:AL163832 EMBL:DQ132634 EMBL:AY034950 EMBL:AY070026 EMBL:AY085394 IPI:IPI00532415 PIR:T49196 RefSeq:NP_191143.1 UniGene:At.19788 UniGene:At.70251 ProteinModelPortal:Q9LY61 IntAct:Q9LY61 PRIDE:Q9LY61 GeneID:824750 KEGG:ath:AT3G55840 TAIR:At3g55840 eggNOG:NOG286983 InParanoid:Q9LY61 OMA:EANANRT PhylomeDB:Q9LY61 ProtClustDB:CLSN2683387 ArrayExpress:Q9LY61 Genevestigator:Q9LY61 InterPro:IPR009743 InterPro:IPR009869 Pfam:PF07014 Pfam:PF07231 Uniprot:Q9LY61

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig04714	85	36	1.110	5.11E-05	ZFIN|ZDB-GENE-070410-9 - symbol:zgc:158463 "zgc:158463" species:7955 "Danio rerio" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] ZFIN:ZDB-GENE-070410-9 EMBL:BX296557 EMBL:BX537263 EMBL:BC129240 IPI:IPI00837201 RefSeq:NP_001091866.1 RefSeq:XP_003200836.1 UniGene:Dr.155369 Ensembl:ENSDART00000102863 Ensembl:ENSDART00000126982 GeneID:100037361 GeneID:100151188 KEGG:dre:100037361 KEGG:dre:100151188 eggNOG:NOG298153 GeneTree:ENSGT00390000016898 InParanoid:A2VD29 OMA:ACHQHAL OrthoDB:EOG4FJ8BF Bgee:A2VD29 Uniprot:A2VD29
Root	Isotig04715	85	36	1.110	5.11E-05	ZFIN|ZDB-GENE-070410-9 - symbol:zgc:158463 "zgc:158463" species:7955 "Danio rerio" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] ZFIN:ZDB-GENE-070410-9 EMBL:BX296557 EMBL:BX537263 EMBL:BC129240 IPI:IPI00837201 RefSeq:NP_001091866.1 RefSeq:XP_003200836.1 UniGene:Dr.155369 Ensembl:ENSDART00000102863 Ensembl:ENSDART00000126982 GeneID:100037361 GeneID:100151188 KEGG:dre:100037361 KEGG:dre:100151188 eggNOG:NOG298153 GeneTree:ENSGT00390000016898 InParanoid:A2VD29 OMA:ACHQHAL OrthoDB:EOG4FJ8BF Bgee:A2VD29 Uniprot:A2VD29
Root	Isotig04716	82	32	1.229	1.62E-05	ZFIN|ZDB-GENE-070410-9 - symbol:zgc:158463 "zgc:158463" species:7955 "Danio rerio" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] ZFIN:ZDB-GENE-070410-9 EMBL:BX296557 EMBL:BX537263 EMBL:BC129240 IPI:IPI00837201 RefSeq:NP_001091866.1 RefSeq:XP_003200836.1 UniGene:Dr.155369 Ensembl:ENSDART00000102863 Ensembl:ENSDART00000126982 GeneID:100037361 GeneID:100151188 KEGG:dre:100037361 KEGG:dre:100151188 eggNOG:NOG298153 GeneTree:ENSGT00390000016898 InParanoid:A2VD29 OMA:ACHQHAL OrthoDB:EOG4FJ8BF Bgee:A2VD29 Uniprot:A2VD29
Root	Isotig04720	0	22	-5.588	6.01E-07	TAIR|locus:2087368 - symbol:scpl40 "serine carboxypeptidase-like 40" species:3702 "Arabidopsis thaliana" [GO:0004185 "serine-type carboxypeptidase activity" evidence=IEA;ISS] [GO:0006508 "proteolysis" evidence=IEA;ISS] InterPro:IPR001563 InterPro:IPR018202 Pfam:PF00450 PRINTS:PR00724 PROSITE:PS00131 PROSITE:PS00560 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005576 GO:GO:0006508 EMBL:AL163818 GO:GO:0004185 eggNOG:COG2939 PANTHER:PTHR11802 HOGENOM:HBG588032 EMBL:AY087589 EMBL:AK228170 EMBL:BT003126 IPI:IPI00536894 PIR:T49188 RefSeq:NP_191906.1 UniGene:At.33917 UniGene:At.71216 ProteinModelPortal:Q0WRX3 SMR:Q0WRX3 MEROPS:S10.A41 PRIDE:Q0WRX3 EnsemblPlants:AT3G63470.1 GeneID:825522 KEGG:ath:AT3G63470 TAIR:At3g63470 InParanoid:Q0WRX3 OMA:WNNAANV PhylomeDB:Q0WRX3 ProtClustDB:CLSN2914723 Genevestigator:Q0WRX3 Uniprot:Q0WRX3
Root	Isotig04721	0	21	-5.521	1.09E-06	TAIR|locus:2087368 - symbol:scpl40 "serine carboxypeptidase-like 40" species:3702 "Arabidopsis thaliana" [GO:0004185 "serine-type carboxypeptidase activity" evidence=IEA;ISS] [GO:0006508 "proteolysis" evidence=IEA;ISS] InterPro:IPR001563 InterPro:IPR018202 Pfam:PF00450 PRINTS:PR00724 PROSITE:PS00131 PROSITE:PS00560 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005576 GO:GO:0006508 EMBL:AL163818 GO:GO:0004185 eggNOG:COG2939 PANTHER:PTHR11802 HOGENOM:HBG588032 EMBL:AY087589 EMBL:AK228170 EMBL:BT003126 IPI:IPI00536894 PIR:T49188 RefSeq:NP_191906.1 UniGene:At.33917 UniGene:At.71216 ProteinModelPortal:Q0WRX3 SMR:Q0WRX3 MEROPS:S10.A41 PRIDE:Q0WRX3 EnsemblPlants:AT3G63470.1 GeneID:825522 KEGG:ath:AT3G63470 TAIR:At3g63470 InParanoid:Q0WRX3 OMA:WNNAANV PhylomeDB:Q0WRX3 ProtClustDB:CLSN2914723 Genevestigator:Q0WRX3 Uniprot:Q0WRX3
Root	Isotig04722	0	22	-5.588	6.01E-07	TAIR|locus:2087368 - symbol:scpl40 "serine carboxypeptidase-like 40" species:3702 "Arabidopsis thaliana" [GO:0004185 "serine-type carboxypeptidase activity" evidence=IEA;ISS] [GO:0006508 "proteolysis" evidence=IEA;ISS] InterPro:IPR001563 InterPro:IPR018202 Pfam:PF00450 PRINTS:PR00724 PROSITE:PS00131 PROSITE:PS00560 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005576 GO:GO:0006508 EMBL:AL163818 GO:GO:0004185 eggNOG:COG2939 PANTHER:PTHR11802 HOGENOM:HBG588032 EMBL:AY087589 EMBL:AK228170 EMBL:BT003126 IPI:IPI00536894 PIR:T49188 RefSeq:NP_191906.1 UniGene:At.33917 UniGene:At.71216 ProteinModelPortal:Q0WRX3 SMR:Q0WRX3 MEROPS:S10.A41 PRIDE:Q0WRX3 EnsemblPlants:AT3G63470.1 GeneID:825522 KEGG:ath:AT3G63470 TAIR:At3g63470 InParanoid:Q0WRX3 OMA:WNNAANV PhylomeDB:Q0WRX3 ProtClustDB:CLSN2914723 Genevestigator:Q0WRX3 Uniprot:Q0WRX3

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig04723	10	57	-2.640	2.52E-10	TAIR|locus:2181665 - symbol:AT5G13420 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004801 "sedoheptulose-7-phosphate:D-glyceraldehyde-3-phosphate glyceronetransferase activity" evidence=IEA;ISS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005829 "cytosol" evidence=RCA] HAMAP:MF_00493 InterPro:IPR001585 InterPro:IPR004732 InterPro:IPR013785 InterPro:IPR018225 Pfam:PF00923 PIRSF:PIRSF036915 PROSITE:PS01054 GO:GO:0005739 GO:GO:0009570 GO:GO:0046686 EMBL:CP002688 GenomeReviews:BA000015_GR Gene3D:G3DSA:3.20.20.70 GO:GO:0006098 EMBL:AL163572 eggNOG:COG0176 PANTHER:PTHR10683 KO:K00616 GO:GO:0004801 HOGENOM:HBG321149 TIGRFAMs:TIGR00876 OMA:MPEKTLD EMBL:AY056296 EMBL:AY114075 EMBL:AY087135 IPI:IPI00531555 PIR:T48589 RefSeq:NP_196846.1 UniGene:At.22457 ProteinModelPortal:Q9LYR4 SMR:Q9LYR4 IntAct:Q9LYR4 STRING:Q9LYR4 PRIDE:Q9LYR4 EnsemblPlants:AT5G13420.1 GeneID:831183 KEGG:ath:AT5G13420 TAIR:At5g13420 InParanoid:Q9LYR4 PhylomeDB:Q9LYR4 ProtClustDB:CLSN2687015 ArrayExpress:Q9LYR4 Genevestigator:Q9LYR4 Uniprot:Q9LYR4
Root	Isotig04724	10	57	-2.640	2.52E-10	TAIR|locus:2181665 - symbol:AT5G13420 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004801 "sedoheptulose-7-phosphate:D-glyceraldehyde-3-phosphate glyceronetransferase activity" evidence=IEA;ISS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005829 "cytosol" evidence=RCA] HAMAP:MF_00493 InterPro:IPR001585 InterPro:IPR004732 InterPro:IPR013785 InterPro:IPR018225 Pfam:PF00923 PIRSF:PIRSF036915 PROSITE:PS01054 GO:GO:0005739 GO:GO:0009570 GO:GO:0046686 EMBL:CP002688 GenomeReviews:BA000015_GR Gene3D:G3DSA:3.20.20.70 GO:GO:0006098 EMBL:AL163572 eggNOG:COG0176 PANTHER:PTHR10683 KO:K00616 GO:GO:0004801 HOGENOM:HBG321149 TIGRFAMs:TIGR00876 OMA:MPEKTLD EMBL:AY056296 EMBL:AY114075 EMBL:AY087135 IPI:IPI00531555 PIR:T48589 RefSeq:NP_196846.1 UniGene:At.22457 ProteinModelPortal:Q9LYR4 SMR:Q9LYR4 IntAct:Q9LYR4 STRING:Q9LYR4 PRIDE:Q9LYR4 EnsemblPlants:AT5G13420.1 GeneID:831183 KEGG:ath:AT5G13420 TAIR:At5g13420 InParanoid:Q9LYR4 PhylomeDB:Q9LYR4 ProtClustDB:CLSN2687015 ArrayExpress:Q9LYR4 Genevestigator:Q9LYR4 Uniprot:Q9LYR4
Root	Isotig04725	9	40	-2.281	1.10E-06	TAIR|locus:2181665 - symbol:AT5G13420 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004801 "sedoheptulose-7-phosphate:D-glyceraldehyde-3-phosphate glyceronetransferase activity" evidence=IEA;ISS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005829 "cytosol" evidence=RCA] HAMAP:MF_00493 InterPro:IPR001585 InterPro:IPR004732 InterPro:IPR013785 InterPro:IPR018225 Pfam:PF00923 PIRSF:PIRSF036915 PROSITE:PS01054 GO:GO:0005739 GO:GO:0009570 GO:GO:0046686 EMBL:CP002688 GenomeReviews:BA000015_GR Gene3D:G3DSA:3.20.20.70 GO:GO:0006098 EMBL:AL163572 eggNOG:COG0176 PANTHER:PTHR10683 KO:K00616 GO:GO:0004801 HOGENOM:HBG321149 TIGRFAMs:TIGR00876 OMA:MPEKTLD EMBL:AY056296 EMBL:AY114075 EMBL:AY087135 IPI:IPI00531555 PIR:T48589 RefSeq:NP_196846.1 UniGene:At.22457 ProteinModelPortal:Q9LYR4 SMR:Q9LYR4 IntAct:Q9LYR4 STRING:Q9LYR4 PRIDE:Q9LYR4 EnsemblPlants:AT5G13420.1 GeneID:831183 KEGG:ath:AT5G13420 TAIR:At5g13420 InParanoid:Q9LYR4 PhylomeDB:Q9LYR4 ProtClustDB:CLSN2687015 ArrayExpress:Q9LYR4 Genevestigator:Q9LYR4 Uniprot:Q9LYR4
Root	Isotig04732	6	24	-2.129	0.00029855	TAIR|locus:2183730 - symbol:AT5G10770 "AT5G10770" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=ISS] [GO:0004190 "aspartic-type endopeptidase activity" evidence=IEA] [GO:0006508 "proteolysis" evidence=IEA] InterPro:IPR001461 InterPro:IPR009007 Pfam:PF00026 PRINTS:PR00792 EMBL:CP002688 GO:GO:0006508 GO:GO:0004190 InterPro:IPR021109 SUPFAM:SSF50630 Gene3D:G3DSA:2.40.70.10 PANTHER:PTHR13683 HSSP:P00799 EMBL:AY075656 EMBL:BT001004 IPI:IPI00543783 RefSeq:NP_196638.2 UniGene:At.32336 ProteinModelPortal:Q8S9J6 MEROPS:A01.A15 PRIDE:Q8S9J6 EnsemblPlants:AT5G10770.1 GeneID:830944 KEGG:ath:AT5G10770 TAIR:At5g10770 InParanoid:Q8S9J6 OMA:LEVVYDG PhylomeDB:Q8S9J6 ProtClustDB:CLSN2686424 Genevestigator:Q8S9J6 Uniprot:Q8S9J6
Root	Isotig04733	5	22	-2.266	0.000318925	TAIR|locus:2183730 - symbol:AT5G10770 "AT5G10770" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=ISS] [GO:0004190 "aspartic-type endopeptidase activity" evidence=IEA] [GO:0006508 "proteolysis" evidence=IEA] InterPro:IPR001461 InterPro:IPR009007 Pfam:PF00026 PRINTS:PR00792 EMBL:CP002688 GO:GO:0006508 GO:GO:0004190 InterPro:IPR021109 SUPFAM:SSF50630

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						Gene3D:G3DSA:2.40.70.10 PANTHER:PTHR13683 HSSP:P00799 EMBL:AY075656 EMBL:BT001004 IPI:IPI00543783 RefSeq:NP_196638.2 UniGene:At.32336 ProteinModelPortal:Q8S9J6 MEROPS:A01.A15 PRIDE:Q8S9J6 EnsemblPlants:AT5G10770.1 GeneID:830944 KEGG:ath:AT5G10770 TAIR:At5g10770 InParanoid:Q8S9J6 OMA:LEVVYDG PhylomeDB:Q8S9J6 ProtClustDB:CLSN2686424 Genevestigator:Q8S9J6 Uniprot:Q8S9J6
Root	Isotig04734	5	23	-2.331	0.000182103	TAIR|locus:2183730 - symbol:AT5G10770 "AT5G10770" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=ISS] [GO:0004190 "aspartic-type endopeptidase activity" evidence=IEA] [GO:0006508 "proteolysis" evidence=IEA] InterPro:IPR001461 InterPro:IPR009007 Pfam:PF00026 PRINTS:PR00792 EMBL:CP002688 GO:GO:0006508 GO:GO:0004190 InterPro:IPR021109 SUPFAM:SSF50630 Gene3D:G3DSA:2.40.70.10 PANTHER:PTHR13683 HSSP:P00799 EMBL:AY075656 EMBL:BT001004 IPI:IPI00543783 RefSeq:NP_196638.2 UniGene:At.32336 ProteinModelPortal:Q8S9J6 MEROPS:A01.A15 PRIDE:Q8S9J6 EnsemblPlants:AT5G10770.1 GeneID:830944 KEGG:ath:AT5G10770 TAIR:At5g10770 InParanoid:Q8S9J6 OMA:LEVVYDG PhylomeDB:Q8S9J6 ProtClustDB:CLSN2686424 Genevestigator:Q8S9J6 Uniprot:Q8S9J6
Root	Isotig04750	49	17	1.398	0.000229772	TAIR|locus:2127173 - symbol:GSH1 "AT4G23100" species:3702 "Arabidopsis thaliana" [GO:0009908 "flower development" evidence=IMP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0004357 "glutamate-cysteine ligase activity" evidence=IMP;IDA] [GO:0006750 "glutathione biosynthetic process" evidence=IMP;IDA;TAS] [GO:0009408 "response to heat" evidence=IMP] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0009753 "response to jasmonic acid stimulus" evidence=IEP] [GO:0010193 "response to ozone" evidence=IEP] [GO:0046686 "response to cadmium ion" evidence=IEP;IMP] [GO:0050832 "defense response to fungus" evidence=IMP] [GO:0002213 "defense response to insect" evidence=IMP] [GO:0019761 "glucosinolate biosynthetic process" evidence=IMP] [GO:0042742 "defense response to bacterium" evidence=IMP] [GO:0052544 "defense response by callose deposition in cell wall" evidence=IMP] [GO:0009700 "indole phytoalexin biosynthetic process" evidence=IMP] [GO:0009816 "defense response to bacterium, incompatible interaction" evidence=IMP] InterPro:IPR006336 InterPro:IPR011556 Pfam:PF04107 GO:GO:0005524 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0009570 GO:GO:0046686 GO:GO:0009753 GO:GO:0050832 GO:GO:0019761 GO:GO:0052544 GO:GO:0010193 GO:GO:0009408 GO:GO:0002213 GO:GO:0009908 EMBL:AL031018 EMBL:AL161558 GO:GO:0009816 GO:GO:0004357 GO:GO:0006750 BRENDA:6.3.2.2 EMBL:Z29490 EMBL:Y09944 EMBL:AF068299 EMBL:DQ993178 EMBL:AF419576 EMBL:AF428393 EMBL:AY056372 EMBL:AY143970 IPI:IPI00536188 PIR:T05142 RefSeq:NP_001190808.1 RefSeq:NP_194041.1 UniGene:At.25074 ProteinModelPortal:P46309 SMR:P46309 STRING:P46309 PRIDE:P46309 EnsemblPlants:AT4G23100.1 EnsemblPlants:AT4G23100.3 GeneID:828409 KEGG:ath:AT4G23100 TAIR:At4g23100 eggNOG:COG3572 HOGENOM:HBG294235 InParanoid:P46309 KO:K01919 OMA:SIEPGGQ PhylomeDB:P46309 ProtClustDB:PLN02611 BioCyc:ARA:AT4G23100-MONOMER BioCyc:MetaCyc:AT4G23100-MONOMER ArrayExpress:P46309 Genevestigator:P46309 GO:GO:0009700 TIGRFAMs:TIGR01436 Uniprot:P46309
Root	Isotig04751	48	14	1.649	3.85E-05	TAIR|locus:2127173 - symbol:GSH1 "AT4G23100" species:3702 "Arabidopsis thaliana" [GO:0009908 "flower development" evidence=IMP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0004357 "glutamate-cysteine ligase activity" evidence=IMP;IDA] [GO:0006750 "glutathione biosynthetic process" evidence=IMP;IDA;TAS] [GO:0009408 "response to heat" evidence=IMP] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0009753 "response to jasmonic acid stimulus" evidence=IEP] [GO:0010193 "response to ozone" evidence=IEP] [GO:0046686 "response to cadmium ion" evidence=IEP;IMP] [GO:0050832 "defense response to fungus" evidence=IMP] [GO:0002213 "defense response to insect" evidence=IMP] [GO:0019761 "glucosinolate biosynthetic process" evidence=IMP] [GO:0042742 "defense response to bacterium" evidence=IMP] [GO:0052544 "defense response by callose deposition in cell wall" evidence=IMP] [GO:0009700 "indole phytoalexin biosynthetic process" evidence=IMP] [GO:0009816 "defense response to bacterium, incompatible interaction" evidence=IMP] InterPro:IPR006336 InterPro:IPR011556 Pfam:PF04107 GO:GO:0005524 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0009570 GO:GO:0046686 GO:GO:0009753 GO:GO:0050832 GO:GO:0019761 GO:GO:0052544 GO:GO:0010193 GO:GO:0009408 GO:GO:0002213 GO:GO:0009908 EMBL:AL031018 EMBL:AL161558 GO:GO:0009816 GO:GO:0004357 GO:GO:0006750 BRENDA:6.3.2.2 EMBL:Z29490 EMBL:Y09944 EMBL:AF068299 EMBL:DQ993178 EMBL:AF419576 EMBL:AF428393 EMBL:AY056372 EMBL:AY143970 IPI:IPI00536188 PIR:T05142 RefSeq:NP_001190808.1 RefSeq:NP_194041.1 UniGene:At.25074 ProteinModelPortal:P46309 SMR:P46309 STRING:P46309 PRIDE:P46309 EnsemblPlants:AT4G23100.1

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EnsemblPlants:AT4G23100.3 GeneID:828409 KEGG:ath:AT4G23100 TAIR:At4g23100 eggNOG:COG3572 HOGENOM:HBG294235 InParanoid:P46309 KO:K01919 OMA:SIEPGGQ PhylomeDB:P46309 ProtClustDB:PLN02611 BioCyc:ARA:AT4G23100-MONOMER BioCyc:MetaCyc:AT4G23100-MONOMER ArrayExpress:P46309 Genevestigator:P46309 GO:GO:0009700 TIGRFAMs:TIGR01436 Uniprot:P46309
Root	Isotig04765	24	4	2.456	0.000163328	TAIR|locus:2198646 - symbol:AT1G20110 "AT1G20110" species:3702 "Arabidopsis thaliana" [GO:0007165 "signal transduction" evidence=ISS] [GO:0035091 "phosphatidylinositol binding" evidence=ISS] InterPro:IPR000306 Pfam:PF01363 SMART:SM00064 InterPro:IPR011011 EMBL:CP002684 GO:GO:0046872 InterPro:IPR017455 InterPro:IPR013083 Gene3D:G3DSA:3.30.40.10 SUPFAM:SSF57903 PROSITE:PS50178 HSSP:Q15075 EMBL:AF367315 EMBL:AF428277 EMBL:AY143942 IPI:IPI00537339 RefSeq:NP_564103.1 UniGene:At.15444 ProteinModelPortal:Q9ASS2 SMR:Q9ASS2 IntAct:Q9ASS2 PRIDE:Q9ASS2 EnsemblPlants:AT1G20110.1 GeneID:838600 KEGG:ath:AT1G20110 TAIR:At1g20110 InParanoid:Q9ASS2 OMA:ENITRCE PhylomeDB:Q9ASS2 ProtClustDB:CLSN2917026 Genevestigator:Q9ASS2 Uniprot:Q9ASS2
Root	Isotig04766	24	4	2.456	0.000163328	TAIR|locus:2198646 - symbol:AT1G20110 "AT1G20110" species:3702 "Arabidopsis thaliana" [GO:0007165 "signal transduction" evidence=ISS] [GO:0035091 "phosphatidylinositol binding" evidence=ISS] InterPro:IPR000306 Pfam:PF01363 SMART:SM00064 InterPro:IPR011011 EMBL:CP002684 GO:GO:0046872 InterPro:IPR017455 InterPro:IPR013083 Gene3D:G3DSA:3.30.40.10 SUPFAM:SSF57903 PROSITE:PS50178 HSSP:Q15075 EMBL:AF367315 EMBL:AF428277 EMBL:AY143942 IPI:IPI00537339 RefSeq:NP_564103.1 UniGene:At.15444 ProteinModelPortal:Q9ASS2 SMR:Q9ASS2 IntAct:Q9ASS2 PRIDE:Q9ASS2 EnsemblPlants:AT1G20110.1 GeneID:838600 KEGG:ath:AT1G20110 TAIR:At1g20110 InParanoid:Q9ASS2 OMA:ENITRCE PhylomeDB:Q9ASS2 ProtClustDB:CLSN2917026 Genevestigator:Q9ASS2 Uniprot:Q9ASS2
Root	Isotig04767	24	5	2.134	0.000532871	TAIR|locus:2198646 - symbol:AT1G20110 "AT1G20110" species:3702 "Arabidopsis thaliana" [GO:0007165 "signal transduction" evidence=ISS] [GO:0035091 "phosphatidylinositol binding" evidence=ISS] InterPro:IPR000306 Pfam:PF01363 SMART:SM00064 InterPro:IPR011011 EMBL:CP002684 GO:GO:0046872 InterPro:IPR017455 InterPro:IPR013083 Gene3D:G3DSA:3.30.40.10 SUPFAM:SSF57903 PROSITE:PS50178 HSSP:Q15075 EMBL:AF367315 EMBL:AF428277 EMBL:AY143942 IPI:IPI00537339 RefSeq:NP_564103.1 UniGene:At.15444 ProteinModelPortal:Q9ASS2 SMR:Q9ASS2 IntAct:Q9ASS2 PRIDE:Q9ASS2 EnsemblPlants:AT1G20110.1 GeneID:838600 KEGG:ath:AT1G20110 TAIR:At1g20110 InParanoid:Q9ASS2 OMA:ENITRCE PhylomeDB:Q9ASS2 ProtClustDB:CLSN2917026 Genevestigator:Q9ASS2 Uniprot:Q9ASS2
Root	Isotig04792	24	53	-1.272	0.000195269	TAIR|locus:2091965 - symbol:AT3G27090 "AT3G27090" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] GenomeReviews:BA000014_GR InterPro:IPR013989 Pfam:PF10539 SMART:SM00767 PROSITE:PS51222 EMBL:AY087011 IPI:IPI00536337 PRIDE:Q8LBT1 TAIR:At3g27090 eggNOG:NOG302982 PhylomeDB:Q8LBT1 Genevestigator:Q8LBT1 Uniprot:Q8LBT1
Root	Isotig04793	17	69	-2.150	6.81E-10	TAIR|locus:2091965 - symbol:AT3G27090 "AT3G27090" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] GenomeReviews:BA000014_GR InterPro:IPR013989 Pfam:PF10539 SMART:SM00767 PROSITE:PS51222 EMBL:AY087011 IPI:IPI00536337 PRIDE:Q8LBT1 TAIR:At3g27090 eggNOG:NOG302982 PhylomeDB:Q8LBT1 Genevestigator:Q8LBT1 Uniprot:Q8LBT1
Root	Isotig04794	14	64	-2.322	4.70E-10	TAIR|locus:2091965 - symbol:AT3G27090 "AT3G27090" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] GenomeReviews:BA000014_GR InterPro:IPR013989 Pfam:PF10539 SMART:SM00767 PROSITE:PS51222 EMBL:AY087011 IPI:IPI00536337 PRIDE:Q8LBT1 TAIR:At3g27090 eggNOG:NOG302982 PhylomeDB:Q8LBT1 Genevestigator:Q8LBT1 Uniprot:Q8LBT1
Root	Isotig04795	124	14	3.018	1.26E-21	TAIR|locus:2206405 - symbol:ALDH5F1 "AT1G79440" species:3702 "Arabidopsis thaliana" [GO:0004028 "3-chloroallyl aldehyde dehydrogenase activity" evidence=ISS] [GO:0004777 "succinate-semialdehyde dehydrogenase activity" evidence=ISS;IDA] [GO:0005759 "mitochondrial matrix" evidence=IDA] [GO:0006540 "glutamate decarboxylation to succinate" evidence=IMP;IDA] [GO:0009450 "gamma-aminobutyric acid catabolic process" evidence=IDA] [GO:0051287 "NAD binding" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0006950 "response to stress" evidence=IMP] [GO:0009408 "response to heat" evidence=IMP] [GO:0009416 "response to light stimulus" evidence=IMP] [GO:0072593 "reactive oxygen species metabolic process" evidence=IMP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] InterPro:IPR010102 InterPro:IPR015590 InterPro:IPR016160

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						InterPro:IPR016161 InterPro:IPR016162 InterPro:IPR016163 Pfam:PF00171 PROSITE:PS00070 PROSITE:PS00687 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009570 GO:GO:0051287 GO:GO:0005759 eggNOG:COG1012 Gene3D:G3DSA:3.40.309.10 Gene3D:G3DSA:3.40.605.10 SUPFAM:SSF53720 HOGENOM:HBG752218 GO:GO:0005507 GO:GO:0009408 GO:GO:0009416 GO:GO:0072593 HSSP:P05091 EMBL:AC007202 GO:GO:0009450 GO:GO:0006540 KO:K00135 TIGRFAMs:TIGR01780 GO:GO:0004777 OMA:MIQNKDD EMBL:AF117335 EMBL:AF428367 EMBL:AY056147 IPI:IPI00532908 PIR:E96825 RefSeq:NP_178062.1 UniGene:At.11884 ProteinModelPortal:Q9SAK4 SMR:Q9SAK4 STRING:Q9SAK4 PRIDE:Q9SAK4 EnsemblPlants:AT1G79440.1 GeneID:844282 KEGG:ath:AT1G79440 GeneFarm:4340 TAIR:At1g79440 InParanoid:Q9SAK4 PhylomeDB:Q9SAK4 ProtClustDB:PLN02278 ArrayExpress:Q9SEK4 Genevestigator:Q9SAK4 Uniprot:Q9SAK4
Root	Isotig04796	121	13	3.089	1.41E-21	TAIR|locus:2206405 - symbol:ALDH5F1 "AT1G79440" species:3702 "Arabidopsis thaliana" [GO:0004028 "3-chloroallyl aldehyde dehydrogenase activity" evidence=ISS] [GO:0004777 "succinate-semialdehyde dehydrogenase activity" evidence=ISS;IDA] [GO:0005759 "mitochondrial matrix" evidence=IDA] [GO:0006540 "glutamate decarboxylation to succinate" evidence=IMP;IDA] [GO:0009450 "gamma-aminobutyric acid catabolic process" evidence=IDA] [GO:0051287 "NAD binding" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0006950 "response to stress" evidence=IMP] [GO:0009408 "response to heat" evidence=IMP] [GO:0009416 "response to light stimulus" evidence=IMP] [GO:0072593 "reactive oxygen species metabolic process" evidence=IMP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] InterPro:IPR010102 InterPro:IPR015590 InterPro:IPR016160 InterPro:IPR016161 InterPro:IPR016162 InterPro:IPR016163 Pfam:PF00171 PROSITE:PS00070 PROSITE:PS00687 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009570 GO:GO:0051287 GO:GO:0005759 eggNOG:COG1012 Gene3D:G3DSA:3.40.309.10 Gene3D:G3DSA:3.40.605.10 SUPFAM:SSF53720 HOGENOM:HBG752218 GO:GO:0005507 GO:GO:0009408 GO:GO:0009416 GO:GO:0072593 HSSP:P05091 EMBL:AC007202 GO:GO:0009450 GO:GO:0006540 KO:K00135 TIGRFAMs:TIGR01780 GO:GO:0004777 OMA:MIQNKDD EMBL:AF117335 EMBL:AF428367 EMBL:AY056147 IPI:IPI00532908 PIR:E96825 RefSeq:NP_178062.1 UniGene:At.11884 ProteinModelPortal:Q9SAK4 SMR:Q9SAK4 STRING:Q9SAK4 PRIDE:Q9SAK4 EnsemblPlants:AT1G79440.1 GeneID:844282 KEGG:ath:AT1G79440 GeneFarm:4340 TAIR:At1g79440 InParanoid:Q9SAK4 PhylomeDB:Q9SAK4 ProtClustDB:PLN02278 ArrayExpress:Q9SEK4 Genevestigator:Q9SAK4 Uniprot:Q9SAK4
Root	Isotig04801	2	18	-3.299	7.42E-05	TAIR|locus:2051859 - symbol:MLO15 "AT2G44110" species:3702 "Arabidopsis thaliana" [GO:0005516 "calmodulin binding" evidence=ISS] [GO:0006952 "defense response" evidence=ISS] [GO:0008219 "cell death" evidence=IEA;ISS] [GO:0016021 "integral to membrane" evidence=IEA;ISS] InterPro:IPR004326 Pfam:PF03094 GO:GO:0016021 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0006952 GO:GO:0008219 GO:GO:0005516 GO:GO:0009607 EMBL:AC004005 HOGENOM:HBG319688 KO:K08472 eggNOG:NOG307472 EMBL:AF369576 IPI:IPI00536590 PIR:T00691 RefSeq:NP_181939.1 UniGene:At.19505 PRIDE:O80580 EnsemblPlants:AT2G44110.1 GeneID:819017 KEGG:ath:AT2G44110 TAIR:At2g44110 InParanoid:O80580 PhylomeDB:O80580 ProtClustDB:CLSN2683190 ArrayExpress:O80580 Genevestigator:O80580 Uniprot:O80580
Root	Isotig04802	2	18	-3.299	7.42E-05	TAIR|locus:2051859 - symbol:MLO15 "AT2G44110" species:3702 "Arabidopsis thaliana" [GO:0005516 "calmodulin binding" evidence=ISS] [GO:0006952 "defense response" evidence=ISS] [GO:0008219 "cell death" evidence=IEA;ISS] [GO:0016021 "integral to membrane" evidence=IEA;ISS] InterPro:IPR004326 Pfam:PF03094 GO:GO:0016021 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0006952 GO:GO:0008219 GO:GO:0005516 GO:GO:0009607 EMBL:AC004005 HOGENOM:HBG319688 KO:K08472 eggNOG:NOG307472 EMBL:AF369576 IPI:IPI00536590 PIR:T00691 RefSeq:NP_181939.1 UniGene:At.19505 PRIDE:O80580 EnsemblPlants:AT2G44110.1 GeneID:819017 KEGG:ath:AT2G44110 TAIR:At2g44110 InParanoid:O80580 PhylomeDB:O80580 ProtClustDB:CLSN2683190 ArrayExpress:O80580 Genevestigator:O80580 Uniprot:O80580
Root	Isotig04810	44	6	2.745	5.73E-08	TAIR|locus:2178128 - symbol:ACT7 "AT5G09810" species:3702 "Arabidopsis thaliana" [GO:0007010 "cytoskeleton organization" evidence=TAS] [GO:0009733 "response to auxin stimulus" evidence=IEP] [GO:0009845 "seed germination" evidence=IMP] [GO:0048364 "root development" evidence=IMP] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0010053 "root epidermal cell differentiation" evidence=IMP] [GO:0048767 "root hair elongation" evidence=IMP] [GO:0051301 "cell division" evidence=IMP] [GO:0005515 "protein binding" evidence=IPI] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA]

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						[GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005200 "structural constituent of cytoskeleton" evidence=ISS] [GO:0005856 "cytoskeleton" evidence=ISS] [GO:0009416 "response to light stimulus" evidence=IEP] [GO:0009611 "response to wounding" evidence=IEP] InterPro:IPR004001 PROSITE:PS00406 PROSITE:PS00432 InterPro:IPR004000 GO:GO:0005829 GO:GO:0005739 GO:GO:0005886 GO:GO:0009506 GO:GO:0005524 GO:GO:0009570 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005618 GO:GO:0005515 GO:GO:0009733 GO:GO:0009611 GO:GO:0005730 GO:GO:0005856 GO:GO:0051301 GO:GO:0009941 EMBL:AB016893 GO:GO:0048767 GO:GO:0009845 GO:GO:0009416 HOGENOM:HBG559892 PANTHER:PTHR11937 Pfam:PF00022 PRINTS:PR00190 SMART:SM00268 KO:K10355 InterPro:IPR020902 PROSITE:PS01132 ProtClustDB:CLSN2682469 UniGene:At.23346 EMBL:U37281 EMBL:U27811 EMBL:AY062702 EMBL:AY063980 EMBL:AY096397 EMBL:AY114679 EMBL:AY120779 IPI:IPI00524611 PIR:S68107 RefSeq:NP_196543.1 UniGene:At.23605 UniGene:At.24396 ProteinModelPortal:P53492 SMR:P53492 IntAct:P53492 STRING:P53492 PRIDE:P53492 ProMEX:P53492 EnsemblPlants:AT5G09810.1 GeneID:830841 KEGG:ath:AT5G09810 TAIR:At5g09810 InParanoid:P53492 OMA:NSICVIL PhylomeDB:P53492 ArrayExpress:P53492 Genevestigator:P53492 GermOnline:AT5G09810 Uniprot:P53492
Root	Isotig04811	46	11	1.935	6.77E-06	TAIR|locus:2178128 - symbol:ACT7 "AT5G09810" species:3702 "Arabidopsis thaliana" [GO:0007010 "cytoskeleton organization" evidence=TAS] [GO:0009733 "response to auxin stimulus" evidence=IEP] [GO:0009845 "seed germination" evidence=IMP] [GO:0048364 "root development" evidence=IMP] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0010053 "root epidermal cell differentiation" evidence=IMP] [GO:0048767 "root hair elongation" evidence=IMP] [GO:0051301 "cell division" evidence=IMP] [GO:0005515 "protein binding" evidence=IPI] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005200 "structural constituent of cytoskeleton" evidence=ISS] [GO:0005856 "cytoskeleton" evidence=ISS] [GO:0009416 "response to light stimulus" evidence=IEP] [GO:0009611 "response to wounding" evidence=IEP] InterPro:IPR004001 PROSITE:PS00406 PROSITE:PS00432 InterPro:IPR004000 GO:GO:0005829 GO:GO:0005739 GO:GO:0005886 GO:GO:0009506 GO:GO:0005524 GO:GO:0009570 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005618 GO:GO:0005515 GO:GO:0009733 GO:GO:0009611 GO:GO:0005730 GO:GO:0005856 GO:GO:0051301 GO:GO:0009941 EMBL:AB016893 GO:GO:0048767 GO:GO:0009845 GO:GO:0009416 HOGENOM:HBG559892 PANTHER:PTHR11937 Pfam:PF00022 PRINTS:PR00190 SMART:SM00268 KO:K10355 InterPro:IPR020902 PROSITE:PS01132 ProtClustDB:CLSN2682469 UniGene:At.23346 EMBL:U37281 EMBL:U27811 EMBL:AY062702 EMBL:AY063980 EMBL:AY096397 EMBL:AY114679 EMBL:AY120779 IPI:IPI00524611 PIR:S68107 RefSeq:NP_196543.1 UniGene:At.23605 UniGene:At.24396 ProteinModelPortal:P53492 SMR:P53492 IntAct:P53492 STRING:P53492 PRIDE:P53492 ProMEX:P53492 EnsemblPlants:AT5G09810.1 GeneID:830841 KEGG:ath:AT5G09810 TAIR:At5g09810 InParanoid:P53492 OMA:NSICVIL PhylomeDB:P53492 ArrayExpress:P53492 Genevestigator:P53492 GermOnline:AT5G09810 Uniprot:P53492
Root	Isotig04812	39	5	2.835	2.06E-07	TAIR|locus:2178128 - symbol:ACT7 "AT5G09810" species:3702 "Arabidopsis thaliana" [GO:0007010 "cytoskeleton organization" evidence=TAS] [GO:0009733 "response to auxin stimulus" evidence=IEP] [GO:0009845 "seed germination" evidence=IMP] [GO:0048364 "root development" evidence=IMP] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0010053 "root epidermal cell differentiation" evidence=IMP] [GO:0048767 "root hair elongation" evidence=IMP] [GO:0051301 "cell division" evidence=IMP] [GO:0005515 "protein binding" evidence=IPI] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005200 "structural constituent of cytoskeleton" evidence=ISS] [GO:0005856 "cytoskeleton" evidence=ISS] [GO:0009416 "response to light stimulus" evidence=IEP] [GO:0009611 "response to wounding" evidence=IEP] InterPro:IPR004001 PROSITE:PS00406 PROSITE:PS00432 InterPro:IPR004000 GO:GO:0005829 GO:GO:0005739 GO:GO:0005886 GO:GO:0009506 GO:GO:0005524 GO:GO:0009570 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005618 GO:GO:0005515 GO:GO:0009733 GO:GO:0009611 GO:GO:0005730 GO:GO:0005856 GO:GO:0051301 GO:GO:0009941 EMBL:AB016893 GO:GO:0048767 GO:GO:0009845 GO:GO:0009416 HOGENOM:HBG559892 PANTHER:PTHR11937 Pfam:PF00022 PRINTS:PR00190 SMART:SM00268 KO:K10355 InterPro:IPR020902 PROSITE:PS01132 ProtClustDB:CLSN2682469 UniGene:At.23346 EMBL:U37281

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EMBL:U27811 EMBL:AY062702 EMBL:AY063980 EMBL:AY096397 EMBL:AY114679 EMBL:AY120779 IPI:IPI00524611 PIR:S68107 RefSeq:NP_196543.1 UniGene:At.23605 UniGene:At.24396 ProteinModelPortal:P53492 SMR:P53492 IntAct:P53492 STRING:P53492 PRIDE:P53492 ProMEX:P53492 EnsemblPlants:AT5G09810.1 GeneID:830841 KEGG:ath:AT5G09810 TAIR:At5g09810 InParanoid:P53492 OMA:NSICVIL PhylomeDB:P53492 ArrayExpress:P53492 Genevestigator:P53492 GermOnline:AT5G09810 Uniprot:P53492
Root	Isotig04826	2	15	-3.036	0.000493759	TAIR|locus:2125766 - symbol:CRK40 "cysteine-rich RLK (RECEPTOR-like protein kinase) 40" species:3702 "Arabidopsis thaliana" [GO:0006468 "protein phosphorylation" evidence=IEA] [GO:0016301 "kinase activity" evidence=ISS] InterPro:IPR000719 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 Pfam:PF00069 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 GO:GO:0016021 GO:GO:0005524 EMBL:CP002687 GenomeReviews:CT486007_GR eggNOG:COG0515 GO:GO:0004872 SUPFAM:SSF56112 GO:GO:0004674 HOGENOM:HBG755340 EMBL:AL161501 EMBL:AF074021 InterPro:IPR002902 Pfam:PF01657 PROSITE:PS51473 ProtClustDB:CLSN2685351 EMBL:AY127017 IPI:IPI00540978 PIR:F85057 RefSeq:NP_192366.1 UniGene:At.33996 ProteinModelPortal:Q9SYS3 SMR:Q9SYS3 IntAct:Q9SYS3 STRING:Q9SYS3 PRIDE:Q9SYS3 EnsemblPlants:AT4G04570.1 GeneID:825789 KEGG:ath:AT4G04570 GeneFarm:748 TAIR:At4g04570 InParanoid:Q9SYS3 OMA:QSESGAM PhylomeDB:Q9SYS3 Genevestigator:Q9SYS3 Uniprot:Q9SYS3
Root	Isotig04832	27	5	2.304	0.000117535	TAIR|locus:2027082 - symbol:SKP2A "AT1G21410" species:3702 "Arabidopsis thaliana" [GO:0005515 "protein binding" evidence=IPI] [GO:0019005 "SCF ubiquitin ligase complex" evidence=IDA;IPI] [GO:0031146 "SCF-dependent proteasomal ubiquitin-dependent protein catabolic process" evidence=IDA;IPI] [GO:0005634 "nucleus" evidence=IDA] [GO:0010386 "lateral root primordium development" evidence=IMP] [GO:0051781 "positive regulation of cell division" evidence=IMP] [GO:0004842 "ubiquitin-protein ligase activity" evidence=IDA] [GO:0016567 "protein ubiquitination" evidence=IDA] [GO:0071365 "cellular response to auxin stimulus" evidence=IDA] InterPro:IPR001810 Pfam:PF00646 PROSITE:PS50181 SMART:SM00256 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005634 GO:GO:0005515 GO:GO:0009734 GO:GO:0051781 SUPFAM:SSF81383 GO:GO:0019005 GO:GO:0031146 EMBL:AC015447 GO:GO:0004842 InterPro:IPR006553 SMART:SM00367 GO:GO:0010386 EMBL:AY058081 EMBL:AY090308 EMBL:AY085898 IPI:IPI00519620 PIR:B86347 RefSeq:NP_564139.1 UniGene:At.25230 ProteinModelPortal:Q9LPL4 SMR:Q9LPL4 IntAct:Q9LPL4 STRING:Q9LPL4 EnsemblPlants:AT1G21410.1 GeneID:838740 KEGG:ath:AT1G21410 TAIR:At1g21410 eggNOG:NOG257455 InParanoid:Q9LPL4 OMA:NLNISQC PhylomeDB:Q9LPL4 ProtClustDB:CLSN2687892 Genevestigator:Q9LPL4 Uniprot:Q9LPL4
Root	Isotig04833	27	5	2.304	0.000117535	TAIR|locus:2027082 - symbol:SKP2A "AT1G21410" species:3702 "Arabidopsis thaliana" [GO:0005515 "protein binding" evidence=IPI] [GO:0019005 "SCF ubiquitin ligase complex" evidence=IDA;IPI] [GO:0031146 "SCF-dependent proteasomal ubiquitin-dependent protein catabolic process" evidence=IDA;IPI] [GO:0005634 "nucleus" evidence=IDA] [GO:0010386 "lateral root primordium development" evidence=IMP] [GO:0051781 "positive regulation of cell division" evidence=IMP] [GO:0004842 "ubiquitin-protein ligase activity" evidence=IDA] [GO:0016567 "protein ubiquitination" evidence=IDA] [GO:0071365 "cellular response to auxin stimulus" evidence=IDA] InterPro:IPR001810 Pfam:PF00646 PROSITE:PS50181 SMART:SM00256 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005634 GO:GO:0005515 GO:GO:0009734 GO:GO:0051781 SUPFAM:SSF81383 GO:GO:0019005 GO:GO:0031146 EMBL:AC015447 GO:GO:0004842 InterPro:IPR006553 SMART:SM00367 GO:GO:0010386 EMBL:AY058081 EMBL:AY090308 EMBL:AY085898 IPI:IPI00519620 PIR:B86347 RefSeq:NP_564139.1 UniGene:At.25230 ProteinModelPortal:Q9LPL4 SMR:Q9LPL4 IntAct:Q9LPL4 STRING:Q9LPL4 EnsemblPlants:AT1G21410.1 GeneID:838740 KEGG:ath:AT1G21410 TAIR:At1g21410 eggNOG:NOG257455 InParanoid:Q9LPL4 OMA:NLNISQC PhylomeDB:Q9LPL4 ProtClustDB:CLSN2687892 Genevestigator:Q9LPL4 Uniprot:Q9LPL4
Root	Isotig04837	9	28	-1.766	0.000557996	TAIR|locus:2007253 - symbol:MTK "AT1G49820" species:3702 "Arabidopsis thaliana" [GO:0046522 "S-methyl-5-thioribose kinase activity" evidence=ISS;IDA;IMP] [GO:0019509 "L-methionine salvage from methylthioadenosine" evidence=TAS] [GO:0042802 "identical protein binding" evidence=IPI] [GO:0071281 "cellular response to iron ion" evidence=IEP] [GO:0071369 "cellular response to ethylene stimulus" evidence=IEP] [GO:0071732 "cellular response to nitric oxide" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR009212 InterPro:IPR011009 PIRSF:PIRSF031134 Pfam:PF01636 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0005524 GO:GO:0042802 GO:GO:0071281 SUPFAM:SSF56112 GO:GO:0019509

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0071732 InterPro:IPR002575 GO:GO:0071369 EMBL:AC079674 EMBL:AY057512 EMBL:AY090315 IPI:IPI00544339 PIR:A96535 RefSeq:NP_564555.1 UniGene:At.20360 PDB:2PYW PDBsum:2PYW ProteinModelPortal:Q9C6D2 SMR:Q9C6D2 STRING:Q9C6D2 PRIDE:Q9C6D2 EnsemblPlants:AT1G49820.1 GeneID:841405 KEGG:ath:AT1G49820 TAIR:At1g49820 eggNOG:COG4857 HOGENOM:HBG305135 InParanoid:Q9C6D2 OMA:REIGDGN PhylomeDB:Q9C6D2 ProtClustDB:PLN02756 Genevestigator:Q9C6D2 GO:GO:0046522 TIGRFAMs:TIGR01767 Uniprot:Q9C6D2
Root	Isotig04838	8	30	-2.036	8.51E-05	TAIR|locus:2007253 - symbol:MTK "AT1G49820" species:3702 "Arabidopsis thaliana" [GO:0046522 "S-methyl-5-thioribose kinase activity" evidence=ISS;IDA;IMP] [GO:0019509 "L-methionine salvage from methylthioadenosine" evidence=TAS] [GO:0042802 "identical protein binding" evidence=IPI] [GO:0071281 "cellular response to iron ion" evidence=IEP] [GO:0071369 "cellular response to ethylene stimulus" evidence=IEP] [GO:0071732 "cellular response to nitric oxide" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR009212 InterPro:IPR011009 PIRSF:PIRSF031134 Pfam:PF01636 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0005524 GO:GO:0042802 GO:GO:0071281 SUPFAM:SSF56112 GO:GO:0019509 GO:GO:0071732 InterPro:IPR002575 GO:GO:0071369 EMBL:AC079674 EMBL:AY057512 EMBL:AY090315 IPI:IPI00544339 PIR:A96535 RefSeq:NP_564555.1 UniGene:At.20360 PDB:2PYW PDBsum:2PYW ProteinModelPortal:Q9C6D2 SMR:Q9C6D2 STRING:Q9C6D2 PRIDE:Q9C6D2 EnsemblPlants:AT1G49820.1 GeneID:841405 KEGG:ath:AT1G49820 TAIR:At1g49820 eggNOG:COG4857 HOGENOM:HBG305135 InParanoid:Q9C6D2 OMA:REIGDGN PhylomeDB:Q9C6D2 ProtClustDB:PLN02756 Genevestigator:Q9C6D2 GO:GO:0046522 TIGRFAMs:TIGR01767 Uniprot:Q9C6D2
Root	Isotig04855	0	35	-6.258	3.45E-10	UNIPROTKB|P29717 - symbol:XOG1 "Glucan 1,3-beta-glucosidase" species:237561 "Candida albicans SC5314" [GO:0004338 "glucan exo-1,3-beta-glucosidase activity" evidence=IMP;IDA] [GO:0005576 "extracellular region" evidence=IDA] [GO:0006073 "cellular glucan metabolic process" evidence=IMP] [GO:0009986 "cell surface" evidence=IDA] [GO:0031505 "fungal-type cell wall organization" evidence=IMP] [GO:0031589 "cell-substrate adhesion" evidence=IDA] [GO:0050839 "cell adhesion molecule binding" evidence=IDA] InterPro:IPR001547 InterPro:IPR013781 InterPro:IPR018087 Pfam:PF00150 PROSITE:PS00659 GO:GO:0005576 EMBL:AACQ01000015 GO:GO:0009986 GO:GO:0043169 InterPro:IPR017853 Gene3D:G3DSA:3.20.20.80 SUPFAM:SSF51445 CAZy:GH5 GO:GO:0031505 GO:GO:0050839 GO:GO:0031589 EMBL:AL033497 KO:K01210 GO:GO:0004338 eggNOG:COG2730 GO:GO:0006073 EMBL:X56556 PIR:A47702 PIR:T52149 RefSeq:XP_721488.1 PDB:1CZ1 PDB:1EQC PDB:1EQP PDB:2PB1 PDB:2PBO PDB:2PC8 PDB:2PF0 PDB:3N9K PDB:3O6A PDBsum:1CZ1 PDBsum:1EQC PDBsum:1EQP PDBsum:2PB1 PDBsum:2PBO PDBsum:2PC8 PDBsum:2PF0 PDBsum:3N9K PDBsum:3O6A ProteinModelPortal:P29717 SMR:P29717 STRING:P29717 GeneID:3636837 KEGG:cal:CaO19.2990 PhylomeDB:P29717 PMAP-CutDB:P29717 Uniprot:P29717
Root	Isotig04856	0	35	-6.258	3.45E-10	UNIPROTKB|P29717 - symbol:XOG1 "Glucan 1,3-beta-glucosidase" species:237561 "Candida albicans SC5314" [GO:0004338 "glucan exo-1,3-beta-glucosidase activity" evidence=IMP;IDA] [GO:0005576 "extracellular region" evidence=IDA] [GO:0006073 "cellular glucan metabolic process" evidence=IMP] [GO:0009986 "cell surface" evidence=IDA] [GO:0031505 "fungal-type cell wall organization" evidence=IMP] [GO:0031589 "cell-substrate adhesion" evidence=IDA] [GO:0050839 "cell adhesion molecule binding" evidence=IDA] InterPro:IPR001547 InterPro:IPR013781 InterPro:IPR018087 Pfam:PF00150 PROSITE:PS00659 GO:GO:0005576 EMBL:AACQ01000015 GO:GO:0009986 GO:GO:0043169 InterPro:IPR017853 Gene3D:G3DSA:3.20.20.80 SUPFAM:SSF51445 CAZy:GH5 GO:GO:0031505 GO:GO:0050839 GO:GO:0031589 EMBL:AL033497 KO:K01210 GO:GO:0004338 eggNOG:COG2730 GO:GO:0006073 EMBL:X56556 PIR:A47702 PIR:T52149 RefSeq:XP_721488.1 PDB:1CZ1 PDB:1EQC PDB:1EQP PDB:2PB1 PDB:2PBO PDB:2PC8 PDB:2PF0 PDB:3N9K PDB:3O6A PDBsum:1CZ1 PDBsum:1EQC PDBsum:1EQP PDBsum:2PB1 PDBsum:2PBO PDBsum:2PC8 PDBsum:2PF0 PDBsum:3N9K PDBsum:3O6A ProteinModelPortal:P29717 SMR:P29717 STRING:P29717 GeneID:3636837 KEGG:cal:CaO19.2990 PhylomeDB:P29717 PMAP-CutDB:P29717 Uniprot:P29717
Root	Isotig04857	0	15	-5.036	4.38E-05	No hit
Root	Isotig04879	30	6	2.193	8.18E-05	TAIR|locus:2009650 - symbol:DJ1B "AT1G53280" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] INTERPRO:IPR002818 EMBL:CP002684 GO:GO:0009570 EMBL:AC008007 UniGene:At.66897 Pfam:PF01965 HSSP:Q99497 InterPro:IPR006287 TIGRFAMs:TIGR01383 KO:K03152 ProtClustDB:CLSN2685087 EMBL:AY056268 EMBL:AY091184 IPI:IPI00532024 RefSeq:NP_564626.1 UniGene:At.24375 ProteinModelPortal:Q9MAH3 SMR:Q9MAH3 IntAct:Q9MAH3 PRIDE:Q9MAH3 EnsemblPlants:AT1G53280.1

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GeneID:841762 KEGG:ath:AT1G53280 TAIR:At1g53280 InParanoid:Q9MAH3 OMA:MIIDILR PhylomeDB:Q9MAH3 ArrayExpress:Q9MAH3 Genevestigator:Q9MAH3 Uniprot:Q9MAH3
Root	Isotig04880	29	7	1.922	0.000375107	TAIR|locus:2009650 - symbol:DJ1B "AT1G53280" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] INTERPRO:IPR002818 EMBL:CP002684 GO:GO:0009570 EMBL:AC008007 UniGene:At.66897 Pfam:PF01965 HSSP:Q99497 InterPro:IPR006287 TIGRFAMs:TIGR01383 KO:K03152 ProtClustDB:CLSN2685087 EMBL:AY056268 EMBL:AY091184 IPI:IPI00532024 RefSeq:NP_564626.1 UniGene:At.24375 ProteinModelPortal:Q9MAH3 SMR:Q9MAH3 IntAct:Q9MAH3 PRIDE:Q9MAH3 EnsemblPlants:AT1G53280.1 GeneID:841762 KEGG:ath:AT1G53280 TAIR:At1g53280 InParanoid:Q9MAH3 OMA:MIIDILR PhylomeDB:Q9MAH3 ArrayExpress:Q9MAH3 Genevestigator:Q9MAH3 Uniprot:Q9MAH3
Root	Isotig04881	29	6	2.144	0.000134201	TAIR|locus:2009650 - symbol:DJ1B "AT1G53280" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] INTERPRO:IPR002818 EMBL:CP002684 GO:GO:0009570 EMBL:AC008007 UniGene:At.66897 Pfam:PF01965 HSSP:Q99497 InterPro:IPR006287 TIGRFAMs:TIGR01383 KO:K03152 ProtClustDB:CLSN2685087 EMBL:AY056268 EMBL:AY091184 IPI:IPI00532024 RefSeq:NP_564626.1 UniGene:At.24375 ProteinModelPortal:Q9MAH3 SMR:Q9MAH3 IntAct:Q9MAH3 PRIDE:Q9MAH3 EnsemblPlants:AT1G53280.1 GeneID:841762 KEGG:ath:AT1G53280 TAIR:At1g53280 InParanoid:Q9MAH3 OMA:MIIDILR PhylomeDB:Q9MAH3 ArrayExpress:Q9MAH3 Genevestigator:Q9MAH3 Uniprot:Q9MAH3
Root	Isotig04890	7	24	-1.907	0.000762598	TAIR|locus:2172214 - symbol:TUB3 "tubulin beta chain 3" species:3702 "Arabidopsis thaliana" [GO:0003924 "GTPase activity" evidence=IEA] [GO:0005198 "structural molecule activity" evidence=IEA;ISS] [GO:0005525 "GTP binding" evidence=IEA] [GO:0045298 "tubulin complex" evidence=TAS] [GO:0005618 "cell wall" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR000217 InterPro:IPR002453 InterPro:IPR003008 InterPro:IPR008280 InterPro:IPR017975 InterPro:IPR018316 Pfam:PF00091 Pfam:PF03953 PRINTS:PR01161 PRINTS:PR01163 PROSITE:PS00227 SMART:SM00864 SMART:SM00865 GO:GO:0005525 GO:GO:0005886 GO:GO:0009506 GO:GO:0046686 GO:GO:0005737 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005618 GO:GO:0005515 GO:GO:0005730 GO:GO:0005198 GO:GO:0003924 GO:GO:0009651 GO:GO:0005874 GO:GO:0051258 Gene3D:G3DSA:3.40.50.1440 SUPFAM:SSF52490 GO:GO:0007018 EMBL:AB009053 EMBL:AB020751 Gene3D:G3DSA:3.30.1330.20 SUPFAM:SSF55307 GO:GO:0045298 eggNOG:COG5023 HOGENOM:HBG750007 InterPro:IPR023123 Gene3D:G3DSA:1.10.287.600 PANTHER:PTHR11588 InterPro:IPR013838 KO:K07375 ProtClustDB:PLN00220 PROSITE:PS00228 OMA:ADEMGEY EMBL:M84700 EMBL:M84701 EMBL:AK117431 EMBL:AY056411 EMBL:AY060550 EMBL:AY062614 EMBL:AY062742 EMBL:AY128785 EMBL:BT002587 EMBL:AY087859 IPI:IPI00525001 PIR:JQ1587 RefSeq:NP_568959.1 RefSeq:NP_568960.1 UniGene:At.24202 UniGene:At.49208 ProteinModelPortal:P29512 SMR:P29512 IntAct:P29512 STRING:P29512 PRIDE:P29512 EnsemblPlants:AT5G62690.1 EnsemblPlants:AT5G62700.1 GeneID:836390 GeneID:836391 KEGG:ath:AT5G62690 KEGG:ath:AT5G62700 TAIR:At5g62690 TAIR:At5g62700 InParanoid:P29512 PhylomeDB:P29512 ArrayExpress:P29512 Genevestigator:P29512 GermOnline:AT5G62690 Uniprot:P29512
Root	Isotig04894	5	21	-2.199	0.000555521	TAIR|locus:2175088 - symbol:ALP "AT5G60360" species:3702 "Arabidopsis thaliana" [GO:0006508 "proteolysis" evidence=ISS] [GO:0008234 "cysteine-type peptidase activity" evidence=ISS] [GO:0009723 "response to ethylene stimulus" evidence=IEP] [GO:0005773 "vacuole" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] [GO:0007568 "aging" evidence=IEP] InterPro:IPR000668 InterPro:IPR013128 Pfam:PF00112 PRINTS:PR00705 SMART:SM00645 InterPro:IPR000169 GO:GO:0005773 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0007568 eggNOG:COG4870 HOGENOM:HBG746690 GO:GO:0004197 GO:GO:0006508 InterPro:IPR013201 PANTHER:PTHR12411 Pfam:PF08246 SMART:SM00848 PROSITE:PS00640 PROSITE:PS00139 PROSITE:PS00639 EMBL:AB011483 KO:K01366 ProtClustDB:CLSN2689015 EMBL:AF233883 EMBL:AF083703 EMBL:AF360273 EMBL:BT000673 EMBL:BT000674 EMBL:BT000676 EMBL:AY088662 IPI:IPI00537494 PIR:PQ0650 RefSeq:NP_568921.1 UniGene:At.25414 UniGene:At.73165 ProteinModelPortal:Q8H166 SMR:Q8H166 IntAct:Q8H166 STRING:Q8H166 MEROPS:C01.A08 PRIDE:Q8H166 EnsemblPlants:AT5G60360.1 GeneID:836158 KEGG:ath:AT5G60360 GeneFarm:5031 TAIR:At5g60360 InParanoid:Q8H166 OMA:CGSTPMD PhylomeDB:Q8H166 Genevestigator:Q8H166 Uniprot:Q8H166
Root	Isotig04908	5	24	-2.392	0.000103464	TAIR|locus:2035619 - symbol:AT1G32780 species:3702 "Arabidopsis thaliana" [GO:0008270 "zinc ion binding" evidence=IEA] [GO:0016491 "oxidoreductase activity" evidence=IEA] [GO:0055114 "oxidation-reduction process"

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						evidence=IEA] InterPro:IPR002085 InterPro:IPR002328 InterPro:IPR013149 InterPro:IPR013154 InterPro:IPR016040 Pfam:PF00107 Pfam:PF08240 PROSITE:PS00059 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005737 GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 GO:GO:0008270 HOGENOM:HBG753318 InterPro:IPR011032 PANTHER:PTHR11695 SUPFAM:SSF50129 eggNOG:COG1062 GO:GO:0004022 KO:K00001 EMBL:AC017118 EMBL:BT029769 EMBL:AY087044 IPI:IPI00541581 RefSeq:NP_564409.1 UniGene:At.40067 ProteinModelPortal:A1L4Y2 SMR:A1L4Y2 STRING:A1L4Y2 PRIDE:A1L4Y2 EnsemblPlants:AT1G32780.1 GeneID:840172 KEGG:ath:AT1G32780 TAIR:At1g32780 InParanoid:A1L4Y2 OMA:TCKAAVV PhylomeDB:A1L4Y2 ProtClustDB:PLN02740 Genevestigator:A1L4Y2 Uniprot:A1L4Y2
Root	Isotig04909	5	26	-2.507	3.30E-05	TAIR|locus:2035619 - symbol:AT1G32780 species:3702 "Arabidopsis thaliana" [GO:0008270 "zinc ion binding" evidence=IEA] [GO:0016491 "oxidoreductase activity" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] InterPro:IPR002085 InterPro:IPR002328 InterPro:IPR013149 InterPro:IPR013154 InterPro:IPR016040 Pfam:PF00107 Pfam:PF08240 PROSITE:PS00059 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005737 GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 GO:GO:0008270 HOGENOM:HBG753318 InterPro:IPR011032 PANTHER:PTHR11695 SUPFAM:SSF50129 eggNOG:COG1062 GO:GO:0004022 KO:K00001 EMBL:AC017118 EMBL:BT029769 EMBL:AY087044 IPI:IPI00541581 RefSeq:NP_564409.1 UniGene:At.40067 ProteinModelPortal:A1L4Y2 SMR:A1L4Y2 STRING:A1L4Y2 PRIDE:A1L4Y2 EnsemblPlants:AT1G32780.1 GeneID:840172 KEGG:ath:AT1G32780 TAIR:At1g32780 InParanoid:A1L4Y2 OMA:TCKAAVV PhylomeDB:A1L4Y2 ProtClustDB:PLN02740 Genevestigator:A1L4Y2 Uniprot:A1L4Y2
Root	Isotig04910	5	26	-2.507	3.30E-05	TAIR|locus:2035619 - symbol:AT1G32780 species:3702 "Arabidopsis thaliana" [GO:0008270 "zinc ion binding" evidence=IEA] [GO:0016491 "oxidoreductase activity" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] InterPro:IPR002085 InterPro:IPR002328 InterPro:IPR013149 InterPro:IPR013154 InterPro:IPR016040 Pfam:PF00107 Pfam:PF08240 PROSITE:PS00059 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005737 GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 GO:GO:0008270 HOGENOM:HBG753318 InterPro:IPR011032 PANTHER:PTHR11695 SUPFAM:SSF50129 eggNOG:COG1062 GO:GO:0004022 KO:K00001 EMBL:AC017118 EMBL:BT029769 EMBL:AY087044 IPI:IPI00541581 RefSeq:NP_564409.1 UniGene:At.40067 ProteinModelPortal:A1L4Y2 SMR:A1L4Y2 STRING:A1L4Y2 PRIDE:A1L4Y2 EnsemblPlants:AT1G32780.1 GeneID:840172 KEGG:ath:AT1G32780 TAIR:At1g32780 InParanoid:A1L4Y2 OMA:TCKAAVV PhylomeDB:A1L4Y2 ProtClustDB:PLN02740 Genevestigator:A1L4Y2 Uniprot:A1L4Y2
Root	Isotig04915	9	27	-1.714	0.000905257	TAIR|locus:505006345 - symbol:AT3G14205 "AT3G14205" species:3702 "Arabidopsis thaliana" [GO:0004439 "phosphatidylinositol-4,5-bisphosphate 5-phosphatase activity" evidence=ISS] [GO:0008150 "biological_process" evidence=ND] InterPro:IPR002013 Pfam:PF02383 PROSITE:PS50275 EMBL:CP002686 GO:GO:0042578 OMA:IESEICV EMBL:AY050432 EMBL:AY093999 EMBL:AY227245 IPI:IPI00525545 RefSeq:NP_566481.1 UniGene:At.26576 ProteinModelPortal:Q94A27 SMR:Q94A27 PRIDE:Q94A27 EnsemblPlants:AT3G14205.1 GeneID:820638 KEGG:ath:AT3G14205 TAIR:At3g14205 InParanoid:Q94A27 PhylomeDB:Q94A27 ProtClustDB:CLSN2914997 Genevestigator:Q94A27 Uniprot:Q94A27
Root	Isotig04920	29	3	3.144	2.49E-06	TAIR|locus:2121363 - symbol:AAC3 "AT4G28390" species:3702 "Arabidopsis thaliana" [GO:0005471 "ATP:ADP antiporter activity" evidence=ISS;IDA] [GO:0005743 "mitochondrial inner membrane" evidence=ISS] [GO:0006810 "transport" evidence=ISS] [GO:0006839 "mitochondrial transport" evidence=ISS] [GO:0015865 "purine nucleotide transport" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] InterPro:IPR002067 InterPro:IPR002113 PRINTS:PR00926 PRINTS:PR00927 Pfam:PF00153 GO:GO:0016021 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005488 GO:GO:0005743 GO:GO:0009941 eggNOG:NOG238123 HOGENOM:HBG610399 KO:K05863 ProtClustDB:CLSN2684949 GO:GO:0005471 GO:GO:0015865 InterPro:IPR018108 InterPro:IPR023395 Gene3D:G3DSA:1.50.40.10 SUPFAM:SSF103506 PROSITE:PS50920 OMA:QREFNGL EMBL:AL021749 EMBL:AL161572 EMBL:AK118017 EMBL:AY088151 IPI:IPI00517177 PIR:T04608 RefSeq:NP_194568.1 UniGene:At.44823 UniGene:At.69694 HSSP:P02722 ProteinModelPortal:O49447 SMR:O49447 STRING:O49447 PRIDE:O49447 GeneID:828955 KEGG:ath:AT4G28390 GeneFarm:3748 TAIR:At4g28390 InParanoid:O49447 PhylomeDB:O49447 ArrayExpress:O49447 Genevestigator:O49447 Uniprot:O49447

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig04921	26	3	2.987	1.35E-05	TAIR|locus:2121363 - symbol:AAC3 "AT4G28390" species:3702 "Arabidopsis thaliana" [GO:0005471 "ATP:ADP antiporter activity" evidence=ISS;IDA] [GO:0005743 "mitochondrial inner membrane" evidence=ISS] [GO:0006810 "transport" evidence=ISS] [GO:0006839 "mitochondrial transport" evidence=ISS] [GO:0015865 "purine nucleotide transport" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] InterPro:IPR002067 InterPro:IPR002113 PRINTS:PR00926 PRINTS:PR00927 Pfam:PF00153 GO:GO:0016021 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005488 GO:GO:0005743 GO:GO:0009941 eggNOG:NOG238123 HOGENOM:HBG610399 KO:K05863 ProtClustDB:CLSN2684949 GO:GO:0005471 GO:GO:0015865 InterPro:IPR018108 InterPro:IPR023395 Gene3D:G3DSA:1.50.40.10 SUPFAM:SSF103506 PROSITE:PS50920 OMA:QREFNGL EMBL:AL021749 EMBL:AL161572 EMBL:AK118017 EMBL:AY088151 IPI:IPI00517177 PIR:T04608 RefSeq:NP_194568.1 UniGene:At.44823 UniGene:At.69694 HSSP:P02722 ProteinModelPortal:O49447 SMR:O49447 STRING:O49447 PRIDE:O49447 GeneID:828955 KEGG:ath:AT4G28390 GeneFarm:3748 TAIR:At4g28390 InParanoid:O49447 PhylomeDB:O49447 ArrayExpress:O49447 Genevestigator:O49447 Uniprot:O49447
Root	Isotig04922	27	3	3.041	7.69E-06	TAIR|locus:2121363 - symbol:AAC3 "AT4G28390" species:3702 "Arabidopsis thaliana" [GO:0005471 "ATP:ADP antiporter activity" evidence=ISS;IDA] [GO:0005743 "mitochondrial inner membrane" evidence=ISS] [GO:0006810 "transport" evidence=ISS] [GO:0006839 "mitochondrial transport" evidence=ISS] [GO:0015865 "purine nucleotide transport" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] InterPro:IPR002067 InterPro:IPR002113 PRINTS:PR00926 PRINTS:PR00927 Pfam:PF00153 GO:GO:0016021 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005488 GO:GO:0005743 GO:GO:0009941 eggNOG:NOG238123 HOGENOM:HBG610399 KO:K05863 ProtClustDB:CLSN2684949 GO:GO:0005471 GO:GO:0015865 InterPro:IPR018108 InterPro:IPR023395 Gene3D:G3DSA:1.50.40.10 SUPFAM:SSF103506 PROSITE:PS50920 OMA:QREFNGL EMBL:AL021749 EMBL:AL161572 EMBL:AK118017 EMBL:AY088151 IPI:IPI00517177 PIR:T04608 RefSeq:NP_194568.1 UniGene:At.44823 UniGene:At.69694 HSSP:P02722 ProteinModelPortal:O49447 SMR:O49447 STRING:O49447 PRIDE:O49447 GeneID:828955 KEGG:ath:AT4G28390 GeneFarm:3748 TAIR:At4g28390 InParanoid:O49447 PhylomeDB:O49447 ArrayExpress:O49447 Genevestigator:O49447 Uniprot:O49447
Root	Isotig04923	37	2	4.080	4.39E-09	TAIR|locus:2027317 - symbol:AT1G11820 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=IEA;ISS] [GO:0005975 "carbohydrate metabolic process" evidence=IEA] [GO:0043169 "cation binding" evidence=IEA] InterPro:IPR000490 InterPro:IPR013781 Pfam:PF00332 PROSITE:PS00587 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005886 GO:GO:0006952 GO:GO:0043169 InterPro:IPR017853 Gene3D:G3DSA:3.20.20.80 SUPFAM:SSF51445 GO:GO:0005975 GO:GO:0031225 EMBL:AC002131 EMBL:AC007296 CAZy:GH17 GO:GO:0042973 HOGENOM:HBG605194 CAZy:CBM43 InterPro:IPR012946 Pfam:PF07983 SMART:SM00768 EMBL:BT004271 IPI:IPI00548319 PIR:E86252 RefSeq:NP_001184967.1 UniGene:At.10643 ProteinModelPortal:O65399 SMR:O65399 PRIDE:O65399 GeneID:837730 KEGG:ath:AT1G11820 TAIR:At1g11820 eggNOG:NOG329755 InParanoid:O65399 PhylomeDB:O65399 Genevestigator:O65399 Uniprot:O65399
Root	Isotig04924	41	2	4.229	4.38E-10	TAIR|locus:2092855 - symbol:AT3G13560 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=IEA;ISS] [GO:0005975 "carbohydrate metabolic process" evidence=IEA] [GO:0043169 "cation binding" evidence=IEA] [GO:0031225 "anchored to membrane" evidence=TAS] [GO:0046658 "anchored to plasma membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] InterPro:IPR000490 InterPro:IPR013781 Pfam:PF00332 PROSITE:PS00587 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0006952 GO:GO:0043169 InterPro:IPR017853 Gene3D:G3DSA:3.20.20.80 SUPFAM:SSF51445 GO:GO:0005975 EMBL:AP000603 GO:GO:0046658 CAZy:GH17 GO:GO:0042973 HOGENOM:HBG605194 CAZy:CBM43 InterPro:IPR012946 Pfam:PF07983 SMART:SM00768 EMBL:AY034940 EMBL:AY063117 IPI:IPI00537250 RefSeq:NP_187965.1 RefSeq:NP_974302.1 RefSeq:NP_974303.1 UniGene:At.8269 ProteinModelPortal:Q94CD8 SMR:Q94CD8 STRING:Q94CD8 PRIDE:Q94CD8 EnsemblPlants:AT3G13560.1 EnsemblPlants:AT3G13560.2 EnsemblPlants:AT3G13560.3 GeneID:820558 KEGG:ath:AT3G13560 TAIR:At3g13560 eggNOG:NOG310730

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						InParanoid:Q94CD8 OMA:IQPGQPC PhylomeDB:Q94CD8 ProtClustDB:CLSN2684782 ArrayExpress:Q94CD8 Genevestigator:Q94CD8 GermOnline:AT3G13560 Uniprot:Q94CD8
Root	Isotig04926	2	16	-3.129	0.000262867	TAIR|locus:2166086 - symbol:sks3 "SKU5 similar 3" species:3702 "Arabidopsis thaliana" [GO:0005507 "copper ion binding" evidence=IEA;ISS] [GO:0016491 "oxidoreductase activity" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR001117 InterPro:IPR011706 InterPro:IPR011707 Pfam:PF00394 Pfam:PF07731 Pfam:PF07732 GO:GO:0005886 GO:GO:0009506 GenomeReviews:BA000015_GR GO:GO:0016491 GO:GO:0005507 InterPro:IPR008972 Gene3D:G3DSA:2.60.40.420 SUPFAM:SSF49503 EMBL:AB020745 eggNOG:COG2132 HOGENOM:HBG316961 IPI:IPI00536545 ProteinModelPortal:Q9LV68 SMR:Q9LV68 PRIDE:Q9LV68 TAIR:At5g48450 InParanoid:Q9LV68 PhylomeDB:Q9LV68 Genevestigator:Q9LV68 Uniprot:Q9LV68
Root	Isotig04932	81	0	7.211	4.65E-19	TAIR|locus:2040646 - symbol:ChlAKR "AT2G37770" species:3702 "Arabidopsis thaliana" [GO:0004033 "aldo-keto reductase (NADP) activity" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0009414 "response to water deprivation" evidence=IEP] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0016229 "steroid dehydrogenase activity" evidence=IDA] [GO:0070401 "NADP+ binding" evidence=IDA] [GO:0008106 "alcohol dehydrogenase (NADP+) activity" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0055114 "oxidation-reduction process" evidence=IDA] InterPro:IPR018170 InterPro:IPR020471 PIRSF:PIRSF000097 PRINTS:PR00069 PROSITE:PS00062 PROSITE:PS00063 PROSITE:PS00798 InterPro:IPR001395 EMBL:AC004684 Pfam:PF00248 GO:GO:0009507 EMBL:CP002685 GenomeReviews:CT485783_GR eggNOG:COG0656 GO:GO:0008106 InterPro:IPR023210 Gene3D:G3DSA:3.20.20.100 PANTHER:PTHR11732 SUPFAM:SSF51430 HOGENOM:HBG605727 GO:GO:0009409 GO:GO:0009651 GO:GO:0009414 GO:GO:0009636 GO:GO:0070401 GO:GO:0016229 EMBL:DQ837654 EMBL:BX820913 EMBL:BT004098 IPI:IPI00541607 IPI:IPI00657326 PIR:T02543 RefSeq:NP_001031505.1 RefSeq:NP_181313.3 UniGene:At.12803 PDB:3H7U PDBsum:3H7U ProteinModelPortal:Q0PGJ6 SMR:Q0PGJ6 STRING:Q0PGJ6 PRIDE:Q0PGJ6 EnsemblPlants:AT2G37770.2 GeneID:818354 KEGG:ath:AT2G37770 TAIR:At2g37770 InParanoid:Q2V420 OMA:VDIPSTW PhylomeDB:Q0PGJ6 ProtClustDB:CLSN2681439 BioCyc:MetaCyc:AT2G37770-MONOMER Genevestigator:Q0PGJ6 Uniprot:Q0PGJ6
Root	Isotig04933	78	0	7.156	1.79E-18	TAIR|locus:2040646 - symbol:ChlAKR "AT2G37770" species:3702 "Arabidopsis thaliana" [GO:0004033 "aldo-keto reductase (NADP) activity" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0009414 "response to water deprivation" evidence=IEP] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0016229 "steroid dehydrogenase activity" evidence=IDA] [GO:0070401 "NADP+ binding" evidence=IDA] [GO:0008106 "alcohol dehydrogenase (NADP+) activity" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0055114 "oxidation-reduction process" evidence=IDA] InterPro:IPR018170 InterPro:IPR020471 PIRSF:PIRSF000097 PRINTS:PR00069 PROSITE:PS00062 PROSITE:PS00063 PROSITE:PS00798 InterPro:IPR001395 EMBL:AC004684 Pfam:PF00248 GO:GO:0009507 EMBL:CP002685 GenomeReviews:CT485783_GR eggNOG:COG0656 GO:GO:0008106 InterPro:IPR023210 Gene3D:G3DSA:3.20.20.100 PANTHER:PTHR11732 SUPFAM:SSF51430 HOGENOM:HBG605727 GO:GO:0009409 GO:GO:0009651 GO:GO:0009414 GO:GO:0009636 GO:GO:0070401 GO:GO:0016229 EMBL:DQ837654 EMBL:BX820913 EMBL:BT004098 IPI:IPI00541607 IPI:IPI00657326 PIR:T02543 RefSeq:NP_001031505.1 RefSeq:NP_181313.3 UniGene:At.12803 PDB:3H7U PDBsum:3H7U ProteinModelPortal:Q0PGJ6 SMR:Q0PGJ6 STRING:Q0PGJ6 PRIDE:Q0PGJ6 EnsemblPlants:AT2G37770.2 GeneID:818354 KEGG:ath:AT2G37770 TAIR:At2g37770 InParanoid:Q2V420 OMA:VDIPSTW PhylomeDB:Q0PGJ6 ProtClustDB:CLSN2681439 BioCyc:MetaCyc:AT2G37770-MONOMER Genevestigator:Q0PGJ6 Uniprot:Q0PGJ6
Root	Isotig04934	81	0	7.211	4.65E-19	TAIR|locus:2040646 - symbol:ChlAKR "AT2G37770" species:3702 "Arabidopsis thaliana" [GO:0004033 "aldo-keto reductase (NADP) activity" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0009414 "response to water deprivation" evidence=IEP] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0016229 "steroid dehydrogenase activity" evidence=IDA] [GO:0070401 "NADP+ binding" evidence=IDA] [GO:0008106 "alcohol dehydrogenase (NADP+) activity" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0055114 "oxidation-reduction process" evidence=IDA] InterPro:IPR018170 InterPro:IPR020471 PIRSF:PIRSF000097 PRINTS:PR00069 PROSITE:PS00062 PROSITE:PS00063 PROSITE:PS00798 InterPro:IPR001395 EMBL:AC004684 Pfam:PF00248 GO:GO:0009507 EMBL:CP002685 GenomeReviews:CT485783_GR eggNOG:COG0656 GO:GO:0008106 InterPro:IPR023210 Gene3D:G3DSA:3.20.20.100 PANTHER:PTHR11732

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						SUPFAM:SSF51430 HOGENOM:HBG605727 GO:GO:0009409 GO:GO:0009651 GO:GO:0009414 GO:GO:0009636 GO:GO:0070401 GO:GO:0016229 EMBL:DQ837654 EMBL:BX820913 EMBL:BT004098 IPI:IPI00541607 IPI:IPI00657326 PIR:T02543 RefSeq:NP_001031505.1 RefSeq:NP_181313.3 UniGene:At.12803 PDB:3H7U PDBsum:3H7U ProteinModelPortal:Q0PGJ6 SMR:Q0PGJ6 STRING:Q0PGJ6 PRIDE:Q0PGJ6 EnsemblPlants:AT2G37770.2 GeneID:818354 KEGG:ath:AT2G37770 TAIR:At2g37770 InParanoid:Q2V420 OMA:VDIPSTW PhylomeDB:Q0PGJ6 ProtClustDB:CLSN2681439 BioCyc:MetaCyc:AT2G37770-MONOMER Genevestigator:Q0PGJ6 Uniprot:Q0PGJ6
Root	Isotig04953	5	21	-2.199	0.000555521	TAIR|locus:2025687 - symbol:WRKY40 "AT1G80840" species:3702 "Arabidopsis thaliana" [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS;IDA] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=ISS] [GO:0031347 "regulation of defense response" evidence=IMP] [GO:0009751 "response to salicylic acid stimulus" evidence=IEP] [GO:0042742 "defense response to bacterium" evidence=IEP] [GO:0005634 "nucleus" evidence=IDA] [GO:0050832 "defense response to fungus" evidence=IEP] [GO:0050691 "regulation of defense response to virus by host" evidence=IGI] [GO:0010200 "response to chitin" evidence=IEP] [GO:0009611 "response to wounding" evidence=IEP] [GO:0005515 "protein binding" evidence=IPI] [GO:0002237 "response to molecule of bacterial origin" evidence=IMP] InterPro:IPR003657 Pfam:PF03106 PROSITE:PS50811 SMART:SM00774 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005634 GO:GO:0042742 GO:GO:0005515 GO:GO:0009611 GO:GO:0050832 GO:GO:0043565 GO:GO:0003700 GO:GO:0006351 GO:GO:0009751 GO:GO:0010200 EMBL:AC011713 GO:GO:0050691 Gene3D:G3DSA:2.20.25.80 SUPFAM:SSF118290 HOGENOM:HBG748409 EMBL:AF480149 EMBL:BT001914 IPI:IPI00522578 PIR:A96841 RefSeq:NP_178199.1 UniGene:At.28188 ProteinModelPortal:Q9SAH7 SMR:Q9SAH7 IntAct:Q9SAH7 STRING:Q9SAH7 PRIDE:Q9SAH7 EnsemblPlants:AT1G80840.1 GeneID:844423 KEGG:ath:AT1G80840 TAIR:At1g80840 eggNOG:NOG310042 InParanoid:Q9SAH7 OMA:SNITERD PhylomeDB:Q9SAH7 ProtClustDB:CLSN2914521 ArrayExpress:Q9SAH7 Genevestigator:Q9SAH7 GermOnline:AT1G80840 Uniprot:Q9SAH7
Root	Isotig04954	5	21	-2.199	0.000555521	TAIR|locus:2025687 - symbol:WRKY40 "AT1G80840" species:3702 "Arabidopsis thaliana" [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS;IDA] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=ISS] [GO:0031347 "regulation of defense response" evidence=IMP] [GO:0009751 "response to salicylic acid stimulus" evidence=IEP] [GO:0042742 "defense response to bacterium" evidence=IEP] [GO:0005634 "nucleus" evidence=IDA] [GO:0050832 "defense response to fungus" evidence=IEP] [GO:0050691 "regulation of defense response to virus by host" evidence=IGI] [GO:0010200 "response to chitin" evidence=IEP] [GO:0009611 "response to wounding" evidence=IEP] [GO:0005515 "protein binding" evidence=IPI] [GO:0002237 "response to molecule of bacterial origin" evidence=IMP] InterPro:IPR003657 Pfam:PF03106 PROSITE:PS50811 SMART:SM00774 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005634 GO:GO:0042742 GO:GO:0005515 GO:GO:0009611 GO:GO:0050832 GO:GO:0043565 GO:GO:0003700 GO:GO:0006351 GO:GO:0009751 GO:GO:0010200 EMBL:AC011713 GO:GO:0050691 Gene3D:G3DSA:2.20.25.80 SUPFAM:SSF118290 HOGENOM:HBG748409 EMBL:AF480149 EMBL:BT001914 IPI:IPI00522578 PIR:A96841 RefSeq:NP_178199.1 UniGene:At.28188 ProteinModelPortal:Q9SAH7 SMR:Q9SAH7 IntAct:Q9SAH7 STRING:Q9SAH7 PRIDE:Q9SAH7 EnsemblPlants:AT1G80840.1 GeneID:844423 KEGG:ath:AT1G80840 TAIR:At1g80840 eggNOG:NOG310042 InParanoid:Q9SAH7 OMA:SNITERD PhylomeDB:Q9SAH7 ProtClustDB:CLSN2914521 ArrayExpress:Q9SAH7 Genevestigator:Q9SAH7 GermOnline:AT1G80840 Uniprot:Q9SAH7
Root	Isotig04969	26	2	3.571	2.56E-06	TAIR|locus:2056700 - symbol:ARPN "plantacyanin" species:3702 "Arabidopsis thaliana" [GO:0005507 "copper ion binding" evidence=IEA;ISS] [GO:0009055 "electron carrier activity" evidence=IEA] [GO:0009856 "pollination" evidence=IMP] [GO:0048196 "plant extracellular matrix" evidence=TAS] [GO:0048653 "anther development" evidence=IMP] [GO:0048046 "apoplast" evidence=IDA] InterPro:IPR003245 Pfam:PF02298 ProDom:PD003122 PROSITE:PS00196 PROSITE:PS51485 EMBL:AC004138 GO:GO:0048046 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009055 GO:GO:0006810 GO:GO:0005507 GO:GO:0022900 GO:GO:0048653 EMBL:AC002521 InterPro:IPR008972 Gene3D:G3DSA:2.60.40.420 SUPFAM:SSF49503 EMBL:U76297 EMBL:AF325063 EMBL:AY064141 EMBL:AY097407 EMBL:AY084407 IPI:IPI00540939 PIR:F84441 PIR:T00843 RefSeq:NP_178388.1 UniGene:At.23668 ProteinModelPortal:Q8LG89 SMR:Q8LG89 PRIDE:Q8LG89 ProMEX:Q8LG89 EnsemblPlants:AT2G02850.1 GeneID:814816 KEGG:ath:AT2G02850 TAIR:At2g02850 eggNOG:NOG271220 HOGENOM:HBG748847 InParanoid:Q8LG89 OMA:SWSARAI PhylomeDB:Q8LG89

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						ProtClustDB:CLSN2913208 ArrayExpress:Q8LG89 Genevestigator:Q8LG89 GermOnline:AT2G02850 GO:GO:0048196 GO:GO:0009856 Uniprot:Q8LG89
Root	Isotig04970	20	2	3.193	8.23E-05	TAIR|locus:2056700 - symbol:ARPN "plantacyanin" species:3702 "Arabidopsis thaliana" [GO:0005507 "copper ion binding" evidence=IEA;ISS] [GO:0009055 "electron carrier activity" evidence=IEA] [GO:0009856 "pollination" evidence=IMP] [GO:0048196 "plant extracellular matrix" evidence=TAS] [GO:0048653 "anther development" evidence=IMP] [GO:0048046 "apoplast" evidence=IDA] InterPro:IPR003245 Pfam:PF02298 ProDom:PD003122 PROSITE:PS00196 PROSITE:PS51485 EMBL:AC004138 GO:GO:0048046 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009055 GO:GO:0006810 GO:GO:0005507 GO:GO:0022900 GO:GO:0048653 EMBL:AC002521 InterPro:IPR008972 Gene3D:G3DSA:2.60.40.420 SUPFAM:SSF49503 EMBL:U76297 EMBL:AF325063 EMBL:AY064141 EMBL:AY097407 EMBL:AY084407 IPI:IPI00540939 PIR:F84441 PIR:T00843 RefSeq:NP_178388.1 UniGene:At.23668 ProteinModelPortal:Q8LG89 SMR:Q8LG89 PRIDE:Q8LG89 ProMEX:Q8LG89 EnsemblPlants:AT2G02850.1 GeneID:814816 KEGG:ath:AT2G02850 TAIR:At2g02850 eggNOG:NOG271220 HOGENOM:HBG748847 InParanoid:Q8LG89 OMA:SWSARAI PhylomeDB:Q8LG89 ProtClustDB:CLSN2913208 ArrayExpress:Q8LG89 Genevestigator:Q8LG89 GermOnline:AT2G02850 GO:GO:0048196 GO:GO:0009856 Uniprot:Q8LG89
Root	Isotig04980	317	0	9.179	2.01E-57	TIGR_CMR|BA_1222 - symbol:BA_1222 "conserved hypothetical protein" species:198094 "Bacillus anthracis str. Ames" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:AE016879 EMBL:AE017334 GenomeReviews:AE016879_GR GenomeReviews:AE017334_GR InterPro:IPR008160 Pfam:PF01391 EMBL:AB281483 EMBL:AJ516936 RefSeq:NP_843695.1 RefSeq:YP_017836.1 PDB:2R6Q PDBsum:2R6Q ProteinModelPortal:Q81JD7 SMR:Q81JD7 IntAct:Q81JD7 EnsemblBacteria:EBBACT00000011819 EnsemblBacteria:EBBACT00000016984 GeneID:1084744 GeneID:2814858 KEGG:ban:BA_1222 KEGG:bar:GBAA_1222 PATRIC:18780046 TIGR:BA_1222 TIGR:GBAA1222 HOGENOM:HBG342646 OMA:SDGLNPD ProtClustDB:CLSK824721 Uniprot:Q81JD7
Root	Isotig04981	318	1	8.184	2.01E-64	TIGR_CMR|BA_1222 - symbol:BA_1222 "conserved hypothetical protein" species:198094 "Bacillus anthracis str. Ames" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:AE016879 EMBL:AE017334 GenomeReviews:AE016879_GR GenomeReviews:AE017334_GR InterPro:IPR008160 Pfam:PF01391 EMBL:AB281483 EMBL:AJ516936 RefSeq:NP_843695.1 RefSeq:YP_017836.1 PDB:2R6Q PDBsum:2R6Q ProteinModelPortal:Q81JD7 SMR:Q81JD7 IntAct:Q81JD7 EnsemblBacteria:EBBACT00000011819 EnsemblBacteria:EBBACT00000016984 GeneID:1084744 GeneID:2814858 KEGG:ban:BA_1222 KEGG:bar:GBAA_1222 PATRIC:18780046 TIGR:BA_1222 TIGR:GBAA1222 HOGENOM:HBG342646 OMA:SDGLNPD ProtClustDB:CLSK824721 Uniprot:Q81JD7
Root	Isotig04982	317	1	8.179	2.96E-64	TIGR_CMR|BA_1222 - symbol:BA_1222 "conserved hypothetical protein" species:198094 "Bacillus anthracis str. Ames" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:AE016879 EMBL:AE017334 GenomeReviews:AE016879_GR GenomeReviews:AE017334_GR InterPro:IPR008160 Pfam:PF01391 EMBL:AB281483 EMBL:AJ516936 RefSeq:NP_843695.1 RefSeq:YP_017836.1 PDB:2R6Q PDBsum:2R6Q ProteinModelPortal:Q81JD7 SMR:Q81JD7 IntAct:Q81JD7 EnsemblBacteria:EBBACT00000011819 EnsemblBacteria:EBBACT00000016984 GeneID:1084744 GeneID:2814858 KEGG:ban:BA_1222 KEGG:bar:GBAA_1222 PATRIC:18780046 TIGR:BA_1222 TIGR:GBAA1222 HOGENOM:HBG342646 OMA:SDGLNPD ProtClustDB:CLSK824721 Uniprot:Q81JD7
Root	Isotig04986	0	12	-4.714	0.000297064	TAIR|locus:2200111 - symbol:AT1G11340 species:3702 "Arabidopsis thaliana" [GO:0004672 "protein kinase activity" evidence=IEA] [GO:0004674 "protein serine/threonine kinase activity" evidence=IEA] [GO:0005524 "ATP binding" evidence=IEA] [GO:0006468 "protein phosphorylation" evidence=IEA] [GO:0016301 "kinase activity" evidence=ISS] [GO:0030246 "carbohydrate binding" evidence=ISS] [GO:0048544 "recognition of pollen" evidence=IEA] InterPro:IPR000719 InterPro:IPR000742 InterPro:IPR000858 InterPro:IPR001245 InterPro:IPR006210 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR024171 Pfam:PF00954 Pfam:PF07714 PIRSF:PIRSF000641 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 PROSITE:PS50026 SMART:SM00181 InterPro:IPR001480 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005524 eggNOG:COG0515 GO:GO:0004872 GO:GO:0005529 SUPFAM:SSF56112 GO:GO:0004674 HOGENOM:HBG755340 GO:GO:0005516 PROSITE:PS00022 PROSITE:PS01186 GO:GO:0044459

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0048544 InterPro:IPR013227 InterPro:IPR003609 Gene3D:G3DSA:2.90.10.10 Pfam:PF01453 Pfam:PF08276 SMART:SM00108 SMART:SM00473 SUPFAM:SSF51110 PROSITE:PS50927 PROSITE:PS50948 EMBL:AC011661 EMBL:AC007259 HSSP:P00523 EMBL:AF084035 IPI:IPI00520959 PIR:E86247 ProteinModelPortal:Q9ZT07 SMR:Q9ZT07 PRIDE:Q9ZT07 GeneFarm:2670 TAIR:At1g11340 InParanoid:Q9LQ00 PhylomeDB:Q9ZT07 Genevestigator:Q9ZT07 Uniprot:Q9ZT07
Root	Isotig04987	0	11	-4.588	0.000569522	TAIR|locus:2200111 - symbol:AT1G11340 species:3702 "Arabidopsis thaliana" [GO:0004672 "protein kinase activity" evidence=IEA] [GO:0004674 "protein serine/threonine kinase activity" evidence=IEA] [GO:0005524 "ATP binding" evidence=IEA] [GO:0006468 "protein phosphorylation" evidence=IEA] [GO:0016301 "kinase activity" evidence=ISS] [GO:0030246 "carbohydrate binding" evidence=ISS] [GO:0048544 "recognition of pollen" evidence=IEA] InterPro:IPR000719 InterPro:IPR000742 InterPro:IPR000858 InterPro:IPR001245 InterPro:IPR006210 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR024171 Pfam:PF00954 Pfam:PF07714 PIRSF:PIRSF000641 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 PROSITE:PS50026 SMART:SM00181 InterPro:IPR001480 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005524 eggNOG:COG0515 GO:GO:0004872 GO:GO:0005529 SUPFAM:SSF56112 GO:GO:0004674 HOGENOM:HBG755340 GO:GO:0005516 PROSITE:PS00022 PROSITE:PS01186 GO:GO:0044459 GO:GO:0048544 InterPro:IPR013227 InterPro:IPR003609 Gene3D:G3DSA:2.90.10.10 Pfam:PF01453 Pfam:PF08276 SMART:SM00108 SMART:SM00473 SUPFAM:SSF51110 PROSITE:PS50927 PROSITE:PS50948 EMBL:AC011661 EMBL:AC007259 HSSP:P00523 EMBL:AF084035 IPI:IPI00520959 PIR:E86247 ProteinModelPortal:Q9ZT07 SMR:Q9ZT07 PRIDE:Q9ZT07 GeneFarm:2670 TAIR:At1g11340 InParanoid:Q9LQ00 PhylomeDB:Q9ZT07 Genevestigator:Q9ZT07 Uniprot:Q9ZT07
Root	Isotig04995	17	2	2.958	0.000459627	TAIR|locus:2206825 - symbol:AT1G73480 "AT1G73480" species:3702 "Arabidopsis thaliana" [GO:0016787 "hydrolase activity" evidence=ISS] EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0016787 HOGENOM:HBG748003 InterPro:IPR022742 Pfam:PF12146 EMBL:AY045929 EMBL:BT001959 IPI:IPI00526340 RefSeq:NP_565066.1 UniGene:At.23620 ProteinModelPortal:Q94AM5 SMR:Q94AM5 MEROPS:S33.A12 PRIDE:Q94AM5 EnsemblPlants:AT1G73480.1 GeneID:843683 KEGG:ath:AT1G73480 TAIR:At1g73480 InParanoid:Q94AM5 OMA:VQPSHPI PhylomeDB:Q94AM5 ProtClustDB:CLSN2917439 ArrayExpress:Q94AM5 Genevestigator:Q94AM5 Uniprot:Q94AM5
Root	Isotig04996	18	2	3.041	0.000259481	TAIR|locus:2206825 - symbol:AT1G73480 "AT1G73480" species:3702 "Arabidopsis thaliana" [GO:0016787 "hydrolase activity" evidence=ISS] EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0016787 HOGENOM:HBG748003 InterPro:IPR022742 Pfam:PF12146 EMBL:AY045929 EMBL:BT001959 IPI:IPI00526340 RefSeq:NP_565066.1 UniGene:At.23620 ProteinModelPortal:Q94AM5 SMR:Q94AM5 MEROPS:S33.A12 PRIDE:Q94AM5 EnsemblPlants:AT1G73480.1 GeneID:843683 KEGG:ath:AT1G73480 TAIR:At1g73480 InParanoid:Q94AM5 OMA:VQPSHPI PhylomeDB:Q94AM5 ProtClustDB:CLSN2917439 ArrayExpress:Q94AM5 Genevestigator:Q94AM5 Uniprot:Q94AM5
Root	Isotig04997	17	2	2.958	0.000459627	TAIR|locus:2206825 - symbol:AT1G73480 "AT1G73480" species:3702 "Arabidopsis thaliana" [GO:0016787 "hydrolase activity" evidence=ISS] EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0016787 HOGENOM:HBG748003 InterPro:IPR022742 Pfam:PF12146 EMBL:AY045929 EMBL:BT001959 IPI:IPI00526340 RefSeq:NP_565066.1 UniGene:At.23620 ProteinModelPortal:Q94AM5 SMR:Q94AM5 MEROPS:S33.A12 PRIDE:Q94AM5 EnsemblPlants:AT1G73480.1 GeneID:843683 KEGG:ath:AT1G73480 TAIR:At1g73480 InParanoid:Q94AM5 OMA:VQPSHPI PhylomeDB:Q94AM5 ProtClustDB:CLSN2917439 ArrayExpress:Q94AM5 Genevestigator:Q94AM5 Uniprot:Q94AM5
Root	Isotig05001	2	26	-3.829	4.59E-07	TAIR|locus:2032075 - symbol:SNRK2-8 "SNF1-RELATED PROTEIN KINASE 2-8" species:3702 "Arabidopsis thaliana" [GO:0004672 "protein kinase activity" evidence=IEA] [GO:0004674 "protein serine/threonine kinase activity" evidence=IEA] [GO:0005524 "ATP binding" evidence=IEA] [GO:0016301 "kinase activity" evidence=ISS] [GO:0080167 "response to karrikin" evidence=IEP] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0006970 "response to osmotic stress" evidence=IGI] InterPro:IPR000719 InterPro:IPR002290 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 Pfam:PF00069 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 SMART:SM00220 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005524 GO:GO:0005634 EMBL:AC013430 GO:GO:0005737 eggNOG:COG0515 SUPFAM:SSF56112 GO:GO:0004674 HOGENOM:HBG755340 GO:GO:0080167 HSSP:P06782 UniGene:At.48390 UniGene:At.70998 KO:K14498 EMBL:AF411782 EMBL:BT020608 EMBL:AY088883 IPI:IPI00530546 RefSeq:NP_001077839.1 RefSeq:NP_974170.1 ProteinModelPortal:Q9M9E9

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						SMR:Q9M9E9 DIP:DIP-48987N STRING:Q9M9E9 PRIDE:Q9M9E9 EnsemblPlants:AT1G78290.2 EnsemblPlants:AT1G78290.3 GeneID:844164 KEGG:ath:AT1G78290 TAIR:At1g78290 OMA:ERYEIIK PhylomeDB:Q9M9E9 ProtClustDB:CLSN2681301 Genevestigator:Q9M9E9 Uniprot:Q9M9E9
Root	Isotig05002	2	24	-3.714	1.64E-06	TAIR|locus:2032075 - symbol:SNRK2-8 "SNF1-RELATED PROTEIN KINASE 2-8" species:3702 "Arabidopsis thaliana" [GO:0004672 "protein kinase activity" evidence=IEA] [GO:0004674 "protein serine/threonine kinase activity" evidence=IEA] [GO:0005524 "ATP binding" evidence=IEA] [GO:0016301 "kinase activity" evidence=ISS] [GO:0080167 "response to karrikin" evidence=IEP] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0006970 "response to osmotic stress" evidence=IGI] InterPro:IPR000719 InterPro:IPR002290 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 Pfam:PF00069 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 SMART:SM00220 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005524 GO:GO:0005634 EMBL:AC013430 GO:GO:0005737 eggNOG:COG0515 SUPFAM:SSF56112 GO:GO:0004674 HOGENOM:HBG755340 GO:GO:0080167 HSSP:P06782 UniGene:At.48390 UniGene:At.70998 KO:K14498 EMBL:AF411782 EMBL:BT020608 EMBL:AY088883 IPI:IPI00530546 RefSeq:NP_001077839.1 RefSeq:NP_974170.1 ProteinModelPortal:Q9M9E9 SMR:Q9M9E9 DIP:DIP-48987N STRING:Q9M9E9 PRIDE:Q9M9E9 EnsemblPlants:AT1G78290.2 EnsemblPlants:AT1G78290.3 GeneID:844164 KEGG:ath:AT1G78290 TAIR:At1g78290 OMA:ERYEIIK PhylomeDB:Q9M9E9 ProtClustDB:CLSN2681301 Genevestigator:Q9M9E9 Uniprot:Q9M9E9
Root	Isotig05003	2	24	-3.714	1.64E-06	TAIR|locus:2032075 - symbol:SNRK2-8 "SNF1-RELATED PROTEIN KINASE 2-8" species:3702 "Arabidopsis thaliana" [GO:0004672 "protein kinase activity" evidence=IEA] [GO:0004674 "protein serine/threonine kinase activity" evidence=IEA] [GO:0005524 "ATP binding" evidence=IEA] [GO:0016301 "kinase activity" evidence=ISS] [GO:0080167 "response to karrikin" evidence=IEP] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0006970 "response to osmotic stress" evidence=IGI] InterPro:IPR000719 InterPro:IPR002290 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 Pfam:PF00069 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 SMART:SM00220 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005524 GO:GO:0005634 EMBL:AC013430 GO:GO:0005737 eggNOG:COG0515 SUPFAM:SSF56112 GO:GO:0004674 HOGENOM:HBG755340 GO:GO:0080167 HSSP:P06782 UniGene:At.48390 UniGene:At.70998 KO:K14498 EMBL:AF411782 EMBL:BT020608 EMBL:AY088883 IPI:IPI00530546 RefSeq:NP_001077839.1 RefSeq:NP_974170.1 ProteinModelPortal:Q9M9E9 SMR:Q9M9E9 DIP:DIP-48987N STRING:Q9M9E9 PRIDE:Q9M9E9 EnsemblPlants:AT1G78290.2 EnsemblPlants:AT1G78290.3 GeneID:844164 KEGG:ath:AT1G78290 TAIR:At1g78290 OMA:ERYEIIK PhylomeDB:Q9M9E9 ProtClustDB:CLSN2681301 Genevestigator:Q9M9E9 Uniprot:Q9M9E9
Root	Isotig05007	1	12	-3.714	0.000699736	TAIR|locus:2043699 - symbol:CYP76C1 ""cytochrome P450, family 76, subfamily C, polypeptide 1"" species:3702 "Arabidopsis thaliana" [GO:0004497 "monooxygenase activity" evidence=IEA] [GO:0005506 "iron ion binding" evidence=IEA] [GO:0009055 "electron carrier activity" evidence=IEA] [GO:0020037 "heme binding" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] InterPro:IPR001128 InterPro:IPR002401 InterPro:IPR017972 Pfam:PF00067 PRINTS:PR00385 PRINTS:PR00463 PROSITE:PS00086 GO:GO:0016021 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009055 GO:GO:0004497 eggNOG:COG2124 GO:GO:0020037 Gene3D:G3DSA:1.10.630.10 SUPFAM:SSF48264 EMBL:AC003680 GO:GO:0016705 HOGENOM:HBG749920 EMBL:D78600 EMBL:AY078939 EMBL:AY124874 EMBL:AY085090 IPI:IPI00519972 IPI:IPI00548813 PIR:T00869 PIR:T52168 RefSeq:NP_850439.1 RefSeq:NP_850440.1 UniGene:At.334 UniGene:At.67815 ProteinModelPortal:O64636 SMR:O64636 PRIDE:O64636 EnsemblPlants:AT2G45560.1 GeneID:819164 KEGG:ath:AT2G45560 GeneFarm:1463 TAIR:At2g45560 InParanoid:O64636 OMA:SISDIEH PhylomeDB:O64636 ProtClustDB:CLSN2679301 ArrayExpress:O64636 Genevestigator:O64636 GermOnline:AT2G45560 Uniprot:O64636
Root	Isotig05019	35	3	3.415	8.27E-08	TAIR|locus:2132644 - symbol:AT4G22740 "AT4G22740" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005886 "plasma membrane" evidence=IDA] GO:GO:0005886 EMBL:CP002687 InterPro:IPR019376 Pfam:PF10248 UniGene:At.22243 UniGene:At.32505 EMBL:AY054243 EMBL:AY080635 EMBL:AY117203 IPI:IPI00525351 RefSeq:NP_567666.1 RefSeq:NP_849421.1 PRIDE:Q940N4 ProMEX:Q940N4 EnsemblPlants:AT4G22740.1 EnsemblPlants:AT4G22740.2 GeneID:828370 KEGG:ath:AT4G22740 TAIR:At4g22740 InParanoid:Q940N4 OMA:VNAERRN PhylomeDB:Q940N4 ProtClustDB:CLSN2689561 Genevestigator:Q940N4 Uniprot:Q940N4

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig05020	42	5	2.941	4.00E-08	TAIR|locus:2132644 - symbol:AT4G22740 "AT4G22740" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005886 "plasma membrane" evidence=IDA] GO:GO:0005886 EMBL:CP002687 InterPro:IPR019376 Pfam:PF10248 UniGene:At.22243 UniGene:At.32505 EMBL:AY054243 EMBL:AY080635 EMBL:AY117203 IPI:IPI00525351 RefSeq:NP_567666.1 RefSeq:NP_849421.1 PRIDE:Q940N4 ProMEX:Q940N4 EnsemblPlants:AT4G22740.1 EnsemblPlants:AT4G22740.2 GeneID:828370 KEGG:ath:AT4G22740 TAIR:At4g22740 InParanoid:Q940N4 OMA:VNAERRN PhylomeDB:Q940N4 ProtClustDB:CLSN2689561 Genevestigator:Q940N4 Uniprot:Q940N4
Root	Isotig05022	21	0	5.263	3.38E-06	TAIR|locus:2195623 - symbol:AT1G60420 species:3702 "Arabidopsis thaliana" [GO:0016209 "antioxidant activity" evidence=IEA] [GO:0016491 "oxidoreductase activity" evidence=IEA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0009860 "pollen tube growth" evidence=IMP] [GO:0010183 "pollen tube guidance" evidence=IMP] [GO:0080092 "regulation of pollen tube growth" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR011424 InterPro:IPR017937 Pfam:PF07649 PROSITE:PS00194 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0046686 GO:GO:0009860 InterPro:IPR012336 Gene3D:G3DSA:3.40.30.10 SUPFAM:SSF52833 GO:GO:0045454 PROSITE:PS51352 GO:GO:0080092 GO:GO:0010183 eggNOG:COG0526 GO:GO:0047134 EMBL:AC004473 EMBL:AY065433 EMBL:AY117231 EMBL:AY087396 IPI:IPI00537432 PIR:T02292 RefSeq:NP_564756.1 UniGene:At.10685 UniGene:At.64112 PDB:1V5N PDBsum:1V5N ProteinModelPortal:O80763 SMR:O80763 IntAct:O80763 PRIDE:O80763 EnsemblPlants:AT1G60420.1 GeneID:842337 KEGG:ath:AT1G60420 TAIR:At1g60420 HOGENOM:HBG594354 InParanoid:O80763 OMA:QMPWLAL PhylomeDB:O80763 ProtClustDB:CLSN2917334 ArrayExpress:O80763 Genevestigator:O80763 Uniprot:O80763
Root	Isotig05023	16	0	4.871	5.89E-05	TAIR|locus:2195623 - symbol:AT1G60420 species:3702 "Arabidopsis thaliana" [GO:0016209 "antioxidant activity" evidence=IEA] [GO:0016491 "oxidoreductase activity" evidence=IEA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0009860 "pollen tube growth" evidence=IMP] [GO:0010183 "pollen tube guidance" evidence=IMP] [GO:0080092 "regulation of pollen tube growth" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR011424 InterPro:IPR017937 Pfam:PF07649 PROSITE:PS00194 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0046686 GO:GO:0009860 InterPro:IPR012336 Gene3D:G3DSA:3.40.30.10 SUPFAM:SSF52833 GO:GO:0045454 PROSITE:PS51352 GO:GO:0080092 GO:GO:0010183 eggNOG:COG0526 GO:GO:0047134 EMBL:AC004473 EMBL:AY065433 EMBL:AY117231 EMBL:AY087396 IPI:IPI00537432 PIR:T02292 RefSeq:NP_564756.1 UniGene:At.10685 UniGene:At.64112 PDB:1V5N PDBsum:1V5N ProteinModelPortal:O80763 SMR:O80763 IntAct:O80763 PRIDE:O80763 EnsemblPlants:AT1G60420.1 GeneID:842337 KEGG:ath:AT1G60420 TAIR:At1g60420 HOGENOM:HBG594354 InParanoid:O80763 OMA:QMPWLAL PhylomeDB:O80763 ProtClustDB:CLSN2917334 ArrayExpress:O80763 Genevestigator:O80763 Uniprot:O80763
Root	Isotig05037	105	51	0.913	0.000128333	TAIR|locus:2061231 - symbol:AT2G40010 "AT2G40010" species:3702 "Arabidopsis thaliana" [GO:0003735 "structural constituent of ribosome" evidence=ISS] [GO:0005840 "ribosome" evidence=ISS] [GO:0006412 "translation" evidence=ISS] [GO:0006414 "translational elongation" evidence=IEA;ISS] [GO:0042254 "ribosome biogenesis" evidence=IEA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR001790 InterPro:IPR001813 Pfam:PF00428 Pfam:PF00466 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0005515 GO:GO:0003735 GO:GO:0022626 GO:GO:0042254 EMBL:AF002109 GO:GO:0006414 eggNOG:COG0244 EMBL:BT001919 IPI:IPI00525504 PIR:B84824 RefSeq:NP_181530.1 UniGene:At.28353 UniGene:At.49578 ProteinModelPortal:O04204 SMR:O04204 IntAct:O04204 STRING:O04204 PRIDE:O04204 EnsemblPlants:AT2G40010.1 GeneID:818589 KEGG:ath:AT2G40010 TAIR:At2g40010 HOGENOM:HBG601294 InParanoid:O04204 KO:K02941 OMA:DYEKLLP PhylomeDB:O04204 ProtClustDB:CLSN2683388 ArrayExpress:O04204 Genevestigator:O04204 GermOnline:AT2G40010 Uniprot:O04204
Root	Isotig05038	103	50	0.914	0.000147131	TAIR|locus:2061231 - symbol:AT2G40010 "AT2G40010" species:3702 "Arabidopsis thaliana" [GO:0003735 "structural constituent of ribosome" evidence=ISS] [GO:0005840 "ribosome" evidence=ISS] [GO:0006412 "translation" evidence=ISS] [GO:0006414 "translational elongation" evidence=IEA;ISS] [GO:0042254 "ribosome biogenesis" evidence=IEA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR001790 InterPro:IPR001813 Pfam:PF00428 Pfam:PF00466 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0005515 GO:GO:0003735 GO:GO:0022626 GO:GO:0042254 EMBL:AF002109 GO:GO:0006414 eggNOG:COG0244

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EMBL:BT001919 IPI:IPI00525504 PIR:B84824 RefSeq:NP_181530.1 UniGene:At.28353 UniGene:At.49578 ProteinModelPortal:O04204 SMR:O04204 IntAct:O04204 STRING:O04204 PRIDE:O04204 EnsemblPlants:AT2G40010.1 GeneID:818589 KEGG:ath:AT2G40010 TAIR:At2g40010 HOGENOM:HBG601294 InParanoid:O04204 KO:K02941 OMA:DYEKLLP PhylomeDB:O04204 ProtClustDB:CLSN2683388 ArrayExpress:O04204 Genevestigator:O04204 GermOnline:AT2G40010 Uniprot:O04204
Root	Isotig05039	98	51	0.813	0.000797392	TAIR|locus:2061231 - symbol:AT2G40010 "AT2G40010" species:3702 "Arabidopsis thaliana" [GO:0003735 "structural constituent of ribosome" evidence=ISS] [GO:0005840 "ribosome" evidence=ISS] [GO:0006412 "translation" evidence=ISS] [GO:0006414 "translational elongation" evidence=IEA;ISS] [GO:0042254 "ribosome biogenesis" evidence=IEA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR001790 InterPro:IPR001813 Pfam:PF00428 Pfam:PF00466 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0005515 GO:GO:0003735 GO:GO:0022626 GO:GO:0042254 EMBL:AF002109 GO:GO:0006414 eggNOG:COG0244 EMBL:BT001919 IPI:IPI00525504 PIR:B84824 RefSeq:NP_181530.1 UniGene:At.28353 UniGene:At.49578 ProteinModelPortal:O04204 SMR:O04204 IntAct:O04204 STRING:O04204 PRIDE:O04204 EnsemblPlants:AT2G40010.1 GeneID:818589 KEGG:ath:AT2G40010 TAIR:At2g40010 HOGENOM:HBG601294 InParanoid:O04204 KO:K02941 OMA:DYEKLLP PhylomeDB:O04204 ProtClustDB:CLSN2683388 ArrayExpress:O04204 Genevestigator:O04204 GermOnline:AT2G40010 Uniprot:O04204
Root	Isotig05055	5	28	-2.614	1.03E-05	TAIR|locus:2172309 - symbol:GDH1 "AT5G18170" species:3702 "Arabidopsis thaliana" [GO:0016491 "oxidoreductase activity" evidence=ISS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005524 "ATP binding" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0008270 "zinc ion binding" evidence=IDA] [GO:0050897 "cobalt ion binding" evidence=IDA] [GO:0004353 "glutamate dehydrogenase [NAD(P)+] activity" evidence=IDA;IMP] [GO:0006807 "nitrogen compound metabolic process" evidence=IMP] [GO:0009646 "response to absence of light" evidence=IEP] InterPro:IPR006095 InterPro:IPR006096 InterPro:IPR006097 InterPro:IPR014362 InterPro:IPR016040 Pfam:PF00208 Pfam:PF02812 PIRSF:PIRSF000185 PRINTS:PR00082 PROSITE:PS00074 SMART:SM00839 GO:GO:0005739 GO:GO:0005524 GO:GO:0046686 EMBL:CP002688 GenomeReviews:BA000015_GR Gene3D:G3DSA:3.40.50.720 GO:GO:0008270 GO:GO:0005507 GO:GO:0006520 GO:GO:0009651 GO:GO:0009646 GO:GO:0050897 EMBL:AB012246 EMBL:U37771 EMBL:U53527 IPI:IPI00531762 PIR:S71217 RefSeq:NP_197318.1 UniGene:At.23609 ProteinModelPortal:Q43314 SMR:Q43314 IntAct:Q43314 STRING:Q43314 PRIDE:Q43314 ProMEX:Q43314 EnsemblPlants:AT5G18170.1 GeneID:831935 KEGG:ath:AT5G18170 GeneFarm:2257 TAIR:At5g18170 eggNOG:COG0334 HOGENOM:HBG590661 InParanoid:Q43314 KO:K00261 OMA:NALYDFH PhylomeDB:Q43314 ProtClustDB:PLN02477 ArrayExpress:Q43314 Genevestigator:Q43314 GermOnline:AT5G18170 GO:GO:0004353 Uniprot:Q43314
Root	Isotig05056	5	22	-2.266	0.000318925	TAIR|locus:2079364 - symbol:GDH3 "glutamate dehydrogenase 3" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0016491 "oxidoreductase activity" evidence=IEA;ISS] [GO:0016639 "oxidoreductase activity, acting on the CH-NH2 group of donors, NAD or NADP as acceptor" evidence=IEA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0051171 "regulation of nitrogen compound metabolic process" evidence=IEP] InterPro:IPR006095 InterPro:IPR006096 InterPro:IPR006097 InterPro:IPR014362 InterPro:IPR016040 Pfam:PF00208 Pfam:PF02812 PIRSF:PIRSF000185 PRINTS:PR00082 PROSITE:PS00074 SMART:SM00839 GO:GO:0005739 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 GO:GO:0006520 EMBL:AC009540 eggNOG:COG0334 HOGENOM:HBG590661 KO:K00261 ProtClustDB:PLN02477 GO:GO:0004353 EMBL:AC011698 IPI:IPI00538151 RefSeq:NP_187041.1 UniGene:At.27423 UniGene:At.53173 ProteinModelPortal:Q9S7A0 SMR:Q9S7A0 STRING:Q9S7A0 PRIDE:Q9S7A0 ProMEX:Q9S7A0 EnsemblPlants:AT3G03910.1 GeneID:821072 KEGG:ath:AT3G03910 GeneFarm:2267 TAIR:At3g03910 InParanoid:Q9S7A0 OMA:VPTHEEE PhylomeDB:Q9S7A0 ArrayExpress:Q9S7A0 Genevestigator:Q9S7A0 GermOnline:AT3G03910 GO:GO:0051171 Uniprot:Q9S7A0
Root	Isotig05057	5	22	-2.266	0.000318925	TAIR|locus:2079364 - symbol:GDH3 "glutamate dehydrogenase 3" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0016491 "oxidoreductase activity" evidence=IEA;ISS] [GO:0016639 "oxidoreductase activity, acting on the CH-NH2 group of donors, NAD or NADP as acceptor" evidence=IEA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0051171 "regulation of nitrogen compound metabolic process" evidence=IEP] InterPro:IPR006095 InterPro:IPR006096 InterPro:IPR006097

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						InterPro:IPR014362 InterPro:IPR016040 Pfam:PF00208 Pfam:PF02812 PIRSF:PIRSF000185 PRINTS:PR00082 PROSITE:PS00074 SMART:SM00839 GO:GO:0005739 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 GO:GO:0006520 EMBL:AC009540 eggNOG:COG0334 HOGENOM:HBG590661 KO:K00261 ProtClustDB:PLN02477 GO:GO:0004353 EMBL:AC011698 IPI:IPI00538151 RefSeq:NP_187041.1 UniGene:At.27423 UniGene:At.53173 ProteinModelPortal:Q9S7A0 SMR:Q9S7A0 STRING:Q9S7A0 PRIDE:Q9S7A0 ProMEX:Q9S7A0 EnsemblPlants:AT3G03910.1 GeneID:821072 KEGG:ath:AT3G03910 GeneFarm:2267 TAIR:At3g03910 InParanoid:Q9S7A0 OMA:VPTHEEE PhylomeDB:Q9S7A0 ArrayExpress:Q9S7A0 Genevestigator:Q9S7A0 GermOnline:AT3G03910 GO:GO:0051171 Uniprot:Q9S7A0
Root	Isotig05061	36	9	1.871	9.91E-05	UNIPROTKB|P83304 - symbol:P83304 "Mannose/glucose-specific lectin" species:185447 "Parkia platycephala" [GO:0000771 "agglutination involved in conjugation" evidence=IDA] [GO:0005536 "glucose binding" evidence=IDA] [GO:0005537 "mannose binding" evidence=IDA] [GO:0005575 "cellular_component" evidence=ND] GO:GO:0005537 GO:GO:0005536 InterPro:IPR001229 Gene3D:G3DSA:2.100.10.30 Pfam:PF01419 SMART:SM00915 SUPFAM:SSF51101 GO:GO:0000771 PDB:1ZGR PDB:1ZGS PDBsum:1ZGR PDBsum:1ZGS ProteinModelPortal:P83304 SMR:P83304 Uniprot:P83304
Root	Isotig05062	44	4	3.330	2.70E-09	TAIR|locus:2154885 - symbol:AT5G66540 "AT5G66540" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0006364 "rRNA processing" evidence=IEA] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR012173 PIRSF:PIRSF017300 GO:GO:0005829 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005730 GO:GO:0030529 GO:GO:0006364 EMBL:AB013389 eggNOG:COG5384 KO:K14559 InterPro:IPR007151 PANTHER:PTHR17039 Pfam:PF04006 EMBL:AF389279 EMBL:AY149928 IPI:IPI00539000 RefSeq:NP_569037.1 UniGene:At.8562 STRING:Q9FJY5 PRIDE:Q9FJY5 EnsemblPlants:AT5G66540.1 GeneID:836786 KEGG:ath:AT5G66540 TAIR:At5g66540 HOGENOM:HBG317308 InParanoid:Q9FJY5 OMA:FKAESAN PhylomeDB:Q9FJY5 ProtClustDB:CLSN2690096 Genevestigator:Q9FJY5 Uniprot:Q9FJY5
Root	Isotig05063	34	6	2.374	1.09E-05	UNIPROTKB|P83304 - symbol:P83304 "Mannose/glucose-specific lectin" species:185447 "Parkia platycephala" [GO:0000771 "agglutination involved in conjugation" evidence=IDA] [GO:0005536 "glucose binding" evidence=IDA] [GO:0005537 "mannose binding" evidence=IDA] [GO:0005575 "cellular_component" evidence=ND] GO:GO:0005537 GO:GO:0005536 InterPro:IPR001229 Gene3D:G3DSA:2.100.10.30 Pfam:PF01419 SMART:SM00915 SUPFAM:SSF51101 GO:GO:0000771 PDB:1ZGR PDB:1ZGS PDBsum:1ZGR PDBsum:1ZGS ProteinModelPortal:P83304 SMR:P83304 Uniprot:P83304
Root	Isotig05067	130	22	2.434	2.57E-18	TAIR|locus:2025162 - symbol:DHAR2 "AT1G75270" species:3702 "Arabidopsis thaliana" [GO:0045174 "glutathione dehydrogenase (ascorbate) activity" evidence=ISS;IDA] [GO:0010731 "protein glutathionylation" evidence=IDA] [GO:0043295 "glutathione binding" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR004045 PROSITE:PS50404 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0005886 GO:GO:0006950 GO:GO:0009636 InterPro:IPR012336 Gene3D:G3DSA:3.40.30.10 SUPFAM:SSF52833 InterPro:IPR010987 Gene3D:G3DSA:1.20.1050.10 SUPFAM:SSF47616 PROSITE:PS50405 InterPro:IPR017933 HSSP:Q9ZVQ3 GO:GO:0045174 GO:GO:0004364 GO:GO:0010731 EMBL:AY074785 EMBL:AC025814 EMBL:AY140019 EMBL:BT006257 EMBL:AY087460 IPI:IPI00542474 PIR:B96783 RefSeq:NP_177662.1 UniGene:At.27979 ProteinModelPortal:Q9FRL8 SMR:Q9FRL8 IntAct:Q9FRL8 STRING:Q9FRL8 PRIDE:Q9FRL8 EnsemblPlants:AT1G75270.1 GeneID:843864 KEGG:ath:AT1G75270 TAIR:At1g75270 eggNOG:COG0625 InParanoid:Q9FRL8 OMA:IDVFAKF PhylomeDB:Q9FRL8 ProtClustDB:CLSN2914231 ArrayExpress:Q9FRL8 Genevestigator:Q9FRL8 GO:GO:0043295 Uniprot:Q9FRL8
Root	Isotig05068	107	19	2.365	6.89E-15	TAIR|locus:2025162 - symbol:DHAR2 "AT1G75270" species:3702 "Arabidopsis thaliana" [GO:0045174 "glutathione dehydrogenase (ascorbate) activity" evidence=ISS;IDA] [GO:0010731 "protein glutathionylation" evidence=IDA] [GO:0043295 "glutathione binding" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR004045 PROSITE:PS50404 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0005886 GO:GO:0006950 GO:GO:0009636 InterPro:IPR012336 Gene3D:G3DSA:3.40.30.10 SUPFAM:SSF52833 InterPro:IPR010987 Gene3D:G3DSA:1.20.1050.10 SUPFAM:SSF47616 PROSITE:PS50405 InterPro:IPR017933 HSSP:Q9ZVQ3 GO:GO:0045174 GO:GO:0004364 GO:GO:0010731 EMBL:AY074785 EMBL:AC025814 EMBL:AY140019 EMBL:BT006257 EMBL:AY087460 IPI:IPI00542474 PIR:B96783 RefSeq:NP_177662.1 UniGene:At.27979

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						ProteinModelPortal:Q9FRL8 SMR:Q9FRL8 IntAct:Q9FRL8 STRING:Q9FRL8 PRIDE:Q9FRL8 EnsemblPlants:AT1G75270.1 GeneID:843864 KEGG:ath:AT1G75270 TAIR:At1g75270 eggNOG:COG0625 InParanoid:Q9FRL8 OMA:IDVFAKF PhylomeDB:Q9FRL8 ProtClustDB:CLSN2914231 ArrayExpress:Q9FRL8 Genevestigator:Q9FRL8 GO:GO:0043295 Uniprot:Q9FRL8
Root	Isotig05069	111	19	2.418	9.42E-16	TAIR|locus:2025162 - symbol:DHAR2 "AT1G75270" species:3702 "Arabidopsis thaliana" [GO:0045174 "glutathione dehydrogenase (ascorbate) activity" evidence=ISS;IDA] [GO:0010731 "protein glutathionylation" evidence=IDA] [GO:0043295 "glutathione binding" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR004045 PROSITE:PS50404 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0005886 GO:GO:0006950 GO:GO:0009636 InterPro:IPR012336 Gene3D:G3DSA:3.40.30.10 SUPFAM:SSF52833 InterPro:IPR010987 Gene3D:G3DSA:1.20.1050.10 SUPFAM:SSF47616 PROSITE:PS50405 InterPro:IPR017933 HSSP:Q9ZVQ3 GO:GO:0045174 GO:GO:0004364 GO:GO:0010731 EMBL:AY074785 EMBL:AC025814 EMBL:AY140019 EMBL:BT006257 EMBL:AY087460 IPI:IPI00542474 PIR:B96783 RefSeq:NP_177662.1 UniGene:At.27979 ProteinModelPortal:Q9FRL8 SMR:Q9FRL8 IntAct:Q9FRL8 STRING:Q9FRL8 PRIDE:Q9FRL8 EnsemblPlants:AT1G75270.1 GeneID:843864 KEGG:ath:AT1G75270 TAIR:At1g75270 eggNOG:COG0625 InParanoid:Q9FRL8 OMA:IDVFAKF PhylomeDB:Q9FRL8 ProtClustDB:CLSN2914231 ArrayExpress:Q9FRL8 Genevestigator:Q9FRL8 GO:GO:0043295 Uniprot:Q9FRL8
Root	Isotig05073	68	18	1.789	2.13E-07	TAIR|locus:2128238 - symbol:BTI2 "AT4G11220" species:3702 "Arabidopsis thaliana" [GO:0005783 "endoplasmic reticulum" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005789 "endoplasmic reticulum membrane" evidence=IDA] [GO:0071458 "integral to cytosolic side of endoplasmic reticulum membrane" evidence=IDA] [GO:0071782 "endoplasmic reticulum tubular network" evidence=IDA] [GO:0071786 "endoplasmic reticulum tubular network organization" evidence=IMP] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR003388 Pfam:PF02453 PROSITE:PS50845 GO:GO:0005886 EMBL:CP002687 GenomeReviews:CT486007_GR EMBL:AL096882 EMBL:AL161531 GO:GO:0071458 PANTHER:PTHR10994 GO:GO:0071786 GO:GO:0071782 eggNOG:NOG303514 ProtClustDB:CLSN2685988 EMBL:AY034901 EMBL:AY048273 EMBL:AY057606 EMBL:BT002368 EMBL:AY086294 IPI:IPI00525362 PIR:T13013 RefSeq:NP_192861.1 UniGene:At.3649 ProteinModelPortal:Q9SUT9 SMR:Q9SUT9 IntAct:Q9SUT9 STRING:Q9SUT9 PRIDE:Q9SUT9 EnsemblPlants:AT4G11220.1 GeneID:826724 KEGG:ath:AT4G11220 TAIR:At4g11220 HOGENOM:HBG596795 InParanoid:Q9SUT9 OMA:HEESSPN PhylomeDB:Q9SUT9 Genevestigator:Q9SUT9 Uniprot:Q9SUT9
Root	Isotig05074	68	18	1.789	2.13E-07	TAIR|locus:2128238 - symbol:BTI2 "AT4G11220" species:3702 "Arabidopsis thaliana" [GO:0005783 "endoplasmic reticulum" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005789 "endoplasmic reticulum membrane" evidence=IDA] [GO:0071458 "integral to cytosolic side of endoplasmic reticulum membrane" evidence=IDA] [GO:0071782 "endoplasmic reticulum tubular network" evidence=IDA] [GO:0071786 "endoplasmic reticulum tubular network organization" evidence=IMP] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR003388 Pfam:PF02453 PROSITE:PS50845 GO:GO:0005886 EMBL:CP002687 GenomeReviews:CT486007_GR EMBL:AL096882 EMBL:AL161531 GO:GO:0071458 PANTHER:PTHR10994 GO:GO:0071786 GO:GO:0071782 eggNOG:NOG303514 ProtClustDB:CLSN2685988 EMBL:AY034901 EMBL:AY048273 EMBL:AY057606 EMBL:BT002368 EMBL:AY086294 IPI:IPI00525362 PIR:T13013 RefSeq:NP_192861.1 UniGene:At.3649 ProteinModelPortal:Q9SUT9 SMR:Q9SUT9 IntAct:Q9SUT9 STRING:Q9SUT9 PRIDE:Q9SUT9 EnsemblPlants:AT4G11220.1 GeneID:826724 KEGG:ath:AT4G11220 TAIR:At4g11220 HOGENOM:HBG596795 InParanoid:Q9SUT9 OMA:HEESSPN PhylomeDB:Q9SUT9 Genevestigator:Q9SUT9 Uniprot:Q9SUT9
Root	Isotig05075	61	9	2.632	4.18E-10	TAIR|locus:2128238 - symbol:BTI2 "AT4G11220" species:3702 "Arabidopsis thaliana" [GO:0005783 "endoplasmic reticulum" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005789 "endoplasmic reticulum membrane" evidence=IDA] [GO:0071458 "integral to cytosolic side of endoplasmic reticulum membrane" evidence=IDA] [GO:0071782 "endoplasmic reticulum tubular network" evidence=IDA] [GO:0071786 "endoplasmic reticulum tubular network organization" evidence=IMP] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR003388 Pfam:PF02453 PROSITE:PS50845 GO:GO:0005886 EMBL:CP002687 GenomeReviews:CT486007_GR EMBL:AL096882 EMBL:AL161531 GO:GO:0071458 PANTHER:PTHR10994 GO:GO:0071786 GO:GO:0071782 eggNOG:NOG303514 ProtClustDB:CLSN2685988 EMBL:AY034901 EMBL:AY048273 EMBL:AY057606 EMBL:BT002368 EMBL:AY086294 IPI:IPI00525362 PIR:T13013

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						RefSeq:NP_192861.1 UniGene:At.3649 ProteinModelPortal:Q9SUT9 SMR:Q9SUT9 IntAct:Q9SUT9 STRING:Q9SUT9 PRIDE:Q9SUT9 EnsemblPlants:AT4G11220.1 GeneID:826724 KEGG:ath:AT4G11220 TAIR:At4g11220 HOGENOM:HBG596795 InParanoid:Q9SUT9 OMA:HEESSPN PhylomeDB:Q9SUT9 Genevestigator:Q9SUT9 Uniprot:Q9SUT9
Root	Isotig05082	7	28	-2.129	9.37E-05	TAIR|locus:2154508 - symbol:AT5G58900 "AT5G58900" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] InterPro:IPR001005 InterPro:IPR009057 Pfam:PF00249 SMART:SM00717 GO:GO:0005634 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0006355 GO:GO:0003677 Gene3D:G3DSA:1.10.10.60 SUPFAM:SSF46689 InterPro:IPR017884 PROSITE:PS51293 InterPro:IPR017930 InterPro:IPR006447 TIGRFAMs:TIGR01557 PROSITE:PS51294 EMBL:AB016885 HOGENOM:HBG591154 EMBL:BT005473 EMBL:AY519533 EMBL:AK118891 IPI:IPI00547099 RefSeq:NP_200698.1 UniGene:At.7757 ProteinModelPortal:Q9FIL9 SMR:Q9FIL9 PRIDE:Q9FIL9 DNASU:836007 EnsemblPlants:AT5G58900.1 GeneID:836007 KEGG:ath:AT5G58900 TAIR:At5g58900 eggNOG:NOG325121 InParanoid:Q9FIL9 OMA:PFTLDWA PhylomeDB:Q9FIL9 ProtClustDB:CLSN2914846 ArrayExpress:Q9FIL9 Genevestigator:Q9FIL9 Uniprot:Q9FIL9
Root	Isotig05109	8	33	-2.173	1.74E-05	TAIR|locus:2125239 - symbol:WRKY11 "AT4G31550" species:3702 "Arabidopsis thaliana" [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0005634 "nucleus" evidence=IC] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=ISS] [GO:0005516 "calmodulin binding" evidence=IDA] [GO:0042742 "defense response to bacterium" evidence=IEP] [GO:0010200 "response to chitin" evidence=IEP] InterPro:IPR003657 Pfam:PF03106 PROSITE:PS50811 SMART:SM00774 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005634 GO:GO:0042742 GO:GO:0043565 GO:GO:0003700 GO:GO:0006351 GO:GO:0005516 GO:GO:0010200 EMBL:AL080283 EMBL:AL161579 Gene3D:G3DSA:2.20.25.80 SUPFAM:SSF118290 EMBL:AF404856 EMBL:AY059731 EMBL:AY150394 EMBL:BT001100 EMBL:AY084855 IPI:IPI00516622 IPI:IPI00531377 PIR:T10685 RefSeq:NP_567878.2 RefSeq:NP_849559.1 UniGene:At.24683 ProteinModelPortal:Q9SV15 SMR:Q9SV15 IntAct:Q9SV15 MINT:MINT-1339027 STRING:Q9SV15 EnsemblPlants:AT4G31550.1 GeneID:829282 KEGG:ath:AT4G31550 TAIR:At4g31550 eggNOG:NOG325238 HOGENOM:HBG595203 InParanoid:Q9SV15 OMA:AMQENIS PhylomeDB:Q9SV15 ProtClustDB:CLSN2688388 ArrayExpress:Q9SV15 Genevestigator:Q9SV15 InterPro:IPR018872 Pfam:PF10533 Uniprot:Q9SV15
Root	Isotig05110	9	32	-1.959	7.57E-05	TAIR|locus:2125239 - symbol:WRKY11 "AT4G31550" species:3702 "Arabidopsis thaliana" [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0005634 "nucleus" evidence=IC] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=ISS] [GO:0005516 "calmodulin binding" evidence=IDA] [GO:0042742 "defense response to bacterium" evidence=IEP] [GO:0010200 "response to chitin" evidence=IEP] InterPro:IPR003657 Pfam:PF03106 PROSITE:PS50811 SMART:SM00774 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005634 GO:GO:0042742 GO:GO:0043565 GO:GO:0003700 GO:GO:0006351 GO:GO:0005516 GO:GO:0010200 EMBL:AL080283 EMBL:AL161579 Gene3D:G3DSA:2.20.25.80 SUPFAM:SSF118290 EMBL:AF404856 EMBL:AY059731 EMBL:AY150394 EMBL:BT001100 EMBL:AY084855 IPI:IPI00516622 IPI:IPI00531377 PIR:T10685 RefSeq:NP_567878.2 RefSeq:NP_849559.1 UniGene:At.24683 ProteinModelPortal:Q9SV15 SMR:Q9SV15 IntAct:Q9SV15 MINT:MINT-1339027 STRING:Q9SV15 EnsemblPlants:AT4G31550.1 GeneID:829282 KEGG:ath:AT4G31550 TAIR:At4g31550 eggNOG:NOG325238 HOGENOM:HBG595203 InParanoid:Q9SV15 OMA:AMQENIS PhylomeDB:Q9SV15 ProtClustDB:CLSN2688388 ArrayExpress:Q9SV15 Genevestigator:Q9SV15 InterPro:IPR018872 Pfam:PF10533 Uniprot:Q9SV15
Root	Isotig05111	6	24	-2.129	0.00029855	TAIR|locus:2125239 - symbol:WRKY11 "AT4G31550" species:3702 "Arabidopsis thaliana" [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0005634 "nucleus" evidence=IC] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=ISS] [GO:0005516 "calmodulin binding" evidence=IDA] [GO:0042742 "defense response to bacterium" evidence=IEP] [GO:0010200 "response to chitin" evidence=IEP] InterPro:IPR003657 Pfam:PF03106 PROSITE:PS50811 SMART:SM00774 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005634 GO:GO:0042742 GO:GO:0043565 GO:GO:0003700 GO:GO:0006351 GO:GO:0005516 GO:GO:0010200 EMBL:AL080283 EMBL:AL161579 Gene3D:G3DSA:2.20.25.80 SUPFAM:SSF118290 EMBL:AF404856 EMBL:AY059731 EMBL:AY150394 EMBL:BT001100 EMBL:AY084855 IPI:IPI00516622 IPI:IPI00531377 PIR:T10685 RefSeq:NP_567878.2 RefSeq:NP_849559.1 UniGene:At.24683 ProteinModelPortal:Q9SV15 SMR:Q9SV15 IntAct:Q9SV15 MINT:MINT-1339027 STRING:Q9SV15 EnsemblPlants:AT4G31550.1 GeneID:829282 KEGG:ath:AT4G31550 TAIR:At4g31550 eggNOG:NOG325238

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						HOGENOM:HBG595203 InParanoid:Q9SV15 OMA:AMQENIS PhylomeDB:Q9SV15 ProtClustDB:CLSN2688388 ArrayExpress:Q9SV15 Genevestigator:Q9SV15 InterPro:IPR018872 Pfam:PF10533 Uniprot:Q9SV15
Root	Isotig05116	2	16	-3.129	0.000262867	TAIR|locus:2018027 - symbol:SLAH1 "AT1G62280" species:3702 "Arabidopsis thaliana" [GO:0005215 "transporter activity" evidence=ISS] [GO:0016021 "integral to membrane" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0006873 "cellular ion homeostasis" evidence=IMP] InterPro:IPR004695 Pfam:PF03595 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005886 GO:GO:0006811 GO:GO:0055085 EMBL:AC000375 EMBL:BT004052 EMBL:BT021090 IPI:IPI00517394 PIR:D96649 RefSeq:NP_176418.2 UniGene:At.36280 EnsemblPlants:AT1G62280.1 GeneID:842525 KEGG:ath:AT1G62280 TAIR:At1g62280 eggNOG:NOG130260 InParanoid:Q5E930 OMA:WWAVSFP PhylomeDB:Q5E930 ProtClustDB:CLSN2680771 ArrayExpress:Q84WB2 Genevestigator:Q5E930 Uniprot:Q5E930
Root	Isotig05124	12	34	-1.631	0.000323514	TAIR|locus:2047057 - symbol:SYTA "synaptotagmin A" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0006612 "protein targeting to membrane" evidence=ISS] [GO:0005773 "vacuole" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0001778 "plasma membrane repair" evidence=IMP] [GO:0009409 "response to cold" evidence=IMP] [GO:0009898 "internal side of plasma membrane" evidence=IDA] [GO:0005768 "endosome" evidence=IDA] [GO:0006897 "endocytosis" evidence=IMP] [GO:0009615 "response to virus" evidence=IPI] [GO:0032456 "endocytic recycling" evidence=IMP] [GO:0046740 "spread of virus in host, cell to cell" evidence=IMP] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000008 InterPro:IPR008973 Pfam:PF00168 SMART:SM00239 GO:GO:0009506 GO:GO:0005773 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0005768 GO:GO:0006897 GO:GO:0009409 GO:GO:0009615 InterPro:IPR018029 SUPFAM:SSF49562 PROSITE:PS50004 eggNOG:COG5038 GO:GO:0032456 GO:GO:0009898 EMBL:AC006234 EMBL:AC006264 InterPro:IPR020477 PRINTS:PR00360 HSSP:P47709 GO:GO:0046740 GO:GO:0001778 HOGENOM:HBG316820 ProtClustDB:CLSN2688294 EMBL:AY045836 EMBL:AY087925 EMBL:BT004371 EMBL:AB102951 EMBL:AJ617630 IPI:IPI00517829 PIR:G84595 RefSeq:NP_565495.1 UniGene:At.24916 ProteinModelPortal:Q9SKR2 SMR:Q9SKR2 STRING:Q9SKR2 PRIDE:Q9SKR2 EnsemblPlants:AT2G20990.1 GeneID:816633 KEGG:ath:AT2G20990 TAIR:At2g20990 InParanoid:Q9SKR2 OMA:EYMWPYL PhylomeDB:Q9SKR2 ArrayExpress:Q9SKR2 Genevestigator:Q9SKR2 Uniprot:Q9SKR2
Root	Isotig05125	11	41	-2.027	4.63E-06	TAIR|locus:2047057 - symbol:SYTA "synaptotagmin A" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0006612 "protein targeting to membrane" evidence=ISS] [GO:0005773 "vacuole" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0001778 "plasma membrane repair" evidence=IMP] [GO:0009409 "response to cold" evidence=IMP] [GO:0009898 "internal side of plasma membrane" evidence=IDA] [GO:0005768 "endosome" evidence=IDA] [GO:0006897 "endocytosis" evidence=IMP] [GO:0009615 "response to virus" evidence=IPI] [GO:0032456 "endocytic recycling" evidence=IMP] [GO:0046740 "spread of virus in host, cell to cell" evidence=IMP] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000008 InterPro:IPR008973 Pfam:PF00168 SMART:SM00239 GO:GO:0009506 GO:GO:0005773 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0005768 GO:GO:0006897 GO:GO:0009409 GO:GO:0009615 InterPro:IPR018029 SUPFAM:SSF49562 PROSITE:PS50004 eggNOG:COG5038 GO:GO:0032456 GO:GO:0009898 EMBL:AC006234 EMBL:AC006264 InterPro:IPR020477 PRINTS:PR00360 HSSP:P47709 GO:GO:0046740 GO:GO:0001778 HOGENOM:HBG316820 ProtClustDB:CLSN2688294 EMBL:AY045836 EMBL:AY087925 EMBL:BT004371 EMBL:AB102951 EMBL:AJ617630 IPI:IPI00517829 PIR:G84595 RefSeq:NP_565495.1 UniGene:At.24916 ProteinModelPortal:Q9SKR2 SMR:Q9SKR2 STRING:Q9SKR2 PRIDE:Q9SKR2 EnsemblPlants:AT2G20990.1 GeneID:816633 KEGG:ath:AT2G20990 TAIR:At2g20990 InParanoid:Q9SKR2 OMA:EYMWPYL PhylomeDB:Q9SKR2 ArrayExpress:Q9SKR2 Genevestigator:Q9SKR2 Uniprot:Q9SKR2
Root	Isotig05126	11	42	-2.062	2.76E-06	TAIR|locus:2047057 - symbol:SYTA "synaptotagmin A" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0006612 "protein targeting to membrane" evidence=ISS] [GO:0005773 "vacuole" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0001778 "plasma membrane repair" evidence=IMP] [GO:0009409 "response to cold" evidence=IMP] [GO:0009898 "internal side of plasma membrane" evidence=IDA] [GO:0005768 "endosome" evidence=IDA] [GO:0006897 "endocytosis" evidence=IMP] [GO:0009615 "response to virus" evidence=IPI] [GO:0032456 "endocytic recycling" evidence=IMP] [GO:0046740 "spread of virus in host, cell to cell" evidence=IMP] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000008 InterPro:IPR008973 Pfam:PF00168

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						SMART:SM00239 GO:GO:0009506 GO:GO:0005773 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0005768 GO:GO:0006897 GO:GO:0009409 GO:GO:0009615 InterPro:IPR018029 SUPFAM:SSF49562 PROSITE:PS50004 eggNOG:COG5038 GO:GO:0032456 GO:GO:0009898 EMBL:AC006234 EMBL:AC006264 InterPro:IPR020477 PRINTS:PR00360 HSSP:P47709 GO:GO:0046740 GO:GO:0001778 HOGENOM:HBG316820 ProtClustDB:CLSN2688294 EMBL:AY045836 EMBL:AY087925 EMBL:BT004371 EMBL:AB102951 EMBL:AJ617630 IPI:IPI00517829 PIR:G84595 RefSeq:NP_565495.1 UniGene:At.24916 ProteinModelPortal:Q9SKR2 SMR:Q9SKR2 STRING:Q9SKR2 PRIDE:Q9SKR2 EnsemblPlants:AT2G20990.1 GeneID:816633 KEGG:ath:AT2G20990 TAIR:At2g20990 InParanoid:Q9SKR2 OMA:EYMWPYL PhylomeDB:Q9SKR2 ArrayExpress:Q9SKR2 Genevestigator:Q9SKR2 Uniprot:Q9SKR2
Root	Isotig05133	0	11	-4.588	0.000569522	TAIR|locus:2180454 - symbol:CPN20 "AT5G20720" species:3702 "Arabidopsis thaliana" [GO:0009507 "chloroplast" evidence=ISS;IDA] [GO:0005516 "calmodulin binding" evidence=TAS] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] InterPro:IPR018369 InterPro:IPR020818 Pfam:PF00166 PRINTS:PR00297 PROSITE:PS00681 SMART:SM00883 GO:GO:0005739 GO:GO:0005524 GO:GO:0048046 GO:GO:0009570 GO:GO:0046686 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0006457 GO:GO:0009941 GO:GO:0005507 GO:GO:0009409 InterPro:IPR011032 SUPFAM:SSF50129 GO:GO:0009535 EMBL:AF296832 UniGene:At.49045 UniGene:At.59645 eggNOG:COG0234 Gene3D:G3DSA:2.30.33.40 PANTHER:PTHR10772 EMBL:AJ010818 EMBL:AF268068 EMBL:AF059037 EMBL:AB007130 EMBL:AY062971 EMBL:AY034979 EMBL:AF428366 EMBL:AF428339 IPI:IPI00537354 PIR:T52122 PIR:T52613 RefSeq:NP_001190350.1 RefSeq:NP_197572.1 RefSeq:NP_851045.1 ProteinModelPortal:O65282 SMR:O65282 IntAct:O65282 STRING:O65282 SWISS-2DPAGE:O65282 PRIDE:O65282 ProMEX:O65282 EnsemblPlants:AT5G20720.1 EnsemblPlants:AT5G20720.2 EnsemblPlants:AT5G20720.3 GeneID:832195 KEGG:ath:AT5G20720 TAIR:At5g20720 HOGENOM:HBG606344 InParanoid:O65282 OMA:RVCSSRR PhylomeDB:O65282 ProtClustDB:CLSN2687389 ArrayExpress:O65282 Genevestigator:O65282 GermOnline:AT5G20720 InterPro:IPR017416 PIRSF:PIRSF038157 Uniprot:O65282
Root	Isotig05134	0	11	-4.588	0.000569522	TAIR|locus:2180454 - symbol:CPN20 "AT5G20720" species:3702 "Arabidopsis thaliana" [GO:0009507 "chloroplast" evidence=ISS;IDA] [GO:0005516 "calmodulin binding" evidence=TAS] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] InterPro:IPR018369 InterPro:IPR020818 Pfam:PF00166 PRINTS:PR00297 PROSITE:PS00681 SMART:SM00883 GO:GO:0005739 GO:GO:0005524 GO:GO:0048046 GO:GO:0009570 GO:GO:0046686 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0006457 GO:GO:0009941 GO:GO:0005507 GO:GO:0009409 InterPro:IPR011032 SUPFAM:SSF50129 GO:GO:0009535 EMBL:AF296832 UniGene:At.49045 UniGene:At.59645 eggNOG:COG0234 Gene3D:G3DSA:2.30.33.40 PANTHER:PTHR10772 EMBL:AJ010818 EMBL:AF268068 EMBL:AF059037 EMBL:AB007130 EMBL:AY062971 EMBL:AY034979 EMBL:AF428366 EMBL:AF428339 IPI:IPI00537354 PIR:T52122 PIR:T52613 RefSeq:NP_001190350.1 RefSeq:NP_197572.1 RefSeq:NP_851045.1 ProteinModelPortal:O65282 SMR:O65282 IntAct:O65282 STRING:O65282 SWISS-2DPAGE:O65282 PRIDE:O65282 ProMEX:O65282 EnsemblPlants:AT5G20720.1 EnsemblPlants:AT5G20720.2 EnsemblPlants:AT5G20720.3 GeneID:832195 KEGG:ath:AT5G20720 TAIR:At5g20720 HOGENOM:HBG606344 InParanoid:O65282 OMA:RVCSSRR PhylomeDB:O65282 ProtClustDB:CLSN2687389 ArrayExpress:O65282 Genevestigator:O65282 GermOnline:AT5G20720 InterPro:IPR017416 PIRSF:PIRSF038157 Uniprot:O65282
Root	Isotig05135	0	11	-4.588	0.000569522	TAIR|locus:2180454 - symbol:CPN20 "AT5G20720" species:3702 "Arabidopsis thaliana" [GO:0009507 "chloroplast" evidence=ISS;IDA] [GO:0005516 "calmodulin binding" evidence=TAS] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] InterPro:IPR018369 InterPro:IPR020818 Pfam:PF00166 PRINTS:PR00297 PROSITE:PS00681 SMART:SM00883

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0005739 GO:GO:0005524 GO:GO:0048046 GO:GO:0009570 GO:GO:0046686 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0006457 GO:GO:0009941 GO:GO:0005507 GO:GO:0009409 InterPro:IPR011032 SUPFAM:SSF50129 GO:GO:0009535 EMBL:AF296832 UniGene:At.49045 UniGene:At.59645 eggNOG:COG0234 Gene3D:G3DSA:2.30.33.40 PANTHER:PTHR10772 EMBL:AJ010818 EMBL:AF268068 EMBL:AF059037 EMBL:AB007130 EMBL:AY062971 EMBL:AY034979 EMBL:AF428366 EMBL:AF428339 IPI:IPI00537354 PIR:T52122 PIR:T52613 RefSeq:NP_001190350.1 RefSeq:NP_197572.1 RefSeq:NP_851045.1 ProteinModelPortal:O65282 SMR:O65282 IntAct:O65282 STRING:O65282 SWISS-2DPAGE:O65282 PRIDE:O65282 ProMEX:O65282 EnsemblPlants:AT5G20720.1 EnsemblPlants:AT5G20720.2 EnsemblPlants:AT5G20720.3 GeneID:832195 KEGG:ath:AT5G20720 TAIR:At5g20720 HOGENOM:HBG606344 InParanoid:O65282 OMA:RVCSSRR PhylomeDB:O65282 ProtClustDB:CLSN2687389 ArrayExpress:O65282 Genevestigator:O65282 GermOnline:AT5G20720 InterPro:IPR017416 PIRSF:PIRSF038157 Uniprot:O65282
Root	Isotig05160	11	85	-3.079	6.87E-17	TAIR|locus:2126026 - symbol:PIP1;4 "AT4G00430" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=ISS] [GO:0015250 "water channel activity" evidence=ISS] [GO:0016020 "membrane" evidence=ISS;IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009414 "response to water deprivation" evidence=IEP] InterPro:IPR000425 InterPro:IPR012269 InterPro:IPR022357 Pfam:PF00230 PRINTS:PR00783 PROSITE:PS00221 GO:GO:0016021 GO:GO:0005886 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0055085 GO:GO:0009414 GO:GO:0005215 GO:GO:0006833 EMBL:AF013293 EMBL:AF195115 EMBL:AL161471 InterPro:IPR023271 Gene3D:G3DSA:1.20.1080.10 SUPFAM:SSF81338 eggNOG:COG0580 HOGENOM:HBG705794 PANTHER:PTHR19139 TIGRFAMs:TIGR00861 OMA:ITHNFKD KO:K09872 ProtClustDB:CLSN2682869 UniGene:At.20518 UniGene:At.20892 EMBL:D26609 EMBL:D85192 EMBL:AY099825 EMBL:AY120785 EMBL:BT000330 EMBL:BT006313 IPI:IPI00521990 PIR:T01528 RefSeq:NP_567178.1 ProteinModelPortal:Q39196 SMR:Q39196 IntAct:Q39196 STRING:Q39196 PRIDE:Q39196 EnsemblPlants:AT4G00430.1 GeneID:827956 KEGG:ath:AT4G00430 GeneFarm:2265 TAIR:At4g00430 InParanoid:Q39196 PhylomeDB:Q39196 ArrayExpress:Q39196 Genevestigator:Q39196 Uniprot:Q39196
Root	Isotig05161	7	31	-2.276	1.84E-05	TAIR|locus:2126026 - symbol:PIP1;4 "AT4G00430" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=ISS] [GO:0015250 "water channel activity" evidence=ISS] [GO:0016020 "membrane" evidence=ISS;IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009414 "response to water deprivation" evidence=IEP] InterPro:IPR000425 InterPro:IPR012269 InterPro:IPR022357 Pfam:PF00230 PRINTS:PR00783 PROSITE:PS00221 GO:GO:0016021 GO:GO:0005886 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0055085 GO:GO:0009414 GO:GO:0005215 GO:GO:0006833 EMBL:AF013293 EMBL:AF195115 EMBL:AL161471 InterPro:IPR023271 Gene3D:G3DSA:1.20.1080.10 SUPFAM:SSF81338 eggNOG:COG0580 HOGENOM:HBG705794 PANTHER:PTHR19139 TIGRFAMs:TIGR00861 OMA:ITHNFKD KO:K09872 ProtClustDB:CLSN2682869 UniGene:At.20518 UniGene:At.20892 EMBL:D26609 EMBL:D85192 EMBL:AY099825 EMBL:AY120785 EMBL:BT000330 EMBL:BT006313 IPI:IPI00521990 PIR:T01528 RefSeq:NP_567178.1 ProteinModelPortal:Q39196 SMR:Q39196 IntAct:Q39196 STRING:Q39196 PRIDE:Q39196 EnsemblPlants:AT4G00430.1 GeneID:827956 KEGG:ath:AT4G00430 GeneFarm:2265 TAIR:At4g00430 InParanoid:Q39196 PhylomeDB:Q39196 ArrayExpress:Q39196 Genevestigator:Q39196 Uniprot:Q39196
Root	Isotig05172	31	0	5.825	1.45E-08	TAIR|locus:2035109 - symbol:LEA7 "AT1G52690" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0009793 "embryo development ending in seed dormancy" evidence=ISS] EMBL:CP002684 EMBL:AC008016 EMBL:AF385732 EMBL:AY093968 EMBL:AY087466 EMBL:BT000737 EMBL:BT000739 EMBL:X91919 IPI:IPI00526817 PIR:H96567 RefSeq:NP_175678.1 RefSeq:NP_974009.1 UniGene:At.21275 STRING:Q96270 PRIDE:Q96270 ProMEX:Q96270 DNASU:841701 EnsemblPlants:AT1G52690.1 EnsemblPlants:AT1G52690.2 GeneID:841701 KEGG:ath:AT1G52690 TAIR:At1g52690 InParanoid:Q96270 OMA:MASHQEQ PhylomeDB:Q96270 ProtClustDB:CLSN2679745 ArrayExpress:Q96270 Genevestigator:Q96270 Uniprot:Q96270
Root	Isotig05173	22	0	5.330	1.93E-06	TAIR|locus:2035109 - symbol:LEA7 "AT1G52690" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0009793 "embryo development ending in seed dormancy" evidence=ISS] EMBL:CP002684 EMBL:AC008016 EMBL:AF385732 EMBL:AY093968 EMBL:AY087466 EMBL:BT000737 EMBL:BT000739 EMBL:X91919 IPI:IPI00526817 PIR:H96567 RefSeq:NP_175678.1 RefSeq:NP_974009.1 UniGene:At.21275 STRING:Q96270 PRIDE:Q96270 ProMEX:Q96270 DNASU:841701 EnsemblPlants:AT1G52690.1 EnsemblPlants:AT1G52690.2 GeneID:841701

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						KEGG:ath:AT1G52690 TAIR:At1g52690 InParanoid:Q96270 OMA:MASHQEQ PhylomeDB:Q96270 ProtClustDB:CLSN2679745 ArrayExpress:Q96270 Genevestigator:Q96270 Uniprot:Q96270
Root	Isotig05174	18	0	5.041	1.86E-05	TAIR|locus:2035109 - symbol:LEA7 "AT1G52690" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0009793 "embryo development ending in seed dormancy" evidence=ISS] EMBL:CP002684 EMBL:AC008016 EMBL:AF385732 EMBL:AY093968 EMBL:AY087466 EMBL:BT000737 EMBL:BT000739 EMBL:X91919 IPI:IPI00526817 PIR:H96567 RefSeq:NP_175678.1 RefSeq:NP_974009.1 UniGene:At.21275 STRING:Q96270 PRIDE:Q96270 ProMEX:Q96270 DNASU:841701 EnsemblPlants:AT1G52690.1 EnsemblPlants:AT1G52690.2 GeneID:841701 KEGG:ath:AT1G52690 TAIR:At1g52690 InParanoid:Q96270 OMA:MASHQEQ PhylomeDB:Q96270 ProtClustDB:CLSN2679745 ArrayExpress:Q96270 Genevestigator:Q96270 Uniprot:Q96270
Root	Isotig05179	30	7	1.971	0.000234532	No hit
Root	Isotig05181	32	0	5.871	8.51E-09	TAIR|locus:2010419 - symbol:AT1G27990 "AT1G27990" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002684 GenomeReviews:CT485782_GR EMBL:AC069471 UniGene:At.66881 EMBL:AK317213 IPI:IPI00523350 PIR:D86405 RefSeq:NP_174120.1 PRIDE:Q9C7F4 EnsemblPlants:AT1G27990.1 GeneID:839692 KEGG:ath:AT1G27990 TAIR:At1g27990 HOGENOM:HBG319949 InParanoid:Q9C7F4 OMA:IPRFLPR PhylomeDB:Q9C7F4 ProtClustDB:CLSN2679353 Genevestigator:Q9C7F4 Uniprot:Q9C7F4
Root	Isotig05182	33	0	5.915	5.02E-09	TAIR|locus:2010419 - symbol:AT1G27990 "AT1G27990" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002684 GenomeReviews:CT485782_GR EMBL:AC069471 UniGene:At.66881 EMBL:AK317213 IPI:IPI00523350 PIR:D86405 RefSeq:NP_174120.1 PRIDE:Q9C7F4 EnsemblPlants:AT1G27990.1 GeneID:839692 KEGG:ath:AT1G27990 TAIR:At1g27990 HOGENOM:HBG319949 InParanoid:Q9C7F4 OMA:IPRFLPR PhylomeDB:Q9C7F4 ProtClustDB:CLSN2679353 Genevestigator:Q9C7F4 Uniprot:Q9C7F4
Root	Isotig05183	31	0	5.825	1.45E-08	TAIR|locus:2010419 - symbol:AT1G27990 "AT1G27990" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002684 GenomeReviews:CT485782_GR EMBL:AC069471 UniGene:At.66881 EMBL:AK317213 IPI:IPI00523350 PIR:D86405 RefSeq:NP_174120.1 PRIDE:Q9C7F4 EnsemblPlants:AT1G27990.1 GeneID:839692 KEGG:ath:AT1G27990 TAIR:At1g27990 HOGENOM:HBG319949 InParanoid:Q9C7F4 OMA:IPRFLPR PhylomeDB:Q9C7F4 ProtClustDB:CLSN2679353 Genevestigator:Q9C7F4 Uniprot:Q9C7F4
Root	Isotig05188	12	0	4.456	0.000626491	TAIR|locus:2062754 - symbol:HB-7 "homeobox 7" species:3702 "Arabidopsis thaliana" [GO:0005634 "nucleus" evidence=IEA;ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=ISS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0045893 "positive regulation of transcription, DNA-dependent" evidence=IDA] [GO:0009414 "response to water deprivation" evidence=IEP] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] [GO:0009738 "abscisic acid mediated signaling pathway" evidence=IGI] InterPro:IPR000047 InterPro:IPR001356 InterPro:IPR003106 InterPro:IPR009057 InterPro:IPR017970 Pfam:PF00046 Pfam:PF02183 PRINTS:PR00031 PROSITE:PS00027 PROSITE:PS50071 SMART:SM00389 GO:GO:0005634 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0045893 GO:GO:0009738 GO:GO:0003700 GO:GO:0006351 GO:GO:0009414 Gene3D:G3DSA:1.10.10.60 SUPFAM:SSF46689 GO:GO:0000976 eggNOG:NOG252905 HOGENOM:HBG593038 ProtClustDB:CLSN2683559 EMBL:X67032 EMBL:AC005819 EMBL:AY045826 EMBL:AY091364 IPI:IPI00544746 PIR:H84905 PIR:S47137 RefSeq:NP_182191.1 UniGene:At.136 ProteinModelPortal:P46897 SMR:P46897 STRING:P46897 EnsemblPlants:AT2G46680.1 GeneID:819280 KEGG:ath:AT2G46680 GeneFarm:3966 TAIR:At2g46680 InParanoid:P46897 OMA:ALVIQLQ PhylomeDB:P46897 ArrayExpress:P46897 Genevestigator:P46897 Uniprot:P46897
Root	Isotig05205	54	144	-1.544	1.15E-12	UNIPROTKB|Q43472 - symbol:blt801 "Glycine-rich RNA-binding protein blt801" species:4513 "Hordeum vulgare" [GO:0003697 "single-stranded DNA binding" evidence=IDA] [GO:0003723 "RNA binding" evidence=IDA] [GO:0009409 "response to cold" evidence=IDA] [GO:0009737 "response to abscisic acid stimulus" evidence=IDA] InterPro:IPR000504 InterPro:IPR012677 Pfam:PF00076 PROSITE:PS50102 SMART:SM00360 GO:GO:0009737 GO:GO:0000166 GO:GO:0006397 Gene3D:G3DSA:3.30.70.330 GO:GO:0006351 GO:GO:0009409

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0003723 GO:GO:0003697 EMBL:U49482 PIR:S71453 HSSP:P11940 ProteinModelPortal:Q43472 Gramene:Q43472 Genevestigator:Q43472 Uniprot:Q43472
Root	Isotig05206	57	202	-1.954	3.13E-23	UNIPROTKB|Q43472 - symbol:blt801 "Glycine-rich RNA-binding protein blt801" species:4513 "Hordeum vulgare" [GO:0003697 "single-stranded DNA binding" evidence=IDA] [GO:0003723 "RNA binding" evidence=IDA] [GO:0009409 "response to cold" evidence=IDA] [GO:0009737 "response to abscisic acid stimulus" evidence=IDA] InterPro:IPR000504 InterPro:IPR012677 Pfam:PF00076 PROSITE:PS50102 SMART:SM00360 GO:GO:0009737 GO:GO:0000166 GO:GO:0006397 Gene3D:G3DSA:3.30.70.330 GO:GO:0006351 GO:GO:0009409 GO:GO:0003723 GO:GO:0003697 EMBL:U49482 PIR:S71453 HSSP:P11940 ProteinModelPortal:Q43472 Gramene:Q43472 Genevestigator:Q43472 Uniprot:Q43472
Root	Isotig05207	28	70	-1.451	2.20E-06	UNIPROTKB|Q43472 - symbol:blt801 "Glycine-rich RNA-binding protein blt801" species:4513 "Hordeum vulgare" [GO:0003697 "single-stranded DNA binding" evidence=IDA] [GO:0003723 "RNA binding" evidence=IDA] [GO:0009409 "response to cold" evidence=IDA] [GO:0009737 "response to abscisic acid stimulus" evidence=IDA] InterPro:IPR000504 InterPro:IPR012677 Pfam:PF00076 PROSITE:PS50102 SMART:SM00360 GO:GO:0009737 GO:GO:0000166 GO:GO:0006397 Gene3D:G3DSA:3.30.70.330 GO:GO:0006351 GO:GO:0009409 GO:GO:0003723 GO:GO:0003697 EMBL:U49482 PIR:S71453 HSSP:P11940 ProteinModelPortal:Q43472 Gramene:Q43472 Genevestigator:Q43472 Uniprot:Q43472
Root	Isotig05211	6	56	-3.351	1.97E-12	TAIR|locus:2064332 - symbol:AT2G30620 "AT2G30620" species:3702 "Arabidopsis thaliana" [GO:0000786 "nucleosome" evidence=ISS] [GO:0003677 "DNA binding" evidence=IEA;ISS] [GO:0005634 "nucleus" evidence=ISS] [GO:0006334 "nucleosome assembly" evidence=IEA;ISS] [GO:0005730 "nucleolus" evidence=IDA] InterPro:IPR005818 InterPro:IPR005819 Pfam:PF00538 PRINTS:PR00624 PROSITE:PS51504 SMART:SM00526 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0005730 GO:GO:0003677 InterPro:IPR011991 Gene3D:G3DSA:1.10.10.10 GO:GO:0006334 GO:GO:0000786 EMBL:U93215 KO:K11275 eggNOG:NOG126832 EMBL:X62459 EMBL:AF360211 EMBL:AY040059 EMBL:AY085789 IPI:IPI00532307 PIR:S19699 RefSeq:NP_180620.1 UniGene:At.20406 ProteinModelPortal:P26569 STRING:P26569 PRIDE:P26569 EnsemblPlants:AT2G30620.1 GeneID:817612 KEGG:ath:AT2G30620 TAIR:At2g30620 HOGENOM:HBG184949 InParanoid:P26569 OMA:HRTPSSH PhylomeDB:P26569 ProtClustDB:CLSN2912930 ArrayExpress:P26569 Genevestigator:P26569 GermOnline:AT2G30620 Uniprot:P26569
Root	Isotig05212	5	54	-3.562	1.44E-12	TAIR|locus:2064332 - symbol:AT2G30620 "AT2G30620" species:3702 "Arabidopsis thaliana" [GO:0000786 "nucleosome" evidence=ISS] [GO:0003677 "DNA binding" evidence=IEA;ISS] [GO:0005634 "nucleus" evidence=ISS] [GO:0006334 "nucleosome assembly" evidence=IEA;ISS] [GO:0005730 "nucleolus" evidence=IDA] InterPro:IPR005818 InterPro:IPR005819 Pfam:PF00538 PRINTS:PR00624 PROSITE:PS51504 SMART:SM00526 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0005730 GO:GO:0003677 InterPro:IPR011991 Gene3D:G3DSA:1.10.10.10 GO:GO:0006334 GO:GO:0000786 EMBL:U93215 KO:K11275 eggNOG:NOG126832 EMBL:X62459 EMBL:AF360211 EMBL:AY040059 EMBL:AY085789 IPI:IPI00532307 PIR:S19699 RefSeq:NP_180620.1 UniGene:At.20406 ProteinModelPortal:P26569 STRING:P26569 PRIDE:P26569 EnsemblPlants:AT2G30620.1 GeneID:817612 KEGG:ath:AT2G30620 TAIR:At2g30620 HOGENOM:HBG184949 InParanoid:P26569 OMA:HRTPSSH PhylomeDB:P26569 ProtClustDB:CLSN2912930 ArrayExpress:P26569 Genevestigator:P26569 GermOnline:AT2G30620 Uniprot:P26569
Root	Isotig05213	5	54	-3.562	1.44E-12	TAIR|locus:2064332 - symbol:AT2G30620 "AT2G30620" species:3702 "Arabidopsis thaliana" [GO:0000786 "nucleosome" evidence=ISS] [GO:0003677 "DNA binding" evidence=IEA;ISS] [GO:0005634 "nucleus" evidence=ISS] [GO:0006334 "nucleosome assembly" evidence=IEA;ISS] [GO:0005730 "nucleolus" evidence=IDA] InterPro:IPR005818 InterPro:IPR005819 Pfam:PF00538 PRINTS:PR00624 PROSITE:PS51504 SMART:SM00526 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0005730 GO:GO:0003677 InterPro:IPR011991 Gene3D:G3DSA:1.10.10.10 GO:GO:0006334 GO:GO:0000786 EMBL:U93215 KO:K11275 eggNOG:NOG126832 EMBL:X62459 EMBL:AF360211 EMBL:AY040059 EMBL:AY085789 IPI:IPI00532307 PIR:S19699 RefSeq:NP_180620.1 UniGene:At.20406 ProteinModelPortal:P26569 STRING:P26569 PRIDE:P26569 EnsemblPlants:AT2G30620.1 GeneID:817612 KEGG:ath:AT2G30620 TAIR:At2g30620 HOGENOM:HBG184949 InParanoid:P26569 OMA:HRTPSSH PhylomeDB:P26569 ProtClustDB:CLSN2912930 ArrayExpress:P26569 Genevestigator:P26569 GermOnline:AT2G30620 Uniprot:P26569
Root	Isotig05235	0	64	-7.129	9.20E-17	TAIR|locus:2168953 - symbol:TIP2;3 "AT5G47450" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=ISS] [GO:0015250 "water channel activity" evidence=ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0009705 "plant-type vacuole membrane" evidence=IDA] [GO:0015200 "methylammonium transmembrane

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						transporter activity" evidence=IDA] [GO:0051739 "ammonia transmembrane transporter activity" evidence=IGI] [GO:0042807 "central vacuole" evidence=IDA] InterPro:IPR000425 InterPro:IPR012269 InterPro:IPR022357 Pfam:PF00230 PRINTS:PR00783 PROSITE:PS00221 GO:GO:0016021 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009705 EMBL:AB025628 GO:GO:0006833 GO:GO:0015200 GO:GO:0051739 InterPro:IPR023271 Gene3D:G3DSA:1.20.1080.10 SUPFAM:SSF81338 eggNOG:COG0580 HOGENOM:HBG705794 PANTHER:PTHR19139 TIGRFAMs:TIGR00861 KO:K09873 GO:GO:0042807 ProtClustDB:PLN00166 EMBL:BT011212 EMBL:BT011663 EMBL:AK229341 IPI:IPI00541642 RefSeq:NP_199556.1 UniGene:At.43789 ProteinModelPortal:Q9FGL2 SMR:Q9FGL2 STRING:Q9FGL2 TCDB:1.A.8.10.4 PRIDE:Q9FGL2 EnsemblPlants:AT5G47450.1 GeneID:834794 KEGG:ath:AT5G47450 GeneFarm:4858 TAIR:At5g47450 InParanoid:Q9FGL2 OMA:GHIVACL PhylomeDB:Q9FGL2 ArrayExpress:Q9FGL2 Genevestigator:Q9FGL2 GermOnline:AT5G47450 Uniprot:Q9FGL2
Root	Isotig05236	0	64	-7.129	9.20E-17	TAIR|locus:2168953 - symbol:TIP2;3 "AT5G47450" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=ISS] [GO:0015250 "water channel activity" evidence=ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0009705 "plant-type vacuole membrane" evidence=IDA] [GO:0015200 "methylammonium transmembrane transporter activity" evidence=IDA] [GO:0051739 "ammonia transmembrane transporter activity" evidence=IGI] [GO:0042807 "central vacuole" evidence=IDA] InterPro:IPR000425 InterPro:IPR012269 InterPro:IPR022357 Pfam:PF00230 PRINTS:PR00783 PROSITE:PS00221 GO:GO:0016021 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009705 EMBL:AB025628 GO:GO:0006833 GO:GO:0015200 GO:GO:0051739 InterPro:IPR023271 Gene3D:G3DSA:1.20.1080.10 SUPFAM:SSF81338 eggNOG:COG0580 HOGENOM:HBG705794 PANTHER:PTHR19139 TIGRFAMs:TIGR00861 KO:K09873 GO:GO:0042807 ProtClustDB:PLN00166 EMBL:BT011212 EMBL:BT011663 EMBL:AK229341 IPI:IPI00541642 RefSeq:NP_199556.1 UniGene:At.43789 ProteinModelPortal:Q9FGL2 SMR:Q9FGL2 STRING:Q9FGL2 TCDB:1.A.8.10.4 PRIDE:Q9FGL2 EnsemblPlants:AT5G47450.1 GeneID:834794 KEGG:ath:AT5G47450 GeneFarm:4858 TAIR:At5g47450 InParanoid:Q9FGL2 OMA:GHIVACL PhylomeDB:Q9FGL2 ArrayExpress:Q9FGL2 Genevestigator:Q9FGL2 GermOnline:AT5G47450 Uniprot:Q9FGL2
Root	Isotig05237	0	43	-6.555	4.45E-12	TAIR|locus:2168953 - symbol:TIP2;3 "AT5G47450" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=ISS] [GO:0015250 "water channel activity" evidence=ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0009705 "plant-type vacuole membrane" evidence=IDA] [GO:0015200 "methylammonium transmembrane transporter activity" evidence=IDA] [GO:0051739 "ammonia transmembrane transporter activity" evidence=IGI] [GO:0042807 "central vacuole" evidence=IDA] InterPro:IPR000425 InterPro:IPR012269 InterPro:IPR022357 Pfam:PF00230 PRINTS:PR00783 PROSITE:PS00221 GO:GO:0016021 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009705 EMBL:AB025628 GO:GO:0006833 GO:GO:0015200 GO:GO:0051739 InterPro:IPR023271 Gene3D:G3DSA:1.20.1080.10 SUPFAM:SSF81338 eggNOG:COG0580 HOGENOM:HBG705794 PANTHER:PTHR19139 TIGRFAMs:TIGR00861 KO:K09873 GO:GO:0042807 ProtClustDB:PLN00166 EMBL:BT011212 EMBL:BT011663 EMBL:AK229341 IPI:IPI00541642 RefSeq:NP_199556.1 UniGene:At.43789 ProteinModelPortal:Q9FGL2 SMR:Q9FGL2 STRING:Q9FGL2 TCDB:1.A.8.10.4 PRIDE:Q9FGL2 EnsemblPlants:AT5G47450.1 GeneID:834794 KEGG:ath:AT5G47450 GeneFarm:4858 TAIR:At5g47450 InParanoid:Q9FGL2 OMA:GHIVACL PhylomeDB:Q9FGL2 ArrayExpress:Q9FGL2 Genevestigator:Q9FGL2 GermOnline:AT5G47450 Uniprot:Q9FGL2
Root	Isotig05260	5	20	-2.129	0.000961902	TAIR|locus:2032574 - symbol:GRX480 "AT1G28480" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0005515 "protein binding" evidence=IPI] [GO:0009751 "response to salicylic acid stimulus" evidence=IEP] [GO:0009863 "salicylic acid mediated signaling pathway" evidence=IMP] [GO:0009867 "jasmonic acid mediated signaling pathway" evidence=IMP] InterPro:IPR002109 Pfam:PF00462 PROSITE:PS00195 PROSITE:PS51354 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005634 GO:GO:0005737 GO:GO:0005515 GO:GO:0009055 GO:GO:0006810 GO:GO:0022900 InterPro:IPR012336 Gene3D:G3DSA:3.40.30.10 SUPFAM:SSF52833 GO:GO:0045454 GO:GO:0015035 GO:GO:0009867 GO:GO:0009863 EMBL:AC010155 HOGENOM:HBG728471 HSSP:Q9CQM9 InterPro:IPR011905 TIGRFAMs:TIGR02189 EMBL:FJ611918 EMBL:AF325030 EMBL:AK229369 EMBL:BT029336 IPI:IPI00535123 PIR:H86410 RefSeq:NP_174170.1 UniGene:At.11829 ProteinModelPortal:Q9SGP6 SMR:Q9SGP6 IntAct:Q9SGP6 STRING:Q9SGP6 EnsemblPlants:AT1G28480.1 GeneID:839748 KEGG:ath:AT1G28480 TAIR:At1g28480 eggNOG:NOG318179 InParanoid:Q9SGP6 OMA:MVVEENA PhylomeDB:Q9SGP6 ProtClustDB:CLSN2913511 Genevestigator:Q9SGP6 GermOnline:AT1G28480 Uniprot:Q9SGP6

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig05273	5	24	-2.392	0.000103464	TAIR|locus:2092339 - symbol:ERF7 "AT3G20310" species:3702 "Arabidopsis thaliana" [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS;TAS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=TAS] [GO:0003677 "DNA binding" evidence=TAS] [GO:0005634 "nucleus" evidence=IC;IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0009414 "response to water deprivation" evidence=IMP] [GO:0009737 "response to abscisic acid stimulus" evidence=IMP] [GO:0043565 "sequence-specific DNA binding" evidence=IDA] [GO:0045892 "negative regulation of transcription, DNA-dependent" evidence=IDA] [GO:0009873 "ethylene mediated signaling pathway" evidence=TAS] InterPro:IPR001471 InterPro:IPR016177 Pfam:PF00847 PRINTS:PR00367 PROSITE:PS51032 SMART:SM00380 GO:GO:0009737 GO:GO:0005634 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0045892 GO:GO:0005515 GO:GO:0006952 GO:GO:0009873 GO:GO:0043565 GO:GO:0003700 GO:GO:0006351 GO:GO:0009414 KO:K09286 Gene3D:G3DSA:3.30.730.10 SUPFAM:SSF54171 EMBL:AB024036 HOGENOM:HBG744062 ProtClustDB:CLSN2682907 EMBL:AB032201 EMBL:AY037254 EMBL:AY094001 EMBL:AY085023 EMBL:AK228460 IPI:IPI00537654 RefSeq:NP_188666.1 UniGene:At.20161 ProteinModelPortal:Q9LDE4 SMR:Q9LDE4 IntAct:Q9LDE4 STRING:Q9LDE4 PRIDE:Q9LDE4 EnsemblPlants:AT3G20310.1 GeneID:821575 KEGG:ath:AT3G20310 TAIR:At3g20310 eggNOG:NOG322216 InParanoid:Q9LDE4 OMA:VAPEDCH PhylomeDB:Q9LDE4 ArrayExpress:Q9LDE4 Genevestigator:Q9LDE4 GermOnline:AT3G20310 Uniprot:Q9LDE4
Root	Isotig05274	5	24	-2.392	0.000103464	TAIR|locus:2092339 - symbol:ERF7 "AT3G20310" species:3702 "Arabidopsis thaliana" [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS;TAS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=TAS] [GO:0003677 "DNA binding" evidence=TAS] [GO:0005634 "nucleus" evidence=IC;IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0009414 "response to water deprivation" evidence=IMP] [GO:0009737 "response to abscisic acid stimulus" evidence=IMP] [GO:0043565 "sequence-specific DNA binding" evidence=IDA] [GO:0045892 "negative regulation of transcription, DNA-dependent" evidence=IDA] [GO:0009873 "ethylene mediated signaling pathway" evidence=TAS] InterPro:IPR001471 InterPro:IPR016177 Pfam:PF00847 PRINTS:PR00367 PROSITE:PS51032 SMART:SM00380 GO:GO:0009737 GO:GO:0005634 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0045892 GO:GO:0005515 GO:GO:0006952 GO:GO:0009873 GO:GO:0043565 GO:GO:0003700 GO:GO:0006351 GO:GO:0009414 KO:K09286 Gene3D:G3DSA:3.30.730.10 SUPFAM:SSF54171 EMBL:AB024036 HOGENOM:HBG744062 ProtClustDB:CLSN2682907 EMBL:AB032201 EMBL:AY037254 EMBL:AY094001 EMBL:AY085023 EMBL:AK228460 IPI:IPI00537654 RefSeq:NP_188666.1 UniGene:At.20161 ProteinModelPortal:Q9LDE4 SMR:Q9LDE4 IntAct:Q9LDE4 STRING:Q9LDE4 PRIDE:Q9LDE4 EnsemblPlants:AT3G20310.1 GeneID:821575 KEGG:ath:AT3G20310 TAIR:At3g20310 eggNOG:NOG322216 InParanoid:Q9LDE4 OMA:VAPEDCH PhylomeDB:Q9LDE4 ArrayExpress:Q9LDE4 Genevestigator:Q9LDE4 GermOnline:AT3G20310 Uniprot:Q9LDE4
Root	Isotig05275	3	22	-3.003	2.69E-05	TAIR|locus:2092339 - symbol:ERF7 "AT3G20310" species:3702 "Arabidopsis thaliana" [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS;TAS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=TAS] [GO:0003677 "DNA binding" evidence=TAS] [GO:0005634 "nucleus" evidence=IC;IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0009414 "response to water deprivation" evidence=IMP] [GO:0009737 "response to abscisic acid stimulus" evidence=IMP] [GO:0043565 "sequence-specific DNA binding" evidence=IDA] [GO:0045892 "negative regulation of transcription, DNA-dependent" evidence=IDA] [GO:0009873 "ethylene mediated signaling pathway" evidence=TAS] InterPro:IPR001471 InterPro:IPR016177 Pfam:PF00847 PRINTS:PR00367 PROSITE:PS51032 SMART:SM00380 GO:GO:0009737 GO:GO:0005634 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0045892 GO:GO:0005515 GO:GO:0006952 GO:GO:0009873 GO:GO:0043565 GO:GO:0003700 GO:GO:0006351 GO:GO:0009414 KO:K09286 Gene3D:G3DSA:3.30.730.10 SUPFAM:SSF54171 EMBL:AB024036 HOGENOM:HBG744062 ProtClustDB:CLSN2682907 EMBL:AB032201 EMBL:AY037254 EMBL:AY094001 EMBL:AY085023 EMBL:AK228460 IPI:IPI00537654 RefSeq:NP_188666.1 UniGene:At.20161 ProteinModelPortal:Q9LDE4 SMR:Q9LDE4 IntAct:Q9LDE4 STRING:Q9LDE4 PRIDE:Q9LDE4 EnsemblPlants:AT3G20310.1 GeneID:821575 KEGG:ath:AT3G20310 TAIR:At3g20310 eggNOG:NOG322216 InParanoid:Q9LDE4 OMA:VAPEDCH PhylomeDB:Q9LDE4 ArrayExpress:Q9LDE4 Genevestigator:Q9LDE4 GermOnline:AT3G20310 Uniprot:Q9LDE4
Root	Isotig05276	257	6	5.292	1.85E-59	TAIR|locus:2123919 - symbol:CFIM-25 "AT4G29820" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] InterPro:IPR000086 InterPro:IPR015797 InterPro:IPR016706 PIRSF:PIRSF017888 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005515 Gene3D:G3DSA:3.90.79.10 SUPFAM:SSF55811 GO:GO:0016787 PANTHER:PTHR13047

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						HOGENOM:HBG629877 ProtClustDB:CLSN2689678 EMBL:AY048229 EMBL:AY091704 EMBL:AY085984 IPI:IPI00532079 RefSeq:NP_567835.1 UniGene:At.26190 ProteinModelPortal:Q94AF0 IntAct:Q94AF0 STRING:Q94AF0 PRIDE:Q94AF0 EnsemblPlants:AT4G29820.1 GeneID:829104 KEGG:ath:AT4G29820 TAIR:At4g29820 eggNOG:NOG303614 InParanoid:Q94AF0 OMA:GECIGMW PhylomeDB:Q94AF0 Genevestigator:Q94AF0 Uniprot:Q94AF0
Root	Isotig05277	257	6	5.292	1.85E-59	TAIR|locus:2123919 - symbol:CFIM-25 "AT4G29820" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] InterPro:IPR000086 InterPro:IPR015797 InterPro:IPR016706 PIRSF:PIRSF017888 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005515 Gene3D:G3DSA:3.90.79.10 SUPFAM:SSF55811 GO:GO:0016787 PANTHER:PTHR13047 HOGENOM:HBG629877 ProtClustDB:CLSN2689678 EMBL:AY048229 EMBL:AY091704 EMBL:AY085984 IPI:IPI00532079 RefSeq:NP_567835.1 UniGene:At.26190 ProteinModelPortal:Q94AF0 IntAct:Q94AF0 STRING:Q94AF0 PRIDE:Q94AF0 EnsemblPlants:AT4G29820.1 GeneID:829104 KEGG:ath:AT4G29820 TAIR:At4g29820 eggNOG:NOG303614 InParanoid:Q94AF0 OMA:GECIGMW PhylomeDB:Q94AF0 Genevestigator:Q94AF0 Uniprot:Q94AF0
Root	Isotig05291	1	21	-4.521	2.07E-06	TAIR|locus:2009130 - symbol:AT1G06620 "AT1G06620" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0016706 "oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors" evidence=ISS] InterPro:IPR005123 Pfam:PF03171 PROSITE:PS51471 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0046872 EMBL:AC007592 EMBL:BT006430 EMBL:AK227676 IPI:IPI00533375 PIR:D86201 RefSeq:NP_172147.2 UniGene:At.42332 HSSP:Q08506 ProteinModelPortal:Q84MB3 SMR:Q84MB3 PRIDE:Q84MB3 EnsemblPlants:AT1G06620.1 GeneID:837171 KEGG:ath:AT1G06620 TAIR:At1g06620 eggNOG:COG3491 HOGENOM:HBG749762 InParanoid:Q84MB3 OMA:CEMMIEY PhylomeDB:Q84MB3 ProtClustDB:CLSN2685246 Genevestigator:Q84MB3 GO:GO:0016706 Uniprot:Q84MB3
Root	Isotig05292	1	17	-4.216	2.69E-05	TAIR|locus:2009130 - symbol:AT1G06620 "AT1G06620" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0016706 "oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors" evidence=ISS] InterPro:IPR005123 Pfam:PF03171 PROSITE:PS51471 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0046872 EMBL:AC007592 EMBL:BT006430 EMBL:AK227676 IPI:IPI00533375 PIR:D86201 RefSeq:NP_172147.2 UniGene:At.42332 HSSP:Q08506 ProteinModelPortal:Q84MB3 SMR:Q84MB3 PRIDE:Q84MB3 EnsemblPlants:AT1G06620.1 GeneID:837171 KEGG:ath:AT1G06620 TAIR:At1g06620 eggNOG:COG3491 HOGENOM:HBG749762 InParanoid:Q84MB3 OMA:CEMMIEY PhylomeDB:Q84MB3 ProtClustDB:CLSN2685246 Genevestigator:Q84MB3 GO:GO:0016706 Uniprot:Q84MB3
Root	Isotig05318	1	28	-4.936	2.57E-08	TAIR|locus:2086445 - symbol:NQR "AT3G27890" species:3702 "Arabidopsis thaliana" [GO:0008752 "FMN reductase activity" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0042742 "defense response to bacterium" evidence=IEP] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] Pfam:PF03358 GO:GO:0005829 GO:GO:0005886 GO:GO:0009570 GO:GO:0042742 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0009651 EMBL:AP000371 GO:GO:0003955 eggNOG:COG0431 HOGENOM:HBG697130 InterPro:IPR005025 EMBL:AF145234 IPI:IPI00522027 RefSeq:NP_189427.1 UniGene:At.5735 ProteinModelPortal:Q9LK88 SMR:Q9LK88 PRIDE:Q9LK88 EnsemblPlants:AT3G27890.1 GeneID:822411 KEGG:ath:AT3G27890 TAIR:At3g27890 InParanoid:Q9LK88 OMA:ASPEYNF PhylomeDB:Q9LK88 ProtClustDB:CLSN2685191 Genevestigator:Q9LK88 GermOnline:AT3G27890 Uniprot:Q9LK88
Root	Isotig05319	1	18	-4.299	1.41E-05	TAIR|locus:2086445 - symbol:NQR "AT3G27890" species:3702 "Arabidopsis thaliana" [GO:0008752 "FMN reductase activity" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0042742 "defense response to bacterium" evidence=IEP] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] Pfam:PF03358 GO:GO:0005829 GO:GO:0005886 GO:GO:0009570 GO:GO:0042742 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0009651 EMBL:AP000371 GO:GO:0003955 eggNOG:COG0431 HOGENOM:HBG697130 InterPro:IPR005025 EMBL:AF145234 IPI:IPI00522027

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						RefSeq:NP_189427.1 UniGene:At.5735 ProteinModelPortal:Q9LK88 SMR:Q9LK88 PRIDE:Q9LK88 EnsemblPlants:AT3G27890.1 GeneID:822411 KEGG:ath:AT3G27890 TAIR:At3g27890 InParanoid:Q9LK88 OMA:ASPEYNF PhylomeDB:Q9LK88 ProtClustDB:CLSN2685191 Genevestigator:Q9LK88 GermOnline:AT3G27890 Uniprot:Q9LK88
Root	Isotig05320	1	18	-4.299	1.41E-05	TAIR|locus:2086445 - symbol:NQR "AT3G27890" species:3702 "Arabidopsis thaliana" [GO:0008752 "FMN reductase activity" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0042742 "defense response to bacterium" evidence=IEP] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] Pfam:PF03358 GO:GO:0005829 GO:GO:0005886 GO:GO:0009570 GO:GO:0042742 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0009651 EMBL:AP000371 GO:GO:0003955 eggNOG:COG0431 HOGENOM:HBG697130 InterPro:IPR005025 EMBL:AF145234 IPI:IPI00522027 RefSeq:NP_189427.1 UniGene:At.5735 ProteinModelPortal:Q9LK88 SMR:Q9LK88 PRIDE:Q9LK88 EnsemblPlants:AT3G27890.1 GeneID:822411 KEGG:ath:AT3G27890 TAIR:At3g27890 InParanoid:Q9LK88 OMA:ASPEYNF PhylomeDB:Q9LK88 ProtClustDB:CLSN2685191 Genevestigator:Q9LK88 GermOnline:AT3G27890 Uniprot:Q9LK88
Root	Isotig05321	0	16	-5.129	2.34E-05	TAIR|locus:2195733 - symbol:BAN "AT1G61720" species:3702 "Arabidopsis thaliana" [GO:0033729 "anthocyanidin reductase activity" evidence=IDA] [GO:0009964 "negative regulation of flavonoid biosynthetic process" evidence=IMP] [GO:0016491 "oxidoreductase activity" evidence=ISS] InterPro:IPR001509 InterPro:IPR016040 Pfam:PF01370 EMBL:CP002684 GenomeReviews:CT485782_GR eggNOG:COG0451 GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 HOGENOM:HBG755066 GO:GO:0050662 EMBL:AF092912 EMBL:AC005882 EMBL:DQ446384 EMBL:AK175960 IPI:IPI00523362 PIR:H96642 RefSeq:NP_176365.1 UniGene:At.11057 ProteinModelPortal:Q9SEV0 SMR:Q9SEV0 STRING:Q9SEV0 PRIDE:Q9SEV0 EnsemblPlants:AT1G61720.1 GeneID:842469 KEGG:ath:AT1G61720 TAIR:At1g61720 InParanoid:Q9SEV0 KO:K08695 OMA:ICCAYNT PhylomeDB:Q9SEV0 ProtClustDB:PLN00198 Genevestigator:Q9SEV0 GO:GO:0033729 GO:GO:0009813 GO:GO:0009964 Uniprot:Q9SEV0
Root	Isotig05322	0	18	-5.299	6.77E-06	TAIR|locus:2195733 - symbol:BAN "AT1G61720" species:3702 "Arabidopsis thaliana" [GO:0033729 "anthocyanidin reductase activity" evidence=IDA] [GO:0009964 "negative regulation of flavonoid biosynthetic process" evidence=IMP] [GO:0016491 "oxidoreductase activity" evidence=ISS] InterPro:IPR001509 InterPro:IPR016040 Pfam:PF01370 EMBL:CP002684 GenomeReviews:CT485782_GR eggNOG:COG0451 GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 HOGENOM:HBG755066 GO:GO:0050662 EMBL:AF092912 EMBL:AC005882 EMBL:DQ446384 EMBL:AK175960 IPI:IPI00523362 PIR:H96642 RefSeq:NP_176365.1 UniGene:At.11057 ProteinModelPortal:Q9SEV0 SMR:Q9SEV0 STRING:Q9SEV0 PRIDE:Q9SEV0 EnsemblPlants:AT1G61720.1 GeneID:842469 KEGG:ath:AT1G61720 TAIR:At1g61720 InParanoid:Q9SEV0 KO:K08695 OMA:ICCAYNT PhylomeDB:Q9SEV0 ProtClustDB:PLN00198 Genevestigator:Q9SEV0 GO:GO:0033729 GO:GO:0009813 GO:GO:0009964 Uniprot:Q9SEV0
Root	Isotig05325	1	20	-4.451	3.92E-06	No hit
Root	Isotig05326	1	20	-4.451	3.92E-06	No hit
Root	Isotig05333	13	141	-3.568	2.37E-30	TAIR|locus:2057906 - symbol:GAMMA-TIP "AT2G36830" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=ISS] [GO:0009740 "gibberellic acid mediated signaling pathway" evidence=TAS] [GO:0015250 "water channel activity" evidence=ISS;IDA] [GO:0016020 "membrane" evidence=ISS] [GO:0009705 "plant-type vacuole membrane" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0015204 "urea transmembrane transporter activity" evidence=IGI] [GO:0015840 "urea transport" evidence=IGI] [GO:0005773 "vacuole" evidence=IDA] [GO:0080170 "hydrogen peroxide transmembrane transport" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0000326 "protein storage vacuole" evidence=IDA] [GO:0042807 "central vacuole" evidence=IDA] [GO:0006833 "water transport" evidence=IDA] InterPro:IPR000425 InterPro:IPR022357 Pfam:PF00230 PRINTS:PR00783 PROSITE:PS00221 GO:GO:0016021 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009941 EMBL:AC006922 GO:GO:0009705 InterPro:IPR023271 Gene3D:G3DSA:1.20.1080.10 SUPFAM:SSF81338 eggNOG:COG0580 HOGENOM:HBG705794 PANTHER:PTHR19139 GO:GO:0015250 GO:GO:0000326 GO:GO:0015204 GO:GO:0080170 EMBL:X54854 EMBL:X63552 EMBL:M84344 EMBL:X72581 EMBL:AF370172 EMBL:AY059134 EMBL:AY087558 EMBL:Z18124 EMBL:Z18771 EMBL:Z26215 IPI:IPI00531328 PIR:S13718 PIR:S22202 RefSeq:NP_181221.1 UniGene:At.25221 UniGene:At.43252 UniGene:At.67051 ProteinModelPortal:P25818 SMR:P25818 IntAct:P25818 STRING:P25818

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						TCDB:1.A.8.10.3 PRIDE:P25818 EnsemblPlants:AT2G36830.1 GeneID:818255 KEGG:ath:AT2G36830 GeneFarm:4855 TAIR:At2g36830 InParanoid:P25818 KO:K09873 OMA:INTTHEQ PhylomeDB:P25818 ProtClustDB:PLN00027 ArrayExpress:P25818 Genevestigator:P25818 GermOnline:AT2G36830 GO:GO:0042807 Uniprot:P25818
Root	Isotig05334	17	119	-2.936	4.58E-22	TAIR|locus:2057906 - symbol:GAMMA-TIP "AT2G36830" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=ISS] [GO:0009740 "gibberellic acid mediated signaling pathway" evidence=TAS] [GO:0015250 "water channel activity" evidence=ISS;IDA] [GO:0016020 "membrane" evidence=ISS] [GO:0009705 "plant-type vacuole membrane" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0015204 "urea transmembrane transporter activity" evidence=IGI] [GO:0015840 "urea transport" evidence=IGI] [GO:0005773 "vacuole" evidence=IDA] [GO:0080170 "hydrogen peroxide transmembrane transport" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0000326 "protein storage vacuole" evidence=IDA] [GO:0042807 "central vacuole" evidence=IDA] [GO:0006833 "water transport" evidence=IDA] InterPro:IPR000425 InterPro:IPR022357 Pfam:PF00230 PRINTS:PR00783 PROSITE:PS00221 GO:GO:0016021 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009941 EMBL:AC006922 GO:GO:0009705 InterPro:IPR023271 Gene3D:G3DSA:1.20.1080.10 SUPFAM:SSF81338 eggNOG:COG0580 HOGENOM:HBG705794 PANTHER:PTHR19139 GO:GO:0015250 GO:GO:0000326 GO:GO:0015204 GO:GO:0080170 EMBL:X54854 EMBL:X63552 EMBL:M84344 EMBL:X72581 EMBL:AF370172 EMBL:AY059134 EMBL:AY087558 EMBL:Z18124 EMBL:Z18771 EMBL:Z26215 IPI:IPI00531328 PIR:S13718 PIR:S22202 RefSeq:NP_181221.1 UniGene:At.25221 UniGene:At.43252 UniGene:At.67051 ProteinModelPortal:P25818 SMR:P25818 IntAct:P25818 STRING:P25818 TCDB:1.A.8.10.3 PRIDE:P25818 EnsemblPlants:AT2G36830.1 GeneID:818255 KEGG:ath:AT2G36830 GeneFarm:4855 TAIR:At2g36830 InParanoid:P25818 KO:K09873 OMA:INTTHEQ PhylomeDB:P25818 ProtClustDB:PLN00027 ArrayExpress:P25818 Genevestigator:P25818 GermOnline:AT2G36830 GO:GO:0042807 Uniprot:P25818
Root	Isotig05339	0	22	-5.588	6.01E-07	TAIR|locus:2195301 - symbol:NAS3 "AT1G09240" species:3702 "Arabidopsis thaliana" [GO:0030410 "nicotianamine synthase activity" evidence=IDA] [GO:0030418 "nicotianamine biosynthetic process" evidence=IDA] InterPro:IPR004298 Pfam:PF03059 PROSITE:PS51142 EMBL:CP002684 GenomeReviews:CT485782_GR EMBL:AC003114 HOGENOM:HBG594037 KO:K05953 ProtClustDB:PLN03075 GO:GO:0030410 GO:GO:0030418 EMBL:AB021936 EMBL:AY140031 EMBL:BT008817 EMBL:AY087620 IPI:IPI00518527 PIR:C86225 RefSeq:NP_172395.1 UniGene:At.42234 ProteinModelPortal:O80483 SMR:O80483 STRING:O80483 PRIDE:O80483 EnsemblPlants:AT1G09240.1 GeneID:837444 KEGG:ath:AT1G09240 TAIR:At1g09240 eggNOG:NOG139408 InParanoid:O80483 OMA:DISQRMF PhylomeDB:O80483 ArrayExpress:O80483 Genevestigator:O80483 GermOnline:AT1G09240 Uniprot:O80483
Root	Isotig05340	0	19	-5.377	3.67E-06	TAIR|locus:2195301 - symbol:NAS3 "AT1G09240" species:3702 "Arabidopsis thaliana" [GO:0030410 "nicotianamine synthase activity" evidence=IDA] [GO:0030418 "nicotianamine biosynthetic process" evidence=IDA] InterPro:IPR004298 Pfam:PF03059 PROSITE:PS51142 EMBL:CP002684 GenomeReviews:CT485782_GR EMBL:AC003114 HOGENOM:HBG594037 KO:K05953 ProtClustDB:PLN03075 GO:GO:0030410 GO:GO:0030418 EMBL:AB021936 EMBL:AY140031 EMBL:BT008817 EMBL:AY087620 IPI:IPI00518527 PIR:C86225 RefSeq:NP_172395.1 UniGene:At.42234 ProteinModelPortal:O80483 SMR:O80483 STRING:O80483 PRIDE:O80483 EnsemblPlants:AT1G09240.1 GeneID:837444 KEGG:ath:AT1G09240 TAIR:At1g09240 eggNOG:NOG139408 InParanoid:O80483 OMA:DISQRMF PhylomeDB:O80483 ArrayExpress:O80483 Genevestigator:O80483 GermOnline:AT1G09240 Uniprot:O80483
Root	Isotig05341	0	18	-5.299	6.77E-06	TAIR|locus:2195301 - symbol:NAS3 "AT1G09240" species:3702 "Arabidopsis thaliana" [GO:0030410 "nicotianamine synthase activity" evidence=IDA] [GO:0030418 "nicotianamine biosynthetic process" evidence=IDA] InterPro:IPR004298 Pfam:PF03059 PROSITE:PS51142 EMBL:CP002684 GenomeReviews:CT485782_GR EMBL:AC003114 HOGENOM:HBG594037 KO:K05953 ProtClustDB:PLN03075 GO:GO:0030410 GO:GO:0030418 EMBL:AB021936 EMBL:AY140031 EMBL:BT008817 EMBL:AY087620 IPI:IPI00518527 PIR:C86225 RefSeq:NP_172395.1 UniGene:At.42234 ProteinModelPortal:O80483 SMR:O80483 STRING:O80483 PRIDE:O80483 EnsemblPlants:AT1G09240.1 GeneID:837444 KEGG:ath:AT1G09240 TAIR:At1g09240 eggNOG:NOG139408 InParanoid:O80483 OMA:DISQRMF PhylomeDB:O80483 ArrayExpress:O80483 Genevestigator:O80483 GermOnline:AT1G09240 Uniprot:O80483
Root	Isotig05354	1	12	-3.714	0.000699736	TAIR|locus:2024122 - symbol:FLA9 "AT1G03870" species:3702 "Arabidopsis thaliana" [GO:0031225 "anchored to membrane" evidence=TAS] [GO:0046658 "anchored to plasma membrane" evidence=IDA] [GO:0005886 "plasma

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						membrane" evidence=IDA] Pfam:PF02469 InterPro:IPR000782 EMBL:CP002684 GenomeReviews:CT485782_GR EMBL:AC003027 GO:GO:0046658 Gene3D:G3DSA:2.30.180.10 SMART:SM00554 SUPFAM:SSF82153 PROSITE:PS50213 HOGENOM:HBG750250 ProtClustDB:CLSN2687227 EMBL:AF333974 EMBL:AF083781 EMBL:AY087938 EMBL:AK227010 IPI:IPI00540701 PIR:D86169 RefSeq:NP_563692.1 UniGene:At.23966 UniGene:At.73148 ProteinModelPortal:Q9ZWA8 SMR:Q9ZWA8 PRIDE:Q9ZWA8 EnsemblPlants:AT1G03870.1 GeneID:839384 KEGG:ath:AT1G03870 GeneFarm:3781 TAIR:At1g03870 eggNOG:NOG299573 InParanoid:Q9ZWA8 OMA:VNSSSEG PhylomeDB:Q9ZWA8 Genevestigator:Q9ZWA8 GermOnline:AT1G03870 Uniprot:Q9ZWA8
Root	Isotig05355	1	12	-3.714	0.000699736	TAIR|locus:2024122 - symbol:FLA9 "AT1G03870" species:3702 "Arabidopsis thaliana" [GO:0031225 "anchored to membrane" evidence=TAS] [GO:0046658 "anchored to plasma membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] Pfam:PF02469 InterPro:IPR000782 EMBL:CP002684 GenomeReviews:CT485782_GR EMBL:AC003027 GO:GO:0046658 Gene3D:G3DSA:2.30.180.10 SMART:SM00554 SUPFAM:SSF82153 PROSITE:PS50213 HOGENOM:HBG750250 ProtClustDB:CLSN2687227 EMBL:AF333974 EMBL:AF083781 EMBL:AY087938 EMBL:AK227010 IPI:IPI00540701 PIR:D86169 RefSeq:NP_563692.1 UniGene:At.23966 UniGene:At.73148 ProteinModelPortal:Q9ZWA8 SMR:Q9ZWA8 PRIDE:Q9ZWA8 EnsemblPlants:AT1G03870.1 GeneID:839384 KEGG:ath:AT1G03870 GeneFarm:3781 TAIR:At1g03870 eggNOG:NOG299573 InParanoid:Q9ZWA8 OMA:VNSSSEG PhylomeDB:Q9ZWA8 Genevestigator:Q9ZWA8 GermOnline:AT1G03870 Uniprot:Q9ZWA8
Root	Isotig05366	6	25	-2.188	0.000173532	TAIR|locus:2038593 - symbol:FD3 "ferredoxin 3" species:3702 "Arabidopsis thaliana" [GO:0009055 "electron carrier activity" evidence=IEA;ISS] [GO:0022900 "electron transport chain" evidence=IEA] [GO:0051536 "iron-sulfur cluster binding" evidence=IEA] [GO:0051537 "2 iron, 2 sulfur cluster binding" evidence=IEA] InterPro:IPR001041 InterPro:IPR006058 InterPro:IPR010241 Pfam:PF00111 PROSITE:PS00197 PROSITE:PS51085 GO:GO:0009507 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009055 GO:GO:0046872 GO:GO:0006810 GO:GO:0022900 GO:GO:0051537 InterPro:IPR012675 Gene3D:G3DSA:3.10.20.30 SUPFAM:SSF54292 eggNOG:COG0633 EMBL:AC006232 TIGRFAMs:TIGR02008 HOGENOM:HBG748855 KO:K02639 EMBL:AY086622 EMBL:BT004187 EMBL:BT005393 IPI:IPI00548374 PIR:G84673 RefSeq:NP_180320.1 UniGene:At.38754 HSSP:P00248 ProteinModelPortal:Q9ZQG8 SMR:Q9ZQG8 STRING:Q9ZQG8 PRIDE:Q9ZQG8 EnsemblPlants:AT2G27510.1 GeneID:817297 KEGG:ath:AT2G27510 TAIR:At2g27510 InParanoid:Q9ZQG8 OMA:YPQSDCV PhylomeDB:Q9ZQG8 ProtClustDB:CLSN2913085 ArrayExpress:Q9ZQG8 Genevestigator:Q9ZQG8 Uniprot:Q9ZQG8
Root	Isotig05367	6	25	-2.188	0.000173532	TAIR|locus:2038593 - symbol:FD3 "ferredoxin 3" species:3702 "Arabidopsis thaliana" [GO:0009055 "electron carrier activity" evidence=IEA;ISS] [GO:0022900 "electron transport chain" evidence=IEA] [GO:0051536 "iron-sulfur cluster binding" evidence=IEA] [GO:0051537 "2 iron, 2 sulfur cluster binding" evidence=IEA] InterPro:IPR001041 InterPro:IPR006058 InterPro:IPR010241 Pfam:PF00111 PROSITE:PS00197 PROSITE:PS51085 GO:GO:0009507 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009055 GO:GO:0046872 GO:GO:0006810 GO:GO:0022900 GO:GO:0051537 InterPro:IPR012675 Gene3D:G3DSA:3.10.20.30 SUPFAM:SSF54292 eggNOG:COG0633 EMBL:AC006232 TIGRFAMs:TIGR02008 HOGENOM:HBG748855 KO:K02639 EMBL:AY086622 EMBL:BT004187 EMBL:BT005393 IPI:IPI00548374 PIR:G84673 RefSeq:NP_180320.1 UniGene:At.38754 HSSP:P00248 ProteinModelPortal:Q9ZQG8 SMR:Q9ZQG8 STRING:Q9ZQG8 PRIDE:Q9ZQG8 EnsemblPlants:AT2G27510.1 GeneID:817297 KEGG:ath:AT2G27510 TAIR:At2g27510 InParanoid:Q9ZQG8 OMA:YPQSDCV PhylomeDB:Q9ZQG8 ProtClustDB:CLSN2913085 ArrayExpress:Q9ZQG8 Genevestigator:Q9ZQG8 Uniprot:Q9ZQG8
Root	Isotig05411	1	23	-4.653	5.84E-07	TAIR|locus:505006681 - symbol:DIR1 "AT5G48485" species:3702 "Arabidopsis thaliana" [GO:0006869 "lipid transport" evidence=ISS] [GO:0008289 "lipid binding" evidence=ISS] [GO:0005319 "lipid transporter activity" evidence=ISS] [GO:0009862 "systemic acquired resistance, salicylic acid mediated signaling pathway" evidence=IMP] [GO:0005504 "fatty acid binding" evidence=IDA] [GO:0008270 "zinc ion binding" evidence=IDA] InterPro:IPR013770 GO:GO:0048046 EMBL:CP002688 GenomeReviews:BA000015_GR InterPro:IPR016140 SMART:SM00499 SUPFAM:SSF47699 GO:GO:0008270 GO:GO:0006869 GO:GO:0005504 Gene3D:G3DSA:1.10.110.10 EMBL:AB020745 GO:GO:0009862 EMBL:AF342726 EMBL:AY062857 EMBL:BT006510 EMBL:AY085224 IPI:IPI00525511 RefSeq:NP_568699.1 UniGene:At.27209 PDB:2RKN PDBsum:2RKN ProteinModelPortal:Q8W453 SMR:Q8W453 PRIDE:Q8W453 EnsemblPlants:AT5G48485.1 GeneID:834904 KEGG:ath:AT5G48485 TAIR:At5g48485 eggNOG:NOG297830 InParanoid:Q8W453

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						OMA:NECKPAV PhylomeDB:Q8W453 ProtClustDB:CLSN2686599 Genevestigator:Q8W453 Pfam:PF14368 Uniprot:Q8W453
Root	Isotig05412	1	23	-4.653	5.84E-07	TAIR|locus:505006681 - symbol:DIR1 "AT5G48485" species:3702 "Arabidopsis thaliana" [GO:0006869 "lipid transport" evidence=ISS] [GO:0008289 "lipid binding" evidence=ISS] [GO:0005319 "lipid transporter activity" evidence=ISS] [GO:0009862 "systemic acquired resistance, salicylic acid mediated signaling pathway" evidence=IMP] [GO:0005504 "fatty acid binding" evidence=IDA] [GO:0008270 "zinc ion binding" evidence=IDA] InterPro:IPR013770 GO:GO:0048046 EMBL:CP002688 GenomeReviews:BA000015_GR InterPro:IPR016140 SMART:SM00499 SUPFAM:SSF47699 GO:GO:0008270 GO:GO:0006869 GO:GO:0005504 Gene3D:G3DSA:1.10.110.10 EMBL:AB020745 GO:GO:0009862 EMBL:AF342726 EMBL:AY062857 EMBL:BT006510 EMBL:AY085224 IPI:IPI00525511 RefSeq:NP_568699.1 UniGene:At.27209 PDB:2RKN PDBsum:2RKN ProteinModelPortal:Q8W453 SMR:Q8W453 PRIDE:Q8W453 EnsemblPlants:AT5G48485.1 GeneID:834904 KEGG:ath:AT5G48485 TAIR:At5g48485 eggNOG:NOG297830 InParanoid:Q8W453 OMA:NECKPAV PhylomeDB:Q8W453 ProtClustDB:CLSN2686599 Genevestigator:Q8W453 Pfam:PF14368 Uniprot:Q8W453
Root	Isotig05435	5	21	-2.199	0.000555521	TAIR|locus:2181823 - symbol:AT5G02570 species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=IEA;ISS] [GO:0006334 "nucleosome assembly" evidence=IEA] [GO:0005730 "nucleolus" evidence=IDA] InterPro:IPR000558 InterPro:IPR007125 InterPro:IPR009072 Pfam:PF00125 PRINTS:PR00621 PROSITE:PS00357 SMART:SM00427 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005730 GO:GO:0003677 Gene3D:G3DSA:1.10.20.10 SUPFAM:SSF47113 GO:GO:0006334 GO:GO:0000786 HOGENOM:HBG715487 EMBL:AL162971 eggNOG:NOG289161 KO:K11252 PANTHER:PTHR23428 OMA:RMPEPAK IPI:IPI00527484 PIR:T48278 RefSeq:NP_195877.1 UniGene:At.65481 ProteinModelPortal:Q9LZ45 SMR:Q9LZ45 PRIDE:Q9LZ45 EnsemblPlants:AT5G02570.1 GeneID:831878 KEGG:ath:AT5G02570 TAIR:At5g02570 InParanoid:Q9LZ45 PhylomeDB:Q9LZ45 ProtClustDB:CLSN2916781 Genevestigator:Q9LZ45 GermOnline:AT5G02570 Uniprot:Q9LZ45
Root	Isotig05436	5	21	-2.199	0.000555521	TAIR|locus:2181823 - symbol:AT5G02570 species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=IEA;ISS] [GO:0006334 "nucleosome assembly" evidence=IEA] [GO:0005730 "nucleolus" evidence=IDA] InterPro:IPR000558 InterPro:IPR007125 InterPro:IPR009072 Pfam:PF00125 PRINTS:PR00621 PROSITE:PS00357 SMART:SM00427 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005730 GO:GO:0003677 Gene3D:G3DSA:1.10.20.10 SUPFAM:SSF47113 GO:GO:0006334 GO:GO:0000786 HOGENOM:HBG715487 EMBL:AL162971 eggNOG:NOG289161 KO:K11252 PANTHER:PTHR23428 OMA:RMPEPAK IPI:IPI00527484 PIR:T48278 RefSeq:NP_195877.1 UniGene:At.65481 ProteinModelPortal:Q9LZ45 SMR:Q9LZ45 PRIDE:Q9LZ45 EnsemblPlants:AT5G02570.1 GeneID:831878 KEGG:ath:AT5G02570 TAIR:At5g02570 InParanoid:Q9LZ45 PhylomeDB:Q9LZ45 ProtClustDB:CLSN2916781 Genevestigator:Q9LZ45 GermOnline:AT5G02570 Uniprot:Q9LZ45
Root	Isotig05437	5	21	-2.199	0.000555521	TAIR|locus:2181823 - symbol:AT5G02570 species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=IEA;ISS] [GO:0006334 "nucleosome assembly" evidence=IEA] [GO:0005730 "nucleolus" evidence=IDA] InterPro:IPR000558 InterPro:IPR007125 InterPro:IPR009072 Pfam:PF00125 PRINTS:PR00621 PROSITE:PS00357 SMART:SM00427 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005730 GO:GO:0003677 Gene3D:G3DSA:1.10.20.10 SUPFAM:SSF47113 GO:GO:0006334 GO:GO:0000786 HOGENOM:HBG715487 EMBL:AL162971 eggNOG:NOG289161 KO:K11252 PANTHER:PTHR23428 OMA:RMPEPAK IPI:IPI00527484 PIR:T48278 RefSeq:NP_195877.1 UniGene:At.65481 ProteinModelPortal:Q9LZ45 SMR:Q9LZ45 PRIDE:Q9LZ45 EnsemblPlants:AT5G02570.1 GeneID:831878 KEGG:ath:AT5G02570 TAIR:At5g02570 InParanoid:Q9LZ45 PhylomeDB:Q9LZ45 ProtClustDB:CLSN2916781 Genevestigator:Q9LZ45 GermOnline:AT5G02570 Uniprot:Q9LZ45
Root	Isotig05506	27	6	2.041	0.000356109	TAIR|locus:2014736 - symbol:AT1G35660 "AT1G35660" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0005886 "plasma membrane" evidence=IDA] GenomeReviews:CT485782_GR GO:GO:0005886 EMBL:AC007887 eggNOG:NOG79617 IPI:IPI00544757 PIR:D86478 ProteinModelPortal:Q9LQH4 PRIDE:Q9LQH4 TAIR:At1g35660 HOGENOM:HBG591637 InParanoid:Q9LQH4 PhylomeDB:Q9LQH4 Genevestigator:Q9LQH4 Uniprot:Q9LQH4
Root	Isotig05507	26	6	1.987	0.000575837	TAIR|locus:2014736 - symbol:AT1G35660 "AT1G35660" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0005886 "plasma membrane" evidence=IDA] GenomeReviews:CT485782_GR GO:GO:0005886 EMBL:AC007887 eggNOG:NOG79617 IPI:IPI00544757 PIR:D86478 ProteinModelPortal:Q9LQH4 PRIDE:Q9LQH4 TAIR:At1g35660 HOGENOM:HBG591637 InParanoid:Q9LQH4 PhylomeDB:Q9LQH4 Genevestigator:Q9LQH4 Uniprot:Q9LQH4

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig05530	0	23	-5.653	3.32E-07	TAIR|locus:2195850 - symbol:AT1G51860 species:3702 "Arabidopsis thaliana" [GO:0006468 "protein phosphorylation" evidence=IEA] [GO:0016301 "kinase activity" evidence=ISS] Pfam:PF00560 InterPro:IPR001611 InterPro:IPR000719 InterPro:IPR001245 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 Pfam:PF07714 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005524 eggNOG:COG0515 GO:GO:0004872 SUPFAM:SSF56112 GO:GO:0004674 HOGENOM:HBG755340 InterPro:IPR024788 Pfam:PF12819 EMBL:AC015448 EMBL:FJ708653 IPI:IPI00532293 PIR:A96558 RefSeq:NP_175598.1 UniGene:At.52143 ProteinModelPortal:C0LGG4 SMR:C0LGG4 PRIDE:C0LGG4 EnsemblPlants:AT1G51860.1 GeneID:841613 KEGG:ath:AT1G51860 GeneFarm:343 TAIR:At1g51860 InParanoid:Q9FZB3 OMA:ERPHIND PhylomeDB:C0LGG4 ProtClustDB:CLSN2679439 Uniprot:C0LGG4
Root	Isotig05531	0	16	-5.129	2.34E-05	TAIR|locus:2089483 - symbol:AT3G21340 species:3702 "Arabidopsis thaliana" [GO:0006468 "protein phosphorylation" evidence=IEA] [GO:0016301 "kinase activity" evidence=ISS] InterPro:IPR000719 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 Pfam:PF00069 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 GO:GO:0016021 GO:GO:0005886 GO:GO:0005524 EMBL:CP002686 GenomeReviews:BA000014_GR eggNOG:COG0515 GO:GO:0004714 SUPFAM:SSF56112 GO:GO:0004674 HOGENOM:HBG755340 EMBL:AP001305 InterPro:IPR024788 Pfam:PF12819 EMBL:FJ708725 IPI:IPI00518645 RefSeq:NP_188771.2 UniGene:At.38075 ProteinModelPortal:Q9LIG2 SMR:Q9LIG2 IntAct:Q9LIG2 PRIDE:Q9LIG2 EnsemblPlants:AT3G21340.1 GeneID:821688 KEGG:ath:AT3G21340 GeneFarm:418 TAIR:At3g21340 InParanoid:Q9LIG2 PhylomeDB:Q9LIG2 Genevestigator:Q9LIG2 Uniprot:Q9LIG2
Root	Isotig05533	5	22	-2.266	0.000318925	TAIR|locus:2064712 - symbol:RIPK "AT2G05940" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0016301 "kinase activity" evidence=ISS] [GO:0004674 "protein serine/threonine kinase activity" evidence=IDA] [GO:0042742 "defense response to bacterium" evidence=IMP] InterPro:IPR000719 InterPro:IPR001245 InterPro:IPR008271 InterPro:IPR011009 Pfam:PF07714 PROSITE:PS00108 PROSITE:PS50011 GO:GO:0005524 GO:GO:0042742 EMBL:CP002685 GenomeReviews:CT485783_GR eggNOG:COG0515 SUPFAM:SSF56112 GO:GO:0004674 HOGENOM:HBG755340 EMBL:AC005970 EMBL:AY056245 EMBL:AY113963 IPI:IPI00547996 PIR:C84473 RefSeq:NP_178651.1 UniGene:At.23011 ProteinModelPortal:Q9ZUF4 SMR:Q9ZUF4 STRING:Q9ZUF4 PRIDE:Q9ZUF4 EnsemblPlants:AT2G05940.1 GeneID:815147 KEGG:ath:AT2G05940 TAIR:At2g05940 InParanoid:Q9ZUF4 OMA:MLNDPRK PhylomeDB:Q9ZUF4 ProtClustDB:CLSN2912989 ArrayExpress:Q9ZUF4 Genevestigator:Q9ZUF4 Uniprot:Q9ZUF4
Root	Isotig05534	5	22	-2.266	0.000318925	TAIR|locus:2064712 - symbol:RIPK "AT2G05940" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0016301 "kinase activity" evidence=ISS] [GO:0004674 "protein serine/threonine kinase activity" evidence=IDA] [GO:0042742 "defense response to bacterium" evidence=IMP] InterPro:IPR000719 InterPro:IPR001245 InterPro:IPR008271 InterPro:IPR011009 Pfam:PF07714 PROSITE:PS00108 PROSITE:PS50011 GO:GO:0005524 GO:GO:0042742 EMBL:CP002685 GenomeReviews:CT485783_GR eggNOG:COG0515 SUPFAM:SSF56112 GO:GO:0004674 HOGENOM:HBG755340 EMBL:AC005970 EMBL:AY056245 EMBL:AY113963 IPI:IPI00547996 PIR:C84473 RefSeq:NP_178651.1 UniGene:At.23011 ProteinModelPortal:Q9ZUF4 SMR:Q9ZUF4 STRING:Q9ZUF4 PRIDE:Q9ZUF4 EnsemblPlants:AT2G05940.1 GeneID:815147 KEGG:ath:AT2G05940 TAIR:At2g05940 InParanoid:Q9ZUF4 OMA:MLNDPRK PhylomeDB:Q9ZUF4 ProtClustDB:CLSN2912989 ArrayExpress:Q9ZUF4 Genevestigator:Q9ZUF4 Uniprot:Q9ZUF4
Root	Isotig05535	5	22	-2.266	0.000318925	TAIR|locus:2064712 - symbol:RIPK "AT2G05940" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0016301 "kinase activity" evidence=ISS] [GO:0004674 "protein serine/threonine kinase activity" evidence=IDA] [GO:0042742 "defense response to bacterium" evidence=IMP] InterPro:IPR000719 InterPro:IPR001245 InterPro:IPR008271 InterPro:IPR011009 Pfam:PF07714 PROSITE:PS00108 PROSITE:PS50011 GO:GO:0005524 GO:GO:0042742 EMBL:CP002685 GenomeReviews:CT485783_GR eggNOG:COG0515 SUPFAM:SSF56112 GO:GO:0004674 HOGENOM:HBG755340 EMBL:AC005970 EMBL:AY056245 EMBL:AY113963 IPI:IPI00547996 PIR:C84473 RefSeq:NP_178651.1 UniGene:At.23011 ProteinModelPortal:Q9ZUF4 SMR:Q9ZUF4 STRING:Q9ZUF4 PRIDE:Q9ZUF4 EnsemblPlants:AT2G05940.1 GeneID:815147 KEGG:ath:AT2G05940 TAIR:At2g05940 InParanoid:Q9ZUF4 OMA:MLNDPRK PhylomeDB:Q9ZUF4 ProtClustDB:CLSN2912989 ArrayExpress:Q9ZUF4 Genevestigator:Q9ZUF4 Uniprot:Q9ZUF4

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig05536	2	78	-5.414	6.38E-21	TAIR|locus:2168988 - symbol:TDT "AT5G47560" species:3702 "Arabidopsis thaliana" [GO:0006814 "sodium ion transport" evidence=ISS] [GO:0006835 "dicarboxylic acid transport" evidence=ISS] [GO:0017153 "sodium:dicarboxylate symporter activity" evidence=ISS] [GO:0005773 "vacuole" evidence=IDA] [GO:0015140 "malate transmembrane transporter activity" evidence=IMP;IDA] [GO:0015743 "malate transport" evidence=TAS] [GO:0051453 "regulation of intracellular pH" evidence=TAS] InterPro:IPR001898 Pfam:PF00939 GO:GO:0016021 GO:GO:0005774 EMBL:CP002688 GenomeReviews:BA000015_GR EMBL:AB025628 GO:GO:0006814 GO:GO:0015140 GO:GO:0051453 eggNOG:COG0471 TIGRFAMs:TIGR00785 KO:K14445 HOGENOM:HBG616159 EMBL:AJ223445 EMBL:AB043024 EMBL:AY072145 EMBL:AY133792 EMBL:AY084408 IPI:IPI00534224 RefSeq:NP_199567.1 UniGene:At.21038 UniGene:At.68515 UniGene:At.71618 STRING:Q8LG88 TCDB:2.A.47.1.6 PRIDE:Q8LG88 EnsemblPlants:AT5G47560.1 GeneID:834806 KEGG:ath:AT5G47560 GeneFarm:4980 TAIR:At5g47560 InParanoid:Q8LG88 OMA:TECMPLA PhylomeDB:Q8LG88 ProtClustDB:CLSN2686388 ArrayExpress:Q9MAW4 Genevestigator:Q8LG88 GermOnline:AT5G47560 Uniprot:Q8LG88
Root	Isotig05537	2	77	-5.396	1.15E-20	TAIR|locus:2168988 - symbol:TDT "AT5G47560" species:3702 "Arabidopsis thaliana" [GO:0006814 "sodium ion transport" evidence=ISS] [GO:0006835 "dicarboxylic acid transport" evidence=ISS] [GO:0017153 "sodium:dicarboxylate symporter activity" evidence=ISS] [GO:0005773 "vacuole" evidence=IDA] [GO:0015140 "malate transmembrane transporter activity" evidence=IMP;IDA] [GO:0015743 "malate transport" evidence=TAS] [GO:0051453 "regulation of intracellular pH" evidence=TAS] InterPro:IPR001898 Pfam:PF00939 GO:GO:0016021 GO:GO:0005774 EMBL:CP002688 GenomeReviews:BA000015_GR EMBL:AB025628 GO:GO:0006814 GO:GO:0015140 GO:GO:0051453 eggNOG:COG0471 TIGRFAMs:TIGR00785 KO:K14445 HOGENOM:HBG616159 EMBL:AJ223445 EMBL:AB043024 EMBL:AY072145 EMBL:AY133792 EMBL:AY084408 IPI:IPI00534224 RefSeq:NP_199567.1 UniGene:At.21038 UniGene:At.68515 UniGene:At.71618 STRING:Q8LG88 TCDB:2.A.47.1.6 PRIDE:Q8LG88 EnsemblPlants:AT5G47560.1 GeneID:834806 KEGG:ath:AT5G47560 GeneFarm:4980 TAIR:At5g47560 InParanoid:Q8LG88 OMA:TECMPLA PhylomeDB:Q8LG88 ProtClustDB:CLSN2686388 ArrayExpress:Q9MAW4 Genevestigator:Q8LG88 GermOnline:AT5G47560 Uniprot:Q8LG88
Root	Isotig05538	2	64	-5.129	2.68E-17	TAIR|locus:2168988 - symbol:TDT "AT5G47560" species:3702 "Arabidopsis thaliana" [GO:0006814 "sodium ion transport" evidence=ISS] [GO:0006835 "dicarboxylic acid transport" evidence=ISS] [GO:0017153 "sodium:dicarboxylate symporter activity" evidence=ISS] [GO:0005773 "vacuole" evidence=IDA] [GO:0015140 "malate transmembrane transporter activity" evidence=IMP;IDA] [GO:0015743 "malate transport" evidence=TAS] [GO:0051453 "regulation of intracellular pH" evidence=TAS] InterPro:IPR001898 Pfam:PF00939 GO:GO:0016021 GO:GO:0005774 EMBL:CP002688 GenomeReviews:BA000015_GR EMBL:AB025628 GO:GO:0006814 GO:GO:0015140 GO:GO:0051453 eggNOG:COG0471 TIGRFAMs:TIGR00785 KO:K14445 HOGENOM:HBG616159 EMBL:AJ223445 EMBL:AB043024 EMBL:AY072145 EMBL:AY133792 EMBL:AY084408 IPI:IPI00534224 RefSeq:NP_199567.1 UniGene:At.21038 UniGene:At.68515 UniGene:At.71618 STRING:Q8LG88 TCDB:2.A.47.1.6 PRIDE:Q8LG88 EnsemblPlants:AT5G47560.1 GeneID:834806 KEGG:ath:AT5G47560 GeneFarm:4980 TAIR:At5g47560 InParanoid:Q8LG88 OMA:TECMPLA PhylomeDB:Q8LG88 ProtClustDB:CLSN2686388 ArrayExpress:Q9MAW4 Genevestigator:Q8LG88 GermOnline:AT5G47560 Uniprot:Q8LG88
Root	Isotig05542	54	7	2.819	1.10E-09	TAIR|locus:2005543 - symbol:TSB2 "AT4G27070" species:3702 "Arabidopsis thaliana" [GO:0000162 "tryptophan biosynthetic process" evidence=TAS] [GO:0004834 "tryptophan synthase activity" evidence=ISS;IMP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] InterPro:IPR001926 InterPro:IPR006653 InterPro:IPR006654 InterPro:IPR023026 Pfam:PF00291 PIRSF:PIRSF001413 PROSITE:PS00168 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0009570 GO:GO:0030170 SUPFAM:SSF53686 EMBL:AL035680 EMBL:AL161566 GO:GO:0009941 EMBL:M81620 EMBL:BT003144 EMBL:AY084334 IPI:IPI00547656 PIR:JQ1073 PIR:T06037 RefSeq:NP_194437.1 UniGene:At.327 ProteinModelPortal:P25269 SMR:P25269 STRING:P25269 PRIDE:P25269 EnsemblPlants:AT4G27070.1 GeneID:828815 KEGG:ath:AT4G27070 TAIR:At4g27070 eggNOG:COG0133 HOGENOM:HBG303148 InParanoid:P25269 KO:K01696 OMA:IMVINLS PhylomeDB:P25269 ProtClustDB:PLN02618 ArrayExpress:P25269 Genevestigator:P25269 GermOnline:AT4G27070 GO:GO:0004834 PANTHER:PTHR10314:SF3 TIGRFAMs:TIGR00263 Uniprot:P25269

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig05543	49	8	2.486	5.83E-08	TAIR|locus:2005543 - symbol:TSB2 "AT4G27070" species:3702 "Arabidopsis thaliana" [GO:0000162 "tryptophan biosynthetic process" evidence=TAS] [GO:0004834 "tryptophan synthase activity" evidence=ISS;IMP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] InterPro:IPR001926 InterPro:IPR006653 InterPro:IPR006654 InterPro:IPR023026 Pfam:PF00291 PIRSF:PIRSF001413 PROSITE:PS00168 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0009570 GO:GO:0030170 SUPFAM:SSF53686 EMBL:AL035680 EMBL:AL161566 GO:GO:0009941 EMBL:M81620 EMBL:BT003144 EMBL:AY084334 IPI:IPI00547656 PIR:JQ1073 PIR:T06037 RefSeq:NP_194437.1 UniGene:At.327 ProteinModelPortal:P25269 SMR:P25269 STRING:P25269 PRIDE:P25269 EnsemblPlants:AT4G27070.1 GeneID:828815 KEGG:ath:AT4G27070 TAIR:At4g27070 eggNOG:COG0133 HOGENOM:HBG303148 InParanoid:P25269 KO:K01696 OMA:IMVINLS PhylomeDB:P25269 ProtClustDB:PLN02618 ArrayExpress:P25269 Genevestigator:P25269 GermOnline:AT4G27070 GO:GO:0004834 PANTHER:PTHR10314:SF3 TIGRFAMs:TIGR00263 Uniprot:P25269
Root	Isotig05544	41	7	2.421	1.02E-06	TAIR|locus:2005543 - symbol:TSB2 "AT4G27070" species:3702 "Arabidopsis thaliana" [GO:0000162 "tryptophan biosynthetic process" evidence=TAS] [GO:0004834 "tryptophan synthase activity" evidence=ISS;IMP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] InterPro:IPR001926 InterPro:IPR006653 InterPro:IPR006654 InterPro:IPR023026 Pfam:PF00291 PIRSF:PIRSF001413 PROSITE:PS00168 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0009570 GO:GO:0030170 SUPFAM:SSF53686 EMBL:AL035680 EMBL:AL161566 GO:GO:0009941 EMBL:M81620 EMBL:BT003144 EMBL:AY084334 IPI:IPI00547656 PIR:JQ1073 PIR:T06037 RefSeq:NP_194437.1 UniGene:At.327 ProteinModelPortal:P25269 SMR:P25269 STRING:P25269 PRIDE:P25269 EnsemblPlants:AT4G27070.1 GeneID:828815 KEGG:ath:AT4G27070 TAIR:At4g27070 eggNOG:COG0133 HOGENOM:HBG303148 InParanoid:P25269 KO:K01696 OMA:IMVINLS PhylomeDB:P25269 ProtClustDB:PLN02618 ArrayExpress:P25269 Genevestigator:P25269 GermOnline:AT4G27070 GO:GO:0004834 PANTHER:PTHR10314:SF3 TIGRFAMs:TIGR00263 Uniprot:P25269
Root	Isotig05560	32	1	4.871	1.34E-08	TAIR|locus:2030230 - symbol:HAB1 "AT1G72770" species:3702 "Arabidopsis thaliana" [GO:0004722 "protein serine/threonine phosphatase activity" evidence=ISS;IDA] [GO:0006470 "protein dephosphorylation" evidence=IEA] [GO:0008287 "protein serine/threonine phosphatase complex" evidence=IEA] [GO:0005515 "protein binding" evidence=IPI] InterPro:IPR000222 InterPro:IPR001932 Pfam:PF00481 PROSITE:PS01032 SMART:SM00331 SMART:SM00332 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005634 GO:GO:0005737 GO:GO:0005515 GO:GO:0006470 GO:GO:0009738 GO:GO:0004722 GO:GO:0046872 EMBL:AC010926 eggNOG:COG0631 Gene3D:G3DSA:3.60.40.10 SUPFAM:SSF81606 GO:GO:0008287 InterPro:IPR015655 PANTHER:PTHR13832 HOGENOM:HBG747569 ProtClustDB:CLSN2679602 EMBL:AJ003119 EMBL:BT015409 EMBL:AK230171 EMBL:AK318665 IPI:IPI00538917 IPI:IPI00846864 PIR:F96752 RefSeq:NP_001077815.1 RefSeq:NP_001185385.1 RefSeq:NP_177421.1 UniGene:At.46635 UniGene:At.67356 PDB:3KB3 PDB:3NMT PDB:3QN1 PDB:3RT0 PDBsum:3KB3 PDBsum:3NMT PDBsum:3QN1 PDBsum:3RT0 ProteinModelPortal:Q9CAJ0 SMR:Q9CAJ0 DIP:DIP-48988N IntAct:Q9CAJ0 STRING:Q9CAJ0 PRIDE:Q9CAJ0 EnsemblPlants:AT1G72770.1 EnsemblPlants:AT1G72770.3 GeneID:843609 KEGG:ath:AT1G72770 TAIR:At1g72770 InParanoid:Q9CAJ0 OMA:YARIENA PhylomeDB:Q9CAJ0 Genevestigator:Q9CAJ0 Uniprot:Q9CAJ0
Root	Isotig05561	23	0	5.395	1.11E-06	TAIR|locus:2007943 - symbol:HAB2 "homology to ABI2" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004722 "protein serine/threonine phosphatase activity" evidence=IEA;ISS] [GO:0006470 "protein dephosphorylation" evidence=IEA] InterPro:IPR000222 InterPro:IPR001932 Pfam:PF00481 PROSITE:PS01032 SMART:SM00331 SMART:SM00332 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0006470 GO:GO:0009738 GO:GO:0004722 GO:GO:0046872 EMBL:AC022492 eggNOG:COG0631 Gene3D:G3DSA:3.60.40.10 SUPFAM:SSF81606 GO:GO:0008287 InterPro:IPR015655 PANTHER:PTHR13832 HSSP:P35813 HOGENOM:HBG747569 KO:K14497 EMBL:AK118656 IPI:IPI00532752 RefSeq:NP_173199.2 UniGene:At.41827 ProteinModelPortal:Q9LNP9 SMR:Q9LNP9 DIP:DIP-48989N PRIDE:Q9LNP9 EnsemblPlants:AT1G17550.1 GeneID:838330 KEGG:ath:AT1G17550 TAIR:At1g17550 InParanoid:Q8GWS8 OMA:RRILAWH PhylomeDB:Q9LNP9 ProtClustDB:CLSN2679602 Genevestigator:Q9LNP9 Uniprot:Q9LNP9
Root	Isotig05562	20	1	4.193	1.37E-05	TAIR|locus:2030230 - symbol:HAB1 "AT1G72770" species:3702 "Arabidopsis thaliana" [GO:0004722 "protein serine/threonine phosphatase activity" evidence=ISS;IDA] [GO:0006470 "protein dephosphorylation" evidence=IEA] [GO:0008287 "protein serine/threonine phosphatase complex" evidence=IEA] [GO:0005515 "protein binding" evidence=IPI] InterPro:IPR000222 InterPro:IPR001932 Pfam:PF00481 PROSITE:PS01032 SMART:SM00331

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						SMART:SM00332 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005634 GO:GO:0005737 GO:GO:0005515 GO:GO:0006470 GO:GO:0009738 GO:GO:0004722 GO:GO:0046872 EMBL:AC010926 eggNOG:COG0631 Gene3D:G3DSA:3.60.40.10 SUPFAM:SSF81606 GO:GO:0008287 InterPro:IPR015655 PANTHER:PTHR13832 HOGENOM:HBG747569 ProtClustDB:CLSN2679602 EMBL:AJ003119 EMBL:BT015409 EMBL:AK230171 EMBL:AK318665 IPI:IPI00538917 IPI:IPI00846864 PIR:F96752 RefSeq:NP_001077815.1 RefSeq:NP_001185385.1 RefSeq:NP_177421.1 UniGene:At.46635 UniGene:At.67356 PDB:3KB3 PDB:3NMT PDB:3QN1 PDB:3RT0 PDBsum:3KB3 PDBsum:3NMT PDBsum:3QN1 PDBsum:3RT0 ProteinModelPortal:Q9CAJ0 SMR:Q9CAJ0 DIP:DIP-48988N IntAct:Q9CAJ0 STRING:Q9CAJ0 PRIDE:Q9CAJ0 EnsemblPlants:AT1G72770.1 EnsemblPlants:AT1G72770.3 GeneID:843609 KEGG:ath:AT1G72770 TAIR:At1g72770 InParanoid:Q9CAJ0 OMA:YARIENA PhylomeDB:Q9CAJ0 Genevestigator:Q9CAJ0 Uniprot:Q9CAJ0
Root	Isotig05574	9	39	-2.244	1.90E-06	No hit
Root	Isotig05581	9	27	-1.714	0.000905257	No hit
Root	Isotig05583	4	20	-2.451	0.000325095	No hit
Root	Isotig05613	13	1	3.571	0.000882483	TAIR|locus:2091117 - symbol:IBM1 "AT3G07610" species:3702 "Arabidopsis thaliana" [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0005575 "cellular_component" evidence=ND] [GO:0009555 "pollen development" evidence=IMP] [GO:0009908 "flower development" evidence=IMP] [GO:0032454 "histone demethylase activity (H3-K9 specific)" evidence=ISS] [GO:0032776 "DNA methylation on cytosine" evidence=IGI;IMP] [GO:0033169 "histone H3-K9 demethylation" evidence=IGI;IMP] [GO:0048366 "leaf development" evidence=IMP] InterPro:IPR003347 Pfam:PF02373 PROSITE:PS51184 SMART:SM00558 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0009555 GO:GO:0048366 GO:GO:0009908 EMBL:AC009176 GO:GO:0033169 InterPro:IPR013129 HOGENOM:HBG633312 IPI:IPI00530050 RefSeq:NP_187418.1 UniGene:At.18334 ProteinModelPortal:Q9SSE9 STRING:Q9SSE9 PRIDE:Q9SSE9 EnsemblPlants:AT3G07610.1 GeneID:819952 KEGG:ath:AT3G07610 TAIR:At3g07610 InParanoid:Q9SSE9 OMA:PDDKPKG PhylomeDB:Q9SSE9 ProtClustDB:CLSN2684849 Genevestigator:Q9SSE9 GO:GO:0032776 Uniprot:Q9SSE9
Root	Isotig05614	15	1	3.778	0.000266457	TAIR|locus:2091117 - symbol:IBM1 "AT3G07610" species:3702 "Arabidopsis thaliana" [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0005575 "cellular_component" evidence=ND] [GO:0009555 "pollen development" evidence=IMP] [GO:0009908 "flower development" evidence=IMP] [GO:0032454 "histone demethylase activity (H3-K9 specific)" evidence=ISS] [GO:0032776 "DNA methylation on cytosine" evidence=IGI;IMP] [GO:0033169 "histone H3-K9 demethylation" evidence=IGI;IMP] [GO:0048366 "leaf development" evidence=IMP] InterPro:IPR003347 Pfam:PF02373 PROSITE:PS51184 SMART:SM00558 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0009555 GO:GO:0048366 GO:GO:0009908 EMBL:AC009176 GO:GO:0033169 InterPro:IPR013129 HOGENOM:HBG633312 IPI:IPI00530050 RefSeq:NP_187418.1 UniGene:At.18334 ProteinModelPortal:Q9SSE9 STRING:Q9SSE9 PRIDE:Q9SSE9 EnsemblPlants:AT3G07610.1 GeneID:819952 KEGG:ath:AT3G07610 TAIR:At3g07610 InParanoid:Q9SSE9 OMA:PDDKPKG PhylomeDB:Q9SSE9 ProtClustDB:CLSN2684849 Genevestigator:Q9SSE9 GO:GO:0032776 Uniprot:Q9SSE9
Root	Isotig05634	15	44	-1.682	2.92E-05	TAIR|locus:2043844 - symbol:SPX2 "AT2G26660" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005634 "nucleus" evidence=IDA] [GO:0016036 "cellular response to phosphate starvation" evidence=IEP] GO:GO:0005634 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0016036 EMBL:AC003105 InterPro:IPR004331 Pfam:PF03105 PROSITE:PS51382 ProtClustDB:CLSN2683415 EMBL:AK118537 EMBL:BT003688 IPI:IPI00529925 PIR:C84663 RefSeq:NP_180234.1 UniGene:At.38863 PRIDE:O48781 EnsemblPlants:AT2G26660.1 GeneID:817207 KEGG:ath:AT2G26660 TAIR:At2g26660 eggNOG:NOG311509 HOGENOM:HBG593729 InParanoid:O48781 OMA:EMINIKK PhylomeDB:O48781 Genevestigator:O48781 Uniprot:O48781
Root	Isotig05635	10	35	-1.936	4.01E-05	TAIR|locus:2149254 - symbol:SPX1 "AT5G20150" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005634 "nucleus" evidence=IDA] [GO:0016036 "cellular response to phosphate starvation" evidence=IEP] [GO:0080040 "positive regulation of cellular response to phosphate starvation" evidence=IMP] GO:GO:0005634 EMBL:CP002688 GenomeReviews:BA000015_GR EMBL:AF296825 InterPro:IPR004331 Pfam:PF03105 PROSITE:PS51382 EMBL:AY075605 EMBL:BT000868 EMBL:AY087206 IPI:IPI00537462 RefSeq:NP_197515.1 UniGene:At.19659 IntAct:Q8LBH4 STRING:Q8LBH4 PRIDE:Q8LBH4 DNASU:832137 EnsemblPlants:AT5G20150.1 GeneID:832137 KEGG:ath:AT5G20150 TAIR:At5g20150

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						eggNOG:NOG289536 InParanoid:Q8RY68 OMA:NGLDETW PhylomeDB:Q8LBH4 ProtClustDB:CLSN2683415 Genevestigator:Q8LBH4 Uniprot:Q8LBH4
Root	Isotig05636	14	40	-1.644	8.83E-05	TAIR|locus:2043844 - symbol:SPX2 "AT2G26660" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005634 "nucleus" evidence=IDA] [GO:0016036 "cellular response to phosphate starvation" evidence=IEP] GO:GO:0005634 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0016036 EMBL:AC003105 InterPro:IPR004331 Pfam:PF03105 PROSITE:PS51382 ProtClustDB:CLSN2683415 EMBL:AK118537 EMBL:BT003688 IPI:IPI00529925 PIR:C84663 RefSeq:NP_180234.1 UniGene:At.38863 PRIDE:O48781 EnsemblPlants:AT2G26660.1 GeneID:817207 KEGG:ath:AT2G26660 TAIR:At2g26660 eggNOG:NOG311509 HOGENOM:HBG593729 InParanoid:O48781 OMA:EMINIKK PhylomeDB:O48781 Genevestigator:O48781 Uniprot:O48781
Root	Isotig05649	2	22	-3.588	5.84E-06	TAIR|locus:2181082 - symbol:AT5G01750 "AT5G01750" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0009507 "chloroplast" evidence=IDA] INTERPRO:IPR000007 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009507 EMBL:AL162351 InterPro:IPR007612 Pfam:PF04525 SUPFAM:SSF54518 HOGENOM:HBG595263 EMBL:AF372877 EMBL:AY142034 EMBL:AY085369 IPI:IPI00516693 IPI:IPI00533737 PIR:T48196 RefSeq:NP_568095.1 RefSeq:NP_850751.1 UniGene:At.21392 PDB:1ZXU PDB:2Q4M PDBsum:1ZXU PDBsum:2Q4M ProteinModelPortal:Q9LZX1 SMR:Q9LZX1 IntAct:Q9LZX1 STRING:Q9LZX1 PRIDE:Q9LZX1 DNASU:831684 EnsemblPlants:AT5G01750.2 GeneID:831684 KEGG:ath:AT5G01750 TAIR:At5g01750 eggNOG:NOG242955 InParanoid:Q9LZX1 OMA:QMHRKHT PhylomeDB:Q9LZX1 ProtClustDB:CLSN2689401 Genevestigator:Q9LZX1 GermOnline:AT5G01750 Uniprot:Q9LZX1
Root	Isotig05650	2	22	-3.588	5.84E-06	TAIR|locus:2181082 - symbol:AT5G01750 "AT5G01750" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0009507 "chloroplast" evidence=IDA] INTERPRO:IPR000007 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009507 EMBL:AL162351 InterPro:IPR007612 Pfam:PF04525 SUPFAM:SSF54518 HOGENOM:HBG595263 EMBL:AF372877 EMBL:AY142034 EMBL:AY085369 IPI:IPI00516693 IPI:IPI00533737 PIR:T48196 RefSeq:NP_568095.1 RefSeq:NP_850751.1 UniGene:At.21392 PDB:1ZXU PDB:2Q4M PDBsum:1ZXU PDBsum:2Q4M ProteinModelPortal:Q9LZX1 SMR:Q9LZX1 IntAct:Q9LZX1 STRING:Q9LZX1 PRIDE:Q9LZX1 DNASU:831684 EnsemblPlants:AT5G01750.2 GeneID:831684 KEGG:ath:AT5G01750 TAIR:At5g01750 eggNOG:NOG242955 InParanoid:Q9LZX1 OMA:QMHRKHT PhylomeDB:Q9LZX1 ProtClustDB:CLSN2689401 Genevestigator:Q9LZX1 GermOnline:AT5G01750 Uniprot:Q9LZX1
Root	Isotig05651	2	22	-3.588	5.84E-06	TAIR|locus:2181082 - symbol:AT5G01750 "AT5G01750" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0009507 "chloroplast" evidence=IDA] INTERPRO:IPR000007 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009507 EMBL:AL162351 InterPro:IPR007612 Pfam:PF04525 SUPFAM:SSF54518 HOGENOM:HBG595263 EMBL:AF372877 EMBL:AY142034 EMBL:AY085369 IPI:IPI00516693 IPI:IPI00533737 PIR:T48196 RefSeq:NP_568095.1 RefSeq:NP_850751.1 UniGene:At.21392 PDB:1ZXU PDB:2Q4M PDBsum:1ZXU PDBsum:2Q4M ProteinModelPortal:Q9LZX1 SMR:Q9LZX1 IntAct:Q9LZX1 STRING:Q9LZX1 PRIDE:Q9LZX1 DNASU:831684 EnsemblPlants:AT5G01750.2 GeneID:831684 KEGG:ath:AT5G01750 TAIR:At5g01750 eggNOG:NOG242955 InParanoid:Q9LZX1 OMA:QMHRKHT PhylomeDB:Q9LZX1 ProtClustDB:CLSN2689401 Genevestigator:Q9LZX1 GermOnline:AT5G01750 Uniprot:Q9LZX1
Root	Isotig05658	0	83	-7.504	9.65E-21	TAIR|locus:2009769 - symbol:AT1G65870 "AT1G65870" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0006952 "defense response" evidence=ISS] [GO:0009807 "lignan biosynthetic process" evidence=ISS] [GO:0005618 "cell wall" evidence=IDA] Pfam:PF03018 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005618 EMBL:AC009513 InterPro:IPR004265 HOGENOM:HBG605442 IPI:IPI00539166 PIR:G96682 RefSeq:NP_176762.1 UniGene:At.66110 EnsemblPlants:AT1G65870.1 GeneID:842898 KEGG:ath:AT1G65870 TAIR:At1g65870 eggNOG:NOG288717 InParanoid:Q9SS03 OMA:ATVEYNI PhylomeDB:Q9SS03 Genevestigator:Q9SS03 Uniprot:Q9SS03
Root	Isotig05659	0	20	-5.451	2.00E-06	TAIR|locus:2009769 - symbol:AT1G65870 "AT1G65870" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0006952 "defense response" evidence=ISS] [GO:0009807 "lignan biosynthetic process" evidence=ISS] [GO:0005618 "cell wall" evidence=IDA] Pfam:PF03018 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005618 EMBL:AC009513 InterPro:IPR004265 HOGENOM:HBG605442 IPI:IPI00539166 PIR:G96682 RefSeq:NP_176762.1 UniGene:At.66110 EnsemblPlants:AT1G65870.1

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GeneID:842898 KEGG:ath:AT1G65870 TAIR:At1g65870 eggNOG:NOG288717 InParanoid:Q9SS03 OMA:ATVEYNI PhylomeDB:Q9SS03 Genevestigator:Q9SS03 Uniprot:Q9SS03
Root	Isotig05660	0	85	-7.538	3.78E-21	TAIR|locus:2009769 - symbol:AT1G65870 "AT1G65870" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0006952 "defense response" evidence=ISS] [GO:0009807 "lignan biosynthetic process" evidence=ISS] [GO:0005618 "cell wall" evidence=IDA] Pfam:PF03018 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005618 EMBL:AC009513 InterPro:IPR004265 HOGENOM:HBG605442 IPI:IPI00539166 PIR:G96682 RefSeq:NP_176762.1 UniGene:At.66110 EnsemblPlants:AT1G65870.1 GeneID:842898 KEGG:ath:AT1G65870 TAIR:At1g65870 eggNOG:NOG288717 InParanoid:Q9SS03 OMA:ATVEYNI PhylomeDB:Q9SS03 Genevestigator:Q9SS03 Uniprot:Q9SS03
Root	Isotig05712	0	19	-5.377	3.67E-06	TAIR|locus:4010713753 - symbol:AT3G17675 species:3702 "Arabidopsis thaliana" [GO:0005507 "copper ion binding" evidence=IEA] [GO:0009055 "electron carrier activity" evidence=IEA] InterPro:IPR003245 Pfam:PF02298 ProDom:PD003122 PROSITE:PS51485 GenomeReviews:BA000014_GR GO:GO:0009055 GO:GO:0005507 EMBL:AB022219 InterPro:IPR008972 Gene3D:G3DSA:2.60.40.420 SUPFAM:SSF49503 HOGENOM:HBG748847 HSSP:P29602 IPI:IPI00534093 ProteinModelPortal:Q9LUM8 SMR:Q9LUM8 PRIDE:Q9LUM8 TAIR:At3g17675 eggNOG:NOG261136 PhylomeDB:Q9LUM8 Genevestigator:Q9LUM8 Uniprot:Q9LUM8
Root	Isotig05713	0	18	-5.299	6.77E-06	TAIR|locus:4010713753 - symbol:AT3G17675 species:3702 "Arabidopsis thaliana" [GO:0005507 "copper ion binding" evidence=IEA] [GO:0009055 "electron carrier activity" evidence=IEA] InterPro:IPR003245 Pfam:PF02298 ProDom:PD003122 PROSITE:PS51485 GenomeReviews:BA000014_GR GO:GO:0009055 GO:GO:0005507 EMBL:AB022219 InterPro:IPR008972 Gene3D:G3DSA:2.60.40.420 SUPFAM:SSF49503 HOGENOM:HBG748847 HSSP:P29602 IPI:IPI00534093 ProteinModelPortal:Q9LUM8 SMR:Q9LUM8 PRIDE:Q9LUM8 TAIR:At3g17675 eggNOG:NOG261136 PhylomeDB:Q9LUM8 Genevestigator:Q9LUM8 Uniprot:Q9LUM8
Root	Isotig05714	0	18	-5.299	6.77E-06	TAIR|locus:4010713753 - symbol:AT3G17675 species:3702 "Arabidopsis thaliana" [GO:0005507 "copper ion binding" evidence=IEA] [GO:0009055 "electron carrier activity" evidence=IEA] InterPro:IPR003245 Pfam:PF02298 ProDom:PD003122 PROSITE:PS51485 GenomeReviews:BA000014_GR GO:GO:0009055 GO:GO:0005507 EMBL:AB022219 InterPro:IPR008972 Gene3D:G3DSA:2.60.40.420 SUPFAM:SSF49503 HOGENOM:HBG748847 HSSP:P29602 IPI:IPI00534093 ProteinModelPortal:Q9LUM8 SMR:Q9LUM8 PRIDE:Q9LUM8 TAIR:At3g17675 eggNOG:NOG261136 PhylomeDB:Q9LUM8 Genevestigator:Q9LUM8 Uniprot:Q9LUM8
Root	Isotig05718	0	16	-5.129	2.34E-05	TAIR|locus:2143651 - symbol:HTA7 "histone H2A 7" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=IEA;ISS] [GO:0006334 "nucleosome assembly" evidence=IEA] [GO:0005730 "nucleolus" evidence=IDA] InterPro:IPR002119 InterPro:IPR007125 InterPro:IPR009072 Pfam:PF00125 PRINTS:PR00620 PROSITE:PS00046 SMART:SM00414 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005730 GO:GO:0003677 Gene3D:G3DSA:1.10.20.10 SUPFAM:SSF47113 EMBL:AC007478 GO:GO:0006334 GO:GO:0000786 EMBL:AC069556 eggNOG:COG5262 HOGENOM:HBG610736 KO:K11251 EMBL:AF385711 EMBL:AY078019 IPI:IPI00533679 RefSeq:NP_198119.1 UniGene:At.19946 ProteinModelPortal:Q94F49 SMR:Q94F49 STRING:Q94F49 PRIDE:Q94F49 EnsemblPlants:AT5G27670.1 GeneID:832829 KEGG:ath:AT5G27670 TAIR:At5g27670 InParanoid:Q94F49 OMA:CLAIRND PhylomeDB:Q94F49 ProtClustDB:CLSN2916652 Genevestigator:Q94F49 GermOnline:AT5G27670 Uniprot:Q94F49
Root	Isotig05719	0	16	-5.129	2.34E-05	TAIR|locus:2143651 - symbol:HTA7 "histone H2A 7" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=IEA;ISS] [GO:0006334 "nucleosome assembly" evidence=IEA] [GO:0005730 "nucleolus" evidence=IDA] InterPro:IPR002119 InterPro:IPR007125 InterPro:IPR009072 Pfam:PF00125 PRINTS:PR00620 PROSITE:PS00046 SMART:SM00414 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005730 GO:GO:0003677 Gene3D:G3DSA:1.10.20.10 SUPFAM:SSF47113 EMBL:AC007478 GO:GO:0006334 GO:GO:0000786 EMBL:AC069556 eggNOG:COG5262 HOGENOM:HBG610736 KO:K11251 EMBL:AF385711 EMBL:AY078019 IPI:IPI00533679 RefSeq:NP_198119.1 UniGene:At.19946 ProteinModelPortal:Q94F49 SMR:Q94F49 STRING:Q94F49 PRIDE:Q94F49 EnsemblPlants:AT5G27670.1 GeneID:832829 KEGG:ath:AT5G27670 TAIR:At5g27670 InParanoid:Q94F49 OMA:CLAIRND PhylomeDB:Q94F49 ProtClustDB:CLSN2916652 Genevestigator:Q94F49 GermOnline:AT5G27670 Uniprot:Q94F49
Root	Isotig05720	0	17	-5.216	1.26E-05	TAIR|locus:2143651 - symbol:HTA7 "histone H2A 7" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=IEA;ISS] [GO:0006334 "nucleosome assembly" evidence=IEA] [GO:0005730 "nucleolus" evidence=IDA] InterPro:IPR002119 InterPro:IPR007125 InterPro:IPR009072 Pfam:PF00125 PRINTS:PR00620 PROSITE:PS00046 SMART:SM00414 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005730 GO:GO:0003677 Gene3D:G3DSA:1.10.20.10 SUPFAM:SSF47113 EMBL:AC007478 GO:GO:0006334

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0000786 EMBL:AC069556 eggNOG:COG5262 HOGENOM:HBG610736 KO:K11251 EMBL:AF385711 EMBL:AY078019 IPI:IPI00533679 RefSeq:NP_198119.1 UniGene:At.19946 ProteinModelPortal:Q94F49 SMR:Q94F49 STRING:Q94F49 PRIDE:Q94F49 EnsemblPlants:AT5G27670.1 GeneID:832829 KEGG:ath:AT5G27670 TAIR:At5g27670 InParanoid:Q94F49 OMA:CLAIRND PhylomeDB:Q94F49 ProtClustDB:CLSN2916652 Genevestigator:Q94F49 GermOnline:AT5G27670 Uniprot:Q94F49
Root	Isotig05744	34	10	1.637	0.000568537	TAIR|locus:2005614 - symbol:XRN3 "AT1G75660" species:3702 "Arabidopsis thaliana" [GO:0004534 "5'-3' exoribonuclease activity" evidence=IGI;ISS] [GO:0005634 "nucleus" evidence=IDA] [GO:0010587 "miRNA catabolic process" evidence=IMP] InterPro:IPR001878 InterPro:IPR004859 InterPro:IPR017151 Pfam:PF00098 Pfam:PF03159 PIRSF:PIRSF037239 PROSITE:PS50158 SMART:SM00343 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005634 GO:GO:0008270 GO:GO:0006397 GO:GO:0003676 Gene3D:G3DSA:4.10.60.10 GO:GO:0010587 EMBL:AC006434 eggNOG:COG5049 GO:GO:0004534 HOGENOM:HBG592534 KO:K12619 EMBL:AF286719 EMBL:AY136383 EMBL:BT000175 IPI:IPI00542756 IPI:IPI00903453 PIR:D96786 RefSeq:NP_565114.1 UniGene:At.23685 ProteinModelPortal:Q9FQ03 SMR:Q9FQ03 STRING:Q9FQ03 PRIDE:Q9FQ03 EnsemblPlants:AT1G75660.1 GeneID:843900 KEGG:ath:AT1G75660 TAIR:At1g75660 InParanoid:Q9FQ03 OMA:ILREVVY PhylomeDB:Q9FQ03 ArrayExpress:Q8L7A3 Genevestigator:Q9FQ03 Uniprot:Q9FQ03
Root	Isotig05745	34	10	1.637	0.000568537	TAIR|locus:2005614 - symbol:XRN3 "AT1G75660" species:3702 "Arabidopsis thaliana" [GO:0004534 "5'-3' exoribonuclease activity" evidence=IGI;ISS] [GO:0005634 "nucleus" evidence=IDA] [GO:0010587 "miRNA catabolic process" evidence=IMP] InterPro:IPR001878 InterPro:IPR004859 InterPro:IPR017151 Pfam:PF00098 Pfam:PF03159 PIRSF:PIRSF037239 PROSITE:PS50158 SMART:SM00343 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005634 GO:GO:0008270 GO:GO:0006397 GO:GO:0003676 Gene3D:G3DSA:4.10.60.10 GO:GO:0010587 EMBL:AC006434 eggNOG:COG5049 GO:GO:0004534 HOGENOM:HBG592534 KO:K12619 EMBL:AF286719 EMBL:AY136383 EMBL:BT000175 IPI:IPI00542756 IPI:IPI00903453 PIR:D96786 RefSeq:NP_565114.1 UniGene:At.23685 ProteinModelPortal:Q9FQ03 SMR:Q9FQ03 STRING:Q9FQ03 PRIDE:Q9FQ03 EnsemblPlants:AT1G75660.1 GeneID:843900 KEGG:ath:AT1G75660 TAIR:At1g75660 InParanoid:Q9FQ03 OMA:ILREVVY PhylomeDB:Q9FQ03 ArrayExpress:Q8L7A3 Genevestigator:Q9FQ03 Uniprot:Q9FQ03
Root	Isotig05794	6	38	-2.792	1.04E-07	TAIR|locus:2827943 - symbol:STY8 "AT2G17700" species:3702 "Arabidopsis thaliana" [GO:0004672 "protein kinase activity" evidence=ISS] [GO:0004712 "protein serine/threonine/tyrosine kinase activity" evidence=ISS] [GO:0005829 "cytosol" evidence=IDA] [GO:0004674 "protein serine/threonine kinase activity" evidence=IDA] [GO:0009658 "chloroplast organization" evidence=IGI] InterPro:IPR000719 InterPro:IPR001245 InterPro:IPR002912 InterPro:IPR008271 InterPro:IPR011009 Pfam:PF01842 Pfam:PF07714 PRINTS:PR00109 PROSITE:PS00108 PROSITE:PS50011 GO:GO:0005829 GO:GO:0005524 EMBL:CP002685 GenomeReviews:CT485783_GR eggNOG:COG0515 SUPFAM:SSF56112 GO:GO:0004674 HOGENOM:HBG755340 GO:GO:0016597 GO:GO:0009658 HSSP:P41240 EMBL:AY070086 EMBL:AY096470 IPI:IPI00530122 PIR:D84555 PIR:T08864 RefSeq:NP_179361.1 UniGene:At.14679 ProteinModelPortal:O22558 SMR:O22558 PRIDE:O22558 EnsemblPlants:AT2G17700.1 GeneID:816278 KEGG:ath:AT2G17700 TAIR:At2g17700 InParanoid:O22558 OMA:DESESCG PhylomeDB:O22558 ProtClustDB:CLSN2683904 ArrayExpress:O22558 Genevestigator:O22558 Uniprot:O22558
Root	Isotig05795	6	38	-2.792	1.04E-07	TAIR|locus:2827943 - symbol:STY8 "AT2G17700" species:3702 "Arabidopsis thaliana" [GO:0004672 "protein kinase activity" evidence=ISS] [GO:0004712 "protein serine/threonine/tyrosine kinase activity" evidence=ISS] [GO:0005829 "cytosol" evidence=IDA] [GO:0004674 "protein serine/threonine kinase activity" evidence=IDA] [GO:0009658 "chloroplast organization" evidence=IGI] InterPro:IPR000719 InterPro:IPR001245 InterPro:IPR002912 InterPro:IPR008271 InterPro:IPR011009 Pfam:PF01842 Pfam:PF07714 PRINTS:PR00109 PROSITE:PS00108 PROSITE:PS50011 GO:GO:0005829 GO:GO:0005524 EMBL:CP002685 GenomeReviews:CT485783_GR eggNOG:COG0515 SUPFAM:SSF56112 GO:GO:0004674 HOGENOM:HBG755340 GO:GO:0016597 GO:GO:0009658 HSSP:P41240 EMBL:AY070086 EMBL:AY096470 IPI:IPI00530122 PIR:D84555 PIR:T08864 RefSeq:NP_179361.1 UniGene:At.14679 ProteinModelPortal:O22558 SMR:O22558 PRIDE:O22558 EnsemblPlants:AT2G17700.1 GeneID:816278 KEGG:ath:AT2G17700 TAIR:At2g17700 InParanoid:O22558 OMA:DESESCG PhylomeDB:O22558 ProtClustDB:CLSN2683904 ArrayExpress:O22558 Genevestigator:O22558 Uniprot:O22558

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig05862	65	0	6.893	6.96E-16	TAIR|locus:2156652 - symbol:LTI65 "AT5G52300" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0009738 "abscisic acid mediated signaling pathway" evidence=IEP] [GO:0009414 "response to water deprivation" evidence=IEP] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] [GO:0010150 "leaf senescence" evidence=IMP] [GO:0009409 "response to cold" evidence=IEP] EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009738 GO:GO:0010150 GO:GO:0009409 GO:GO:0009651 GO:GO:0009414 EMBL:AB019226 EMBL:X67670 EMBL:D13044 EMBL:AY081282 EMBL:AY128731 EMBL:Z34014 IPI:IPI00526103 PIR:S30153 RefSeq:NP_200043.2 UniGene:At.43012 STRING:Q04980 PRIDE:Q04980 EnsemblPlants:AT5G52300.1 GeneID:835306 KEGG:ath:AT5G52300 TAIR:At5g52300 eggNOG:NOG281420 HOGENOM:HBG027913 InParanoid:Q04980 OMA:APVYESS PhylomeDB:Q04980 ProtClustDB:PLN03021 ArrayExpress:Q04980 Genevestigator:Q04980 InterPro:IPR012418 Pfam:PF07918 Uniprot:Q04980
Root	Isotig05863	72	0	7.041	2.73E-17	TAIR|locus:2156652 - symbol:LTI65 "AT5G52300" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0009738 "abscisic acid mediated signaling pathway" evidence=IEP] [GO:0009414 "response to water deprivation" evidence=IEP] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] [GO:0010150 "leaf senescence" evidence=IMP] [GO:0009409 "response to cold" evidence=IEP] EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009738 GO:GO:0010150 GO:GO:0009409 GO:GO:0009651 GO:GO:0009414 EMBL:AB019226 EMBL:X67670 EMBL:D13044 EMBL:AY081282 EMBL:AY128731 EMBL:Z34014 IPI:IPI00526103 PIR:S30153 RefSeq:NP_200043.2 UniGene:At.43012 STRING:Q04980 PRIDE:Q04980 EnsemblPlants:AT5G52300.1 GeneID:835306 KEGG:ath:AT5G52300 TAIR:At5g52300 eggNOG:NOG281420 HOGENOM:HBG027913 InParanoid:Q04980 OMA:APVYESS PhylomeDB:Q04980 ProtClustDB:PLN03021 ArrayExpress:Q04980 Genevestigator:Q04980 InterPro:IPR012418 Pfam:PF07918 Uniprot:Q04980
Root	Isotig05870	2	30	-4.036	3.63E-08	UNIPROTKB|Q70KG3 - symbol:RAFTIN1B "Protein RAFTIN 1B" species:4565 "Triticum aestivum" [GO:0009555 "pollen development" evidence=ISS] [GO:0043668 "exine" evidence=IDA] GO:GO:0009555 InterPro:IPR004873 Pfam:PF03181 PROSITE:PS51277 GO:GO:0043668 EMBL:AJ575664 EMBL:AJ575665 UniGene:Ta.4176 Gramene:Q70KG3 Uniprot:Q70KG3
Root	Isotig05871	2	35	-4.258	1.54E-09	UNIPROTKB|Q70KG3 - symbol:RAFTIN1B "Protein RAFTIN 1B" species:4565 "Triticum aestivum" [GO:0009555 "pollen development" evidence=ISS] [GO:0043668 "exine" evidence=IDA] GO:GO:0009555 InterPro:IPR004873 Pfam:PF03181 PROSITE:PS51277 GO:GO:0043668 EMBL:AJ575664 EMBL:AJ575665 UniGene:Ta.4176 Gramene:Q70KG3 Uniprot:Q70KG3
Root	Isotig05876	4	86	-4.555	6.56E-22	TAIR|locus:2053654 - symbol:NIR1 "AT2G15620" species:3702 "Arabidopsis thaliana" [GO:0047889 "ferredoxin-nitrate reductase activity" evidence=ISS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0010167 "response to nitrate" evidence=IEP] [GO:0005829 "cytosol" evidence=RCA] [GO:0050421 "nitrite reductase (NO-forming) activity" evidence=ISS] InterPro:IPR005117 InterPro:IPR006066 InterPro:IPR006067 Pfam:PF01077 Pfam:PF03460 PRINTS:PR00397 PROSITE:PS00365 GO:GO:0005739 GO:GO:0048046 GO:GO:0009570 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0016020 GO:GO:0006810 GO:GO:0051539 GO:GO:0020037 GO:GO:0022900 GO:GO:0042128 GO:GO:0010167 EMBL:AC006248 eggNOG:COG0155 Gene3D:G3DSA:3.90.480.10 SUPFAM:SSF55124 EMBL:D14824 EMBL:AB006032 EMBL:AF360320 EMBL:AY045608 EMBL:AY093995 EMBL:AY142685 EMBL:BT000685 EMBL:BT000686 IPI:IPI00533476 PIR:C84531 RefSeq:NP_179164.1 UniGene:At.21870 ProteinModelPortal:Q39161 SMR:Q39161 IntAct:Q39161 STRING:Q39161 PRIDE:Q39161 EnsemblPlants:AT2G15620.1 GeneID:816055 KEGG:ath:AT2G15620 GeneFarm:4362 TAIR:At2g15620 HOGENOM:HBG578916 InParanoid:Q39161 KO:K00366 OMA:DKYFMLR PhylomeDB:Q39161 ProtClustDB:PLN02431 ArrayExpress:Q39161 Genevestigator:Q39161 GermOnline:AT2G15620 GO:GO:0048307 Uniprot:Q39161
Root	Isotig05877	4	80	-4.451	2.67E-20	TAIR|locus:2053654 - symbol:NIR1 "AT2G15620" species:3702 "Arabidopsis thaliana" [GO:0047889 "ferredoxin-nitrate reductase activity" evidence=ISS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0010167 "response to nitrate" evidence=IEP] [GO:0005829 "cytosol"

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						evidence=RCA] [GO:0050421 "nitrite reductase (NO-forming) activity" evidence=ISS] InterPro:IPR005117 InterPro:IPR006066 InterPro:IPR006067 Pfam:PF01077 Pfam:PF03460 PRINTS:PR00397 PROSITE:PS00365 GO:GO:0005739 GO:GO:0048046 GO:GO:0009570 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0016020 GO:GO:0006810 GO:GO:0051539 GO:GO:0020037 GO:GO:0022900 GO:GO:0042128 GO:GO:0010167 EMBL:AC006248 eggNOG:COG0155 Gene3D:G3DSA:3.90.480.10 SUPFAM:SSF55124 EMBL:D14824 EMBL:AB006032 EMBL:AF360320 EMBL:AY045608 EMBL:AY093995 EMBL:AY142685 EMBL:BT000685 EMBL:BT000686 IPI:IPI00533476 PIR:C84531 RefSeq:NP_179164.1 UniGene:At.21870 ProteinModelPortal:Q39161 SMR:Q39161 IntAct:Q39161 STRING:Q39161 PRIDE:Q39161 EnsemblPlants:AT2G15620.1 GeneID:816055 KEGG:ath:AT2G15620 GeneFarm:4362 TAIR:At2g15620 HOGENOM:HBG578916 InParanoid:Q39161 KO:K00366 OMA:DKYFMLR PhylomeDB:Q39161 ProtClustDB:PLN02431 ArrayExpress:Q39161 Genevestigator:Q39161 GermOnline:AT2G15620 GO:GO:0048307 Uniprot:Q39161
Root	Isotig05884	36	7	2.234	1.28E-05	TAIR|locus:2155806 - symbol:FIP1[V] "AT5G58040" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0003723 "RNA binding" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] GenomeReviews:BA000015_GR GO:GO:0042802 GO:GO:0003723 EMBL:AB024029 InterPro:IPR007854 Pfam:PF05182 IPI:IPI00524599 IntAct:Q9FGU0 STRING:Q9FGU0 PRIDE:Q9FGU0 TAIR:At5g58040 HOGENOM:HBG595008 InParanoid:Q9FGU0 PhylomeDB:Q9FGU0 Genevestigator:Q9FGU0 Uniprot:Q9FGU0
Root	Isotig05885	6	23	-2.068	0.000510704	No hit
Root	Isotig05886	6	23	-2.068	0.000510704	No hit
Root	Isotig05911	57	20	1.382	8.22E-05	TAIR|locus:2037863 - symbol:MBD10 "AT1G15340" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=ISS] [GO:0008150 "biological_process" evidence=ND] [GO:0008327 "methyl-CpG binding" evidence=ISS] [GO:0005634 "nucleus" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001739 InterPro:IPR016177 Pfam:PF01429 PROSITE:PS50982 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0005634 GO:GO:0006355 GO:GO:0003677 GO:GO:0006351 EMBL:AC007591 SUPFAM:SSF54171 Gene3D:G3DSA:3.30.890.10 EMBL:AY094439 EMBL:BT020367 EMBL:AK230256 IPI:IPI00519005 IPI:IPI00785822 PIR:G86287 RefSeq:NP_001185003.1 RefSeq:NP_563971.1 UniGene:At.27594 UniGene:At.70811 ProteinModelPortal:Q9XI36 SMR:Q9XI36 STRING:Q9XI36 PRIDE:Q9XI36 ProMEX:Q9XI36 EnsemblPlants:AT1G15340.1 GeneID:838103 KEGG:ath:AT1G15340 TAIR:At1g15340 eggNOG:NOG328305 InParanoid:Q9XI36 OMA:VTTEANG PhylomeDB:Q9XI36 ProtClustDB:CLSN2917009 Genevestigator:Q9XI36 Uniprot:Q9XI36
Root	Isotig05912	61	20	1.480	1.80E-05	TAIR|locus:2037863 - symbol:MBD10 "AT1G15340" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=ISS] [GO:0008150 "biological_process" evidence=ND] [GO:0008327 "methyl-CpG binding" evidence=ISS] [GO:0005634 "nucleus" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001739 InterPro:IPR016177 Pfam:PF01429 PROSITE:PS50982 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0005634 GO:GO:0006355 GO:GO:0003677 GO:GO:0006351 EMBL:AC007591 SUPFAM:SSF54171 Gene3D:G3DSA:3.30.890.10 EMBL:AY094439 EMBL:BT020367 EMBL:AK230256 IPI:IPI00519005 IPI:IPI00785822 PIR:G86287 RefSeq:NP_001185003.1 RefSeq:NP_563971.1 UniGene:At.27594 UniGene:At.70811 ProteinModelPortal:Q9XI36 SMR:Q9XI36 STRING:Q9XI36 PRIDE:Q9XI36 ProMEX:Q9XI36 EnsemblPlants:AT1G15340.1 GeneID:838103 KEGG:ath:AT1G15340 TAIR:At1g15340 eggNOG:NOG328305 InParanoid:Q9XI36 OMA:VTTEANG PhylomeDB:Q9XI36 ProtClustDB:CLSN2917009 Genevestigator:Q9XI36 Uniprot:Q9XI36
Root	Isotig05948	0	46	-6.653	9.06E-13	UNIPROTKB|P47787 - symbol:TBXAS1 "Thromboxane-A synthase" species:9823 "Sus scrofa" [GO:0001516 "prostaglandin biosynthetic process" evidence=IEA] [GO:0004497 "monooxygenase activity" evidence=IEA] [GO:0004796 "thromboxane-A synthase activity" evidence=IEA] [GO:0005789 "endoplasmic reticulum membrane" evidence=IEA] [GO:0009055 "electron carrier activity" evidence=IEA] [GO:0016021 "integral to membrane" evidence=IEA] [GO:0016705 "oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen" evidence=IEA] [GO:0020037 "heme binding" evidence=IEA] InterPro:IPR001128 InterPro:IPR002401 InterPro:IPR017972 Pfam:PF00067 PRINTS:PR00385 PRINTS:PR00463 PROSITE:PS00086 GO:GO:0016021 GO:GO:0005789 GO:GO:0009055 GO:GO:0004497 GO:GO:0020037 Gene3D:G3DSA:1.10.630.10 SUPFAM:SSF48264 GO:GO:0016705 HOVERGEN:HBG108567 GO:GO:0001516 CTD:6916 KO:K01832 OrthoDB:EOG415GDB GO:GO:0004796 EMBL:L13128 RefSeq:NP_999211.1

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						UniGene:Ssc.158 ProteinModelPortal:P47787 STRING:P47787 GeneID:397112 KEGG:ssc:397112 eggNOG:NOG308437 Uniprot:P47787
Root	Isotig05949	0	46	-6.653	9.06E-13	UNIPROTKB|P47787 - symbol:TBXAS1 "Thromboxane-A synthase" species:9823 "Sus scrofa" [GO:0001516 "prostaglandin biosynthetic process" evidence=IEA] [GO:0004497 "monooxygenase activity" evidence=IEA] [GO:0004796 "thromboxane-A synthase activity" evidence=IEA] [GO:0005789 "endoplasmic reticulum membrane" evidence=IEA] [GO:0009055 "electron carrier activity" evidence=IEA] [GO:0016021 "integral to membrane" evidence=IEA] [GO:0016705 "oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen" evidence=IEA] [GO:0020037 "heme binding" evidence=IEA] InterPro:IPR001128 InterPro:IPR002401 InterPro:IPR017972 Pfam:PF00067 PRINTS:PR00385 PRINTS:PR00463 PROSITE:PS00086 GO:GO:0016021 GO:GO:0005789 GO:GO:0009055 GO:GO:0004497 GO:GO:0020037 Gene3D:G3DSA:1.10.630.10 SUPFAM:SSF48264 GO:GO:0016705 HOVERGEN:HBG108567 GO:GO:0001516 CTD:6916 KO:K01832 OrthoDB:EOG415GDB GO:GO:0004796 EMBL:L13128 RefSeq:NP_999211.1 UniGene:Ssc.158 ProteinModelPortal:P47787 STRING:P47787 GeneID:397112 KEGG:ssc:397112 eggNOG:NOG308437 Uniprot:P47787
Root	Isotig05988	0	77	-7.396	1.66E-19	TAIR|locus:2183730 - symbol:AT5G10770 "AT5G10770" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=ISS] [GO:0004190 "aspartic-type endopeptidase activity" evidence=IEA] [GO:0006508 "proteolysis" evidence=IEA] InterPro:IPR001461 InterPro:IPR009007 Pfam:PF00026 PRINTS:PR00792 EMBL:CP002688 GO:GO:0006508 GO:GO:0004190 InterPro:IPR021109 SUPFAM:SSF50630 Gene3D:G3DSA:2.40.70.10 PANTHER:PTHR13683 HSSP:P00799 EMBL:AY075656 EMBL:BT001004 IPI:IPI00543783 RefSeq:NP_196638.2 UniGene:At.32336 ProteinModelPortal:Q8S9J6 MEROPS:A01.A15 PRIDE:Q8S9J6 EnsemblPlants:AT5G10770.1 GeneID:830944 KEGG:ath:AT5G10770 TAIR:At5g10770 InParanoid:Q8S9J6 OMA:LEVVYDG PhylomeDB:Q8S9J6 ProtClustDB:CLSN2686424 Genevestigator:Q8S9J6 Uniprot:Q8S9J6
Root	Isotig05989	0	78	-7.414	1.03E-19	TAIR|locus:2183730 - symbol:AT5G10770 "AT5G10770" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=ISS] [GO:0004190 "aspartic-type endopeptidase activity" evidence=IEA] [GO:0006508 "proteolysis" evidence=IEA] InterPro:IPR001461 InterPro:IPR009007 Pfam:PF00026 PRINTS:PR00792 EMBL:CP002688 GO:GO:0006508 GO:GO:0004190 InterPro:IPR021109 SUPFAM:SSF50630 Gene3D:G3DSA:2.40.70.10 PANTHER:PTHR13683 HSSP:P00799 EMBL:AY075656 EMBL:BT001004 IPI:IPI00543783 RefSeq:NP_196638.2 UniGene:At.32336 ProteinModelPortal:Q8S9J6 MEROPS:A01.A15 PRIDE:Q8S9J6 EnsemblPlants:AT5G10770.1 GeneID:830944 KEGG:ath:AT5G10770 TAIR:At5g10770 InParanoid:Q8S9J6 OMA:LEVVYDG PhylomeDB:Q8S9J6 ProtClustDB:CLSN2686424 Genevestigator:Q8S9J6 Uniprot:Q8S9J6
Root	Isotig06010	0	28	-5.936	1.79E-08	TAIR|locus:2181950 - symbol:AT5G11650 "AT5G11650" species:3702 "Arabidopsis thaliana" [GO:0016787 "hydrolase activity" evidence=ISS] EMBL:CP002688 GO:GO:0016787 EMBL:AL163814 InterPro:IPR022742 Pfam:PF12146 EMBL:BT026426 EMBL:AK229263 IPI:IPI00517172 PIR:T48524 RefSeq:NP_196726.1 UniGene:At.32229 ProteinModelPortal:Q9LYG5 SMR:Q9LYG5 IntAct:Q9LYG5 STRING:Q9LYG5 MEROPS:S33.A11 PRIDE:Q9LYG5 ProMEX:Q9LYG5 EnsemblPlants:AT5G11650.1 GeneID:831037 KEGG:ath:AT5G11650 TAIR:At5g11650 InParanoid:Q9LYG5 OMA:RAWVERF PhylomeDB:Q9LYG5 ProtClustDB:PLN02652 Genevestigator:Q9LYG5 Uniprot:Q9LYG5
Root	Isotig06011	0	28	-5.936	1.79E-08	TAIR|locus:2181950 - symbol:AT5G11650 "AT5G11650" species:3702 "Arabidopsis thaliana" [GO:0016787 "hydrolase activity" evidence=ISS] EMBL:CP002688 GO:GO:0016787 EMBL:AL163814 InterPro:IPR022742 Pfam:PF12146 EMBL:BT026426 EMBL:AK229263 IPI:IPI00517172 PIR:T48524 RefSeq:NP_196726.1 UniGene:At.32229 ProteinModelPortal:Q9LYG5 SMR:Q9LYG5 IntAct:Q9LYG5 STRING:Q9LYG5 MEROPS:S33.A11 PRIDE:Q9LYG5 ProMEX:Q9LYG5 EnsemblPlants:AT5G11650.1 GeneID:831037 KEGG:ath:AT5G11650 TAIR:At5g11650 InParanoid:Q9LYG5 OMA:RAWVERF PhylomeDB:Q9LYG5 ProtClustDB:PLN02652 Genevestigator:Q9LYG5 Uniprot:Q9LYG5
Root	Isotig06048	3	17	-2.631	0.00056383	TAIR|locus:2061748 - symbol:IRX9 "AT2G37090" species:3702 "Arabidopsis thaliana" [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0009834 "secondary cell wall biogenesis" evidence=IMP] [GO:0010417 "glucuronoxylan biosynthetic process" evidence=IGI] [GO:0005794 "Golgi apparatus" evidence=IDA] [GO:0010413 "glucuronoxylan metabolic process" evidence=IMP] [GO:0042285 "xylosyltransferase activity" evidence=IMP] InterPro:IPR005027 Pfam:PF03360 GO:GO:0016021 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0000139 GO:GO:0007047 CAZy:GT43 GO:GO:0015018

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						PANTHER:PTHR10896 GO:GO:0009834 EMBL:AC006260 GO:GO:0010417 GO:GO:0042285 EMBL:BT015044 EMBL:BT015838 IPI:IPI00532147 PIR:D84788 RefSeq:NP_181246.1 UniGene:At.26964 UniGene:At.67134 ProteinModelPortal:Q9ZQC6 SMR:Q9ZQC6 STRING:Q9ZQC6 PRIDE:Q9ZQC6 EnsemblPlants:AT2G37090.1 GeneID:818285 KEGG:ath:AT2G37090 TAIR:At2g37090 eggNOG:NOG308705 HOGENOM:HBG600303 InParanoid:Q9ZQC6 OMA:FSLCFVM PhylomeDB:Q9ZQC6 ProtClustDB:PLN02458 ArrayExpress:Q9ZQC6 Genevestigator:Q9ZQC6 Uniprot:Q9ZQC6
Root	Isotig06049	3	17	-2.631	0.00056383	TAIR|locus:2061748 - symbol:IRX9 "AT2G37090" species:3702 "Arabidopsis thaliana" [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0009834 "secondary cell wall biogenesis" evidence=IMP] [GO:0010417 "glucuronoxylan biosynthetic process" evidence=IGI] [GO:0005794 "Golgi apparatus" evidence=IDA] [GO:0010413 "glucuronoxylan metabolic process" evidence=IMP] [GO:0042285 "xylosyltransferase activity" evidence=IMP] InterPro:IPR005027 Pfam:PF03360 GO:GO:0016021 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0000139 GO:GO:0007047 CAZy:GT43 GO:GO:0015018 PANTHER:PTHR10896 GO:GO:0009834 EMBL:AC006260 GO:GO:0010417 GO:GO:0042285 EMBL:BT015044 EMBL:BT015838 IPI:IPI00532147 PIR:D84788 RefSeq:NP_181246.1 UniGene:At.26964 UniGene:At.67134 ProteinModelPortal:Q9ZQC6 SMR:Q9ZQC6 STRING:Q9ZQC6 PRIDE:Q9ZQC6 EnsemblPlants:AT2G37090.1 GeneID:818285 KEGG:ath:AT2G37090 TAIR:At2g37090 eggNOG:NOG308705 HOGENOM:HBG600303 InParanoid:Q9ZQC6 OMA:FSLCFVM PhylomeDB:Q9ZQC6 ProtClustDB:PLN02458 ArrayExpress:Q9ZQC6 Genevestigator:Q9ZQC6 Uniprot:Q9ZQC6
Root	Isotig06054	0	15	-5.036	4.38E-05	TAIR|locus:2092950 - symbol:AT3G20980 "AT3G20980" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] GenomeReviews:BA000014_GR EMBL:AP000604 eggNOG:KOG0017 IPI:IPI01020495 PRIDE:Q9LJD3 TAIR:At3g20980 InParanoid:Q9LJD3 PhylomeDB:Q9LJD3 Genevestigator:Q9LJD3 Uniprot:Q9LJD3
Root	Isotig06055	0	12	-4.714	0.000297064	TAIR|locus:2092950 - symbol:AT3G20980 "AT3G20980" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] GenomeReviews:BA000014_GR EMBL:AP000604 eggNOG:KOG0017 IPI:IPI01020495 PRIDE:Q9LJD3 TAIR:At3g20980 InParanoid:Q9LJD3 PhylomeDB:Q9LJD3 Genevestigator:Q9LJD3 Uniprot:Q9LJD3
Root	Isotig06056	3	66	-4.588	3.16E-17	TAIR|locus:2150763 - symbol:AGAL2 "alpha-galactosidase 2" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=IEA] [GO:0004557 "alpha-galactosidase activity" evidence=ISS;IBA] [GO:0005737 "cytoplasm" evidence=IBA] [GO:0009311 "oligosaccharide metabolic process" evidence=IBA] [GO:0016139 "glycoside catabolic process" evidence=IBA] [GO:0046477 "glycosylceramide catabolic process" evidence=IBA] [GO:0009505 "plant-type cell wall" evidence=IDA] [GO:0009911 "positive regulation of flower development" evidence=IMP] [GO:0009965 "leaf morphogenesis" evidence=IMP] InterPro:IPR000111 InterPro:IPR002241 InterPro:IPR013780 InterPro:IPR013785 Pfam:PF02065 PRINTS:PR00740 PROSITE:PS00512 EMBL:CP002688 GenomeReviews:BA000015_GR Gene3D:G3DSA:3.20.20.70 GO:GO:0043169 InterPro:IPR017853 SUPFAM:SSF51445 GO:GO:0005975 Gene3D:G3DSA:2.60.40.1180 GO:GO:0004553 GO:GO:0009505 GO:GO:0009911 CAZy:GH27 KO:K07407 HOGENOM:HBG424315 OMA:DMMEVGN GO:GO:0009965 UniGene:At.32587 UniGene:At.48997 EMBL:AY090238 EMBL:AY085529 EMBL:BT000619 IPI:IPI00547726 RefSeq:NP_568193.1 HSSP:Q9FXT4 ProteinModelPortal:Q8RX86 SMR:Q8RX86 PRIDE:Q8RX86 EnsemblPlants:AT5G08370.1 GeneID:830735 KEGG:ath:AT5G08370 TAIR:At5g08370 InParanoid:Q8RX86 PhylomeDB:Q8RX86 ProtClustDB:PLN02808 Genevestigator:Q8RX86 Uniprot:Q8RX86
Root	Isotig06057	3	70	-4.673	2.69E-18	TAIR|locus:2150763 - symbol:AGAL2 "alpha-galactosidase 2" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=IEA] [GO:0004557 "alpha-galactosidase activity" evidence=ISS;IBA] [GO:0005737 "cytoplasm" evidence=IBA] [GO:0009311 "oligosaccharide metabolic process" evidence=IBA] [GO:0016139 "glycoside catabolic process" evidence=IBA] [GO:0046477 "glycosylceramide catabolic process" evidence=IBA] [GO:0009505 "plant-type cell wall" evidence=IDA] [GO:0009911 "positive regulation of flower development" evidence=IMP] [GO:0009965 "leaf morphogenesis" evidence=IMP] InterPro:IPR000111 InterPro:IPR002241 InterPro:IPR013780 InterPro:IPR013785 Pfam:PF02065 PRINTS:PR00740 PROSITE:PS00512 EMBL:CP002688 GenomeReviews:BA000015_GR Gene3D:G3DSA:3.20.20.70 GO:GO:0043169 InterPro:IPR017853 SUPFAM:SSF51445 GO:GO:0005975

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						Gene3D:G3DSA:2.60.40.1180 GO:GO:0004553 GO:GO:0009505 GO:GO:0009911 CAZy:GH27 KO:K07407 HOGENOM:HBG424315 OMA:DMMEVGN GO:GO:0009965 UniGene:At.32587 UniGene:At.48997 EMBL:AY090238 EMBL:AY085529 EMBL:BT000619 IPI:IPI00547726 RefSeq:NP_568193.1 HSSP:Q9FXT4 ProteinModelPortal:Q8RX86 SMR:Q8RX86 PRIDE:Q8RX86 EnsemblPlants:AT5G08370.1 GeneID:830735 KEGG:ath:AT5G08370 TAIR:At5g08370 InParanoid:Q8RX86 PhylomeDB:Q8RX86 ProtClustDB:PLN02808 Genevestigator:Q8RX86 Uniprot:Q8RX86
Root	Isotig06064	17	163	-3.390	1.66E-33	TAIR|locus:2084031 - symbol:PIP2A "AT3G53420" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=ISS] [GO:0015250 "water channel activity" evidence=ISS;IDA] [GO:0016020 "membrane" evidence=ISS;IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA;TAS] [GO:0005773 "vacuole" evidence=IDA] [GO:0009414 "response to water deprivation" evidence=IEP] [GO:0080170 "hydrogen peroxide transmembrane transport" evidence=IDA] [GO:0031625 "ubiquitin protein ligase binding" evidence=IPI] [GO:0009737 "response to abscisic acid stimulus" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0006833 "water transport" evidence=IDA] InterPro:IPR000425 InterPro:IPR012269 InterPro:IPR022357 Pfam:PF00230 PRINTS:PR00783 PROSITE:PS00221 GO:GO:0016021 GO:GO:0005886 GO:GO:0009506 GO:GO:0009737 GO:GO:0005773 GO:GO:0009507 EMBL:CP002686 GenomeReviews:BA000014_GR EMBL:AL132966 GO:GO:0009414 GO:GO:0031625 InterPro:IPR023271 Gene3D:G3DSA:1.20.1080.10 SUPFAM:SSF81338 eggNOG:COG0580 HOGENOM:HBG705794 PANTHER:PTHR19139 TIGRFAMs:TIGR00861 GO:GO:0015250 GO:GO:0080170 KO:K09872 EMBL:X75883 EMBL:AY039579 EMBL:AY044327 EMBL:AY056085 EMBL:AF428426 EMBL:AY072374 EMBL:AY087854 IPI:IPI00532482 PIR:S44084 RefSeq:NP_001030851.1 RefSeq:NP_190910.1 UniGene:At.47609 ProteinModelPortal:P43286 SMR:P43286 MINT:MINT-6951259 STRING:P43286 TCDB:1.A.8.11.4 PRIDE:P43286 ProMEX:P43286 EnsemblPlants:AT3G53420.1 EnsemblPlants:AT3G53420.2 GeneID:824510 KEGG:ath:AT3G53420 GeneFarm:4866 TAIR:At3g53420 InParanoid:P43286 OMA:VFMAITI PhylomeDB:P43286 ProtClustDB:CLSN2683965 ArrayExpress:P43286 Genevestigator:P43286 GermOnline:AT3G53420 Uniprot:P43286
Root	Isotig06065	17	163	-3.390	1.66E-33	TAIR|locus:2084031 - symbol:PIP2A "AT3G53420" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=ISS] [GO:0015250 "water channel activity" evidence=ISS;IDA] [GO:0016020 "membrane" evidence=ISS;IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA;TAS] [GO:0005773 "vacuole" evidence=IDA] [GO:0009414 "response to water deprivation" evidence=IEP] [GO:0080170 "hydrogen peroxide transmembrane transport" evidence=IDA] [GO:0031625 "ubiquitin protein ligase binding" evidence=IPI] [GO:0009737 "response to abscisic acid stimulus" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0006833 "water transport" evidence=IDA] InterPro:IPR000425 InterPro:IPR012269 InterPro:IPR022357 Pfam:PF00230 PRINTS:PR00783 PROSITE:PS00221 GO:GO:0016021 GO:GO:0005886 GO:GO:0009506 GO:GO:0009737 GO:GO:0005773 GO:GO:0009507 EMBL:CP002686 GenomeReviews:BA000014_GR EMBL:AL132966 GO:GO:0009414 GO:GO:0031625 InterPro:IPR023271 Gene3D:G3DSA:1.20.1080.10 SUPFAM:SSF81338 eggNOG:COG0580 HOGENOM:HBG705794 PANTHER:PTHR19139 TIGRFAMs:TIGR00861 GO:GO:0015250 GO:GO:0080170 KO:K09872 EMBL:X75883 EMBL:AY039579 EMBL:AY044327 EMBL:AY056085 EMBL:AF428426 EMBL:AY072374 EMBL:AY087854 IPI:IPI00532482 PIR:S44084 RefSeq:NP_001030851.1 RefSeq:NP_190910.1 UniGene:At.47609 ProteinModelPortal:P43286 SMR:P43286 MINT:MINT-6951259 STRING:P43286 TCDB:1.A.8.11.4 PRIDE:P43286 ProMEX:P43286 EnsemblPlants:AT3G53420.1 EnsemblPlants:AT3G53420.2 GeneID:824510 KEGG:ath:AT3G53420 GeneFarm:4866 TAIR:At3g53420 InParanoid:P43286 OMA:VFMAITI PhylomeDB:P43286 ProtClustDB:CLSN2683965 ArrayExpress:P43286 Genevestigator:P43286 GermOnline:AT3G53420 Uniprot:P43286
Root	Isotig06082	15	0	4.778	0.000105609	TAIR|locus:2158544 - symbol:AT5G63350 "AT5G63350" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0005515 "protein binding" evidence=IPI] EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005515 EMBL:AB023035 EMBL:BT002821 EMBL:BT004383 IPI:IPI00523793 RefSeq:NP_201140.1 UniGene:At.29001 IntAct:Q9FGW7 PRIDE:Q9FGW7 EnsemblPlants:AT5G63350.1 GeneID:836455 KEGG:ath:AT5G63350 TAIR:At5g63350 eggNOG:NOG314236 HOGENOM:HBG745108 InParanoid:Q9FGW7 OMA:DINIPME PhylomeDB:Q9FGW7 ProtClustDB:CLSN2687559 Genevestigator:Q9FGW7 Uniprot:Q9FGW7

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig06083	15	0	4.778	0.000105609	TAIR|locus:2158544 - symbol:AT5G63350 "AT5G63350" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0005515 "protein binding" evidence=IPI] EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005515 EMBL:AB023035 EMBL:BT002821 EMBL:BT004383 IPI:IPI00523793 RefSeq:NP_201140.1 UniGene:At.29001 IntAct:Q9FGW7 PRIDE:Q9FGW7 EnsemblPlants:AT5G63350.1 GeneID:836455 KEGG:ath:AT5G63350 TAIR:At5g63350 eggNOG:NOG314236 HOGENOM:HBG745108 InParanoid:Q9FGW7 OMA:DINIPME PhylomeDB:Q9FGW7 ProtClustDB:CLSN2687559 Genevestigator:Q9FGW7 Uniprot:Q9FGW7
Root	Isotig06108	14	1	3.678	0.000484579	TAIR|locus:2055155 - symbol:AT2G14520 "AT2G14520" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] InterPro:IPR000644 Pfam:PF00571 PROSITE:PS51371 GO:GO:0016021 EMBL:CP002685 GenomeReviews:CT485783_GR eggNOG:COG1253 InterPro:IPR002550 Pfam:PF01595 EMBL:AC006067 HOGENOM:HBG317049 EMBL:AY080819 IPI:IPI01019762 PIR:B84518 RefSeq:NP_179058.3 UniGene:At.40534 ProteinModelPortal:Q9ZQR4 SMR:Q9ZQR4 PRIDE:Q9ZQR4 GeneID:815939 KEGG:ath:AT2G14520 TAIR:At2g14520 InParanoid:Q9ZQR4 PhylomeDB:Q9ZQR4 ArrayExpress:Q9ZQR4 Genevestigator:Q9ZQR4 Uniprot:Q9ZQR4
Root	Isotig06109	14	1	3.678	0.000484579	TAIR|locus:2055155 - symbol:AT2G14520 "AT2G14520" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] InterPro:IPR000644 Pfam:PF00571 PROSITE:PS51371 GO:GO:0016021 EMBL:CP002685 GenomeReviews:CT485783_GR eggNOG:COG1253 InterPro:IPR002550 Pfam:PF01595 EMBL:AC006067 HOGENOM:HBG317049 EMBL:AY080819 IPI:IPI01019762 PIR:B84518 RefSeq:NP_179058.3 UniGene:At.40534 ProteinModelPortal:Q9ZQR4 SMR:Q9ZQR4 PRIDE:Q9ZQR4 GeneID:815939 KEGG:ath:AT2G14520 TAIR:At2g14520 InParanoid:Q9ZQR4 PhylomeDB:Q9ZQR4 ArrayExpress:Q9ZQR4 Genevestigator:Q9ZQR4 Uniprot:Q9ZQR4
Root	Isotig06112	0	18	-5.299	6.77E-06	TAIR|locus:2183229 - symbol:AT5G19740 species:3702 "Arabidopsis thaliana" [GO:0006508 "proteolysis" evidence=IEA;ISS] [GO:0016805 "dipeptidase activity" evidence=ISS] [GO:0005773 "vacuole" evidence=IDA] InterPro:IPR007484 Pfam:PF04389 InterPro:IPR003137 Pfam:PF02225 GO:GO:0005773 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0006508 GO:GO:0008233 eggNOG:NOG74799 HOGENOM:HBG713441 InterPro:IPR007365 Gene3D:G3DSA:1.20.930.40 Pfam:PF04253 SUPFAM:SSF47672 EMBL:BT008323 IPI:IPI00537808 RefSeq:NP_197475.2 UniGene:At.31257 HSSP:P80561 ProteinModelPortal:Q7Y228 SMR:Q7Y228 MEROPS:M28.A02 PRIDE:Q7Y228 EnsemblPlants:AT5G19740.1 GeneID:832094 KEGG:ath:AT5G19740 TAIR:At5g19740 InParanoid:Q7Y228 OMA:FLQHLGI PhylomeDB:Q7Y228 ProtClustDB:CLSN2918628 Genevestigator:Q7Y228 Uniprot:Q7Y228
Root	Isotig06113	0	18	-5.299	6.77E-06	TAIR|locus:2183229 - symbol:AT5G19740 species:3702 "Arabidopsis thaliana" [GO:0006508 "proteolysis" evidence=IEA;ISS] [GO:0016805 "dipeptidase activity" evidence=ISS] [GO:0005773 "vacuole" evidence=IDA] InterPro:IPR007484 Pfam:PF04389 InterPro:IPR003137 Pfam:PF02225 GO:GO:0005773 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0006508 GO:GO:0008233 eggNOG:NOG74799 HOGENOM:HBG713441 InterPro:IPR007365 Gene3D:G3DSA:1.20.930.40 Pfam:PF04253 SUPFAM:SSF47672 EMBL:BT008323 IPI:IPI00537808 RefSeq:NP_197475.2 UniGene:At.31257 HSSP:P80561 ProteinModelPortal:Q7Y228 SMR:Q7Y228 MEROPS:M28.A02 PRIDE:Q7Y228 EnsemblPlants:AT5G19740.1 GeneID:832094 KEGG:ath:AT5G19740 TAIR:At5g19740 InParanoid:Q7Y228 OMA:FLQHLGI PhylomeDB:Q7Y228 ProtClustDB:CLSN2918628 Genevestigator:Q7Y228 Uniprot:Q7Y228
Root	Isotig06144	18	1	4.041	4.47E-05	TAIR|locus:2054809 - symbol:AT2G20560 species:3702 "Arabidopsis thaliana" [GO:0006457 "protein folding" evidence=IEA;ISS] [GO:0031072 "heat shock protein binding" evidence=IEA] [GO:0051082 "unfolded protein binding" evidence=IEA] InterPro:IPR001623 InterPro:IPR002939 InterPro:IPR003095 InterPro:IPR008971 InterPro:IPR018253 Pfam:PF00226 Pfam:PF01556 PRINTS:PR00625 PROSITE:PS00636 PROSITE:PS50076 SMART:SM00271 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0006457 GO:GO:0006950 GO:GO:0051082 eggNOG:COG0484 HOGENOM:HBG635315 GO:GO:0031072 Gene3D:G3DSA:1.10.287.110 SUPFAM:SSF46565 SUPFAM:SSF49493 HSSP:P25685 EMBL:AC007109 ProtClustDB:CLSN2683325 EMBL:AY057555 EMBL:AY086509 EMBL:AY133644 IPI:IPI00547861 PIR:G84590 RefSeq:NP_179646.1 UniGene:At.26315 ProteinModelPortal:Q9SIL3 SMR:Q9SIL3 STRING:Q9SIL3 PRIDE:Q9SIL3 EnsemblPlants:AT2G20560.1 GeneID:816578 KEGG:ath:AT2G20560 TAIR:At2g20560 InParanoid:Q9SIL3 OMA:TKKMRIS PhylomeDB:Q9SIL3 ArrayExpress:Q9SIL3 Genevestigator:Q9SIL3 Uniprot:Q9SIL3

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig06145	18	1	4.041	4.47E-05	TAIR|locus:2097638 - symbol:AT3G08910 "AT3G08910" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0006457 "protein folding" evidence=IEA;ISS] [GO:0031072 "heat shock protein binding" evidence=IEA] [GO:0051082 "unfolded protein binding" evidence=IEA] InterPro:IPR001623 InterPro:IPR002939 InterPro:IPR003095 InterPro:IPR008971 InterPro:IPR018253 Pfam:PF00226 Pfam:PF01556 PRINTS:PR00625 PROSITE:PS00636 PROSITE:PS50076 SMART:SM00271 EMBL:CP002686 GO:GO:0006457 GO:GO:0006950 GO:GO:0051082 EMBL:AC010871 GO:GO:0031072 Gene3D:G3DSA:1.10.287.110 SUPFAM:SSF46565 SUPFAM:SSF49493 HSSP:P25685 EMBL:BT044615 IPI:IPI00530981 RefSeq:NP_187503.1 UniGene:At.40199 ProteinModelPortal:Q9SR91 SMR:Q9SR91 PRIDE:Q9SR91 EnsemblPlants:AT3G08910.1 GeneID:820040 KEGG:ath:AT3G08910 TAIR:At3g08910 InParanoid:Q9SR91 OMA:FRFNGRS PhylomeDB:Q9SR91 ProtClustDB:CLSN2915586 Genevestigator:Q9SR91 Uniprot:Q9SR91
Root	Isotig06176	7	57	-3.155	4.72E-12	TAIR|locus:2122829 - symbol:NIP5;1 "AT4G10380" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=ISS] [GO:0015250 "water channel activity" evidence=ISS;IDA] [GO:0016020 "membrane" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0010036 "response to boron-containing substance" evidence=IEP;IMP] [GO:0046713 "borate transport" evidence=IDA] [GO:0046715 "borate transmembrane transporter activity" evidence=IDA] [GO:0080138 "borate uptake transmembrane transporter activity" evidence=IDA] [GO:0080029 "cellular response to boron-containing substance levels" evidence=IEP] [GO:0015105 "arsenite transmembrane transporter activity" evidence=IDA] [GO:0015700 "arsenite transport" evidence=IDA] [GO:0046685 "response to arsenic-containing substance" evidence=IMP] [GO:0016328 "lateral plasma membrane" evidence=IDA] InterPro:IPR000425 InterPro:IPR022357 Pfam:PF00230 PRINTS:PR00783 PROSITE:PS00221 GO:GO:0016021 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0046685 GO:GO:0016328 InterPro:IPR023271 Gene3D:G3DSA:1.20.1080.10 SUPFAM:SSF81338 eggNOG:COG0580 HOGENOM:HBG705794 PANTHER:PTHR19139 GO:GO:0015250 GO:GO:0015105 GO:GO:0046715 GO:GO:0080029 EMBL:AL049488 EMBL:AL161517 KO:K09874 EMBL:AY087560 IPI:IPI00536883 PIR:T04053 RefSeq:NP_192776.1 UniGene:At.33633 ProteinModelPortal:Q9SV84 SMR:Q9SV84 TCDB:1.A.8.12.3 EnsemblPlants:AT4G10380.1 GeneID:826630 KEGG:ath:AT4G10380 GeneFarm:4878 TAIR:At4g10380 InParanoid:Q9SV84 OMA:PRCKCLP PhylomeDB:Q9SV84 ProtClustDB:PLN00026 ArrayExpress:Q9SV84 Genevestigator:Q9SV84 GermOnline:AT4G10380 GO:GO:0080138 Uniprot:Q9SV84
Root	Isotig06177	7	57	-3.155	4.72E-12	TAIR|locus:2122829 - symbol:NIP5;1 "AT4G10380" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=ISS] [GO:0015250 "water channel activity" evidence=ISS;IDA] [GO:0016020 "membrane" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0010036 "response to boron-containing substance" evidence=IEP;IMP] [GO:0046713 "borate transport" evidence=IDA] [GO:0046715 "borate transmembrane transporter activity" evidence=IDA] [GO:0080138 "borate uptake transmembrane transporter activity" evidence=IDA] [GO:0080029 "cellular response to boron-containing substance levels" evidence=IEP] [GO:0015105 "arsenite transmembrane transporter activity" evidence=IDA] [GO:0015700 "arsenite transport" evidence=IDA] [GO:0046685 "response to arsenic-containing substance" evidence=IMP] [GO:0016328 "lateral plasma membrane" evidence=IDA] InterPro:IPR000425 InterPro:IPR022357 Pfam:PF00230 PRINTS:PR00783 PROSITE:PS00221 GO:GO:0016021 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0046685 GO:GO:0016328 InterPro:IPR023271 Gene3D:G3DSA:1.20.1080.10 SUPFAM:SSF81338 eggNOG:COG0580 HOGENOM:HBG705794 PANTHER:PTHR19139 GO:GO:0015250 GO:GO:0015105 GO:GO:0046715 GO:GO:0080029 EMBL:AL049488 EMBL:AL161517 KO:K09874 EMBL:AY087560 IPI:IPI00536883 PIR:T04053 RefSeq:NP_192776.1 UniGene:At.33633 ProteinModelPortal:Q9SV84 SMR:Q9SV84 TCDB:1.A.8.12.3 EnsemblPlants:AT4G10380.1 GeneID:826630 KEGG:ath:AT4G10380 GeneFarm:4878 TAIR:At4g10380 InParanoid:Q9SV84 OMA:PRCKCLP PhylomeDB:Q9SV84 ProtClustDB:PLN00026 ArrayExpress:Q9SV84 Genevestigator:Q9SV84 GermOnline:AT4G10380 GO:GO:0080138 Uniprot:Q9SV84
Root	Isotig06181	0	11	-4.588	0.000569522	TAIR|locus:2207210 - symbol:RCI3 "AT1G05260" species:3702 "Arabidopsis thaliana" [GO:0004601 "peroxidase activity" evidence=ISS;IDA] [GO:0005783 "endoplasmic reticulum" evidence=ISS] [GO:0009269 "response to desiccation" evidence=IMP] [GO:0009409 "response to cold" evidence=IEP] [GO:0042538 "hyperosmotic salinity response" evidence=IMP] InterPro:IPR000823 InterPro:IPR002016 InterPro:IPR010255 InterPro:IPR019793 InterPro:IPR019794 Pfam:PF00141 PRINTS:PR00458 PRINTS:PR00461 PROSITE:PS00435 PROSITE:PS00436 PROSITE:PS50873 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005576 GO:GO:0009409 GO:GO:0020037 GO:GO:0004601 GO:GO:0009269 GO:GO:0042744 HOGENOM:HBG597790 SUPFAM:SSF48113 GO:GO:0042538 EMBL:AC000098 KO:K00430 eggNOG:NOG242082

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						ProtClustDB:CLSN2681995 EMBL:U97684 EMBL:BT004817 EMBL:AY084678 IPI:IPI00521040 PIR:B86187 RefSeq:NP_172018.1 UniGene:At.23986 ProteinModelPortal:O23044 SMR:O23044 IntAct:O23044 STRING:O23044 PeroxiBase:79 PRIDE:O23044 EnsemblPlants:AT1G05260.1 GeneID:837028 KEGG:ath:AT1G05260 GeneFarm:1833 TAIR:At1g05260 InParanoid:O23044 OMA:ANIPPPT PhylomeDB:O23044 ArrayExpress:O23044 Genevestigator:O23044 GermOnline:AT1G05260 Uniprot:O23044
Root	Isotig06182	0	11	-4.588	0.000569522	TAIR|locus:2128308 - symbol:AT4G11290 species:3702 "Arabidopsis thaliana" [GO:0004601 "peroxidase activity" evidence=IEA;ISS] [GO:0006979 "response to oxidative stress" evidence=IEA] [GO:0020037 "heme binding" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] InterPro:IPR000823 InterPro:IPR002016 InterPro:IPR010255 InterPro:IPR019793 InterPro:IPR019794 Pfam:PF00141 PRINTS:PR00458 PRINTS:PR00461 PROSITE:PS00435 PROSITE:PS00436 PROSITE:PS50873 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005576 EMBL:AL096882 EMBL:AL161531 GO:GO:0020037 GO:GO:0004601 GO:GO:0042744 HOGENOM:HBG597790 SUPFAM:SSF48113 KO:K00430 eggNOG:NOG242082 ProtClustDB:CLSN2681995 EMBL:X98805 IPI:IPI00531288 PIR:T13020 RefSeq:NP_192868.1 UniGene:At.22642 ProteinModelPortal:Q9SUT2 SMR:Q9SUT2 STRING:Q9SUT2 PeroxiBase:205 PRIDE:Q9SUT2 EnsemblPlants:AT4G11290.1 GeneID:826731 KEGG:ath:AT4G11290 GeneFarm:1868 TAIR:At4g11290 InParanoid:Q9SUT2 OMA:QLKMGFY PhylomeDB:Q9SUT2 ArrayExpress:Q9SUT2 Genevestigator:Q9SUT2 GermOnline:AT4G11290 Uniprot:Q9SUT2
Root	Isotig06236	0	19	-5.377	3.67E-06	TAIR|locus:2040939 - symbol:CYP710A1 "AT2G34500" species:3702 "Arabidopsis thaliana" [GO:0019825 "oxygen binding" evidence=ISS] [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0000249 "C-22 sterol desaturase activity" evidence=IDA] InterPro:IPR001128 InterPro:IPR002401 InterPro:IPR017972 Pfam:PF00067 PRINTS:PR00385 PRINTS:PR00463 PROSITE:PS00086 GO:GO:0016021 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009055 GO:GO:0004497 GO:GO:0016126 eggNOG:COG2124 GO:GO:0020037 Gene3D:G3DSA:1.10.630.10 SUPFAM:SSF48264 HOGENOM:HBG592092 OMA:CLGQTYA EMBL:AB219423 EMBL:AC004077 EMBL:AC004481 EMBL:BT002069 EMBL:BT010554 IPI:IPI00537608 PIR:T02337 RefSeq:NP_180997.1 UniGene:At.27806 UniGene:At.67747 ProteinModelPortal:O64697 SMR:O64697 STRING:O64697 PRIDE:O64697 GeneID:818013 KEGG:ath:AT2G34500 GeneFarm:1168 TAIR:At2g34500 InParanoid:O64697 KO:K09832 PhylomeDB:O64697 ProtClustDB:CLSN2683644 BioCyc:ARA:AT2G34500-MONOMER BioCyc:MetaCyc:AT2G34500-MONOMER ArrayExpress:O64697 Genevestigator:O64697 GO:GO:0000249 Uniprot:O64697
Root	Isotig06237	0	19	-5.377	3.67E-06	TAIR|locus:2040939 - symbol:CYP710A1 "AT2G34500" species:3702 "Arabidopsis thaliana" [GO:0019825 "oxygen binding" evidence=ISS] [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0000249 "C-22 sterol desaturase activity" evidence=IDA] InterPro:IPR001128 InterPro:IPR002401 InterPro:IPR017972 Pfam:PF00067 PRINTS:PR00385 PRINTS:PR00463 PROSITE:PS00086 GO:GO:0016021 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009055 GO:GO:0004497 GO:GO:0016126 eggNOG:COG2124 GO:GO:0020037 Gene3D:G3DSA:1.10.630.10 SUPFAM:SSF48264 HOGENOM:HBG592092 OMA:CLGQTYA EMBL:AB219423 EMBL:AC004077 EMBL:AC004481 EMBL:BT002069 EMBL:BT010554 IPI:IPI00537608 PIR:T02337 RefSeq:NP_180997.1 UniGene:At.27806 UniGene:At.67747 ProteinModelPortal:O64697 SMR:O64697 STRING:O64697 PRIDE:O64697 GeneID:818013 KEGG:ath:AT2G34500 GeneFarm:1168 TAIR:At2g34500 InParanoid:O64697 KO:K09832 PhylomeDB:O64697 ProtClustDB:CLSN2683644 BioCyc:ARA:AT2G34500-MONOMER BioCyc:MetaCyc:AT2G34500-MONOMER ArrayExpress:O64697 Genevestigator:O64697 GO:GO:0000249 Uniprot:O64697
Root	Isotig06238	2	23	-3.653	3.09E-06	TAIR|locus:2132303 - symbol:UNE12 "AT4G02590" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=ISS] [GO:0005634 "nucleus" evidence=IEA] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=TAS] [GO:0009567 "double fertilization forming a zygote and endosperm" evidence=IMP] [GO:0031347 "regulation of defense response" evidence=IMP] InterPro:IPR011598 Pfam:PF00010 GO:GO:0007275 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005634 GO:GO:0006355 GO:GO:0003677 GO:GO:0006351 Gene3D:G3DSA:4.10.280.10 SMART:SM00353 SUPFAM:SSF47459 PROSITE:PS50888 HOGENOM:HBG602703 ProtClustDB:CLSN2687635 EMBL:AC002330 EMBL:AL161494 GO:GO:0031347 GO:GO:0009567 EMBL:AF488592 EMBL:AF367328 EMBL:AY143951 EMBL:AY088218 IPI:IPI00545077 IPI:IPI00892352 PIR:T01090 RefSeq:NP_001031577.1 RefSeq:NP_001118919.1 RefSeq:NP_567245.1 UniGene:At.20028 ProteinModelPortal:O22768 SMR:O22768 IntAct:O22768 PRIDE:O22768 EnsemblPlants:AT4G02590.1 EnsemblPlants:AT4G02590.2 GeneID:828126 KEGG:ath:AT4G02590

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						TAIR:At4g02590 eggNOG:euNOG02041 InParanoid:O22768 OMA:FHGQPMQ PhylomeDB:O22768 ArrayExpress:O22768 Genevestigator:O22768 Uniprot:O22768
Root	Isotig06239	2	21	-3.521	1.10E-05	TAIR|locus:2132303 - symbol:UNE12 "AT4G02590" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=ISS] [GO:0005634 "nucleus" evidence=IEA] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=TAS] [GO:0009567 "double fertilization forming a zygote and endosperm" evidence=IMP] [GO:0031347 "regulation of defense response" evidence=IMP] InterPro:IPR011598 Pfam:PF00010 GO:GO:0007275 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005634 GO:GO:0006355 GO:GO:0003677 GO:GO:0006351 Gene3D:G3DSA:4.10.280.10 SMART:SM00353 SUPFAM:SSF47459 PROSITE:PS50888 HOGENOM:HBG602703 ProtClustDB:CLSN2687635 EMBL:AC002330 EMBL:AL161494 GO:GO:0031347 GO:GO:0009567 EMBL:AF488592 EMBL:AF367328 EMBL:AY143951 EMBL:AY088218 IPI:IPI00545077 IPI:IPI00892352 PIR:T01090 RefSeq:NP_001031577.1 RefSeq:NP_001118919.1 RefSeq:NP_567245.1 UniGene:At.20028 ProteinModelPortal:O22768 SMR:O22768 IntAct:O22768 PRIDE:O22768 EnsemblPlants:AT4G02590.1 EnsemblPlants:AT4G02590.2 GeneID:828126 KEGG:ath:AT4G02590 TAIR:At4g02590 eggNOG:euNOG02041 InParanoid:O22768 OMA:FHGQPMQ PhylomeDB:O22768 ArrayExpress:O22768 Genevestigator:O22768 Uniprot:O22768
Root	Isotig06240	112	45	1.187	9.44E-07	TAIR|locus:2149194 - symbol:AT5G20290 "AT5G20290" species:3702 "Arabidopsis thaliana" [GO:0000462 "maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)" evidence=IBA] [GO:0003735 "structural constituent of ribosome" evidence=ISS;IBA] [GO:0005840 "ribosome" evidence=ISS] [GO:0006412 "translation" evidence=ISS] [GO:0006414 "translational elongation" evidence=IBA] [GO:0042254 "ribosome biogenesis" evidence=ISS] [GO:0022627 "cytosolic small ribosomal subunit" evidence=ISS;IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005730 "nucleolus" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR001047 InterPro:IPR018283 PROSITE:PS01193 Pfam:PF01201 PANTHER:PTHR10394 GO:GO:0005886 GO:GO:0009506 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005618 GO:GO:0009507 GO:GO:0005730 GO:GO:0006412 GO:GO:0003735 EMBL:AF296825 GO:GO:0022627 eggNOG:COG2007 InterPro:IPR022309 UniGene:At.24020 EMBL:AY050937 EMBL:AY052338 EMBL:AY061909 EMBL:AY091172 EMBL:AK226280 EMBL:AY086963 IPI:IPI00524577 RefSeq:NP_197529.1 UniGene:At.24724 ProteinModelPortal:Q93VG5 SMR:Q93VG5 IntAct:Q93VG5 STRING:Q93VG5 PRIDE:Q93VG5 EnsemblPlants:AT5G20290.1 GeneID:832151 KEGG:ath:AT5G20290 TAIR:At5g20290 HOGENOM:HBG745393 InParanoid:Q93VG5 KO:K02995 OMA:AWASEGC PhylomeDB:Q93VG5 ProtClustDB:CLSN2687206 ArrayExpress:Q93VG5 Genevestigator:Q93VG5 GermOnline:AT5G20290 TIGRFAMs:TIGR00307 Uniprot:Q93VG5
Root	Isotig06241	112	45	1.187	9.44E-07	TAIR|locus:2149194 - symbol:AT5G20290 "AT5G20290" species:3702 "Arabidopsis thaliana" [GO:0000462 "maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)" evidence=IBA] [GO:0003735 "structural constituent of ribosome" evidence=ISS;IBA] [GO:0005840 "ribosome" evidence=ISS] [GO:0006412 "translation" evidence=ISS] [GO:0006414 "translational elongation" evidence=IBA] [GO:0042254 "ribosome biogenesis" evidence=ISS] [GO:0022627 "cytosolic small ribosomal subunit" evidence=ISS;IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005730 "nucleolus" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR001047 InterPro:IPR018283 PROSITE:PS01193 Pfam:PF01201 PANTHER:PTHR10394 GO:GO:0005886 GO:GO:0009506 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005618 GO:GO:0009507 GO:GO:0005730 GO:GO:0006412 GO:GO:0003735 EMBL:AF296825 GO:GO:0022627 eggNOG:COG2007 InterPro:IPR022309 UniGene:At.24020 EMBL:AY050937 EMBL:AY052338 EMBL:AY061909 EMBL:AY091172 EMBL:AK226280 EMBL:AY086963 IPI:IPI00524577 RefSeq:NP_197529.1 UniGene:At.24724 ProteinModelPortal:Q93VG5 SMR:Q93VG5 IntAct:Q93VG5 STRING:Q93VG5 PRIDE:Q93VG5 EnsemblPlants:AT5G20290.1 GeneID:832151 KEGG:ath:AT5G20290 TAIR:At5g20290 HOGENOM:HBG745393 InParanoid:Q93VG5 KO:K02995 OMA:AWASEGC PhylomeDB:Q93VG5 ProtClustDB:CLSN2687206 ArrayExpress:Q93VG5 Genevestigator:Q93VG5 GermOnline:AT5G20290 TIGRFAMs:TIGR00307 Uniprot:Q93VG5

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig06244	25	77	-1.752	1.26E-08	No hit
Root	Isotig06245	23	66	-1.650	4.42E-07	No hit
Root	Isotig06343	18	0	5.041	1.86E-05	DICTYBASE|DDB_G0267846 - symbol:expl1 "expansin-like protein" species:44689 "Dictyostelium discoideum" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] dictyBase:DDB_G0267846 GO:GO:0016021 GenomeReviews:CM000150_GR EMBL:AAFI02000003 InterPro:IPR014733 InterPro:IPR009009 InterPro:IPR007112 Gene3D:G3DSA:2.40.40.10 Pfam:PF03330 SMART:SM00837 SUPFAM:SSF50685 PROSITE:PS50842 InterPro:IPR007117 Gene3D:G3DSA:2.60.40.760 SUPFAM:SSF49590 RefSeq:XP_647352.1 HSSP:P43213 ProteinModelPortal:Q55G31 EnsemblProtists:DDB0231629 GeneID:8616163 KEGG:ddi:DDB_G0267846 eggNOG:COG4305 HOGENOM:HBG077223 InParanoid:Q55G31 OMA:ISKSETC ProtClustDB:CLSZ2430666 Uniprot:Q55G31
Root	Isotig06344	18	0	5.041	1.86E-05	DICTYBASE|DDB_G0267846 - symbol:expl1 "expansin-like protein" species:44689 "Dictyostelium discoideum" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] dictyBase:DDB_G0267846 GO:GO:0016021 GenomeReviews:CM000150_GR EMBL:AAFI02000003 InterPro:IPR014733 InterPro:IPR009009 InterPro:IPR007112 Gene3D:G3DSA:2.40.40.10 Pfam:PF03330 SMART:SM00837 SUPFAM:SSF50685 PROSITE:PS50842 InterPro:IPR007117 Gene3D:G3DSA:2.60.40.760 SUPFAM:SSF49590 RefSeq:XP_647352.1 HSSP:P43213 ProteinModelPortal:Q55G31 EnsemblProtists:DDB0231629 GeneID:8616163 KEGG:ddi:DDB_G0267846 eggNOG:COG4305 HOGENOM:HBG077223 InParanoid:Q55G31 OMA:ISKSETC ProtClustDB:CLSZ2430666 Uniprot:Q55G31
Root	Isotig06361	2	14	-2.936	0.000925454	TAIR|locus:2168656 - symbol:YSL3 "AT5G53550" species:3702 "Arabidopsis thaliana" [GO:0006857 "oligopeptide transport" evidence=ISS] [GO:0015198 "oligopeptide transporter activity" evidence=ISS] [GO:0009624 "response to nematode" evidence=IEP] [GO:0003006 "developmental process involved in reproduction" evidence=IGI] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0048316 "seed development" evidence=IGI] [GO:0051980 "iron-nicotianamine transmembrane transporter activity" evidence=IGI] InterPro:IPR004813 Pfam:PF03169 GO:GO:0016021 GO:GO:0005886 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009624 GO:GO:0048316 GO:GO:0055072 EMBL:AB015476 TIGRFAMs:TIGR00728 eggNOG:COG1297 HOGENOM:HBG606963 GO:GO:0051980 EMBL:DQ385057 EMBL:AK226687 IPI:IPI00523096 RefSeq:NP_001190532.1 RefSeq:NP_200167.2 UniGene:At.49426 TCDB:2.A.67.2.4 EnsemblPlants:AT5G53550.1 EnsemblPlants:AT5G53550.2 GeneID:835437 KEGG:ath:AT5G53550 TAIR:At5g53550 InParanoid:Q2EF88 PhylomeDB:Q2EF88 ProtClustDB:CLSN2681646 Genevestigator:Q2EF88 Uniprot:Q2EF88
Root	Isotig06424	0	26	-5.829	5.70E-08	No hit
Root	Isotig06425	0	25	-5.773	1.02E-07	No hit
Root	Isotig06619	39	11	1.697	0.000152266	TAIR|locus:2149179 - symbol:SPS1F "sucrose phosphate synthase 1F" species:3702 "Arabidopsis thaliana" [GO:0005985 "sucrose metabolic process" evidence=IEA] [GO:0009058 "biosynthetic process" evidence=IEA] [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0046524 "sucrose-phosphate synthase activity" evidence=RCA;IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR001296 InterPro:IPR012819 Pfam:PF00534 Pfam:PF05116 GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 EMBL:CP002688 GO:GO:0009058 eggNOG:COG0438 CAZy:GT4 GO:GO:0005985 InterPro:IPR006380 EMBL:AY039911 EMBL:AY079334 EMBL:AK230113 IPI:IPI00528074 RefSeq:NP_197528.1 UniGene:At.22681 ProteinModelPortal:Q94BT0 SMR:Q94BT0 IntAct:Q94BT0 STRING:Q94BT0 PRIDE:Q94BT0 ProMEX:Q94BT0 EnsemblPlants:AT5G20280.1 GeneID:832150 KEGG:ath:AT5G20280 TAIR:At5g20280 InParanoid:Q94BT0 KO:K00696 OMA:ESGDTDY PhylomeDB:Q94BT0 ProtClustDB:CLSN2687205 ArrayExpress:Q94BT0 Genevestigator:Q94BT0 GO:GO:0046524 TIGRFAMs:TIGR02468 Uniprot:Q94BT0
Root	Isotig06620	44	11	1.871	1.68E-05	TAIR|locus:2149179 - symbol:SPS1F "sucrose phosphate synthase 1F" species:3702 "Arabidopsis thaliana" [GO:0005985 "sucrose metabolic process" evidence=IEA] [GO:0009058 "biosynthetic process" evidence=IEA] [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0046524 "sucrose-phosphate synthase activity" evidence=RCA;IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR001296 InterPro:IPR012819 Pfam:PF00534 Pfam:PF05116 GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 EMBL:CP002688 GO:GO:0009058 eggNOG:COG0438 CAZy:GT4 GO:GO:0005985 InterPro:IPR006380 EMBL:AY039911

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EMBL:AY079334 EMBL:AK230113 IPI:IPI00528074 RefSeq:NP_197528.1 UniGene:At.22681 ProteinModelPortal:Q94BT0 SMR:Q94BT0 IntAct:Q94BT0 STRING:Q94BT0 PRIDE:Q94BT0 ProMEX:Q94BT0 EnsemblPlants:AT5G20280.1 GeneID:832150 KEGG:ath:AT5G20280 TAIR:At5g20280 InParanoid:Q94BT0 KO:K00696 OMA:ESGDTDY PhylomeDB:Q94BT0 ProtClustDB:CLSN2687205 ArrayExpress:Q94BT0 Genevestigator:Q94BT0 GO:GO:0046524 TIGRFAMs:TIGR02468 Uniprot:Q94BT0
Root	Isotig06621	31	6	2.240	4.97E-05	TAIR|locus:2156030 - symbol:OXP1 "AT5G37830" species:3702 "Arabidopsis thaliana" [GO:0016787 "hydrolase activity" evidence=ISS] [GO:0005737 "cytoplasm" evidence=NAS] [GO:0006751 "glutathione catabolic process" evidence=IMP] [GO:0017168 "5-oxoprolinase (ATP-hydrolyzing) activity" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR002821 InterPro:IPR003692 Pfam:PF01968 Pfam:PF02538 Pfam:PF05378 GO:GO:0005829 GO:GO:0009506 GO:GO:0005524 EMBL:CP002688 GenomeReviews:BA000015_GR InterPro:IPR008040 eggNOG:COG0146 EMBL:AB016873 GO:GO:0006751 EMBL:AY102096 EMBL:BT004510 EMBL:AK228904 IPI:IPI00543587 RefSeq:NP_198599.1 UniGene:At.30461 ProteinModelPortal:Q9FIZ7 STRING:Q9FIZ7 PRIDE:Q9FIZ7 EnsemblPlants:AT5G37830.1 GeneID:833761 KEGG:ath:AT5G37830 TAIR:At5g37830 InParanoid:Q9FIZ7 KO:K01469 OMA:PLTVTDC PhylomeDB:Q9FIZ7 ProtClustDB:PLN02666 Genevestigator:Q9FIZ7 GO:GO:0017168 Uniprot:Q9FIZ7
Root	Isotig06622	32	6	2.286	3.01E-05	TAIR|locus:2156030 - symbol:OXP1 "AT5G37830" species:3702 "Arabidopsis thaliana" [GO:0016787 "hydrolase activity" evidence=ISS] [GO:0005737 "cytoplasm" evidence=NAS] [GO:0006751 "glutathione catabolic process" evidence=IMP] [GO:0017168 "5-oxoprolinase (ATP-hydrolyzing) activity" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR002821 InterPro:IPR003692 Pfam:PF01968 Pfam:PF02538 Pfam:PF05378 GO:GO:0005829 GO:GO:0009506 GO:GO:0005524 EMBL:CP002688 GenomeReviews:BA000015_GR InterPro:IPR008040 eggNOG:COG0146 EMBL:AB016873 GO:GO:0006751 EMBL:AY102096 EMBL:BT004510 EMBL:AK228904 IPI:IPI00543587 RefSeq:NP_198599.1 UniGene:At.30461 ProteinModelPortal:Q9FIZ7 STRING:Q9FIZ7 PRIDE:Q9FIZ7 EnsemblPlants:AT5G37830.1 GeneID:833761 KEGG:ath:AT5G37830 TAIR:At5g37830 InParanoid:Q9FIZ7 KO:K01469 OMA:PLTVTDC PhylomeDB:Q9FIZ7 ProtClustDB:PLN02666 Genevestigator:Q9FIZ7 GO:GO:0017168 Uniprot:Q9FIZ7
Root	Isotig06630	32	9	1.701	0.000589296	UNIPROTKB|E1B7V8 - symbol:PLEKHA4 "Uncharacterized protein" species:9913 "Bos taurus" [GO:0005543 "phospholipid binding" evidence=IEA] Pfam:PF00169 InterPro:IPR001849 PROSITE:PS50003 SMART:SM00233 InterPro:IPR011993 Gene3D:G3DSA:2.30.29.30 GeneTree:ENSGT00530000063012 EMBL:DAAA02047467 IPI:IPI00923864 Ensembl:ENSBTAT00000061135 Uniprot:E1B7V8
Root	Isotig06643	2	31	-4.083	1.93E-08	TAIR|locus:2100367 - symbol:ABCA2 "AT3G47730" species:3702 "Arabidopsis thaliana" [GO:0005215 "transporter activity" evidence=ISS] [GO:0042626 "ATPase activity, coupled to transmembrane movement of substances" evidence=ISS] InterPro:IPR003439 InterPro:IPR003593 InterPro:IPR017871 Pfam:PF00005 PROSITE:PS00211 PROSITE:PS50893 SMART:SM00382 GO:GO:0016021 GO:GO:0005524 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0006810 eggNOG:COG1131 GO:GO:0016887 EMBL:AL049746 EMBL:BT004197 EMBL:BT005456 IPI:IPI00534264 PIR:T07712 RefSeq:NP_190357.2 UniGene:At.23005 ProteinModelPortal:Q84K47 SMR:Q84K47 PRIDE:Q84K47 EnsemblPlants:AT3G47730.1 GeneID:823927 KEGG:ath:AT3G47730 TAIR:At3g47730 HOGENOM:HBG317214 InParanoid:Q84K47 OMA:SLCISGH PhylomeDB:Q84K47 ProtClustDB:CLSN2686937 ArrayExpress:Q84K47 Genevestigator:Q84K47 GermOnline:AT3G47730 Uniprot:Q84K47
Root	Isotig06644	4	19	-2.377	0.000578515	TAIR|locus:2100367 - symbol:ABCA2 "AT3G47730" species:3702 "Arabidopsis thaliana" [GO:0005215 "transporter activity" evidence=ISS] [GO:0042626 "ATPase activity, coupled to transmembrane movement of substances" evidence=ISS] InterPro:IPR003439 InterPro:IPR003593 InterPro:IPR017871 Pfam:PF00005 PROSITE:PS00211 PROSITE:PS50893 SMART:SM00382 GO:GO:0016021 GO:GO:0005524 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0006810 eggNOG:COG1131 GO:GO:0016887 EMBL:AL049746 EMBL:BT004197 EMBL:BT005456 IPI:IPI00534264 PIR:T07712 RefSeq:NP_190357.2 UniGene:At.23005 ProteinModelPortal:Q84K47 SMR:Q84K47 PRIDE:Q84K47 EnsemblPlants:AT3G47730.1 GeneID:823927 KEGG:ath:AT3G47730 TAIR:At3g47730 HOGENOM:HBG317214 InParanoid:Q84K47 OMA:SLCISGH PhylomeDB:Q84K47 ProtClustDB:CLSN2686937 ArrayExpress:Q84K47 Genevestigator:Q84K47 GermOnline:AT3G47730 Uniprot:Q84K47
Root	Isotig06647	4	21	-2.521	0.000181802	TAIR|locus:2019863 - symbol:AT1G79620 "AT1G79620" species:3702 "Arabidopsis thaliana" [GO:0004674 "protein serine/threonine kinase activity" evidence=ISS] [GO:0005524 "ATP binding" evidence=ISS] [GO:0006468 "protein phosphorylation" evidence=IEA;ISS] [GO:0007169 "transmembrane receptor protein tyrosine kinase signaling

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						pathway" evidence=ISS] [GO:0016301 "kinase activity" evidence=ISS] Pfam:PF00560 InterPro:IPR001611 InterPro:IPR000719 InterPro:IPR001245 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 Pfam:PF07714 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005524 eggNOG:COG0515 GO:GO:0004872 SUPFAM:SSF56112 GO:GO:0004674 HSSP:P36897 InterPro:IPR013210 Pfam:PF08263 HOGENOM:HBG316990 EMBL:FJ708684 EMBL:AK117863 IPI:IPI00517320 RefSeq:NP_178080.2 UniGene:At.46098 ProteinModelPortal:Q8GY50 SMR:Q8GY50 PRIDE:Q8GY50 EnsemblPlants:AT1G79620.1 GeneID:844301 KEGG:ath:AT1G79620 TAIR:At1g79620 InParanoid:Q8GY50 OMA:YFIASPY PhylomeDB:Q8GY50 ProtClustDB:CLSN2680668 Genevestigator:Q8GY50 Uniprot:Q8GY50
Root	Isotig06648	4	21	-2.521	0.000181802	TAIR|locus:2019863 - symbol:AT1G79620 "AT1G79620" species:3702 "Arabidopsis thaliana" [GO:0004674 "protein serine/threonine kinase activity" evidence=ISS] [GO:0005524 "ATP binding" evidence=ISS] [GO:0006468 "protein phosphorylation" evidence=IEA;ISS] [GO:0007169 "transmembrane receptor protein tyrosine kinase signaling pathway" evidence=ISS] [GO:0016301 "kinase activity" evidence=ISS] Pfam:PF00560 InterPro:IPR001611 InterPro:IPR000719 InterPro:IPR001245 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 Pfam:PF07714 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005524 eggNOG:COG0515 GO:GO:0004872 SUPFAM:SSF56112 GO:GO:0004674 HSSP:P36897 InterPro:IPR013210 Pfam:PF08263 HOGENOM:HBG316990 EMBL:FJ708684 EMBL:AK117863 IPI:IPI00517320 RefSeq:NP_178080.2 UniGene:At.46098 ProteinModelPortal:Q8GY50 SMR:Q8GY50 PRIDE:Q8GY50 EnsemblPlants:AT1G79620.1 GeneID:844301 KEGG:ath:AT1G79620 TAIR:At1g79620 InParanoid:Q8GY50 OMA:YFIASPY PhylomeDB:Q8GY50 ProtClustDB:CLSN2680668 Genevestigator:Q8GY50 Uniprot:Q8GY50
Root	Isotig06659	12	61	-2.475	2.75E-10	TAIR|locus:2007760 - symbol:AGO1 "AT1G48410" species:3702 "Arabidopsis thaliana" [GO:0016441 "posttranscriptional gene silencing" evidence=IEP] [GO:0035195 "gene silencing by miRNA" evidence=IGI;IEP;IMP] [GO:0009733 "response to auxin stimulus" evidence=IGI] [GO:0009850 "auxin metabolic process" evidence=IGI] [GO:0010218 "response to far red light" evidence=IGI] [GO:0048830 "adventitious root development" evidence=IMP] [GO:0004521 "endoribonuclease activity" evidence=IDA] [GO:0035197 "siRNA binding" evidence=IPI] [GO:0035198 "miRNA binding" evidence=IPI] [GO:0009616 "virus induced gene silencing" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA;TAS] [GO:0016246 "RNA interference" evidence=IMP] [GO:0005515 "protein binding" evidence=IPI] [GO:0005829 "cytosol" evidence=IDA] [GO:0048864 "stem cell development" evidence=IGI] [GO:0045087 "innate immune response" evidence=IMP] [GO:0000300 "peripheral to membrane of membrane fraction" evidence=IDA] [GO:0009965 "leaf morphogenesis" evidence=IMP] [GO:0009793 "embryo development ending in seed dormancy" evidence=IGI] InterPro:IPR003100 InterPro:IPR003165 InterPro:IPR012337 Pfam:PF02170 Pfam:PF02171 PROSITE:PS50821 PROSITE:PS50822 SMART:SM00949 SMART:SM00950 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0005634 GO:GO:0005515 GO:GO:0009733 GO:GO:0006417 GO:GO:0016246 GO:GO:0006355 GO:GO:0006351 GO:GO:0010218 GO:GO:0009793 GO:GO:0030529 GO:GO:0009850 SUPFAM:SSF53098 GO:GO:0009965 eggNOG:NOG279895 HOGENOM:HBG717005 KO:K11596 GO:GO:0035198 InterPro:IPR014811 Pfam:PF08699 SUPFAM:SSF101690 EMBL:U91995 EMBL:AC007932 EMBL:AC020889 EMBL:BT000941 EMBL:AK227868 IPI:IPI00522985 IPI:IPI00523962 RefSeq:NP_001185169.1 RefSeq:NP_175274.1 RefSeq:NP_849784.1 UniGene:At.21124 ProteinModelPortal:O04379 SMR:O04379 STRING:O04379 PRIDE:O04379 EnsemblPlants:AT1G48410.1 GeneID:841262 KEGG:ath:AT1G48410 TAIR:At1g48410 InParanoid:O04379 OMA:RANHFQI PhylomeDB:O04379 ProtClustDB:CLSN2693050 ArrayExpress:O04379 Genevestigator:O04379 GO:GO:0004521 GO:GO:0035197 GO:GO:0048830 GO:GO:0035195 GO:GO:0048864 GO:GO:0009616 InterPro:IPR024357 Pfam:PF12764 Uniprot:O04379
Root	Isotig06660	12	62	-2.498	1.57E-10	TAIR|locus:2007760 - symbol:AGO1 "AT1G48410" species:3702 "Arabidopsis thaliana" [GO:0016441 "posttranscriptional gene silencing" evidence=IEP] [GO:0035195 "gene silencing by miRNA" evidence=IGI;IEP;IMP] [GO:0009733 "response to auxin stimulus" evidence=IGI] [GO:0009850 "auxin metabolic process" evidence=IGI] [GO:0010218 "response to far red light" evidence=IGI] [GO:0048830 "adventitious root development" evidence=IMP] [GO:0004521 "endoribonuclease activity" evidence=IDA] [GO:0035197 "siRNA binding" evidence=IPI] [GO:0035198 "miRNA binding" evidence=IPI] [GO:0009616 "virus induced gene silencing" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA;TAS] [GO:0016246 "RNA interference" evidence=IMP] [GO:0005515 "protein binding" evidence=IPI] [GO:0005829 "cytosol" evidence=IDA] [GO:0048864 "stem cell

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						development" evidence=IGI] [GO:0045087 "innate immune response" evidence=IMP] [GO:0000300 "peripheral to membrane of membrane fraction" evidence=IDA] [GO:0009965 "leaf morphogenesis" evidence=IMP] [GO:0009793 "embryo development ending in seed dormancy" evidence=IGI] InterPro:IPR003100 InterPro:IPR003165 InterPro:IPR012337 Pfam:PF02170 Pfam:PF02171 PROSITE:PS50821 PROSITE:PS50822 SMART:SM00949 SMART:SM00950 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0005634 GO:GO:0005515 GO:GO:0009733 GO:GO:0006417 GO:GO:0016246 GO:GO:0006355 GO:GO:0006351 GO:GO:0010218 GO:GO:0009793 GO:GO:0030529 GO:GO:0009850 SUPFAM:SSF53098 GO:GO:0009965 eggNOG:NOG279895 HOGENOM:HBG717005 KO:K11596 GO:GO:0035198 InterPro:IPR014811 Pfam:PF08699 SUPFAM:SSF101690 EMBL:U91995 EMBL:AC007932 EMBL:AC020889 EMBL:BT000941 EMBL:AK227868 IPI:IPI00522985 IPI:IPI00523962 RefSeq:NP_001185169.1 RefSeq:NP_175274.1 RefSeq:NP_849784.1 UniGene:At.21124 ProteinModelPortal:O04379 SMR:O04379 STRING:O04379 PRIDE:O04379 EnsemblPlants:AT1G48410.1 GeneID:841262 KEGG:ath:AT1G48410 TAIR:At1g48410 InParanoid:O04379 OMA:RANHFQI PhylomeDB:O04379 ProtClustDB:CLSN2693050 ArrayExpress:O04379 Genevestigator:O04379 GO:GO:0004521 GO:GO:0035197 GO:GO:0048830 GO:GO:0035195 GO:GO:0048864 GO:GO:0009616 InterPro:IPR024357 Pfam:PF12764 Uniprot:O04379
Root	Isotig06663	15	38	-1.470	0.00042777	TAIR|locus:2182397 - symbol:AT5G35160 "AT5G35160" species:3702 "Arabidopsis thaliana" [GO:0016021 "integral to membrane" evidence=ISS] [GO:0005794 "Golgi apparatus" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] InterPro:IPR004240 Pfam:PF02990 GO:GO:0016021 EMBL:CP002688 GO:GO:0005794 PANTHER:PTHR10766 EMBL:AP000421 IPI:IPI00992767 RefSeq:NP_001190420.1 UniGene:At.1657 STRING:Q9FYQ8 PRIDE:Q9FYQ8 EnsemblPlants:AT5G35160.2 GeneID:833470 KEGG:ath:AT5G35160 TAIR:At5g35160 InParanoid:Q9FYQ8 PhylomeDB:Q9FYQ8 Genevestigator:Q9FYQ8 Uniprot:Q9FYQ8
Root	Isotig06667	19	48	-1.466	7.79E-05	TAIR|locus:2123777 - symbol:GLDP1 "AT4G33010" species:3702 "Arabidopsis thaliana" [GO:0004375 "glycine dehydrogenase (decarboxylating) activity" evidence=ISS] [GO:0005960 "glycine cleavage complex" evidence=ISS] [GO:0019464 "glycine decarboxylation via glycine cleavage system" evidence=ISS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0006546 "glycine catabolic process" evidence=IMP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] InterPro:IPR003437 InterPro:IPR015421 InterPro:IPR020580 InterPro:IPR020581 Pfam:PF02347 GO:GO:0005739 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0048046 GO:GO:0009570 GO:GO:0046686 GO:GO:0005515 GO:GO:0030170 InterPro:IPR015424 Gene3D:G3DSA:3.40.640.10 SUPFAM:SSF53383 GO:GO:0009941 GO:GO:0009534 EMBL:AL031804 EMBL:AL161582 GO:GO:0006546 GO:GO:0004375 UniGene:At.24550 HOGENOM:HBG286723 KO:K00281 ProtClustDB:PLN02414 PANTHER:PTHR11773 TIGRFAMs:TIGR00461 EMBL:AY063903 EMBL:AY091186 EMBL:AY042800 EMBL:AY128922 EMBL:AY065004 EMBL:BT001132 EMBL:BT000446 IPI:IPI00536025 PIR:T05309 RefSeq:NP_195027.1 UniGene:At.22214 ProteinModelPortal:Q94B78 SMR:Q94B78 IntAct:Q94B78 STRING:Q94B78 PRIDE:Q94B78 ProMEX:Q94B78 EnsemblPlants:AT4G33010.1 GeneID:829438 KEGG:ath:AT4G33010 GeneFarm:1737 TAIR:At4g33010 InParanoid:Q94B78 OMA:VPMSEYQ PhylomeDB:Q94B78 ArrayExpress:Q94B78 Genevestigator:Q94B78 GermOnline:AT4G33010 Uniprot:Q94B78
Root	Isotig06668	19	51	-1.553	2.13E-05	TAIR|locus:2123777 - symbol:GLDP1 "AT4G33010" species:3702 "Arabidopsis thaliana" [GO:0004375 "glycine dehydrogenase (decarboxylating) activity" evidence=ISS] [GO:0005960 "glycine cleavage complex" evidence=ISS] [GO:0019464 "glycine decarboxylation via glycine cleavage system" evidence=ISS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0006546 "glycine catabolic process" evidence=IMP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] InterPro:IPR003437 InterPro:IPR015421 InterPro:IPR020580 InterPro:IPR020581 Pfam:PF02347 GO:GO:0005739 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0048046 GO:GO:0009570 GO:GO:0046686 GO:GO:0005515 GO:GO:0030170 InterPro:IPR015424 Gene3D:G3DSA:3.40.640.10 SUPFAM:SSF53383 GO:GO:0009941 GO:GO:0009534 EMBL:AL031804 EMBL:AL161582 GO:GO:0006546 GO:GO:0004375 UniGene:At.24550 HOGENOM:HBG286723 KO:K00281 ProtClustDB:PLN02414 PANTHER:PTHR11773 TIGRFAMs:TIGR00461 EMBL:AY063903 EMBL:AY091186 EMBL:AY042800 EMBL:AY128922 EMBL:AY065004 EMBL:BT001132

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EMBL:BT000446 IPI:IPI00536025 PIR:T05309 RefSeq:NP_195027.1 UniGene:At.22214 ProteinModelPortal:Q94B78 SMR:Q94B78 IntAct:Q94B78 STRING:Q94B78 PRIDE:Q94B78 ProMEX:Q94B78 EnsemblPlants:AT4G33010.1 GeneID:829438 KEGG:ath:AT4G33010 GeneFarm:1737 TAIR:At4g33010 InParanoid:Q94B78 OMA:VPMSEYQ PhylomeDB:Q94B78 ArrayExpress:Q94B78 Genevestigator:Q94B78 GermOnline:AT4G33010 Uniprot:Q94B78
Root	Isotig06683	15	44	-1.682	2.92E-05	TAIR|locus:2011030 - symbol:LOX1 "AT1G55020" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0010386 "lateral root primordium development" evidence=IMP] [GO:0048364 "root development" evidence=IMP] [GO:0016165 "lipoxygenase activity" evidence=ISS;IMP;IDA] [GO:0006952 "defense response" evidence=TAS] [GO:0009611 "response to wounding" evidence=TAS] [GO:0009695 "jasmonic acid biosynthetic process" evidence=TAS] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] [GO:0009753 "response to jasmonic acid stimulus" evidence=IEP] [GO:0009816 "defense response to bacterium, incompatible interaction" evidence=IEP] [GO:0030397 "membrane disassembly" evidence=TAS] [GO:0040007 "growth" evidence=TAS] InterPro:IPR000907 InterPro:IPR001024 InterPro:IPR001246 InterPro:IPR013819 InterPro:IPR020833 InterPro:IPR020834 Pfam:PF00305 Pfam:PF01477 PRINTS:PR00087 PRINTS:PR00468 PROSITE:PS00081 PROSITE:PS00711 PROSITE:PS50095 PROSITE:PS51393 SMART:SM00308 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009737 GO:GO:0005737 GO:GO:0009753 GO:GO:0005506 GO:GO:0031408 GO:GO:0010386 EMBL:AC064840 EMBL:AC069144 InterPro:IPR008976 Gene3D:G3DSA:2.60.60.20 SUPFAM:SSF49723 GO:GO:0016165 PANTHER:PTHR11771 SUPFAM:SSF48484 eggNOG:NOG69653 EMBL:L04637 EMBL:U01843 EMBL:AY093104 EMBL:BT010358 IPI:IPI00547307 PIR:JQ2267 RefSeq:NP_175900.1 UniGene:At.19984 UniGene:At.67309 ProteinModelPortal:Q06327 SMR:Q06327 STRING:Q06327 PRIDE:Q06327 EnsemblPlants:AT1G55020.1 GeneID:841944 KEGG:ath:AT1G55020 TAIR:At1g55020 HOGENOM:HBG749429 InParanoid:Q06327 KO:K15718 OMA:TPKEFDS PhylomeDB:Q06327 ProtClustDB:PLN02337 ArrayExpress:Q06327 Genevestigator:Q06327 GermOnline:AT1G55020 Uniprot:Q06327
Root	Isotig06684	15	43	-1.648	4.63E-05	TAIR|locus:2011030 - symbol:LOX1 "AT1G55020" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0010386 "lateral root primordium development" evidence=IMP] [GO:0048364 "root development" evidence=IMP] [GO:0016165 "lipoxygenase activity" evidence=ISS;IMP;IDA] [GO:0006952 "defense response" evidence=TAS] [GO:0009611 "response to wounding" evidence=TAS] [GO:0009695 "jasmonic acid biosynthetic process" evidence=TAS] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] [GO:0009753 "response to jasmonic acid stimulus" evidence=IEP] [GO:0009816 "defense response to bacterium, incompatible interaction" evidence=IEP] [GO:0030397 "membrane disassembly" evidence=TAS] [GO:0040007 "growth" evidence=TAS] InterPro:IPR000907 InterPro:IPR001024 InterPro:IPR001246 InterPro:IPR013819 InterPro:IPR020833 InterPro:IPR020834 Pfam:PF00305 Pfam:PF01477 PRINTS:PR00087 PRINTS:PR00468 PROSITE:PS00081 PROSITE:PS00711 PROSITE:PS50095 PROSITE:PS51393 SMART:SM00308 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009737 GO:GO:0005737 GO:GO:0009753 GO:GO:0005506 GO:GO:0031408 GO:GO:0010386 EMBL:AC064840 EMBL:AC069144 InterPro:IPR008976 Gene3D:G3DSA:2.60.60.20 SUPFAM:SSF49723 GO:GO:0016165 PANTHER:PTHR11771 SUPFAM:SSF48484 eggNOG:NOG69653 EMBL:L04637 EMBL:U01843 EMBL:AY093104 EMBL:BT010358 IPI:IPI00547307 PIR:JQ2267 RefSeq:NP_175900.1 UniGene:At.19984 UniGene:At.67309 ProteinModelPortal:Q06327 SMR:Q06327 STRING:Q06327 PRIDE:Q06327 EnsemblPlants:AT1G55020.1 GeneID:841944 KEGG:ath:AT1G55020 TAIR:At1g55020 HOGENOM:HBG749429 InParanoid:Q06327 KO:K15718 OMA:TPKEFDS PhylomeDB:Q06327 ProtClustDB:PLN02337 ArrayExpress:Q06327 Genevestigator:Q06327 GermOnline:AT1G55020 Uniprot:Q06327
Root	Isotig06693	4	31	-3.083	4.53E-07	TAIR|locus:2133995 - symbol:AK-HSDH II "AT4G19710" species:3702 "Arabidopsis thaliana" [GO:0004072 "aspartate kinase activity" evidence=IDA] [GO:0004412 "homoserine dehydrogenase activity" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0009067 "aspartate family amino acid biosynthetic process" evidence=TAS] InterPro:IPR001048 InterPro:IPR001341 InterPro:IPR001342 InterPro:IPR002912 InterPro:IPR005106 InterPro:IPR011147 InterPro:IPR016040 InterPro:IPR018042 InterPro:IPR019811 Pfam:PF00696 Pfam:PF00742 Pfam:PF01842 Pfam:PF03447 PIRSF:PIRSF000727 PROSITE:PS00324 PROSITE:PS01042 GO:GO:0005524 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0009570 Gene3D:G3DSA:3.40.50.720 GO:GO:0050661 GO:GO:0016597 eggNOG:COG0527 HOGENOM:HBG298754 KO:K12524 OMA:GANEMNI GO:GO:0004072 GO:GO:0004412

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						Gene3D:G3DSA:3.40.1160.10 SUPFAM:SSF53633 TIGRFAMs:TIGR00657 GO:GO:0009086 ProtClustDB:CLSN2682367 EMBL:AL024486 EMBL:AL161551 EMBL:BX827863 IPI:IPI00521909 IPI:IPI00539074 PIR:T04752 RefSeq:NP_193706.2 RefSeq:NP_974576.1 UniGene:At.32787 ProteinModelPortal:O81852 SMR:O81852 STRING:O81852 PRIDE:O81852 EnsemblPlants:AT4G19710.2 GeneID:827715 KEGG:ath:AT4G19710 TAIR:At4g19710 InParanoid:O81852 PhylomeDB:O81852 BRENDA:1.1.1.3 ArrayExpress:O81852 Genevestigator:O81852 GermOnline:AT4G19710 Uniprot:O81852
Root	Isotig06694	4	32	-3.129	2.46E-07	TAIR|locus:2133995 - symbol:AK-HSDH II "AT4G19710" species:3702 "Arabidopsis thaliana" [GO:0004072 "aspartate kinase activity" evidence=IDA] [GO:0004412 "homoserine dehydrogenase activity" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0009067 "aspartate family amino acid biosynthetic process" evidence=TAS] InterPro:IPR001048 InterPro:IPR001341 InterPro:IPR001342 InterPro:IPR002912 InterPro:IPR005106 InterPro:IPR011147 InterPro:IPR016040 InterPro:IPR018042 InterPro:IPR019811 Pfam:PF00696 Pfam:PF00742 Pfam:PF01842 Pfam:PF03447 PIRSF:PIRSF000727 PROSITE:PS00324 PROSITE:PS01042 GO:GO:0005524 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0009570 Gene3D:G3DSA:3.40.50.720 GO:GO:0050661 GO:GO:0016597 eggNOG:COG0527 HOGENOM:HBG298754 KO:K12524 OMA:GANEMNI GO:GO:0004072 GO:GO:0004412 Gene3D:G3DSA:3.40.1160.10 SUPFAM:SSF53633 TIGRFAMs:TIGR00657 GO:GO:0009086 ProtClustDB:CLSN2682367 EMBL:AL024486 EMBL:AL161551 EMBL:BX827863 IPI:IPI00521909 IPI:IPI00539074 PIR:T04752 RefSeq:NP_193706.2 RefSeq:NP_974576.1 UniGene:At.32787 ProteinModelPortal:O81852 SMR:O81852 STRING:O81852 PRIDE:O81852 EnsemblPlants:AT4G19710.2 GeneID:827715 KEGG:ath:AT4G19710 TAIR:At4g19710 InParanoid:O81852 PhylomeDB:O81852 BRENDA:1.1.1.3 ArrayExpress:O81852 Genevestigator:O81852 GermOnline:AT4G19710 Uniprot:O81852
Root	Isotig06697	68	6	3.374	1.04E-13	TAIR|locus:2175579 - symbol:ACA8 "AT5G57110" species:3702 "Arabidopsis thaliana" [GO:0005388 "calcium-transporting ATPase activity" evidence=ISS;IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005516 "calmodulin binding" evidence=TAS] [GO:0043621 "protein self-association" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0009624 "response to nematode" evidence=IEP] [GO:0016020 "membrane" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000695 InterPro:IPR001757 InterPro:IPR005834 InterPro:IPR006408 InterPro:IPR008250 InterPro:IPR024750 Pfam:PF00122 Pfam:PF00702 Pfam:PF12515 PRINTS:PR00119 PRINTS:PR00120 InterPro:IPR018303 InterPro:IPR004014 InterPro:IPR006068 Pfam:PF00690 Pfam:PF00689 Prosite:PS00154 GO:GO:0016021 GO:GO:0005886 GO:GO:0009506 GO:GO:0005524 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0046872 InterPro:IPR023214 SUPFAM:SSF56784 GO:GO:0006754 GO:GO:0009624 GO:GO:0005516 GO:GO:0043621 eggNOG:COG0474 HOGENOM:HBG456486 GO:GO:0005388 InterPro:IPR023300 InterPro:IPR023299 InterPro:IPR023298 Gene3D:G3DSA:2.70.150.10 Gene3D:G3DSA:3.40.1110.10 Gene3D:G3DSA:1.20.1110.10 SMART:SM00831 TIGRFAMs:TIGR01517 TIGRFAMs:TIGR01494 EMBL:AJ249352 EMBL:AB023042 EMBL:AY069869 IPI:IPI00540817 PIR:T52654 RefSeq:NP_200521.3 RefSeq:NP_851200.1 UniGene:At.9676 ProteinModelPortal:Q9LF79 SMR:Q9LF79 IntAct:Q9LF79 TCDB:3.A.3.2.10 PRIDE:Q9LF79 EnsemblPlants:AT5G57110.1 EnsemblPlants:AT5G57110.2 GeneID:835815 KEGG:ath:AT5G57110 TAIR:At5g57110 InParanoid:Q9LF79 OMA:VAFVGAC PhylomeDB:Q9LF79 ProtClustDB:CLSN2685405 ArrayExpress:Q9LF79 Genevestigator:Q9LF79 GermOnline:AT5G57110 Uniprot:Q9LF79
Root	Isotig06698	35	2	4.000	1.39E-08	TAIR|locus:2175579 - symbol:ACA8 "AT5G57110" species:3702 "Arabidopsis thaliana" [GO:0005388 "calcium-transporting ATPase activity" evidence=ISS;IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005516 "calmodulin binding" evidence=TAS] [GO:0043621 "protein self-association" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0009624 "response to nematode" evidence=IEP] [GO:0016020 "membrane" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000695 InterPro:IPR001757 InterPro:IPR005834 InterPro:IPR006408 InterPro:IPR008250 InterPro:IPR024750 Pfam:PF00122 Pfam:PF00702 Pfam:PF12515 PRINTS:PR00119 PRINTS:PR00120 InterPro:IPR018303 InterPro:IPR004014 InterPro:IPR006068 Pfam:PF00690 Pfam:PF00689 Prosite:PS00154 GO:GO:0016021 GO:GO:0005886 GO:GO:0009506 GO:GO:0005524 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0046872 InterPro:IPR023214 SUPFAM:SSF56784 GO:GO:0006754 GO:GO:0009624 GO:GO:0005516 GO:GO:0043621 eggNOG:COG0474 HOGENOM:HBG456486 GO:GO:0005388 InterPro:IPR023300 InterPro:IPR023299 InterPro:IPR023298 Gene3D:G3DSA:2.70.150.10 Gene3D:G3DSA:3.40.1110.10 Gene3D:G3DSA:1.20.1110.10 SMART:SM00831 TIGRFAMs:TIGR01517 TIGRFAMs:TIGR01494 EMBL:AJ249352 EMBL:AB023042 EMBL:AY069869

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						IPI:IPI00540817 PIR:T52654 RefSeq:NP_200521.3 RefSeq:NP_851200.1 UniGene:At.9676 ProteinModelPortal:Q9LF79 SMR:Q9LF79 IntAct:Q9LF79 TCDB:3.A.3.2.10 PRIDE:Q9LF79 EnsemblPlants:AT5G57110.1 EnsemblPlants:AT5G57110.2 GeneID:835815 KEGG:ath:AT5G57110 TAIR:At5g57110 InParanoid:Q9LF79 OMA:VAFVGAC PhylomeDB:Q9LF79 ProtClustDB:CLSN2685405 ArrayExpress:Q9LF79 Genevestigator:Q9LF79 GermOnline:AT5G57110 Uniprot:Q9LF79
Root	Isotig06705	12	32	-1.544	0.000803022	TAIR|locus:2025991 - symbol:ARF1 "AT1G59750" species:3702 "Arabidopsis thaliana" [GO:0005634 "nucleus" evidence=ISS] [GO:0003677 "DNA binding" evidence=IDA;IPI] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS;TAS] [GO:0010150 "leaf senescence" evidence=IGI] [GO:0045892 "negative regulation of transcription, DNA-dependent" evidence=IEP] [GO:0005515 "protein binding" evidence=IPI] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=TAS] [GO:0009733 "response to auxin stimulus" evidence=IEP] InterPro:IPR003311 InterPro:IPR003340 InterPro:IPR010525 InterPro:IPR011525 Pfam:PF02309 Pfam:PF02362 Pfam:PF06507 PROSITE:PS50863 PROSITE:PS50962 SMART:SM01019 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005634 GO:GO:0045892 GO:GO:0009734 GO:GO:0003677 GO:GO:0006351 GO:GO:0010150 EMBL:AC007258 GO:GO:0046983 InterPro:IPR015300 Gene3D:G3DSA:2.40.330.10 SUPFAM:SSF101936 EMBL:U83245 EMBL:AY133723 EMBL:BT002748 IPI:IPI00518211 IPI:IPI00520405 PIR:D96621 RefSeq:NP_001031208.1 RefSeq:NP_176184.1 RefSeq:NP_849830.1 UniGene:At.74832 ProteinModelPortal:Q8L7G0 SMR:Q8L7G0 IntAct:Q8L7G0 STRING:Q8L7G0 PRIDE:Q8L7G0 EnsemblPlants:AT1G59750.1 EnsemblPlants:AT1G59750.3 GeneID:842268 KEGG:ath:AT1G59750 GeneFarm:3363 TAIR:At1g59750 eggNOG:NOG257828 HOGENOM:HBG746399 InParanoid:Q8L7G0 KO:K14486 OMA:NEFCGMV PhylomeDB:Q8L7G0 ProtClustDB:CLSN2679699 ArrayExpress:Q8L7G0 Genevestigator:Q8L7G0 GermOnline:AT1G59750 Uniprot:Q8L7G0
Root	Isotig06706	12	32	-1.544	0.000803022	TAIR|locus:2025991 - symbol:ARF1 "AT1G59750" species:3702 "Arabidopsis thaliana" [GO:0005634 "nucleus" evidence=ISS] [GO:0003677 "DNA binding" evidence=IDA;IPI] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS;TAS] [GO:0010150 "leaf senescence" evidence=IGI] [GO:0045892 "negative regulation of transcription, DNA-dependent" evidence=IEP] [GO:0005515 "protein binding" evidence=IPI] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=TAS] [GO:0009733 "response to auxin stimulus" evidence=IEP] InterPro:IPR003311 InterPro:IPR003340 InterPro:IPR010525 InterPro:IPR011525 Pfam:PF02309 Pfam:PF02362 Pfam:PF06507 PROSITE:PS50863 PROSITE:PS50962 SMART:SM01019 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005634 GO:GO:0045892 GO:GO:0009734 GO:GO:0003677 GO:GO:0006351 GO:GO:0010150 EMBL:AC007258 GO:GO:0046983 InterPro:IPR015300 Gene3D:G3DSA:2.40.330.10 SUPFAM:SSF101936 EMBL:U83245 EMBL:AY133723 EMBL:BT002748 IPI:IPI00518211 IPI:IPI00520405 PIR:D96621 RefSeq:NP_001031208.1 RefSeq:NP_176184.1 RefSeq:NP_849830.1 UniGene:At.74832 ProteinModelPortal:Q8L7G0 SMR:Q8L7G0 IntAct:Q8L7G0 STRING:Q8L7G0 PRIDE:Q8L7G0 EnsemblPlants:AT1G59750.1 EnsemblPlants:AT1G59750.3 GeneID:842268 KEGG:ath:AT1G59750 GeneFarm:3363 TAIR:At1g59750 eggNOG:NOG257828 HOGENOM:HBG746399 InParanoid:Q8L7G0 KO:K14486 OMA:NEFCGMV PhylomeDB:Q8L7G0 ProtClustDB:CLSN2679699 ArrayExpress:Q8L7G0 Genevestigator:Q8L7G0 GermOnline:AT1G59750 Uniprot:Q8L7G0
Root	Isotig06707	69	4	3.980	1.80E-15	TAIR|locus:2155894 - symbol:SUS2 "AT5G49190" species:3702 "Arabidopsis thaliana" [GO:0005986 "sucrose biosynthetic process" evidence=ISS] [GO:0008194 "UDP-glycosyltransferase activity" evidence=ISS] [GO:0016157 "sucrose synthase activity" evidence=ISS;IMP] [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0001666 "response to hypoxia" evidence=IEP] [GO:0009505 "plant-type cell wall" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0005982 "starch metabolic process" evidence=IMP] [GO:0005985 "sucrose metabolic process" evidence=IMP] [GO:0010431 "seed maturation" evidence=IMP] InterPro:IPR000368 InterPro:IPR001296 InterPro:IPR012820 Pfam:PF00534 Pfam:PF00862 GO:GO:0005829 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0016020 GO:GO:0001666 GO:GO:0009058 GO:GO:0009505 eggNOG:COG0438 GO:GO:0010431 CAZy:GT4 EMBL:AB016872 GO:GO:0005985 GO:GO:0005982 HOGENOM:HBG286768 GO:GO:0016157 PANTHER:PTHR12526:SF27 TIGRFAMs:TIGR02470 EMBL:X60987 IPI:IPI00539012 PIR:S19125 RefSeq:NP_199730.1 UniGene:At.8597 ProteinModelPortal:Q00917 STRING:Q00917 PRIDE:Q00917 GeneID:834978 KEGG:ath:AT5G49190 TAIR:At5g49190 InParanoid:Q00917 PhylomeDB:Q00917 ArrayExpress:Q00917 Genevestigator:Q00917 GermOnline:AT5G49190 Uniprot:Q00917

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig06708	62	4	3.825	9.77E-14	TAIR|locus:2155894 - symbol:SUS2 "AT5G49190" species:3702 "Arabidopsis thaliana" [GO:0005986 "sucrose biosynthetic process" evidence=ISS] [GO:0008194 "UDP-glycosyltransferase activity" evidence=ISS] [GO:0016157 "sucrose synthase activity" evidence=ISS;IMP] [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0001666 "response to hypoxia" evidence=IEP] [GO:0009505 "plant-type cell wall" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0005982 "starch metabolic process" evidence=IMP] [GO:0005985 "sucrose metabolic process" evidence=IMP] [GO:0010431 "seed maturation" evidence=IMP] InterPro:IPR000368 InterPro:IPR001296 InterPro:IPR012820 Pfam:PF00534 Pfam:PF00862 GO:GO:0005829 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0016020 GO:GO:0001666 GO:GO:0009058 GO:GO:0009505 eggNOG:COG0438 GO:GO:0010431 CAZy:GT4 EMBL:AB016872 GO:GO:0005985 GO:GO:0005982 HOGENOM:HBG286768 GO:GO:0016157 PANTHER:PTHR12526:SF27 TIGRFAMs:TIGR02470 EMBL:X60987 IPI:IPI00539012 PIR:S19125 RefSeq:NP_199730.1 UniGene:At.8597 ProteinModelPortal:Q00917 STRING:Q00917 PRIDE:Q00917 GeneID:834978 KEGG:ath:AT5G49190 TAIR:At5g49190 InParanoid:Q00917 PhylomeDB:Q00917 ArrayExpress:Q00917 Genevestigator:Q00917 GermOnline:AT5G49190 Uniprot:Q00917
Root	Isotig06711	3	32	-3.544	5.33E-08	TAIR|locus:2117343 - symbol:AT4G25160 species:3702 "Arabidopsis thaliana" [GO:0000151 "ubiquitin ligase complex" evidence=IEA] [GO:0006468 "protein phosphorylation" evidence=IEA] [GO:0006950 "response to stress" evidence=IEA] [GO:0016301 "kinase activity" evidence=ISS] [GO:0016567 "protein ubiquitination" evidence=IEA] [GO:0005515 "protein binding" evidence=IPI] InterPro:IPR000719 InterPro:IPR001245 InterPro:IPR003613 InterPro:IPR006016 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 Pfam:PF00582 Pfam:PF04564 Pfam:PF07714 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 SMART:SM00504 GO:GO:0005524 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005515 GO:GO:0006950 eggNOG:COG0515 SUPFAM:SSF56112 GO:GO:0004674 InterPro:IPR013083 Gene3D:G3DSA:3.30.40.10 EMBL:AL161562 GO:GO:0004842 InterPro:IPR014729 Gene3D:G3DSA:3.40.50.620 GO:GO:0000151 EMBL:AL035523 EMBL:AL035396 HSSP:Q8VZ40 HOGENOM:HBG590743 EMBL:BX828107 IPI:IPI00540343 PIR:T05537 RefSeq:NP_194246.2 UniGene:At.32287 ProteinModelPortal:Q9SW11 SMR:Q9SW11 IntAct:Q9SW11 PRIDE:Q9SW11 EnsemblPlants:AT4G25160.1 GeneID:828619 KEGG:ath:AT4G25160 GeneFarm:2015 TAIR:At4g25160 InParanoid:Q9SW11 OMA:FQQELEI PhylomeDB:Q9SW11 ProtClustDB:CLSN2918598 ArrayExpress:Q9SW11 Genevestigator:Q9SW11 Uniprot:Q9SW11
Root	Isotig06712	3	32	-3.544	5.33E-08	TAIR|locus:2117343 - symbol:AT4G25160 species:3702 "Arabidopsis thaliana" [GO:0000151 "ubiquitin ligase complex" evidence=IEA] [GO:0006468 "protein phosphorylation" evidence=IEA] [GO:0006950 "response to stress" evidence=IEA] [GO:0016301 "kinase activity" evidence=ISS] [GO:0016567 "protein ubiquitination" evidence=IEA] [GO:0005515 "protein binding" evidence=IPI] InterPro:IPR000719 InterPro:IPR001245 InterPro:IPR003613 InterPro:IPR006016 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 Pfam:PF00582 Pfam:PF04564 Pfam:PF07714 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 SMART:SM00504 GO:GO:0005524 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005515 GO:GO:0006950 eggNOG:COG0515 SUPFAM:SSF56112 GO:GO:0004674 InterPro:IPR013083 Gene3D:G3DSA:3.30.40.10 EMBL:AL161562 GO:GO:0004842 InterPro:IPR014729 Gene3D:G3DSA:3.40.50.620 GO:GO:0000151 EMBL:AL035523 EMBL:AL035396 HSSP:Q8VZ40 HOGENOM:HBG590743 EMBL:BX828107 IPI:IPI00540343 PIR:T05537 RefSeq:NP_194246.2 UniGene:At.32287 ProteinModelPortal:Q9SW11 SMR:Q9SW11 IntAct:Q9SW11 PRIDE:Q9SW11 EnsemblPlants:AT4G25160.1 GeneID:828619 KEGG:ath:AT4G25160 GeneFarm:2015 TAIR:At4g25160 InParanoid:Q9SW11 OMA:FQQELEI PhylomeDB:Q9SW11 ProtClustDB:CLSN2918598 ArrayExpress:Q9SW11 Genevestigator:Q9SW11 Uniprot:Q9SW11
Root	Isotig06715	31	8	1.825	0.000382406	TAIR|locus:2035893 - symbol:AT1G42440 "AT1G42440" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005634 "nucleus" evidence=IEA] [GO:0042254 "ribosome biogenesis" evidence=IEA] InterPro:IPR012948 Pfam:PF08142 SMART:SM00785 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005634 GO:GO:0042254 InterPro:IPR007034 Pfam:PF04950 eggNOG:COG5177 HOGENOM:HBG330634 KO:K14799 OMA:DAEQTWP EMBL:AF361826 EMBL:AY133551 EMBL:BT000755 IPI:IPI00527453 RefSeq:NP_564480.1 UniGene:At.19120 UniGene:At.67019 ProteinModelPortal:Q9ASU6 IntAct:Q9ASU6 STRING:Q9ASU6 PRIDE:Q9ASU6 EnsemblPlants:AT1G42440.1 GeneID:840848 KEGG:ath:AT1G42440 TAIR:At1g42440 InParanoid:Q9ASU6 PhylomeDB:Q9ASU6 ProtClustDB:CLSN2688391 ArrayExpress:Q9ASU6 Genevestigator:Q9ASU6 Uniprot:Q9ASU6

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig06716	31	8	1.825	0.000382406	TAIR|locus:2035893 - symbol:AT1G42440 "AT1G42440" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005634 "nucleus" evidence=IEA] [GO:0042254 "ribosome biogenesis" evidence=IEA] InterPro:IPR012948 Pfam:PF08142 SMART:SM00785 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005634 GO:GO:0042254 InterPro:IPR007034 Pfam:PF04950 eggNOG:COG5177 HOGENOM:HBG330634 KO:K14799 OMA:DAEQTWP EMBL:AF361826 EMBL:AY133551 EMBL:BT000755 IPI:IPI00527453 RefSeq:NP_564480.1 UniGene:At.19120 UniGene:At.67019 ProteinModelPortal:Q9ASU6 IntAct:Q9ASU6 STRING:Q9ASU6 PRIDE:Q9ASU6 EnsemblPlants:AT1G42440.1 GeneID:840848 KEGG:ath:AT1G42440 TAIR:At1g42440 InParanoid:Q9ASU6 PhylomeDB:Q9ASU6 ProtClustDB:CLSN2688391 ArrayExpress:Q9ASU6 Genevestigator:Q9ASU6 Uniprot:Q9ASU6
Root	Isotig06719	162	15	3.304	5.50E-30	No hit
Root	Isotig06720	87	10	2.992	1.60E-15	No hit
Root	Isotig06723	13	34	-1.516	0.00065265	TAIR|locus:2175851 - symbol:HDS "AT5G60600" species:3702 "Arabidopsis thaliana" [GO:0008299 "isoprenoid biosynthetic process" evidence=ISS] [GO:0046429 "4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase activity" evidence=IGI;ISS;IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0019288 "isopentenyl diphosphate biosynthetic process, mevalonate-independent pathway" evidence=TAS] [GO:0051539 "4 iron, 4 sulfur cluster binding" evidence=IDA] [GO:0009617 "response to bacterium" evidence=IMP] [GO:0009862 "systemic acquired resistance, salicylic acid mediated signaling pathway" evidence=IMP] [GO:0009570 "chloroplast stroma" evidence=IDA] InterPro:IPR004588 InterPro:IPR017178 Pfam:PF04551 PIRSF:PIRSF037336 GO:GO:0009570 GenomeReviews:BA000015_GR GO:GO:0009617 GO:GO:0005506 GO:GO:0009941 GO:GO:0051539 GO:GO:0009862 GO:GO:0019288 GO:GO:0016114 HOGENOM:HBG335271 GO:GO:0046429 HAMAP:MF_00159 TIGRFAMs:TIGR00612 EMBL:AY094472 IPI:IPI00530209 ProteinModelPortal:Q8LPQ4 STRING:Q8LPQ4 PRIDE:Q8LPQ4 TAIR:At5g60600 InParanoid:Q8LPQ4 PhylomeDB:Q8LPQ4 Genevestigator:Q8LPQ4 Uniprot:Q8LPQ4
Root	Isotig06725	20	2	3.193	8.23E-05	TAIR|locus:2142788 - symbol:DGK1 "AT5G07920" species:3702 "Arabidopsis thaliana" [GO:0004143 "diacylglycerol kinase activity" evidence=ISS;TAS] [GO:0007205 "activation of protein kinase C activity by G-protein coupled receptor protein signaling pathway" evidence=IEA;ISS] [GO:0035556 "intracellular signal transduction" evidence=IEA] [GO:0005509 "calcium ion binding" evidence=ISS] InterPro:IPR000756 InterPro:IPR001206 InterPro:IPR002219 Pfam:PF00130 Pfam:PF00609 Pfam:PF00781 PROSITE:PS00479 PROSITE:PS50081 PROSITE:PS50146 SMART:SM00045 SMART:SM00046 SMART:SM00109 GO:GO:0016021 GO:GO:0005524 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0035556 GO:GO:0046872 GO:GO:0007205 InterPro:IPR013083 Gene3D:G3DSA:3.30.40.10 GO:GO:0004143 EMBL:AL133421 EMBL:AB005249 EMBL:D63787 EMBL:BT004148 IPI:IPI00527797 PIR:S71467 RefSeq:NP_196409.1 UniGene:At.260 ProteinModelPortal:Q39017 SMR:Q39017 STRING:Q39017 PRIDE:Q39017 EnsemblPlants:AT5G07920.1 GeneID:830686 KEGG:ath:AT5G07920 TAIR:At5g07920 eggNOG:NOG47311 HOGENOM:HBG317349 InParanoid:Q39017 KO:K00901 OMA:VDLWQNE PhylomeDB:Q39017 ProtClustDB:CLSN2687236 ArrayExpress:Q39017 Genevestigator:Q39017 GermOnline:AT5G07920 Uniprot:Q39017
Root	Isotig06726	20	2	3.193	8.23E-05	TAIR|locus:2142788 - symbol:DGK1 "AT5G07920" species:3702 "Arabidopsis thaliana" [GO:0004143 "diacylglycerol kinase activity" evidence=ISS;TAS] [GO:0007205 "activation of protein kinase C activity by G-protein coupled receptor protein signaling pathway" evidence=IEA;ISS] [GO:0035556 "intracellular signal transduction" evidence=IEA] [GO:0005509 "calcium ion binding" evidence=ISS] InterPro:IPR000756 InterPro:IPR001206 InterPro:IPR002219 Pfam:PF00130 Pfam:PF00609 Pfam:PF00781 PROSITE:PS00479 PROSITE:PS50081 PROSITE:PS50146 SMART:SM00045 SMART:SM00046 SMART:SM00109 GO:GO:0016021 GO:GO:0005524 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0035556 GO:GO:0046872 GO:GO:0007205 InterPro:IPR013083 Gene3D:G3DSA:3.30.40.10 GO:GO:0004143 EMBL:AL133421 EMBL:AB005249 EMBL:D63787 EMBL:BT004148 IPI:IPI00527797 PIR:S71467 RefSeq:NP_196409.1 UniGene:At.260 ProteinModelPortal:Q39017 SMR:Q39017 STRING:Q39017 PRIDE:Q39017 EnsemblPlants:AT5G07920.1 GeneID:830686 KEGG:ath:AT5G07920 TAIR:At5g07920 eggNOG:NOG47311 HOGENOM:HBG317349 InParanoid:Q39017 KO:K00901 OMA:VDLWQNE PhylomeDB:Q39017 ProtClustDB:CLSN2687236 ArrayExpress:Q39017 Genevestigator:Q39017 GermOnline:AT5G07920 Uniprot:Q39017
Root	Isotig06743	7	33	-2.366	6.09E-06	TAIR|locus:2050669 - symbol:AT2G45910 species:3702 "Arabidopsis thaliana" [GO:0000151 "ubiquitin ligase complex" evidence=IEA] [GO:0004672 "protein kinase activity" evidence=IEA] [GO:0004674 "protein serine/threonine kinase activity" evidence=IEA] [GO:0004842 "ubiquitin-protein ligase activity" evidence=IEA]

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						[GO:0005524 "ATP binding" evidence=IEA] [GO:0006468 "protein phosphorylation" evidence=IEA] [GO:0006950 "response to stress" evidence=IEA] [GO:0016301 "kinase activity" evidence=ISS] [GO:0016567 "protein ubiquitination" evidence=IEA] InterPro:IPR000719 InterPro:IPR003613 InterPro:IPR006016 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 Pfam:PF00069 Pfam:PF00582 Pfam:PF04564 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 SMART:SM00504 GO:GO:0005524 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0006950 eggNOG:COG0515 SUPFAM:SSF56112 GO:GO:0004674 HOGENOM:HBG755340 InterPro:IPR013083 Gene3D:G3DSA:3.30.40.10 GO:GO:0004842 InterPro:IPR014729 Gene3D:G3DSA:3.40.50.620 GO:GO:0000151 EMBL:AC004665 HSSP:Q8VZ40 EMBL:BT002512 EMBL:AK227123 IPI:IPI00542046 PIR:T02456 RefSeq:NP_182115.2 UniGene:At.36571 ProteinModelPortal:Q8GUH1 SMR:Q8GUH1 PRIDE:Q8GUH1 EnsemblPlants:AT2G45910.1 GeneID:819199 KEGG:ath:AT2G45910 GeneFarm:1984 TAIR:At2g45910 InParanoid:Q8GUH1 OMA:SQMIPLM PhylomeDB:Q8GUH1 ProtClustDB:CLSN2680270 Genevestigator:Q8GUH1 Uniprot:Q8GUH1
Root	Isotig06744	8	33	-2.173	1.74E-05	TAIR|locus:2050669 - symbol:AT2G45910 species:3702 "Arabidopsis thaliana" [GO:0000151 "ubiquitin ligase complex" evidence=IEA] [GO:0004672 "protein kinase activity" evidence=IEA] [GO:0004674 "protein serine/threonine kinase activity" evidence=IEA] [GO:0004842 "ubiquitin-protein ligase activity" evidence=IEA] [GO:0005524 "ATP binding" evidence=IEA] [GO:0006468 "protein phosphorylation" evidence=IEA] [GO:0006950 "response to stress" evidence=IEA] [GO:0016301 "kinase activity" evidence=ISS] [GO:0016567 "protein ubiquitination" evidence=IEA] InterPro:IPR000719 InterPro:IPR003613 InterPro:IPR006016 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 Pfam:PF00069 Pfam:PF00582 Pfam:PF04564 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 SMART:SM00504 GO:GO:0005524 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0006950 eggNOG:COG0515 SUPFAM:SSF56112 GO:GO:0004674 HOGENOM:HBG755340 InterPro:IPR013083 Gene3D:G3DSA:3.30.40.10 GO:GO:0004842 InterPro:IPR014729 Gene3D:G3DSA:3.40.50.620 GO:GO:0000151 EMBL:AC004665 HSSP:Q8VZ40 EMBL:BT002512 EMBL:AK227123 IPI:IPI00542046 PIR:T02456 RefSeq:NP_182115.2 UniGene:At.36571 ProteinModelPortal:Q8GUH1 SMR:Q8GUH1 PRIDE:Q8GUH1 EnsemblPlants:AT2G45910.1 GeneID:819199 KEGG:ath:AT2G45910 GeneFarm:1984 TAIR:At2g45910 InParanoid:Q8GUH1 OMA:SQMIPLM PhylomeDB:Q8GUH1 ProtClustDB:CLSN2680270 Genevestigator:Q8GUH1 Uniprot:Q8GUH1
Root	Isotig06745	21	59	-1.619	2.46E-06	TAIR|locus:2198656 - symbol:ATSBT5.2 "AT1G20160" species:3702 "Arabidopsis thaliana" [GO:0004252 "serine-type endopeptidase activity" evidence=IEA;IBA] [GO:0005618 "cell wall" evidence=IBA] [GO:0006508 "proteolysis" evidence=ISS] [GO:0008152 "metabolic process" evidence=IBA] [GO:0042802 "identical protein binding" evidence=IEA] [GO:0048046 "apoplast" evidence=IDA] InterPro:IPR000209 InterPro:IPR010259 Pfam:PF00082 Pfam:PF05922 InterPro:IPR003137 Prosite:PS00137 Prosite:PS00138 PANTHER:PTHR10795 Pfam:PF02225 EMBL:CP002684 GO:GO:0048046 GO:GO:0042802 GO:GO:0006508 GO:GO:0004252 GO:GO:0043086 InterPro:IPR022398 InterPro:IPR023828 InterPro:IPR015500 Gene3D:G3DSA:3.40.50.200 PRINTS:PR00723 SUPFAM:SSF52743 EMBL:AC022472 HSSP:Q45670 EMBL:AK228874 IPI:IPI00518804 PIR:D86335 RefSeq:NP_564107.1 UniGene:At.24841 ProteinModelPortal:Q9LNU1 SMR:Q9LNU1 MEROPS:S08.A22 PRIDE:Q9LNU1 ProMEX:Q9LNU1 EnsemblPlants:AT1G20160.1 GeneID:838606 KEGG:ath:AT1G20160 TAIR:At1g20160 InParanoid:Q9LNU1 OMA:GGNKVIK PhylomeDB:Q9LNU1 ProtClustDB:CLSN2687878 Genevestigator:Q9LNU1 Uniprot:Q9LNU1
Root	Isotig06746	21	59	-1.619	2.46E-06	TAIR|locus:2198656 - symbol:ATSBT5.2 "AT1G20160" species:3702 "Arabidopsis thaliana" [GO:0004252 "serine-type endopeptidase activity" evidence=IEA;IBA] [GO:0005618 "cell wall" evidence=IBA] [GO:0006508 "proteolysis" evidence=ISS] [GO:0008152 "metabolic process" evidence=IBA] [GO:0042802 "identical protein binding" evidence=IEA] [GO:0048046 "apoplast" evidence=IDA] InterPro:IPR000209 InterPro:IPR010259 Pfam:PF00082 Pfam:PF05922 InterPro:IPR003137 Prosite:PS00137 Prosite:PS00138 PANTHER:PTHR10795 Pfam:PF02225 EMBL:CP002684 GO:GO:0048046 GO:GO:0042802 GO:GO:0006508 GO:GO:0004252 GO:GO:0043086 InterPro:IPR022398 InterPro:IPR023828 InterPro:IPR015500 Gene3D:G3DSA:3.40.50.200 PRINTS:PR00723 SUPFAM:SSF52743 EMBL:AC022472 HSSP:Q45670 EMBL:AK228874 IPI:IPI00518804 PIR:D86335 RefSeq:NP_564107.1 UniGene:At.24841 ProteinModelPortal:Q9LNU1 SMR:Q9LNU1 MEROPS:S08.A22 PRIDE:Q9LNU1 ProMEX:Q9LNU1 EnsemblPlants:AT1G20160.1 GeneID:838606 KEGG:ath:AT1G20160 TAIR:At1g20160 InParanoid:Q9LNU1 OMA:GGNKVIK PhylomeDB:Q9LNU1 ProtClustDB:CLSN2687878 Genevestigator:Q9LNU1 Uniprot:Q9LNU1

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig06753	18	2	3.041	0.000259481	TAIR|locus:2125541 - symbol:AT4G03200 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0009507 "chloroplast" evidence=IDA] InterPro:IPR008928 InterPro:IPR012341 GenomeReviews:CT486007_GR GO:GO:0009507 GO:GO:0003824 Gene3D:G3DSA:1.50.10.10 SUPFAM:SSF48208 InterPro:IPR012336 Gene3D:G3DSA:3.40.30.10 SUPFAM:SSF52833 InterPro:IPR004879 InterPro:IPR024705 Pfam:PF03190 PIRSF:PIRSF006402 HOGENOM:HBG756603 EMBL:AY062530 EMBL:BT010343 IPI:IPI00528599 ProteinModelPortal:Q8W4J1 SMR:Q8W4J1 STRING:Q8W4J1 PRIDE:Q8W4J1 TAIR:At4g03200 InParanoid:Q8W4J1 PhylomeDB:Q8W4J1 Genevestigator:Q8W4J1 Uniprot:Q8W4J1
Root	Isotig06754	18	2	3.041	0.000259481	TAIR|locus:2125541 - symbol:AT4G03200 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0009507 "chloroplast" evidence=IDA] InterPro:IPR008928 InterPro:IPR012341 GenomeReviews:CT486007_GR GO:GO:0009507 GO:GO:0003824 Gene3D:G3DSA:1.50.10.10 SUPFAM:SSF48208 InterPro:IPR012336 Gene3D:G3DSA:3.40.30.10 SUPFAM:SSF52833 InterPro:IPR004879 InterPro:IPR024705 Pfam:PF03190 PIRSF:PIRSF006402 HOGENOM:HBG756603 EMBL:AY062530 EMBL:BT010343 IPI:IPI00528599 ProteinModelPortal:Q8W4J1 SMR:Q8W4J1 STRING:Q8W4J1 PRIDE:Q8W4J1 TAIR:At4g03200 InParanoid:Q8W4J1 PhylomeDB:Q8W4J1 Genevestigator:Q8W4J1 Uniprot:Q8W4J1
Root	Isotig06757	23	5	2.073	0.000873448	TAIR|locus:2152965 - symbol:AT5G41770 species:3702 "Arabidopsis thaliana" [GO:0005622 "intracellular" evidence=IEA;ISS] [GO:0006396 "RNA processing" evidence=IEA;ISS] InterPro:IPR003107 InterPro:IPR011990 InterPro:IPR013026 Pfam:PF02184 PROSITE:PS50293 SMART:SM00386 GenomeReviews:BA000015_GR GO:GO:0005488 Gene3D:G3DSA:1.25.40.10 GO:GO:0006396 GO:GO:0005622 eggNOG:NOG327505 HOGENOM:HBG611628 EMBL:BT002040 IPI:IPI00530971 ProteinModelPortal:Q8GTX9 SMR:Q8GTX9 IntAct:Q8GTX9 STRING:Q8GTX9 PRIDE:Q8GTX9 TAIR:At5g41770 InParanoid:Q8GTX9 PhylomeDB:Q8GTX9 ArrayExpress:Q8GTX9 Genevestigator:Q8GTX9 Uniprot:Q8GTX9
Root	Isotig06758	23	5	2.073	0.000873448	TAIR|locus:2152965 - symbol:AT5G41770 species:3702 "Arabidopsis thaliana" [GO:0005622 "intracellular" evidence=IEA;ISS] [GO:0006396 "RNA processing" evidence=IEA;ISS] InterPro:IPR003107 InterPro:IPR011990 InterPro:IPR013026 Pfam:PF02184 PROSITE:PS50293 SMART:SM00386 GenomeReviews:BA000015_GR GO:GO:0005488 Gene3D:G3DSA:1.25.40.10 GO:GO:0006396 GO:GO:0005622 eggNOG:NOG327505 HOGENOM:HBG611628 EMBL:BT002040 IPI:IPI00530971 ProteinModelPortal:Q8GTX9 SMR:Q8GTX9 IntAct:Q8GTX9 STRING:Q8GTX9 PRIDE:Q8GTX9 TAIR:At5g41770 InParanoid:Q8GTX9 PhylomeDB:Q8GTX9 ArrayExpress:Q8GTX9 Genevestigator:Q8GTX9 Uniprot:Q8GTX9
Root	Isotig06761	25	0	5.515	3.68E-07	No hit
Root	Isotig06762	25	0	5.515	3.68E-07	No hit
Root	Isotig06765	1	24	-4.714	3.11E-07	TIGR_CMR|GSU_0686 - symbol:GSU_0686 "deoxyxylulose-5-phosphate synthase" species:243231 "Geobacter sulfurreducens PCA" [GO:0008299 "isoprenoid biosynthetic process" evidence=ISS] [GO:0008615 "pyridoxine biosynthetic process" evidence=ISS] [GO:0008661 "1-deoxy-D-xylulose-5-phosphate synthase activity" evidence=ISS] [GO:0009228 "thiamine biosynthetic process" evidence=ISS] HAMAP:MF_00315 InterPro:IPR005476 InterPro:IPR005477 InterPro:IPR009014 InterPro:IPR015941 Pfam:PF02780 InterPro:IPR005475 Pfam:PF02779 InterPro:IPR005474 EMBL:AE017180 GenomeReviews:AE017180_GR GO:GO:0009228 SMART:SM00861 RefSeq:NP_951743.1 ProteinModelPortal:Q74FC3 GeneID:2685342 KEGG:gsu:GSU0686 PATRIC:22024127 TIGR:GSU0686 eggNOG:COG1154 HOGENOM:HBG571647 KO:K01662 OMA:DPILYHG PhylomeDB:Q74FC3 ProtClustDB:PRK05444 BioCyc:GSUL243231:GSU_0686-MONOMER GO:GO:0008661 GO:GO:0016114 InterPro:IPR020826 Gene3D:G3DSA:3.40.50.920 SUPFAM:SSF52922 TIGRFAMs:TIGR00204 PROSITE:PS00801 PROSITE:PS00802 Uniprot:Q74FC3
Root	Isotig06766	1	19	-4.377	7.43E-06	TAIR|locus:2130374 - symbol:CLA1 "AT4G15560" species:3702 "Arabidopsis thaliana" [GO:0008661 "1-deoxy-D-xylulose-5-phosphate synthase activity" evidence=IDA] [GO:0015995 "chlorophyll biosynthetic process" evidence=IMP] [GO:0019288 "isopentenyl diphosphate biosynthetic process, mevalonate-independent pathway" evidence=TAS] [GO:0009507 "chloroplast" evidence=IDA] InterPro:IPR005476 InterPro:IPR005477 InterPro:IPR009014 InterPro:IPR015941 Pfam:PF02780 InterPro:IPR005475 Pfam:PF02779 InterPro:IPR005474 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0009507 GO:GO:0015995 GO:GO:0009228 EMBL:AL161542 EMBL:Z97339 SMART:SM00861 GO:GO:0019288 eggNOG:COG1154 HOGENOM:HBG571647 KO:K01662 OMA:DPILYHG GO:GO:0008661 GO:GO:0016114 InterPro:IPR020826 Gene3D:G3DSA:3.40.50.920 SUPFAM:SSF52922 TIGRFAMs:TIGR00204 PROSITE:PS00801 PROSITE:PS00802 EMBL:U27099 EMBL:Y14333 EMBL:BT002340 IPI:IPI00516684 PIR:H85171 PIR:T52289 RefSeq:NP_193291.1 UniGene:At.23240 ProteinModelPortal:Q38854 SMR:Q38854 STRING:Q38854 PRIDE:Q38854 EnsemblPlants:AT4G15560.1

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GeneID:827230 KEGG:ath:AT4G15560 TAIR:At4g15560 InParanoid:Q38854 PhylomeDB:Q38854 ProtClustDB:PLN02582 BioCyc:ARA:AT4G15560-MONOMER BioCyc:MetaCyc:AT4G15560-MONOMER Genevestigator:Q38854 GermOnline:AT4G15560 Uniprot:Q38854
Root	Isotig06771	5	24	-2.392	0.000103464	TAIR|locus:2007760 - symbol:AGO1 "AT1G48410" species:3702 "Arabidopsis thaliana" [GO:0016441 "posttranscriptional gene silencing" evidence=IEP] [GO:0035195 "gene silencing by miRNA" evidence=IGI;IEP;IMP] [GO:0009733 "response to auxin stimulus" evidence=IGI] [GO:0009850 "auxin metabolic process" evidence=IGI] [GO:0010218 "response to far red light" evidence=IGI] [GO:0048830 "adventitious root development" evidence=IMP] [GO:0004521 "endoribonuclease activity" evidence=IDA] [GO:0035197 "siRNA binding" evidence=IPI] [GO:0035198 "miRNA binding" evidence=IPI] [GO:0009616 "virus induced gene silencing" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA;TAS] [GO:0016246 "RNA interference" evidence=IMP] [GO:0005515 "protein binding" evidence=IPI] [GO:0005829 "cytosol" evidence=IDA] [GO:0048864 "stem cell development" evidence=IGI] [GO:0045087 "innate immune response" evidence=IMP] [GO:0000300 "peripheral to membrane of membrane fraction" evidence=IDA] [GO:0009965 "leaf morphogenesis" evidence=IMP] [GO:0009793 "embryo development ending in seed dormancy" evidence=IGI] InterPro:IPR003100 InterPro:IPR003165 InterPro:IPR012337 Pfam:PF02170 Pfam:PF02171 PROSITE:PS50821 PROSITE:PS50822 SMART:SM00949 SMART:SM00950 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0005634 GO:GO:0005515 GO:GO:0009733 GO:GO:0006417 GO:GO:0016246 GO:GO:0006355 GO:GO:0006351 GO:GO:0010218 GO:GO:0009793 GO:GO:0030529 GO:GO:0009850 SUPFAM:SSF53098 GO:GO:0009965 eggNOG:NOG279895 HOGENOM:HBG717005 KO:K11596 GO:GO:0035198 InterPro:IPR014811 Pfam:PF08699 SUPFAM:SSF101690 EMBL:U91995 EMBL:AC007932 EMBL:AC020889 EMBL:BT000941 EMBL:AK227868 IPI:IPI00522985 IPI:IPI00523962 RefSeq:NP_001185169.1 RefSeq:NP_175274.1 RefSeq:NP_849784.1 UniGene:At.21124 ProteinModelPortal:O04379 SMR:O04379 STRING:O04379 PRIDE:O04379 EnsemblPlants:AT1G48410.1 GeneID:841262 KEGG:ath:AT1G48410 TAIR:At1g48410 InParanoid:O04379 OMA:RANHFQI PhylomeDB:O04379 ProtClustDB:CLSN2693050 ArrayExpress:O04379 Genevestigator:O04379 GO:GO:0004521 GO:GO:0035197 GO:GO:0048830 GO:GO:0035195 GO:GO:0048864 GO:GO:0009616 InterPro:IPR024357 Pfam:PF12764 Uniprot:O04379
Root	Isotig06772	2	23	-3.653	3.09E-06	TAIR|locus:2007760 - symbol:AGO1 "AT1G48410" species:3702 "Arabidopsis thaliana" [GO:0016441 "posttranscriptional gene silencing" evidence=IEP] [GO:0035195 "gene silencing by miRNA" evidence=IGI;IEP;IMP] [GO:0009733 "response to auxin stimulus" evidence=IGI] [GO:0009850 "auxin metabolic process" evidence=IGI] [GO:0010218 "response to far red light" evidence=IGI] [GO:0048830 "adventitious root development" evidence=IMP] [GO:0004521 "endoribonuclease activity" evidence=IDA] [GO:0035197 "siRNA binding" evidence=IPI] [GO:0035198 "miRNA binding" evidence=IPI] [GO:0009616 "virus induced gene silencing" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA;TAS] [GO:0016246 "RNA interference" evidence=IMP] [GO:0005515 "protein binding" evidence=IPI] [GO:0005829 "cytosol" evidence=IDA] [GO:0048864 "stem cell development" evidence=IGI] [GO:0045087 "innate immune response" evidence=IMP] [GO:0000300 "peripheral to membrane of membrane fraction" evidence=IDA] [GO:0009965 "leaf morphogenesis" evidence=IMP] [GO:0009793 "embryo development ending in seed dormancy" evidence=IGI] InterPro:IPR003100 InterPro:IPR003165 InterPro:IPR012337 Pfam:PF02170 Pfam:PF02171 PROSITE:PS50821 PROSITE:PS50822 SMART:SM00949 SMART:SM00950 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0005634 GO:GO:0005515 GO:GO:0009733 GO:GO:0006417 GO:GO:0016246 GO:GO:0006355 GO:GO:0006351 GO:GO:0010218 GO:GO:0009793 GO:GO:0030529 GO:GO:0009850 SUPFAM:SSF53098 GO:GO:0009965 eggNOG:NOG279895 HOGENOM:HBG717005 KO:K11596 GO:GO:0035198 InterPro:IPR014811 Pfam:PF08699 SUPFAM:SSF101690 EMBL:U91995 EMBL:AC007932 EMBL:AC020889 EMBL:BT000941 EMBL:AK227868 IPI:IPI00522985 IPI:IPI00523962 RefSeq:NP_001185169.1 RefSeq:NP_175274.1 RefSeq:NP_849784.1 UniGene:At.21124 ProteinModelPortal:O04379 SMR:O04379 STRING:O04379 PRIDE:O04379 EnsemblPlants:AT1G48410.1 GeneID:841262 KEGG:ath:AT1G48410 TAIR:At1g48410 InParanoid:O04379 OMA:RANHFQI PhylomeDB:O04379 ProtClustDB:CLSN2693050 ArrayExpress:O04379 Genevestigator:O04379 GO:GO:0004521 GO:GO:0035197 GO:GO:0048830 GO:GO:0035195 GO:GO:0048864 GO:GO:0009616 InterPro:IPR024357 Pfam:PF12764 Uniprot:O04379
Root	Isotig06782	5	22	-2.266	0.000318925	TAIR|locus:2199512 - symbol:ATG18H "AT1G54710" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0042594 "response to starvation" evidence=IEP] InterPro:IPR017986 InterPro:IPR001680 InterPro:IPR015943 Pfam:PF00400 SMART:SM00320 EMBL:CP002684

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						Gene3D:G3DSA:2.130.10.10 SUPFAM:SSF50978 GO:GO:0042594 eggNOG:NOG321894 InterPro:IPR022175 Pfam:PF12490 ProtClustDB:CLSN2686780 EMBL:AY142626 IPI:IPI00534724 RefSeq:NP_564664.1 UniGene:At.21107 UniGene:At.52203 UniGene:At.64867 ProteinModelPortal:Q8H1Q5 SMR:Q8H1Q5 PRIDE:Q8H1Q5 EnsemblPlants:AT1G54710.1 GeneID:841912 KEGG:ath:AT1G54710 TAIR:At1g54710 InParanoid:Q8H1Q5 OMA:HRGMTSA PhylomeDB:Q8H1Q5 Genevestigator:Q8H1Q5 Uniprot:Q8H1Q5
Root	Isotig06787	44	96	-1.255	7.06E-07	TAIR|locus:2057981 - symbol:PAL1 "PHE ammonia lyase 1" species:3702 "Arabidopsis thaliana" [GO:0005737 "cytoplasm" evidence=IEA] [GO:0009699 "phenylpropanoid biosynthetic process" evidence=TAS] [GO:0045548 "phenylalanine ammonia-lyase activity" evidence=ISS;IDA;TAS] [GO:0006979 "response to oxidative stress" evidence=IEP] [GO:0080167 "response to karrikin" evidence=IEP] [GO:0009555 "pollen development" evidence=IMP] [GO:0009819 "drought recovery" evidence=IMP] [GO:0010224 "response to UV-B" evidence=IMP] [GO:0046244 "salicylic acid catabolic process" evidence=IMP] [GO:0046274 "lignin catabolic process" evidence=IMP] [GO:0006952 "defense response" evidence=TAS] [GO:0009611 "response to wounding" evidence=TAS] InterPro:IPR001106 InterPro:IPR005922 InterPro:IPR008948 InterPro:IPR022313 Pfam:PF00221 PROSITE:PS00488 GO:GO:0005737 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0006979 GO:GO:0009058 GO:GO:0080167 EMBL:AC006922 GO:GO:0009555 SUPFAM:SSF48557 GO:GO:0006559 InterPro:IPR024083 Gene3D:G3DSA:1.10.275.10 GO:GO:0010224 eggNOG:COG2986 GO:GO:0046274 EMBL:L33677 EMBL:AY303128 EMBL:AY045919 EMBL:AY079363 EMBL:BT003330 EMBL:X62747 IPI:IPI00519512 PIR:G84787 PIR:S52990 RefSeq:NP_181241.1 UniGene:At.21614 UniGene:At.22705 ProteinModelPortal:P35510 SMR:P35510 IntAct:P35510 STRING:P35510 PRIDE:P35510 EnsemblPlants:AT2G37040.1 GeneID:818280 KEGG:ath:AT2G37040 TAIR:At2g37040 HOGENOM:HBG318028 InParanoid:P35510 KO:K10775 OMA:QRGADFL PhylomeDB:P35510 ProtClustDB:PLN02457 BRENDA:4.3.1.24 Genevestigator:P35510 GermOnline:AT2G37040 GO:GO:0045548 GO:GO:0009819 GO:GO:0046244 InterPro:IPR023144 Gene3D:G3DSA:1.10.274.20 TIGRFAMs:TIGR01226 Uniprot:P35510
Root	Isotig06796	9	39	-2.244	1.90E-06	TAIR|locus:2012763 - symbol:ADL6 "AT1G10290" species:3702 "Arabidopsis thaliana" [GO:0003924 "GTPase activity" evidence=ISS] [GO:0005794 "Golgi apparatus" evidence=IDA] [GO:0006896 "Golgi to vacuole transport" evidence=IMP] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] Pfam:PF00169 InterPro:IPR000375 InterPro:IPR001401 InterPro:IPR001849 InterPro:IPR003130 Pfam:PF00350 Pfam:PF01031 Pfam:PF02212 PROSITE:PS50003 SMART:SM00053 SMART:SM00233 GO:GO:0005525 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 GO:GO:0005774 GO:GO:0000139 InterPro:IPR011993 Gene3D:G3DSA:2.30.29.30 GO:GO:0003924 GO:GO:0008289 GO:GO:0005874 GO:GO:0006896 eggNOG:COG0699 InterPro:IPR022812 PRINTS:PR00195 PROSITE:PS00410 EMBL:AC005489 GO:GO:0009524 InterPro:IPR020850 PROSITE:PS51388 InterPro:IPR019762 EMBL:AF180732 EMBL:AK221193 EMBL:AK228995 IPI:IPI00539942 PIR:B86237 RefSeq:NP_172500.1 UniGene:At.11881 ProteinModelPortal:Q9SE83 SMR:Q9SE83 STRING:Q9SE83 PRIDE:Q9SE83 EnsemblPlants:AT1G10290.1 GeneID:837568 KEGG:ath:AT1G10290 GeneFarm:4740 TAIR:At1g10290 HOGENOM:HBG593279 InParanoid:Q9SE83 OMA:ESTRTIG PhylomeDB:Q9SE83 ProtClustDB:CLSN2679567 BRENDA:3.6.5.5 ArrayExpress:Q9SE83 Genevestigator:Q9SE83 GermOnline:AT1G10290 Uniprot:Q9SE83
Root	Isotig06805	1	30	-5.036	7.50E-09	TAIR|locus:2019693 - symbol:ABCG39 "AT1G66950" species:3702 "Arabidopsis thaliana" [GO:0042626 "ATPase activity, coupled to transmembrane movement of substances" evidence=ISS] [GO:0006855 "drug transmembrane transport" evidence=ISS;IMP] [GO:0000302 "response to reactive oxygen species" evidence=IEP] [GO:0005886 "plasma membrane" evidence=IDA] InterPro:IPR003439 InterPro:IPR003593 InterPro:IPR013525 Pfam:PF00005 Pfam:PF01061 PROSITE:PS00211 PROSITE:PS50893 SMART:SM00382 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005886 GO:GO:0005524 eggNOG:COG1131 GO:GO:0016887 HOGENOM:HBG750535 InterPro:IPR013581 Pfam:PF08370 ProtClustDB:CLSN2690483 EMBL:AC007152 EMBL:AC083891 EMBL:BK001010 IPI:IPI00531524 PIR:D96693 RefSeq:NP_176867.2 UniGene:At.35712 ProteinModelPortal:Q7PC84 SMR:Q7PC84 PRIDE:Q7PC84 EnsemblPlants:AT1G66950.1 GeneID:843013 KEGG:ath:AT1G66950 TAIR:At1g66950 InParanoid:Q7PC84 OMA:AKFLWFY PhylomeDB:Q7PC84 ArrayExpress:Q7PC84 Genevestigator:Q7PC84 GermOnline:AT1G66950 GO:GO:0006855 GO:GO:0000302 Uniprot:Q7PC84

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig06806	1	26	-4.829	8.91E-08	TAIR|locus:2019693 - symbol:ABCG39 "AT1G66950" species:3702 "Arabidopsis thaliana" [GO:0042626 "ATPase activity, coupled to transmembrane movement of substances" evidence=ISS] [GO:0006855 "drug transmembrane transport" evidence=ISS;IMP] [GO:0000302 "response to reactive oxygen species" evidence=IEP] [GO:0005886 "plasma membrane" evidence=IDA] InterPro:IPR003439 InterPro:IPR003593 InterPro:IPR013525 Pfam:PF00005 Pfam:PF01061 PROSITE:PS00211 PROSITE:PS50893 SMART:SM00382 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005886 GO:GO:0005524 eggNOG:COG1131 GO:GO:0016887 HOGENOM:HBG750535 InterPro:IPR013581 Pfam:PF08370 ProtClustDB:CLSN2690483 EMBL:AC007152 EMBL:AC083891 EMBL:BK001010 IPI:IPI00531524 PIR:D96693 RefSeq:NP_176867.2 UniGene:At.35712 ProteinModelPortal:Q7PC84 SMR:Q7PC84 PRIDE:Q7PC84 EnsemblPlants:AT1G66950.1 GeneID:843013 KEGG:ath:AT1G66950 TAIR:At1g66950 InParanoid:Q7PC84 OMA:AKFLWFY PhylomeDB:Q7PC84 ArrayExpress:Q7PC84 Genevestigator:Q7PC84 GermOnline:AT1G66950 GO:GO:0006855 GO:GO:0000302 Uniprot:Q7PC84
Root	Isotig06813	3	28	-3.351	6.51E-07	TAIR|locus:2145643 - symbol:RGLG2 "AT5G14420" species:3702 "Arabidopsis thaliana" [GO:0004842 "ubiquitin-protein ligase activity" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009690 "cytokinin metabolic process" evidence=IGI] [GO:0009850 "auxin metabolic process" evidence=IGI] [GO:0005634 "nucleus" evidence=IDA] [GO:0080148 "negative regulation of response to water deprivation" evidence=IGI] InterPro:IPR001841 InterPro:IPR002035 PROSITE:PS50089 PROSITE:PS50234 SMART:SM00184 SMART:SM00327 Prosite:PS00518 GO:GO:0005886 GO:GO:0005634 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0008270 InterPro:IPR013083 Gene3D:G3DSA:3.30.40.10 GO:GO:0009850 EMBL:AL163817 GO:GO:0004842 InterPro:IPR010734 Pfam:PF07002 GO:GO:0009690 GO:GO:0080148 eggNOG:NOG278119 HOGENOM:HBG746179 EMBL:DQ086862 EMBL:AY099597 EMBL:BT000249 IPI:IPI00535253 PIR:T48615 RefSeq:NP_196946.1 RefSeq:NP_850818.1 RefSeq:NP_974779.1 RefSeq:NP_974780.1 UniGene:At.5177 ProteinModelPortal:Q9LY87 SMR:Q9LY87 STRING:Q9LY87 PRIDE:Q9LY87 EnsemblPlants:AT5G14420.1 EnsemblPlants:AT5G14420.2 EnsemblPlants:AT5G14420.3 EnsemblPlants:AT5G14420.4 GeneID:831293 KEGG:ath:AT5G14420 TAIR:At5g14420 InParanoid:Q9LY87 OMA:EMATTIV PhylomeDB:Q9LY87 ProtClustDB:CLSN2687222 ArrayExpress:Q9LY87 Genevestigator:Q9LY87 Uniprot:Q9LY87
Root	Isotig06817	13	41	-1.786	2.57E-05	TAIR|locus:2005496 - symbol:AUX1 "AT2G38120" species:3702 "Arabidopsis thaliana" [GO:0005215 "transporter activity" evidence=ISS] [GO:0006865 "amino acid transport" evidence=ISS] [GO:0009723 "response to ethylene stimulus" evidence=NAS] [GO:0009733 "response to auxin stimulus" evidence=NAS] [GO:0015171 "amino acid transmembrane transporter activity" evidence=ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0009986 "cell surface" evidence=IDA] [GO:0009624 "response to nematode" evidence=IEP] [GO:0010328 "auxin influx transmembrane transporter activity" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009926 "auxin polar transport" evidence=TAS] [GO:0001736 "establishment of planar polarity" evidence=IGI] [GO:0048765 "root hair cell differentiation" evidence=IGI] [GO:0005768 "endosome" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] [GO:0010311 "lateral root formation" evidence=IGI;IMP] [GO:0010011 "auxin binding" evidence=IDA] [GO:0048829 "root cap development" evidence=IMP] [GO:0009958 "positive gravitropism" evidence=IMP] GO:GO:0016021 GO:GO:0005886 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009986 GO:GO:0009734 GO:GO:0009926 GO:GO:0005794 GO:GO:0005768 GO:GO:0015293 GO:GO:0009624 InterPro:IPR013057 Pfam:PF01490 GO:GO:0006865 GO:GO:0009958 GO:GO:0010011 GO:GO:0010311 GO:GO:0048829 EMBL:AC003028 EMBL:X98772 EMBL:AY054488 EMBL:AY093300 EMBL:AY087092 IPI:IPI00525677 PIR:T01244 RefSeq:NP_565882.1 UniGene:At.24295 ProteinModelPortal:Q96247 STRING:Q96247 TCDB:2.A.18.1.1 PRIDE:Q96247 EnsemblPlants:AT2G38120.1 GeneID:818390 KEGG:ath:AT2G38120 TAIR:At2g38120 eggNOG:NOG319329 HOGENOM:HBG320564 InParanoid:Q96247 KO:K13946 OMA:ASARMNA PhylomeDB:Q96247 ProtClustDB:PLN03074 ArrayExpress:Q96247 Genevestigator:Q96247 GermOnline:AT2G38120 GO:GO:0010328 Uniprot:Q96247
Root	Isotig06818	8	33	-2.173	1.74E-05	TAIR|locus:2005496 - symbol:AUX1 "AT2G38120" species:3702 "Arabidopsis thaliana" [GO:0005215 "transporter activity" evidence=ISS] [GO:0006865 "amino acid transport" evidence=ISS] [GO:0009723 "response to ethylene stimulus" evidence=NAS] [GO:0009733 "response to auxin stimulus" evidence=NAS] [GO:0015171 "amino acid transmembrane transporter activity" evidence=ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0009986 "cell surface" evidence=IDA] [GO:0009624 "response to nematode" evidence=IEP] [GO:0010328 "auxin influx transmembrane transporter activity" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009926

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						"auxin polar transport" evidence=TAS] [GO:0001736 "establishment of planar polarity" evidence=IGI] [GO:0048765 "root hair cell differentiation" evidence=IGI] [GO:0005768 "endosome" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] [GO:0010311 "lateral root formation" evidence=IGI;IMP] [GO:0010011 "auxin binding" evidence=IDA] [GO:0048829 "root cap development" evidence=IMP] [GO:0009958 "positive gravitropism" evidence=IMP] GO:GO:0016021 GO:GO:0005886 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009986 GO:GO:0009734 GO:GO:0009926 GO:GO:0005794 GO:GO:0005768 GO:GO:0015293 GO:GO:0009624 InterPro:IPR013057 Pfam:PF01490 GO:GO:0006865 GO:GO:0009958 GO:GO:0010011 GO:GO:0010311 GO:GO:0048829 EMBL:AC003028 EMBL:X98772 EMBL:AY054488 EMBL:AY093300 EMBL:AY087092 IPI:IPI00525677 PIR:T01244 RefSeq:NP_565882.1 UniGene:At.24295 ProteinModelPortal:Q96247 STRING:Q96247 TCDB:2.A.18.1.1 PRIDE:Q96247 EnsemblPlants:AT2G38120.1 GeneID:818390 KEGG:ath:AT2G38120 TAIR:At2g38120 eggNOG:NOG319329 HOGENOM:HBG320564 InParanoid:Q96247 KO:K13946 OMA:ASARMNA PhylomeDB:Q96247 ProtClustDB:PLN03074 ArrayExpress:Q96247 Genevestigator:Q96247 GermOnline:AT2G38120 GO:GO:0010328 Uniprot:Q96247
Root	Isotig06821	66	0	6.915	4.37E-16	TAIR|locus:2084756 - symbol:SUS4 "AT3G43190" species:3702 "Arabidopsis thaliana" [GO:0005986 "sucrose biosynthetic process" evidence=ISS] [GO:0008194 "UDP-glycosyltransferase activity" evidence=ISS] [GO:0016157 "sucrose synthase activity" evidence=IGI;ISS;IDA] [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0005773 "vacuole" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR000368 InterPro:IPR001296 InterPro:IPR012820 Pfam:PF00534 Pfam:PF00862 GO:GO:0005829 GO:GO:0005886 GO:GO:0005773 EMBL:CP002686 GO:GO:0009058 CAZy:GT4 EMBL:AL353871 GO:GO:0005985 KO:K00695 ProtClustDB:PLN00142 GO:GO:0016157 PANTHER:PTHR12526:SF27 TIGRFAMs:TIGR02470 IPI:IPI00540190 PIR:T49233 RefSeq:NP_566865.2 UniGene:At.1720 ProteinModelPortal:Q9LXL5 SMR:Q9LXL5 STRING:Q9LXL5 PRIDE:Q9LXL5 EnsemblPlants:AT3G43190.1 GeneID:823393 KEGG:ath:AT3G43190 TAIR:At3g43190 InParanoid:Q9LXL5 OMA:KAEEYLM PhylomeDB:Q9LXL5 Genevestigator:Q9LXL5 Uniprot:Q9LXL5
Root	Isotig06822	62	0	6.825	2.85E-15	TAIR|locus:2084756 - symbol:SUS4 "AT3G43190" species:3702 "Arabidopsis thaliana" [GO:0005986 "sucrose biosynthetic process" evidence=ISS] [GO:0008194 "UDP-glycosyltransferase activity" evidence=ISS] [GO:0016157 "sucrose synthase activity" evidence=IGI;ISS;IDA] [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0005773 "vacuole" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR000368 InterPro:IPR001296 InterPro:IPR012820 Pfam:PF00534 Pfam:PF00862 GO:GO:0005829 GO:GO:0005886 GO:GO:0005773 EMBL:CP002686 GO:GO:0009058 CAZy:GT4 EMBL:AL353871 GO:GO:0005985 KO:K00695 ProtClustDB:PLN00142 GO:GO:0016157 PANTHER:PTHR12526:SF27 TIGRFAMs:TIGR02470 IPI:IPI00540190 PIR:T49233 RefSeq:NP_566865.2 UniGene:At.1720 ProteinModelPortal:Q9LXL5 SMR:Q9LXL5 STRING:Q9LXL5 PRIDE:Q9LXL5 EnsemblPlants:AT3G43190.1 GeneID:823393 KEGG:ath:AT3G43190 TAIR:At3g43190 InParanoid:Q9LXL5 OMA:KAEEYLM PhylomeDB:Q9LXL5 Genevestigator:Q9LXL5 Uniprot:Q9LXL5
Root	Isotig06825	41	0	6.229	8.08E-11	UNIPROTKB|Q43848 - symbol:Q43848 "Transketolase, chloroplastic" species:4113 "Solanum tuberosum" [GO:0004802 "transketolase activity" evidence=ISS] [GO:0009535 "chloroplast thylakoid membrane" evidence=ISS] InterPro:IPR005476 InterPro:IPR005478 InterPro:IPR009014 InterPro:IPR015941 Pfam:PF02780 InterPro:IPR005475 Pfam:PF00456 Pfam:PF02779 InterPro:IPR005474 GO:GO:0046872 GO:GO:0009535 SMART:SM00861 InterPro:IPR020826 Gene3D:G3DSA:3.40.50.920 SUPFAM:SSF52922 PROSITE:PS00801 PROSITE:PS00802 GO:GO:0004802 TIGRFAMs:TIGR00232 EMBL:Z50099 PIR:S58083 ProteinModelPortal:Q43848 SMR:Q43848 PRIDE:Q43848 Uniprot:Q43848
Root	Isotig06826	45	0	6.363	1.08E-11	UNIPROTKB|Q43848 - symbol:Q43848 "Transketolase, chloroplastic" species:4113 "Solanum tuberosum" [GO:0004802 "transketolase activity" evidence=ISS] [GO:0009535 "chloroplast thylakoid membrane" evidence=ISS] InterPro:IPR005476 InterPro:IPR005478 InterPro:IPR009014 InterPro:IPR015941 Pfam:PF02780 InterPro:IPR005475 Pfam:PF00456 Pfam:PF02779 InterPro:IPR005474 GO:GO:0046872 GO:GO:0009535 SMART:SM00861 InterPro:IPR020826 Gene3D:G3DSA:3.40.50.920 SUPFAM:SSF52922 PROSITE:PS00801 PROSITE:PS00802 GO:GO:0004802 TIGRFAMs:TIGR00232 EMBL:Z50099 PIR:S58083 ProteinModelPortal:Q43848 SMR:Q43848 PRIDE:Q43848 Uniprot:Q43848
Root	Isotig06827	26	60	-1.335	3.86E-05	TAIR|locus:2121894 - symbol:ATR1 "AT4G24520" species:3702 "Arabidopsis thaliana" [GO:0009737 "response to abscisic acid stimulus" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0003958 "NADPH-hemoprotein reductase activity" evidence=IDA] [GO:0005783 "endoplasmic reticulum" evidence=IDA] [GO:0009698

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						"phenylpropanoid metabolic process" evidence=IDA] [GO:0006979 "response to oxidative stress" evidence=IEP] InterPro:IPR001094 InterPro:IPR001433 InterPro:IPR001709 InterPro:IPR003097 InterPro:IPR008254 InterPro:IPR017927 InterPro:IPR017938 InterPro:IPR023173 InterPro:IPR023208 Pfam:PF00175 Pfam:PF00258 Pfam:PF00667 PIRSF:PIRSF000208 PRINTS:PR00369 PRINTS:PR00371 PROSITE:PS50902 PROSITE:PS51384 GO:GO:0005829 GO:GO:0009737 EMBL:CP002687 GO:GO:0006979 GO:GO:0005789 GO:GO:0005506 GO:GO:0009698 EMBL:AL161561 EMBL:AL035356 SUPFAM:SSF63380 GO:GO:0010181 Gene3D:G3DSA:1.20.990.10 OMA:KIQPRYY HSSP:P00388 GO:GO:0003958 KO:K00327 EMBL:AY054688 EMBL:BT008426 IPI:IPI00541592 PIR:T05582 RefSeq:NP_194183.1 UniGene:At.144 UniGene:At.70123 ProteinModelPortal:Q9SB48 SMR:Q9SB48 STRING:Q9SB48 PRIDE:Q9SB48 EnsemblPlants:AT4G24520.1 GeneID:828554 KEGG:ath:AT4G24520 TAIR:At4g24520 InParanoid:Q9SB48 PhylomeDB:Q9SB48 ProtClustDB:CLSN2685426 ArrayExpress:Q9SB48 Genevestigator:Q9SB48 Uniprot:Q9SB48
Root	Isotig06828	26	61	-1.359	2.59E-05	TAIR|locus:2121894 - symbol:ATR1 "AT4G24520" species:3702 "Arabidopsis thaliana" [GO:0009737 "response to abscisic acid stimulus" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0003958 "NADPH-hemoprotein reductase activity" evidence=IDA] [GO:0005783 "endoplasmic reticulum" evidence=IDA] [GO:0009698 "phenylpropanoid metabolic process" evidence=IDA] [GO:0006979 "response to oxidative stress" evidence=IEP] InterPro:IPR001094 InterPro:IPR001433 InterPro:IPR001709 InterPro:IPR003097 InterPro:IPR008254 InterPro:IPR017927 InterPro:IPR017938 InterPro:IPR023173 InterPro:IPR023208 Pfam:PF00175 Pfam:PF00258 Pfam:PF00667 PIRSF:PIRSF000208 PRINTS:PR00369 PRINTS:PR00371 PROSITE:PS50902 PROSITE:PS51384 GO:GO:0005829 GO:GO:0009737 EMBL:CP002687 GO:GO:0006979 GO:GO:0005789 GO:GO:0005506 GO:GO:0009698 EMBL:AL161561 EMBL:AL035356 SUPFAM:SSF63380 GO:GO:0010181 Gene3D:G3DSA:1.20.990.10 OMA:KIQPRYY HSSP:P00388 GO:GO:0003958 KO:K00327 EMBL:AY054688 EMBL:BT008426 IPI:IPI00541592 PIR:T05582 RefSeq:NP_194183.1 UniGene:At.144 UniGene:At.70123 ProteinModelPortal:Q9SB48 SMR:Q9SB48 STRING:Q9SB48 PRIDE:Q9SB48 EnsemblPlants:AT4G24520.1 GeneID:828554 KEGG:ath:AT4G24520 TAIR:At4g24520 InParanoid:Q9SB48 PhylomeDB:Q9SB48 ProtClustDB:CLSN2685426 ArrayExpress:Q9SB48 Genevestigator:Q9SB48 Uniprot:Q9SB48
Root	Isotig06829	10	29	-1.665	0.000753212	TAIR|locus:2036778 - symbol:GPT2 "AT1G61800" species:3702 "Arabidopsis thaliana" [GO:0015152 "glucose-6-phosphate transmembrane transporter activity" evidence=ISS;IDA] [GO:0015297 "antiporter activity" evidence=ISS] [GO:0015712 "hexose phosphate transport" evidence=ISS] [GO:0005315 "inorganic phosphate transmembrane transporter activity" evidence=IDA] [GO:0007276 "gamete generation" evidence=IMP] [GO:0015120 "phosphoglycerate transmembrane transporter activity" evidence=IDA] [GO:0015713 "phosphoglycerate transport" evidence=IDA] [GO:0015714 "phosphoenolpyruvate transport" evidence=IDA] [GO:0015760 "glucose-6-phosphate transport" evidence=IDA] [GO:0035436 "triose phosphate transmembrane transport" evidence=IDA] [GO:0071917 "triose-phosphate transmembrane transporter activity" evidence=IDA] [GO:0009744 "response to sucrose stimulus" evidence=IEP] [GO:0009749 "response to glucose stimulus" evidence=IEP] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0009624 "response to nematode" evidence=IEP] [GO:0009643 "photosynthetic acclimation" evidence=IMP] [GO:0010109 "regulation of photosynthesis" evidence=IMP] [GO:0015979 "photosynthesis" evidence=IMP] [GO:0080167 "response to karrikin" evidence=IEP] InterPro:IPR000620 InterPro:IPR004696 Pfam:PF00892 Pfam:PF03151 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005774 GO:GO:0009624 GO:GO:0080167 GO:GO:0005315 GO:GO:0031969 GO:GO:0009749 GO:GO:0009744 GO:GO:0015979 EMBL:AC004392 InterPro:IPR004853 GO:GO:0015152 eggNOG:NOG312636 HOGENOM:HBG745150 KO:K15283 GO:GO:0015120 GO:GO:0071917 GO:GO:0015714 TIGRFAMs:TIGR00817 EMBL:AY042874 EMBL:AY081479 IPI:IPI00535228 PIR:T02126 RefSeq:NP_564785.1 UniGene:At.10733 STRING:Q94B38 PRIDE:Q94B38 EnsemblPlants:AT1G61800.1 GeneID:842477 KEGG:ath:AT1G61800 TAIR:At1g61800 InParanoid:Q94B38 OMA:PDEQSAQ ArrayExpress:Q94B38 Genevestigator:Q94B38 GermOnline:AT1G61800 GO:GO:0009643 GO:GO:0010109 Uniprot:Q94B38
Root	Isotig06831	2	19	-3.377	3.93E-05	TAIR|locus:2088500 - symbol:RLK902 "AT3G17840" species:3702 "Arabidopsis thaliana" [GO:0004674 "protein serine/threonine kinase activity" evidence=ISS] [GO:0005524 "ATP binding" evidence=ISS] [GO:0006468 "protein phosphorylation" evidence=ISS] [GO:0007169 "transmembrane receptor protein tyrosine kinase signaling pathway" evidence=ISS] [GO:0016301 "kinase activity" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000719 InterPro:IPR011009 InterPro:IPR017441 Pfam:PF00069 PROSITE:PS00107 PROSITE:PS50011 GO:GO:0016021 GO:GO:0005886 GO:GO:0009506 GO:GO:0005524 EMBL:CP002686 GenomeReviews:BA000014_GR eggNOG:COG0515 GO:GO:0004872

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						SUPFAM:SSF56112 HOGENOM:HBG755340 GO:GO:0004672 InterPro:IPR013210 Pfam:PF08263 EMBL:AB019230 EMBL:AY095994 EMBL:BT002283 EMBL:AY086189 IPI:IPI00521331 RefSeq:NP_566589.1 UniGene:At.38651 ProteinModelPortal:Q9LVI6 SMR:Q9LVI6 IntAct:Q9LVI6 STRING:Q9LVI6 PRIDE:Q9LVI6 EnsemblPlants:AT3G17840.1 GeneID:821053 KEGG:ath:AT3G17840 GeneFarm:530 TAIR:At3g17840 InParanoid:Q9LVI6 OMA:YYYSGDE PhylomeDB:Q9LVI6 ProtClustDB:CLSN2688502 Genevestigator:Q9LVI6 Uniprot:Q9LVI6
Root	Isotig06832	2	19	-3.377	3.93E-05	TAIR|locus:2088500 - symbol:RLK902 "AT3G17840" species:3702 "Arabidopsis thaliana" [GO:0004674 "protein serine/threonine kinase activity" evidence=ISS] [GO:0005524 "ATP binding" evidence=ISS] [GO:0006468 "protein phosphorylation" evidence=ISS] [GO:0007169 "transmembrane receptor protein tyrosine kinase signaling pathway" evidence=ISS] [GO:0016301 "kinase activity" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000719 InterPro:IPR011009 InterPro:IPR017441 Pfam:PF00069 PROSITE:PS00107 PROSITE:PS50011 GO:GO:0016021 GO:GO:0005886 GO:GO:0009506 GO:GO:0005524 EMBL:CP002686 GenomeReviews:BA000014_GR eggNOG:COG0515 GO:GO:0004872 SUPFAM:SSF56112 HOGENOM:HBG755340 GO:GO:0004672 InterPro:IPR013210 Pfam:PF08263 EMBL:AB019230 EMBL:AY095994 EMBL:BT002283 EMBL:AY086189 IPI:IPI00521331 RefSeq:NP_566589.1 UniGene:At.38651 ProteinModelPortal:Q9LVI6 SMR:Q9LVI6 IntAct:Q9LVI6 STRING:Q9LVI6 PRIDE:Q9LVI6 EnsemblPlants:AT3G17840.1 GeneID:821053 KEGG:ath:AT3G17840 GeneFarm:530 TAIR:At3g17840 InParanoid:Q9LVI6 OMA:YYYSGDE PhylomeDB:Q9LVI6 ProtClustDB:CLSN2688502 Genevestigator:Q9LVI6 Uniprot:Q9LVI6
Root	Isotig06839	8	28	-1.936	0.000239276	TAIR|locus:2091960 - symbol:AT3G26935 "AT3G26935" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0008270 "zinc ion binding" evidence=IEA] [GO:0005886 "plasma membrane" evidence=IDA] InterPro:IPR001594 Pfam:PF01529 PROSITE:PS50216 GO:GO:0016021 GO:GO:0005886 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0008270 GO:GO:0016746 EMBL:AB026649 EMBL:AP000602 eggNOG:COG5273 HOGENOM:HBG744542 EMBL:AK228693 IPI:IPI00526912 RefSeq:NP_850638.1 UniGene:At.47119 STRING:Q0WQK2 PRIDE:Q0WQK2 EnsemblPlants:AT3G26935.1 GeneID:822311 KEGG:ath:AT3G26935 TAIR:At3g26935 InParanoid:Q0WQK2 OMA:AVGDIEM PhylomeDB:Q0WQK2 ProtClustDB:CLSN2918228 Genevestigator:Q0WQK2 Uniprot:Q0WQK2
Root	Isotig06845	17	51	-1.714	5.10E-06	TAIR|locus:2156789 - symbol:CEV1 "AT5G05170" species:3702 "Arabidopsis thaliana" [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0016759 "cellulose synthase activity" evidence=ISS;IMP] [GO:0005886 "plasma membrane" evidence=IDA;TAS] [GO:0009834 "secondary cell wall biogenesis" evidence=IMP] [GO:0009833 "primary cell wall biogenesis" evidence=IMP;TAS] [GO:0030244 "cellulose biosynthetic process" evidence=IMP] [GO:0009809 "lignin biosynthetic process" evidence=IGI] [GO:0043255 "regulation of carbohydrate biosynthetic process" evidence=IGI] [GO:0006952 "defense response" evidence=TAS] [GO:0005794 "Golgi apparatus" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR001841 InterPro:IPR005150 Pfam:PF03552 PROSITE:PS50089 SMART:SM00184 Prosite:PS00518 GO:GO:0016021 GO:GO:0005886 GO:GO:0009506 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0006952 GO:GO:0005794 GO:GO:0008270 InterPro:IPR013083 Gene3D:G3DSA:3.30.40.10 GO:GO:0007047 CAZy:GT2 eggNOG:COG1215 GO:GO:0016760 GO:GO:0030244 HOGENOM:HBG744549 KO:K10999 GO:GO:0009833 EMBL:AF027174 EMBL:AB018111 EMBL:AY045960 EMBL:BT002335 EMBL:AK230097 IPI:IPI00528019 PIR:T52054 RefSeq:NP_196136.1 UniGene:At.24338 ProteinModelPortal:Q941L0 SMR:Q941L0 DIP:DIP-46437N IntAct:Q941L0 STRING:Q941L0 PRIDE:Q941L0 EnsemblPlants:AT5G05170.1 GeneID:830399 KEGG:ath:AT5G05170 GeneFarm:5086 TAIR:At5g05170 InParanoid:Q941L0 OMA:DVNQSPN PhylomeDB:Q941L0 ProtClustDB:PLN02638 Genevestigator:Q941L0 GermOnline:AT5G05170 Uniprot:Q941L0
Root	Isotig06846	8	29	-1.987	0.000143108	TAIR|locus:2156789 - symbol:CEV1 "AT5G05170" species:3702 "Arabidopsis thaliana" [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0016759 "cellulose synthase activity" evidence=ISS;IMP] [GO:0005886 "plasma membrane" evidence=IDA;TAS] [GO:0009834 "secondary cell wall biogenesis" evidence=IMP] [GO:0009833 "primary cell wall biogenesis" evidence=IMP;TAS] [GO:0030244 "cellulose biosynthetic process" evidence=IMP] [GO:0009809 "lignin biosynthetic process" evidence=IGI] [GO:0043255 "regulation of carbohydrate biosynthetic process" evidence=IGI] [GO:0006952 "defense response" evidence=TAS] [GO:0005794 "Golgi apparatus" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR001841 InterPro:IPR005150 Pfam:PF03552 PROSITE:PS50089 SMART:SM00184 Prosite:PS00518 GO:GO:0016021 GO:GO:0005886 GO:GO:0009506 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0006952

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0005794 GO:GO:0008270 InterPro:IPR013083 Gene3D:G3DSA:3.30.40.10 GO:GO:0007047 CAZy:GT2 eggNOG:COG1215 GO:GO:0016760 GO:GO:0030244 HOGENOM:HBG744549 KO:K10999 GO:GO:0009833 EMBL:AF027174 EMBL:AB018111 EMBL:AY045960 EMBL:BT002335 EMBL:AK230097 IPI:IPI00528019 PIR:T52054 RefSeq:NP_196136.1 UniGene:At.24338 ProteinModelPortal:Q941L0 SMR:Q941L0 DIP:DIP-46437N IntAct:Q941L0 STRING:Q941L0 PRIDE:Q941L0 EnsemblPlants:AT5G05170.1 GeneID:830399 KEGG:ath:AT5G05170 GeneFarm:5086 TAIR:At5g05170 InParanoid:Q941L0 OMA:DVNQSPN PhylomeDB:Q941L0 ProtClustDB:PLN02638 Genevestigator:Q941L0 GermOnline:AT5G05170 Uniprot:Q941L0
Root	Isotig06849	8	29	-1.987	0.000143108	TAIR|locus:2129650 - symbol:AT4G14350 "AT4G14350" species:3702 "Arabidopsis thaliana" [GO:0004672 "protein kinase activity" evidence=ISS] [GO:0005524 "ATP binding" evidence=ISS] [GO:0006468 "protein phosphorylation" evidence=IEA;ISS] [GO:0016301 "kinase activity" evidence=ISS] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0009524 "phragmoplast" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR000719 InterPro:IPR000961 InterPro:IPR002290 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 InterPro:IPR017892 Pfam:PF00069 Pfam:PF00433 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 PROSITE:PS51285 SMART:SM00133 SMART:SM00220 GO:GO:0005829 GO:GO:0005886 GO:GO:0005524 EMBL:CP002687 GO:GO:0005634 SUPFAM:SSF56112 GO:GO:0004674 GO:GO:0009524 HSSP:P31751 OMA:IFPPEIP EMBL:AY128279 EMBL:BT000628 IPI:IPI00546199 RefSeq:NP_193171.2 RefSeq:NP_849380.1 UniGene:At.23938 UniGene:At.68891 ProteinModelPortal:Q8L7S7 SMR:Q8L7S7 PRIDE:Q8L7S7 EnsemblPlants:AT4G14350.1 EnsemblPlants:AT4G14350.2 GeneID:827078 KEGG:ath:AT4G14350 TAIR:At4g14350 InParanoid:Q8L7S7 PhylomeDB:Q8L7S7 ProtClustDB:CLSN2690563 Genevestigator:Q8L7S7 Uniprot:Q8L7S7
Root	Isotig06850	8	29	-1.987	0.000143108	TAIR|locus:2129650 - symbol:AT4G14350 "AT4G14350" species:3702 "Arabidopsis thaliana" [GO:0004672 "protein kinase activity" evidence=ISS] [GO:0005524 "ATP binding" evidence=ISS] [GO:0006468 "protein phosphorylation" evidence=IEA;ISS] [GO:0016301 "kinase activity" evidence=ISS] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0009524 "phragmoplast" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR000719 InterPro:IPR000961 InterPro:IPR002290 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 InterPro:IPR017892 Pfam:PF00069 Pfam:PF00433 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 PROSITE:PS51285 SMART:SM00133 SMART:SM00220 GO:GO:0005829 GO:GO:0005886 GO:GO:0005524 EMBL:CP002687 GO:GO:0005634 SUPFAM:SSF56112 GO:GO:0004674 GO:GO:0009524 HSSP:P31751 OMA:IFPPEIP EMBL:AY128279 EMBL:BT000628 IPI:IPI00546199 RefSeq:NP_193171.2 RefSeq:NP_849380.1 UniGene:At.23938 UniGene:At.68891 ProteinModelPortal:Q8L7S7 SMR:Q8L7S7 PRIDE:Q8L7S7 EnsemblPlants:AT4G14350.1 EnsemblPlants:AT4G14350.2 GeneID:827078 KEGG:ath:AT4G14350 TAIR:At4g14350 InParanoid:Q8L7S7 PhylomeDB:Q8L7S7 ProtClustDB:CLSN2690563 Genevestigator:Q8L7S7 Uniprot:Q8L7S7
Root	Isotig06853	13	42	-1.821	1.59E-05	TAIR|locus:2103172 - symbol:ASD1 "AT3G10740" species:3702 "Arabidopsis thaliana" [GO:0016798 "hydrolase activity, acting on glycosyl bonds" evidence=ISS] [GO:0009044 "xylan 1,4-beta-xylosidase activity" evidence=IDA] [GO:0045493 "xylan catabolic process" evidence=IDA] [GO:0046556 "alpha-N-arabinofuranosidase activity" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0009505 "plant-type cell wall" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] InterPro:IPR010720 Pfam:PF06964 SMART:SM00813 GO:GO:0048046 GO:GO:0005773 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0045493 InterPro:IPR017853 SUPFAM:SSF51445 GO:GO:0005578 EMBL:AC011708 CAZy:GH51 GO:GO:0046556 GO:GO:0046373 eggNOG:COG3534 GO:GO:0009505 EMBL:AY243509 EMBL:AF372949 EMBL:AY143944 EMBL:AK222175 EMBL:AK220766 IPI:IPI00526411 RefSeq:NP_187685.1 UniGene:At.20271 ProteinModelPortal:Q9SG80 SMR:Q9SG80 STRING:Q9SG80 PRIDE:Q9SG80 EnsemblPlants:AT3G10740.1 GeneID:820243 KEGG:ath:AT3G10740 TAIR:At3g10740 InParanoid:Q9SG80 OMA:LEYLGIG PhylomeDB:Q9SG80 ProtClustDB:CLSN2684036 Genevestigator:Q9SG80 GO:GO:0009044 Uniprot:Q9SG80
Root	Isotig06854	12	34	-1.631	0.000323514	TAIR|locus:2103172 - symbol:ASD1 "AT3G10740" species:3702 "Arabidopsis thaliana" [GO:0016798 "hydrolase activity, acting on glycosyl bonds" evidence=ISS] [GO:0009044 "xylan 1,4-beta-xylosidase activity" evidence=IDA] [GO:0045493 "xylan catabolic process" evidence=IDA] [GO:0046556 "alpha-N-arabinofuranosidase activity" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0009505 "plant-type cell wall" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] InterPro:IPR010720 Pfam:PF06964 SMART:SM00813 GO:GO:0048046 GO:GO:0005773 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0045493 InterPro:IPR017853 SUPFAM:SSF51445 GO:GO:0005578 EMBL:AC011708 CAZy:GH51 GO:GO:0046556 GO:GO:0046373

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						eggNOG:COG3534 GO:GO:0009505 EMBL:AY243509 EMBL:AF372949 EMBL:AY143944 EMBL:AK222175 EMBL:AK220766 IPI:IPI00526411 RefSeq:NP_187685.1 UniGene:At.20271 ProteinModelPortal:Q9SG80 SMR:Q9SG80 STRING:Q9SG80 PRIDE:Q9SG80 EnsemblPlants:AT3G10740.1 GeneID:820243 KEGG:ath:AT3G10740 TAIR:At3g10740 InParanoid:Q9SG80 OMA:LEYLGIG PhylomeDB:Q9SG80 ProtClustDB:CLSN2684036 Genevestigator:Q9SG80 GO:GO:0009044 Uniprot:Q9SG80
Root	Isotig06875	17	50	-1.685	8.10E-06	TAIR|locus:2026177 - symbol:AT1G62660 species:3702 "Arabidopsis thaliana" [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=IEA;ISS] [GO:0071370 "cellular response to gibberellin stimulus" evidence=IEP] [GO:0000325 "plant-type vacuole" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0009617 "response to bacterium" evidence=IEP] InterPro:IPR001362 InterPro:IPR018053 InterPro:IPR021792 Pfam:PF11837 PROSITE:PS00609 SMART:SM00640 EMBL:CP002684 GO:GO:0005975 InterPro:IPR008985 SUPFAM:SSF49899 InterPro:IPR023296 SUPFAM:SSF75005 CAZy:GH32 KO:K01193 GO:GO:0004575 InterPro:IPR013189 InterPro:IPR013148 Pfam:PF08244 Pfam:PF00251 ProtClustDB:CLSN2687777 EMBL:AY048269 EMBL:AY062481 EMBL:AY063904 EMBL:AY114066 EMBL:X99111 IPI:IPI00517592 PIR:S71268 RefSeq:NP_564798.1 UniGene:At.24113 UniGene:At.67066 ProteinModelPortal:Q43348 SMR:Q43348 STRING:Q43348 PRIDE:Q43348 ProMEX:Q43348 EnsemblPlants:AT1G62660.1 GeneID:842563 KEGG:ath:AT1G62660 TAIR:At1g62660 InParanoid:Q43348 OMA:HSIVEGF PhylomeDB:Q43348 ArrayExpress:Q43348 Genevestigator:Q43348 Uniprot:Q43348
Root	Isotig06876	12	47	-2.099	5.30E-07	TAIR|locus:2026177 - symbol:AT1G62660 species:3702 "Arabidopsis thaliana" [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=IEA;ISS] [GO:0071370 "cellular response to gibberellin stimulus" evidence=IEP] [GO:0000325 "plant-type vacuole" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0009617 "response to bacterium" evidence=IEP] InterPro:IPR001362 InterPro:IPR018053 InterPro:IPR021792 Pfam:PF11837 PROSITE:PS00609 SMART:SM00640 EMBL:CP002684 GO:GO:0005975 InterPro:IPR008985 SUPFAM:SSF49899 InterPro:IPR023296 SUPFAM:SSF75005 CAZy:GH32 KO:K01193 GO:GO:0004575 InterPro:IPR013189 InterPro:IPR013148 Pfam:PF08244 Pfam:PF00251 ProtClustDB:CLSN2687777 EMBL:AY048269 EMBL:AY062481 EMBL:AY063904 EMBL:AY114066 EMBL:X99111 IPI:IPI00517592 PIR:S71268 RefSeq:NP_564798.1 UniGene:At.24113 UniGene:At.67066 ProteinModelPortal:Q43348 SMR:Q43348 STRING:Q43348 PRIDE:Q43348 ProMEX:Q43348 EnsemblPlants:AT1G62660.1 GeneID:842563 KEGG:ath:AT1G62660 TAIR:At1g62660 InParanoid:Q43348 OMA:HSIVEGF PhylomeDB:Q43348 ArrayExpress:Q43348 Genevestigator:Q43348 Uniprot:Q43348
Root	Isotig06893	12	50	-2.188	1.10E-07	TAIR|locus:2080722 - symbol:SPY "AT3G11540" species:3702 "Arabidopsis thaliana" [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0016262 "protein N-acetylglucosaminyltransferase activity" evidence=TAS] [GO:0009938 "negative regulation of gibberellic acid mediated signaling pathway" evidence=IGI] [GO:0005634 "nucleus" evidence=IDA;TAS] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0009740 "gibberellic acid mediated signaling pathway" evidence=TAS] [GO:0005515 "protein binding" evidence=IPI] [GO:0009736 "cytokinin mediated signaling pathway" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] [GO:2000377 "regulation of reactive oxygen species metabolic process" evidence=IMP] InterPro:IPR001440 InterPro:IPR011990 InterPro:IPR013026 InterPro:IPR019734 Pfam:PF00515 PROSITE:PS50005 PROSITE:PS50293 SMART:SM00028 GO:GO:0005829 GO:GO:0005634 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005515 GO:GO:0030154 GO:GO:0048511 GO:GO:0009736 InterPro:IPR006597 Gene3D:G3DSA:1.25.40.10 SMART:SM00671 GO:GO:0009908 GO:GO:0016262 EMBL:AC008153 GO:GO:0009740 GO:GO:2000377 GO:GO:0009938 CAZy:GT41 eggNOG:COG3914 EMBL:U62135 EMBL:AK220931 EMBL:AK221192 EMBL:AK221314 IPI:IPI00544177 RefSeq:NP_187761.1 UniGene:At.17656 ProteinModelPortal:Q96301 SMR:Q96301 IntAct:Q96301 STRING:Q96301 PRIDE:Q96301 ProMEX:Q96301 EnsemblPlants:AT3G11540.1 GeneID:820327 KEGG:ath:AT3G11540 GeneFarm:5156 TAIR:At3g11540 HOGENOM:HBG684498 InParanoid:Q96301 OMA:GVPCVTM PhylomeDB:Q96301 ProtClustDB:CLSN2684418 Genevestigator:Q96301 Uniprot:Q96301
Root	Isotig06894	15	54	-1.977	2.32E-07	TAIR|locus:2080722 - symbol:SPY "AT3G11540" species:3702 "Arabidopsis thaliana" [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0016262 "protein N-acetylglucosaminyltransferase activity" evidence=TAS] [GO:0009938 "negative regulation of gibberellic acid mediated signaling pathway" evidence=IGI] [GO:0005634 "nucleus" evidence=IDA;TAS] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0009740 "gibberellic acid mediated signaling pathway" evidence=TAS] [GO:0005515 "protein binding" evidence=IPI] [GO:0009736 "cytokinin mediated signaling pathway" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] [GO:2000377 "regulation of

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						reactive oxygen species metabolic process" evidence=IMP] InterPro:IPR001440 InterPro:IPR011990 InterPro:IPR013026 InterPro:IPR019734 Pfam:PF00515 PROSITE:PS50005 PROSITE:PS50293 SMART:SM00028 GO:GO:0005829 GO:GO:0005634 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005515 GO:GO:0030154 GO:GO:0048511 GO:GO:0009736 InterPro:IPR006597 Gene3D:G3DSA:1.25.40.10 SMART:SM00671 GO:GO:0009908 GO:GO:0016262 EMBL:AC008153 GO:GO:0009740 GO:GO:2000377 GO:GO:0009938 CAZy:GT41 eggNOG:COG3914 EMBL:U62135 EMBL:AK220931 EMBL:AK221192 EMBL:AK221314 IPI:IPI00544177 RefSeq:NP_187761.1 UniGene:At.17656 ProteinModelPortal:Q96301 SMR:Q96301 IntAct:Q96301 STRING:Q96301 PRIDE:Q96301 ProMEX:Q96301 EnsemblPlants:AT3G11540.1 GeneID:820327 KEGG:ath:AT3G11540 GeneFarm:5156 TAIR:At3g11540 HOGENOM:HBG684498 InParanoid:Q96301 OMA:GVPCVTM PhylomeDB:Q96301 ProtClustDB:CLSN2684418 Genevestigator:Q96301 Uniprot:Q96301
Root	Isotig06895	35	2	4.000	1.39E-08	TAIR|locus:2076086 - symbol:BAM1 "AT3G23920" species:3702 "Arabidopsis thaliana" [GO:0016161 "beta-amylase activity" evidence=ISS;IDA] [GO:0005983 "starch catabolic process" evidence=IMP] [GO:0005634 "nucleus" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009414 "response to water deprivation" evidence=IEP] BRENDA:3.2.1.2 InterPro:IPR001371 InterPro:IPR001554 InterPro:IPR013781 InterPro:IPR018238 Pfam:PF01373 PRINTS:PR00750 PRINTS:PR00842 PROSITE:PS00506 PROSITE:PS00679 GO:GO:0005829 GO:GO:0005634 GO:GO:0009507 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0043169 InterPro:IPR017853 Gene3D:G3DSA:3.20.20.80 SUPFAM:SSF51445 GO:GO:0009414 GO:GO:0005983 EMBL:AP001297 EMBL:AF367293 EMBL:AY074393 EMBL:AY078046 EMBL:AY096517 EMBL:AK226274 IPI:IPI00518242 RefSeq:NP_189034.1 UniGene:At.8278 HSSP:P16098 ProteinModelPortal:Q9LIR6 SMR:Q9LIR6 STRING:Q9LIR6 CAZy:GH14 PRIDE:Q9LIR6 EnsemblPlants:AT3G23920.1 GeneID:821975 KEGG:ath:AT3G23920 TAIR:At3g23920 eggNOG:NOG77898 InParanoid:Q9LIR6 KO:K01177 OMA:DKDQDLA PhylomeDB:Q9LIR6 ProtClustDB:PLN00197 ArrayExpress:Q9LIR6 Genevestigator:Q9LIR6 GO:GO:0016161 Uniprot:Q9LIR6
Root	Isotig06896	33	2	3.915	4.43E-08	TAIR|locus:2076086 - symbol:BAM1 "AT3G23920" species:3702 "Arabidopsis thaliana" [GO:0016161 "beta-amylase activity" evidence=ISS;IDA] [GO:0005983 "starch catabolic process" evidence=IMP] [GO:0005634 "nucleus" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009414 "response to water deprivation" evidence=IEP] BRENDA:3.2.1.2 InterPro:IPR001371 InterPro:IPR001554 InterPro:IPR013781 InterPro:IPR018238 Pfam:PF01373 PRINTS:PR00750 PRINTS:PR00842 PROSITE:PS00506 PROSITE:PS00679 GO:GO:0005829 GO:GO:0005634 GO:GO:0009507 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0043169 InterPro:IPR017853 Gene3D:G3DSA:3.20.20.80 SUPFAM:SSF51445 GO:GO:0009414 GO:GO:0005983 EMBL:AP001297 EMBL:AF367293 EMBL:AY074393 EMBL:AY078046 EMBL:AY096517 EMBL:AK226274 IPI:IPI00518242 RefSeq:NP_189034.1 UniGene:At.8278 HSSP:P16098 ProteinModelPortal:Q9LIR6 SMR:Q9LIR6 STRING:Q9LIR6 CAZy:GH14 PRIDE:Q9LIR6 EnsemblPlants:AT3G23920.1 GeneID:821975 KEGG:ath:AT3G23920 TAIR:At3g23920 eggNOG:NOG77898 InParanoid:Q9LIR6 KO:K01177 OMA:DKDQDLA PhylomeDB:Q9LIR6 ProtClustDB:PLN00197 ArrayExpress:Q9LIR6 Genevestigator:Q9LIR6 GO:GO:0016161 Uniprot:Q9LIR6
Root	Isotig06907	7	33	-2.366	6.09E-06	TAIR|locus:2175143 - symbol:AT5G60570 "AT5G60570" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0005634 "nucleus" evidence=IDA] InterPro:IPR006652 Pfam:PF01344 PROSITE:PS50181 SMART:SM00612 GO:GO:0005634 EMBL:CP002688 GenomeReviews:BA000015_GR InterPro:IPR015916 Gene3D:G3DSA:2.130.10.80 EMBL:AB011483 eggNOG:NOG312724 EMBL:AK221729 EMBL:BT029765 IPI:IPI00533154 RefSeq:NP_200865.1 UniGene:At.43004 ProteinModelPortal:Q9FKJ0 SMR:Q9FKJ0 IntAct:Q9FKJ0 PRIDE:Q9FKJ0 EnsemblPlants:AT5G60570.1 GeneID:836178 KEGG:ath:AT5G60570 TAIR:At5g60570 InParanoid:Q9FKJ0 OMA:SSSGRWE PhylomeDB:Q9FKJ0 ProtClustDB:CLSN2916403 Genevestigator:Q9FKJ0 Uniprot:Q9FKJ0
Root	Isotig06908	6	31	-2.498	6.06E-06	TAIR|locus:2175143 - symbol:AT5G60570 "AT5G60570" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0005634 "nucleus" evidence=IDA] InterPro:IPR006652 Pfam:PF01344 PROSITE:PS50181 SMART:SM00612 GO:GO:0005634 EMBL:CP002688 GenomeReviews:BA000015_GR InterPro:IPR015916 Gene3D:G3DSA:2.130.10.80 EMBL:AB011483 eggNOG:NOG312724 EMBL:AK221729 EMBL:BT029765 IPI:IPI00533154 RefSeq:NP_200865.1 UniGene:At.43004 ProteinModelPortal:Q9FKJ0 SMR:Q9FKJ0 IntAct:Q9FKJ0 PRIDE:Q9FKJ0 EnsemblPlants:AT5G60570.1 GeneID:836178 KEGG:ath:AT5G60570 TAIR:At5g60570 InParanoid:Q9FKJ0 OMA:SSSGRWE PhylomeDB:Q9FKJ0 ProtClustDB:CLSN2916403 Genevestigator:Q9FKJ0 Uniprot:Q9FKJ0

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig06911	21	4	2.263	0.000779124	TAIR|locus:2138947 - symbol:ABCI8 "AT4G04770" species:3702 "Arabidopsis thaliana" [GO:0005215 "transporter activity" evidence=ISS] [GO:0009507 "chloroplast" evidence=IDA] [GO:0042626 "ATPase activity, coupled to transmembrane movement of substances" evidence=ISS;IDA] [GO:2000030 "regulation of response to red or far red light" evidence=IMP] [GO:0005515 "protein binding" evidence=IPI] [GO:0006879 "cellular iron ion homeostasis" evidence=IDA;TAS] [GO:0016226 "iron-sulfur cluster assembly" evidence=IGI] [GO:0009570 "chloroplast stroma" evidence=IDA] InterPro:IPR000825 InterPro:IPR010231 Pfam:PF01458 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0009570 GO:GO:0005515 GO:GO:0042626 GO:GO:0006879 GO:GO:0016226 eggNOG:COG0719 HOGENOM:HBG711081 EMBL:AF118223 EMBL:AL161501 EMBL:AY052195 EMBL:AY056410 EMBL:AY142069 EMBL:BK001497 IPI:IPI00526234 PIR:A85060 RefSeq:NP_192386.1 UniGene:At.4040 UniGene:At.67960 ProteinModelPortal:Q9ZS97 IntAct:Q9ZS97 STRING:Q9ZS97 PRIDE:Q9ZS97 EnsemblPlants:AT4G04770.1 GeneID:825814 KEGG:ath:AT4G04770 GeneFarm:2674 TAIR:At4g04770 InParanoid:Q9ZS97 KO:K07033 OMA:CTAPMFD PhylomeDB:Q9ZS97 ProtClustDB:CLSN2685558 ArrayExpress:Q9ZS97 Genevestigator:Q9ZS97 GermOnline:AT4G04770 GO:GO:2000030 TIGRFAMs:TIGR01980 Uniprot:Q9ZS97
Root	Isotig06943	12	62	-2.498	1.57E-10	TAIR|locus:2157022 - symbol:GH9A1 "AT5G49720" species:3702 "Arabidopsis thaliana" [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=ISS] [GO:0009504 "cell plate" evidence=IDA] [GO:0009826 "unidimensional cell growth" evidence=IMP] [GO:0009735 "response to cytokinin stimulus" evidence=IMP] [GO:0048367 "shoot development" evidence=IMP] [GO:0030244 "cellulose biosynthetic process" evidence=IMP;TAS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005769 "early endosome" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] [GO:0042538 "hyperosmotic salinity response" evidence=IMP] [GO:0043622 "cortical microtubule organization" evidence=IMP] [GO:0008810 "cellulase activity" evidence=ISS] InterPro:IPR001701 InterPro:IPR008928 InterPro:IPR012341 InterPro:IPR018221 Pfam:PF00759 PROSITE:PS00592 PROSITE:PS00698 GO:GO:0016021 GO:GO:0005886 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009735 GO:GO:0005794 GO:GO:0030245 GO:GO:0009826 GO:GO:0007047 Gene3D:G3DSA:1.50.10.10 SUPFAM:SSF48208 GO:GO:0048367 GO:GO:0005769 GO:GO:0042538 GO:GO:0043622 UniGene:At.23416 GO:GO:0009504 GO:GO:0030244 GO:GO:0008810 CAZy:GH9 EMBL:AB025613 HSSP:P26221 HOGENOM:HBG746347 ProtClustDB:CLSN2679649 EMBL:U37702 EMBL:AF073875 EMBL:AF074092 EMBL:AF074375 EMBL:AY037218 EMBL:BT002221 EMBL:AY086165 EMBL:AK221941 EMBL:AK222193 IPI:IPI00523242 PIR:S71215 RefSeq:NP_199783.1 UniGene:At.21098 ProteinModelPortal:Q38890 SMR:Q38890 STRING:Q38890 PRIDE:Q38890 EnsemblPlants:AT5G49720.1 GeneID:835035 KEGG:ath:AT5G49720 TAIR:At5g49720 eggNOG:NOG257354 InParanoid:Q38890 OMA:DEFIWGG PhylomeDB:Q38890 Genevestigator:Q38890 GermOnline:AT5G49720 Uniprot:Q38890
Root	Isotig06944	12	60	-2.451	4.79E-10	TAIR|locus:2157022 - symbol:GH9A1 "AT5G49720" species:3702 "Arabidopsis thaliana" [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=ISS] [GO:0009504 "cell plate" evidence=IDA] [GO:0009826 "unidimensional cell growth" evidence=IMP] [GO:0009735 "response to cytokinin stimulus" evidence=IMP] [GO:0048367 "shoot development" evidence=IMP] [GO:0030244 "cellulose biosynthetic process" evidence=IMP;TAS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005769 "early endosome" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] [GO:0042538 "hyperosmotic salinity response" evidence=IMP] [GO:0043622 "cortical microtubule organization" evidence=IMP] [GO:0008810 "cellulase activity" evidence=ISS] InterPro:IPR001701 InterPro:IPR008928 InterPro:IPR012341 InterPro:IPR018221 Pfam:PF00759 PROSITE:PS00592 PROSITE:PS00698 GO:GO:0016021 GO:GO:0005886 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009735 GO:GO:0005794 GO:GO:0030245 GO:GO:0009826 GO:GO:0007047 Gene3D:G3DSA:1.50.10.10 SUPFAM:SSF48208 GO:GO:0048367 GO:GO:0005769 GO:GO:0042538 GO:GO:0043622 UniGene:At.23416 GO:GO:0009504 GO:GO:0030244 GO:GO:0008810 CAZy:GH9 EMBL:AB025613 HSSP:P26221 HOGENOM:HBG746347 ProtClustDB:CLSN2679649 EMBL:U37702 EMBL:AF073875 EMBL:AF074092 EMBL:AF074375 EMBL:AY037218 EMBL:BT002221 EMBL:AY086165 EMBL:AK221941 EMBL:AK222193 IPI:IPI00523242 PIR:S71215 RefSeq:NP_199783.1 UniGene:At.21098 ProteinModelPortal:Q38890 SMR:Q38890 STRING:Q38890 PRIDE:Q38890 EnsemblPlants:AT5G49720.1 GeneID:835035 KEGG:ath:AT5G49720 TAIR:At5g49720 eggNOG:NOG257354 InParanoid:Q38890 OMA:DEFIWGG PhylomeDB:Q38890 Genevestigator:Q38890 GermOnline:AT5G49720 Uniprot:Q38890
Root	Isotig06957	28	6	2.093	0.000219123	ZFIN|ZDB-GENE-030131-1473 - symbol:ubr3 "ubiquitin protein ligase E3 component n-recognin 3" species:7955 "Danio rerio" [GO:0008270 "zinc ion binding" evidence=IEA] [GO:0046872 "metal ion binding" evidence=IEA]

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						InterPro:IPR001841 PROSITE:PS50089 SMART:SM00184 ZFIN:ZDB-GENE-030131-1473 GO:GO:0008270 InterPro:IPR013083 Gene3D:G3DSA:3.30.40.10 GeneTree:ENSGT00530000063055 EMBL:CU639483 EMBL:CU986282 EMBL:FP089512 IPI:IPI00897370 Ensembl:ENSDART00000129091 Bgee:F1QJX5 Uniprot:F1QJX5
Root	Isotig06958	28	5	2.356	7.04E-05	ZFIN|ZDB-GENE-030131-1473 - symbol:ubr3 "ubiquitin protein ligase E3 component n-recognin 3" species:7955 "Danio rerio" [GO:0008270 "zinc ion binding" evidence=IEA] [GO:0046872 "metal ion binding" evidence=IEA] InterPro:IPR001841 PROSITE:PS50089 SMART:SM00184 ZFIN:ZDB-GENE-030131-1473 GO:GO:0008270 InterPro:IPR013083 Gene3D:G3DSA:3.30.40.10 GeneTree:ENSGT00530000063055 EMBL:CU639483 EMBL:CU986282 EMBL:FP089512 IPI:IPI00897370 Ensembl:ENSDART00000129091 Bgee:F1QJX5 Uniprot:F1QJX5
Root	Isotig06963	7	24	-1.907	0.000762598	TAIR|locus:2149104 - symbol:ACS "AT5G36880" species:3702 "Arabidopsis thaliana" [GO:0008152 "metabolic process" evidence=ISS] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA;IDA] [GO:0003987 "acetate-CoA ligase activity" evidence=IMP] [GO:0006083 "acetate metabolic process" evidence=IMP] InterPro:IPR000873 InterPro:IPR011904 Pfam:PF00501 Prosite:PS00455 GO:GO:0005829 GO:GO:0009570 EMBL:CP002688 HOGENOM:HBG547964 InterPro:IPR020845 InterPro:IPR025110 Pfam:PF13193 eggNOG:COG0365 InterPro:IPR024597 Pfam:PF11930 GO:GO:0016208 GO:GO:0006083 KO:K01895 GO:GO:0003987 PANTHER:PTHR24095:SF42 TIGRFAMs:TIGR02188 EMBL:AF036618 EMBL:AB025605 EMBL:AY045880 EMBL:BT002371 EMBL:AK317115 IPI:IPI00846476 RefSeq:NP_001031974.2 RefSeq:NP_198504.1 UniGene:At.21024 ProteinModelPortal:B9DGD6 STRING:B9DGD6 PRIDE:O49063 EnsemblPlants:AT5G36880.2 GeneID:833655 KEGG:ath:AT5G36880 TAIR:At5g36880 PhylomeDB:B9DGD6 ProtClustDB:PLN02654 Genevestigator:B9DGD6 Uniprot:B9DGD6
Root	Isotig06964	6	24	-2.129	0.00029855	TAIR|locus:2149104 - symbol:ACS "AT5G36880" species:3702 "Arabidopsis thaliana" [GO:0008152 "metabolic process" evidence=ISS] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA;IDA] [GO:0003987 "acetate-CoA ligase activity" evidence=IMP] [GO:0006083 "acetate metabolic process" evidence=IMP] InterPro:IPR000873 InterPro:IPR011904 Pfam:PF00501 Prosite:PS00455 GO:GO:0005829 GO:GO:0009570 EMBL:CP002688 HOGENOM:HBG547964 InterPro:IPR020845 InterPro:IPR025110 Pfam:PF13193 eggNOG:COG0365 InterPro:IPR024597 Pfam:PF11930 GO:GO:0016208 GO:GO:0006083 KO:K01895 GO:GO:0003987 PANTHER:PTHR24095:SF42 TIGRFAMs:TIGR02188 EMBL:AF036618 EMBL:AB025605 EMBL:AY045880 EMBL:BT002371 EMBL:AK317115 IPI:IPI00846476 RefSeq:NP_001031974.2 RefSeq:NP_198504.1 UniGene:At.21024 ProteinModelPortal:B9DGD6 STRING:B9DGD6 PRIDE:O49063 EnsemblPlants:AT5G36880.2 GeneID:833655 KEGG:ath:AT5G36880 TAIR:At5g36880 PhylomeDB:B9DGD6 ProtClustDB:PLN02654 Genevestigator:B9DGD6 Uniprot:B9DGD6
Root	Isotig06965	26	5	2.250	0.000195402	TAIR|locus:2034235 - symbol:NTT1 "AT1G80300" species:3702 "Arabidopsis thaliana" [GO:0005471 "ATP:ADP antiporter activity" evidence=ISS] [GO:0006810 "transport" evidence=IEA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] InterPro:IPR004667 Pfam:PF03219 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005524 GO:GO:0031969 GO:GO:0005471 EMBL:AC018848 EMBL:Z49227 EMBL:AF428316 EMBL:AY045903 IPI:IPI00527573 PIR:E96834 PIR:S68205 RefSeq:NP_178146.1 UniGene:At.23897 UniGene:At.72668 ProteinModelPortal:Q39002 IntAct:Q39002 STRING:Q39002 TCDB:2.A.12.2.1 PRIDE:Q39002 EnsemblPlants:AT1G80300.1 GeneID:844370 KEGG:ath:AT1G80300 GeneFarm:3067 TAIR:At1g80300 eggNOG:COG3202 HOGENOM:HBG586333 InParanoid:Q39002 OMA:AYPNFKW PhylomeDB:Q39002 ProtClustDB:CLSN2679486 ArrayExpress:Q39002 Genevestigator:Q39002 GermOnline:AT1G80300 TIGRFAMs:TIGR00769 Uniprot:Q39002
Root	Isotig06966	27	5	2.304	0.000117535	TAIR|locus:2034235 - symbol:NTT1 "AT1G80300" species:3702 "Arabidopsis thaliana" [GO:0005471 "ATP:ADP antiporter activity" evidence=ISS] [GO:0006810 "transport" evidence=IEA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] InterPro:IPR004667 Pfam:PF03219 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005524 GO:GO:0031969 GO:GO:0005471 EMBL:AC018848 EMBL:Z49227 EMBL:AF428316 EMBL:AY045903 IPI:IPI00527573 PIR:E96834 PIR:S68205 RefSeq:NP_178146.1 UniGene:At.23897 UniGene:At.72668 ProteinModelPortal:Q39002 IntAct:Q39002 STRING:Q39002 TCDB:2.A.12.2.1 PRIDE:Q39002 EnsemblPlants:AT1G80300.1 GeneID:844370 KEGG:ath:AT1G80300 GeneFarm:3067 TAIR:At1g80300 eggNOG:COG3202 HOGENOM:HBG586333 InParanoid:Q39002 OMA:AYPNFKW PhylomeDB:Q39002 ProtClustDB:CLSN2679486 ArrayExpress:Q39002 Genevestigator:Q39002 GermOnline:AT1G80300 TIGRFAMs:TIGR00769 Uniprot:Q39002

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig06980	46	14	1.587	8.82E-05	TAIR|locus:2154094 - symbol:ALDH12A1 "AT5G62530" species:3702 "Arabidopsis thaliana" [GO:0004028 "3-chloroallyl aldehyde dehydrogenase activity" evidence=ISS] [GO:0003842 "1-pyrroline-5-carboxylate dehydrogenase activity" evidence=IGI;IMP] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0006560 "proline metabolic process" evidence=TAS] [GO:0009507 "chloroplast" evidence=IDA] [GO:0010133 "proline catabolic process to glutamate" evidence=IMP] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0072593 "reactive oxygen species metabolic process" evidence=IMP] [GO:0008270 "zinc ion binding" evidence=IDA] [GO:0050897 "cobalt ion binding" evidence=IDA] InterPro:IPR015590 InterPro:IPR016160 InterPro:IPR016161 InterPro:IPR016162 InterPro:IPR016163 Pfam:PF00171 PROSITE:PS00070 PROSITE:PS00687 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009507 GO:GO:0005759 GO:GO:0008270 GO:GO:0016620 Gene3D:G3DSA:3.40.309.10 Gene3D:G3DSA:3.40.605.10 SUPFAM:SSF53720 GO:GO:0009651 GO:GO:0050897 GO:GO:0072593 EMBL:AY039787 EMBL:AB015469 EMBL:AY065072 EMBL:BT000746 EMBL:BT010391 IPI:IPI00520602 RefSeq:NP_568955.1 UniGene:At.75205 UniGene:At.9309 ProteinModelPortal:Q8VZC3 IntAct:Q8VZC3 STRING:Q8VZC3 PRIDE:Q8VZC3 EnsemblPlants:AT5G62530.1 GeneID:836373 KEGG:ath:AT5G62530 GeneFarm:4315 TAIR:At5g62530 eggNOG:COG4230 HOGENOM:HBG317230 InParanoid:Q8VZC3 KO:K00294 OMA:DAYACSG PhylomeDB:Q8VZC3 ProtClustDB:CLSN2690065 ArrayExpress:Q8VZC3 Genevestigator:Q8VZC3 GermOnline:AT5G62530 GO:GO:0003842 GO:GO:0010133 Uniprot:Q8VZC3
Root	Isotig06997	7	39	-2.607	2.03E-07	TAIR|locus:2044340 - symbol:AT2G46750 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0003885 "D-arabinono-1,4-lactone oxidase activity" evidence=IEA] [GO:0016020 "membrane" evidence=IEA] [GO:0016491 "oxidoreductase activity" evidence=IEA] [GO:0050660 "flavin adenine dinucleotide binding" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] InterPro:IPR006094 InterPro:IPR007173 InterPro:IPR016166 InterPro:IPR016168 Pfam:PF01565 Pfam:PF04030 PROSITE:PS51387 EMBL:CP002685 GO:GO:0016020 GO:GO:0050660 GO:GO:0008762 Gene3D:G3DSA:3.30.465.20 SUPFAM:SSF56176 GO:GO:0003885 ProtClustDB:CLSN2683562 InterPro:IPR010030 TIGRFAMs:TIGR01677 EMBL:BT010596 IPI:IPI00538609 RefSeq:NP_182198.2 UniGene:At.36462 ProteinModelPortal:Q6NQ66 PRIDE:Q6NQ66 EnsemblPlants:AT2G46750.1 GeneID:819288 KEGG:ath:AT2G46750 TAIR:At2g46750 InParanoid:Q6NQ66 OMA:LELHYGI PhylomeDB:Q6NQ66 Genevestigator:Q6NQ66 Uniprot:Q6NQ66
Root	Isotig07001	83	0	7.246	1.90E-19	No hit
Root	Isotig07002	83	0	7.246	1.90E-19	No hit
Root	Isotig07019	36	7	2.234	1.28E-05	TAIR|locus:2075845 - symbol:SCPL49 "SERINE CARBOXYPEPTIDASE-LIKE 49" species:3702 "Arabidopsis thaliana" [GO:0004185 "serine-type carboxypeptidase activity" evidence=IEA;ISS] [GO:0006508 "proteolysis" evidence=IEA;ISS] [GO:0005773 "vacuole" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001563 InterPro:IPR018202 Pfam:PF00450 PRINTS:PR00724 PROSITE:PS00131 PROSITE:PS00560 GO:GO:0005829 GO:GO:0005773 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005576 GO:GO:0006508 EMBL:AC011560 GO:GO:0004185 eggNOG:COG2939 KO:K13289 PANTHER:PTHR11802 HOGENOM:HBG588032 ProtClustDB:CLSN2684010 EMBL:M81130 EMBL:AY091767 EMBL:AY149954 EMBL:Z25955 EMBL:Z26528 IPI:IPI00547765 RefSeq:NP_187652.1 UniGene:At.20528 UniGene:At.45878 UniGene:At.72674 ProteinModelPortal:P32826 SMR:P32826 STRING:P32826 MEROPS:S10.A45 PRIDE:P32826 EnsemblPlants:AT3G10410.1 GeneID:820205 KEGG:ath:AT3G10410 TAIR:At3g10410 InParanoid:P32826 OMA:AYPDYAL PhylomeDB:P32826 ArrayExpress:P32826 Genevestigator:P32826 GermOnline:AT3G10410 Uniprot:P32826
Root	Isotig07020	34	7	2.151	3.42E-05	TAIR|locus:2075845 - symbol:SCPL49 "SERINE CARBOXYPEPTIDASE-LIKE 49" species:3702 "Arabidopsis thaliana" [GO:0004185 "serine-type carboxypeptidase activity" evidence=IEA;ISS] [GO:0006508 "proteolysis" evidence=IEA;ISS] [GO:0005773 "vacuole" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001563 InterPro:IPR018202 Pfam:PF00450 PRINTS:PR00724 PROSITE:PS00131 PROSITE:PS00560 GO:GO:0005829 GO:GO:0005773 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005576 GO:GO:0006508 EMBL:AC011560 GO:GO:0004185 eggNOG:COG2939 KO:K13289 PANTHER:PTHR11802 HOGENOM:HBG588032 ProtClustDB:CLSN2684010 EMBL:M81130 EMBL:AY091767 EMBL:AY149954 EMBL:Z25955 EMBL:Z26528 IPI:IPI00547765 RefSeq:NP_187652.1 UniGene:At.20528 UniGene:At.45878 UniGene:At.72674 ProteinModelPortal:P32826 SMR:P32826 STRING:P32826 MEROPS:S10.A45 PRIDE:P32826 EnsemblPlants:AT3G10410.1 GeneID:820205 KEGG:ath:AT3G10410 TAIR:At3g10410 InParanoid:P32826

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						OMA:AYPDYAL PhylomeDB:P32826 ArrayExpress:P32826 Genevestigator:P32826 GermOnline:AT3G10410 Uniprot:P32826
Root	Isotig07025	52	20	1.250	0.000501794	TAIR|locus:2076371 - symbol:AT3G58610 "AT3G58610" species:3702 "Arabidopsis thaliana" [GO:0004455 "ketol-acid reductoisomerase activity" evidence=ISS] [GO:0009082 "branched chain family amino acid biosynthetic process" evidence=ISS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0048046 "apoplast" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] InterPro:IPR000506 InterPro:IPR008927 InterPro:IPR013023 InterPro:IPR013116 InterPro:IPR013328 InterPro:IPR016040 InterPro:IPR016206 Pfam:PF01450 Pfam:PF07991 PIRSF:PIRSF000118 GO:GO:0005739 GO:GO:0048046 GO:GO:0009570 GO:GO:0046686 GO:GO:0005618 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 Gene3D:G3DSA:1.10.1040.10 SUPFAM:SSF48179 GO:GO:0009941 GO:GO:0005507 GO:GO:0050662 GO:GO:0009082 EMBL:AL137082 UniGene:At.480 EMBL:X68150 EMBL:X69880 EMBL:AF324671 EMBL:AF329500 EMBL:AY062094 EMBL:AY065398 EMBL:AY096556 EMBL:BT000669 EMBL:BT000822 IPI:IPI00533630 PIR:S30145 PIR:T45681 RefSeq:NP_001078309.1 RefSeq:NP_001190127.1 RefSeq:NP_191420.1 UniGene:At.46637 UniGene:At.69012 ProteinModelPortal:Q05758 SMR:Q05758 STRING:Q05758 PRIDE:Q05758 EnsemblPlants:AT3G58610.1 EnsemblPlants:AT3G58610.2 EnsemblPlants:AT3G58610.3 GeneID:825030 KEGG:ath:AT3G58610 GeneFarm:4243 TAIR:At3g58610 eggNOG:COG0059 HOGENOM:HBG743920 InParanoid:Q05758 KO:K00053 OMA:EAYSAAY PhylomeDB:Q05758 ProtClustDB:CLSN2684737 ArrayExpress:Q05758 Genevestigator:Q05758 GermOnline:AT3G58610 GO:GO:0004455 PANTHER:PTHR21371 Uniprot:Q05758
Root	Isotig07026	52	20	1.250	0.000501794	TAIR|locus:2076371 - symbol:AT3G58610 "AT3G58610" species:3702 "Arabidopsis thaliana" [GO:0004455 "ketol-acid reductoisomerase activity" evidence=ISS] [GO:0009082 "branched chain family amino acid biosynthetic process" evidence=ISS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0048046 "apoplast" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] InterPro:IPR000506 InterPro:IPR008927 InterPro:IPR013023 InterPro:IPR013116 InterPro:IPR013328 InterPro:IPR016040 InterPro:IPR016206 Pfam:PF01450 Pfam:PF07991 PIRSF:PIRSF000118 GO:GO:0005739 GO:GO:0048046 GO:GO:0009570 GO:GO:0046686 GO:GO:0005618 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 Gene3D:G3DSA:1.10.1040.10 SUPFAM:SSF48179 GO:GO:0009941 GO:GO:0005507 GO:GO:0050662 GO:GO:0009082 EMBL:AL137082 UniGene:At.480 EMBL:X68150 EMBL:X69880 EMBL:AF324671 EMBL:AF329500 EMBL:AY062094 EMBL:AY065398 EMBL:AY096556 EMBL:BT000669 EMBL:BT000822 IPI:IPI00533630 PIR:S30145 PIR:T45681 RefSeq:NP_001078309.1 RefSeq:NP_001190127.1 RefSeq:NP_191420.1 UniGene:At.46637 UniGene:At.69012 ProteinModelPortal:Q05758 SMR:Q05758 STRING:Q05758 PRIDE:Q05758 EnsemblPlants:AT3G58610.1 EnsemblPlants:AT3G58610.2 EnsemblPlants:AT3G58610.3 GeneID:825030 KEGG:ath:AT3G58610 GeneFarm:4243 TAIR:At3g58610 eggNOG:COG0059 HOGENOM:HBG743920 InParanoid:Q05758 KO:K00053 OMA:EAYSAAY PhylomeDB:Q05758 ProtClustDB:CLSN2684737 ArrayExpress:Q05758 Genevestigator:Q05758 GermOnline:AT3G58610 GO:GO:0004455 PANTHER:PTHR21371 Uniprot:Q05758
Root	Isotig07033	28	56	-1.129	0.000494096	TAIR|locus:2007357 - symbol:NPC1 "non-specific phospholipase C1" species:3702 "Arabidopsis thaliana" [GO:0016788 "hydrolase activity, acting on ester bonds" evidence=IEA;ISS] InterPro:IPR007312 Pfam:PF04185 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0016788 eggNOG:COG3511 KO:K01114 ProtClustDB:CLSN2683426 EMBL:AY124005 EMBL:BT020583 EMBL:AB084291 IPI:IPI00522350 RefSeq:NP_172203.2 UniGene:At.43894 ProteinModelPortal:Q8L7Y9 STRING:Q8L7Y9 PRIDE:Q8L7Y9 EnsemblPlants:AT1G07230.1 GeneID:837234 KEGG:ath:AT1G07230 TAIR:At1g07230 InParanoid:Q8L7Y9 PhylomeDB:Q8L7Y9 Genevestigator:Q8L7Y9 Uniprot:Q8L7Y9
Root	Isotig07034	28	56	-1.129	0.000494096	TAIR|locus:2007357 - symbol:NPC1 "non-specific phospholipase C1" species:3702 "Arabidopsis thaliana" [GO:0016788 "hydrolase activity, acting on ester bonds" evidence=IEA;ISS] InterPro:IPR007312 Pfam:PF04185 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0016788 eggNOG:COG3511 KO:K01114 ProtClustDB:CLSN2683426 EMBL:AY124005 EMBL:BT020583 EMBL:AB084291 IPI:IPI00522350 RefSeq:NP_172203.2 UniGene:At.43894 ProteinModelPortal:Q8L7Y9 STRING:Q8L7Y9 PRIDE:Q8L7Y9

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EnsemblPlants:AT1G07230.1 GeneID:837234 KEGG:ath:AT1G07230 TAIR:At1g07230 InParanoid:Q8L7Y9 PhylomeDB:Q8L7Y9 Genevestigator:Q8L7Y9 Uniprot:Q8L7Y9
Root	Isotig07037	5	24	-2.392	0.000103464	TAIR|locus:2084500 - symbol:AT3G53960 "AT3G53960" species:3702 "Arabidopsis thaliana" [GO:0005215 "transporter activity" evidence=ISS] [GO:0006857 "oligopeptide transport" evidence=IEA;ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] InterPro:IPR000109 InterPro:IPR018456 Pfam:PF00854 PROSITE:PS01022 PROSITE:PS01023 GO:GO:0016021 GO:GO:0005886 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005215 InterPro:IPR016196 SUPFAM:SSF103473 EMBL:AL132960 eggNOG:COG3104 OMA:GAFLMAV GO:GO:0006857 EMBL:AF361587 IPI:IPI00532128 PIR:T45936 RefSeq:NP_190964.2 UniGene:At.27522 ProteinModelPortal:Q9M331 PRIDE:Q9M331 EnsemblPlants:AT3G53960.1 GeneID:824563 KEGG:ath:AT3G53960 TAIR:At3g53960 InParanoid:Q9M331 PhylomeDB:Q9M331 Genevestigator:Q9M331 Uniprot:Q9M331
Root	Isotig07038	5	21	-2.199	0.000555521	TAIR|locus:2084500 - symbol:AT3G53960 "AT3G53960" species:3702 "Arabidopsis thaliana" [GO:0005215 "transporter activity" evidence=ISS] [GO:0006857 "oligopeptide transport" evidence=IEA;ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] InterPro:IPR000109 InterPro:IPR018456 Pfam:PF00854 PROSITE:PS01022 PROSITE:PS01023 GO:GO:0016021 GO:GO:0005886 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005215 InterPro:IPR016196 SUPFAM:SSF103473 EMBL:AL132960 eggNOG:COG3104 OMA:GAFLMAV GO:GO:0006857 EMBL:AF361587 IPI:IPI00532128 PIR:T45936 RefSeq:NP_190964.2 UniGene:At.27522 ProteinModelPortal:Q9M331 PRIDE:Q9M331 EnsemblPlants:AT3G53960.1 GeneID:824563 KEGG:ath:AT3G53960 TAIR:At3g53960 InParanoid:Q9M331 PhylomeDB:Q9M331 Genevestigator:Q9M331 Uniprot:Q9M331
Root	Isotig07041	270	365	-0.564	9.51E-07	TAIR|locus:2094473 - symbol:AT3G25570 species:3702 "Arabidopsis thaliana" [GO:0004014 "adenosylmethionine decarboxylase activity" evidence=IEA;ISS] [GO:0005575 "cellular_component" evidence=ND] [GO:0006597 "spermine biosynthetic process" evidence=IEA] [GO:0008295 "spermidine biosynthetic process" evidence=IEA] InterPro:IPR001985 InterPro:IPR016067 InterPro:IPR018166 InterPro:IPR018167 Pfam:PF01536 PIRSF:PIRSF001355 PROSITE:PS01336 EMBL:CP002686 GenomeReviews:BA000014_GR eggNOG:NOG77566 HOGENOM:HBG610629 KO:K01611 ProtClustDB:PLN02524 GO:GO:0004014 GO:GO:0008295 GO:GO:0006597 Gene3D:G3DSA:3.60.90.10 PANTHER:PTHR11570 SUPFAM:SSF56276 TIGRFAMs:TIGR00535 HSSP:P17707 OMA:TSELLMY EMBL:AB025639 EMBL:BT012654 IPI:IPI00546639 RefSeq:NP_001189972.1 RefSeq:NP_189184.1 UniGene:At.49653 ProteinModelPortal:Q9LSU6 SMR:Q9LSU6 STRING:Q9LSU6 PRIDE:Q9LSU6 EnsemblPlants:AT3G25570.1 EnsemblPlants:AT3G25570.2 GeneID:822144 KEGG:ath:AT3G25570 TAIR:At3g25570 InParanoid:Q9LSU6 PhylomeDB:Q9LSU6 Genevestigator:Q9LSU6 Uniprot:Q9LSU6
Root	Isotig07042	237	317	-0.549	8.38E-06	TAIR|locus:2094473 - symbol:AT3G25570 species:3702 "Arabidopsis thaliana" [GO:0004014 "adenosylmethionine decarboxylase activity" evidence=IEA;ISS] [GO:0005575 "cellular_component" evidence=ND] [GO:0006597 "spermine biosynthetic process" evidence=IEA] [GO:0008295 "spermidine biosynthetic process" evidence=IEA] InterPro:IPR001985 InterPro:IPR016067 InterPro:IPR018166 InterPro:IPR018167 Pfam:PF01536 PIRSF:PIRSF001355 PROSITE:PS01336 EMBL:CP002686 GenomeReviews:BA000014_GR eggNOG:NOG77566 HOGENOM:HBG610629 KO:K01611 ProtClustDB:PLN02524 GO:GO:0004014 GO:GO:0008295 GO:GO:0006597 Gene3D:G3DSA:3.60.90.10 PANTHER:PTHR11570 SUPFAM:SSF56276 TIGRFAMs:TIGR00535 HSSP:P17707 OMA:TSELLMY EMBL:AB025639 EMBL:BT012654 IPI:IPI00546639 RefSeq:NP_001189972.1 RefSeq:NP_189184.1 UniGene:At.49653 ProteinModelPortal:Q9LSU6 SMR:Q9LSU6 STRING:Q9LSU6 PRIDE:Q9LSU6 EnsemblPlants:AT3G25570.1 EnsemblPlants:AT3G25570.2 GeneID:822144 KEGG:ath:AT3G25570 TAIR:At3g25570 InParanoid:Q9LSU6 PhylomeDB:Q9LSU6 Genevestigator:Q9LSU6 Uniprot:Q9LSU6
Root	Isotig07043	13	38	-1.676	0.000106259	TAIR|locus:2059456 - symbol:ALDH6B2 "AT2G14170" species:3702 "Arabidopsis thaliana" [GO:0004028 "3-chloroallyl aldehyde dehydrogenase activity" evidence=ISS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0006979 "response to oxidative stress" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] InterPro:IPR010061 InterPro:IPR015590 InterPro:IPR016160 InterPro:IPR016161 InterPro:IPR016162 InterPro:IPR016163 Pfam:PF00171 PROSITE:PS00070 PROSITE:PS00687 GO:GO:0005739 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0006979 eggNOG:COG1012 Gene3D:G3DSA:3.40.309.10 Gene3D:G3DSA:3.40.605.10 SUPFAM:SSF53720 HOGENOM:HBG752218 GO:GO:0005507 KO:K00140 GO:GO:0004491 PANTHER:PTHR11699:SF27 TIGRFAMs:TIGR01722 EMBL:AC007197 EMBL:AK230004

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						IPI:IPI00518167 PIR:H84514 RefSeq:NP_179032.1 UniGene:At.43851 ProteinModelPortal:Q0WM29 SMR:Q0WM29 STRING:Q0WM29 PRIDE:Q0WM29 EnsemblPlants:AT2G14170.1 GeneID:815903 KEGG:ath:AT2G14170 GeneFarm:4385 TAIR:At2g14170 InParanoid:Q0WM29 OMA:IISNVKP PhylomeDB:Q0WM29 ProtClustDB:PLN02419 ArrayExpress:Q9SI43 Genevestigator:Q0WM29 Uniprot:Q0WM29
Root	Isotig07044	13	39	-1.714	6.66E-05	TAIR|locus:2059456 - symbol:ALDH6B2 "AT2G14170" species:3702 "Arabidopsis thaliana" [GO:0004028 "3-chloroallyl aldehyde dehydrogenase activity" evidence=ISS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0006979 "response to oxidative stress" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] InterPro:IPR010061 InterPro:IPR015590 InterPro:IPR016160 InterPro:IPR016161 InterPro:IPR016162 InterPro:IPR016163 Pfam:PF00171 PROSITE:PS00070 PROSITE:PS00687 GO:GO:0005739 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0006979 eggNOG:COG1012 Gene3D:G3DSA:3.40.309.10 Gene3D:G3DSA:3.40.605.10 SUPFAM:SSF53720 HOGENOM:HBG752218 GO:GO:0005507 KO:K00140 GO:GO:0004491 PANTHER:PTHR11699:SF27 TIGRFAMs:TIGR01722 EMBL:AC007197 EMBL:AK230004 IPI:IPI00518167 PIR:H84514 RefSeq:NP_179032.1 UniGene:At.43851 ProteinModelPortal:Q0WM29 SMR:Q0WM29 STRING:Q0WM29 PRIDE:Q0WM29 EnsemblPlants:AT2G14170.1 GeneID:815903 KEGG:ath:AT2G14170 GeneFarm:4385 TAIR:At2g14170 InParanoid:Q0WM29 OMA:IISNVKP PhylomeDB:Q0WM29 ProtClustDB:PLN02419 ArrayExpress:Q9SI43 Genevestigator:Q0WM29 Uniprot:Q0WM29
Root	Isotig07053	11	33	-1.714	0.000243809	TAIR|locus:2087418 - symbol:CCD1 "AT3G63520" species:3702 "Arabidopsis thaliana" [GO:0009414 "response to water deprivation" evidence=IEP] [GO:0016118 "carotenoid catabolic process" evidence=IDA] [GO:0045549 "9-cis-epoxycarotenoid dioxygenase activity" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0016121 "carotene catabolic process" evidence=IMP] [GO:0016124 "xanthophyll catabolic process" evidence=IMP] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] GO:GO:0005886 GO:GO:0009506 GO:GO:0005774 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0006950 GO:GO:0046872 EMBL:AL163818 eggNOG:COG3670 InterPro:IPR004294 PANTHER:PTHR10543 Pfam:PF03055 GO:GO:0016121 EMBL:AJ005813 EMBL:BT000436 EMBL:BT002102 IPI:IPI00517969 PIR:T49193 PIR:T51734 RefSeq:NP_191911.1 UniGene:At.22615 UniGene:At.43820 ProteinModelPortal:O65572 SMR:O65572 STRING:O65572 PRIDE:O65572 EnsemblPlants:AT3G63520.1 GeneID:825527 KEGG:ath:AT3G63520 TAIR:At3g63520 HOGENOM:HBG559594 InParanoid:O65572 KO:K11159 OMA:IKFDLHA PhylomeDB:O65572 ProtClustDB:PLN02491 ArrayExpress:Q8GRI2 Genevestigator:O65572 GO:GO:0045549 GO:GO:0016124 Uniprot:O65572
Root	Isotig07054	11	30	-1.576	0.000984585	TAIR|locus:2087418 - symbol:CCD1 "AT3G63520" species:3702 "Arabidopsis thaliana" [GO:0009414 "response to water deprivation" evidence=IEP] [GO:0016118 "carotenoid catabolic process" evidence=IDA] [GO:0045549 "9-cis-epoxycarotenoid dioxygenase activity" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0016121 "carotene catabolic process" evidence=IMP] [GO:0016124 "xanthophyll catabolic process" evidence=IMP] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] GO:GO:0005886 GO:GO:0009506 GO:GO:0005774 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0006950 GO:GO:0046872 EMBL:AL163818 eggNOG:COG3670 InterPro:IPR004294 PANTHER:PTHR10543 Pfam:PF03055 GO:GO:0016121 EMBL:AJ005813 EMBL:BT000436 EMBL:BT002102 IPI:IPI00517969 PIR:T49193 PIR:T51734 RefSeq:NP_191911.1 UniGene:At.22615 UniGene:At.43820 ProteinModelPortal:O65572 SMR:O65572 STRING:O65572 PRIDE:O65572 EnsemblPlants:AT3G63520.1 GeneID:825527 KEGG:ath:AT3G63520 TAIR:At3g63520 HOGENOM:HBG559594 InParanoid:O65572 KO:K11159 OMA:IKFDLHA PhylomeDB:O65572 ProtClustDB:PLN02491 ArrayExpress:Q8GRI2 Genevestigator:O65572 GO:GO:0045549 GO:GO:0016124 Uniprot:O65572
Root	Isotig07057	39	8	2.156	8.81E-06	TAIR|locus:2201036 - symbol:NTMC2T2.1 "AT1G05500" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0012505 "endomembrane system" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000008 InterPro:IPR008973 Pfam:PF00168 SMART:SM00239 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005886 GO:GO:0009506 GO:GO:0012505 InterPro:IPR018029 SUPFAM:SSF49562 PROSITE:PS50004 eggNOG:COG5038 InterPro:IPR020477 PRINTS:PR00360 HSSP:P04410 ProtClustDB:CLSN2697228 EMBL:AY140038 EMBL:BT008907 EMBL:AK228581 IPI:IPI00548718 RefSeq:NP_172041.2 UniGene:At.27942 ProteinModelPortal:Q8L706 SMR:Q8L706 PRIDE:Q8L706

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EnsemblPlants:AT1G05500.1 GeneID:837052 KEGG:ath:AT1G05500 TAIR:At1g05500 HOGENOM:HBG320331 InParanoid:Q8L706 PhylomeDB:Q8L706 ArrayExpress:Q8L706 Genevestigator:Q8L706 Uniprot:Q8L706
Root	Isotig07058	41	9	2.059	9.66E-06	TAIR|locus:2201036 - symbol:NTMC2T2.1 "AT1G05500" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0012505 "endomembrane system" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000008 InterPro:IPR008973 Pfam:PF00168 SMART:SM00239 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005886 GO:GO:0009506 GO:GO:0012505 InterPro:IPR018029 SUPFAM:SSF49562 PROSITE:PS50004 eggNOG:COG5038 InterPro:IPR020477 PRINTS:PR00360 HSSP:P04410 ProtClustDB:CLSN2697228 EMBL:AY140038 EMBL:BT008907 EMBL:AK228581 IPI:IPI00548718 RefSeq:NP_172041.2 UniGene:At.27942 ProteinModelPortal:Q8L706 SMR:Q8L706 PRIDE:Q8L706 EnsemblPlants:AT1G05500.1 GeneID:837052 KEGG:ath:AT1G05500 TAIR:At1g05500 HOGENOM:HBG320331 InParanoid:Q8L706 PhylomeDB:Q8L706 ArrayExpress:Q8L706 Genevestigator:Q8L706 Uniprot:Q8L706
Root	Isotig07067	29	7	1.922	0.000375107	SGD|S000028422 - symbol:TAR1 "Mitochondrial protein potentially involved in respiratory metabolism" species:4932 "Saccharomyces cerevisiae" [GO:0003674 "molecular_function" evidence=ND] [GO:0043457 "regulation of cellular respiration" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IEA;IMP] SGD:S000028422 GO:GO:0005739 EMBL:BK006945 EMBL:U53879 GO:GO:0043457 EMBL:Z73326 EMBL:AF479964 RefSeq:NP_690845.1 ProteinModelPortal:Q8TGM6 STRING:Q8TGM6 EnsemblFungi:YLR154W-C GeneID:1466405 KEGG:sce:YLR154W-C CYGD:YLR154w-c eggNOG:NOG79861 OMA:SCSKEHR OrthoDB:EOG466ZX8 NextBio:967146 Genevestigator:Q8TGM6 GermOnline:YLR154W-C Uniprot:Q8TGM6
Root	Isotig07068	23	3	2.810	7.16E-05	No hit
Root	Isotig07075	25	1	4.515	7.40E-07	TAIR|locus:2009580 - symbol:AT1G53210 species:3702 "Arabidopsis thaliana" [GO:0005509 "calcium ion binding" evidence=IEA;ISS] [GO:0055085 "transmembrane transport" evidence=IEA] [GO:0016020 "membrane" evidence=ISS;IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0000325 "plant-type vacuole" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR002048 InterPro:IPR004837 InterPro:IPR011992 Pfam:PF01699 SMART:SM00054 Prosite:PS00018 GO:GO:0016021 EMBL:CP002684 GO:GO:0009506 GO:GO:0005774 GO:GO:0005509 InterPro:IPR018247 InterPro:IPR018249 Gene3D:G3DSA:1.10.238.10 PROSITE:PS50222 GO:GO:0055085 GO:GO:0000325 EMBL:AY099550 IPI:IPI00521295 RefSeq:NP_564623.2 UniGene:At.23754 ProteinModelPortal:Q8L636 SMR:Q8L636 PRIDE:Q8L636 EnsemblPlants:AT1G53210.1 GeneID:841755 KEGG:ath:AT1G53210 TAIR:At1g53210 InParanoid:Q8L636 OMA:CEQTYGF PhylomeDB:Q8L636 ProtClustDB:CLSN2680479 Genevestigator:Q8L636 Uniprot:Q8L636
Root	Isotig07076	25	1	4.515	7.40E-07	TAIR|locus:2009580 - symbol:AT1G53210 species:3702 "Arabidopsis thaliana" [GO:0005509 "calcium ion binding" evidence=IEA;ISS] [GO:0055085 "transmembrane transport" evidence=IEA] [GO:0016020 "membrane" evidence=ISS;IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0000325 "plant-type vacuole" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR002048 InterPro:IPR004837 InterPro:IPR011992 Pfam:PF01699 SMART:SM00054 Prosite:PS00018 GO:GO:0016021 EMBL:CP002684 GO:GO:0009506 GO:GO:0005774 GO:GO:0005509 InterPro:IPR018247 InterPro:IPR018249 Gene3D:G3DSA:1.10.238.10 PROSITE:PS50222 GO:GO:0055085 GO:GO:0000325 EMBL:AY099550 IPI:IPI00521295 RefSeq:NP_564623.2 UniGene:At.23754 ProteinModelPortal:Q8L636 SMR:Q8L636 PRIDE:Q8L636 EnsemblPlants:AT1G53210.1 GeneID:841755 KEGG:ath:AT1G53210 TAIR:At1g53210 InParanoid:Q8L636 OMA:CEQTYGF PhylomeDB:Q8L636 ProtClustDB:CLSN2680479 Genevestigator:Q8L636 Uniprot:Q8L636
Root	Isotig07107	43	1	5.297	2.89E-11	TAIR|locus:2164047 - symbol:AT5G53770 "AT5G53770" species:3702 "Arabidopsis thaliana" [GO:0003676 "nucleic acid binding" evidence=ISS] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0016779 "nucleotidyltransferase activity" evidence=IEA] InterPro:IPR002934 Pfam:PF01909 Pfam:PF03828 EMBL:CP002688 eggNOG:COG5260 InterPro:IPR002058 GO:GO:0016779 EMBL:BT002764 IPI:IPI00522291 RefSeq:NP_568798.1 UniGene:At.6981 ProteinModelPortal:Q84WU1 SMR:Q84WU1 PRIDE:Q84WU1 EnsemblPlants:AT5G53770.1 GeneID:835458 KEGG:ath:AT5G53770 TAIR:At5g53770 InParanoid:Q84WU1 OMA:IVDFCDF PhylomeDB:Q84WU1 ProtClustDB:CLSN2690011 ArrayExpress:Q84WU1 Genevestigator:Q84WU1 Uniprot:Q84WU1
Root	Isotig07108	43	1	5.297	2.89E-11	TAIR|locus:2164047 - symbol:AT5G53770 "AT5G53770" species:3702 "Arabidopsis thaliana" [GO:0003676 "nucleic acid binding" evidence=ISS] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process"

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						evidence=ND] [GO:0016779 "nucleotidyltransferase activity" evidence=IEA] InterPro:IPR002934 Pfam:PF01909 Pfam:PF03828 EMBL:CP002688 eggNOG:COG5260 InterPro:IPR002058 GO:GO:0016779 EMBL:BT002764 IPI:IPI00522291 RefSeq:NP_568798.1 UniGene:At.6981 ProteinModelPortal:Q84WU1 SMR:Q84WU1 PRIDE:Q84WU1 EnsemblPlants:AT5G53770.1 GeneID:835458 KEGG:ath:AT5G53770 TAIR:At5g53770 InParanoid:Q84WU1 OMA:IVDFCDF PhylomeDB:Q84WU1 ProtClustDB:CLSN2690011 ArrayExpress:Q84WU1 Genevestigator:Q84WU1 Uniprot:Q84WU1
Root	Isotig07109	1	20	-4.451	3.92E-06	TAIR|locus:2171402 - symbol:AAE5 "acyl activating enzyme 5" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0008152 "metabolic process" evidence=IEA] [GO:0005777 "peroxisome" evidence=IDA] InterPro:IPR000873 Pfam:PF00501 Prosite:PS00455 EMBL:CP002688 GO:GO:0005777 InterPro:IPR020845 InterPro:IPR025110 Pfam:PF13193 HSSP:P08659 GO:GO:0003824 EMBL:AF503764 EMBL:AB005242 IPI:IPI00539798 RefSeq:NP_197141.1 UniGene:At.28787 UniGene:At.43181 ProteinModelPortal:Q9FFE6 SMR:Q9FFE6 STRING:Q9FFE6 PRIDE:Q9FFE6 EnsemblPlants:AT5G16370.1 GeneID:831498 KEGG:ath:AT5G16370 TAIR:At5g16370 InParanoid:Q9FFE6 OMA:SCAWKPQ PhylomeDB:Q9FFE6 ProtClustDB:CLSN2913637 Genevestigator:Q9FFE6 Uniprot:Q9FFE6
Root	Isotig07110	1	20	-4.451	3.92E-06	TAIR|locus:2171402 - symbol:AAE5 "acyl activating enzyme 5" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0008152 "metabolic process" evidence=IEA] [GO:0005777 "peroxisome" evidence=IDA] InterPro:IPR000873 Pfam:PF00501 Prosite:PS00455 EMBL:CP002688 GO:GO:0005777 InterPro:IPR020845 InterPro:IPR025110 Pfam:PF13193 HSSP:P08659 GO:GO:0003824 EMBL:AF503764 EMBL:AB005242 IPI:IPI00539798 RefSeq:NP_197141.1 UniGene:At.28787 UniGene:At.43181 ProteinModelPortal:Q9FFE6 SMR:Q9FFE6 STRING:Q9FFE6 PRIDE:Q9FFE6 EnsemblPlants:AT5G16370.1 GeneID:831498 KEGG:ath:AT5G16370 TAIR:At5g16370 InParanoid:Q9FFE6 OMA:SCAWKPQ PhylomeDB:Q9FFE6 ProtClustDB:CLSN2913637 Genevestigator:Q9FFE6 Uniprot:Q9FFE6
Root	Isotig07113	0	14	-4.936	8.24E-05	TAIR|locus:2132609 - symbol:ACR7 "ACT domain repeat 7" species:3702 "Arabidopsis thaliana" [GO:0008152 "metabolic process" evidence=IEA] [GO:0005829 "cytosol" evidence=ISS] [GO:0016597 "amino acid binding" evidence=ISS] InterPro:IPR002912 Pfam:PF01842 EMBL:CP002687 GO:GO:0016597 GO:GO:0008152 EMBL:AF528063 EMBL:BT029176 IPI:IPI00537192 RefSeq:NP_194009.2 UniGene:At.32498 ProteinModelPortal:Q8LJW1 PRIDE:Q8LJW1 EnsemblPlants:AT4G22780.1 GeneID:828377 KEGG:ath:AT4G22780 TAIR:At4g22780 InParanoid:Q8LJW1 OMA:VLADLEC PhylomeDB:Q8LJW1 ProtClustDB:CLSN2682266 Genevestigator:Q8LJW1 Uniprot:Q8LJW1
Root	Isotig07114	0	14	-4.936	8.24E-05	TAIR|locus:2132609 - symbol:ACR7 "ACT domain repeat 7" species:3702 "Arabidopsis thaliana" [GO:0008152 "metabolic process" evidence=IEA] [GO:0005829 "cytosol" evidence=ISS] [GO:0016597 "amino acid binding" evidence=ISS] InterPro:IPR002912 Pfam:PF01842 EMBL:CP002687 GO:GO:0016597 GO:GO:0008152 EMBL:AF528063 EMBL:BT029176 IPI:IPI00537192 RefSeq:NP_194009.2 UniGene:At.32498 ProteinModelPortal:Q8LJW1 PRIDE:Q8LJW1 EnsemblPlants:AT4G22780.1 GeneID:828377 KEGG:ath:AT4G22780 TAIR:At4g22780 InParanoid:Q8LJW1 OMA:VLADLEC PhylomeDB:Q8LJW1 ProtClustDB:CLSN2682266 Genevestigator:Q8LJW1 Uniprot:Q8LJW1
Root	Isotig07123	4	28	-2.936	2.81E-06	TAIR|locus:2039270 - symbol:FLA16 "AT2G35860" species:3702 "Arabidopsis thaliana" [GO:0007155 "cell adhesion" evidence=ISS] Pfam:PF02469 InterPro:IPR000782 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0005576 EMBL:AC007017 Gene3D:G3DSA:2.30.180.10 SMART:SM00554 SUPFAM:SSF82153 PROSITE:PS50213 HOGENOM:HBG595175 ProtClustDB:CLSN2915491 EMBL:AY093189 EMBL:BT006590 IPI:IPI00537255 PIR:H84773 RefSeq:NP_850253.1 UniGene:At.27800 ProteinModelPortal:Q8RWC5 SMR:Q8RWC5 STRING:Q8RWC5 PRIDE:Q8RWC5 EnsemblPlants:AT2G35860.1 GeneID:818159 KEGG:ath:AT2G35860 GeneFarm:3813 TAIR:At2g35860 eggNOG:NOG302692 InParanoid:Q8RWC5 OMA:ATEIKPA PhylomeDB:Q8RWC5 Genevestigator:Q8RWC5 GermOnline:AT2G35860 Uniprot:Q8RWC5
Root	Isotig07124	3	29	-3.402	3.49E-07	TAIR|locus:2164290 - symbol:FLA17 "AT5G06390" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0007155 "cell adhesion" evidence=ISS] [GO:0005773 "vacuole" evidence=IDA] Pfam:PF02469 InterPro:IPR000782 GO:GO:0005773 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005576 EMBL:AB006700 Gene3D:G3DSA:2.30.180.10 SMART:SM00554 SUPFAM:SSF82153 PROSITE:PS50213 HOGENOM:HBG595175 eggNOG:NOG302692 EMBL:BT015342 EMBL:BT020253 IPI:IPI00521755 RefSeq:NP_196257.2 UniGene:At.32865 ProteinModelPortal:Q66GR0 SMR:Q66GR0 PRIDE:Q66GR0 EnsemblPlants:AT5G06390.1 GeneID:830527

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						KEGG:ath:AT5G06390 GeneFarm:3814 TAIR:At5g06390 InParanoid:Q66GR0 OMA:IQSAMAP PhylomeDB:Q66GR0 ProtClustDB:CLSN2914955 Genevestigator:Q66GR0 Uniprot:Q66GR0
Root	Isotig07131	5	23	-2.331	0.000182103	No hit
Root	Isotig07149	4	24	-2.714	3.10E-05	TAIR|locus:2015791 - symbol:GlcNAc1pUT1 "N-acetylglucosamine-1-phosphate uridylyltransferase 1" species:3702 "Arabidopsis thaliana" [GO:0005886 "plasma membrane" evidence=IDA] [GO:0003977 "UDP-N-acetylglucosamine diphosphorylase activity" evidence=IDA] [GO:0006047 "UDP-N-acetylglucosamine metabolic process" evidence=IDA] [GO:0019276 "UDP-N-acetylgalactosamine metabolic process" evidence=IDA] [GO:0052630 "UDP-N-acetylgalactosamine diphosphorylase activity" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR002618 Pfam:PF01704 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0005886 GO:GO:0019276 GO:GO:0006047 GO:GO:0003977 HSSP:Q16222 eggNOG:COG4284 HOGENOM:HBG527090 KO:K00972 PANTHER:PTHR11952 ProtClustDB:PLN02435 GO:GO:0052630 OMA:YFDIFRY EMBL:AY053411 IPI:IPI00517047 RefSeq:NP_564372.3 UniGene:At.15935 ProteinModelPortal:Q940S3 SMR:Q940S3 STRING:Q940S3 PRIDE:Q940S3 EnsemblPlants:AT1G31070.2 GeneID:839993 KEGG:ath:AT1G31070 TAIR:At1g31070 InParanoid:Q940S3 PhylomeDB:Q940S3 Genevestigator:Q940S3 Uniprot:Q940S3
Root	Isotig07150	4	24	-2.714	3.10E-05	TAIR|locus:2015791 - symbol:GlcNAc1pUT1 "N-acetylglucosamine-1-phosphate uridylyltransferase 1" species:3702 "Arabidopsis thaliana" [GO:0005886 "plasma membrane" evidence=IDA] [GO:0003977 "UDP-N-acetylglucosamine diphosphorylase activity" evidence=IDA] [GO:0006047 "UDP-N-acetylglucosamine metabolic process" evidence=IDA] [GO:0019276 "UDP-N-acetylgalactosamine metabolic process" evidence=IDA] [GO:0052630 "UDP-N-acetylgalactosamine diphosphorylase activity" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR002618 Pfam:PF01704 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0005886 GO:GO:0019276 GO:GO:0006047 GO:GO:0003977 HSSP:Q16222 eggNOG:COG4284 HOGENOM:HBG527090 KO:K00972 PANTHER:PTHR11952 ProtClustDB:PLN02435 GO:GO:0052630 OMA:YFDIFRY EMBL:AY053411 IPI:IPI00517047 RefSeq:NP_564372.3 UniGene:At.15935 ProteinModelPortal:Q940S3 SMR:Q940S3 STRING:Q940S3 PRIDE:Q940S3 EnsemblPlants:AT1G31070.2 GeneID:839993 KEGG:ath:AT1G31070 TAIR:At1g31070 InParanoid:Q940S3 PhylomeDB:Q940S3 Genevestigator:Q940S3 Uniprot:Q940S3
Root	Isotig07151	4	31	-3.083	4.53E-07	TAIR|locus:2147117 - symbol:AT5G20950 species:3702 "Arabidopsis thaliana" [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=IEA;ISS] [GO:0005975 "carbohydrate metabolic process" evidence=IEA;ISS] [GO:0005618 "cell wall" evidence=IDA] [GO:0009505 "plant-type cell wall" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR001764 InterPro:IPR002772 Pfam:PF00933 Pfam:PF01915 PRINTS:PR00133 GO:GO:0009506 EMBL:CP002688 GO:GO:0016020 InterPro:IPR017853 SUPFAM:SSF51445 GO:GO:0005975 GO:GO:0004553 GO:GO:0009505 Gene3D:G3DSA:3.40.50.1700 Gene3D:G3DSA:3.20.20.300 SUPFAM:SSF52279 CAZy:GH3 HSSP:Q9XEI3 EMBL:AF462808 EMBL:AY091027 EMBL:AY142679 IPI:IPI00528669 RefSeq:NP_197595.2 RefSeq:NP_851048.1 UniGene:At.23560 ProteinModelPortal:Q8W112 SMR:Q8W112 PRIDE:Q8W112 EnsemblPlants:AT5G20950.1 EnsemblPlants:AT5G20950.2 GeneID:832220 KEGG:ath:AT5G20950 TAIR:At5g20950 InParanoid:Q8W112 OMA:THNGINE PhylomeDB:Q8W112 ProtClustDB:CLSN2690178 ArrayExpress:Q8W112 Genevestigator:Q8W112 Uniprot:Q8W112
Root	Isotig07152	4	23	-2.653	5.61E-05	TAIR|locus:2147117 - symbol:AT5G20950 species:3702 "Arabidopsis thaliana" [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=IEA;ISS] [GO:0005975 "carbohydrate metabolic process" evidence=IEA;ISS] [GO:0005618 "cell wall" evidence=IDA] [GO:0009505 "plant-type cell wall" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR001764 InterPro:IPR002772 Pfam:PF00933 Pfam:PF01915 PRINTS:PR00133 GO:GO:0009506 EMBL:CP002688 GO:GO:0016020 InterPro:IPR017853 SUPFAM:SSF51445 GO:GO:0005975 GO:GO:0004553 GO:GO:0009505 Gene3D:G3DSA:3.40.50.1700 Gene3D:G3DSA:3.20.20.300 SUPFAM:SSF52279 CAZy:GH3 HSSP:Q9XEI3 EMBL:AF462808 EMBL:AY091027 EMBL:AY142679 IPI:IPI00528669 RefSeq:NP_197595.2 RefSeq:NP_851048.1 UniGene:At.23560 ProteinModelPortal:Q8W112 SMR:Q8W112 PRIDE:Q8W112 EnsemblPlants:AT5G20950.1 EnsemblPlants:AT5G20950.2 GeneID:832220 KEGG:ath:AT5G20950 TAIR:At5g20950 InParanoid:Q8W112 OMA:THNGINE PhylomeDB:Q8W112 ProtClustDB:CLSN2690178 ArrayExpress:Q8W112 Genevestigator:Q8W112 Uniprot:Q8W112

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig07165	2	17	-3.216	0.000139706	TAIR|locus:2167240 - symbol:GAD "AT5G17330" species:3702 "Arabidopsis thaliana" [GO:0005516 "calmodulin binding" evidence=IDA;TAS;IPI] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA] [GO:0004351 "glutamate decarboxylase activity" evidence=IDA] InterPro:IPR002129 InterPro:IPR010107 InterPro:IPR015421 Pfam:PF00282 PROSITE:PS00392 GO:GO:0005829 GO:GO:0046686 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0030170 InterPro:IPR015424 Gene3D:G3DSA:3.40.640.10 SUPFAM:SSF53383 GO:GO:0006536 GO:GO:0005516 EMBL:AB005238 eggNOG:COG0076 PANTHER:PTHR11999 EMBL:U10034 EMBL:AY094464 EMBL:BT001047 IPI:IPI00530557 RefSeq:NP_197235.1 UniGene:At.25228 PDB:3HBX PDBsum:3HBX ProteinModelPortal:Q42521 SMR:Q42521 STRING:Q42521 PRIDE:Q42521 EnsemblPlants:AT5G17330.1 GeneID:831599 KEGG:ath:AT5G17330 TAIR:At5g17330 HOGENOM:HBG365574 InParanoid:Q42521 KO:K01580 OMA:RRWQNKM PhylomeDB:Q42521 ProtClustDB:CLSN2683665 ArrayExpress:Q42521 Genevestigator:Q42521 GermOnline:AT5G17330 GO:GO:0004351 PANTHER:PTHR11999:SF1 TIGRFAMs:TIGR01788 Uniprot:Q42521
Root	Isotig07166	2	17	-3.216	0.000139706	TAIR|locus:2167240 - symbol:GAD "AT5G17330" species:3702 "Arabidopsis thaliana" [GO:0005516 "calmodulin binding" evidence=IDA;TAS;IPI] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA] [GO:0004351 "glutamate decarboxylase activity" evidence=IDA] InterPro:IPR002129 InterPro:IPR010107 InterPro:IPR015421 Pfam:PF00282 PROSITE:PS00392 GO:GO:0005829 GO:GO:0046686 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0030170 InterPro:IPR015424 Gene3D:G3DSA:3.40.640.10 SUPFAM:SSF53383 GO:GO:0006536 GO:GO:0005516 EMBL:AB005238 eggNOG:COG0076 PANTHER:PTHR11999 EMBL:U10034 EMBL:AY094464 EMBL:BT001047 IPI:IPI00530557 RefSeq:NP_197235.1 UniGene:At.25228 PDB:3HBX PDBsum:3HBX ProteinModelPortal:Q42521 SMR:Q42521 STRING:Q42521 PRIDE:Q42521 EnsemblPlants:AT5G17330.1 GeneID:831599 KEGG:ath:AT5G17330 TAIR:At5g17330 HOGENOM:HBG365574 InParanoid:Q42521 KO:K01580 OMA:RRWQNKM PhylomeDB:Q42521 ProtClustDB:CLSN2683665 ArrayExpress:Q42521 Genevestigator:Q42521 GermOnline:AT5G17330 GO:GO:0004351 PANTHER:PTHR11999:SF1 TIGRFAMs:TIGR01788 Uniprot:Q42521
Root	Isotig07185	0	14	-4.936	8.24E-05	TAIR|locus:2148171 - symbol:CSLD2 "AT5G16910" species:3702 "Arabidopsis thaliana" [GO:0000271 "polysaccharide biosynthetic process" evidence=ISS] [GO:0009832 "plant-type cell wall biogenesis" evidence=ISS] [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0016759 "cellulose synthase activity" evidence=ISS] [GO:0005794 "Golgi apparatus" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0030173 "integral to Golgi membrane" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0048767 "root hair elongation" evidence=IMP] InterPro:IPR005150 Pfam:PF03552 GO:GO:0005886 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0030173 GO:GO:0009409 GO:GO:0048767 InterPro:IPR013083 Gene3D:G3DSA:3.30.40.10 GO:GO:0007047 CAZy:GT2 eggNOG:COG1215 GO:GO:0016760 GO:GO:0030244 HOGENOM:HBG744549 ProtClustDB:PLN02248 EMBL:AL391141 IPI:IPI00532872 PIR:T51546 RefSeq:NP_197193.1 UniGene:At.20318 ProteinModelPortal:Q9LFL0 SMR:Q9LFL0 PRIDE:Q9LFL0 EnsemblPlants:AT5G16910.1 GeneID:831554 KEGG:ath:AT5G16910 TAIR:At5g16910 InParanoid:Q9LFL0 OMA:WRIKHQN PhylomeDB:Q9LFL0 Genevestigator:Q9LFL0 Uniprot:Q9LFL0
Root	Isotig07187	28	6	2.093	0.000219123	TAIR|locus:2091618 - symbol:AT3G22270 "AT3G22270" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] GenomeReviews:BA000014_GR HOGENOM:HBG318375 EMBL:AK228960 IPI:IPI00533404 ProteinModelPortal:Q0WPV0 PRIDE:Q0WPV0 TAIR:At3g22270 eggNOG:NOG323978 InParanoid:Q0WPV0 PhylomeDB:Q0WPV0 Genevestigator:Q0WPV0 Uniprot:Q0WPV0
Root	Isotig07188	27	5	2.304	0.000117535	TAIR|locus:2091618 - symbol:AT3G22270 "AT3G22270" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] GenomeReviews:BA000014_GR HOGENOM:HBG318375 EMBL:AK228960 IPI:IPI00533404 ProteinModelPortal:Q0WPV0 PRIDE:Q0WPV0 TAIR:At3g22270 eggNOG:NOG323978 InParanoid:Q0WPV0 PhylomeDB:Q0WPV0 Genevestigator:Q0WPV0 Uniprot:Q0WPV0
Root	Isotig07193	7	28	-2.129	9.37E-05	TAIR|locus:2118791 - symbol:DGK7 "AT4G30340" species:3702 "Arabidopsis thaliana" [GO:0004143 "diacylglycerol kinase activity" evidence=ISS;IDA] [GO:0007205 "activation of protein kinase C activity by G-protein coupled receptor protein signaling pathway" evidence=ISS] [GO:0048364 "root development" evidence=IMP] [GO:0048366 "leaf development" evidence=IMP] [GO:0005886 "plasma membrane" evidence=IDA] InterPro:IPR000756 InterPro:IPR001206 Pfam:PF00609 Pfam:PF00781 PROSITE:PS50146 SMART:SM00045 SMART:SM00046 GO:GO:0005886 GenomeReviews:CT486007_GR GO:GO:0007205 GO:GO:0048364

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0048366 GO:GO:0004143 eggNOG:NOG47311 EMBL:DQ350135 IPI:IPI00538842 ProteinModelPortal:B0KYU1 PRIDE:B0KYU1 TAIR:At4g30340 HOGENOM:HBG317142 PhylomeDB:B0KYU1 Genevestigator:B0KYU1 InterPro:IPR016961 PIRSF:PIRSF030829 Uniprot:B0KYU1
Root	Isotig07194	7	28	-2.129	9.37E-05	TAIR|locus:2118791 - symbol:DGK7 "AT4G30340" species:3702 "Arabidopsis thaliana" [GO:0004143 "diacylglycerol kinase activity" evidence=ISS;IDA] [GO:0007205 "activation of protein kinase C activity by G-protein coupled receptor protein signaling pathway" evidence=ISS] [GO:0048364 "root development" evidence=IMP] [GO:0048366 "leaf development" evidence=IMP] [GO:0005886 "plasma membrane" evidence=IDA] InterPro:IPR000756 InterPro:IPR001206 Pfam:PF00609 Pfam:PF00781 PROSITE:PS50146 SMART:SM00045 SMART:SM00046 GO:GO:0005886 GenomeReviews:CT486007_GR GO:GO:0007205 GO:GO:0048364 GO:GO:0048366 GO:GO:0004143 eggNOG:NOG47311 EMBL:DQ350135 IPI:IPI00538842 ProteinModelPortal:B0KYU1 PRIDE:B0KYU1 TAIR:At4g30340 HOGENOM:HBG317142 PhylomeDB:B0KYU1 Genevestigator:B0KYU1 InterPro:IPR016961 PIRSF:PIRSF030829 Uniprot:B0KYU1
Root	Isotig07217	38	7	2.312	4.70E-06	TAIR|locus:2089521 - symbol:CYP72A15 ""cytochrome P450, family 72, subfamily A, polypeptide 15"" species:3702 "Arabidopsis thaliana" [GO:0004497 "monooxygenase activity" evidence=IEA] [GO:0005506 "iron ion binding" evidence=IEA] [GO:0009055 "electron carrier activity" evidence=IEA] [GO:0019825 "oxygen binding" evidence=ISS] [GO:0020037 "heme binding" evidence=IEA] InterPro:IPR001128 InterPro:IPR002401 Pfam:PF00067 PRINTS:PR00385 PRINTS:PR00463 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0009055 GO:GO:0004497 eggNOG:COG2124 GO:GO:0020037 Gene3D:G3DSA:1.10.630.10 SUPFAM:SSF48264 GO:GO:0016705 HSSP:P14779 HOGENOM:HBG715383 EMBL:AB023038 EMBL:AY050827 EMBL:AY096748 IPI:IPI00542070 RefSeq:NP_188087.1 UniGene:At.19957 UniGene:At.23975 ProteinModelPortal:Q9LUC5 SMR:Q9LUC5 STRING:Q9LUC5 PRIDE:Q9LUC5 EnsemblPlants:AT3G14690.1 GeneID:820697 KEGG:ath:AT3G14690 TAIR:At3g14690 InParanoid:Q9LUC5 OMA:TVITIHP PhylomeDB:Q9LUC5 ProtClustDB:CLSN2684942 ArrayExpress:Q9LUC5 Genevestigator:Q9LUC5 Uniprot:Q9LUC5
Root	Isotig07218	38	5	2.797	3.54E-07	TAIR|locus:2089521 - symbol:CYP72A15 ""cytochrome P450, family 72, subfamily A, polypeptide 15"" species:3702 "Arabidopsis thaliana" [GO:0004497 "monooxygenase activity" evidence=IEA] [GO:0005506 "iron ion binding" evidence=IEA] [GO:0009055 "electron carrier activity" evidence=IEA] [GO:0019825 "oxygen binding" evidence=ISS] [GO:0020037 "heme binding" evidence=IEA] InterPro:IPR001128 InterPro:IPR002401 Pfam:PF00067 PRINTS:PR00385 PRINTS:PR00463 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0009055 GO:GO:0004497 eggNOG:COG2124 GO:GO:0020037 Gene3D:G3DSA:1.10.630.10 SUPFAM:SSF48264 GO:GO:0016705 HSSP:P14779 HOGENOM:HBG715383 EMBL:AB023038 EMBL:AY050827 EMBL:AY096748 IPI:IPI00542070 RefSeq:NP_188087.1 UniGene:At.19957 UniGene:At.23975 ProteinModelPortal:Q9LUC5 SMR:Q9LUC5 STRING:Q9LUC5 PRIDE:Q9LUC5 EnsemblPlants:AT3G14690.1 GeneID:820697 KEGG:ath:AT3G14690 TAIR:At3g14690 InParanoid:Q9LUC5 OMA:TVITIHP PhylomeDB:Q9LUC5 ProtClustDB:CLSN2684942 ArrayExpress:Q9LUC5 Genevestigator:Q9LUC5 Uniprot:Q9LUC5
Root	Isotig07225	5	47	-3.362	1.09E-10	TAIR|locus:2166645 - symbol:AT5G38710 species:3702 "Arabidopsis thaliana" [GO:0004657 "proline dehydrogenase activity" evidence=IEA;IGI;ISS] [GO:0006537 "glutamate biosynthetic process" evidence=IEA;ISS] [GO:0006562 "proline catabolic process" evidence=IEA;IGI;ISS] [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0006970 "response to osmotic stress" evidence=IEP] [GO:0009414 "response to water deprivation" evidence=IEP] InterPro:IPR002872 InterPro:IPR015659 Pfam:PF01619 GO:GO:0005739 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009414 GO:GO:0006970 GO:GO:0006537 GO:GO:0006562 EMBL:AB011478 eggNOG:COG0506 KO:K00318 ProtClustDB:PLN02681 GO:GO:0004657 PANTHER:PTHR13914 EMBL:BT012572 EMBL:AK221601 IPI:IPI00544454 RefSeq:NP_198687.1 UniGene:At.50494 ProteinModelPortal:Q6NKX1 PRIDE:Q6NKX1 EnsemblPlants:AT5G38710.1 GeneID:833862 KEGG:ath:AT5G38710 TAIR:At5g38710 InParanoid:Q6NKX1 OMA:GQTGREL PhylomeDB:Q6NKX1 BioCyc:MetaCyc:AT5G38710-MONOMER Genevestigator:Q6NKX1 Uniprot:Q6NKX1
Root	Isotig07226	4	47	-3.684	2.25E-11	TAIR|locus:2166645 - symbol:AT5G38710 species:3702 "Arabidopsis thaliana" [GO:0004657 "proline dehydrogenase activity" evidence=IEA;IGI;ISS] [GO:0006537 "glutamate biosynthetic process" evidence=IEA;ISS] [GO:0006562 "proline catabolic process" evidence=IEA;IGI;ISS] [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0006970 "response to osmotic stress" evidence=IEP] [GO:0009414 "response to water deprivation" evidence=IEP] InterPro:IPR002872 InterPro:IPR015659 Pfam:PF01619 GO:GO:0005739 EMBL:CP002688 GenomeReviews:BA000015_GR

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0009414 GO:GO:0006970 GO:GO:0006537 GO:GO:0006562 EMBL:AB011478 eggNOG:COG0506 KO:K00318 ProtClustDB:PLN02681 GO:GO:0004657 PANTHER:PTHR13914 EMBL:BT012572 EMBL:AK221601 IPI:IPI00544454 RefSeq:NP_198687.1 UniGene:At.50494 ProteinModelPortal:Q6NKX1 PRIDE:Q6NKX1 EnsemblPlants:AT5G38710.1 GeneID:833862 KEGG:ath:AT5G38710 TAIR:At5g38710 InParanoid:Q6NKX1 OMA:GQTGREL PhylomeDB:Q6NKX1 BioCyc:MetaCyc:AT5G38710-MONOMER Genevestigator:Q6NKX1 Uniprot:Q6NKX1
Root	Isotig07229	0	20	-5.451	2.00E-06	TAIR|locus:2161710 - symbol:AT5G55180 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=IEA;ISS] [GO:0005975 "carbohydrate metabolic process" evidence=IEA] [GO:0043169 "cation binding" evidence=IEA] InterPro:IPR000490 InterPro:IPR013781 Pfam:PF00332 PROSITE:PS00587 GO:GO:0043169 InterPro:IPR017853 Gene3D:G3DSA:3.20.20.80 SUPFAM:SSF51445 GO:GO:0005975 GO:GO:0004553 CAZy:GH17 EMBL:AB010071 HSSP:P15737 CAZy:CBM43 InterPro:IPR012946 Pfam:PF07983 SMART:SM00768 IPI:IPI00531642 ProteinModelPortal:Q9FLP4 SMR:Q9FLP4 PRIDE:Q9FLP4 TAIR:At5g55180 PhylomeDB:Q9FLP4 Genevestigator:Q9FLP4 Uniprot:Q9FLP4
Root	Isotig07230	0	16	-5.129	2.34E-05	TAIR|locus:2161710 - symbol:AT5G55180 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=IEA;ISS] [GO:0005975 "carbohydrate metabolic process" evidence=IEA] [GO:0043169 "cation binding" evidence=IEA] InterPro:IPR000490 InterPro:IPR013781 Pfam:PF00332 PROSITE:PS00587 GO:GO:0043169 InterPro:IPR017853 Gene3D:G3DSA:3.20.20.80 SUPFAM:SSF51445 GO:GO:0005975 GO:GO:0004553 CAZy:GH17 EMBL:AB010071 HSSP:P15737 CAZy:CBM43 InterPro:IPR012946 Pfam:PF07983 SMART:SM00768 IPI:IPI00531642 ProteinModelPortal:Q9FLP4 SMR:Q9FLP4 PRIDE:Q9FLP4 TAIR:At5g55180 PhylomeDB:Q9FLP4 Genevestigator:Q9FLP4 Uniprot:Q9FLP4
Root	Isotig07231	23	99	-2.235	3.72E-14	RGD|727924 - symbol:LOC257642 "rRNA promoter binding protein" species:10116 "Rattus norvegicus" [GO:0003690 "double-stranded DNA binding" evidence=IDA] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=IDA] [GO:0008134 "transcription factor binding" evidence=IDA] [GO:0008283 "cell proliferation" evidence=IDA] [GO:0009303 "rRNA transcription" evidence=IDA] RGD:727924 GO:GO:0008134 GO:GO:0008283 GO:GO:0003700 GO:GO:0003690 GO:GO:0009303 EMBL:U77931 IPI:IPI00195015 RefSeq:NP_671477.1 GeneID:257642 KEGG:rno:257642 NextBio:624170 Genevestigator:Q99JC0 Uniprot:Q99JC0
Root	Isotig07232	23	98	-2.220	6.29E-14	RGD|727924 - symbol:LOC257642 "rRNA promoter binding protein" species:10116 "Rattus norvegicus" [GO:0003690 "double-stranded DNA binding" evidence=IDA] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=IDA] [GO:0008134 "transcription factor binding" evidence=IDA] [GO:0008283 "cell proliferation" evidence=IDA] [GO:0009303 "rRNA transcription" evidence=IDA] RGD:727924 GO:GO:0008134 GO:GO:0008283 GO:GO:0003700 GO:GO:0003690 GO:GO:0009303 EMBL:U77931 IPI:IPI00195015 RefSeq:NP_671477.1 GeneID:257642 KEGG:rno:257642 NextBio:624170 Genevestigator:Q99JC0 Uniprot:Q99JC0
Root	Isotig07235	4	20	-2.451	0.000325095	TAIR|locus:2064402 - symbol:C4H "AT2G30490" species:3702 "Arabidopsis thaliana" [GO:0009505 "plant-type cell wall" evidence=IDA] [GO:0005783 "endoplasmic reticulum" evidence=IDA;TAS] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009555 "pollen development" evidence=IMP] [GO:0009698 "phenylpropanoid metabolic process" evidence=IMP] [GO:0009808 "lignin metabolic process" evidence=IMP] [GO:0032502 "developmental process" evidence=IMP] [GO:0040007 "growth" evidence=IMP] [GO:0080167 "response to karrikin" evidence=IEP] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] [GO:0009416 "response to light stimulus" evidence=IEP] [GO:0009611 "response to wounding" evidence=IMP] [GO:0009699 "phenylpropanoid biosynthetic process" evidence=TAS] [GO:0016710 "trans-cinnamate 4-monooxygenase activity" evidence=IDA] InterPro:IPR001128 InterPro:IPR002401 InterPro:IPR017972 Pfam:PF00067 PRINTS:PR00385 PRINTS:PR00463 PROSITE:PS00086 GO:GO:0005783 GO:GO:0016021 GO:GO:0005886 GO:GO:0009506 GO:GO:0005774 GO:GO:0040007 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009055 GO:GO:0080167 GO:GO:0009555 eggNOG:COG2124 GO:GO:0020037 Gene3D:G3DSA:1.10.630.10 SUPFAM:SSF48264 GO:GO:0009505 HOGENOM:HBG749920 GO:GO:0009808 EMBL:U93215 EMBL:U71081 EMBL:U71080 EMBL:D78596 EMBL:AY065145 EMBL:BT008875 IPI:IPI00525264 PIR:A84709 RefSeq:NP_180607.1 UniGene:At.23450 ProteinModelPortal:P92994 SMR:P92994 IntAct:P92994 STRING:P92994 PRIDE:P92994 EnsemblPlants:AT2G30490.1 GeneID:817599 KEGG:ath:AT2G30490 GeneFarm:1333

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						TAIR:At2g30490 InParanoid:P92994 KO:K00487 OMA:GITIGRM PhylomeDB:P92994 ProtClustDB:PLN02394 ArrayExpress:P92994 Genevestigator:P92994 GermOnline:AT2G30490 GO:GO:0016710 Uniprot:P92994
Root	Isotig07236	4	21	-2.521	0.000181802	TAIR|locus:2064402 - symbol:C4H "AT2G30490" species:3702 "Arabidopsis thaliana" [GO:0009505 "plant-type cell wall" evidence=IDA] [GO:0005783 "endoplasmic reticulum" evidence=IDA;TAS] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009555 "pollen development" evidence=IMP] [GO:0009698 "phenylpropanoid metabolic process" evidence=IMP] [GO:0009808 "lignin metabolic process" evidence=IMP] [GO:0032502 "developmental process" evidence=IMP] [GO:0040007 "growth" evidence=IMP] [GO:0080167 "response to karrikin" evidence=IEP] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] [GO:0009416 "response to light stimulus" evidence=IEP] [GO:0009611 "response to wounding" evidence=IMP] [GO:0009699 "phenylpropanoid biosynthetic process" evidence=TAS] [GO:0016710 "trans-cinnamate 4-monooxygenase activity" evidence=IDA] InterPro:IPR001128 InterPro:IPR002401 InterPro:IPR017972 Pfam:PF00067 PRINTS:PR00385 PRINTS:PR00463 PROSITE:PS00086 GO:GO:0005783 GO:GO:0016021 GO:GO:0005886 GO:GO:0009506 GO:GO:0005774 GO:GO:0040007 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009055 GO:GO:0080167 GO:GO:0009555 eggNOG:COG2124 GO:GO:0020037 Gene3D:G3DSA:1.10.630.10 SUPFAM:SSF48264 GO:GO:0009505 HOGENOM:HBG749920 GO:GO:0009808 EMBL:U93215 EMBL:U71081 EMBL:U71080 EMBL:D78596 EMBL:AY065145 EMBL:BT008875 IPI:IPI00525264 PIR:A84709 RefSeq:NP_180607.1 UniGene:At.23450 ProteinModelPortal:P92994 SMR:P92994 IntAct:P92994 STRING:P92994 PRIDE:P92994 EnsemblPlants:AT2G30490.1 GeneID:817599 KEGG:ath:AT2G30490 GeneFarm:1333 TAIR:At2g30490 InParanoid:P92994 KO:K00487 OMA:GITIGRM PhylomeDB:P92994 ProtClustDB:PLN02394 ArrayExpress:P92994 Genevestigator:P92994 GermOnline:AT2G30490 GO:GO:0016710 Uniprot:P92994
Root	Isotig07239	0	17	-5.216	1.26E-05	No hit
Root	Isotig07240	0	13	-4.829	0.000155955	TAIR|locus:2097380 - symbol:AT3G49720 "AT3G49720" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] GO:GO:0016021 GO:GO:0005886 GO:GO:0005774 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0000139 EMBL:AL132965 GO:GO:0009535 UniGene:At.22445 EMBL:AY087451 EMBL:AY059938 EMBL:AY114597 IPI:IPI00546242 PIR:T46038 RefSeq:NP_001078265.1 RefSeq:NP_566924.1 STRING:Q9M2Y6 PRIDE:Q9M2Y6 EnsemblPlants:AT3G49720.1 EnsemblPlants:AT3G49720.2 GeneID:824134 KEGG:ath:AT3G49720 TAIR:At3g49720 eggNOG:NOG327425 HOGENOM:HBG317293 InParanoid:Q9M2Y6 OMA:IEDADSH PhylomeDB:Q9M2Y6 ProtClustDB:CLSN2689079 ArrayExpress:Q93YM8 Genevestigator:Q9M2Y6 Uniprot:Q9M2Y6
Root	Isotig07248	12	0	4.456	0.000626491	TAIR|locus:2095833 - symbol:AT3G58030 species:3702 "Arabidopsis thaliana" [GO:0008270 "zinc ion binding" evidence=IEA;ISS] InterPro:IPR001841 PROSITE:PS50089 SMART:SM00184 Prosite:PS00518 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0008270 InterPro:IPR013083 Gene3D:G3DSA:3.30.40.10 InterPro:IPR017907 HOGENOM:HBG749996 ProtClustDB:CLSN2683808 EMBL:AY081289 EMBL:BT006585 IPI:IPI00546255 RefSeq:NP_001190122.1 RefSeq:NP_191362.2 RefSeq:NP_974453.1 RefSeq:NP_974454.1 UniGene:At.34773 ProteinModelPortal:Q8RXF2 SMR:Q8RXF2 PRIDE:Q8RXF2 EnsemblPlants:AT3G58030.1 EnsemblPlants:AT3G58030.2 EnsemblPlants:AT3G58030.3 EnsemblPlants:AT3G58030.4 GeneID:824972 KEGG:ath:AT3G58030 TAIR:At3g58030 eggNOG:NOG244906 InParanoid:Q8RXF2 OMA:HARRIES PhylomeDB:Q8RXF2 Genevestigator:Q8RXF2 Uniprot:Q8RXF2
Root	Isotig07259	49	7	2.678	1.58E-08	RGD|727924 - symbol:LOC257642 "rRNA promoter binding protein" species:10116 "Rattus norvegicus" [GO:0003690 "double-stranded DNA binding" evidence=IDA] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=IDA] [GO:0008134 "transcription factor binding" evidence=IDA] [GO:0008283 "cell proliferation" evidence=IDA] [GO:0009303 "rRNA transcription" evidence=IDA] RGD:727924 GO:GO:0008134 GO:GO:0008283 GO:GO:0003700 GO:GO:0003690 GO:GO:0009303 EMBL:U77931 IPI:IPI00195015 RefSeq:NP_671477.1 GeneID:257642 KEGG:rno:257642 NextBio:624170 Genevestigator:Q99JC0 Uniprot:Q99JC0
Root	Isotig07281	92	0	7.395	3.60E-21	TAIR|locus:2092990 - symbol:AT3G21000 "AT3G21000" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002686 EMBL:DQ446681 IPI:IPI00522289 RefSeq:NP_188737.1

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						UniGene:At.53413 PRIDE:Q1PEN6 EnsemblPlants:AT3G21000.1 GeneID:821651 KEGG:ath:AT3G21000 TAIR:At3g21000 InParanoid:Q1PEN6 OMA:ATANIRD Genevestigator:Q1PEN6 Uniprot:Q1PEN6
Root	Isotig07282	88	0	7.330	2.08E-20	TAIR|locus:2092990 - symbol:AT3G21000 "AT3G21000" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002686 EMBL:DQ446681 IPI:IPI00522289 RefSeq:NP_188737.1 UniGene:At.53413 PRIDE:Q1PEN6 EnsemblPlants:AT3G21000.1 GeneID:821651 KEGG:ath:AT3G21000 TAIR:At3g21000 InParanoid:Q1PEN6 OMA:ATANIRD Genevestigator:Q1PEN6 Uniprot:Q1PEN6
Root	Isotig07301	16	0	4.871	5.89E-05	TAIR|locus:2129351 - symbol:SBP1 "selenium-binding protein 1" species:3702 "Arabidopsis thaliana" [GO:0008430 "selenium binding" evidence=IEA;ISS] [GO:0046686 "response to cadmium ion" evidence=IEP;IDA] [GO:0000103 "sulfate assimilation" evidence=IEP] [GO:0042542 "response to hydrogen peroxide" evidence=IDA] [GO:0071291 "cellular response to selenium ion" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR008826 InterPro:IPR015943 Pfam:PF05694 GO:GO:0005829 GO:GO:0009506 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0046686 Gene3D:G3DSA:2.130.10.10 EMBL:Z97335 GO:GO:0042542 GO:GO:0000103 GO:GO:0008430 EMBL:AL161537 eggNOG:NOG84363 PANTHER:PTHR23300 HOGENOM:HBG318348 EMBL:AY062634 EMBL:AY128727 EMBL:Z27257 EMBL:AJ401229 IPI:IPI00543374 PIR:D71401 RefSeq:NP_001190723.1 RefSeq:NP_193139.1 UniGene:At.4249 ProteinModelPortal:O23264 SMR:O23264 PRIDE:O23264 EnsemblPlants:AT4G14030.1 EnsemblPlants:AT4G14030.2 GeneID:827039 KEGG:ath:AT4G14030 TAIR:At4g14030 InParanoid:O23264 OMA:MATETEV PhylomeDB:O23264 ProtClustDB:CLSN2684339 ArrayExpress:O23264 Genevestigator:O23264 GermOnline:AT4G14030 GO:GO:0071291 Uniprot:O23264
Root	Isotig07302	16	0	4.871	5.89E-05	TAIR|locus:2129351 - symbol:SBP1 "selenium-binding protein 1" species:3702 "Arabidopsis thaliana" [GO:0008430 "selenium binding" evidence=IEA;ISS] [GO:0046686 "response to cadmium ion" evidence=IEP;IDA] [GO:0000103 "sulfate assimilation" evidence=IEP] [GO:0042542 "response to hydrogen peroxide" evidence=IDA] [GO:0071291 "cellular response to selenium ion" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR008826 InterPro:IPR015943 Pfam:PF05694 GO:GO:0005829 GO:GO:0009506 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0046686 Gene3D:G3DSA:2.130.10.10 EMBL:Z97335 GO:GO:0042542 GO:GO:0000103 GO:GO:0008430 EMBL:AL161537 eggNOG:NOG84363 PANTHER:PTHR23300 HOGENOM:HBG318348 EMBL:AY062634 EMBL:AY128727 EMBL:Z27257 EMBL:AJ401229 IPI:IPI00543374 PIR:D71401 RefSeq:NP_001190723.1 RefSeq:NP_193139.1 UniGene:At.4249 ProteinModelPortal:O23264 SMR:O23264 PRIDE:O23264 EnsemblPlants:AT4G14030.1 EnsemblPlants:AT4G14030.2 GeneID:827039 KEGG:ath:AT4G14030 TAIR:At4g14030 InParanoid:O23264 OMA:MATETEV PhylomeDB:O23264 ProtClustDB:CLSN2684339 ArrayExpress:O23264 Genevestigator:O23264 GermOnline:AT4G14030 GO:GO:0071291 Uniprot:O23264
Root	Isotig07315	7	31	-2.276	1.84E-05	TAIR|locus:3439219 - symbol:TUA6 "AT4G14960" species:3702 "Arabidopsis thaliana" [GO:0005874 "microtubule" evidence=IDA] [GO:0045298 "tubulin complex" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005200 "structural constituent of cytoskeleton" evidence=ISS] [GO:0005730 "nucleolus" evidence=IDA] [GO:0000226 "microtubule cytoskeleton organization" evidence=IMP] [GO:0005618 "cell wall" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0071258 "cellular response to gravity" evidence=IMP] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000217 InterPro:IPR002452 InterPro:IPR003008 InterPro:IPR008280 InterPro:IPR017975 InterPro:IPR018316 Pfam:PF00091 Pfam:PF03953 PRINTS:PR01161 PRINTS:PR01162 PROSITE:PS00227 SMART:SM00864 SMART:SM00865 GO:GO:0005525 GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005773 GO:GO:0005618 GO:GO:0005515 GO:GO:0005730 GO:GO:0005198 GO:GO:0003924 GO:GO:0009651 EMBL:AL161540 GO:GO:0000226 GO:GO:0005874 GO:GO:0051258 Gene3D:G3DSA:3.40.50.1440 SUPFAM:SSF52490 GO:GO:0007018 EMBL:Z97337 Gene3D:G3DSA:3.30.1330.20 SUPFAM:SSF55307 GO:GO:0045298 eggNOG:COG5023 GO:GO:0071258 HOGENOM:HBG750007 KO:K07374 InterPro:IPR023123 Gene3D:G3DSA:1.10.287.600 PANTHER:PTHR11588 ProtClustDB:PLN00221 UniGene:At.22368 UniGene:At.48153 EMBL:M84699 EMBL:AY058858 EMBL:AY065347 EMBL:AY079036 EMBL:AY117174 IPI:IPI00520226 PIR:JQ1597 RefSeq:NP_193232.1 ProteinModelPortal:P29511 SMR:P29511 IntAct:P29511 STRING:P29511 PRIDE:P29511

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EnsemblPlants:AT4G14960.2 GeneID:827154 KEGG:ath:AT4G14960 TAIR:At4g14960 InParanoid:P29511 OMA:MPSDKAI PhylomeDB:P29511 ArrayExpress:P29511 Genevestigator:P29511 Uniprot:P29511
Root	Isotig07316	5	34	-2.895	2.97E-07	TAIR|locus:3439219 - symbol:TUA6 "AT4G14960" species:3702 "Arabidopsis thaliana" [GO:0005874 "microtubule" evidence=IDA] [GO:0045298 "tubulin complex" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005200 "structural constituent of cytoskeleton" evidence=ISS] [GO:0005730 "nucleolus" evidence=IDA] [GO:0000226 "microtubule cytoskeleton organization" evidence=IMP] [GO:0005618 "cell wall" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0071258 "cellular response to gravity" evidence=IMP] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000217 InterPro:IPR002452 InterPro:IPR003008 InterPro:IPR008280 InterPro:IPR017975 InterPro:IPR018316 Pfam:PF00091 Pfam:PF03953 PRINTS:PR01161 PRINTS:PR01162 PROSITE:PS00227 SMART:SM00864 SMART:SM00865 GO:GO:0005525 GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005773 GO:GO:0005618 GO:GO:0005515 GO:GO:0005730 GO:GO:0005198 GO:GO:0003924 GO:GO:0009651 EMBL:AL161540 GO:GO:0000226 GO:GO:0005874 GO:GO:0051258 Gene3D:G3DSA:3.40.50.1440 SUPFAM:SSF52490 GO:GO:0007018 EMBL:Z97337 Gene3D:G3DSA:3.30.1330.20 SUPFAM:SSF55307 GO:GO:0045298 eggNOG:COG5023 GO:GO:0071258 HOGENOM:HBG750007 KO:K07374 InterPro:IPR023123 Gene3D:G3DSA:1.10.287.600 PANTHER:PTHR11588 ProtClustDB:PLN00221 UniGene:At.22368 UniGene:At.48153 EMBL:M84699 EMBL:AY058858 EMBL:AY065347 EMBL:AY079036 EMBL:AY117174 IPI:IPI00520226 PIR:JQ1597 RefSeq:NP_193232.1 ProteinModelPortal:P29511 SMR:P29511 IntAct:P29511 STRING:P29511 PRIDE:P29511 EnsemblPlants:AT4G14960.2 GeneID:827154 KEGG:ath:AT4G14960 TAIR:At4g14960 InParanoid:P29511 OMA:MPSDKAI PhylomeDB:P29511 ArrayExpress:P29511 Genevestigator:P29511 Uniprot:P29511
Root	Isotig07323	18	0	5.041	1.86E-05	TAIR|locus:2014109 - symbol:EBS5 "AT1G18260" species:3702 "Arabidopsis thaliana" [GO:0005783 "endoplasmic reticulum" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0030433 "ER-associated protein catabolic process" evidence=IMP] [GO:0042538 "hyperosmotic salinity response" evidence=IMP] InterPro:IPR011990 GO:GO:0005783 EMBL:CP002684 GO:GO:0005488 GO:GO:0016020 KO:K07126 InterPro:IPR006597 Gene3D:G3DSA:1.25.40.10 Pfam:PF08238 SMART:SM00671 GO:GO:0030433 GO:GO:0042538 EMBL:AC069551 ProtClustDB:CLSN2679872 EMBL:AB189471 IPI:IPI00542104 RefSeq:NP_564049.1 UniGene:At.14948 UniGene:At.67114 ProteinModelPortal:Q9LM25 SMR:Q9LM25 PRIDE:Q9LM25 EnsemblPlants:AT1G18260.1 GeneID:838406 KEGG:ath:AT1G18260 TAIR:At1g18260 InParanoid:Q9LM25 OMA:HGQGLPF PhylomeDB:Q9LM25 Genevestigator:Q9LM25 Uniprot:Q9LM25
Root	Isotig07324	18	0	5.041	1.86E-05	TAIR|locus:2014109 - symbol:EBS5 "AT1G18260" species:3702 "Arabidopsis thaliana" [GO:0005783 "endoplasmic reticulum" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0030433 "ER-associated protein catabolic process" evidence=IMP] [GO:0042538 "hyperosmotic salinity response" evidence=IMP] InterPro:IPR011990 GO:GO:0005783 EMBL:CP002684 GO:GO:0005488 GO:GO:0016020 KO:K07126 InterPro:IPR006597 Gene3D:G3DSA:1.25.40.10 Pfam:PF08238 SMART:SM00671 GO:GO:0030433 GO:GO:0042538 EMBL:AC069551 ProtClustDB:CLSN2679872 EMBL:AB189471 IPI:IPI00542104 RefSeq:NP_564049.1 UniGene:At.14948 UniGene:At.67114 ProteinModelPortal:Q9LM25 SMR:Q9LM25 PRIDE:Q9LM25 EnsemblPlants:AT1G18260.1 GeneID:838406 KEGG:ath:AT1G18260 TAIR:At1g18260 InParanoid:Q9LM25 OMA:HGQGLPF PhylomeDB:Q9LM25 Genevestigator:Q9LM25 Uniprot:Q9LM25
Root	Isotig07347	32	6	2.286	3.01E-05	TAIR|locus:2016254 - symbol:GLYI7 "AT1G80160" species:3702 "Arabidopsis thaliana" [GO:0004462 "lactoylglutathione lyase activity" evidence=ISS] [GO:0005975 "carbohydrate metabolic process" evidence=ISS] EMBL:AC009322 IPI:IPI00532356 PIR:C96833 ProteinModelPortal:Q9SSC3 SMR:Q9SSC3 STRING:Q9SSC3 PRIDE:Q9SSC3 TAIR:At1g80160 InParanoid:Q9SSC3 PhylomeDB:Q9SSC3 Genevestigator:Q9SSC3 Uniprot:Q9SSC3
Root	Isotig07348	32	5	2.549	8.76E-06	TAIR|locus:2016254 - symbol:GLYI7 "AT1G80160" species:3702 "Arabidopsis thaliana" [GO:0004462 "lactoylglutathione lyase activity" evidence=ISS] [GO:0005975 "carbohydrate metabolic process" evidence=ISS] EMBL:AC009322 IPI:IPI00532356 PIR:C96833 ProteinModelPortal:Q9SSC3 SMR:Q9SSC3 STRING:Q9SSC3 PRIDE:Q9SSC3 TAIR:At1g80160 InParanoid:Q9SSC3 PhylomeDB:Q9SSC3 Genevestigator:Q9SSC3 Uniprot:Q9SSC3
Root	Isotig07355	0	33	-6.173	1.05E-09	TAIR|locus:2141201 - symbol:CRK29 "AT4G21410" species:3702 "Arabidopsis thaliana" [GO:0016301 "kinase activity" evidence=ISS] [GO:0005773 "vacuole" evidence=IDA] [GO:0009737 "response to abscisic acid stimulus"

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						evidence=IEP] [GO:0005886 "plasma membrane" evidence=IDA] InterPro:IPR000719 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 Pfam:PF00069 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 GO:GO:0016021 GO:GO:0005886 GO:GO:0005524 GO:GO:0009737 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005773 eggNOG:COG0515 GO:GO:0004872 SUPFAM:SSF56112 GO:GO:0004674 HOGENOM:HBG755340 EMBL:AL161555 EMBL:AL022603 EMBL:AL031187 InterPro:IPR002902 Pfam:PF01657 PROSITE:PS51473 ProtClustDB:CLSN2685554 EMBL:AY074844 IPI:IPI00516505 PIR:T05149 RefSeq:NP_193872.2 UniGene:At.43984 ProteinModelPortal:Q8S9L6 SMR:Q8S9L6 PRIDE:Q8S9L6 EnsemblPlants:AT4G21410.1 GeneID:827893 KEGG:ath:AT4G21410 GeneFarm:237 TAIR:At4g21410 InParanoid:Q8S9L6 OMA:ISANRDD PhylomeDB:Q8S9L6 ArrayExpress:O65406 Genevestigator:Q8S9L6 Uniprot:Q8S9L6
Root	Isotig07356	0	12	-4.714	0.000297064	TAIR|locus:2115728 - symbol:CRK25 "cysteine-rich RLK (RECEPTOR-like protein kinase) 25" species:3702 "Arabidopsis thaliana" [GO:0006468 "protein phosphorylation" evidence=IEA] [GO:0016301 "kinase activity" evidence=ISS] InterPro:IPR000719 InterPro:IPR001245 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 Pfam:PF07714 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 GO:GO:0016021 GO:GO:0005524 EMBL:CP002687 GenomeReviews:CT486007_GR eggNOG:COG0515 GO:GO:0004872 SUPFAM:SSF56112 GO:GO:0004674 HOGENOM:HBG755340 EMBL:AL161503 InterPro:IPR002902 Pfam:PF01657 PROSITE:PS51473 HSSP:P19525 EMBL:AC012477 IPI:IPI00521065 PIR:D85065 RefSeq:NP_192429.1 UniGene:At.33905 ProteinModelPortal:Q9M0X5 SMR:Q9M0X5 PRIDE:Q9M0X5 EnsemblPlants:AT4G05200.1 GeneID:825868 KEGG:ath:AT4G05200 GeneFarm:203 TAIR:At4g05200 InParanoid:Q9M0X5 OMA:LMETEIA PhylomeDB:Q9M0X5 ArrayExpress:Q9M0X5 Genevestigator:Q9M0X5 Uniprot:Q9M0X5
Root	Isotig07357	0	15	-5.036	4.38E-05	TAIR|locus:2126540 - symbol:AT4G29990 species:3702 "Arabidopsis thaliana" [GO:0004672 "protein kinase activity" evidence=IEA;ISS] [GO:0004674 "protein serine/threonine kinase activity" evidence=IEA] [GO:0005524 "ATP binding" evidence=IEA;ISS] [GO:0006468 "protein phosphorylation" evidence=IEA;ISS] InterPro:IPR000719 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 Pfam:PF00069 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 GO:GO:0016021 GO:GO:0005524 EMBL:CP002687 GO:GO:0004872 SUPFAM:SSF56112 GO:GO:0004674 EMBL:AL161576 EMBL:AL078464 InterPro:IPR024788 Pfam:PF12819 HSSP:Q62838 ProtClustDB:CLSN2683161 IPI:IPI00537051 PIR:D85350 RefSeq:NP_194728.1 UniGene:At.5387 ProteinModelPortal:Q9SZV2 SMR:Q9SZV2 PRIDE:Q9SZV2 EnsemblPlants:AT4G29990.1 GeneID:829122 KEGG:ath:AT4G29990 TAIR:At4g29990 InParanoid:Q9SZV2 OMA:INETAIM PhylomeDB:Q9SZV2 ArrayExpress:Q9SZV2 Genevestigator:Q9SZV2 Uniprot:Q9SZV2
Root	Isotig07358	0	16	-5.129	2.34E-05	TAIR|locus:2126540 - symbol:AT4G29990 species:3702 "Arabidopsis thaliana" [GO:0004672 "protein kinase activity" evidence=IEA;ISS] [GO:0004674 "protein serine/threonine kinase activity" evidence=IEA] [GO:0005524 "ATP binding" evidence=IEA;ISS] [GO:0006468 "protein phosphorylation" evidence=IEA;ISS] InterPro:IPR000719 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 Pfam:PF00069 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 GO:GO:0016021 GO:GO:0005524 EMBL:CP002687 GO:GO:0004872 SUPFAM:SSF56112 GO:GO:0004674 EMBL:AL161576 EMBL:AL078464 InterPro:IPR024788 Pfam:PF12819 HSSP:Q62838 ProtClustDB:CLSN2683161 IPI:IPI00537051 PIR:D85350 RefSeq:NP_194728.1 UniGene:At.5387 ProteinModelPortal:Q9SZV2 SMR:Q9SZV2 PRIDE:Q9SZV2 EnsemblPlants:AT4G29990.1 GeneID:829122 KEGG:ath:AT4G29990 TAIR:At4g29990 InParanoid:Q9SZV2 OMA:INETAIM PhylomeDB:Q9SZV2 ArrayExpress:Q9SZV2 Genevestigator:Q9SZV2 Uniprot:Q9SZV2
Root	Isotig07379	24	57	-1.377	4.02E-05	TAIR|locus:2061136 - symbol:COI1 "AT2G39940" species:3702 "Arabidopsis thaliana" [GO:0006511 "ubiquitin-dependent protein catabolic process" evidence=TAS] [GO:0009861 "jasmonic acid and ethylene-dependent systemic resistance" evidence=TAS] [GO:0005515 "protein binding" evidence=IPI] [GO:0009867 "jasmonic acid mediated signaling pathway" evidence=IGI;TAS] [GO:0009625 "response to insect" evidence=IMP] [GO:0009611 "response to wounding" evidence=IMP] [GO:0009753 "response to jasmonic acid stimulus" evidence=IMP] [GO:0019005 "SCF ubiquitin ligase complex" evidence=IPI] [GO:0031348 "negative regulation of defense response" evidence=IMP] [GO:0010118 "stomatal movement" evidence=IMP] [GO:0042742 "defense response to bacterium" evidence=IMP] [GO:0050832 "defense response to fungus" evidence=IMP] [GO:0031146 "SCF-dependent proteasomal ubiquitin-dependent protein catabolic process" evidence=IMP] [GO:0009641 "shade avoidance" evidence=IMP] [GO:0009909 "regulation of flower development" evidence=IMP] [GO:0010218 "response to far red light" evidence=IMP] [GO:0004842 "ubiquitin-protein ligase activity" evidence=ISS] [GO:0006952 "defense

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						response" evidence=TAS] PROSITE:PS50181 GO:GO:0042742 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0005515 GO:GO:0031348 GO:GO:0050832 GO:GO:0010218 GO:GO:0010118 GO:GO:0019005 GO:GO:0031146 HOGENOM:HBG319412 GO:GO:0009625 GO:GO:0009909 GO:GO:0009641 GO:GO:0009867 EMBL:AF002109 EMBL:AF036340 EMBL:EF470606 EMBL:EF470607 EMBL:EF470608 EMBL:EF470609 EMBL:EF470610 EMBL:EF470611 EMBL:EF470612 EMBL:EF470613 EMBL:EF470614 EMBL:EF470615 EMBL:EF470616 EMBL:EF470617 EMBL:EF470619 EMBL:EF470620 EMBL:EF470621 EMBL:EF470622 EMBL:EF470623 EMBL:EF470624 EMBL:AY045625 EMBL:AY133556 IPI:IPI00516922 PIR:T52139 RefSeq:NP_565919.1 UniGene:At.20831 UniGene:At.71018 PDB:3OGK PDB:3OGL PDB:3OGM PDBsum:3OGK PDBsum:3OGL PDBsum:3OGM ProteinModelPortal:O04197 SMR:O04197 DIP:DIP-31324N IntAct:O04197 STRING:O04197 PRIDE:O04197 EnsemblPlants:AT2G39940.1 GeneID:818581 KEGG:ath:AT2G39940 GeneFarm:4758 TAIR:At2g39940 eggNOG:NOG262527 InParanoid:O04197 KO:K13463 OMA:ARNCRSL PhylomeDB:O04197 ProtClustDB:CLSN2688817 ArrayExpress:O04197 Genevestigator:O04197 GermOnline:AT2G39940 GO:GO:0009861 Uniprot:O04197
Root	Isotig07386	1	12	-3.714	0.000699736	TAIR|locus:2036504 - symbol:ATB2 species:3702 "Arabidopsis thaliana" [GO:0016491 "oxidoreductase activity" evidence=IEA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR020471 PRINTS:PR00069 PROSITE:PS00062 PROSITE:PS00063 PROSITE:PS00798 InterPro:IPR001395 Pfam:PF00248 EMBL:CP002684 GO:GO:0005829 GO:GO:0046686 InterPro:IPR023210 Gene3D:G3DSA:3.20.20.100 PANTHER:PTHR11732 SUPFAM:SSF51430 GO:GO:0016491 eggNOG:COG0667 EMBL:AC002292 HSSP:P38918 ProtClustDB:CLSN2681811 EMBL:AJ608277 EMBL:AF057715 EMBL:AY056440 EMBL:AY099655 EMBL:BT000251 EMBL:Z26233 IPI:IPI00523400 IPI:IPI00533262 PIR:E96632 RefSeq:NP_564761.1 UniGene:At.22690 ProteinModelPortal:Q93ZN2 SMR:Q93ZN2 STRING:Q93ZN2 ANU-2DPAGE:Q9SEX1 PRIDE:Q93ZN2 EnsemblPlants:AT1G60710.1 GeneID:842365 KEGG:ath:AT1G60710 TAIR:At1g60710 InParanoid:Q93ZN2 OMA:ELGINFL PhylomeDB:Q93ZN2 ArrayExpress:Q93ZN2 Genevestigator:Q93ZN2 Uniprot:Q93ZN2
Root	Isotig07391	5	26	-2.507	3.30E-05	TAIR|locus:2080432 - symbol:AT3G59940 "AT3G59940" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] InterPro:IPR001810 InterPro:IPR006652 Pfam:PF01344 PROSITE:PS50181 SMART:SM00256 SMART:SM00612 GO:GO:0005634 EMBL:CP002686 GenomeReviews:BA000014_GR SUPFAM:SSF81383 InterPro:IPR015916 Gene3D:G3DSA:2.130.10.80 EMBL:AL138647 UniGene:At.1165 UniGene:At.48785 HOGENOM:HBG593750 eggNOG:NOG282025 ProtClustDB:CLSN2685021 EMBL:AY074382 EMBL:AY081325 EMBL:AY091240 EMBL:AY088575 IPI:IPI00534118 PIR:T47818 RefSeq:NP_191553.1 ProteinModelPortal:Q9M1Y1 SMR:Q9M1Y1 IntAct:Q9M1Y1 STRING:Q9M1Y1 PRIDE:Q9M1Y1 EnsemblPlants:AT3G59940.1 GeneID:825164 KEGG:ath:AT3G59940 TAIR:At3g59940 InParanoid:Q9M1Y1 OMA:CFIDSER PhylomeDB:Q9M1Y1 ArrayExpress:Q9M1Y1 Genevestigator:Q9M1Y1 Uniprot:Q9M1Y1
Root	Isotig07392	5	26	-2.507	3.30E-05	TAIR|locus:2080432 - symbol:AT3G59940 "AT3G59940" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] InterPro:IPR001810 InterPro:IPR006652 Pfam:PF01344 PROSITE:PS50181 SMART:SM00256 SMART:SM00612 GO:GO:0005634 EMBL:CP002686 GenomeReviews:BA000014_GR SUPFAM:SSF81383 InterPro:IPR015916 Gene3D:G3DSA:2.130.10.80 EMBL:AL138647 UniGene:At.1165 UniGene:At.48785 HOGENOM:HBG593750 eggNOG:NOG282025 ProtClustDB:CLSN2685021 EMBL:AY074382 EMBL:AY081325 EMBL:AY091240 EMBL:AY088575 IPI:IPI00534118 PIR:T47818 RefSeq:NP_191553.1 ProteinModelPortal:Q9M1Y1 SMR:Q9M1Y1 IntAct:Q9M1Y1 STRING:Q9M1Y1 PRIDE:Q9M1Y1 EnsemblPlants:AT3G59940.1 GeneID:825164 KEGG:ath:AT3G59940 TAIR:At3g59940 InParanoid:Q9M1Y1 OMA:CFIDSER PhylomeDB:Q9M1Y1 ArrayExpress:Q9M1Y1 Genevestigator:Q9M1Y1 Uniprot:Q9M1Y1
Root	Isotig07393	804	976	-0.409	2.35E-09	No hit
Root	Isotig07394	752	909	-0.403	1.33E-08	No hit
Root	Isotig07399	18	0	5.041	1.86E-05	TAIR|locus:2029486 - symbol:AT1G78070 "AT1G78070" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0080008 "CUL4 RING ubiquitin ligase complex" evidence=ISS] InterPro:IPR017986 InterPro:IPR001680 InterPro:IPR015943 Pfam:PF00400 PROSITE:PS50082 PROSITE:PS50294 SMART:SM00320 EMBL:CP002684 InterPro:IPR019775 Gene3D:G3DSA:2.130.10.10 PROSITE:PS00678 EMBL:AF372951 EMBL:BT002231 IPI:IPI00528231 RefSeq:NP_565168.4 UniGene:At.19130 ProteinModelPortal:Q94JT6 SMR:Q94JT6 IntAct:Q94JT6

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						STRING:Q94JT6 EnsemblPlants:AT1G78070.1 GeneID:844142 KEGG:ath:AT1G78070 TAIR:At1g78070 InParanoid:Q94JT6 PhylomeDB:Q94JT6 ProtClustDB:CLSN2714470 Genevestigator:Q94JT6 Uniprot:Q94JT6
Root	Isotig07400	18	0	5.041	1.86E-05	TAIR|locus:2029486 - symbol:AT1G78070 "AT1G78070" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0080008 "CUL4 RING ubiquitin ligase complex" evidence=ISS] InterPro:IPR017986 InterPro:IPR001680 InterPro:IPR015943 Pfam:PF00400 PROSITE:PS50082 PROSITE:PS50294 SMART:SM00320 EMBL:CP002684 InterPro:IPR019775 Gene3D:G3DSA:2.130.10.10 PROSITE:PS00678 EMBL:AF372951 EMBL:BT002231 IPI:IPI00528231 RefSeq:NP_565168.4 UniGene:At.19130 ProteinModelPortal:Q94JT6 SMR:Q94JT6 IntAct:Q94JT6 STRING:Q94JT6 EnsemblPlants:AT1G78070.1 GeneID:844142 KEGG:ath:AT1G78070 TAIR:At1g78070 InParanoid:Q94JT6 PhylomeDB:Q94JT6 ProtClustDB:CLSN2714470 Genevestigator:Q94JT6 Uniprot:Q94JT6
Root	Isotig07423	16	0	4.871	5.89E-05	TAIR|locus:2176501 - symbol:AT5G43400 "AT5G43400" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002688 GenomeReviews:BA000015_GR EMBL:AB025638 InterPro:IPR024553 Pfam:PF11443 eggNOG:NOG75724 HOGENOM:HBG589557 InterPro:IPR011205 PIRSF:PIRSF015417 EMBL:AY048243 EMBL:BT002275 IPI:IPI00546502 RefSeq:NP_199153.1 UniGene:At.7153 ProteinModelPortal:Q94AE4 IntAct:Q94AE4 PRIDE:Q94AE4 EnsemblPlants:AT5G43400.1 GeneID:834358 KEGG:ath:AT5G43400 TAIR:At5g43400 InParanoid:Q94AE4 OMA:EDRILEN PhylomeDB:Q94AE4 ProtClustDB:CLSN2686815 Genevestigator:Q94AE4 Uniprot:Q94AE4
Root	Isotig07427	2	24	-3.714	1.64E-06	TAIR|locus:2170773 - symbol:DXR "AT5G62790" species:3702 "Arabidopsis thaliana" [GO:0008299 "isoprenoid biosynthetic process" evidence=TAS] [GO:0009507 "chloroplast" evidence=IDA] [GO:0019288 "isopentenyl diphosphate biosynthetic process, mevalonate-independent pathway" evidence=IDA;TAS] [GO:0030604 "1-deoxy-D-xylulose-5-phosphate reductoisomerase activity" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0009570 "chloroplast stroma" evidence=IDA] InterPro:IPR003821 InterPro:IPR013512 InterPro:IPR013644 InterPro:IPR016040 Pfam:PF02670 Pfam:PF08436 PIRSF:PIRSF006205 GO:GO:0009570 GO:GO:0046686 EMBL:CP002688 GenomeReviews:BA000015_GR Gene3D:G3DSA:3.40.50.720 GO:GO:0046872 GO:GO:0070402 EMBL:AB009053 eggNOG:COG0743 HOGENOM:HBG430762 KO:K00099 GO:GO:0030604 TIGRFAMs:TIGR00243 OMA:IHSMVEY EMBL:AF148852 EMBL:AY045634 EMBL:AY050802 EMBL:AY054682 EMBL:AY081453 EMBL:AY091405 EMBL:AY098952 EMBL:AY084775 EMBL:AJ242588 IPI:IPI00519417 PIR:T52570 RefSeq:NP_201085.1 UniGene:At.23021 ProteinModelPortal:Q9XFS9 SMR:Q9XFS9 STRING:Q9XFS9 PRIDE:Q9XFS9 EnsemblPlants:AT5G62790.1 GeneID:836400 KEGG:ath:AT5G62790 TAIR:At5g62790 InParanoid:Q9XFS9 PhylomeDB:Q9XFS9 ProtClustDB:PLN02696 BioCyc:ARA:AT5G62790-MONOMER BioCyc:MetaCyc:AT5G62790-MONOMER BRENDA:1.1.1.267 ArrayExpress:Q9XFS9 Genevestigator:Q9XFS9 GermOnline:AT5G62790 GO:GO:0019288 Uniprot:Q9XFS9
Root	Isotig07428	2	24	-3.714	1.64E-06	TAIR|locus:2170773 - symbol:DXR "AT5G62790" species:3702 "Arabidopsis thaliana" [GO:0008299 "isoprenoid biosynthetic process" evidence=TAS] [GO:0009507 "chloroplast" evidence=IDA] [GO:0019288 "isopentenyl diphosphate biosynthetic process, mevalonate-independent pathway" evidence=IDA;TAS] [GO:0030604 "1-deoxy-D-xylulose-5-phosphate reductoisomerase activity" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0009570 "chloroplast stroma" evidence=IDA] InterPro:IPR003821 InterPro:IPR013512 InterPro:IPR013644 InterPro:IPR016040 Pfam:PF02670 Pfam:PF08436 PIRSF:PIRSF006205 GO:GO:0009570 GO:GO:0046686 EMBL:CP002688 GenomeReviews:BA000015_GR Gene3D:G3DSA:3.40.50.720 GO:GO:0046872 GO:GO:0070402 EMBL:AB009053 eggNOG:COG0743 HOGENOM:HBG430762 KO:K00099 GO:GO:0030604 TIGRFAMs:TIGR00243 OMA:IHSMVEY EMBL:AF148852 EMBL:AY045634 EMBL:AY050802 EMBL:AY054682 EMBL:AY081453 EMBL:AY091405 EMBL:AY098952 EMBL:AY084775 EMBL:AJ242588 IPI:IPI00519417 PIR:T52570 RefSeq:NP_201085.1 UniGene:At.23021 ProteinModelPortal:Q9XFS9 SMR:Q9XFS9 STRING:Q9XFS9 PRIDE:Q9XFS9 EnsemblPlants:AT5G62790.1 GeneID:836400 KEGG:ath:AT5G62790 TAIR:At5g62790 InParanoid:Q9XFS9 PhylomeDB:Q9XFS9 ProtClustDB:PLN02696 BioCyc:ARA:AT5G62790-MONOMER BioCyc:MetaCyc:AT5G62790-MONOMER BRENDA:1.1.1.267 ArrayExpress:Q9XFS9 Genevestigator:Q9XFS9 GermOnline:AT5G62790 GO:GO:0019288 Uniprot:Q9XFS9
Root	Isotig07431	4	41	-3.487	9.45E-10	TAIR|locus:505006632 - symbol:TUB8 "AT5G23860" species:3702 "Arabidopsis thaliana" [GO:0005200 "structural constituent of cytoskeleton" evidence=ISS] [GO:0007017 "microtubule-based process" evidence=ISS] [GO:0045298 "tubulin complex" evidence=ISS] [GO:0016020 "membrane" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0005515 "protein binding" evidence=IPI] [GO:0005794 "Golgi apparatus" evidence=IDA]

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						InterPro:IPR000217 InterPro:IPR002453 InterPro:IPR003008 InterPro:IPR008280 InterPro:IPR017975 InterPro:IPR018316 Pfam:PF00091 Pfam:PF03953 PRINTS:PR01161 PRINTS:PR01163 PROSITE:PS00227 SMART:SM00864 SMART:SM00865 GO:GO:0005525 GO:GO:0005737 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005515 GO:GO:0016020 GO:GO:0005198 GO:GO:0003924 EMBL:AB005244 GO:GO:0009651 GO:GO:0005874 GO:GO:0051258 Gene3D:G3DSA:3.40.50.1440 SUPFAM:SSF52490 GO:GO:0007018 Gene3D:G3DSA:3.30.1330.20 SUPFAM:SSF55307 eggNOG:COG5023 HOGENOM:HBG750007 InterPro:IPR023123 Gene3D:G3DSA:1.10.287.600 InterPro:IPR013838 KO:K07375 ProtClustDB:PLN00220 PROSITE:PS00228 OMA:RYQGEND EMBL:M84705 EMBL:AY054693 EMBL:AY081473 IPI:IPI00539093 PIR:JQ1592 RefSeq:NP_001190373.1 RefSeq:NP_568437.1 UniGene:At.330 UniGene:At.67084 ProteinModelPortal:P29516 SMR:P29516 IntAct:P29516 STRING:P29516 PRIDE:P29516 EnsemblPlants:AT5G23860.1 EnsemblPlants:AT5G23860.2 GeneID:832451 KEGG:ath:AT5G23860 TAIR:At5g23860 InParanoid:P29516 PhylomeDB:P29516 Genevestigator:P29516 GermOnline:AT5G23860 Uniprot:P29516
Root	Isotig07432	4	42	-3.521	5.08E-10	TAIR|locus:505006632 - symbol:TUB8 "AT5G23860" species:3702 "Arabidopsis thaliana" [GO:0005200 "structural constituent of cytoskeleton" evidence=ISS] [GO:0007017 "microtubule-based process" evidence=ISS] [GO:0045298 "tubulin complex" evidence=ISS] [GO:0016020 "membrane" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0005515 "protein binding" evidence=IPI] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR000217 InterPro:IPR002453 InterPro:IPR003008 InterPro:IPR008280 InterPro:IPR017975 InterPro:IPR018316 Pfam:PF00091 Pfam:PF03953 PRINTS:PR01161 PRINTS:PR01163 PROSITE:PS00227 SMART:SM00864 SMART:SM00865 GO:GO:0005525 GO:GO:0005737 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005515 GO:GO:0016020 GO:GO:0005198 GO:GO:0003924 EMBL:AB005244 GO:GO:0009651 GO:GO:0005874 GO:GO:0051258 Gene3D:G3DSA:3.40.50.1440 SUPFAM:SSF52490 GO:GO:0007018 Gene3D:G3DSA:3.30.1330.20 SUPFAM:SSF55307 eggNOG:COG5023 HOGENOM:HBG750007 InterPro:IPR023123 Gene3D:G3DSA:1.10.287.600 InterPro:IPR013838 KO:K07375 ProtClustDB:PLN00220 PROSITE:PS00228 OMA:RYQGEND EMBL:M84705 EMBL:AY054693 EMBL:AY081473 IPI:IPI00539093 PIR:JQ1592 RefSeq:NP_001190373.1 RefSeq:NP_568437.1 UniGene:At.330 UniGene:At.67084 ProteinModelPortal:P29516 SMR:P29516 IntAct:P29516 STRING:P29516 PRIDE:P29516 EnsemblPlants:AT5G23860.1 EnsemblPlants:AT5G23860.2 GeneID:832451 KEGG:ath:AT5G23860 TAIR:At5g23860 InParanoid:P29516 PhylomeDB:P29516 Genevestigator:P29516 GermOnline:AT5G23860 Uniprot:P29516
Root	Isotig07439	0	27	-5.884	3.19E-08	TAIR|locus:2173219 - symbol:PAO1 "polyamine oxidase 1" species:3702 "Arabidopsis thaliana" [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0046592 "polyamine oxidase activity" evidence=IDA] [GO:0050660 "flavin adenine dinucleotide binding" evidence=IDA] InterPro:IPR001613 InterPro:IPR002937 Pfam:PF01593 PRINTS:PR00757 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0050660 EMBL:AB006704 eggNOG:COG1231 GO:GO:0046592 EMBL:AK118627 EMBL:BT026370 IPI:IPI00526970 RefSeq:NP_196874.1 UniGene:At.49017 UniGene:At.6477 HSSP:O64411 ProteinModelPortal:Q9FNA2 SMR:Q9FNA2 STRING:Q9FNA2 PRIDE:Q9FNA2 EnsemblPlants:AT5G13700.1 GeneID:831215 KEGG:ath:AT5G13700 TAIR:At5g13700 HOGENOM:HBG325057 InParanoid:Q9FNA2 KO:K13366 OMA:EPISTYV PhylomeDB:Q9FNA2 ProtClustDB:PLN02676 BioCyc:ARA:AT5G13700-MONOMER BioCyc:MetaCyc:AT5G13700-MONOMER Genevestigator:Q9FNA2 Uniprot:Q9FNA2
Root	Isotig07440	0	24	-5.714	1.84E-07	TAIR|locus:2173219 - symbol:PAO1 "polyamine oxidase 1" species:3702 "Arabidopsis thaliana" [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0046592 "polyamine oxidase activity" evidence=IDA] [GO:0050660 "flavin adenine dinucleotide binding" evidence=IDA] InterPro:IPR001613 InterPro:IPR002937 Pfam:PF01593 PRINTS:PR00757 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0050660 EMBL:AB006704 eggNOG:COG1231 GO:GO:0046592 EMBL:AK118627 EMBL:BT026370 IPI:IPI00526970 RefSeq:NP_196874.1 UniGene:At.49017 UniGene:At.6477 HSSP:O64411 ProteinModelPortal:Q9FNA2 SMR:Q9FNA2 STRING:Q9FNA2 PRIDE:Q9FNA2 EnsemblPlants:AT5G13700.1 GeneID:831215 KEGG:ath:AT5G13700 TAIR:At5g13700 HOGENOM:HBG325057 InParanoid:Q9FNA2 KO:K13366 OMA:EPISTYV PhylomeDB:Q9FNA2 ProtClustDB:PLN02676 BioCyc:ARA:AT5G13700-MONOMER BioCyc:MetaCyc:AT5G13700-MONOMER Genevestigator:Q9FNA2 Uniprot:Q9FNA2
Root	Isotig07441	30	0	5.778	2.46E-08	TAIR|locus:2179867 - symbol:SAG29 "senescence-associated gene 29" species:3702 "Arabidopsis thaliana" [GO:0016020 "membrane" evidence=IEA;ISS] [GO:0016021 "integral to membrane" evidence=IEA] [GO:0010150

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						"leaf senescence" evidence=IEP;IMP] [GO:0071446 "cellular response to salicylic acid stimulus" evidence=IEP] [GO:0005887 "integral to plasma membrane" evidence=IDA] [GO:0071215 "cellular response to abscisic acid stimulus" evidence=IEP] [GO:0071470 "cellular response to osmotic stress" evidence=IMP] [GO:0051119 "sugar transmembrane transporter activity" evidence=ISS] InterPro:IPR004316 Pfam:PF03083 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005887 GO:GO:0010150 EMBL:AL391711 GO:GO:0071470 GO:GO:0071215 GO:GO:0071446 GO:GO:0051119 PANTHER:PTHR10791 KO:K15382 eggNOG:NOG308353 EMBL:AY045949 EMBL:AY113934 EMBL:AY087836 EMBL:AF118824 IPI:IPI00530310 RefSeq:NP_196821.1 UniGene:At.46857 TCDB:9.A.58.1.3 EnsemblPlants:AT5G13170.1 GeneID:831156 KEGG:ath:AT5G13170 TAIR:At5g13170 InParanoid:Q9FY94 OMA:WFAYGLF PhylomeDB:Q9FY94 ProtClustDB:CLSN2916510 ArrayExpress:Q9FY94 Genevestigator:Q9FY94 Uniprot:Q9FY94
Root	Isotig07442	30	0	5.778	2.46E-08	TAIR|locus:2179867 - symbol:SAG29 "senescence-associated gene 29" species:3702 "Arabidopsis thaliana" [GO:0016020 "membrane" evidence=IEA;ISS] [GO:0016021 "integral to membrane" evidence=IEA] [GO:0010150 "leaf senescence" evidence=IEP;IMP] [GO:0071446 "cellular response to salicylic acid stimulus" evidence=IEP] [GO:0005887 "integral to plasma membrane" evidence=IDA] [GO:0071215 "cellular response to abscisic acid stimulus" evidence=IEP] [GO:0071470 "cellular response to osmotic stress" evidence=IMP] [GO:0051119 "sugar transmembrane transporter activity" evidence=ISS] InterPro:IPR004316 Pfam:PF03083 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005887 GO:GO:0010150 EMBL:AL391711 GO:GO:0071470 GO:GO:0071215 GO:GO:0071446 GO:GO:0051119 PANTHER:PTHR10791 KO:K15382 eggNOG:NOG308353 EMBL:AY045949 EMBL:AY113934 EMBL:AY087836 EMBL:AF118824 IPI:IPI00530310 RefSeq:NP_196821.1 UniGene:At.46857 TCDB:9.A.58.1.3 EnsemblPlants:AT5G13170.1 GeneID:831156 KEGG:ath:AT5G13170 TAIR:At5g13170 InParanoid:Q9FY94 OMA:WFAYGLF PhylomeDB:Q9FY94 ProtClustDB:CLSN2916510 ArrayExpress:Q9FY94 Genevestigator:Q9FY94 Uniprot:Q9FY94
Root	Isotig07449	33	7	2.108	5.57E-05	TAIR|locus:2026242 - symbol:BETA-VPE "AT1G62710" species:3702 "Arabidopsis thaliana" [GO:0004197 "cysteine-type endopeptidase activity" evidence=ISS] [GO:0006508 "proteolysis" evidence=ISS] [GO:0006624 "vacuolar protein processing" evidence=ISS] InterPro:IPR001096 Pfam:PF01650 PIRSF:PIRSF019663 PRINTS:PR00776 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005773 GO:GO:0004197 GO:GO:0006508 EMBL:AC007190 eggNOG:COG5206 PANTHER:PTHR12000 KO:K01369 HOGENOM:HBG318720 ProtClustDB:CLSN2682340 EMBL:D61394 EMBL:AY059156 EMBL:AF367254 IPI:IPI00519485 PIR:C96652 PIR:S60050 RefSeq:NP_176458.1 UniGene:At.16374 ProteinModelPortal:Q39044 STRING:Q39044 MEROPS:C13.001 PRIDE:Q39044 EnsemblPlants:AT1G62710.1 GeneID:842569 KEGG:ath:AT1G62710 TAIR:At1g62710 InParanoid:Q39044 OMA:PPSEYIT PhylomeDB:Q39044 ArrayExpress:Q39044 Genevestigator:Q39044 GermOnline:AT1G62710 Uniprot:Q39044
Root	Isotig07450	35	7	2.193	2.09E-05	TAIR|locus:2123782 - symbol:GAMMA-VPE "AT4G32940" species:3702 "Arabidopsis thaliana" [GO:0004197 "cysteine-type endopeptidase activity" evidence=ISS;IDA] [GO:0006508 "proteolysis" evidence=ISS] [GO:0000323 "lytic vacuole" evidence=IDA] [GO:0006624 "vacuolar protein processing" evidence=ISS] InterPro:IPR001096 Pfam:PF01650 PIRSF:PIRSF019663 PRINTS:PR00776 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0004197 GO:GO:0006508 EMBL:AL031804 EMBL:AL161582 eggNOG:COG5206 PANTHER:PTHR12000 KO:K01369 HOGENOM:HBG318720 GO:GO:0000323 ProtClustDB:CLSN2682340 EMBL:D61395 EMBL:AF370160 EMBL:AF424619 EMBL:AY059104 EMBL:AY133531 IPI:IPI00537536 PIR:T05302 RefSeq:NP_195020.1 UniGene:At.21567 UniGene:At.48929 UniGene:At.75206 ProteinModelPortal:Q39119 STRING:Q39119 MEROPS:C13.006 PRIDE:Q39119 EnsemblPlants:AT4G32940.1 GeneID:829431 KEGG:ath:AT4G32940 TAIR:At4g32940 InParanoid:Q39119 OMA:ICHAYQL PhylomeDB:Q39119 Genevestigator:Q39119 Uniprot:Q39119
Root	Isotig07453	0	17	-5.216	1.26E-05	TAIR|locus:2064945 - symbol:AT2G38970 "AT2G38970" species:3702 "Arabidopsis thaliana" [GO:0004842 "ubiquitin-protein ligase activity" evidence=ISS] [GO:0008270 "zinc ion binding" evidence=IEA;ISS] InterPro:IPR001841 InterPro:IPR002035 PROSITE:PS50089 PROSITE:PS50234 SMART:SM00184 SMART:SM00327 GenomeReviews:CT485783_GR GO:GO:0008270 InterPro:IPR013083 Gene3D:G3DSA:3.30.40.10 eggNOG:COG2304 EMBL:AY075691 IPI:IPI00529574 ProteinModelPortal:Q8S9I2 SMR:Q8S9I2 PRIDE:Q8S9I2 TAIR:At2g38970 HOGENOM:HBG317190 InParanoid:Q8S9I2 PhylomeDB:Q8S9I2 Genevestigator:Q8S9I2 Uniprot:Q8S9I2
Root	Isotig07454	0	14	-4.936	8.24E-05	TAIR|locus:2175796 - symbol:AT5G60710 "AT5G60710" species:3702 "Arabidopsis thaliana" [GO:0004842 "ubiquitin-protein ligase activity" evidence=ISS] [GO:0008270 "zinc ion binding" evidence=IEA;ISS] [GO:0005886

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						"plasma membrane" evidence=IDA] InterPro:IPR001841 InterPro:IPR002035 Pfam:PF00092 PROSITE:PS50089 PROSITE:PS50234 SMART:SM00184 SMART:SM00327 GO:GO:0005886 EMBL:CP002688 GO:GO:0008270 EMBL:AB005246 InterPro:IPR013083 Gene3D:G3DSA:3.30.40.10 IPI:IPI00533797 RefSeq:NP_200879.1 UniGene:At.21965 ProteinModelPortal:Q9FF49 SMR:Q9FF49 PRIDE:Q9FF49 EnsemblPlants:AT5G60710.1 GeneID:836192 KEGG:ath:AT5G60710 TAIR:At5g60710 InParanoid:Q9FF49 OMA:QGHAIFT PhylomeDB:Q9FF49 Genevestigator:Q9FF49 Uniprot:Q9FF49
Root	Isotig07475	1	26	-4.829	8.91E-08	UNIPROTKB|Q9ST02 - symbol:naat-A "Nicotianamine aminotransferase A" species:4513 "Hordeum vulgare" [GO:0033855 "nicotianamine aminotransferase activity" evidence=IDA] InterPro:IPR001176 InterPro:IPR004839 InterPro:IPR005958 InterPro:IPR015421 InterPro:IPR015422 InterPro:IPR021178 Pfam:PF00155 PIRSF:PIRSF000517 PRINTS:PR00753 PROSITE:PS00105 GO:GO:0016847 GO:GO:0030170 InterPro:IPR015424 Gene3D:G3DSA:3.40.640.10 Gene3D:G3DSA:3.90.1150.10 SUPFAM:SSF53383 TIGRFAMs:TIGR01265 EMBL:AB024006 EMBL:D88273 ProteinModelPortal:Q9ST02 Gramene:Q9ST02 BRENDA:2.6.1.80 Genevestigator:Q9ST02 GO:GO:0033855 Uniprot:Q9ST02
Root	Isotig07476	1	26	-4.829	8.91E-08	UNIPROTKB|Q9ST02 - symbol:naat-A "Nicotianamine aminotransferase A" species:4513 "Hordeum vulgare" [GO:0033855 "nicotianamine aminotransferase activity" evidence=IDA] InterPro:IPR001176 InterPro:IPR004839 InterPro:IPR005958 InterPro:IPR015421 InterPro:IPR015422 InterPro:IPR021178 Pfam:PF00155 PIRSF:PIRSF000517 PRINTS:PR00753 PROSITE:PS00105 GO:GO:0016847 GO:GO:0030170 InterPro:IPR015424 Gene3D:G3DSA:3.40.640.10 Gene3D:G3DSA:3.90.1150.10 SUPFAM:SSF53383 TIGRFAMs:TIGR01265 EMBL:AB024006 EMBL:D88273 ProteinModelPortal:Q9ST02 Gramene:Q9ST02 BRENDA:2.6.1.80 Genevestigator:Q9ST02 GO:GO:0033855 Uniprot:Q9ST02
Root	Isotig07509	3	43	-3.970	5.33E-11	TAIR|locus:2178067 - symbol:AATP1 "AT5G40010" species:3702 "Arabidopsis thaliana" [GO:0005524 "ATP binding" evidence=ISS] [GO:0016887 "ATPase activity" evidence=ISS;IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0010154 "fruit development" evidence=IMP] [GO:0010431 "seed maturation" evidence=IMP] InterPro:IPR003593 InterPro:IPR003959 InterPro:IPR003960 Pfam:PF00004 PROSITE:PS00674 SMART:SM00382 GO:GO:0005739 GO:GO:0005524 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0016887 eggNOG:COG0465 GO:GO:0010431 EMBL:AB010077 HOGENOM:HBG744315 IPI:IPI00538441 RefSeq:NP_198817.1 UniGene:At.65609 ProteinModelPortal:Q9FLD5 SMR:Q9FLD5 PRIDE:Q9FLD5 EnsemblPlants:AT5G40010.1 GeneID:833998 KEGG:ath:AT5G40010 TAIR:At5g40010 InParanoid:Q9FLD5 OMA:LRLESHH PhylomeDB:Q9FLD5 ProtClustDB:CLSN2685235 Genevestigator:Q9FLD5 Uniprot:Q9FLD5
Root	Isotig07510	3	32	-3.544	5.33E-08	TAIR|locus:2178067 - symbol:AATP1 "AT5G40010" species:3702 "Arabidopsis thaliana" [GO:0005524 "ATP binding" evidence=ISS] [GO:0016887 "ATPase activity" evidence=ISS;IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0010154 "fruit development" evidence=IMP] [GO:0010431 "seed maturation" evidence=IMP] InterPro:IPR003593 InterPro:IPR003959 InterPro:IPR003960 Pfam:PF00004 PROSITE:PS00674 SMART:SM00382 GO:GO:0005739 GO:GO:0005524 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0016887 eggNOG:COG0465 GO:GO:0010431 EMBL:AB010077 HOGENOM:HBG744315 IPI:IPI00538441 RefSeq:NP_198817.1 UniGene:At.65609 ProteinModelPortal:Q9FLD5 SMR:Q9FLD5 PRIDE:Q9FLD5 EnsemblPlants:AT5G40010.1 GeneID:833998 KEGG:ath:AT5G40010 TAIR:At5g40010 InParanoid:Q9FLD5 OMA:LRLESHH PhylomeDB:Q9FLD5 ProtClustDB:CLSN2685235 Genevestigator:Q9FLD5 Uniprot:Q9FLD5
Root	Isotig07514	24	53	-1.272	0.000195269	TAIR|locus:2044851 - symbol:LOS2 "AT2G36530" species:3702 "Arabidopsis thaliana" [GO:0004634 "phosphopyruvate hydratase activity" evidence=ISS;IDA] [GO:0003677 "DNA binding" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0009409 "response to cold" evidence=IMP] [GO:0009416 "response to light stimulus" evidence=IMP] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0005740 "mitochondrial envelope" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000941 InterPro:IPR020809 InterPro:IPR020810 InterPro:IPR020811 Pfam:PF00113 Pfam:PF03952 PIRSF:PIRSF001400 PRINTS:PR00148 PROSITE:PS00164 PANTHER:PTHR11902 GO:GO:0005886 GO:GO:0009506 GO:GO:0009737 GO:GO:0048046 GO:GO:0005634 GO:GO:0046686 GO:GO:0009507 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0006355 GO:GO:0003677 GO:GO:0000287 GO:GO:0006351 GO:GO:0005507 GO:GO:0009409 GO:GO:0009651 EMBL:AC006919 GO:GO:0005740

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0009416 GO:GO:0006096 eggNOG:COG0148 HOGENOM:HBG726599 KO:K01689 GO:GO:0000015 GO:GO:0004634 TIGRFAMs:TIGR01060 ProtClustDB:PLN00191 EMBL:X58107 EMBL:AF424603 EMBL:AY054253 EMBL:AY072095 EMBL:AY092986 EMBL:AY150418 IPI:IPI00526310 PIR:JQ1187 RefSeq:NP_181192.1 UniGene:At.24124 UniGene:At.25354 UniGene:At.74012 ProteinModelPortal:P25696 SMR:P25696 STRING:P25696 SWISS-2DPAGE:P25696 PRIDE:P25696 ProMEX:P25696 EnsemblPlants:AT2G36530.1 GeneID:818226 KEGG:ath:AT2G36530 TAIR:At2g36530 InParanoid:P25696 OMA:GELYKNF PhylomeDB:P25696 BioCyc:ARA:AT2G36530-MONOMER BioCyc:MetaCyc:AT2G36530-MONOMER Genevestigator:P25696 GermOnline:AT2G36530 Uniprot:P25696
Root	Isotig07533	2	16	-3.129	0.000262867	TAIR|locus:2055165 - symbol:AT2G14510 species:3702 "Arabidopsis thaliana" [GO:0006468 "protein phosphorylation" evidence=IEA] [GO:0016301 "kinase activity" evidence=ISS] InterPro:IPR000719 InterPro:IPR001245 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 Pfam:PF07714 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 GO:GO:0016021 GO:GO:0005886 GO:GO:0005524 EMBL:CP002685 GenomeReviews:CT485783_GR eggNOG:COG0515 GO:GO:0004872 SUPFAM:SSF56112 GO:GO:0004674 HOGENOM:HBG755340 InterPro:IPR024788 Pfam:PF12819 EMBL:AC006067 ProtClustDB:CLSN2683452 EMBL:FJ708693 IPI:IPI00521096 PIR:A84518 RefSeq:NP_179057.1 UniGene:At.52739 ProteinModelPortal:Q9ZQR3 SMR:Q9ZQR3 PRIDE:Q9ZQR3 EnsemblPlants:AT2G14510.1 GeneID:815938 KEGG:ath:AT2G14510 GeneFarm:454 TAIR:At2g14510 InParanoid:Q9ZQR3 PhylomeDB:Q9ZQR3 ArrayExpress:Q9ZQR3 Genevestigator:Q9ZQR3 Uniprot:Q9ZQR3
Root	Isotig07534	1	15	-4.036	9.83E-05	TAIR|locus:2017537 - symbol:AT1G51810 species:3702 "Arabidopsis thaliana" [GO:0004672 "protein kinase activity" evidence=IEA] [GO:0004674 "protein serine/threonine kinase activity" evidence=IEA] [GO:0005524 "ATP binding" evidence=IEA] [GO:0006468 "protein phosphorylation" evidence=IEA] [GO:0016301 "kinase activity" evidence=ISS] InterPro:IPR000719 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 Pfam:PF00069 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005524 EMBL:AC025294 eggNOG:COG0515 GO:GO:0004872 SUPFAM:SSF56112 GO:GO:0004674 HSSP:P36897 InterPro:IPR024788 Pfam:PF12819 EMBL:AC015448 EMBL:DQ459169 EMBL:FJ708651 IPI:IPI00546436 IPI:IPI00953809 PIR:D96557 RefSeq:NP_175593.2 UniGene:At.52140 ProteinModelPortal:Q9FZB8 SMR:Q9FZB8 PRIDE:Q9FZB8 GeneID:841608 KEGG:ath:AT1G51810 GeneFarm:337 TAIR:At1g51810 InParanoid:Q9C8I8 PhylomeDB:Q9FZB8 Uniprot:Q9FZB8
Root	Isotig07543	66	9	2.745	3.00E-11	TAIR|locus:2025237 - symbol:ADH1 "AT1G77120" species:3702 "Arabidopsis thaliana" [GO:0045333 "cellular respiration" evidence=TAS] [GO:0006970 "response to osmotic stress" evidence=IGI] [GO:0001666 "response to hypoxia" evidence=IEP] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] [GO:0004022 "alcohol dehydrogenase (NAD) activity" evidence=ISS;IMP] InterPro:IPR002085 InterPro:IPR002328 InterPro:IPR013149 InterPro:IPR013154 InterPro:IPR016040 Pfam:PF00107 Pfam:PF08240 PROSITE:PS00059 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0005886 GO:GO:0046686 GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 GO:GO:0008270 GO:GO:0001666 GO:GO:0009651 InterPro:IPR011032 PANTHER:PTHR11695 SUPFAM:SSF50129 eggNOG:COG1062 GO:GO:0004022 EMBL:M12196 EMBL:X77943 EMBL:D84240 EMBL:D84241 EMBL:D84242 EMBL:D84243 EMBL:D84244 EMBL:D84245 EMBL:D84246 EMBL:D84247 EMBL:D84248 EMBL:D84249 EMBL:D63460 EMBL:D63461 EMBL:D63462 EMBL:D63463 EMBL:D63464 EMBL:AF110456 EMBL:AB048394 EMBL:AB048395 EMBL:AY536888 EMBL:AC002291 EMBL:AY045612 EMBL:AY090330 EMBL:AY088010 IPI:IPI00539119 PIR:A23815 RefSeq:NP_177837.1 UniGene:At.22653 UniGene:At.64099 ProteinModelPortal:P06525 SMR:P06525 STRING:P06525 PRIDE:P06525 EnsemblPlants:AT1G77120.1 GeneID:844047 KEGG:ath:AT1G77120 TAIR:At1g77120 InParanoid:P06525 KO:K00001 OMA:ECTGSVQ PhylomeDB:P06525 ProtClustDB:CLSN2717044 ArrayExpress:P06525 Genevestigator:P06525 Uniprot:P06525
Root	Isotig07544	63	9	2.678	1.46E-10	TAIR|locus:2025237 - symbol:ADH1 "AT1G77120" species:3702 "Arabidopsis thaliana" [GO:0045333 "cellular respiration" evidence=TAS] [GO:0006970 "response to osmotic stress" evidence=IGI] [GO:0001666 "response to hypoxia" evidence=IEP] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] [GO:0004022 "alcohol dehydrogenase (NAD) activity" evidence=ISS;IMP] InterPro:IPR002085 InterPro:IPR002328 InterPro:IPR013149 InterPro:IPR013154

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						InterPro:IPR016040 Pfam:PF00107 Pfam:PF08240 PROSITE:PS00059 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0005886 GO:GO:0046686 GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 GO:GO:0008270 GO:GO:0001666 GO:GO:0009651 InterPro:IPR011032 PANTHER:PTHR11695 SUPFAM:SSF50129 eggNOG:COG1062 GO:GO:0004022 EMBL:M12196 EMBL:X77943 EMBL:D84240 EMBL:D84241 EMBL:D84242 EMBL:D84243 EMBL:D84244 EMBL:D84245 EMBL:D84246 EMBL:D84247 EMBL:D84248 EMBL:D84249 EMBL:D63460 EMBL:D63461 EMBL:D63462 EMBL:D63463 EMBL:D63464 EMBL:AF110456 EMBL:AB048394 EMBL:AB048395 EMBL:AY536888 EMBL:AC002291 EMBL:AY045612 EMBL:AY090330 EMBL:AY088010 IPI:IPI00539119 PIR:A23815 RefSeq:NP_177837.1 UniGene:At.22653 UniGene:At.64099 ProteinModelPortal:P06525 SMR:P06525 STRING:P06525 PRIDE:P06525 EnsemblPlants:AT1G77120.1 GeneID:844047 KEGG:ath:AT1G77120 TAIR:At1g77120 InParanoid:P06525 KO:K00001 OMA:ECTGSVQ PhylomeDB:P06525 ProtClustDB:CLSN2717044 ArrayExpress:P06525 Genevestigator:P06525 Uniprot:P06525
Root	Isotig07554	10	29	-1.665	0.000753212	TAIR|locus:2039037 - symbol:AT2G20420 "AT2G20420" species:3702 "Arabidopsis thaliana" [GO:0004776 "succinate-CoA ligase (GDP-forming) activity" evidence=ISS] [GO:0008152 "metabolic process" evidence=ISS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005524 "ATP binding" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR005809 InterPro:IPR005811 InterPro:IPR011761 InterPro:IPR013815 InterPro:IPR013816 Pfam:PF00549 PIRSF:PIRSF001554 PROSITE:PS50975 Prosite:PS01217 GO:GO:0005739 GO:GO:0005524 GO:GO:0046686 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0005507 Gene3D:G3DSA:3.30.1490.20 Gene3D:G3DSA:3.30.470.20 GO:GO:0006099 InterPro:IPR017866 InterPro:IPR016102 Gene3D:G3DSA:3.40.50.261 eggNOG:COG0045 InterPro:IPR013650 Pfam:PF08442 SUPFAM:SSF52210 GO:GO:0004775 EMBL:AC006569 KO:K01900 PANTHER:PTHR11815 TIGRFAMs:TIGR01016 HOGENOM:HBG315432 EMBL:AJ001808 EMBL:AY099707 EMBL:AY128889 IPI:IPI00532524 PIR:T51809 RefSeq:NP_179632.1 UniGene:At.21151 ProteinModelPortal:O82662 SMR:O82662 STRING:O82662 PRIDE:O82662 EnsemblPlants:AT2G20420.1 GeneID:816561 KEGG:ath:AT2G20420 GeneFarm:2004 TAIR:At2g20420 InParanoid:O82662 OMA:MIIKVPI PhylomeDB:O82662 ProtClustDB:PLN00124 ArrayExpress:O82662 Genevestigator:O82662 GermOnline:AT2G20420 Uniprot:O82662
Root	Isotig07565	78	133	-0.899	8.63E-06	TAIR|locus:2141385 - symbol:SAM-2 "AT4G01850" species:3702 "Arabidopsis thaliana" [GO:0004478 "methionine adenosyltransferase activity" evidence=ISS] [GO:0006556 "S-adenosylmethionine biosynthetic process" evidence=ISS] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0071281 "cellular response to iron ion" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA;RCA] [GO:0070062 "extracellular vesicular exosome" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR002133 InterPro:IPR022628 InterPro:IPR022629 InterPro:IPR022630 InterPro:IPR022631 InterPro:IPR022636 Pfam:PF00438 Pfam:PF02772 Pfam:PF02773 PIRSF:PIRSF000497 PROSITE:PS00376 PROSITE:PS00377 GO:GO:0005829 GO:GO:0009506 GO:GO:0005524 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005618 GO:GO:0071281 GO:GO:0005730 GO:GO:0005507 EMBL:AC007138 EMBL:AL161493 GO:GO:0070062 GO:GO:0006730 KO:K00789 GO:GO:0006556 UniGene:At.24731 eggNOG:COG0192 HOGENOM:HBG443662 ProtClustDB:PLN02243 GO:GO:0004478 PANTHER:PTHR11964 SUPFAM:SSF55973 TIGRFAMs:TIGR01034 EMBL:M33217 EMBL:AY072327 EMBL:AY094454 EMBL:BT000575 EMBL:Z33778 EMBL:Z29136 IPI:IPI00529348 PIR:JQ0410 RefSeq:NP_001078345.1 RefSeq:NP_192094.1 UniGene:At.24433 UniGene:At.71920 ProteinModelPortal:P17562 SMR:P17562 STRING:P17562 PRIDE:P17562 ProMEX:P17562 EnsemblPlants:AT4G01850.1 EnsemblPlants:AT4G01850.2 GeneID:826987 KEGG:ath:AT4G01850 TAIR:At4g01850 InParanoid:P17562 OMA:ATIDYEK PhylomeDB:P17562 ArrayExpress:P17562 Genevestigator:P17562 GermOnline:AT4G01850 Uniprot:P17562
Root	Isotig07566	62	126	-1.152	1.09E-07	TAIR|locus:2141385 - symbol:SAM-2 "AT4G01850" species:3702 "Arabidopsis thaliana" [GO:0004478 "methionine adenosyltransferase activity" evidence=ISS] [GO:0006556 "S-adenosylmethionine biosynthetic process" evidence=ISS] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0071281 "cellular response to iron ion" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA;RCA] [GO:0070062 "extracellular vesicular exosome" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR002133 InterPro:IPR022628 InterPro:IPR022629 InterPro:IPR022630 InterPro:IPR022631 InterPro:IPR022636 Pfam:PF00438 Pfam:PF02772 Pfam:PF02773 PIRSF:PIRSF000497

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						PROSITE:PS00376 PROSITE:PS00377 GO:GO:0005829 GO:GO:0009506 GO:GO:0005524 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005618 GO:GO:0071281 GO:GO:0005730 GO:GO:0005507 EMBL:AC007138 EMBL:AL161493 GO:GO:0070062 GO:GO:0006730 KO:K00789 GO:GO:0006556 UniGene:At.24731 eggNOG:COG0192 HOGENOM:HBG443662 ProtClustDB:PLN02243 GO:GO:0004478 PANTHER:PTHR11964 SUPFAM:SSF55973 TIGRFAMs:TIGR01034 EMBL:M33217 EMBL:AY072327 EMBL:AY094454 EMBL:BT000575 EMBL:Z33778 EMBL:Z29136 IPI:IPI00529348 PIR:JQ0410 RefSeq:NP_001078345.1 RefSeq:NP_192094.1 UniGene:At.24433 UniGene:At.71920 ProteinModelPortal:P17562 SMR:P17562 STRING:P17562 PRIDE:P17562 ProMEX:P17562 EnsemblPlants:AT4G01850.1 EnsemblPlants:AT4G01850.2 GeneID:826987 KEGG:ath:AT4G01850 TAIR:At4g01850 InParanoid:P17562 OMA:ATIDYEK PhylomeDB:P17562 ArrayExpress:P17562 Genevestigator:P17562 GermOnline:AT4G01850 Uniprot:P17562
Root	Isotig07569	5	33	-2.851	5.40E-07	TAIR|locus:2103040 - symbol:APY1 "AT3G04080" species:3702 "Arabidopsis thaliana" [GO:0005516 "calmodulin binding" evidence=ISS;IDA] [GO:0016887 "ATPase activity" evidence=IDA] [GO:0017110 "nucleoside-diphosphatase activity" evidence=IGI;IDA] [GO:0009846 "pollen germination" evidence=IGI] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR000407 Pfam:PF01150 PROSITE:PS01238 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0016787 EMBL:AC016829 GO:GO:0009846 eggNOG:COG5371 PANTHER:PTHR11782 OMA:MATSWGA HOGENOM:HBG444677 EMBL:AF093604 EMBL:BT029157 IPI:IPI00522459 RefSeq:NP_187058.1 UniGene:At.16940 ProteinModelPortal:Q9SQG2 SMR:Q9SQG2 STRING:Q9SQG2 PRIDE:Q9SQG2 EnsemblPlants:AT3G04080.1 GeneID:819563 KEGG:ath:AT3G04080 TAIR:At3g04080 InParanoid:Q9SQG2 KO:K14641 PhylomeDB:Q9SQG2 ProtClustDB:CLSN2684264 Genevestigator:Q9SQG2 Uniprot:Q9SQG2
Root	Isotig07570	5	30	-2.714	3.20E-06	TAIR|locus:2103040 - symbol:APY1 "AT3G04080" species:3702 "Arabidopsis thaliana" [GO:0005516 "calmodulin binding" evidence=ISS;IDA] [GO:0016887 "ATPase activity" evidence=IDA] [GO:0017110 "nucleoside-diphosphatase activity" evidence=IGI;IDA] [GO:0009846 "pollen germination" evidence=IGI] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR000407 Pfam:PF01150 PROSITE:PS01238 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0016787 EMBL:AC016829 GO:GO:0009846 eggNOG:COG5371 PANTHER:PTHR11782 OMA:MATSWGA HOGENOM:HBG444677 EMBL:AF093604 EMBL:BT029157 IPI:IPI00522459 RefSeq:NP_187058.1 UniGene:At.16940 ProteinModelPortal:Q9SQG2 SMR:Q9SQG2 STRING:Q9SQG2 PRIDE:Q9SQG2 EnsemblPlants:AT3G04080.1 GeneID:819563 KEGG:ath:AT3G04080 TAIR:At3g04080 InParanoid:Q9SQG2 KO:K14641 PhylomeDB:Q9SQG2 ProtClustDB:CLSN2684264 Genevestigator:Q9SQG2 Uniprot:Q9SQG2
Root	Isotig07592	1	13	-3.829	0.000362856	TAIR|locus:2016407 - symbol:AT1G19450 "AT1G19450" species:3702 "Arabidopsis thaliana" [GO:0005351 "sugar:hydrogen symporter activity" evidence=ISS] [GO:0006810 "transport" evidence=IEA] [GO:0015144 "carbohydrate transmembrane transporter activity" evidence=ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0055085 "transmembrane transport" evidence=IEA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] InterPro:IPR003663 InterPro:IPR005828 InterPro:IPR005829 Pfam:PF00083 PRINTS:PR00171 PROSITE:PS00216 PROSITE:PS00217 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005774 eggNOG:COG0477 InterPro:IPR016196 SUPFAM:SSF103473 GO:GO:0008643 InterPro:IPR020846 PROSITE:PS50850 HOGENOM:HBG744444 GO:GO:0022891 TIGRFAMs:TIGR00879 EMBL:AC025808 EMBL:AY059848 EMBL:AY093274 IPI:IPI00534617 RefSeq:NP_173377.1 UniGene:At.22941 ProteinModelPortal:Q93YP9 IntAct:Q93YP9 PRIDE:Q93YP9 EnsemblPlants:AT1G19450.1 GeneID:838529 KEGG:ath:AT1G19450 TAIR:At1g19450 InParanoid:Q93YP9 OMA:SIGMTIS PhylomeDB:Q93YP9 ProtClustDB:CLSN2682491 ArrayExpress:Q93YP9 Genevestigator:Q93YP9 GermOnline:AT1G19450 Uniprot:Q93YP9
Root	Isotig07593	2	17	-3.216	0.000139706	TAIR|locus:2009323 - symbol:AT1G34580 "AT1G34580" species:3702 "Arabidopsis thaliana" [GO:0005351 "sugar:hydrogen symporter activity" evidence=ISS] [GO:0006810 "transport" evidence=IEA] [GO:0015144 "carbohydrate transmembrane transporter activity" evidence=ISS] [GO:0016020 "membrane" evidence=IEA;ISS] [GO:0016021 "integral to membrane" evidence=IEA] [GO:0055085 "transmembrane transport" evidence=IEA] InterPro:IPR003663 InterPro:IPR005828 InterPro:IPR005829 Pfam:PF00083 PRINTS:PR00171 PROSITE:PS00216 PROSITE:PS00217 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0015293 eggNOG:COG0477 InterPro:IPR016196 SUPFAM:SSF103473 GO:GO:0008643 InterPro:IPR020846 PROSITE:PS50850 HOGENOM:HBG744444 GO:GO:0022891 TIGRFAMs:TIGR00879 EMBL:AC023279

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EMBL:AJ344335 EMBL:AK118511 EMBL:BT005898 IPI:IPI00529432 PIR:F86469 RefSeq:NP_174718.1 UniGene:At.15065 ProteinModelPortal:Q93Y91 PRIDE:Q93Y91 EnsemblPlants:AT1G34580.1 GeneID:840362 KEGG:ath:AT1G34580 TAIR:At1g34580 InParanoid:Q93Y91 OMA:SMYQVWE PhylomeDB:Q93Y91 ProtClustDB:CLSN2679632 Genevestigator:Q93Y91 GermOnline:AT1G34580 Uniprot:Q93Y91
Root	Isotig07594	2	16	-3.129	0.000262867	TAIR|locus:2009323 - symbol:AT1G34580 "AT1G34580" species:3702 "Arabidopsis thaliana" [GO:0005351 "sugar:hydrogen symporter activity" evidence=ISS] [GO:0006810 "transport" evidence=IEA] [GO:0015144 "carbohydrate transmembrane transporter activity" evidence=ISS] [GO:0016020 "membrane" evidence=IEA;ISS] [GO:0016021 "integral to membrane" evidence=IEA] [GO:0055085 "transmembrane transport" evidence=IEA] InterPro:IPR003663 InterPro:IPR005828 InterPro:IPR005829 Pfam:PF00083 PRINTS:PR00171 PROSITE:PS00216 PROSITE:PS00217 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0015293 eggNOG:COG0477 InterPro:IPR016196 SUPFAM:SSF103473 GO:GO:0008643 InterPro:IPR020846 PROSITE:PS50850 HOGENOM:HBG744444 GO:GO:0022891 TIGRFAMs:TIGR00879 EMBL:AC023279 EMBL:AJ344335 EMBL:AK118511 EMBL:BT005898 IPI:IPI00529432 PIR:F86469 RefSeq:NP_174718.1 UniGene:At.15065 ProteinModelPortal:Q93Y91 PRIDE:Q93Y91 EnsemblPlants:AT1G34580.1 GeneID:840362 KEGG:ath:AT1G34580 TAIR:At1g34580 InParanoid:Q93Y91 OMA:SMYQVWE PhylomeDB:Q93Y91 ProtClustDB:CLSN2679632 Genevestigator:Q93Y91 GermOnline:AT1G34580 Uniprot:Q93Y91
Root	Isotig07625	13	0	4.571	0.000344357	CGD|CAL0004433 - symbol:orf19.2051 species:5476 "Candida albicans" [GO:0008150 "biological_process" evidence=ND] [GO:0005622 "intracellular" evidence=IEA] [GO:0008270 "zinc ion binding" evidence=IEA] InterPro:IPR007087 InterPro:IPR015880 PROSITE:PS50157 SMART:SM00355 GO:GO:0008270 GO:GO:0005622 EMBL:AACQ01000030 RefSeq:XP_719625.1 GeneID:3638749 KEGG:cal:CaO19.9599 CGD:CAL0072124 Uniprot:Q5ADE8
Root	Isotig07639	6	37	-2.753	1.87E-07	TAIR|locus:2165580 - symbol:AT5G57330 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004034 "aldose 1-epimerase activity" evidence=ISS] [GO:0006012 "galactose metabolic process" evidence=ISS] [GO:0016853 "isomerase activity" evidence=IEA] [GO:0030246 "carbohydrate binding" evidence=IEA] [GO:0009737 "response to abscisic acid stimulus" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR008183 InterPro:IPR011013 InterPro:IPR014718 Pfam:PF01263 GO:GO:0005829 GO:GO:0009737 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005975 GO:GO:0016853 GO:GO:0030246 SUPFAM:SSF74650 Gene3D:G3DSA:2.70.98.10 EMBL:AB019233 eggNOG:COG0676 HOGENOM:HBG737737 KO:K01792 InterPro:IPR025532 PIRSF:PIRSF016020 EMBL:AY093119 EMBL:BT003381 IPI:IPI00546569 RefSeq:NP_200543.1 UniGene:At.9593 HSSP:Q9RP27 ProteinModelPortal:Q9LVC5 SMR:Q9LVC5 STRING:Q9LVC5 PRIDE:Q9LVC5 EnsemblPlants:AT5G57330.1 GeneID:835838 KEGG:ath:AT5G57330 TAIR:At5g57330 InParanoid:Q9LVC5 OMA:EYREMVC PhylomeDB:Q9LVC5 ProtClustDB:CLSN2916812 ArrayExpress:Q9LVC5 Genevestigator:Q9LVC5 Uniprot:Q9LVC5
Root	Isotig07640	6	39	-2.829	5.74E-08	TAIR|locus:2165580 - symbol:AT5G57330 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004034 "aldose 1-epimerase activity" evidence=ISS] [GO:0006012 "galactose metabolic process" evidence=ISS] [GO:0016853 "isomerase activity" evidence=IEA] [GO:0030246 "carbohydrate binding" evidence=IEA] [GO:0009737 "response to abscisic acid stimulus" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR008183 InterPro:IPR011013 InterPro:IPR014718 Pfam:PF01263 GO:GO:0005829 GO:GO:0009737 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005975 GO:GO:0016853 GO:GO:0030246 SUPFAM:SSF74650 Gene3D:G3DSA:2.70.98.10 EMBL:AB019233 eggNOG:COG0676 HOGENOM:HBG737737 KO:K01792 InterPro:IPR025532 PIRSF:PIRSF016020 EMBL:AY093119 EMBL:BT003381 IPI:IPI00546569 RefSeq:NP_200543.1 UniGene:At.9593 HSSP:Q9RP27 ProteinModelPortal:Q9LVC5 SMR:Q9LVC5 STRING:Q9LVC5 PRIDE:Q9LVC5 EnsemblPlants:AT5G57330.1 GeneID:835838 KEGG:ath:AT5G57330 TAIR:At5g57330 InParanoid:Q9LVC5 OMA:EYREMVC PhylomeDB:Q9LVC5 ProtClustDB:CLSN2916812 ArrayExpress:Q9LVC5 Genevestigator:Q9LVC5 Uniprot:Q9LVC5
Root	Isotig07645	6	22	-2.003	0.00086822	TAIR|locus:2098343 - symbol:AT3G11680 species:3702 "Arabidopsis thaliana" [GO:0010044 "response to aluminum ion" evidence=IEA] InterPro:IPR020966 Pfam:PF11744 GO:GO:0016021 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0010044 GO:GO:0005216 eggNOG:NOG318607 HOGENOM:HBG749623 EMBL:AC009918 IPI:IPI00517606 RefSeq:NP_187774.1 UniGene:At.50172 PRIDE:Q9SRM9 EnsemblPlants:AT3G11680.1 GeneID:820340 KEGG:ath:AT3G11680 TAIR:At3g11680 InParanoid:Q9SRM9 OMA:MIANNIN PhylomeDB:Q9SRM9 ProtClustDB:CLSN2914776 Genevestigator:Q9SRM9 Uniprot:Q9SRM9

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig07667	2	44	-4.588	5.52E-12	TAIR|locus:2015021 - symbol:AT1G22170 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA;ISS] [GO:0006096 "glycolysis" evidence=IEA] [GO:0008152 "metabolic process" evidence=IEA;ISS] [GO:0016868 "intramolecular transferase activity, phosphotransferases" evidence=IEA] HAMAP:MF_01039 InterPro:IPR001345 InterPro:IPR005952 PROSITE:PS00175 Pfam:PF00300 EMBL:CP002684 InterPro:IPR013078 SMART:SM00855 GO:GO:0006096 EMBL:AC073942 KO:K01834 PANTHER:PTHR11931 OMA:YWNDVII GO:GO:0016868 HSSP:P00950 EMBL:BT020337 IPI:IPI00547090 PIR:C86354 RefSeq:NP_564161.1 UniGene:At.41618 UniGene:At.43225 ProteinModelPortal:Q9LM13 SMR:Q9LM13 PRIDE:Q9LM13 EnsemblPlants:AT1G22170.1 GeneID:838822 KEGG:ath:AT1G22170 TAIR:At1g22170 InParanoid:Q9LM13 PhylomeDB:Q9LM13 ProtClustDB:CLSN2687909 Genevestigator:Q9LM13 Uniprot:Q9LM13
Root	Isotig07668	2	44	-4.588	5.52E-12	TAIR|locus:2015021 - symbol:AT1G22170 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA;ISS] [GO:0006096 "glycolysis" evidence=IEA] [GO:0008152 "metabolic process" evidence=IEA;ISS] [GO:0016868 "intramolecular transferase activity, phosphotransferases" evidence=IEA] HAMAP:MF_01039 InterPro:IPR001345 InterPro:IPR005952 PROSITE:PS00175 Pfam:PF00300 EMBL:CP002684 InterPro:IPR013078 SMART:SM00855 GO:GO:0006096 EMBL:AC073942 KO:K01834 PANTHER:PTHR11931 OMA:YWNDVII GO:GO:0016868 HSSP:P00950 EMBL:BT020337 IPI:IPI00547090 PIR:C86354 RefSeq:NP_564161.1 UniGene:At.41618 UniGene:At.43225 ProteinModelPortal:Q9LM13 SMR:Q9LM13 PRIDE:Q9LM13 EnsemblPlants:AT1G22170.1 GeneID:838822 KEGG:ath:AT1G22170 TAIR:At1g22170 InParanoid:Q9LM13 PhylomeDB:Q9LM13 ProtClustDB:CLSN2687909 Genevestigator:Q9LM13 Uniprot:Q9LM13
Root	Isotig07673	4	23	-2.653	5.61E-05	TAIR|locus:2170428 - symbol:KASI "3-ketoacyl-acyl carrier protein synthase I" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004312 "fatty acid synthase activity" evidence=ISS] [GO:0016747 "transferase activity, transferring acyl groups other than amino-acyl groups" evidence=IEA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009790 "embryo development" evidence=IMP] [GO:0010020 "chloroplast fission" evidence=IMP] InterPro:IPR000794 InterPro:IPR016038 InterPro:IPR016039 InterPro:IPR017568 Pfam:PF02801 Pfam:PF00109 Prosite:PS00606 GO:GO:0009570 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0016020 GO:GO:0009790 GO:GO:0009941 GO:GO:0006633 GO:GO:0010020 Gene3D:G3DSA:3.40.47.10 SUPFAM:SSF53901 PANTHER:PTHR11712 eggNOG:COG0304 HOGENOM:HBG757733 GO:GO:0004315 InterPro:IPR018201 InterPro:IPR014031 InterPro:IPR014030 TIGRFAMs:TIGR03150 EMBL:AB010698 EMBL:U24177 EMBL:AY037261 EMBL:AY094005 EMBL:AY123979 EMBL:AY087843 IPI:IPI00541557 IPI:IPI00657465 RefSeq:NP_001032018.1 RefSeq:NP_199441.1 UniGene:At.9183 ProteinModelPortal:P52410 SMR:P52410 STRING:P52410 PRIDE:P52410 EnsemblPlants:AT5G46290.1 GeneID:834671 KEGG:ath:AT5G46290 TAIR:At5g46290 InParanoid:P52410 OMA:NAQNTSQ PhylomeDB:P52410 ProtClustDB:CLSN2715653 BioCyc:MetaCyc:MONOMER-14117 ArrayExpress:P52410 Genevestigator:P52410 Uniprot:P52410
Root	Isotig07674	4	23	-2.653	5.61E-05	TAIR|locus:2170428 - symbol:KASI "3-ketoacyl-acyl carrier protein synthase I" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004312 "fatty acid synthase activity" evidence=ISS] [GO:0016747 "transferase activity, transferring acyl groups other than amino-acyl groups" evidence=IEA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009790 "embryo development" evidence=IMP] [GO:0010020 "chloroplast fission" evidence=IMP] InterPro:IPR000794 InterPro:IPR016038 InterPro:IPR016039 InterPro:IPR017568 Pfam:PF02801 Pfam:PF00109 Prosite:PS00606 GO:GO:0009570 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0016020 GO:GO:0009790 GO:GO:0009941 GO:GO:0006633 GO:GO:0010020 Gene3D:G3DSA:3.40.47.10 SUPFAM:SSF53901 PANTHER:PTHR11712 eggNOG:COG0304 HOGENOM:HBG757733 GO:GO:0004315 InterPro:IPR018201 InterPro:IPR014031 InterPro:IPR014030 TIGRFAMs:TIGR03150 EMBL:AB010698 EMBL:U24177 EMBL:AY037261 EMBL:AY094005 EMBL:AY123979 EMBL:AY087843 IPI:IPI00541557 IPI:IPI00657465 RefSeq:NP_001032018.1 RefSeq:NP_199441.1 UniGene:At.9183 ProteinModelPortal:P52410 SMR:P52410 STRING:P52410 PRIDE:P52410 EnsemblPlants:AT5G46290.1 GeneID:834671 KEGG:ath:AT5G46290 TAIR:At5g46290 InParanoid:P52410 OMA:NAQNTSQ PhylomeDB:P52410 ProtClustDB:CLSN2715653 BioCyc:MetaCyc:MONOMER-14117 ArrayExpress:P52410 Genevestigator:P52410 Uniprot:P52410
Root	Isotig07675	2	29	-3.987	6.83E-08	TAIR|locus:2007651 - symbol:TPPD "trehalose-6-phosphate phosphatase D" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004805 "trehalose-phosphatase activity" evidence=ISS]

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						[GO:0005992 "trehalose biosynthetic process" evidence=IEA;ISS] [GO:0008152 "metabolic process" evidence=IEA] InterPro:IPR003337 InterPro:IPR006379 Pfam:PF02358 EMBL:CP002684 GenomeReviews:CT485782_GR InterPro:IPR023214 Gene3D:G3DSA:3.40.50.1000 SUPFAM:SSF56784 GO:GO:0016787 GO:GO:0005992 TIGRFAMs:TIGR01484 eggNOG:COG1877 HOGENOM:HBG686849 OMA:EGANVEN TIGRFAMs:TIGR00685 EMBL:AK176890 IPI:IPI00519798 RefSeq:NP_564464.1 UniGene:At.39452 ProteinModelPortal:Q67XC9 PRIDE:Q67XC9 EnsemblPlants:AT1G35910.1 GeneID:840493 KEGG:ath:AT1G35910 TAIR:At1g35910 InParanoid:Q67XC9 PhylomeDB:Q67XC9 ProtClustDB:CLSN2914984 ArrayExpress:Q67XC9 Genevestigator:Q67XC9 Uniprot:Q67XC9
Root	Isotig07676	2	29	-3.987	6.83E-08	TAIR|locus:2007651 - symbol:TPPD "trehalose-6-phosphate phosphatase D" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004805 "trehalose-phosphatase activity" evidence=ISS] [GO:0005992 "trehalose biosynthetic process" evidence=IEA;ISS] [GO:0008152 "metabolic process" evidence=IEA] InterPro:IPR003337 InterPro:IPR006379 Pfam:PF02358 EMBL:CP002684 GenomeReviews:CT485782_GR InterPro:IPR023214 Gene3D:G3DSA:3.40.50.1000 SUPFAM:SSF56784 GO:GO:0016787 GO:GO:0005992 TIGRFAMs:TIGR01484 eggNOG:COG1877 HOGENOM:HBG686849 OMA:EGANVEN TIGRFAMs:TIGR00685 EMBL:AK176890 IPI:IPI00519798 RefSeq:NP_564464.1 UniGene:At.39452 ProteinModelPortal:Q67XC9 PRIDE:Q67XC9 EnsemblPlants:AT1G35910.1 GeneID:840493 KEGG:ath:AT1G35910 TAIR:At1g35910 InParanoid:Q67XC9 PhylomeDB:Q67XC9 ProtClustDB:CLSN2914984 ArrayExpress:Q67XC9 Genevestigator:Q67XC9 Uniprot:Q67XC9
Root	Isotig07685	0	32	-6.129	1.84E-09	TAIR|locus:2165897 - symbol:GS2 "AT5G35630" species:3702 "Arabidopsis thaliana" [GO:0004356 "glutamate-ammonia ligase activity" evidence=ISS;IDA;TAS;IPI] [GO:0007568 "aging" evidence=TAS] [GO:0009507 "chloroplast" evidence=IDA;NAS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0019676 "ammonia assimilation cycle" evidence=TAS] [GO:0009579 "thylakoid" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0048046 "apoplast" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] InterPro:IPR008146 InterPro:IPR008147 InterPro:IPR014746 Pfam:PF00120 Pfam:PF03951 PROSITE:PS00180 PROSITE:PS00181 GO:GO:0005739 GO:GO:0005524 GO:GO:0048046 GO:GO:0009570 GO:GO:0046686 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0007568 GO:GO:0009941 GO:GO:0009651 GO:GO:0009535 GO:GO:0022626 GO:GO:0019676 eggNOG:COG0174 HOGENOM:HBG299709 KO:K01915 GO:GO:0004356 GO:GO:0006542 Gene3D:G3DSA:3.30.590.10 SUPFAM:SSF54368 EMBL:S69727 EMBL:AB015045 EMBL:AB013393 EMBL:AF428319 EMBL:AF428461 EMBL:AY081252 EMBL:AY091114 EMBL:AY122977 EMBL:AY088222 IPI:IPI00534852 PIR:S18600 RefSeq:NP_001031969.1 RefSeq:NP_001078639.1 RefSeq:NP_198413.1 UniGene:At.24218 ProteinModelPortal:Q43127 SMR:Q43127 DIP:DIP-32735N IntAct:Q43127 STRING:Q43127 SWISS-2DPAGE:Q43127 PRIDE:Q43127 EnsemblPlants:AT5G35630.1 EnsemblPlants:AT5G35630.2 EnsemblPlants:AT5G35630.3 GeneID:833535 KEGG:ath:AT5G35630 TAIR:At5g35630 InParanoid:Q43127 OMA:TLDPKPI PhylomeDB:Q43127 ProtClustDB:PLN03036 ArrayExpress:Q43127 Genevestigator:Q43127 GermOnline:AT5G35630 Uniprot:Q43127
Root	Isotig07686	0	29	-5.987	1.01E-08	TAIR|locus:2165897 - symbol:GS2 "AT5G35630" species:3702 "Arabidopsis thaliana" [GO:0004356 "glutamate-ammonia ligase activity" evidence=ISS;IDA;TAS;IPI] [GO:0007568 "aging" evidence=TAS] [GO:0009507 "chloroplast" evidence=IDA;NAS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0019676 "ammonia assimilation cycle" evidence=TAS] [GO:0009579 "thylakoid" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0048046 "apoplast" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] InterPro:IPR008146 InterPro:IPR008147 InterPro:IPR014746 Pfam:PF00120 Pfam:PF03951 PROSITE:PS00180 PROSITE:PS00181 GO:GO:0005739 GO:GO:0005524 GO:GO:0048046 GO:GO:0009570 GO:GO:0046686 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0007568 GO:GO:0009941 GO:GO:0009651 GO:GO:0009535 GO:GO:0022626 GO:GO:0019676 eggNOG:COG0174 HOGENOM:HBG299709 KO:K01915 GO:GO:0004356 GO:GO:0006542 Gene3D:G3DSA:3.30.590.10 SUPFAM:SSF54368 EMBL:S69727 EMBL:AB015045 EMBL:AB013393 EMBL:AF428319 EMBL:AF428461 EMBL:AY081252 EMBL:AY091114 EMBL:AY122977 EMBL:AY088222 IPI:IPI00534852 PIR:S18600

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						RefSeq:NP_001031969.1 RefSeq:NP_001078639.1 RefSeq:NP_198413.1 UniGene:At.24218 ProteinModelPortal:Q43127 SMR:Q43127 DIP:DIP-32735N IntAct:Q43127 STRING:Q43127 SWISS-2DPAGE:Q43127 PRIDE:Q43127 EnsemblPlants:AT5G35630.1 EnsemblPlants:AT5G35630.2 EnsemblPlants:AT5G35630.3 GeneID:833535 KEGG:ath:AT5G35630 TAIR:At5g35630 InParanoid:Q43127 OMA:TLDPKPI PhylomeDB:Q43127 ProtClustDB:PLN03036 ArrayExpress:Q43127 Genevestigator:Q43127 GermOnline:AT5G35630 Uniprot:Q43127
Root	Isotig07703	12	50	-2.188	1.10E-07	TAIR|locus:2028145 - symbol:RFNR2 "AT1G30510" species:3702 "Arabidopsis thaliana" [GO:0016491 "oxidoreductase activity" evidence=ISS] [GO:0042651 "thylakoid membrane" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0005507 "copper ion binding" evidence=IDA] InterPro:IPR001433 InterPro:IPR001709 InterPro:IPR012146 InterPro:IPR015701 InterPro:IPR017927 InterPro:IPR017938 Pfam:PF00175 PIRSF:PIRSF000361 PRINTS:PR00371 PROSITE:PS51384 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009507 GO:GO:0050660 GO:GO:0006810 GO:GO:0050661 GO:GO:0005507 EMBL:AC009917 GO:GO:0022900 GO:GO:0004324 SUPFAM:SSF63380 GO:GO:0015979 GO:GO:0042651 eggNOG:COG0369 PANTHER:PTHR19384:SF1 HOGENOM:HBG353752 KO:K02641 HSSP:P00455 ProtClustDB:PLN03116 EMBL:AF424594 EMBL:AY140017 EMBL:BT008468 EMBL:AY088018 IPI:IPI00525557 IPI:IPI00529741 IPI:IPI00534215 PIR:B86430 RefSeq:NP_564355.1 RefSeq:NP_849734.1 RefSeq:NP_973942.1 UniGene:At.25172 ProteinModelPortal:Q9S9P8 SMR:Q9S9P8 PRIDE:Q9S9P8 EnsemblPlants:AT1G30510.2 GeneID:839930 KEGG:ath:AT1G30510 TAIR:At1g30510 InParanoid:Q9S9P8 OMA:FLCDSKP PhylomeDB:Q9S9P8 ArrayExpress:Q9S9P8 Genevestigator:Q9S9P8 Uniprot:Q9S9P8
Root	Isotig07704	12	49	-2.159	1.86E-07	TAIR|locus:2028145 - symbol:RFNR2 "AT1G30510" species:3702 "Arabidopsis thaliana" [GO:0016491 "oxidoreductase activity" evidence=ISS] [GO:0042651 "thylakoid membrane" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0005507 "copper ion binding" evidence=IDA] InterPro:IPR001433 InterPro:IPR001709 InterPro:IPR012146 InterPro:IPR015701 InterPro:IPR017927 InterPro:IPR017938 Pfam:PF00175 PIRSF:PIRSF000361 PRINTS:PR00371 PROSITE:PS51384 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009507 GO:GO:0050660 GO:GO:0006810 GO:GO:0050661 GO:GO:0005507 EMBL:AC009917 GO:GO:0022900 GO:GO:0004324 SUPFAM:SSF63380 GO:GO:0015979 GO:GO:0042651 eggNOG:COG0369 PANTHER:PTHR19384:SF1 HOGENOM:HBG353752 KO:K02641 HSSP:P00455 ProtClustDB:PLN03116 EMBL:AF424594 EMBL:AY140017 EMBL:BT008468 EMBL:AY088018 IPI:IPI00525557 IPI:IPI00529741 IPI:IPI00534215 PIR:B86430 RefSeq:NP_564355.1 RefSeq:NP_849734.1 RefSeq:NP_973942.1 UniGene:At.25172 ProteinModelPortal:Q9S9P8 SMR:Q9S9P8 PRIDE:Q9S9P8 EnsemblPlants:AT1G30510.2 GeneID:839930 KEGG:ath:AT1G30510 TAIR:At1g30510 InParanoid:Q9S9P8 OMA:FLCDSKP PhylomeDB:Q9S9P8 ArrayExpress:Q9S9P8 Genevestigator:Q9S9P8 Uniprot:Q9S9P8
Root	Isotig07713	175	19	3.074	2.39E-30	ZFIN|ZDB-GENE-070410-9 - symbol:zgc:158463 "zgc:158463" species:7955 "Danio rerio" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] ZFIN:ZDB-GENE-070410-9 EMBL:BX296557 EMBL:BX537263 EMBL:BC129240 IPI:IPI00837201 RefSeq:NP_001091866.1 RefSeq:XP_003200836.1 UniGene:Dr.155369 Ensembl:ENSDART00000102863 Ensembl:ENSDART00000126982 GeneID:100037361 GeneID:100151188 KEGG:dre:100037361 KEGG:dre:100151188 eggNOG:NOG298153 GeneTree:ENSGT00390000016898 InParanoid:A2VD29 OMA:ACHQHAL OrthoDB:EOG4FJ8BF Bgee:A2VD29 Uniprot:A2VD29
Root	Isotig07714	124	12	3.240	5.66E-23	No hit
Root	Isotig07721	31	140	-2.304	4.67E-20	TAIR|locus:2075236 - symbol:MYB48 "AT3G46130" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=ISS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=ISS;TAS] [GO:0009751 "response to salicylic acid stimulus" evidence=IEP] [GO:0005634 "nucleus" evidence=IDA] InterPro:IPR001005 InterPro:IPR009057 Pfam:PF00249 SMART:SM00717 GO:GO:0005634 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0006355 GO:GO:0003677 GO:GO:0006351 GO:GO:0009751 Gene3D:G3DSA:1.10.10.60 SUPFAM:SSF46689 InterPro:IPR017930 PROSITE:PS51294 eggNOG:COG5147 InterPro:IPR015495 PANTHER:PTHR10641 EMBL:AL355775 HOGENOM:HBG750380 EMBL:AF272733 EMBL:AY519594 EMBL:DQ075255 EMBL:DQ075256 EMBL:DQ075257 EMBL:AK176475 IPI:IPI00528378 IPI:IPI00656574 IPI:IPI00759334 IPI:IPI00759367 PIR:T49254 RefSeq:NP_001030816.1 RefSeq:NP_001078249.1 RefSeq:NP_190199.1 UniGene:At.1475 UniGene:At.72744 ProteinModelPortal:Q9LX82 SMR:Q9LX82 STRING:Q9LX82 EnsemblPlants:AT3G46130.1 GeneID:823756 KEGG:ath:AT3G46130 GeneFarm:1132

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						TAIR:At3g46130 InParanoid:Q9LX82 OMA:REIDHSA PhylomeDB:Q9LX82 ProtClustDB:CLSN2684805 Genevestigator:Q9LX82 GermOnline:AT3G46130 Uniprot:Q9LX82
Root	Isotig07722	33	137	-2.183	1.68E-18	TAIR|locus:2174324 - symbol:MYB59 "AT5G59780" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=ISS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0009723 "response to ethylene stimulus" evidence=IEP] [GO:0009739 "response to gibberellin stimulus" evidence=IEP] [GO:0009751 "response to salicylic acid stimulus" evidence=IEP] [GO:0009753 "response to jasmonic acid stimulus" evidence=IEP] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005634 "nucleus" evidence=IDA] [GO:0010200 "response to chitin" evidence=IEP] InterPro:IPR001005 InterPro:IPR009057 Pfam:PF00249 SMART:SM00717 GO:GO:0005634 GO:GO:0046686 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009753 GO:GO:0006355 GO:GO:0003677 GO:GO:0006351 GO:GO:0009723 GO:GO:0009751 Gene3D:G3DSA:1.10.10.60 SUPFAM:SSF46689 GO:GO:0010200 GO:GO:0009739 InterPro:IPR017930 PROSITE:PS51294 eggNOG:COG5147 KO:K09422 InterPro:IPR015495 PANTHER:PTHR10641 EMBL:AB006705 EMBL:AF062894 EMBL:AY519641 EMBL:DQ075252 EMBL:DQ075253 EMBL:DQ075254 EMBL:AK229048 EMBL:Z95781 EMBL:Z95772 IPI:IPI00528791 IPI:IPI00545664 IPI:IPI00548069 IPI:IPI00759289 PIR:T51666 RefSeq:NP_200786.1 RefSeq:NP_851225.1 RefSeq:NP_851226.1 UniGene:At.22428 UniGene:At.70065 ProteinModelPortal:Q4JL84 SMR:Q4JL84 STRING:Q4JL84 PRIDE:Q4JL84 EnsemblPlants:AT5G59780.3 GeneID:836099 KEGG:ath:AT5G59780 GeneFarm:952 TAIR:At5g59780 InParanoid:Q4JL84 OMA:WESSLES PhylomeDB:Q4JL84 ProtClustDB:CLSN2916286 ArrayExpress:Q9FN86 Genevestigator:Q4JL84 GermOnline:AT5G59780 Uniprot:Q4JL84
Root	Isotig07739	22	54	-1.424	4.11E-05	TAIR|locus:2064965 - symbol:EULS3 "AT2G39050" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0030246 "carbohydrate binding" evidence=IDA] GO:GO:0005634 GO:GO:0005737 EMBL:CP002685 GenomeReviews:CT485783_GR InterPro:IPR000772 SUPFAM:SSF50370 PROSITE:PS50231 GO:GO:0030246 EMBL:AC005770 Pfam:PF14200 EMBL:AF411801 EMBL:AY093795 EMBL:AY087909 IPI:IPI00536641 PIR:E84812 RefSeq:NP_565899.1 UniGene:At.22599 ProteinModelPortal:Q945P1 SMR:Q945P1 PRIDE:Q945P1 EnsemblPlants:AT2G39050.1 GeneID:818491 KEGG:ath:AT2G39050 TAIR:At2g39050 eggNOG:NOG254161 HOGENOM:HBG750017 InParanoid:Q945P1 OMA:GYRTIRM PhylomeDB:Q945P1 ProtClustDB:CLSN2681741 ArrayExpress:Q945P1 Genevestigator:Q945P1 Uniprot:Q945P1
Root	Isotig07740	21	57	-1.570	5.97E-06	TAIR|locus:2064965 - symbol:EULS3 "AT2G39050" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0030246 "carbohydrate binding" evidence=IDA] GO:GO:0005634 GO:GO:0005737 EMBL:CP002685 GenomeReviews:CT485783_GR InterPro:IPR000772 SUPFAM:SSF50370 PROSITE:PS50231 GO:GO:0030246 EMBL:AC005770 Pfam:PF14200 EMBL:AF411801 EMBL:AY093795 EMBL:AY087909 IPI:IPI00536641 PIR:E84812 RefSeq:NP_565899.1 UniGene:At.22599 ProteinModelPortal:Q945P1 SMR:Q945P1 PRIDE:Q945P1 EnsemblPlants:AT2G39050.1 GeneID:818491 KEGG:ath:AT2G39050 TAIR:At2g39050 eggNOG:NOG254161 HOGENOM:HBG750017 InParanoid:Q945P1 OMA:GYRTIRM PhylomeDB:Q945P1 ProtClustDB:CLSN2681741 ArrayExpress:Q945P1 Genevestigator:Q945P1 Uniprot:Q945P1
Root	Isotig07745	19	52	-1.581	1.37E-05	TAIR|locus:2119251 - symbol:AT4G33420 species:3702 "Arabidopsis thaliana" [GO:0004601 "peroxidase activity" evidence=IEA;ISS] [GO:0006979 "response to oxidative stress" evidence=IEA] [GO:0020037 "heme binding" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] InterPro:IPR000823 InterPro:IPR002016 InterPro:IPR010255 InterPro:IPR019793 InterPro:IPR019794 Pfam:PF00141 PRINTS:PR00458 PRINTS:PR00461 PROSITE:PS00435 PROSITE:PS00436 PROSITE:PS50873 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005576 GO:GO:0006979 EMBL:AL161583 EMBL:AL035678 GO:GO:0020037 GO:GO:0004601 HOGENOM:HBG597790 SUPFAM:SSF48113 KO:K00430 EMBL:AF451951 EMBL:BT044614 IPI:IPI00539387 PIR:T05993 RefSeq:NP_567919.1 UniGene:At.28650 ProteinModelPortal:Q9SZB9 SMR:Q9SZB9 STRING:Q9SZB9 PeroxiBase:213 PRIDE:Q9SZB9 EnsemblPlants:AT4G33420.1 GeneID:829479 KEGG:ath:AT4G33420 GeneFarm:1879 TAIR:At4g33420 eggNOG:NOG276365 InParanoid:Q9SZB9 ProtClustDB:CLSN2689733 Genevestigator:Q9SZB9 GermOnline:AT4G33420 Uniprot:Q9SZB9
Root	Isotig07747	1	14	-3.936	0.000188601	TAIR|locus:2183379 - symbol:GDH2 "AT5G07440" species:3702 "Arabidopsis thaliana" [GO:0016491 "oxidoreductase activity" evidence=ISS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005524 "ATP binding" evidence=IDA] [GO:0005774 "vacuolar membrane"

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0004352 "glutamate dehydrogenase (NAD+) activity" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0008270 "zinc ion binding" evidence=IDA] [GO:0050897 "cobalt ion binding" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] [GO:0004353 "glutamate dehydrogenase [NAD(P)+] activity" evidence=IDA] InterPro:IPR006095 InterPro:IPR006096 InterPro:IPR006097 InterPro:IPR014362 InterPro:IPR016040 Pfam:PF00208 Pfam:PF02812 PIRSF:PIRSF000185 PRINTS:PR00082 PROSITE:PS00074 SMART:SM00839 GO:GO:0005739 GO:GO:0005524 GO:GO:0046686 GO:GO:0005774 EMBL:CP002688 GenomeReviews:BA000015_GR Gene3D:G3DSA:3.40.50.720 GO:GO:0008270 GO:GO:0005507 GO:GO:0006520 GO:GO:0009651 GO:GO:0050897 EMBL:AL163912 eggNOG:COG0334 HOGENOM:HBG590661 KO:K00261 ProtClustDB:PLN02477 GO:GO:0004353 EMBL:U56635 IPI:IPI00543481 PIR:T49883 RefSeq:NP_001119183.1 RefSeq:NP_196361.1 UniGene:At.21712 ProteinModelPortal:Q38946 SMR:Q38946 STRING:Q38946 PRIDE:Q38946 ProMEX:Q38946 EnsemblPlants:AT5G07440.1 EnsemblPlants:AT5G07440.2 GeneID:830635 KEGG:ath:AT5G07440 GeneFarm:2247 TAIR:At5g07440 InParanoid:Q38946 OMA:NTGHTEE PhylomeDB:Q38946 ArrayExpress:Q38946 Genevestigator:Q38946 GermOnline:AT5G07440 GO:GO:0004352 Uniprot:Q38946
Root	Isotig07773	4	126	-5.106	1.81E-32	UNIPROTKB|A8QW53 - symbol:OMT3 "5-pentadecatrienyl resorcinol O-methyltransferase" species:4558 "Sorghum bicolor" [GO:0008171 "O-methyltransferase activity" evidence=IDA] [GO:0008757 "S-adenosylmethionine-dependent methyltransferase activity" evidence=IDA] [GO:0032259 "methylation" evidence=IDA] InterPro:IPR001077 InterPro:IPR012967 InterPro:IPR016461 Pfam:PF00891 Pfam:PF08100 PIRSF:PIRSF005739 InterPro:IPR011991 Gene3D:G3DSA:1.10.10.10 GO:GO:0046983 GO:GO:0008171 GO:GO:0008757 EMBL:EF189708 EMBL:CM000765 RefSeq:XP_002447425.1 UniGene:Sbi.19698 ProteinModelPortal:A8QW53 EnsemblPlants:Sb06g000820.1 GeneID:8080259 KEGG:sbi:SORBI_06g000820 eggNOG:NOG272168 PhylomeDB:A8QW53 ProtClustDB:CLSN2725062 Uniprot:A8QW53
Root	Isotig07774	5	112	-4.614	3.50E-28	UNIPROTKB|A8QW53 - symbol:OMT3 "5-pentadecatrienyl resorcinol O-methyltransferase" species:4558 "Sorghum bicolor" [GO:0008171 "O-methyltransferase activity" evidence=IDA] [GO:0008757 "S-adenosylmethionine-dependent methyltransferase activity" evidence=IDA] [GO:0032259 "methylation" evidence=IDA] InterPro:IPR001077 InterPro:IPR012967 InterPro:IPR016461 Pfam:PF00891 Pfam:PF08100 PIRSF:PIRSF005739 InterPro:IPR011991 Gene3D:G3DSA:1.10.10.10 GO:GO:0046983 GO:GO:0008171 GO:GO:0008757 EMBL:EF189708 EMBL:CM000765 RefSeq:XP_002447425.1 UniGene:Sbi.19698 ProteinModelPortal:A8QW53 EnsemblPlants:Sb06g000820.1 GeneID:8080259 KEGG:sbi:SORBI_06g000820 eggNOG:NOG272168 PhylomeDB:A8QW53 ProtClustDB:CLSN2725062 Uniprot:A8QW53
Root	Isotig07783	3	21	-2.936	4.98E-05	UNIPROTKB|P29717 - symbol:XOG1 "Glucan 1,3-beta-glucosidase" species:237561 "Candida albicans SC5314" [GO:0004338 "glucan exo-1,3-beta-glucosidase activity" evidence=IMP;IDA] [GO:0005576 "extracellular region" evidence=IDA] [GO:0006073 "cellular glucan metabolic process" evidence=IMP] [GO:0009986 "cell surface" evidence=IDA] [GO:0031505 "fungal-type cell wall organization" evidence=IMP] [GO:0031589 "cell-substrate adhesion" evidence=IDA] [GO:0050839 "cell adhesion molecule binding" evidence=IDA] InterPro:IPR001547 InterPro:IPR013781 InterPro:IPR018087 Pfam:PF00150 PROSITE:PS00659 GO:GO:0005576 EMBL:AACQ01000015 GO:GO:0009986 GO:GO:0043169 InterPro:IPR017853 Gene3D:G3DSA:3.20.20.80 SUPFAM:SSF51445 CAZy:GH5 GO:GO:0031505 GO:GO:0050839 GO:GO:0031589 EMBL:AL033497 KO:K01210 GO:GO:0004338 eggNOG:COG2730 GO:GO:0006073 EMBL:X56556 PIR:A47702 PIR:T52149 RefSeq:XP_721488.1 PDB:1CZ1 PDB:1EQC PDB:1EQP PDB:2PB1 PDB:2PBO PDB:2PC8 PDB:2PF0 PDB:3N9K PDB:3O6A PDBsum:1CZ1 PDBsum:1EQC PDBsum:1EQP PDBsum:2PB1 PDBsum:2PBO PDBsum:2PC8 PDBsum:2PF0 PDBsum:3N9K PDBsum:3O6A ProteinModelPortal:P29717 SMR:P29717 STRING:P29717 GeneID:3636837 KEGG:cal:CaO19.2990 PhylomeDB:P29717 PMAP-CutDB:P29717 Uniprot:P29717
Root	Isotig07784	2	20	-3.451	2.08E-05	UNIPROTKB|P29717 - symbol:XOG1 "Glucan 1,3-beta-glucosidase" species:237561 "Candida albicans SC5314" [GO:0004338 "glucan exo-1,3-beta-glucosidase activity" evidence=IMP;IDA] [GO:0005576 "extracellular region" evidence=IDA] [GO:0006073 "cellular glucan metabolic process" evidence=IMP] [GO:0009986 "cell surface" evidence=IDA] [GO:0031505 "fungal-type cell wall organization" evidence=IMP] [GO:0031589 "cell-substrate adhesion" evidence=IDA] [GO:0050839 "cell adhesion molecule binding" evidence=IDA] InterPro:IPR001547 InterPro:IPR013781 InterPro:IPR018087 Pfam:PF00150 PROSITE:PS00659 GO:GO:0005576 EMBL:AACQ01000015 GO:GO:0009986 GO:GO:0043169 InterPro:IPR017853 Gene3D:G3DSA:3.20.20.80 SUPFAM:SSF51445 CAZy:GH5 GO:GO:0031505 GO:GO:0050839 GO:GO:0031589 EMBL:AL033497 KO:K01210 GO:GO:0004338 eggNOG:COG2730 GO:GO:0006073 EMBL:X56556 PIR:A47702 PIR:T52149

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						RefSeq:XP_721488.1 PDB:1CZ1 PDB:1EQC PDB:1EQP PDB:2PB1 PDB:2PBO PDB:2PC8 PDB:2PF0 PDB:3N9K PDB:3O6A PDBsum:1CZ1 PDBsum:1EQC PDBsum:1EQP PDBsum:2PB1 PDBsum:2PBO PDBsum:2PC8 PDBsum:2PF0 PDBsum:3N9K PDBsum:3O6A ProteinModelPortal:P29717 SMR:P29717 STRING:P29717 GeneID:3636837 KEGG:cal:CaO19.2990 PhylomeDB:P29717 PMAP-CutDB:P29717 Uniprot:P29717
Root	Isotig07789	2	21	-3.521	1.10E-05	TAIR|locus:2200980 - symbol:PDH-E1 ALPHA "AT1G01090" species:3702 "Arabidopsis thaliana" [GO:0004739 "pyruvate dehydrogenase (acetyl-transferring) activity" evidence=ISS] [GO:0006096 "glycolysis" evidence=IEA] [GO:0008152 "metabolic process" evidence=IEA;ISS] [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] [GO:0009536 "plastid" evidence=ISS] InterPro:IPR001017 InterPro:IPR017597 Pfam:PF00676 EMBL:CP002684 GO:GO:0009570 GO:GO:0009941 GO:GO:0006096 GO:GO:0004739 eggNOG:COG1071 KO:K00161 TIGRFAMs:TIGR03182 HSSP:P08559 EMBL:U80185 EMBL:AY052721 EMBL:AY063724 EMBL:AK226909 IPI:IPI00525582 RefSeq:NP_171617.1 UniGene:At.20069 ProteinModelPortal:O24457 IntAct:O24457 STRING:O24457 PRIDE:O24457 ProMEX:O24457 EnsemblPlants:AT1G01090.1 GeneID:839429 KEGG:ath:AT1G01090 TAIR:At1g01090 InParanoid:O24457 OMA:SKEHHLL PhylomeDB:O24457 ProtClustDB:PLN02374 Genevestigator:O24457 Uniprot:O24457
Root	Isotig07790	2	21	-3.521	1.10E-05	TAIR|locus:2200980 - symbol:PDH-E1 ALPHA "AT1G01090" species:3702 "Arabidopsis thaliana" [GO:0004739 "pyruvate dehydrogenase (acetyl-transferring) activity" evidence=ISS] [GO:0006096 "glycolysis" evidence=IEA] [GO:0008152 "metabolic process" evidence=IEA;ISS] [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] [GO:0009536 "plastid" evidence=ISS] InterPro:IPR001017 InterPro:IPR017597 Pfam:PF00676 EMBL:CP002684 GO:GO:0009570 GO:GO:0009941 GO:GO:0006096 GO:GO:0004739 eggNOG:COG1071 KO:K00161 TIGRFAMs:TIGR03182 HSSP:P08559 EMBL:U80185 EMBL:AY052721 EMBL:AY063724 EMBL:AK226909 IPI:IPI00525582 RefSeq:NP_171617.1 UniGene:At.20069 ProteinModelPortal:O24457 IntAct:O24457 STRING:O24457 PRIDE:O24457 ProMEX:O24457 EnsemblPlants:AT1G01090.1 GeneID:839429 KEGG:ath:AT1G01090 TAIR:At1g01090 InParanoid:O24457 OMA:SKEHHLL PhylomeDB:O24457 ProtClustDB:PLN02374 Genevestigator:O24457 Uniprot:O24457
Root	Isotig07811	1	28	-4.936	2.57E-08	TAIR|locus:2082837 - symbol:CYSC1 "AT3G61440" species:3702 "Arabidopsis thaliana" [GO:0004124 "cysteine synthase activity" evidence=ISS;IDA;IMP] [GO:0019344 "cysteine biosynthetic process" evidence=ISS;IDA] [GO:0019499 "cyanide metabolic process" evidence=TAS] [GO:0050017 "L-3-cyanoalanine synthase activity" evidence=IDA] [GO:0051410 "detoxification of nitrogen compound" evidence=TAS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0019500 "cyanide catabolic process" evidence=IMP] [GO:0080147 "root hair cell development" evidence=IMP] InterPro:IPR001216 InterPro:IPR001926 InterPro:IPR005856 InterPro:IPR005859 Pfam:PF00291 PROSITE:PS00901 GO:GO:0005739 GO:GO:0009507 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0030170 EMBL:AL132962 SUPFAM:SSF53686 GO:GO:0016740 GO:GO:0005507 GO:GO:0080147 HOGENOM:HBG748215 GO:GO:0006535 GO:GO:0004124 TIGRFAMs:TIGR01139 TIGRFAMs:TIGR01136 GO:GO:0051410 HSSP:Q9WZD3 EMBL:AY093094 EMBL:AY087208 EMBL:AY128782 EMBL:AB024282 EMBL:AK226606 EMBL:AJ010505 IPI:IPI00534676 PIR:T47936 RefSeq:NP_191703.1 UniGene:At.21833 ProteinModelPortal:Q9S757 SMR:Q9S757 IntAct:Q9S757 STRING:Q9S757 PRIDE:Q9S757 ProMEX:Q9S757 EnsemblPlants:AT3G61440.1 GeneID:825317 KEGG:ath:AT3G61440 TAIR:At3g61440 InParanoid:Q9S757 KO:K13034 OMA:MERDGKG PhylomeDB:Q9S757 ProtClustDB:PLN02556 BRENDA:4.4.1.9 ArrayExpress:Q9S757 Genevestigator:Q9S757 GO:GO:0050017 GO:GO:0019500 Uniprot:Q9S757
Root	Isotig07812	1	37	-5.338	1.07E-10	TAIR|locus:2082837 - symbol:CYSC1 "AT3G61440" species:3702 "Arabidopsis thaliana" [GO:0004124 "cysteine synthase activity" evidence=ISS;IDA;IMP] [GO:0019344 "cysteine biosynthetic process" evidence=ISS;IDA] [GO:0019499 "cyanide metabolic process" evidence=TAS] [GO:0050017 "L-3-cyanoalanine synthase activity" evidence=IDA] [GO:0051410 "detoxification of nitrogen compound" evidence=TAS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0019500 "cyanide catabolic process" evidence=IMP] [GO:0080147 "root hair cell development" evidence=IMP] InterPro:IPR001216 InterPro:IPR001926 InterPro:IPR005856 InterPro:IPR005859 Pfam:PF00291 PROSITE:PS00901 GO:GO:0005739 GO:GO:0009507 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0030170 EMBL:AL132962 SUPFAM:SSF53686 GO:GO:0016740 GO:GO:0005507 GO:GO:0080147 HOGENOM:HBG748215 GO:GO:0006535 GO:GO:0004124 TIGRFAMs:TIGR01139 TIGRFAMs:TIGR01136

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0051410 HSSP:Q9WZD3 EMBL:AY093094 EMBL:AY087208 EMBL:AY128782 EMBL:AB024282 EMBL:AK226606 EMBL:AJ010505 IPI:IPI00534676 PIR:T47936 RefSeq:NP_191703.1 UniGene:At.21833 ProteinModelPortal:Q9S757 SMR:Q9S757 IntAct:Q9S757 STRING:Q9S757 PRIDE:Q9S757 ProMEX:Q9S757 EnsemblPlants:AT3G61440.1 GeneID:825317 KEGG:ath:AT3G61440 TAIR:At3g61440 InParanoid:Q9S757 KO:K13034 OMA:MERDGKG PhylomeDB:Q9S757 ProtClustDB:PLN02556 BRENDA:4.4.1.9 ArrayExpress:Q9S757 Genevestigator:Q9S757 GO:GO:0050017 GO:GO:0019500 Uniprot:Q9S757
Root	Isotig07813	1	18	-4.299	1.41E-05	TAIR|locus:2115065 - symbol:PLP4 "AT4G37050" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0045735 "nutrient reservoir activity" evidence=ISS] [GO:0004620 "phospholipase activity" evidence=IDA] [GO:0009737 "response to abscisic acid stimulus" evidence=IDA] InterPro:IPR002641 InterPro:IPR016035 Pfam:PF01734 GO:GO:0009737 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0006629 EMBL:Z99707 EMBL:AL161590 UniGene:At.4646 SUPFAM:SSF52151 GO:GO:0004620 eggNOG:COG3621 HSSP:Q8LPW4 HOGENOM:HBG581721 IPI:IPI00546583 PIR:F85437 RefSeq:NP_195422.3 UniGene:At.48948 ProteinModelPortal:O23181 SMR:O23181 PRIDE:O23181 EnsemblPlants:AT4G37050.1 GeneID:829859 KEGG:ath:AT4G37050 TAIR:At4g37050 InParanoid:O23181 PhylomeDB:O23181 ProtClustDB:CLSN2914016 Genevestigator:O23181 Uniprot:O23181
Root	Isotig07814	1	18	-4.299	1.41E-05	TAIR|locus:2115065 - symbol:PLP4 "AT4G37050" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0045735 "nutrient reservoir activity" evidence=ISS] [GO:0004620 "phospholipase activity" evidence=IDA] [GO:0009737 "response to abscisic acid stimulus" evidence=IDA] InterPro:IPR002641 InterPro:IPR016035 Pfam:PF01734 GO:GO:0009737 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0006629 EMBL:Z99707 EMBL:AL161590 UniGene:At.4646 SUPFAM:SSF52151 GO:GO:0004620 eggNOG:COG3621 HSSP:Q8LPW4 HOGENOM:HBG581721 IPI:IPI00546583 PIR:F85437 RefSeq:NP_195422.3 UniGene:At.48948 ProteinModelPortal:O23181 SMR:O23181 PRIDE:O23181 EnsemblPlants:AT4G37050.1 GeneID:829859 KEGG:ath:AT4G37050 TAIR:At4g37050 InParanoid:O23181 PhylomeDB:O23181 ProtClustDB:CLSN2914016 Genevestigator:O23181 Uniprot:O23181
Root	Isotig07827	6	25	-2.188	0.000173532	TAIR|locus:2135932 - symbol:VEP1 "AT4G24220" species:3702 "Arabidopsis thaliana" [GO:0009611 "response to wounding" evidence=IEP] [GO:0010051 "xylem and phloem pattern formation" evidence=IMP] [GO:0008202 "steroid metabolic process" evidence=IDA] [GO:0035671 "enone reductase activity" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR016040 GO:GO:0005829 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0009611 GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 GO:GO:0008202 EMBL:AL078637 EMBL:AL161561 UniGene:At.32364 UniGene:At.71005 GO:GO:0010051 GO:GO:0035671 HOGENOM:HBG353845 ProtClustDB:CLSN2685402 EMBL:AY062451 EMBL:AY087323 EMBL:BT008479 EMBL:EF579963 IPI:IPI00524911 PIR:T09885 RefSeq:NP_194153.1 ProteinModelPortal:Q9STX2 SMR:Q9STX2 PRIDE:Q9STX2 EnsemblPlants:AT4G24220.1 GeneID:828523 KEGG:ath:AT4G24220 TAIR:At4g24220 InParanoid:Q9STX2 OMA:GLKHYLG PhylomeDB:Q9STX2 ArrayExpress:Q9STX2 Genevestigator:Q9STX2 Uniprot:Q9STX2
Root	Isotig07828	6	25	-2.188	0.000173532	TAIR|locus:2135932 - symbol:VEP1 "AT4G24220" species:3702 "Arabidopsis thaliana" [GO:0009611 "response to wounding" evidence=IEP] [GO:0010051 "xylem and phloem pattern formation" evidence=IMP] [GO:0008202 "steroid metabolic process" evidence=IDA] [GO:0035671 "enone reductase activity" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR016040 GO:GO:0005829 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0009611 GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 GO:GO:0008202 EMBL:AL078637 EMBL:AL161561 UniGene:At.32364 UniGene:At.71005 GO:GO:0010051 GO:GO:0035671 HOGENOM:HBG353845 ProtClustDB:CLSN2685402 EMBL:AY062451 EMBL:AY087323 EMBL:BT008479 EMBL:EF579963 IPI:IPI00524911 PIR:T09885 RefSeq:NP_194153.1 ProteinModelPortal:Q9STX2 SMR:Q9STX2 PRIDE:Q9STX2 EnsemblPlants:AT4G24220.1 GeneID:828523 KEGG:ath:AT4G24220 TAIR:At4g24220 InParanoid:Q9STX2 OMA:GLKHYLG PhylomeDB:Q9STX2 ArrayExpress:Q9STX2 Genevestigator:Q9STX2 Uniprot:Q9STX2
Root	Isotig07831	3	20	-2.866	9.17E-05	TAIR|locus:2167659 - symbol:ERF9 "AT5G44210" species:3702 "Arabidopsis thaliana" [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS;TAS] [GO:0003677 "DNA binding" evidence=TAS] [GO:0045892 "negative regulation of transcription, DNA-dependent" evidence=TAS] [GO:0016020 "membrane" evidence=IDA] [GO:0009873 "ethylene mediated signaling pathway" evidence=TAS] InterPro:IPR001471 InterPro:IPR016177 Pfam:PF00847 PRINTS:PR00367 PROSITE:PS51032 SMART:SM00380 GO:GO:0005634 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0006952 GO:GO:0009873 GO:GO:0016020 GO:GO:0003677 GO:GO:0003700 GO:GO:0006351 EMBL:AB005239 KO:K09286 Gene3D:G3DSA:3.30.730.10 SUPFAM:SSF54171 HOGENOM:HBG744062 EMBL:AB047648 EMBL:AY560856 EMBL:BT015876

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EMBL:BT020188 IPI:IPI00535860 RefSeq:NP_199234.1 UniGene:At.30087 ProteinModelPortal:Q9FE67 SMR:Q9FE67 IntAct:Q9FE67 STRING:Q9FE67 EnsemblPlants:AT5G44210.1 GeneID:834444 KEGG:ath:AT5G44210 TAIR:At5g44210 eggNOG:NOG249494 InParanoid:Q9FE67 OMA:FACHRER PhylomeDB:Q9FE67 ProtClustDB:CLSN2916712 ArrayExpress:Q9FE67 Genevestigator:Q9FE67 GermOnline:AT5G44210 Uniprot:Q9FE67
Root	Isotig07832	3	18	-2.714	0.000308932	TAIR|locus:2167659 - symbol:ERF9 "AT5G44210" species:3702 "Arabidopsis thaliana" [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS;TAS] [GO:0003677 "DNA binding" evidence=TAS] [GO:0045892 "negative regulation of transcription, DNA-dependent" evidence=TAS] [GO:0016020 "membrane" evidence=IDA] [GO:0009873 "ethylene mediated signaling pathway" evidence=TAS] InterPro:IPR001471 InterPro:IPR016177 Pfam:PF00847 PRINTS:PR00367 PROSITE:PS51032 SMART:SM00380 GO:GO:0005634 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0006952 GO:GO:0009873 GO:GO:0016020 GO:GO:0003677 GO:GO:0003700 GO:GO:0006351 EMBL:AB005239 KO:K09286 Gene3D:G3DSA:3.30.730.10 SUPFAM:SSF54171 HOGENOM:HBG744062 EMBL:AB047648 EMBL:AY560856 EMBL:BT015876 EMBL:BT020188 IPI:IPI00535860 RefSeq:NP_199234.1 UniGene:At.30087 ProteinModelPortal:Q9FE67 SMR:Q9FE67 IntAct:Q9FE67 STRING:Q9FE67 EnsemblPlants:AT5G44210.1 GeneID:834444 KEGG:ath:AT5G44210 TAIR:At5g44210 eggNOG:NOG249494 InParanoid:Q9FE67 OMA:FACHRER PhylomeDB:Q9FE67 ProtClustDB:CLSN2916712 ArrayExpress:Q9FE67 Genevestigator:Q9FE67 GermOnline:AT5G44210 Uniprot:Q9FE67
Root	Isotig07859	6	24	-2.129	0.00029855	TAIR|locus:2134971 - symbol:AT4G24050 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0008152 "metabolic process" evidence=IEA] [GO:0016491 "oxidoreductase activity" evidence=IEA;ISS] [GO:0055114 "oxidation-reduction process" evidence=IEA] InterPro:IPR002198 InterPro:IPR016040 Pfam:PF00106 InterPro:IPR002347 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 GO:GO:0016491 eggNOG:COG1028 HOGENOM:HBG750976 PRINTS:PR00081 EMBL:AC002343 EMBL:AL161560 EMBL:AL109619 OMA:TELARNW EMBL:AF439829 EMBL:AY125561 IPI:IPI00517204 PIR:T13447 RefSeq:NP_194136.1 UniGene:At.3661 ProteinModelPortal:O22985 IntAct:O22985 PRIDE:O22985 ProMEX:O22985 EnsemblPlants:AT4G24050.1 GeneID:828505 KEGG:ath:AT4G24050 TAIR:At4g24050 InParanoid:O22985 PhylomeDB:O22985 ProtClustDB:CLSN2679319 ArrayExpress:O22985 Genevestigator:O22985 Uniprot:O22985
Root	Isotig07861	0	34	-6.216	6.02E-10	TAIR|locus:2119642 - symbol:SPHK1 "AT4G21540" species:3702 "Arabidopsis thaliana" [GO:0004143 "diacylglycerol kinase activity" evidence=ISS] [GO:0007205 "activation of protein kinase C activity by G-protein coupled receptor protein signaling pathway" evidence=ISS] [GO:0005773 "vacuole" evidence=IDA] [GO:0017050 "D-erythro-sphingosine kinase activity" evidence=IDA;TAS] [GO:0008481 "sphinganine kinase activity" evidence=IDA] [GO:0009737 "response to abscisic acid stimulus" evidence=IMP] [GO:0009845 "seed germination" evidence=IMP] [GO:0009705 "plant-type vacuole membrane" evidence=IDA] InterPro:IPR001206 Pfam:PF00781 PROSITE:PS50146 SMART:SM00046 GO:GO:0009737 GO:GO:0007205 GO:GO:0009845 GO:GO:0009705 eggNOG:COG1597 GO:GO:0004143 EMBL:AL161555 EMBL:AL022603 GO:GO:0017050 GO:GO:0008481 IPI:IPI01020462 PIR:T05162 ProteinModelPortal:O65419 STRING:O65419 InParanoid:O65419 PhylomeDB:O65419 Genevestigator:O65419 Uniprot:O65419
Root	Isotig07862	0	34	-6.216	6.02E-10	TAIR|locus:2119642 - symbol:SPHK1 "AT4G21540" species:3702 "Arabidopsis thaliana" [GO:0004143 "diacylglycerol kinase activity" evidence=ISS] [GO:0007205 "activation of protein kinase C activity by G-protein coupled receptor protein signaling pathway" evidence=ISS] [GO:0005773 "vacuole" evidence=IDA] [GO:0017050 "D-erythro-sphingosine kinase activity" evidence=IDA;TAS] [GO:0008481 "sphinganine kinase activity" evidence=IDA] [GO:0009737 "response to abscisic acid stimulus" evidence=IMP] [GO:0009845 "seed germination" evidence=IMP] [GO:0009705 "plant-type vacuole membrane" evidence=IDA] InterPro:IPR001206 Pfam:PF00781 PROSITE:PS50146 SMART:SM00046 GO:GO:0009737 GO:GO:0007205 GO:GO:0009845 GO:GO:0009705 eggNOG:COG1597 GO:GO:0004143 EMBL:AL161555 EMBL:AL022603 GO:GO:0017050 GO:GO:0008481 IPI:IPI01020462 PIR:T05162 ProteinModelPortal:O65419 STRING:O65419 InParanoid:O65419 PhylomeDB:O65419 Genevestigator:O65419 Uniprot:O65419
Root	Isotig07871	0	18	-5.299	6.77E-06	TAIR|locus:2183730 - symbol:AT5G10770 "AT5G10770" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=ISS] [GO:0004190 "aspartic-type endopeptidase activity" evidence=IEA] [GO:0006508 "proteolysis" evidence=IEA] InterPro:IPR001461 InterPro:IPR009007 Pfam:PF00026 PRINTS:PR00792 EMBL:CP002688 GO:GO:0006508 GO:GO:0004190 InterPro:IPR021109 SUPFAM:SSF50630

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						Gene3D:G3DSA:2.40.70.10 PANTHER:PTHR13683 HSSP:P00799 EMBL:AY075656 EMBL:BT001004 IPI:IPI00543783 RefSeq:NP_196638.2 UniGene:At.32336 ProteinModelPortal:Q8S9J6 MEROPS:A01.A15 PRIDE:Q8S9J6 EnsemblPlants:AT5G10770.1 GeneID:830944 KEGG:ath:AT5G10770 TAIR:At5g10770 InParanoid:Q8S9J6 OMA:LEVVYDG PhylomeDB:Q8S9J6 ProtClustDB:CLSN2686424 Genevestigator:Q8S9J6 Uniprot:Q8S9J6
Root	Isotig07881	0	18	-5.299	6.77E-06	UNIPROTKB|B2HIN2 - symbol:fadD26 "Long-chain-fatty-acid--AMP ligase FadD26" species:216594 "Mycobacterium marinum M" [GO:0008610 "lipid biosynthetic process" evidence=ISS] InterPro:IPR000873 Pfam:PF00501 eggNOG:COG0318 HOGENOM:HBG547964 GO:GO:0016874 GO:GO:0008610 GO:GO:0006631 KO:K12426 OMA:PARWIQQ ProtClustDB:PRK05850 EMBL:CP000854 RefSeq:YP_001850081.1 ProteinModelPortal:B2HIN2 STRING:B2HIN2 EnsemblBacteria:EBMYCT00000032275 GeneID:6226036 GenomeReviews:CP000854_GR KEGG:mmi:MMAR_1777 PATRIC:18064429 Uniprot:B2HIN2
Root	Isotig07883	2	52	-4.829	3.94E-14	TAIR|locus:2130329 - symbol:AT4G16260 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=IEA;ISS] [GO:0043169 "cation binding" evidence=IEA] [GO:0005618 "cell wall" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0009817 "defense response to fungus, incompatible interaction" evidence=IDA] InterPro:IPR000490 InterPro:IPR013781 Pfam:PF00332 PROSITE:PS00587 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005774 GO:GO:0005618 GO:GO:0043169 InterPro:IPR017853 Gene3D:G3DSA:3.20.20.80 SUPFAM:SSF51445 GO:GO:0005975 GO:GO:0004553 GO:GO:0009651 GO:GO:0009817 CAZy:GH17 HSSP:P15737 EMBL:AY064130 EMBL:AY143867 IPI:IPI00944240 RefSeq:NP_193361.4 UniGene:At.22570 ProteinModelPortal:Q8VZJ2 SMR:Q8VZJ2 PRIDE:Q8VZJ2 EnsemblPlants:AT4G16260.1 GeneID:827320 KEGG:ath:AT4G16260 TAIR:At4g16260 PhylomeDB:Q8VZJ2 ProtClustDB:CLSN2927419 Genevestigator:Q8VZJ2 Uniprot:Q8VZJ2
Root	Isotig07884	1	44	-5.588	1.69E-12	TAIR|locus:2130329 - symbol:AT4G16260 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=IEA;ISS] [GO:0043169 "cation binding" evidence=IEA] [GO:0005618 "cell wall" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0009817 "defense response to fungus, incompatible interaction" evidence=IDA] InterPro:IPR000490 InterPro:IPR013781 Pfam:PF00332 PROSITE:PS00587 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005774 GO:GO:0005618 GO:GO:0043169 InterPro:IPR017853 Gene3D:G3DSA:3.20.20.80 SUPFAM:SSF51445 GO:GO:0005975 GO:GO:0004553 GO:GO:0009651 GO:GO:0009817 CAZy:GH17 HSSP:P15737 EMBL:AY064130 EMBL:AY143867 IPI:IPI00944240 RefSeq:NP_193361.4 UniGene:At.22570 ProteinModelPortal:Q8VZJ2 SMR:Q8VZJ2 PRIDE:Q8VZJ2 EnsemblPlants:AT4G16260.1 GeneID:827320 KEGG:ath:AT4G16260 TAIR:At4g16260 PhylomeDB:Q8VZJ2 ProtClustDB:CLSN2927419 Genevestigator:Q8VZJ2 Uniprot:Q8VZJ2
Root	Isotig07885	11	33	-1.714	0.000243809	TAIR|locus:2046485 - symbol:ATP3 "gamma subunit of Mt ATP synthase" species:3702 "Arabidopsis thaliana" [GO:0015986 "ATP synthesis coupled proton transport" evidence=IEA;ISS] [GO:0015992 "proton transport" evidence=ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0005753 "mitochondrial proton-transporting ATP synthase complex" evidence=IDA] [GO:0008270 "zinc ion binding" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR000131 Pfam:PF00231 PRINTS:PR00126 GO:GO:0005618 GO:GO:0009507 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0005730 GO:GO:0008270 EMBL:AC003033 GO:GO:0046933 GO:GO:0046961 GO:GO:0015986 eggNOG:COG0224 HOGENOM:HBG586593 ProtClustDB:CLSN2679503 InterPro:IPR023632 InterPro:IPR023633 PANTHER:PTHR11693 SUPFAM:SSF52943 TIGRFAMs:TIGR01146 PROSITE:PS00153 EMBL:D88374 EMBL:AC002334 EMBL:AY039513 EMBL:AY062627 EMBL:AY102152 EMBL:AY086685 IPI:IPI00526529 PIR:F84740 PIR:T01103 RefSeq:NP_180863.1 UniGene:At.25073 ProteinModelPortal:Q96250 SMR:Q96250 IntAct:Q96250 STRING:Q96250 PRIDE:Q96250 EnsemblPlants:AT2G33040.1 GeneID:817866 KEGG:ath:AT2G33040 GeneFarm:3313 TAIR:At2g33040 InParanoid:Q96250 KO:K02136 OMA:SARRNAM PhylomeDB:Q96250 Genevestigator:Q96250 GermOnline:AT2G33040 Uniprot:Q96250
Root	Isotig07886	11	33	-1.714	0.000243809	TAIR|locus:2046485 - symbol:ATP3 "gamma subunit of Mt ATP synthase" species:3702 "Arabidopsis thaliana" [GO:0015986 "ATP synthesis coupled proton transport" evidence=IEA;ISS] [GO:0015992 "proton transport" evidence=ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0005739 "mitochondrion" evidence=IDA]

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						[GO:0009507 "chloroplast" evidence=IDA] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0005753 "mitochondrial proton-transporting ATP synthase complex" evidence=IDA] [GO:0008270 "zinc ion binding" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR000131 Pfam:PF00231 PRINTS:PR00126 GO:GO:0005618 GO:GO:0009507 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0005730 GO:GO:0008270 EMBL:AC003033 GO:GO:0046933 GO:GO:0046961 GO:GO:0015986 eggNOG:COG0224 HOGENOM:HBG586593 ProtClustDB:CLSN2679503 InterPro:IPR023632 InterPro:IPR023633 PANTHER:PTHR11693 SUPFAM:SSF52943 TIGRFAMs:TIGR01146 PROSITE:PS00153 EMBL:D88374 EMBL:AC002334 EMBL:AY039513 EMBL:AY062627 EMBL:AY102152 EMBL:AY086685 IPI:IPI00526529 PIR:F84740 PIR:T01103 RefSeq:NP_180863.1 UniGene:At.25073 ProteinModelPortal:Q96250 SMR:Q96250 IntAct:Q96250 STRING:Q96250 PRIDE:Q96250 EnsemblPlants:AT2G33040.1 GeneID:817866 KEGG:ath:AT2G33040 GeneFarm:3313 TAIR:At2g33040 InParanoid:Q96250 KO:K02136 OMA:SARRNAM PhylomeDB:Q96250 Genevestigator:Q96250 GermOnline:AT2G33040 Uniprot:Q96250
Root	Isotig07893	0	21	-5.521	1.09E-06	RGD|727924 - symbol:LOC257642 "rRNA promoter binding protein" species:10116 "Rattus norvegicus" [GO:0003690 "double-stranded DNA binding" evidence=IDA] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=IDA] [GO:0008134 "transcription factor binding" evidence=IDA] [GO:0008283 "cell proliferation" evidence=IDA] [GO:0009303 "rRNA transcription" evidence=IDA] RGD:727924 GO:GO:0008134 GO:GO:0008283 GO:GO:0003700 GO:GO:0003690 GO:GO:0009303 EMBL:U77931 IPI:IPI00195015 RefSeq:NP_671477.1 GeneID:257642 KEGG:rno:257642 NextBio:624170 Genevestigator:Q99JC0 Uniprot:Q99JC0
Root	Isotig07894	0	16	-5.129	2.34E-05	RGD|727924 - symbol:LOC257642 "rRNA promoter binding protein" species:10116 "Rattus norvegicus" [GO:0003690 "double-stranded DNA binding" evidence=IDA] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=IDA] [GO:0008134 "transcription factor binding" evidence=IDA] [GO:0008283 "cell proliferation" evidence=IDA] [GO:0009303 "rRNA transcription" evidence=IDA] RGD:727924 GO:GO:0008134 GO:GO:0008283 GO:GO:0003700 GO:GO:0003690 GO:GO:0009303 EMBL:U77931 IPI:IPI00195015 RefSeq:NP_671477.1 GeneID:257642 KEGG:rno:257642 NextBio:624170 Genevestigator:Q99JC0 Uniprot:Q99JC0
Root	Isotig07897	0	37	-6.338	1.15E-10	TAIR|locus:2135212 - symbol:GGT1 "AT4G39640" species:3702 "Arabidopsis thaliana" [GO:0003840 "gamma-glutamyltransferase activity" evidence=ISS] [GO:0006751 "glutathione catabolic process" evidence=IDA] [GO:0006979 "response to oxidative stress" evidence=IDA] [GO:0016756 "glutathione gamma-glutamylcysteinyltransferase activity" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009505 "plant-type cell wall" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000101 Pfam:PF01019 PRINTS:PR01210 GO:GO:0009506 EMBL:CP002687 GO:GO:0048046 GO:GO:0006979 GO:GO:0009505 GO:GO:0006751 KO:K00681 GO:GO:0003840 PANTHER:PTHR11686 TIGRFAMs:TIGR00066 GO:GO:0016756 ProtClustDB:PLN02198 EMBL:AY069872 EMBL:BT000495 IPI:IPI00546319 RefSeq:NP_195674.2 RefSeq:NP_974717.1 UniGene:At.21562 ProteinModelPortal:Q8VYW6 SMR:Q8VYW6 STRING:Q8VYW6 MEROPS:T03.008 PRIDE:Q8VYW6 EnsemblPlants:AT4G39640.1 EnsemblPlants:AT4G39640.2 GeneID:830118 KEGG:ath:AT4G39640 TAIR:At4g39640 InParanoid:Q8VYW6 OMA:ANTYQTI PhylomeDB:Q8VYW6 Genevestigator:Q8VYW6 Uniprot:Q8VYW6
Root	Isotig07898	0	21	-5.521	1.09E-06	TAIR|locus:2135212 - symbol:GGT1 "AT4G39640" species:3702 "Arabidopsis thaliana" [GO:0003840 "gamma-glutamyltransferase activity" evidence=ISS] [GO:0006751 "glutathione catabolic process" evidence=IDA] [GO:0006979 "response to oxidative stress" evidence=IDA] [GO:0016756 "glutathione gamma-glutamylcysteinyltransferase activity" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009505 "plant-type cell wall" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000101 Pfam:PF01019 PRINTS:PR01210 GO:GO:0009506 EMBL:CP002687 GO:GO:0048046 GO:GO:0006979 GO:GO:0009505 GO:GO:0006751 KO:K00681 GO:GO:0003840 PANTHER:PTHR11686 TIGRFAMs:TIGR00066 GO:GO:0016756 ProtClustDB:PLN02198 EMBL:AY069872 EMBL:BT000495 IPI:IPI00546319 RefSeq:NP_195674.2 RefSeq:NP_974717.1 UniGene:At.21562 ProteinModelPortal:Q8VYW6 SMR:Q8VYW6 STRING:Q8VYW6 MEROPS:T03.008 PRIDE:Q8VYW6 EnsemblPlants:AT4G39640.1 EnsemblPlants:AT4G39640.2 GeneID:830118 KEGG:ath:AT4G39640 TAIR:At4g39640 InParanoid:Q8VYW6 OMA:ANTYQTI PhylomeDB:Q8VYW6 Genevestigator:Q8VYW6 Uniprot:Q8VYW6
Root	Isotig07923	2	29	-3.987	6.83E-08	TAIR|locus:2151739 - symbol:GSR 1 "glutamine synthase clone R1" species:3702 "Arabidopsis thaliana" [GO:0004356 "glutamate-ammonia ligase activity" evidence=ISS;IDA;IPI] [GO:0005829 "cytosol" evidence=TAS] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0042128 "nitrate

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						assimilation" evidence=TAS] [GO:0005515 "protein binding" evidence=IPI] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR008146 InterPro:IPR008147 InterPro:IPR014746 Pfam:PF00120 Pfam:PF03951 PROSITE:PS00180 PROSITE:PS00181 GO:GO:0005886 GO:GO:0009506 GO:GO:0005524 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005618 GO:GO:0005515 GO:GO:0005507 GO:GO:0022626 GO:GO:0042128 GO:GO:0009399 EMBL:AB018107 EMBL:AF419608 EMBL:AF428386 EMBL:AY079113 EMBL:BT000753 EMBL:AK222005 IPI:IPI00519748 PIR:S18601 RefSeq:NP_198576.1 UniGene:At.7003 ProteinModelPortal:Q56WN1 SMR:Q56WN1 IntAct:Q56WN1 STRING:Q56WN1 PRIDE:Q56WN1 EnsemblPlants:AT5G37600.1 GeneID:833738 KEGG:ath:AT5G37600 TAIR:At5g37600 eggNOG:COG0174 HOGENOM:HBG299709 InParanoid:Q56WN1 KO:K01915 OMA:DPYRVTS PhylomeDB:Q56WN1 ProtClustDB:PLN02284 BRENDA:6.3.1.2 ArrayExpress:Q9FHR0 Genevestigator:Q56WN1 GermOnline:AT5G37600 GO:GO:0004356 GO:GO:0006542 Gene3D:G3DSA:3.30.590.10 Gene3D:G3DSA:3.10.20.70 SUPFAM:SSF54368 Uniprot:Q56WN1
Root	Isotig07924	2	29	-3.987	6.83E-08	TAIR|locus:2151739 - symbol:GSR 1 "glutamine synthase clone R1" species:3702 "Arabidopsis thaliana" [GO:0004356 "glutamate-ammonia ligase activity" evidence=ISS;IDA;IPI] [GO:0005829 "cytosol" evidence=TAS] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0042128 "nitrate assimilation" evidence=TAS] [GO:0005515 "protein binding" evidence=IPI] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR008146 InterPro:IPR008147 InterPro:IPR014746 Pfam:PF00120 Pfam:PF03951 PROSITE:PS00180 PROSITE:PS00181 GO:GO:0005886 GO:GO:0009506 GO:GO:0005524 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005618 GO:GO:0005515 GO:GO:0005507 GO:GO:0022626 GO:GO:0042128 GO:GO:0009399 EMBL:AB018107 EMBL:AF419608 EMBL:AF428386 EMBL:AY079113 EMBL:BT000753 EMBL:AK222005 IPI:IPI00519748 PIR:S18601 RefSeq:NP_198576.1 UniGene:At.7003 ProteinModelPortal:Q56WN1 SMR:Q56WN1 IntAct:Q56WN1 STRING:Q56WN1 PRIDE:Q56WN1 EnsemblPlants:AT5G37600.1 GeneID:833738 KEGG:ath:AT5G37600 TAIR:At5g37600 eggNOG:COG0174 HOGENOM:HBG299709 InParanoid:Q56WN1 KO:K01915 OMA:DPYRVTS PhylomeDB:Q56WN1 ProtClustDB:PLN02284 BRENDA:6.3.1.2 ArrayExpress:Q9FHR0 Genevestigator:Q56WN1 GermOnline:AT5G37600 GO:GO:0004356 GO:GO:0006542 Gene3D:G3DSA:3.30.590.10 Gene3D:G3DSA:3.10.20.70 SUPFAM:SSF54368 Uniprot:Q56WN1
Root	Isotig07925	0	42	-6.521	7.61E-12	TAIR|locus:2101135 - symbol:BT2 "AT3G48360" species:3702 "Arabidopsis thaliana" [GO:0006355 "regulation of transcription, DNA-dependent" evidence=TAS] [GO:0005515 "protein binding" evidence=IPI] [GO:0005516 "calmodulin binding" evidence=IDA] [GO:0009611 "response to wounding" evidence=IEP] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] [GO:0009751 "response to salicylic acid stimulus" evidence=IEP] [GO:0042542 "response to hydrogen peroxide" evidence=IEP] [GO:0009734 "auxin mediated signaling pathway" evidence=IMP] [GO:0051973 "positive regulation of telomerase activity" evidence=IGI;IPI] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0009553 "embryo sac development" evidence=IGI] [GO:0009555 "pollen development" evidence=IGI] [GO:0009733 "response to auxin stimulus" evidence=IEP] [GO:0007623 "circadian rhythm" evidence=IEP] [GO:0009409 "response to cold" evidence=IEP] [GO:0009738 "abscisic acid mediated signaling pathway" evidence=IMP] [GO:0009743 "response to carbohydrate stimulus" evidence=IEP] [GO:0009753 "response to jasmonic acid stimulus" evidence=IEP] [GO:0010167 "response to nitrate" evidence=IEP] [GO:0010182 "sugar mediated signaling pathway" evidence=IMP] [GO:0080134 "regulation of response to stress" evidence=IMP] InterPro:IPR000197 InterPro:IPR000210 InterPro:IPR013069 Pfam:PF00651 Pfam:PF02135 PROSITE:PS50097 PROSITE:PS50134 SMART:SM00225 GO:GO:0005634 GO:GO:0005737 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0009753 GO:GO:0009611 GO:GO:0009738 GO:GO:0009734 GO:GO:0006355 GO:GO:0007623 GO:GO:0008270 GO:GO:0009409 GO:GO:0009651 GO:GO:0005516 GO:GO:0009555 GO:GO:0009751 GO:GO:0010182 InterPro:IPR011333 Gene3D:G3DSA:3.30.710.10 SUPFAM:SSF54695 GO:GO:0051973 GO:GO:0042542 GO:GO:0009553 GO:GO:0003712 GO:GO:0010167 KO:K00517 eggNOG:NOG287613 ProtClustDB:CLSN2687065 GO:GO:0004402 Gene3D:G3DSA:1.20.1020.10 SUPFAM:SSF57933 EMBL:AY316675 EMBL:AL049659 EMBL:AY040015 EMBL:AY079408 EMBL:BT000678 EMBL:AK226596 IPI:IPI00536189 PIR:T06706 RefSeq:NP_566902.1 UniGene:At.21922 UniGene:At.67255 ProteinModelPortal:Q94BN0 SMR:Q94BN0 IntAct:Q94BN0 STRING:Q94BN0 PRIDE:Q94BN0

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EnsemblPlants:AT3G48360.1 GeneID:823994 KEGG:ath:AT3G48360 TAIR:At3g48360 InParanoid:Q94BN0 OMA:RMWQLLR PhylomeDB:Q94BN0 Genevestigator:Q94BN0 GO:GO:0080134 Uniprot:Q94BN0
Root	Isotig07926	0	39	-6.414	3.85E-11	TAIR|locus:2101135 - symbol:BT2 "AT3G48360" species:3702 "Arabidopsis thaliana" [GO:0006355 "regulation of transcription, DNA-dependent" evidence=TAS] [GO:0005515 "protein binding" evidence=IPI] [GO:0005516 "calmodulin binding" evidence=IDA] [GO:0009611 "response to wounding" evidence=IEP] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] [GO:0009751 "response to salicylic acid stimulus" evidence=IEP] [GO:0042542 "response to hydrogen peroxide" evidence=IEP] [GO:0009734 "auxin mediated signaling pathway" evidence=IMP] [GO:0051973 "positive regulation of telomerase activity" evidence=IGI;IPI] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0009553 "embryo sac development" evidence=IGI] [GO:0009555 "pollen development" evidence=IGI] [GO:0009733 "response to auxin stimulus" evidence=IEP] [GO:0007623 "circadian rhythm" evidence=IEP] [GO:0009409 "response to cold" evidence=IEP] [GO:0009738 "abscisic acid mediated signaling pathway" evidence=IMP] [GO:0009743 "response to carbohydrate stimulus" evidence=IEP] [GO:0009753 "response to jasmonic acid stimulus" evidence=IEP] [GO:0010167 "response to nitrate" evidence=IEP] [GO:0010182 "sugar mediated signaling pathway" evidence=IMP] [GO:0080134 "regulation of response to stress" evidence=IMP] InterPro:IPR000197 InterPro:IPR000210 InterPro:IPR013069 Pfam:PF00651 Pfam:PF02135 PROSITE:PS50097 PROSITE:PS50134 SMART:SM00225 GO:GO:0005634 GO:GO:0005737 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0009753 GO:GO:0009611 GO:GO:0009738 GO:GO:0009734 GO:GO:0006355 GO:GO:0007623 GO:GO:0008270 GO:GO:0009409 GO:GO:0009651 GO:GO:0005516 GO:GO:0009555 GO:GO:0009751 GO:GO:0010182 InterPro:IPR011333 Gene3D:G3DSA:3.30.710.10 SUPFAM:SSF54695 GO:GO:0051973 GO:GO:0042542 GO:GO:0009553 GO:GO:0003712 GO:GO:0010167 KO:K00517 eggNOG:NOG287613 ProtClustDB:CLSN2687065 GO:GO:0004402 Gene3D:G3DSA:1.20.1020.10 SUPFAM:SSF57933 EMBL:AY316675 EMBL:AL049659 EMBL:AY040015 EMBL:AY079408 EMBL:BT000678 EMBL:AK226596 IPI:IPI00536189 PIR:T06706 RefSeq:NP_566902.1 UniGene:At.21922 UniGene:At.67255 ProteinModelPortal:Q94BN0 SMR:Q94BN0 IntAct:Q94BN0 STRING:Q94BN0 PRIDE:Q94BN0 EnsemblPlants:AT3G48360.1 GeneID:823994 KEGG:ath:AT3G48360 TAIR:At3g48360 InParanoid:Q94BN0 OMA:RMWQLLR PhylomeDB:Q94BN0 Genevestigator:Q94BN0 GO:GO:0080134 Uniprot:Q94BN0
Root	Isotig07929	0	21	-5.521	1.09E-06	No hit
Root	Isotig07930	0	21	-5.521	1.09E-06	No hit
Root	Isotig07947	17	1	3.958	8.09E-05	TAIR|locus:2144905 - symbol:AT5G18780 "AT5G18780" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] InterPro:IPR001810 Pfam:PF00646 PROSITE:PS50181 SMART:SM00256 EMBL:CP002688 GenomeReviews:BA000015_GR SUPFAM:SSF81383 InterPro:IPR006566 SMART:SM00579 EMBL:AC068655 HOGENOM:HBG316570 Pfam:PF08387 EMBL:AK221350 EMBL:AK230408 IPI:IPI00527938 RefSeq:NP_001190332.1 RefSeq:NP_197379.1 UniGene:At.31380 UniGene:At.54909 ProteinModelPortal:Q56YH2 SMR:Q56YH2 STRING:Q56YH2 GeneID:831996 KEGG:ath:AT5G18780 TAIR:At5g18780 eggNOG:NOG253687 InParanoid:Q56YH2 PhylomeDB:Q56YH2 Genevestigator:Q56YH2 Uniprot:Q56YH2
Root	Isotig07963	0	23	-5.653	3.32E-07	No hit
Root	Isotig07964	0	22	-5.588	6.01E-07	No hit
Root	Isotig07971	46	7	2.587	7.68E-08	TAIR|locus:2100449 - symbol:ALDH10A9 "AT3G48170" species:3702 "Arabidopsis thaliana" [GO:0004028 "3-chloroallyl aldehyde dehydrogenase activity" evidence=ISS] [GO:0005777 "peroxisome" evidence=IDA] [GO:0004029 "aldehyde dehydrogenase (NAD) activity" evidence=IDA] [GO:0008802 "betaine-aldehyde dehydrogenase activity" evidence=IDA] [GO:0009414 "response to water deprivation" evidence=IEP] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] [GO:0055114 "oxidation-reduction process" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] InterPro:IPR015590 InterPro:IPR016160 InterPro:IPR016161 InterPro:IPR016162 InterPro:IPR016163 Pfam:PF00171 PROSITE:PS00070 PROSITE:PS00687 GO:GO:0005739 GO:GO:0009737 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005777 eggNOG:COG1012 Gene3D:G3DSA:3.40.309.10 Gene3D:G3DSA:3.40.605.10 SUPFAM:SSF53720 HOGENOM:HBG752218 GO:GO:0009414 HSSP:P05091 GO:GO:0008802 EMBL:AL096856 KO:K00130 ProtClustDB:PLN02467 EMBL:AF370333 EMBL:AY062987 EMBL:Z29888 IPI:IPI00545825 PIR:T13006 RefSeq:NP_190400.1 UniGene:At.1613 ProteinModelPortal:Q9STS1 SMR:Q9STS1 STRING:Q9STS1 PRIDE:Q9STS1 EnsemblPlants:AT3G48170.1 GeneID:823972 KEGG:ath:AT3G48170 TAIR:At3g48170 InParanoid:Q9STS1

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						OMA:MEIWREE PhylomeDB:Q9STS1 BioCyc:MetaCyc:AT3G48170-MONOMER ArrayExpress:Q9STS1 Genevestigator:Q9STS1 GermOnline:AT3G48170 Uniprot:Q9STS1
Root	Isotig07997	3	56	-4.351	1.56E-14	TAIR|locus:2119251 - symbol:AT4G33420 species:3702 "Arabidopsis thaliana" [GO:0004601 "peroxidase activity" evidence=IEA;ISS] [GO:0006979 "response to oxidative stress" evidence=IEA] [GO:0020037 "heme binding" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] InterPro:IPR000823 InterPro:IPR002016 InterPro:IPR010255 InterPro:IPR019793 InterPro:IPR019794 Pfam:PF00141 PRINTS:PR00458 PRINTS:PR00461 PROSITE:PS00435 PROSITE:PS00436 PROSITE:PS50873 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005576 GO:GO:0006979 EMBL:AL161583 EMBL:AL035678 GO:GO:0020037 GO:GO:0004601 HOGENOM:HBG597790 SUPFAM:SSF48113 KO:K00430 EMBL:AF451951 EMBL:BT044614 IPI:IPI00539387 PIR:T05993 RefSeq:NP_567919.1 UniGene:At.28650 ProteinModelPortal:Q9SZB9 SMR:Q9SZB9 STRING:Q9SZB9 PeroxiBase:213 PRIDE:Q9SZB9 EnsemblPlants:AT4G33420.1 GeneID:829479 KEGG:ath:AT4G33420 GeneFarm:1879 TAIR:At4g33420 eggNOG:NOG276365 InParanoid:Q9SZB9 ProtClustDB:CLSN2689733 Genevestigator:Q9SZB9 GermOnline:AT4G33420 Uniprot:Q9SZB9
Root	Isotig07998	5	64	-3.807	2.88E-15	TAIR|locus:2119251 - symbol:AT4G33420 species:3702 "Arabidopsis thaliana" [GO:0004601 "peroxidase activity" evidence=IEA;ISS] [GO:0006979 "response to oxidative stress" evidence=IEA] [GO:0020037 "heme binding" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] InterPro:IPR000823 InterPro:IPR002016 InterPro:IPR010255 InterPro:IPR019793 InterPro:IPR019794 Pfam:PF00141 PRINTS:PR00458 PRINTS:PR00461 PROSITE:PS00435 PROSITE:PS00436 PROSITE:PS50873 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005576 GO:GO:0006979 EMBL:AL161583 EMBL:AL035678 GO:GO:0020037 GO:GO:0004601 HOGENOM:HBG597790 SUPFAM:SSF48113 KO:K00430 EMBL:AF451951 EMBL:BT044614 IPI:IPI00539387 PIR:T05993 RefSeq:NP_567919.1 UniGene:At.28650 ProteinModelPortal:Q9SZB9 SMR:Q9SZB9 STRING:Q9SZB9 PeroxiBase:213 PRIDE:Q9SZB9 EnsemblPlants:AT4G33420.1 GeneID:829479 KEGG:ath:AT4G33420 GeneFarm:1879 TAIR:At4g33420 eggNOG:NOG276365 InParanoid:Q9SZB9 ProtClustDB:CLSN2689733 Genevestigator:Q9SZB9 GermOnline:AT4G33420 Uniprot:Q9SZB9
Root	Isotig07999	6	52	-3.244	2.28E-11	TAIR|locus:2013001 - symbol:AT1G71695 species:3702 "Arabidopsis thaliana" [GO:0004601 "peroxidase activity" evidence=IEA;ISS] [GO:0006979 "response to oxidative stress" evidence=IEA] [GO:0020037 "heme binding" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0009505 "plant-type cell wall" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000823 InterPro:IPR002016 InterPro:IPR010255 InterPro:IPR019793 InterPro:IPR019794 Pfam:PF00141 PRINTS:PR00458 PRINTS:PR00461 PROSITE:PS00435 PROSITE:PS00436 PROSITE:PS50873 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009506 GO:GO:0005773 GO:GO:0005576 GO:GO:0016020 GO:GO:0020037 GO:GO:0009505 EMBL:AC012654 EMBL:AC016163 GO:GO:0004601 GO:GO:0042744 HOGENOM:HBG597790 SUPFAM:SSF48113 KO:K00430 EMBL:X98318 EMBL:X98773 EMBL:AF334732 EMBL:BT000715 EMBL:AY087964 IPI:IPI00538176 PIR:A96739 RefSeq:NP_177313.1 UniGene:At.67041 UniGene:At.94 ProteinModelPortal:Q96520 SMR:Q96520 STRING:Q96520 PeroxiBase:93 PRIDE:Q96520 EnsemblPlants:AT1G71695.1 GeneID:843498 KEGG:ath:AT1G71695 GeneFarm:1474 TAIR:At1g71695 eggNOG:NOG252730 InParanoid:Q96520 OMA:NCSARNT PhylomeDB:Q96520 ProtClustDB:CLSN2679267 ArrayExpress:Q96520 Genevestigator:Q96520 GermOnline:AT1G71695 Uniprot:Q96520
Root	Isotig08000	8	39	-2.414	6.49E-07	TAIR|locus:2013001 - symbol:AT1G71695 species:3702 "Arabidopsis thaliana" [GO:0004601 "peroxidase activity" evidence=IEA;ISS] [GO:0006979 "response to oxidative stress" evidence=IEA] [GO:0020037 "heme binding" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0009505 "plant-type cell wall" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000823 InterPro:IPR002016 InterPro:IPR010255 InterPro:IPR019793 InterPro:IPR019794 Pfam:PF00141 PRINTS:PR00458 PRINTS:PR00461 PROSITE:PS00435 PROSITE:PS00436 PROSITE:PS50873 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009506 GO:GO:0005773 GO:GO:0005576 GO:GO:0016020 GO:GO:0020037 GO:GO:0009505 EMBL:AC012654 EMBL:AC016163 GO:GO:0004601 GO:GO:0042744 HOGENOM:HBG597790 SUPFAM:SSF48113 KO:K00430 EMBL:X98318 EMBL:X98773 EMBL:AF334732 EMBL:BT000715 EMBL:AY087964 IPI:IPI00538176 PIR:A96739 RefSeq:NP_177313.1 UniGene:At.67041 UniGene:At.94 ProteinModelPortal:Q96520 SMR:Q96520 STRING:Q96520 PeroxiBase:93 PRIDE:Q96520 EnsemblPlants:AT1G71695.1 GeneID:843498 KEGG:ath:AT1G71695 GeneFarm:1474 TAIR:At1g71695

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						eggNOG:NOG252730 InParanoid:Q96520 OMA:NCSARNT PhylomeDB:Q96520 ProtClustDB:CLSN2679267 ArrayExpress:Q96520 Genevestigator:Q96520 GermOnline:AT1G71695 Uniprot:Q96520
Root	Isotig08003	2	14	-2.936	0.000925454	TAIR|locus:2130005 - symbol:AT4G14620 "AT4G14620" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002687 InterPro:IPR006502 Pfam:PF04720 TIGRFAMs:TIGR01615 EMBL:AY133694 IPI:IPI00536806 RefSeq:NP_193198.2 UniGene:At.33259 PRIDE:Q8L7H9 EnsemblPlants:AT4G14620.1 GeneID:827112 KEGG:ath:AT4G14620 TAIR:At4g14620 InParanoid:Q8L7H9 OMA:EENNDKQ PhylomeDB:Q8L7H9 ProtClustDB:CLSN2918097 Genevestigator:Q8L7H9 Uniprot:Q8L7H9
Root	Isotig08004	2	14	-2.936	0.000925454	TAIR|locus:2084593 - symbol:AT3G22970 "AT3G22970" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002686 EMBL:AP001300 InterPro:IPR006502 Pfam:PF04720 TIGRFAMs:TIGR01615 EMBL:BT024897 IPI:IPI00544999 RefSeq:NP_188937.1 UniGene:At.43562 UniGene:At.71498 UniGene:At.72007 PRIDE:Q9LIJ8 EnsemblPlants:AT3G22970.1 GeneID:821871 KEGG:ath:AT3G22970 TAIR:At3g22970 InParanoid:Q9LIJ8 OMA:VIIGEER PhylomeDB:Q9LIJ8 ProtClustDB:CLSN2913460 Genevestigator:Q9LIJ8 Uniprot:Q9LIJ8
Root	Isotig08005	15	45	-1.714	1.83E-05	TAIR|locus:2183254 - symbol:AT5G19760 "AT5G19760" species:3702 "Arabidopsis thaliana" [GO:0005743 "mitochondrial inner membrane" evidence=ISS] [GO:0006810 "transport" evidence=ISS] [GO:0006839 "mitochondrial transport" evidence=ISS] [GO:0017077 "oxidative phosphorylation uncoupler activity" evidence=ISS] [GO:0005310 "dicarboxylic acid transmembrane transporter activity" evidence=IDA] [GO:0006835 "dicarboxylic acid transport" evidence=IDA] [GO:0015142 "tricarboxylic acid transmembrane transporter activity" evidence=IDA] [GO:0035674 "tricarboxylic acid transmembrane transport" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR002067 PRINTS:PR00926 Pfam:PF00153 GO:GO:0016021 GO:GO:0009506 GO:GO:0005774 EMBL:CP002688 GO:GO:0005618 GO:GO:0005488 GO:GO:0005743 GO:GO:0009941 InterPro:IPR018108 InterPro:IPR023395 Gene3D:G3DSA:1.50.40.10 SUPFAM:SSF103506 PROSITE:PS50920 GO:GO:0005310 KO:K15104 UniGene:At.24504 EMBL:AF360153 EMBL:AY056307 EMBL:AY085901 EMBL:AK226470 EMBL:AJ311780 IPI:IPI00545483 RefSeq:NP_197477.1 UniGene:At.24857 UniGene:At.49038 ProteinModelPortal:Q9C5M0 SMR:Q9C5M0 STRING:Q9C5M0 PRIDE:Q9C5M0 ProMEX:Q9C5M0 DNASU:832096 EnsemblPlants:AT5G19760.1 GeneID:832096 KEGG:ath:AT5G19760 TAIR:At5g19760 InParanoid:Q9C5M0 OMA:LRQAVYT PhylomeDB:Q9C5M0 ProtClustDB:CLSN2687170 ArrayExpress:Q9C5M0 Genevestigator:Q9C5M0 GO:GO:0015142 Uniprot:Q9C5M0
Root	Isotig08006	16	44	-1.588	6.01E-05	TAIR|locus:2183254 - symbol:AT5G19760 "AT5G19760" species:3702 "Arabidopsis thaliana" [GO:0005743 "mitochondrial inner membrane" evidence=ISS] [GO:0006810 "transport" evidence=ISS] [GO:0006839 "mitochondrial transport" evidence=ISS] [GO:0017077 "oxidative phosphorylation uncoupler activity" evidence=ISS] [GO:0005310 "dicarboxylic acid transmembrane transporter activity" evidence=IDA] [GO:0006835 "dicarboxylic acid transport" evidence=IDA] [GO:0015142 "tricarboxylic acid transmembrane transporter activity" evidence=IDA] [GO:0035674 "tricarboxylic acid transmembrane transport" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR002067 PRINTS:PR00926 Pfam:PF00153 GO:GO:0016021 GO:GO:0009506 GO:GO:0005774 EMBL:CP002688 GO:GO:0005618 GO:GO:0005488 GO:GO:0005743 GO:GO:0009941 InterPro:IPR018108 InterPro:IPR023395 Gene3D:G3DSA:1.50.40.10 SUPFAM:SSF103506 PROSITE:PS50920 GO:GO:0005310 KO:K15104 UniGene:At.24504 EMBL:AF360153 EMBL:AY056307 EMBL:AY085901 EMBL:AK226470 EMBL:AJ311780 IPI:IPI00545483 RefSeq:NP_197477.1 UniGene:At.24857 UniGene:At.49038 ProteinModelPortal:Q9C5M0 SMR:Q9C5M0 STRING:Q9C5M0 PRIDE:Q9C5M0 ProMEX:Q9C5M0 DNASU:832096 EnsemblPlants:AT5G19760.1 GeneID:832096 KEGG:ath:AT5G19760 TAIR:At5g19760 InParanoid:Q9C5M0 OMA:LRQAVYT PhylomeDB:Q9C5M0 ProtClustDB:CLSN2687170 ArrayExpress:Q9C5M0 Genevestigator:Q9C5M0 GO:GO:0015142 Uniprot:Q9C5M0
Root	Isotig08009	1	14	-3.936	0.000188601	TAIR|locus:2076591 - symbol:AT3G57790 species:3702 "Arabidopsis thaliana" [GO:0004650 "polygalacturonase activity" evidence=IEA;ISS] [GO:0005975 "carbohydrate metabolic process" evidence=IEA;ISS] [GO:0005774

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						"vacuolar membrane" evidence=IDA] InterPro:IPR000743 Pfam:PF00295 GO:GO:0005774 GO:GO:0005576 GO:GO:0005975 GO:GO:0004650 InterPro:IPR006626 InterPro:IPR012334 InterPro:IPR011050 Gene3D:G3DSA:2.160.20.10 SMART:SM00710 SUPFAM:SSF51126 GO:GO:0007047 EMBL:AL049660 InterPro:IPR019329 Pfam:PF10183 IPI:IPI00532018 PIR:T06741 ProteinModelPortal:Q9SVZ3 SMR:Q9SVZ3 STRING:Q9SVZ3 PRIDE:Q9SVZ3 TAIR:At3g57790 InParanoid:Q9SVZ3 PhylomeDB:Q9SVZ3 Genevestigator:Q9SVZ3 Uniprot:Q9SVZ3
Root	Isotig08010	1	13	-3.829	0.000362856	TAIR|locus:2076591 - symbol:AT3G57790 species:3702 "Arabidopsis thaliana" [GO:0004650 "polygalacturonase activity" evidence=IEA;ISS] [GO:0005975 "carbohydrate metabolic process" evidence=IEA;ISS] [GO:0005774 "vacuolar membrane" evidence=IDA] InterPro:IPR000743 Pfam:PF00295 GO:GO:0005774 GO:GO:0005576 GO:GO:0005975 GO:GO:0004650 InterPro:IPR006626 InterPro:IPR012334 InterPro:IPR011050 Gene3D:G3DSA:2.160.20.10 SMART:SM00710 SUPFAM:SSF51126 GO:GO:0007047 EMBL:AL049660 InterPro:IPR019329 Pfam:PF10183 IPI:IPI00532018 PIR:T06741 ProteinModelPortal:Q9SVZ3 SMR:Q9SVZ3 STRING:Q9SVZ3 PRIDE:Q9SVZ3 TAIR:At3g57790 InParanoid:Q9SVZ3 PhylomeDB:Q9SVZ3 Genevestigator:Q9SVZ3 Uniprot:Q9SVZ3
Root	Isotig08021	0	52	-6.829	3.96E-14	TAIR|locus:2168912 - symbol:AAP6 "AT5G49630" species:3702 "Arabidopsis thaliana" [GO:0015171 "amino acid transmembrane transporter activity" evidence=ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0015172 "acidic amino acid transmembrane transporter activity" evidence=IDA] [GO:0015175 "neutral amino acid transmembrane transporter activity" evidence=IDA] [GO:0015810 "aspartate transport" evidence=IDA] [GO:0015827 "tryptophan transport" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] GO:GO:0016021 GO:GO:0005886 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0015175 GO:GO:0015827 GO:GO:0015293 InterPro:IPR013057 Pfam:PF01490 HOGENOM:HBG319901 GO:GO:0015172 EMBL:X95736 EMBL:AB025627 EMBL:AK229102 IPI:IPI00517925 PIR:T50691 RefSeq:NP_199774.1 UniGene:At.163 ProteinModelPortal:P92934 TCDB:2.A.18.2.4 EnsemblPlants:AT5G49630.1 GeneID:835025 KEGG:ath:AT5G49630 TAIR:At5g49630 eggNOG:NOG265519 InParanoid:P92934 OMA:FAYAYST PhylomeDB:P92934 ProtClustDB:CLSN2686986 GO:GO:0015810 Uniprot:P92934
Root	Isotig08022	0	50	-6.773	1.11E-13	TAIR|locus:2168912 - symbol:AAP6 "AT5G49630" species:3702 "Arabidopsis thaliana" [GO:0015171 "amino acid transmembrane transporter activity" evidence=ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0015172 "acidic amino acid transmembrane transporter activity" evidence=IDA] [GO:0015175 "neutral amino acid transmembrane transporter activity" evidence=IDA] [GO:0015810 "aspartate transport" evidence=IDA] [GO:0015827 "tryptophan transport" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] GO:GO:0016021 GO:GO:0005886 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0015175 GO:GO:0015827 GO:GO:0015293 InterPro:IPR013057 Pfam:PF01490 HOGENOM:HBG319901 GO:GO:0015172 EMBL:X95736 EMBL:AB025627 EMBL:AK229102 IPI:IPI00517925 PIR:T50691 RefSeq:NP_199774.1 UniGene:At.163 ProteinModelPortal:P92934 TCDB:2.A.18.2.4 EnsemblPlants:AT5G49630.1 GeneID:835025 KEGG:ath:AT5G49630 TAIR:At5g49630 eggNOG:NOG265519 InParanoid:P92934 OMA:FAYAYST PhylomeDB:P92934 ProtClustDB:CLSN2686986 GO:GO:0015810 Uniprot:P92934
Root	Isotig08041	23	5	2.073	0.000873448	TAIR|locus:2092339 - symbol:ERF7 "AT3G20310" species:3702 "Arabidopsis thaliana" [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS;TAS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=TAS] [GO:0003677 "DNA binding" evidence=TAS] [GO:0005634 "nucleus" evidence=IC;IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0009414 "response to water deprivation" evidence=IMP] [GO:0009737 "response to abscisic acid stimulus" evidence=IMP] [GO:0043565 "sequence-specific DNA binding" evidence=IDA] [GO:0045892 "negative regulation of transcription, DNA-dependent" evidence=IDA] [GO:0009873 "ethylene mediated signaling pathway" evidence=TAS] InterPro:IPR001471 InterPro:IPR016177 Pfam:PF00847 PRINTS:PR00367 PROSITE:PS51032 SMART:SM00380 GO:GO:0009737 GO:GO:0005634 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0045892 GO:GO:0005515 GO:GO:0006952 GO:GO:0009873 GO:GO:0043565 GO:GO:0003700 GO:GO:0006351 GO:GO:0009414 KO:K09286 Gene3D:G3DSA:3.30.730.10 SUPFAM:SSF54171 EMBL:AB024036 HOGENOM:HBG744062 ProtClustDB:CLSN2682907 EMBL:AB032201 EMBL:AY037254 EMBL:AY094001 EMBL:AY085023 EMBL:AK228460 IPI:IPI00537654 RefSeq:NP_188666.1 UniGene:At.20161 ProteinModelPortal:Q9LDE4 SMR:Q9LDE4 IntAct:Q9LDE4 STRING:Q9LDE4 PRIDE:Q9LDE4 EnsemblPlants:AT3G20310.1 GeneID:821575 KEGG:ath:AT3G20310 TAIR:At3g20310 eggNOG:NOG322216 InParanoid:Q9LDE4 OMA:VAPEDCH PhylomeDB:Q9LDE4 ArrayExpress:Q9LDE4 Genevestigator:Q9LDE4 GermOnline:AT3G20310 Uniprot:Q9LDE4

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig08043	1	58	-5.987	5.40E-16	TAIR|locus:2202007 - symbol:AT1G12230 "AT1G12230" species:3702 "Arabidopsis thaliana" [GO:0004801 "sedoheptulose-7-phosphate:D-glyceraldehyde-3-phosphate glyceronetransferase activity" evidence=ISS] [GO:0005975 "carbohydrate metabolic process" evidence=IEA] [GO:0008152 "metabolic process" evidence=IEA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0008270 "zinc ion binding" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] InterPro:IPR001585 InterPro:IPR013785 Pfam:PF00923 EMBL:CP002684 GO:GO:0009570 Gene3D:G3DSA:3.20.20.70 GO:GO:0003824 GO:GO:0005975 GO:GO:0008270 GO:GO:0009941 EMBL:AC022522 PANTHER:PTHR10683 KO:K00616 EMBL:BT002036 EMBL:BT008487 IPI:IPI00518291 PIR:D86257 RefSeq:NP_563900.1 UniGene:At.16219 HSSP:P30148 ProteinModelPortal:Q9FWX0 SMR:Q9FWX0 STRING:Q9FWX0 PRIDE:Q9FWX0 EnsemblPlants:AT1G12230.1 GeneID:837776 KEGG:ath:AT1G12230 TAIR:At1g12230 InParanoid:Q9FWX0 OMA:DWHKAKT PhylomeDB:Q9FWX0 ProtClustDB:CLSN2687776 ArrayExpress:Q9FWX0 Genevestigator:Q9FWX0 Uniprot:Q9FWX0
Root	Isotig08044	1	56	-5.936	1.67E-15	TAIR|locus:2202007 - symbol:AT1G12230 "AT1G12230" species:3702 "Arabidopsis thaliana" [GO:0004801 "sedoheptulose-7-phosphate:D-glyceraldehyde-3-phosphate glyceronetransferase activity" evidence=ISS] [GO:0005975 "carbohydrate metabolic process" evidence=IEA] [GO:0008152 "metabolic process" evidence=IEA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0008270 "zinc ion binding" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] InterPro:IPR001585 InterPro:IPR013785 Pfam:PF00923 EMBL:CP002684 GO:GO:0009570 Gene3D:G3DSA:3.20.20.70 GO:GO:0003824 GO:GO:0005975 GO:GO:0008270 GO:GO:0009941 EMBL:AC022522 PANTHER:PTHR10683 KO:K00616 EMBL:BT002036 EMBL:BT008487 IPI:IPI00518291 PIR:D86257 RefSeq:NP_563900.1 UniGene:At.16219 HSSP:P30148 ProteinModelPortal:Q9FWX0 SMR:Q9FWX0 STRING:Q9FWX0 PRIDE:Q9FWX0 EnsemblPlants:AT1G12230.1 GeneID:837776 KEGG:ath:AT1G12230 TAIR:At1g12230 InParanoid:Q9FWX0 OMA:DWHKAKT PhylomeDB:Q9FWX0 ProtClustDB:CLSN2687776 ArrayExpress:Q9FWX0 Genevestigator:Q9FWX0 Uniprot:Q9FWX0
Root	Isotig08069	1	24	-4.714	3.11E-07	TAIR|locus:2167225 - symbol:PSY "AT5G17230" species:3702 "Arabidopsis thaliana" [GO:0016117 "carotenoid biosynthetic process" evidence=IMP] [GO:0016767 "geranylgeranyl-diphosphate geranylgeranyltransferase activity" evidence=ISS;TAS] [GO:0046905 "phytoene synthase activity" evidence=TAS] [GO:0009507 "chloroplast" evidence=IDA] InterPro:IPR002060 InterPro:IPR019845 Pfam:PF00494 PROSITE:PS01044 PROSITE:PS01045 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009507 InterPro:IPR008949 Gene3D:G3DSA:1.10.600.10 SUPFAM:SSF48576 EMBL:AB005238 eggNOG:COG1562 GO:GO:0016767 GO:GO:0046905 EMBL:L25812 EMBL:AF009954 EMBL:BT000450 EMBL:BT002084 EMBL:AY085565 IPI:IPI00527204 RefSeq:NP_001031895.1 RefSeq:NP_197225.1 UniGene:At.23726 ProteinModelPortal:P37271 SMR:P37271 STRING:P37271 PRIDE:P37271 EnsemblPlants:AT5G17230.1 EnsemblPlants:AT5G17230.2 GeneID:831587 KEGG:ath:AT5G17230 TAIR:At5g17230 HOGENOM:HBG693191 InParanoid:P37271 KO:K02291 OMA:ELKLYCY PhylomeDB:P37271 ProtClustDB:PLN02632 BioCyc:ARA:AT5G17230-MONOMER BioCyc:MetaCyc:AT5G17230-MONOMER ArrayExpress:P37271 Genevestigator:P37271 GermOnline:AT5G17230 Uniprot:P37271
Root	Isotig08070	1	20	-4.451	3.92E-06	TAIR|locus:2167225 - symbol:PSY "AT5G17230" species:3702 "Arabidopsis thaliana" [GO:0016117 "carotenoid biosynthetic process" evidence=IMP] [GO:0016767 "geranylgeranyl-diphosphate geranylgeranyltransferase activity" evidence=ISS;TAS] [GO:0046905 "phytoene synthase activity" evidence=TAS] [GO:0009507 "chloroplast" evidence=IDA] InterPro:IPR002060 InterPro:IPR019845 Pfam:PF00494 PROSITE:PS01044 PROSITE:PS01045 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009507 InterPro:IPR008949 Gene3D:G3DSA:1.10.600.10 SUPFAM:SSF48576 EMBL:AB005238 eggNOG:COG1562 GO:GO:0016767 GO:GO:0046905 EMBL:L25812 EMBL:AF009954 EMBL:BT000450 EMBL:BT002084 EMBL:AY085565 IPI:IPI00527204 RefSeq:NP_001031895.1 RefSeq:NP_197225.1 UniGene:At.23726 ProteinModelPortal:P37271 SMR:P37271 STRING:P37271 PRIDE:P37271 EnsemblPlants:AT5G17230.1 EnsemblPlants:AT5G17230.2 GeneID:831587 KEGG:ath:AT5G17230 TAIR:At5g17230 HOGENOM:HBG693191 InParanoid:P37271 KO:K02291 OMA:ELKLYCY PhylomeDB:P37271 ProtClustDB:PLN02632 BioCyc:ARA:AT5G17230-MONOMER BioCyc:MetaCyc:AT5G17230-MONOMER ArrayExpress:P37271 Genevestigator:P37271 GermOnline:AT5G17230 Uniprot:P37271
Root	Isotig08075	43	121	-1.622	1.44E-11	TAIR|locus:2177386 - symbol:GRF3 "AT5G38480" species:3702 "Arabidopsis thaliana" [GO:0045309 "protein phosphorylated amino acid binding" evidence=TAS] [GO:0005773 "vacuole" evidence=IDA] [GO:0005618 "cell wall"

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						evidence=IDA] [GO:0005524 "ATP binding" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR000308 PIRSF:PIRSF000868 PRINTS:PR00305 eggNOG:COG5040 HOGENOM:HBG611720 GO:GO:0005829 GO:GO:0005739 GO:GO:0005886 GO:GO:0009506 GO:GO:0005524 GO:GO:0019904 InterPro:IPR023409 InterPro:IPR023410 Gene3D:G3DSA:1.20.190.20 PANTHER:PTHR18860 Pfam:PF00244 SMART:SM00101 SUPFAM:SSF48445 PROSITE:PS00796 PROSITE:PS00797 GO:GO:0005773 KO:K06630 EMBL:L09110 EMBL:X74140 EMBL:U09375 EMBL:AB005231 EMBL:AB005248 EMBL:CP002688 EMBL:AF412093 EMBL:AY093976 EMBL:AK226217 EMBL:AK228478 IPI:IPI00538115 PIR:S47969 PIR:S57277 RefSeq:NP_568557.1 UniGene:At.22344 UniGene:At.22949 ProteinModelPortal:P42644 SMR:P42644 IntAct:P42644 STRING:P42644 PRIDE:P42644 EnsemblPlants:AT5G38480.1 GeneID:833836 GenomeReviews:BA000015_GR KEGG:ath:AT5G38480 TAIR:At5g38480 InParanoid:P42644 OMA:KESALIM PhylomeDB:P42644 ProtClustDB:CLSN2689896 ArrayExpress:P42644 Genevestigator:P42644 GO:GO:0005618 GO:GO:0009507 Uniprot:P42644
Root	Isotig08076	43	120	-1.610	2.23E-11	TAIR|locus:2177386 - symbol:GRF3 "AT5G38480" species:3702 "Arabidopsis thaliana" [GO:0045309 "protein phosphorylated amino acid binding" evidence=TAS] [GO:0005773 "vacuole" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0005524 "ATP binding" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR000308 PIRSF:PIRSF000868 PRINTS:PR00305 eggNOG:COG5040 HOGENOM:HBG611720 GO:GO:0005829 GO:GO:0005739 GO:GO:0005886 GO:GO:0009506 GO:GO:0005524 GO:GO:0019904 InterPro:IPR023409 InterPro:IPR023410 Gene3D:G3DSA:1.20.190.20 PANTHER:PTHR18860 Pfam:PF00244 SMART:SM00101 SUPFAM:SSF48445 PROSITE:PS00796 PROSITE:PS00797 GO:GO:0005773 KO:K06630 EMBL:L09110 EMBL:X74140 EMBL:U09375 EMBL:AB005231 EMBL:AB005248 EMBL:CP002688 EMBL:AF412093 EMBL:AY093976 EMBL:AK226217 EMBL:AK228478 IPI:IPI00538115 PIR:S47969 PIR:S57277 RefSeq:NP_568557.1 UniGene:At.22344 UniGene:At.22949 ProteinModelPortal:P42644 SMR:P42644 IntAct:P42644 STRING:P42644 PRIDE:P42644 EnsemblPlants:AT5G38480.1 GeneID:833836 GenomeReviews:BA000015_GR KEGG:ath:AT5G38480 TAIR:At5g38480 InParanoid:P42644 OMA:KESALIM PhylomeDB:P42644 ProtClustDB:CLSN2689896 ArrayExpress:P42644 Genevestigator:P42644 GO:GO:0005618 GO:GO:0009507 Uniprot:P42644
Root	Isotig08091	21	46	-1.260	0.000570291	TAIR|locus:2075236 - symbol:MYB48 "AT3G46130" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=ISS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=ISS;TAS] [GO:0009751 "response to salicylic acid stimulus" evidence=IEP] [GO:0005634 "nucleus" evidence=IDA] InterPro:IPR001005 InterPro:IPR009057 Pfam:PF00249 SMART:SM00717 GO:GO:0005634 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0006355 GO:GO:0003677 GO:GO:0006351 GO:GO:0009751 Gene3D:G3DSA:1.10.10.60 SUPFAM:SSF46689 InterPro:IPR017930 PROSITE:PS51294 eggNOG:COG5147 InterPro:IPR015495 PANTHER:PTHR10641 EMBL:AL355775 HOGENOM:HBG750380 EMBL:AF272733 EMBL:AY519594 EMBL:DQ075255 EMBL:DQ075256 EMBL:DQ075257 EMBL:AK176475 IPI:IPI00528378 IPI:IPI00656574 IPI:IPI00759334 IPI:IPI00759367 PIR:T49254 RefSeq:NP_001030816.1 RefSeq:NP_001078249.1 RefSeq:NP_190199.1 UniGene:At.1475 UniGene:At.72744 ProteinModelPortal:Q9LX82 SMR:Q9LX82 STRING:Q9LX82 EnsemblPlants:AT3G46130.1 GeneID:823756 KEGG:ath:AT3G46130 GeneFarm:1132 TAIR:At3g46130 InParanoid:Q9LX82 OMA:REIDHSA PhylomeDB:Q9LX82 ProtClustDB:CLSN2684805 Genevestigator:Q9LX82 GermOnline:AT3G46130 Uniprot:Q9LX82
Root	Isotig08092	21	46	-1.260	0.000570291	TAIR|locus:2075236 - symbol:MYB48 "AT3G46130" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=ISS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=ISS;TAS] [GO:0009751 "response to salicylic acid stimulus" evidence=IEP] [GO:0005634 "nucleus" evidence=IDA] InterPro:IPR001005 InterPro:IPR009057 Pfam:PF00249 SMART:SM00717 GO:GO:0005634 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0006355 GO:GO:0003677 GO:GO:0006351 GO:GO:0009751 Gene3D:G3DSA:1.10.10.60 SUPFAM:SSF46689 InterPro:IPR017930 PROSITE:PS51294 eggNOG:COG5147 InterPro:IPR015495 PANTHER:PTHR10641 EMBL:AL355775 HOGENOM:HBG750380 EMBL:AF272733 EMBL:AY519594

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EMBL:DQ075255 EMBL:DQ075256 EMBL:DQ075257 EMBL:AK176475 IPI:IPI00528378 IPI:IPI00656574 IPI:IPI00759334 IPI:IPI00759367 PIR:T49254 RefSeq:NP_001030816.1 RefSeq:NP_001078249.1 RefSeq:NP_190199.1 UniGene:At.1475 UniGene:At.72744 ProteinModelPortal:Q9LX82 SMR:Q9LX82 STRING:Q9LX82 EnsemblPlants:AT3G46130.1 GeneID:823756 KEGG:ath:AT3G46130 GeneFarm:1132 TAIR:At3g46130 InParanoid:Q9LX82 OMA:REIDHSA PhylomeDB:Q9LX82 ProtClustDB:CLSN2684805 Genevestigator:Q9LX82 GermOnline:AT3G46130 Uniprot:Q9LX82
Root	Isotig08111	28	2	3.678	8.04E-07	TAIR|locus:2118929 - symbol:OST1 "AT4G33950" species:3702 "Arabidopsis thaliana" [GO:0016301 "kinase activity" evidence=ISS;IDA] [GO:0009414 "response to water deprivation" evidence=IGI;IMP] [GO:0009737 "response to abscisic acid stimulus" evidence=IDA;IMP] [GO:0010119 "regulation of stomatal movement" evidence=IMP] [GO:0004672 "protein kinase activity" evidence=IDA;TAS] [GO:0009931 "calcium-dependent protein serine/threonine kinase activity" evidence=ISS] [GO:0009738 "abscisic acid mediated signaling pathway" evidence=TAS] [GO:2000377 "regulation of reactive oxygen species metabolic process" evidence=IMP] [GO:0006970 "response to osmotic stress" evidence=IGI;IDA] [GO:0009651 "response to salt stress" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0010118 "stomatal movement" evidence=IMP] [GO:0042742 "defense response to bacterium" evidence=IMP] [GO:0005829 "cytosol" evidence=RCA;IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0005985 "sucrose metabolic process" evidence=IMP] [GO:0006636 "unsaturated fatty acid biosynthetic process" evidence=IMP] [GO:0019432 "triglyceride biosynthetic process" evidence=IMP] [GO:0040007 "growth" evidence=IMP] [GO:0048366 "leaf development" evidence=IMP] InterPro:IPR000719 InterPro:IPR002290 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 Pfam:PF00069 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 SMART:SM00220 GO:GO:0005829 GO:GO:0005524 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005634 GO:GO:0040007 GO:GO:0042742 GO:GO:0009738 GO:GO:0010119 eggNOG:COG0515 SUPFAM:SSF56112 GO:GO:0004674 HOGENOM:HBG755340 GO:GO:0009651 GO:GO:0009414 GO:GO:0010118 GO:GO:0019432 GO:GO:0048366 GO:GO:0006636 EMBL:AL031032 EMBL:AL161584 GO:GO:0019903 GO:GO:0010359 GO:GO:0005985 GO:GO:2000377 KO:K14498 EMBL:AJ316009 EMBL:AY054624 EMBL:AY081538 IPI:IPI00547757 IPI:IPI00900499 PIR:T05223 RefSeq:NP_567945.1 UniGene:At.2399 PDB:3UC4 PDB:3UDB PDB:3ZUT PDB:3ZUU PDBsum:3UC4 PDBsum:3UDB PDBsum:3ZUT PDBsum:3ZUU ProteinModelPortal:Q940H6 SMR:Q940H6 DIP:DIP-36705N IntAct:Q940H6 MINT:MINT-7260107 STRING:Q940H6 PRIDE:Q940H6 EnsemblPlants:AT4G33950.1 GeneID:829541 KEGG:ath:AT4G33950 TAIR:At4g33950 InParanoid:Q940H6 OMA:QYEEPEQ PhylomeDB:Q940H6 ProtClustDB:CLSN2917660 Genevestigator:Q940H6 Uniprot:Q940H6
Root	Isotig08112	27	2	3.626	1.44E-06	TAIR|locus:2118929 - symbol:OST1 "AT4G33950" species:3702 "Arabidopsis thaliana" [GO:0016301 "kinase activity" evidence=ISS;IDA] [GO:0009414 "response to water deprivation" evidence=IGI;IMP] [GO:0009737 "response to abscisic acid stimulus" evidence=IDA;IMP] [GO:0010119 "regulation of stomatal movement" evidence=IMP] [GO:0004672 "protein kinase activity" evidence=IDA;TAS] [GO:0009931 "calcium-dependent protein serine/threonine kinase activity" evidence=ISS] [GO:0009738 "abscisic acid mediated signaling pathway" evidence=TAS] [GO:2000377 "regulation of reactive oxygen species metabolic process" evidence=IMP] [GO:0006970 "response to osmotic stress" evidence=IGI;IDA] [GO:0009651 "response to salt stress" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0010118 "stomatal movement" evidence=IMP] [GO:0042742 "defense response to bacterium" evidence=IMP] [GO:0005829 "cytosol" evidence=RCA;IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0005985 "sucrose metabolic process" evidence=IMP] [GO:0006636 "unsaturated fatty acid biosynthetic process" evidence=IMP] [GO:0019432 "triglyceride biosynthetic process" evidence=IMP] [GO:0040007 "growth" evidence=IMP] [GO:0048366 "leaf development" evidence=IMP] InterPro:IPR000719 InterPro:IPR002290 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 Pfam:PF00069 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 SMART:SM00220 GO:GO:0005829 GO:GO:0005524 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005634 GO:GO:0040007 GO:GO:0042742 GO:GO:0009738 GO:GO:0010119 eggNOG:COG0515 SUPFAM:SSF56112 GO:GO:0004674 HOGENOM:HBG755340 GO:GO:0009651 GO:GO:0009414 GO:GO:0010118 GO:GO:0019432 GO:GO:0048366 GO:GO:0006636 EMBL:AL031032 EMBL:AL161584 GO:GO:0019903 GO:GO:0010359 GO:GO:0005985 GO:GO:2000377 KO:K14498 EMBL:AJ316009 EMBL:AY054624 EMBL:AY081538 IPI:IPI00547757 IPI:IPI00900499 PIR:T05223 RefSeq:NP_567945.1 UniGene:At.2399 PDB:3UC4 PDB:3UDB PDB:3ZUT PDB:3ZUU PDBsum:3UC4 PDBsum:3UDB PDBsum:3ZUT PDBsum:3ZUU ProteinModelPortal:Q940H6 SMR:Q940H6 DIP:DIP-36705N IntAct:Q940H6 MINT:MINT-7260107 STRING:Q940H6 PRIDE:Q940H6

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EnsemblPlants:AT4G33950.1 GeneID:829541 KEGG:ath:AT4G33950 TAIR:At4g33950 InParanoid:Q940H6 OMA:QYEEPEQ PhylomeDB:Q940H6 ProtClustDB:CLSN2917660 Genevestigator:Q940H6 Uniprot:Q940H6
Root	Isotig08115	0	39	-6.414	3.85E-11	TAIR|locus:2089423 - symbol:AT3G21360 species:3702 "Arabidopsis thaliana" [GO:0016491 "oxidoreductase activity" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0005634 "nucleus" evidence=IDA] InterPro:IPR003819 Pfam:PF02668 GO:GO:0005634 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0046872 GO:GO:0016491 EMBL:AP001305 UniGene:At.47366 UniGene:At.63567 EMBL:AK117772 IPI:IPI00537078 RefSeq:NP_188773.1 PDB:1Y0Z PDB:2Q4A PDBsum:1Y0Z PDBsum:2Q4A ProteinModelPortal:Q9LIG0 SMR:Q9LIG0 PRIDE:Q9LIG0 DNASU:821690 EnsemblPlants:AT3G21360.1 GeneID:821690 KEGG:ath:AT3G21360 TAIR:At3g21360 eggNOG:NOG13343 HOGENOM:HBG592040 InParanoid:Q9LIG0 OMA:NSMVAAY PhylomeDB:Q9LIG0 ProtClustDB:CLSN2685103 Genevestigator:Q9LIG0 GermOnline:AT3G21360 Uniprot:Q9LIG0
Root	Isotig08116	0	40	-6.451	2.24E-11	TAIR|locus:2089423 - symbol:AT3G21360 species:3702 "Arabidopsis thaliana" [GO:0016491 "oxidoreductase activity" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0005634 "nucleus" evidence=IDA] InterPro:IPR003819 Pfam:PF02668 GO:GO:0005634 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0046872 GO:GO:0016491 EMBL:AP001305 UniGene:At.47366 UniGene:At.63567 EMBL:AK117772 IPI:IPI00537078 RefSeq:NP_188773.1 PDB:1Y0Z PDB:2Q4A PDBsum:1Y0Z PDBsum:2Q4A ProteinModelPortal:Q9LIG0 SMR:Q9LIG0 PRIDE:Q9LIG0 DNASU:821690 EnsemblPlants:AT3G21360.1 GeneID:821690 KEGG:ath:AT3G21360 TAIR:At3g21360 eggNOG:NOG13343 HOGENOM:HBG592040 InParanoid:Q9LIG0 OMA:NSMVAAY PhylomeDB:Q9LIG0 ProtClustDB:CLSN2685103 Genevestigator:Q9LIG0 GermOnline:AT3G21360 Uniprot:Q9LIG0
Root	Isotig08119	52	16	1.571	3.49E-05	TAIR|locus:2013001 - symbol:AT1G71695 species:3702 "Arabidopsis thaliana" [GO:0004601 "peroxidase activity" evidence=IEA;ISS] [GO:0006979 "response to oxidative stress" evidence=IEA] [GO:0020037 "heme binding" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0009505 "plant-type cell wall" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000823 InterPro:IPR002016 InterPro:IPR010255 InterPro:IPR019793 InterPro:IPR019794 Pfam:PF00141 PRINTS:PR00458 PRINTS:PR00461 PROSITE:PS00435 PROSITE:PS00436 PROSITE:PS50873 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009506 GO:GO:0005773 GO:GO:0005576 GO:GO:0016020 GO:GO:0020037 GO:GO:0009505 EMBL:AC012654 EMBL:AC016163 GO:GO:0004601 GO:GO:0042744 HOGENOM:HBG597790 SUPFAM:SSF48113 KO:K00430 EMBL:X98318 EMBL:X98773 EMBL:AF334732 EMBL:BT000715 EMBL:AY087964 IPI:IPI00538176 PIR:A96739 RefSeq:NP_177313.1 UniGene:At.67041 UniGene:At.94 ProteinModelPortal:Q96520 SMR:Q96520 STRING:Q96520 PeroxiBase:93 PRIDE:Q96520 EnsemblPlants:AT1G71695.1 GeneID:843498 KEGG:ath:AT1G71695 GeneFarm:1474 TAIR:At1g71695 eggNOG:NOG252730 InParanoid:Q96520 OMA:NCSARNT PhylomeDB:Q96520 ProtClustDB:CLSN2679267 ArrayExpress:Q96520 Genevestigator:Q96520 GermOnline:AT1G71695 Uniprot:Q96520
Root	Isotig08129	19	0	5.119	1.05E-05	TAIR|locus:2123782 - symbol:GAMMA-VPE "AT4G32940" species:3702 "Arabidopsis thaliana" [GO:0004197 "cysteine-type endopeptidase activity" evidence=ISS;IDA] [GO:0006508 "proteolysis" evidence=ISS] [GO:0000323 "lytic vacuole" evidence=IDA] [GO:0006624 "vacuolar protein processing" evidence=ISS] InterPro:IPR001096 Pfam:PF01650 PIRSF:PIRSF019663 PRINTS:PR00776 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0004197 GO:GO:0006508 EMBL:AL031804 EMBL:AL161582 eggNOG:COG5206 PANTHER:PTHR12000 KO:K01369 HOGENOM:HBG318720 GO:GO:0000323 ProtClustDB:CLSN2682340 EMBL:D61395 EMBL:AF370160 EMBL:AF424619 EMBL:AY059104 EMBL:AY133531 IPI:IPI00537536 PIR:T05302 RefSeq:NP_195020.1 UniGene:At.21567 UniGene:At.48929 UniGene:At.75206 ProteinModelPortal:Q39119 STRING:Q39119 MEROPS:C13.006 PRIDE:Q39119 EnsemblPlants:AT4G32940.1 GeneID:829431 KEGG:ath:AT4G32940 TAIR:At4g32940 InParanoid:Q39119 OMA:ICHAYQL PhylomeDB:Q39119 Genevestigator:Q39119 Uniprot:Q39119
Root	Isotig08130	19	0	5.119	1.05E-05	TAIR|locus:2087625 - symbol:DELTA-VPE "AT3G20210" species:3702 "Arabidopsis thaliana" [GO:0004197 "cysteine-type endopeptidase activity" evidence=ISS;IDA] [GO:0006508 "proteolysis" evidence=ISS] [GO:0006624 "vacuolar protein processing" evidence=ISS] [GO:0005615 "extracellular space" evidence=IDA] [GO:0010214 "seed coat development" evidence=IMP] [GO:0012501 "programmed cell death" evidence=IMP] InterPro:IPR001096 Pfam:PF01650 PIRSF:PIRSF019663 PRINTS:PR00776 EMBL:CP002686 GO:GO:0005615 GO:GO:0004197 GO:GO:0006508 EMBL:AP000383 GO:GO:0010214 GO:GO:0012501 PANTHER:PTHR12000 KO:K01369

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						ProtClustDB:CLSN2682340 UniGene:At.26916 EMBL:AY120765 EMBL:BT000949 EMBL:AF521661 EMBL:AB105106 IPI:IPI00543686 RefSeq:NP_188656.1 ProteinModelPortal:Q9LJX8 MEROPS:C13.A01 PRIDE:Q9LJX8 EnsemblPlants:AT3G20210.1 GeneID:821565 KEGG:ath:AT3G20210 TAIR:At3g20210 InParanoid:Q9LJX8 OMA:SWLEDSD PhylomeDB:Q9LJX8 ArrayExpress:Q9LJX8 Genevestigator:Q9LJX8 Uniprot:Q9LJX8
Root	Isotig08133	3	20	-2.866	9.17E-05	TAIR|locus:2173093 - symbol:AT5G51970 species:3702 "Arabidopsis thaliana" [GO:0008270 "zinc ion binding" evidence=IEA] [GO:0016491 "oxidoreductase activity" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR002085 InterPro:IPR002328 InterPro:IPR013149 InterPro:IPR013154 InterPro:IPR016040 Pfam:PF00107 Pfam:PF08240 PROSITE:PS00059 GO:GO:0005829 GO:GO:0009506 EMBL:CP002688 GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 GO:GO:0008270 GO:GO:0016491 InterPro:IPR011032 PANTHER:PTHR11695 SUPFAM:SSF50129 EMBL:AB015478 UniGene:At.29648 UniGene:At.9328 KO:K00008 OMA:FYKHNAN HSSP:O96496 EMBL:AF370161 EMBL:AY133848 EMBL:AK230367 IPI:IPI00526124 RefSeq:NP_200010.1 RefSeq:NP_974925.1 ProteinModelPortal:Q9FJ95 SMR:Q9FJ95 STRING:Q9FJ95 PRIDE:Q9FJ95 EnsemblPlants:AT5G51970.1 EnsemblPlants:AT5G51970.2 GeneID:835272 KEGG:ath:AT5G51970 TAIR:At5g51970 InParanoid:Q9FJ95 PhylomeDB:Q9FJ95 ProtClustDB:PLN02702 Genevestigator:Q9FJ95 Uniprot:Q9FJ95
Root	Isotig08134	2	28	-3.936	1.29E-07	TAIR|locus:2173093 - symbol:AT5G51970 species:3702 "Arabidopsis thaliana" [GO:0008270 "zinc ion binding" evidence=IEA] [GO:0016491 "oxidoreductase activity" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR002085 InterPro:IPR002328 InterPro:IPR013149 InterPro:IPR013154 InterPro:IPR016040 Pfam:PF00107 Pfam:PF08240 PROSITE:PS00059 GO:GO:0005829 GO:GO:0009506 EMBL:CP002688 GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 GO:GO:0008270 GO:GO:0016491 InterPro:IPR011032 PANTHER:PTHR11695 SUPFAM:SSF50129 EMBL:AB015478 UniGene:At.29648 UniGene:At.9328 KO:K00008 OMA:FYKHNAN HSSP:O96496 EMBL:AF370161 EMBL:AY133848 EMBL:AK230367 IPI:IPI00526124 RefSeq:NP_200010.1 RefSeq:NP_974925.1 ProteinModelPortal:Q9FJ95 SMR:Q9FJ95 STRING:Q9FJ95 PRIDE:Q9FJ95 EnsemblPlants:AT5G51970.1 EnsemblPlants:AT5G51970.2 GeneID:835272 KEGG:ath:AT5G51970 TAIR:At5g51970 InParanoid:Q9FJ95 PhylomeDB:Q9FJ95 ProtClustDB:PLN02702 Genevestigator:Q9FJ95 Uniprot:Q9FJ95
Root	Isotig08135	2	18	-3.299	7.42E-05	TAIR|locus:2103172 - symbol:ASD1 "AT3G10740" species:3702 "Arabidopsis thaliana" [GO:0016798 "hydrolase activity, acting on glycosyl bonds" evidence=ISS] [GO:0009044 "xylan 1,4-beta-xylosidase activity" evidence=IDA] [GO:0045493 "xylan catabolic process" evidence=IDA] [GO:0046556 "alpha-N-arabinofuranosidase activity" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0009505 "plant-type cell wall" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] InterPro:IPR010720 Pfam:PF06964 SMART:SM00813 GO:GO:0048046 GO:GO:0005773 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0045493 InterPro:IPR017853 SUPFAM:SSF51445 GO:GO:0005578 EMBL:AC011708 CAZy:GH51 GO:GO:0046556 GO:GO:0046373 eggNOG:COG3534 GO:GO:0009505 EMBL:AY243509 EMBL:AF372949 EMBL:AY143944 EMBL:AK222175 EMBL:AK220766 IPI:IPI00526411 RefSeq:NP_187685.1 UniGene:At.20271 ProteinModelPortal:Q9SG80 SMR:Q9SG80 STRING:Q9SG80 PRIDE:Q9SG80 EnsemblPlants:AT3G10740.1 GeneID:820243 KEGG:ath:AT3G10740 TAIR:At3g10740 InParanoid:Q9SG80 OMA:LEYLGIG PhylomeDB:Q9SG80 ProtClustDB:CLSN2684036 Genevestigator:Q9SG80 GO:GO:0009044 Uniprot:Q9SG80
Root	Isotig08151	2	15	-3.036	0.000493759	TAIR|locus:2168988 - symbol:TDT "AT5G47560" species:3702 "Arabidopsis thaliana" [GO:0006814 "sodium ion transport" evidence=ISS] [GO:0006835 "dicarboxylic acid transport" evidence=ISS] [GO:0017153 "sodium:dicarboxylate symporter activity" evidence=ISS] [GO:0005773 "vacuole" evidence=IDA] [GO:0015140 "malate transmembrane transporter activity" evidence=IMP;IDA] [GO:0015743 "malate transport" evidence=TAS] [GO:0051453 "regulation of intracellular pH" evidence=TAS] InterPro:IPR001898 Pfam:PF00939 GO:GO:0016021 GO:GO:0005774 EMBL:CP002688 GenomeReviews:BA000015_GR EMBL:AB025628 GO:GO:0006814 GO:GO:0015140 GO:GO:0051453 eggNOG:COG0471 TIGRFAMs:TIGR00785 KO:K14445 HOGENOM:HBG616159 EMBL:AJ223445 EMBL:AB043024 EMBL:AY072145 EMBL:AY133792 EMBL:AY084408 IPI:IPI00534224 RefSeq:NP_199567.1 UniGene:At.21038 UniGene:At.68515 UniGene:At.71618 STRING:Q8LG88 TCDB:2.A.47.1.6 PRIDE:Q8LG88 EnsemblPlants:AT5G47560.1 GeneID:834806 KEGG:ath:AT5G47560 GeneFarm:4980 TAIR:At5g47560 InParanoid:Q8LG88 OMA:TECMPLA PhylomeDB:Q8LG88

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						ProtClustDB:CLSN2686388 ArrayExpress:Q9MAW4 Genevestigator:Q8LG88 GermOnline:AT5G47560 Uniprot:Q8LG88
Root	Isotig08152	2	16	-3.129	0.000262867	TAIR|locus:2168988 - symbol:TDT "AT5G47560" species:3702 "Arabidopsis thaliana" [GO:0006814 "sodium ion transport" evidence=ISS] [GO:0006835 "dicarboxylic acid transport" evidence=ISS] [GO:0017153 "sodium:dicarboxylate symporter activity" evidence=ISS] [GO:0005773 "vacuole" evidence=IDA] [GO:0015140 "malate transmembrane transporter activity" evidence=IMP;IDA] [GO:0015743 "malate transport" evidence=TAS] [GO:0051453 "regulation of intracellular pH" evidence=TAS] InterPro:IPR001898 Pfam:PF00939 GO:GO:0016021 GO:GO:0005774 EMBL:CP002688 GenomeReviews:BA000015_GR EMBL:AB025628 GO:GO:0006814 GO:GO:0015140 GO:GO:0051453 eggNOG:COG0471 TIGRFAMs:TIGR00785 KO:K14445 HOGENOM:HBG616159 EMBL:AJ223445 EMBL:AB043024 EMBL:AY072145 EMBL:AY133792 EMBL:AY084408 IPI:IPI00534224 RefSeq:NP_199567.1 UniGene:At.21038 UniGene:At.68515 UniGene:At.71618 STRING:Q8LG88 TCDB:2.A.47.1.6 PRIDE:Q8LG88 EnsemblPlants:AT5G47560.1 GeneID:834806 KEGG:ath:AT5G47560 GeneFarm:4980 TAIR:At5g47560 InParanoid:Q8LG88 OMA:TECMPLA PhylomeDB:Q8LG88 ProtClustDB:CLSN2686388 ArrayExpress:Q9MAW4 Genevestigator:Q8LG88 GermOnline:AT5G47560 Uniprot:Q8LG88
Root	Isotig08173	39	1	5.156	2.63E-10	TAIR|locus:2167418 - symbol:AT5G24130 "AT5G24130" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002688 GenomeReviews:BA000015_GR EMBL:AB010696 EMBL:BT005307 EMBL:AK118424 IPI:IPI00517115 RefSeq:NP_197801.1 UniGene:At.30976 IntAct:Q9FL61 PRIDE:Q9FL61 EnsemblPlants:AT5G24130.1 GeneID:832478 KEGG:ath:AT5G24130 TAIR:At5g24130 eggNOG:NOG265800 HOGENOM:HBG597859 InParanoid:Q9FL61 OMA:AREIRTY PhylomeDB:Q9FL61 ProtClustDB:CLSN2686316 Genevestigator:Q9FL61 Uniprot:Q9FL61
Root	Isotig08174	39	0	6.156	2.24E-10	TAIR|locus:2167418 - symbol:AT5G24130 "AT5G24130" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002688 GenomeReviews:BA000015_GR EMBL:AB010696 EMBL:BT005307 EMBL:AK118424 IPI:IPI00517115 RefSeq:NP_197801.1 UniGene:At.30976 IntAct:Q9FL61 PRIDE:Q9FL61 EnsemblPlants:AT5G24130.1 GeneID:832478 KEGG:ath:AT5G24130 TAIR:At5g24130 eggNOG:NOG265800 HOGENOM:HBG597859 InParanoid:Q9FL61 OMA:AREIRTY PhylomeDB:Q9FL61 ProtClustDB:CLSN2686316 Genevestigator:Q9FL61 Uniprot:Q9FL61
Root	Isotig08189	1	14	-3.936	0.000188601	TAIR|locus:2183730 - symbol:AT5G10770 "AT5G10770" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=ISS] [GO:0004190 "aspartic-type endopeptidase activity" evidence=IEA] [GO:0006508 "proteolysis" evidence=IEA] InterPro:IPR001461 InterPro:IPR009007 Pfam:PF00026 PRINTS:PR00792 EMBL:CP002688 GO:GO:0006508 GO:GO:0004190 InterPro:IPR021109 SUPFAM:SSF50630 Gene3D:G3DSA:2.40.70.10 PANTHER:PTHR13683 HSSP:P00799 EMBL:AY075656 EMBL:BT001004 IPI:IPI00543783 RefSeq:NP_196638.2 UniGene:At.32336 ProteinModelPortal:Q8S9J6 MEROPS:A01.A15 PRIDE:Q8S9J6 EnsemblPlants:AT5G10770.1 GeneID:830944 KEGG:ath:AT5G10770 TAIR:At5g10770 InParanoid:Q8S9J6 OMA:LEVVYDG PhylomeDB:Q8S9J6 ProtClustDB:CLSN2686424 Genevestigator:Q8S9J6 Uniprot:Q8S9J6
Root	Isotig08213	8	38	-2.377	1.13E-06	UNIPROTKB|Q8I4X0 - symbol:PFL2215w "Actin-1" species:36329 "Plasmodium falciparum 3D7" [GO:0005200 "structural constituent of cytoskeleton" evidence=ISS] [GO:0005884 "actin filament" evidence=ISS] [GO:0007010 "cytoskeleton organization" evidence=ISS] [GO:0070359 "actin polymerization-dependent cell motility involved in migration of symbiont in host" evidence=ISS] InterPro:IPR004001 PROSITE:PS00406 PROSITE:PS00432 InterPro:IPR004000 GO:GO:0005524 GO:GO:0005737 GO:GO:0005200 GO:GO:0005884 HOGENOM:HBG559892 PANTHER:PTHR11937 Pfam:PF00022 PRINTS:PR00190 SMART:SM00268 KO:K10355 OMA:PRHQVRQ InterPro:IPR020902 PROSITE:PS01132 EMBL:AE014188 PIR:S12628 RefSeq:XP_001350847.1 ProteinModelPortal:Q8I4X0 SMR:Q8I4X0 IntAct:Q8I4X0 MINT:MINT-1556031 EnsemblProtists:PFL2215w:mRNA GeneID:811495 KEGG:pfa:PFL2215w EuPathDB:EupathDB:PFL2215w ProtClustDB:PTZ00004 GO:GO:0070359 Uniprot:Q8I4X0
Root	Isotig08214	8	38	-2.377	1.13E-06	TAIR|locus:2099302 - symbol:ACT11 "AT3G12110" species:3702 "Arabidopsis thaliana" [GO:0005200 "structural constituent of cytoskeleton" evidence=ISS] [GO:0030036 "actin cytoskeleton organization" evidence=TAS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009506

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						"plasmodesma" evidence=IDA] [GO:0005856 "cytoskeleton" evidence=ISS] InterPro:IPR004001 PROSITE:PS00406 PROSITE:PS00432 InterPro:IPR004000 GO:GO:0005739 GO:GO:0005886 GO:GO:0009506 GO:GO:0005524 GO:GO:0009570 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005856 EMBL:AC069473 GO:GO:0009941 eggNOG:COG5277 HOGENOM:HBG559892 PANTHER:PTHR11937 Pfam:PF00022 PRINTS:PR00190 SMART:SM00268 KO:K10355 InterPro:IPR020902 PROSITE:PS01132 EMBL:U27981 EMBL:AP002063 EMBL:BT005593 EMBL:AY087740 IPI:IPI00538017 PIR:S68109 RefSeq:NP_187818.1 UniGene:At.28138 ProteinModelPortal:P53496 SMR:P53496 IntAct:P53496 STRING:P53496 PRIDE:P53496 EnsemblPlants:AT3G12110.1 GeneID:820385 KEGG:ath:AT3G12110 TAIR:At3g12110 InParanoid:P53496 OMA:GERFRCP PhylomeDB:P53496 ProtClustDB:CLSN2682469 ArrayExpress:P53496 Genevestigator:P53496 GermOnline:AT3G12110 Uniprot:P53496
Root	Isotig08223	10	29	-1.665	0.000753212	TAIR|locus:2076904 - symbol:GRF7 "AT3G02520" species:3702 "Arabidopsis thaliana" [GO:0005635 "nuclear envelope" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0045309 "protein phosphorylated amino acid binding" evidence=TAS] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] InterPro:IPR000308 PIRSF:PIRSF000868 PRINTS:PR00305 HOGENOM:HBG611720 GO:GO:0005886 GO:GO:0009506 GO:GO:0019904 InterPro:IPR023409 InterPro:IPR023410 Gene3D:G3DSA:1.20.190.20 PANTHER:PTHR18860 Pfam:PF00244 SMART:SM00101 SUPFAM:SSF48445 PROSITE:PS00796 PROSITE:PS00797 GO:GO:0009507 ProtClustDB:CLSN2688003 EMBL:U60445 EMBL:AF145299 EMBL:AC021640 EMBL:CP002686 EMBL:AY065274 EMBL:AY096526 EMBL:AY087723 IPI:IPI00536399 RefSeq:NP_566174.1 UniGene:At.21863 ProteinModelPortal:Q96300 SMR:Q96300 IntAct:Q96300 STRING:Q96300 PRIDE:Q96300 EnsemblPlants:AT3G02520.1 GeneID:821060 GenomeReviews:BA000014_GR KEGG:ath:AT3G02520 TAIR:At3g02520 InParanoid:Q96300 OMA:KVCQDVL PhylomeDB:Q96300 ArrayExpress:Q96300 Genevestigator:Q96300 GermOnline:AT3G02520 Uniprot:Q96300
Root	Isotig08224	8	28	-1.936	0.000239276	TAIR|locus:2076904 - symbol:GRF7 "AT3G02520" species:3702 "Arabidopsis thaliana" [GO:0005635 "nuclear envelope" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0045309 "protein phosphorylated amino acid binding" evidence=TAS] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] InterPro:IPR000308 PIRSF:PIRSF000868 PRINTS:PR00305 HOGENOM:HBG611720 GO:GO:0005886 GO:GO:0009506 GO:GO:0019904 InterPro:IPR023409 InterPro:IPR023410 Gene3D:G3DSA:1.20.190.20 PANTHER:PTHR18860 Pfam:PF00244 SMART:SM00101 SUPFAM:SSF48445 PROSITE:PS00796 PROSITE:PS00797 GO:GO:0009507 ProtClustDB:CLSN2688003 EMBL:U60445 EMBL:AF145299 EMBL:AC021640 EMBL:CP002686 EMBL:AY065274 EMBL:AY096526 EMBL:AY087723 IPI:IPI00536399 RefSeq:NP_566174.1 UniGene:At.21863 ProteinModelPortal:Q96300 SMR:Q96300 IntAct:Q96300 STRING:Q96300 PRIDE:Q96300 EnsemblPlants:AT3G02520.1 GeneID:821060 GenomeReviews:BA000014_GR KEGG:ath:AT3G02520 TAIR:At3g02520 InParanoid:Q96300 OMA:KVCQDVL PhylomeDB:Q96300 ArrayExpress:Q96300 Genevestigator:Q96300 GermOnline:AT3G02520 Uniprot:Q96300
Root	Isotig08225	11	45	-2.161	5.75E-07	TAIR|locus:2013001 - symbol:AT1G71695 species:3702 "Arabidopsis thaliana" [GO:0004601 "peroxidase activity" evidence=IEA;ISS] [GO:0006979 "response to oxidative stress" evidence=IEA] [GO:0020037 "heme binding" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0009505 "plant-type cell wall" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000823 InterPro:IPR002016 InterPro:IPR010255 InterPro:IPR019793 InterPro:IPR019794 Pfam:PF00141 PRINTS:PR00458 PRINTS:PR00461 PROSITE:PS00435 PROSITE:PS00436 PROSITE:PS50873 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009506 GO:GO:0005773 GO:GO:0005576 GO:GO:0016020 GO:GO:0020037 GO:GO:0009505 EMBL:AC012654 EMBL:AC016163 GO:GO:0004601 GO:GO:0042744 HOGENOM:HBG597790 SUPFAM:SSF48113 KO:K00430 EMBL:X98318 EMBL:X98773 EMBL:AF334732 EMBL:BT000715 EMBL:AY087964 IPI:IPI00538176 PIR:A96739 RefSeq:NP_177313.1 UniGene:At.67041 UniGene:At.94 ProteinModelPortal:Q96520 SMR:Q96520 STRING:Q96520 PeroxiBase:93 PRIDE:Q96520 EnsemblPlants:AT1G71695.1 GeneID:843498 KEGG:ath:AT1G71695 GeneFarm:1474 TAIR:At1g71695

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						eggNOG:NOG252730 InParanoid:Q96520 OMA:NCSARNT PhylomeDB:Q96520 ProtClustDB:CLSN2679267 ArrayExpress:Q96520 Genevestigator:Q96520 GermOnline:AT1G71695 Uniprot:Q96520
Root	Isotig08226	11	45	-2.161	5.75E-07	TAIR|locus:2013001 - symbol:AT1G71695 species:3702 "Arabidopsis thaliana" [GO:0004601 "peroxidase activity" evidence=IEA;ISS] [GO:0006979 "response to oxidative stress" evidence=IEA] [GO:0020037 "heme binding" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0009505 "plant-type cell wall" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000823 InterPro:IPR002016 InterPro:IPR010255 InterPro:IPR019793 InterPro:IPR019794 Pfam:PF00141 PRINTS:PR00458 PRINTS:PR00461 PROSITE:PS00435 PROSITE:PS00436 PROSITE:PS50873 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009506 GO:GO:0005773 GO:GO:0005576 GO:GO:0016020 GO:GO:0020037 GO:GO:0009505 EMBL:AC012654 EMBL:AC016163 GO:GO:0004601 GO:GO:0042744 HOGENOM:HBG597790 SUPFAM:SSF48113 KO:K00430 EMBL:X98318 EMBL:X98773 EMBL:AF334732 EMBL:BT000715 EMBL:AY087964 IPI:IPI00538176 PIR:A96739 RefSeq:NP_177313.1 UniGene:At.67041 UniGene:At.94 ProteinModelPortal:Q96520 SMR:Q96520 STRING:Q96520 PeroxiBase:93 PRIDE:Q96520 EnsemblPlants:AT1G71695.1 GeneID:843498 KEGG:ath:AT1G71695 GeneFarm:1474 TAIR:At1g71695 eggNOG:NOG252730 InParanoid:Q96520 OMA:NCSARNT PhylomeDB:Q96520 ProtClustDB:CLSN2679267 ArrayExpress:Q96520 Genevestigator:Q96520 GermOnline:AT1G71695 Uniprot:Q96520
Root	Isotig08239	53	14	1.792	4.53E-06	TAIR|locus:2019574 - symbol:AT1G67280 species:3702 "Arabidopsis thaliana" [GO:0004462 "lactoylglutathione lyase activity" evidence=IEA;ISS] [GO:0005975 "carbohydrate metabolic process" evidence=ISS] [GO:0046872 "metal ion binding" evidence=IEA] [GO:0031977 "thylakoid lumen" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0010319 "stromule" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] InterPro:IPR004361 InterPro:IPR018146 PROSITE:PS00934 PROSITE:PS00935 Pfam:PF00903 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009570 GO:GO:0046872 GO:GO:0010319 GO:GO:0009409 GO:GO:0031977 eggNOG:COG0346 InterPro:IPR004360 EMBL:AC002130 GO:GO:0004462 EMBL:AF419551 EMBL:AY079102 EMBL:AY085148 IPI:IPI00544224 IPI:IPI00846167 PIR:E96696 RefSeq:NP_001077783.1 RefSeq:NP_176896.1 UniGene:At.22738 HSSP:Q59384 ProteinModelPortal:Q8W593 SMR:Q8W593 STRING:Q8W593 PRIDE:Q8W593 EnsemblPlants:AT1G67280.1 GeneID:843048 KEGG:ath:AT1G67280 TAIR:At1g67280 InParanoid:Q8W593 KO:K01759 OMA:GPESSHF PhylomeDB:Q8W593 ProtClustDB:PLN02300 Genevestigator:Q8W593 TIGRFAMs:TIGR00068 Uniprot:Q8W593
Root	Isotig08240	71	16	2.021	8.76E-09	TAIR|locus:2019574 - symbol:AT1G67280 species:3702 "Arabidopsis thaliana" [GO:0004462 "lactoylglutathione lyase activity" evidence=IEA;ISS] [GO:0005975 "carbohydrate metabolic process" evidence=ISS] [GO:0046872 "metal ion binding" evidence=IEA] [GO:0031977 "thylakoid lumen" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0010319 "stromule" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] InterPro:IPR004361 InterPro:IPR018146 PROSITE:PS00934 PROSITE:PS00935 Pfam:PF00903 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009570 GO:GO:0046872 GO:GO:0010319 GO:GO:0009409 GO:GO:0031977 eggNOG:COG0346 InterPro:IPR004360 EMBL:AC002130 GO:GO:0004462 EMBL:AF419551 EMBL:AY079102 EMBL:AY085148 IPI:IPI00544224 IPI:IPI00846167 PIR:E96696 RefSeq:NP_001077783.1 RefSeq:NP_176896.1 UniGene:At.22738 HSSP:Q59384 ProteinModelPortal:Q8W593 SMR:Q8W593 STRING:Q8W593 PRIDE:Q8W593 EnsemblPlants:AT1G67280.1 GeneID:843048 KEGG:ath:AT1G67280 TAIR:At1g67280 InParanoid:Q8W593 KO:K01759 OMA:GPESSHF PhylomeDB:Q8W593 ProtClustDB:PLN02300 Genevestigator:Q8W593 TIGRFAMs:TIGR00068 Uniprot:Q8W593
Root	Isotig08241	12	33	-1.588	0.000511326	TAIR|locus:2147142 - symbol:JAZ12 "AT5G20900" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0005515 "protein binding" evidence=IPI] InterPro:IPR018467 Pfam:PF09425 GO:GO:0005634 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005515 GO:GO:0006952 GO:GO:0006355 GO:GO:0006351 EMBL:AF296834 UniGene:At.1134 UniGene:At.68499 InterPro:IPR010399 Pfam:PF06200 SMART:SM00979 PROSITE:PS51320 KO:K13464 EMBL:AF360184 EMBL:AY051013 IPI:IPI00543677 RefSeq:NP_197590.1 DIP:DIP-53279N IntAct:Q9C5K8 STRING:Q9C5K8 PRIDE:Q9C5K8 EnsemblPlants:AT5G20900.1 GeneID:832214 KEGG:ath:AT5G20900 TAIR:At5g20900 eggNOG:NOG316310 InParanoid:Q9C5K8 OMA:PALNRAP PhylomeDB:Q9C5K8 ProtClustDB:CLSN2916811 ArrayExpress:Q9C5K8 Genevestigator:Q9C5K8 Uniprot:Q9C5K8

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig08242	12	33	-1.588	0.000511326	TAIR|locus:2147142 - symbol:JAZ12 "AT5G20900" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0005515 "protein binding" evidence=IPI] InterPro:IPR018467 Pfam:PF09425 GO:GO:0005634 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005515 GO:GO:0006952 GO:GO:0006355 GO:GO:0006351 EMBL:AF296834 UniGene:At.1134 UniGene:At.68499 InterPro:IPR010399 Pfam:PF06200 SMART:SM00979 PROSITE:PS51320 KO:K13464 EMBL:AF360184 EMBL:AY051013 IPI:IPI00543677 RefSeq:NP_197590.1 DIP:DIP-53279N IntAct:Q9C5K8 STRING:Q9C5K8 PRIDE:Q9C5K8 EnsemblPlants:AT5G20900.1 GeneID:832214 KEGG:ath:AT5G20900 TAIR:At5g20900 eggNOG:NOG316310 InParanoid:Q9C5K8 OMA:PALNRAP PhylomeDB:Q9C5K8 ProtClustDB:CLSN2916811 ArrayExpress:Q9C5K8 Genevestigator:Q9C5K8 Uniprot:Q9C5K8
Root	Isotig08253	29	5	2.407	4.20E-05	TAIR|locus:2146178 - symbol:AT5G18400 "AT5G18400" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0005515 "protein binding" evidence=IPI] GO:GO:0005737 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0006915 InterPro:IPR007785 PANTHER:PTHR13273 Pfam:PF05093 HOGENOM:HBG316506 eggNOG:COG5636 EMBL:AC051626 EMBL:AY080855 EMBL:AY123986 EMBL:BT000943 EMBL:BT001035 EMBL:AY088356 IPI:IPI00544195 RefSeq:NP_001078602.1 RefSeq:NP_568363.1 RefSeq:NP_850844.1 UniGene:At.31429 ProteinModelPortal:Q8L7Z3 SMR:Q8L7Z3 IntAct:Q8L7Z3 STRING:Q8L7Z3 PRIDE:Q8L7Z3 EnsemblPlants:AT5G18400.2 EnsemblPlants:AT5G18400.3 GeneID:831958 KEGG:ath:AT5G18400 TAIR:At5g18400 InParanoid:Q8L7Z3 OMA:CGTCPYK PhylomeDB:Q8L7Z3 ProtClustDB:CLSN2689770 Genevestigator:Q8L7Z3 Uniprot:Q8L7Z3
Root	Isotig08254	29	5	2.407	4.20E-05	TAIR|locus:2146178 - symbol:AT5G18400 "AT5G18400" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0005515 "protein binding" evidence=IPI] GO:GO:0005737 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0006915 InterPro:IPR007785 PANTHER:PTHR13273 Pfam:PF05093 HOGENOM:HBG316506 eggNOG:COG5636 EMBL:AC051626 EMBL:AY080855 EMBL:AY123986 EMBL:BT000943 EMBL:BT001035 EMBL:AY088356 IPI:IPI00544195 RefSeq:NP_001078602.1 RefSeq:NP_568363.1 RefSeq:NP_850844.1 UniGene:At.31429 ProteinModelPortal:Q8L7Z3 SMR:Q8L7Z3 IntAct:Q8L7Z3 STRING:Q8L7Z3 PRIDE:Q8L7Z3 EnsemblPlants:AT5G18400.2 EnsemblPlants:AT5G18400.3 GeneID:831958 KEGG:ath:AT5G18400 TAIR:At5g18400 InParanoid:Q8L7Z3 OMA:CGTCPYK PhylomeDB:Q8L7Z3 ProtClustDB:CLSN2689770 Genevestigator:Q8L7Z3 Uniprot:Q8L7Z3
Root	Isotig08291	0	31	-6.083	3.24E-09	TAIR|locus:2013728 - symbol:AT1G29380 "AT1G29380" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002684 GenomeReviews:CT485782_GR CAZy:CBM43 InterPro:IPR012946 Pfam:PF07983 SMART:SM00768 EMBL:AY648309 EMBL:AY773818 EMBL:AK221467 IPI:IPI00528008 RefSeq:NP_174231.2 UniGene:At.50785 UniGene:At.68810 ProteinModelPortal:Q6DST9 SMR:Q6DST9 STRING:Q6DST9 EnsemblPlants:AT1G29380.1 GeneID:839813 KEGG:ath:AT1G29380 TAIR:At1g29380 eggNOG:NOG246571 HOGENOM:HBG744505 InParanoid:Q6DST9 OMA:WCIAKAN PhylomeDB:Q6DST9 ProtClustDB:CLSN2918796 Genevestigator:Q6DST9 Uniprot:Q6DST9
Root	Isotig08292	0	14	-4.936	8.24E-05	TAIR|locus:2013728 - symbol:AT1G29380 "AT1G29380" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002684 GenomeReviews:CT485782_GR CAZy:CBM43 InterPro:IPR012946 Pfam:PF07983 SMART:SM00768 EMBL:AY648309 EMBL:AY773818 EMBL:AK221467 IPI:IPI00528008 RefSeq:NP_174231.2 UniGene:At.50785 UniGene:At.68810 ProteinModelPortal:Q6DST9 SMR:Q6DST9 STRING:Q6DST9 EnsemblPlants:AT1G29380.1 GeneID:839813 KEGG:ath:AT1G29380 TAIR:At1g29380 eggNOG:NOG246571 HOGENOM:HBG744505 InParanoid:Q6DST9 OMA:WCIAKAN PhylomeDB:Q6DST9 ProtClustDB:CLSN2918796 Genevestigator:Q6DST9 Uniprot:Q6DST9
Root	Isotig08293	0	18	-5.299	6.77E-06	TAIR|locus:2142105 - symbol:LRX3 "AT4G13340" species:3702 "Arabidopsis thaliana" [GO:0005515 "protein binding" evidence=IPI] [GO:0005199 "structural constituent of cell wall" evidence=ISS] [GO:0005618 "cell wall" evidence=IDA] [GO:0009505 "plant-type cell wall" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] PROSITE:PS51450 GO:GO:0009506 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005576 GO:GO:0005515 eggNOG:COG4886 HOGENOM:HBG755340 GO:GO:0009505 GO:GO:0007047 EMBL:AL161536 InterPro:IPR013210 Pfam:PF08263 EMBL:AL049608 IPI:IPI00546699 PIR:T06291 RefSeq:NP_193070.1 UniGene:At.48854 ProteinModelPortal:Q9T0K5 SMR:Q9T0K5 PRIDE:Q9T0K5 EnsemblPlants:AT4G13340.1 GeneID:826964 KEGG:ath:AT4G13340 GeneFarm:1493 TAIR:At4g13340 InParanoid:Q9T0K5 OMA:VHYSSPP PhylomeDB:Q9T0K5 ProtClustDB:CLSN2916045 ArrayExpress:Q9T0K5 Genevestigator:Q9T0K5 Uniprot:Q9T0K5

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig08294	0	18	-5.299	6.77E-06	TAIR|locus:2142105 - symbol:LRX3 "AT4G13340" species:3702 "Arabidopsis thaliana" [GO:0005515 "protein binding" evidence=IPI] [GO:0005199 "structural constituent of cell wall" evidence=ISS] [GO:0005618 "cell wall" evidence=IDA] [GO:0009505 "plant-type cell wall" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] PROSITE:PS51450 GO:GO:0009506 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005576 GO:GO:0005515 eggNOG:COG4886 HOGENOM:HBG755340 GO:GO:0009505 GO:GO:0007047 EMBL:AL161536 InterPro:IPR013210 Pfam:PF08263 EMBL:AL049608 IPI:IPI00546699 PIR:T06291 RefSeq:NP_193070.1 UniGene:At.48854 ProteinModelPortal:Q9T0K5 SMR:Q9T0K5 PRIDE:Q9T0K5 EnsemblPlants:AT4G13340.1 GeneID:826964 KEGG:ath:AT4G13340 GeneFarm:1493 TAIR:At4g13340 InParanoid:Q9T0K5 OMA:VHYSSPP PhylomeDB:Q9T0K5 ProtClustDB:CLSN2916045 ArrayExpress:Q9T0K5 Genevestigator:Q9T0K5 Uniprot:Q9T0K5
Root	Isotig08301	0	11	-4.588	0.000569522	TAIR|locus:2019863 - symbol:AT1G79620 "AT1G79620" species:3702 "Arabidopsis thaliana" [GO:0004674 "protein serine/threonine kinase activity" evidence=ISS] [GO:0005524 "ATP binding" evidence=ISS] [GO:0006468 "protein phosphorylation" evidence=IEA;ISS] [GO:0007169 "transmembrane receptor protein tyrosine kinase signaling pathway" evidence=ISS] [GO:0016301 "kinase activity" evidence=ISS] Pfam:PF00560 InterPro:IPR001611 InterPro:IPR000719 InterPro:IPR001245 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 Pfam:PF07714 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005524 eggNOG:COG0515 GO:GO:0004872 SUPFAM:SSF56112 GO:GO:0004674 HSSP:P36897 InterPro:IPR013210 Pfam:PF08263 HOGENOM:HBG316990 EMBL:FJ708684 EMBL:AK117863 IPI:IPI00517320 RefSeq:NP_178080.2 UniGene:At.46098 ProteinModelPortal:Q8GY50 SMR:Q8GY50 PRIDE:Q8GY50 EnsemblPlants:AT1G79620.1 GeneID:844301 KEGG:ath:AT1G79620 TAIR:At1g79620 InParanoid:Q8GY50 OMA:YFIASPY PhylomeDB:Q8GY50 ProtClustDB:CLSN2680668 Genevestigator:Q8GY50 Uniprot:Q8GY50
Root	Isotig08302	0	11	-4.588	0.000569522	TAIR|locus:2019863 - symbol:AT1G79620 "AT1G79620" species:3702 "Arabidopsis thaliana" [GO:0004674 "protein serine/threonine kinase activity" evidence=ISS] [GO:0005524 "ATP binding" evidence=ISS] [GO:0006468 "protein phosphorylation" evidence=IEA;ISS] [GO:0007169 "transmembrane receptor protein tyrosine kinase signaling pathway" evidence=ISS] [GO:0016301 "kinase activity" evidence=ISS] Pfam:PF00560 InterPro:IPR001611 InterPro:IPR000719 InterPro:IPR001245 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 Pfam:PF07714 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005524 eggNOG:COG0515 GO:GO:0004872 SUPFAM:SSF56112 GO:GO:0004674 HSSP:P36897 InterPro:IPR013210 Pfam:PF08263 HOGENOM:HBG316990 EMBL:FJ708684 EMBL:AK117863 IPI:IPI00517320 RefSeq:NP_178080.2 UniGene:At.46098 ProteinModelPortal:Q8GY50 SMR:Q8GY50 PRIDE:Q8GY50 EnsemblPlants:AT1G79620.1 GeneID:844301 KEGG:ath:AT1G79620 TAIR:At1g79620 InParanoid:Q8GY50 OMA:YFIASPY PhylomeDB:Q8GY50 ProtClustDB:CLSN2680668 Genevestigator:Q8GY50 Uniprot:Q8GY50
Root	Isotig08333	1	23	-4.653	5.84E-07	TAIR|locus:2122113 - symbol:XCP1 "xylem cysteine peptidase 1" species:3702 "Arabidopsis thaliana" [GO:0004197 "cysteine-type endopeptidase activity" evidence=IEA] [GO:0006508 "proteolysis" evidence=ISS] [GO:0008234 "cysteine-type peptidase activity" evidence=IEA;ISS] [GO:0000325 "plant-type vacuole" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0010623 "developmental programmed cell death" evidence=IMP] InterPro:IPR000668 InterPro:IPR013128 Pfam:PF00112 PRINTS:PR00705 SMART:SM00645 InterPro:IPR000169 GO:GO:0005886 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005634 eggNOG:COG4870 HOGENOM:HBG746690 GO:GO:0004197 GO:GO:0006508 InterPro:IPR013201 PANTHER:PTHR12411 Pfam:PF08246 SMART:SM00848 PROSITE:PS00640 PROSITE:PS00139 PROSITE:PS00639 GO:GO:0000325 EMBL:AL161587 EMBL:AL022604 GO:GO:0010623 KO:K01376 EMBL:AF191027 EMBL:AK117394 EMBL:BT005179 IPI:IPI00532220 PIR:T06122 RefSeq:NP_567983.1 UniGene:At.2280 UniGene:At.67622 ProteinModelPortal:O65493 SMR:O65493 STRING:O65493 MEROPS:C01.065 PRIDE:O65493 EnsemblPlants:AT4G35350.1 GeneID:829688 KEGG:ath:AT4G35350 GeneFarm:5033 TAIR:At4g35350 InParanoid:O65493 OMA:FEVFREN PhylomeDB:O65493 ProtClustDB:CLSN2689772 Genevestigator:O65493 Uniprot:O65493
Root	Isotig08334	1	23	-4.653	5.84E-07	TAIR|locus:2122113 - symbol:XCP1 "xylem cysteine peptidase 1" species:3702 "Arabidopsis thaliana" [GO:0004197 "cysteine-type endopeptidase activity" evidence=IEA] [GO:0006508 "proteolysis" evidence=ISS] [GO:0008234 "cysteine-type peptidase activity" evidence=IEA;ISS] [GO:0000325 "plant-type vacuole" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0010623 "developmental programmed cell death" evidence=IMP] InterPro:IPR000668 InterPro:IPR013128 Pfam:PF00112 PRINTS:PR00705 SMART:SM00645

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						InterPro:IPR000169 GO:GO:0005886 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005634 eggNOG:COG4870 HOGENOM:HBG746690 GO:GO:0004197 GO:GO:0006508 InterPro:IPR013201 PANTHER:PTHR12411 Pfam:PF08246 SMART:SM00848 PROSITE:PS00640 PROSITE:PS00139 PROSITE:PS00639 GO:GO:0000325 EMBL:AL161587 EMBL:AL022604 GO:GO:0010623 KO:K01376 EMBL:AF191027 EMBL:AK117394 EMBL:BT005179 IPI:IPI00532220 PIR:T06122 RefSeq:NP_567983.1 UniGene:At.2280 UniGene:At.67622 ProteinModelPortal:O65493 SMR:O65493 STRING:O65493 MEROPS:C01.065 PRIDE:O65493 EnsemblPlants:AT4G35350.1 GeneID:829688 KEGG:ath:AT4G35350 GeneFarm:5033 TAIR:At4g35350 InParanoid:O65493 OMA:FEVFREN PhylomeDB:O65493 ProtClustDB:CLSN2689772 Genevestigator:O65493 Uniprot:O65493
Root	Isotig08353	27	0	5.626	1.24E-07	TAIR|locus:2124784 - symbol:WIN2 "AT4G31750" species:3702 "Arabidopsis thaliana" [GO:0004722 "protein serine/threonine phosphatase activity" evidence=ISS;IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0006470 "protein dephosphorylation" evidence=IDA] [GO:0042742 "defense response to bacterium" evidence=IMP] [GO:0044419 "interspecies interaction between organisms" evidence=IPI] InterPro:IPR000222 InterPro:IPR001932 Pfam:PF00481 PROSITE:PS01032 SMART:SM00331 SMART:SM00332 GO:GO:0005886 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0042742 GO:GO:0044419 GO:GO:0006470 GO:GO:0004722 GO:GO:0046872 eggNOG:COG0631 Gene3D:G3DSA:3.60.40.10 SUPFAM:SSF81606 EMBL:AL161579 EMBL:AL031004 GO:GO:0008287 InterPro:IPR015655 PANTHER:PTHR13832 HSSP:P35813 HOGENOM:HBG747569 EMBL:EU214909 EMBL:AY080658 EMBL:AY133761 IPI:IPI00537408 PIR:T05095 RefSeq:NP_194903.2 UniGene:At.31716 UniGene:At.51039 ProteinModelPortal:Q8RXV3 SMR:Q8RXV3 PRIDE:Q8RXV3 EnsemblPlants:AT4G31750.1 GeneID:829303 KEGG:ath:AT4G31750 TAIR:At4g31750 InParanoid:Q8RXV3 OMA:DIMTFDL PhylomeDB:Q8RXV3 ProtClustDB:CLSN2680208 Genevestigator:Q8RXV3 Uniprot:Q8RXV3
Root	Isotig08354	30	0	5.778	2.46E-08	TAIR|locus:2124784 - symbol:WIN2 "AT4G31750" species:3702 "Arabidopsis thaliana" [GO:0004722 "protein serine/threonine phosphatase activity" evidence=ISS;IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0006470 "protein dephosphorylation" evidence=IDA] [GO:0042742 "defense response to bacterium" evidence=IMP] [GO:0044419 "interspecies interaction between organisms" evidence=IPI] InterPro:IPR000222 InterPro:IPR001932 Pfam:PF00481 PROSITE:PS01032 SMART:SM00331 SMART:SM00332 GO:GO:0005886 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0042742 GO:GO:0044419 GO:GO:0006470 GO:GO:0004722 GO:GO:0046872 eggNOG:COG0631 Gene3D:G3DSA:3.60.40.10 SUPFAM:SSF81606 EMBL:AL161579 EMBL:AL031004 GO:GO:0008287 InterPro:IPR015655 PANTHER:PTHR13832 HSSP:P35813 HOGENOM:HBG747569 EMBL:EU214909 EMBL:AY080658 EMBL:AY133761 IPI:IPI00537408 PIR:T05095 RefSeq:NP_194903.2 UniGene:At.31716 UniGene:At.51039 ProteinModelPortal:Q8RXV3 SMR:Q8RXV3 PRIDE:Q8RXV3 EnsemblPlants:AT4G31750.1 GeneID:829303 KEGG:ath:AT4G31750 TAIR:At4g31750 InParanoid:Q8RXV3 OMA:DIMTFDL PhylomeDB:Q8RXV3 ProtClustDB:CLSN2680208 Genevestigator:Q8RXV3 Uniprot:Q8RXV3
Root	Isotig08367	1	13	-3.829	0.000362856	TAIR|locus:2147117 - symbol:AT5G20950 species:3702 "Arabidopsis thaliana" [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=IEA;ISS] [GO:0005975 "carbohydrate metabolic process" evidence=IEA;ISS] [GO:0005618 "cell wall" evidence=IDA] [GO:0009505 "plant-type cell wall" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR001764 InterPro:IPR002772 Pfam:PF00933 Pfam:PF01915 PRINTS:PR00133 GO:GO:0009506 EMBL:CP002688 GO:GO:0016020 InterPro:IPR017853 SUPFAM:SSF51445 GO:GO:0005975 GO:GO:0004553 GO:GO:0009505 Gene3D:G3DSA:3.40.50.1700 Gene3D:G3DSA:3.20.20.300 SUPFAM:SSF52279 CAZy:GH3 HSSP:Q9XEI3 EMBL:AF462808 EMBL:AY091027 EMBL:AY142679 IPI:IPI00528669 RefSeq:NP_197595.2 RefSeq:NP_851048.1 UniGene:At.23560 ProteinModelPortal:Q8W112 SMR:Q8W112 PRIDE:Q8W112 EnsemblPlants:AT5G20950.1 EnsemblPlants:AT5G20950.2 GeneID:832220 KEGG:ath:AT5G20950 TAIR:At5g20950 InParanoid:Q8W112 OMA:THNGINE PhylomeDB:Q8W112 ProtClustDB:CLSN2690178 ArrayExpress:Q8W112 Genevestigator:Q8W112 Uniprot:Q8W112
Root	Isotig08368	1	13	-3.829	0.000362856	TAIR|locus:2147117 - symbol:AT5G20950 species:3702 "Arabidopsis thaliana" [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=IEA;ISS] [GO:0005975 "carbohydrate metabolic process" evidence=IEA;ISS] [GO:0005618 "cell wall" evidence=IDA] [GO:0009505 "plant-type cell wall" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR001764 InterPro:IPR002772 Pfam:PF00933 Pfam:PF01915 PRINTS:PR00133

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0009506 EMBL:CP002688 GO:GO:0016020 InterPro:IPR017853 SUPFAM:SSF51445 GO:GO:0005975 GO:GO:0004553 GO:GO:0009505 Gene3D:G3DSA:3.40.50.1700 Gene3D:G3DSA:3.20.20.300 SUPFAM:SSF52279 CAZy:GH3 HSSP:Q9XEI3 EMBL:AF462808 EMBL:AY091027 EMBL:AY142679 IPI:IPI00528669 RefSeq:NP_197595.2 RefSeq:NP_851048.1 UniGene:At.23560 ProteinModelPortal:Q8W112 SMR:Q8W112 PRIDE:Q8W112 EnsemblPlants:AT5G20950.1 EnsemblPlants:AT5G20950.2 GeneID:832220 KEGG:ath:AT5G20950 TAIR:At5g20950 InParanoid:Q8W112 OMA:THNGINE PhylomeDB:Q8W112 ProtClustDB:CLSN2690178 ArrayExpress:Q8W112 Genevestigator:Q8W112 Uniprot:Q8W112
Root	Isotig08373	19	0	5.119	1.05E-05	TAIR|locus:2025966 - symbol:E1 ALPHA "pyruvate dehydrogenase complex E1 alpha subunit" species:3702 "Arabidopsis thaliana" [GO:0004739 "pyruvate dehydrogenase (acetyl-transferring) activity" evidence=IEA;ISS] [GO:0008152 "metabolic process" evidence=ISS] [GO:0016624 "oxidoreductase activity, acting on the aldehyde or oxo group of donors, disulfide as acceptor" evidence=IEA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005634 "nucleus" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001017 InterPro:IPR017597 Pfam:PF00676 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0005634 GO:GO:0046686 GO:GO:0005759 EMBL:AC007258 GO:GO:0006096 GO:GO:0004739 eggNOG:COG1071 HOGENOM:HBG753263 EMBL:U21214 EMBL:AF360306 EMBL:BT000974 EMBL:AY087667 IPI:IPI00531318 PIR:B96623 PIR:JC4358 RefSeq:NP_176198.1 UniGene:At.23186 ProteinModelPortal:P52901 SMR:P52901 IntAct:P52901 STRING:P52901 SWISS-2DPAGE:P52901 PRIDE:P52901 EnsemblPlants:AT1G59900.1 GeneID:842284 KEGG:ath:AT1G59900 GeneFarm:4372 TAIR:At1g59900 InParanoid:P52901 KO:K00161 OMA:IVENNRY PhylomeDB:P52901 ProtClustDB:PLN02269 ArrayExpress:P52901 Genevestigator:P52901 GermOnline:AT1G59900 TIGRFAMs:TIGR03182 Uniprot:P52901
Root	Isotig08385	214	0	8.612	5.02E-42	TAIR|locus:2025346 - symbol:LEA14 "AT1G01470" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0009269 "response to desiccation" evidence=ISS] [GO:0009793 "embryo development ending in seed dormancy" evidence=ISS] [GO:0009644 "response to high light intensity" evidence=IEP] [GO:0009611 "response to wounding" evidence=IEP] [GO:0050832 "defense response to fungus" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR013990 SMART:SM00769 InterPro:IPR004864 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 InterPro:IPR013783 Gene3D:G3DSA:2.60.40.10 EMBL:Y12776 EMBL:AC061957 GO:GO:0009611 GO:GO:0050832 GO:GO:0009644 GO:GO:0009269 EMBL:Y10085 EMBL:AY074855 EMBL:BT015111 EMBL:Z37258 IPI:IPI00525938 PIR:D86145 RefSeq:NP_171654.1 UniGene:At.25113 PDB:1XO8 PDBsum:1XO8 ProteinModelPortal:O03983 SMR:O03983 IntAct:O03983 STRING:O03983 PRIDE:O03983 DNASU:837071 EnsemblPlants:AT1G01470.1 GeneID:837071 KEGG:ath:AT1G01470 TAIR:At1g01470 eggNOG:NOG271766 HOGENOM:HBG320411 InParanoid:O03983 OMA:YSHSIPI PhylomeDB:O03983 ProtClustDB:CLSN2682861 Genevestigator:O03983 GermOnline:AT1G01470 Pfam:PF03168 Uniprot:O03983
Root	Isotig08386	215	0	8.619	3.50E-42	TAIR|locus:2025346 - symbol:LEA14 "AT1G01470" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0009269 "response to desiccation" evidence=ISS] [GO:0009793 "embryo development ending in seed dormancy" evidence=ISS] [GO:0009644 "response to high light intensity" evidence=IEP] [GO:0009611 "response to wounding" evidence=IEP] [GO:0050832 "defense response to fungus" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR013990 SMART:SM00769 InterPro:IPR004864 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 InterPro:IPR013783 Gene3D:G3DSA:2.60.40.10 EMBL:Y12776 EMBL:AC061957 GO:GO:0009611 GO:GO:0050832 GO:GO:0009644 GO:GO:0009269 EMBL:Y10085 EMBL:AY074855 EMBL:BT015111 EMBL:Z37258 IPI:IPI00525938 PIR:D86145 RefSeq:NP_171654.1 UniGene:At.25113 PDB:1XO8 PDBsum:1XO8 ProteinModelPortal:O03983 SMR:O03983 IntAct:O03983 STRING:O03983 PRIDE:O03983 DNASU:837071 EnsemblPlants:AT1G01470.1 GeneID:837071 KEGG:ath:AT1G01470 TAIR:At1g01470 eggNOG:NOG271766 HOGENOM:HBG320411 InParanoid:O03983 OMA:YSHSIPI PhylomeDB:O03983 ProtClustDB:CLSN2682861 Genevestigator:O03983 GermOnline:AT1G01470 Pfam:PF03168 Uniprot:O03983
Root	Isotig08411	16	2	2.871	0.000812389	No hit
Root	Isotig08412	17	0	4.958	3.30E-05	TAIR|locus:2154930 - symbol:RAB18 "AT5G66400" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] [GO:0009631 "cold acclimation" evidence=IGI] [GO:0009961 "response to 1-aminocyclopropane-1-carboxylic acid" evidence=IEP] [GO:0009414 "response to water deprivation" evidence=IEP]

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						[GO:0006950 "response to stress" evidence=IEP] InterPro:IPR000167 Pfam:PF00257 PROSITE:PS00315 PROSITE:PS00823 GO:GO:0009737 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009414 GO:GO:0009631 EMBL:AB013389 EMBL:X68042 EMBL:L04173 EMBL:AF428458 EMBL:AY093779 EMBL:BT002226 IPI:IPI00540524 PIR:S28021 RefSeq:NP_201441.1 UniGene:At.20221 UniGene:At.74882 STRING:P30185 PRIDE:P30185 EnsemblPlants:AT5G66400.1 GeneID:836772 KEGG:ath:AT5G66400 TAIR:At5g66400 eggNOG:NOG291924 InParanoid:P30185 OMA:MGTHGTT PhylomeDB:P30185 ProtClustDB:CLSN2686697 ArrayExpress:P30185 Genevestigator:P30185 GO:GO:0009961 Uniprot:P30185
Root	Isotig08431	27	4	2.626	3.31E-05	TAIR|locus:2119682 - symbol:AT4G21580 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0008152 "metabolic process" evidence=IEA] [GO:0008270 "zinc ion binding" evidence=IEA;ISS] [GO:0016491 "oxidoreductase activity" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR002085 InterPro:IPR013149 InterPro:IPR013154 InterPro:IPR016040 Pfam:PF00107 Pfam:PF08240 GO:GO:0005829 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 GO:GO:0008270 GO:GO:0016491 HOGENOM:HBG753318 InterPro:IPR011032 PANTHER:PTHR11695 SUPFAM:SSF50129 EMBL:AL035527 EMBL:AL161555 EMBL:AL022603 OMA:IPEVWLT InterPro:IPR014189 PANTHER:PTHR11695:SF28 TIGRFAMs:TIGR02824 HSSP:Q8L3C8 EMBL:AF411784 EMBL:AY088237 EMBL:AY124814 IPI:IPI00539765 PIR:T05166 RefSeq:NP_193889.1 UniGene:At.2271 ProteinModelPortal:O65423 SMR:O65423 PRIDE:O65423 EnsemblPlants:AT4G21580.1 GeneID:828243 KEGG:ath:AT4G21580 TAIR:At4g21580 InParanoid:O65423 PhylomeDB:O65423 ProtClustDB:CLSN2685583 ArrayExpress:O65423 Genevestigator:O65423 Uniprot:O65423
Root	Isotig08432	27	4	2.626	3.31E-05	TAIR|locus:2119682 - symbol:AT4G21580 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0008152 "metabolic process" evidence=IEA] [GO:0008270 "zinc ion binding" evidence=IEA;ISS] [GO:0016491 "oxidoreductase activity" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR002085 InterPro:IPR013149 InterPro:IPR013154 InterPro:IPR016040 Pfam:PF00107 Pfam:PF08240 GO:GO:0005829 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 GO:GO:0008270 GO:GO:0016491 HOGENOM:HBG753318 InterPro:IPR011032 PANTHER:PTHR11695 SUPFAM:SSF50129 EMBL:AL035527 EMBL:AL161555 EMBL:AL022603 OMA:IPEVWLT InterPro:IPR014189 PANTHER:PTHR11695:SF28 TIGRFAMs:TIGR02824 HSSP:Q8L3C8 EMBL:AF411784 EMBL:AY088237 EMBL:AY124814 IPI:IPI00539765 PIR:T05166 RefSeq:NP_193889.1 UniGene:At.2271 ProteinModelPortal:O65423 SMR:O65423 PRIDE:O65423 EnsemblPlants:AT4G21580.1 GeneID:828243 KEGG:ath:AT4G21580 TAIR:At4g21580 InParanoid:O65423 PhylomeDB:O65423 ProtClustDB:CLSN2685583 ArrayExpress:O65423 Genevestigator:O65423 Uniprot:O65423
Root	Isotig08447	7	85	-3.731	1.62E-19	TAIR|locus:2117939 - symbol:PIP1;5 "AT4G23400" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=ISS] [GO:0015250 "water channel activity" evidence=ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000425 InterPro:IPR012269 InterPro:IPR022357 Pfam:PF00230 PRINTS:PR00783 PROSITE:PS00221 GO:GO:0016021 GO:GO:0005886 GO:GO:0009506 EMBL:CP002687 GenomeReviews:CT486007_GR EMBL:AL161559 GO:GO:0055085 GO:GO:0005215 GO:GO:0006833 EMBL:AL031326 InterPro:IPR023271 Gene3D:G3DSA:1.20.1080.10 SUPFAM:SSF81338 eggNOG:COG0580 HOGENOM:HBG705794 PANTHER:PTHR19139 TIGRFAMs:TIGR00861 KO:K09872 ProtClustDB:CLSN2682869 EMBL:AY059948 EMBL:AY081593 EMBL:AY087945 IPI:IPI00536498 PIR:T05378 RefSeq:NP_194071.1 UniGene:At.2438 ProteinModelPortal:Q8LAA6 SMR:Q8LAA6 IntAct:Q8LAA6 STRING:Q8LAA6 PRIDE:Q8LAA6 EnsemblPlants:AT4G23400.1 GeneID:828439 KEGG:ath:AT4G23400 GeneFarm:4865 TAIR:At4g23400 InParanoid:Q8LAA6 OMA:YDFLLAP PhylomeDB:Q8LAA6 ArrayExpress:Q8LAA6 Genevestigator:Q8LAA6 GermOnline:AT4G23400 Uniprot:Q8LAA6
Root	Isotig08448	7	85	-3.731	1.62E-19	TAIR|locus:2117939 - symbol:PIP1;5 "AT4G23400" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=ISS] [GO:0015250 "water channel activity" evidence=ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000425 InterPro:IPR012269 InterPro:IPR022357 Pfam:PF00230 PRINTS:PR00783 PROSITE:PS00221 GO:GO:0016021 GO:GO:0005886 GO:GO:0009506 EMBL:CP002687 GenomeReviews:CT486007_GR EMBL:AL161559 GO:GO:0055085 GO:GO:0005215 GO:GO:0006833 EMBL:AL031326 InterPro:IPR023271 Gene3D:G3DSA:1.20.1080.10 SUPFAM:SSF81338 eggNOG:COG0580 HOGENOM:HBG705794 PANTHER:PTHR19139 TIGRFAMs:TIGR00861 KO:K09872 ProtClustDB:CLSN2682869 EMBL:AY059948

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EMBL:AY081593 EMBL:AY087945 IPI:IPI00536498 PIR:T05378 RefSeq:NP_194071.1 UniGene:At.2438 ProteinModelPortal:Q8LAA6 SMR:Q8LAA6 IntAct:Q8LAA6 STRING:Q8LAA6 PRIDE:Q8LAA6 EnsemblPlants:AT4G23400.1 GeneID:828439 KEGG:ath:AT4G23400 GeneFarm:4865 TAIR:At4g23400 InParanoid:Q8LAA6 OMA:YDFLLAP PhylomeDB:Q8LAA6 ArrayExpress:Q8LAA6 Genevestigator:Q8LAA6 GermOnline:AT4G23400 Uniprot:Q8LAA6
Root	Isotig08449	0	11	-4.588	0.000569522	No hit
Root	Isotig08450	0	11	-4.588	0.000569522	No hit
Root	Isotig08461	4	25	-2.773	1.71E-05	TAIR|locus:2077502 - symbol:AT3G07720 "AT3G07720" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0010043 "response to zinc ion" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR006652 InterPro:IPR015915 Pfam:PF01344 GO:GO:0005829 GO:GO:0005634 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0010043 Gene3D:G3DSA:2.120.10.80 EMBL:AC013483 EMBL:AC009176 HOGENOM:HBG329174 ProtClustDB:CLSN2688154 EMBL:AF324668 EMBL:AF329503 EMBL:AY039559 EMBL:AY113872 EMBL:BT000850 IPI:IPI00543372 RefSeq:NP_566316.1 UniGene:At.18342 ProteinModelPortal:Q9S7W4 SMR:Q9S7W4 IntAct:Q9S7W4 STRING:Q9S7W4 PRIDE:Q9S7W4 ProMEX:Q9S7W4 DNASU:819963 EnsemblPlants:AT3G07720.1 GeneID:819963 KEGG:ath:AT3G07720 TAIR:At3g07720 eggNOG:NOG293724 InParanoid:Q9S7W4 OMA:DDIFFFT PhylomeDB:Q9S7W4 ArrayExpress:Q9S7W4 Genevestigator:Q9S7W4 Uniprot:Q9S7W4
Root	Isotig08462	3	25	-3.188	4.22E-06	TAIR|locus:2077502 - symbol:AT3G07720 "AT3G07720" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0010043 "response to zinc ion" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR006652 InterPro:IPR015915 Pfam:PF01344 GO:GO:0005829 GO:GO:0005634 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0010043 Gene3D:G3DSA:2.120.10.80 EMBL:AC013483 EMBL:AC009176 HOGENOM:HBG329174 ProtClustDB:CLSN2688154 EMBL:AF324668 EMBL:AF329503 EMBL:AY039559 EMBL:AY113872 EMBL:BT000850 IPI:IPI00543372 RefSeq:NP_566316.1 UniGene:At.18342 ProteinModelPortal:Q9S7W4 SMR:Q9S7W4 IntAct:Q9S7W4 STRING:Q9S7W4 PRIDE:Q9S7W4 ProMEX:Q9S7W4 DNASU:819963 EnsemblPlants:AT3G07720.1 GeneID:819963 KEGG:ath:AT3G07720 TAIR:At3g07720 eggNOG:NOG293724 InParanoid:Q9S7W4 OMA:DDIFFFT PhylomeDB:Q9S7W4 ArrayExpress:Q9S7W4 Genevestigator:Q9S7W4 Uniprot:Q9S7W4
Root	Isotig08465	23	4	2.395	0.000276124	TAIR|locus:2153117 - symbol:AT5G51570 species:3702 "Arabidopsis thaliana" [GO:0005773 "vacuole" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR001972 InterPro:IPR001107 Pfam:PF01145 GO:GO:0005886 GO:GO:0009506 GO:GO:0005774 EMBL:CP002688 GenomeReviews:BA000015_GR eggNOG:COG0330 PANTHER:PTHR10264 SMART:SM00244 EMBL:AB018109 HOGENOM:HBG519201 ProtClustDB:CLSN2682581 EMBL:BT006203 EMBL:AK227961 IPI:IPI00518030 RefSeq:NP_199970.1 UniGene:At.7811 ProteinModelPortal:Q9FHM7 SMR:Q9FHM7 IntAct:Q9FHM7 STRING:Q9FHM7 PRIDE:Q9FHM7 EnsemblPlants:AT5G51570.1 GeneID:835231 KEGG:ath:AT5G51570 TAIR:At5g51570 InParanoid:Q9FHM7 OMA:SIEHILM PhylomeDB:Q9FHM7 Genevestigator:Q9FHM7 Uniprot:Q9FHM7
Root	Isotig08466	23	4	2.395	0.000276124	TAIR|locus:2153117 - symbol:AT5G51570 species:3702 "Arabidopsis thaliana" [GO:0005773 "vacuole" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR001972 InterPro:IPR001107 Pfam:PF01145 GO:GO:0005886 GO:GO:0009506 GO:GO:0005774 EMBL:CP002688 GenomeReviews:BA000015_GR eggNOG:COG0330 PANTHER:PTHR10264 SMART:SM00244 EMBL:AB018109 HOGENOM:HBG519201 ProtClustDB:CLSN2682581 EMBL:BT006203 EMBL:AK227961 IPI:IPI00518030 RefSeq:NP_199970.1 UniGene:At.7811 ProteinModelPortal:Q9FHM7 SMR:Q9FHM7 IntAct:Q9FHM7 STRING:Q9FHM7 PRIDE:Q9FHM7 EnsemblPlants:AT5G51570.1 GeneID:835231 KEGG:ath:AT5G51570 TAIR:At5g51570 InParanoid:Q9FHM7 OMA:SIEHILM PhylomeDB:Q9FHM7 Genevestigator:Q9FHM7 Uniprot:Q9FHM7
Root	Isotig08467	4	37	-3.338	1.13E-08	No hit
Root	Isotig08468	3	33	-3.588	2.85E-08	No hit

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig08501	46	1	5.395	5.60E-12	TAIR|locus:2084598 - symbol:AT3G22850 "AT3G22850" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009737 "response to abscisic acid stimulus" evidence=IDA] GO:GO:0005829 GO:GO:0005886 GO:GO:0009737 GO:GO:0005634 EMBL:CP002686 GenomeReviews:BA000014_GR EMBL:AP001300 eggNOG:COG0367 InterPro:IPR024286 Pfam:PF12481 HOGENOM:HBG605462 ProtClustDB:CLSN2684172 EMBL:AY072385 EMBL:AY114623 IPI:IPI00535884 RefSeq:NP_188925.1 UniGene:At.28093 UniGene:At.67702 ProteinModelPortal:Q9LIL3 SMR:Q9LIL3 PRIDE:Q9LIL3 ProMEX:Q9LIL3 EnsemblPlants:AT3G22850.1 GeneID:821857 KEGG:ath:AT3G22850 TAIR:At3g22850 InParanoid:Q9LIL3 OMA:EVTIVIE PhylomeDB:Q9LIL3 ArrayExpress:Q9LIL3 Genevestigator:Q9LIL3 Uniprot:Q9LIL3
Root	Isotig08502	47	1	5.426	3.25E-12	TAIR|locus:2084598 - symbol:AT3G22850 "AT3G22850" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009737 "response to abscisic acid stimulus" evidence=IDA] GO:GO:0005829 GO:GO:0005886 GO:GO:0009737 GO:GO:0005634 EMBL:CP002686 GenomeReviews:BA000014_GR EMBL:AP001300 eggNOG:COG0367 InterPro:IPR024286 Pfam:PF12481 HOGENOM:HBG605462 ProtClustDB:CLSN2684172 EMBL:AY072385 EMBL:AY114623 IPI:IPI00535884 RefSeq:NP_188925.1 UniGene:At.28093 UniGene:At.67702 ProteinModelPortal:Q9LIL3 SMR:Q9LIL3 PRIDE:Q9LIL3 ProMEX:Q9LIL3 EnsemblPlants:AT3G22850.1 GeneID:821857 KEGG:ath:AT3G22850 TAIR:At3g22850 InParanoid:Q9LIL3 OMA:EVTIVIE PhylomeDB:Q9LIL3 ArrayExpress:Q9LIL3 Genevestigator:Q9LIL3 Uniprot:Q9LIL3
Root	Isotig08509	14	0	4.678	0.000190242	TAIR|locus:2129695 - symbol:CYP97B3 ""cytochrome P450, family 97, subfamily B, polypeptide 3"" species:3702 "Arabidopsis thaliana" [GO:0004497 "monooxygenase activity" evidence=IEA] [GO:0005506 "iron ion binding" evidence=IEA] [GO:0009055 "electron carrier activity" evidence=IEA] [GO:0019825 "oxygen binding" evidence=ISS] [GO:0020037 "heme binding" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] InterPro:IPR001128 InterPro:IPR002401 InterPro:IPR017972 Pfam:PF00067 PRINTS:PR00385 PRINTS:PR00463 PROSITE:PS00086 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0009570 GO:GO:0009055 GO:GO:0004497 GO:GO:0031969 EMBL:AL161540 eggNOG:COG2124 GO:GO:0020037 Gene3D:G3DSA:1.10.630.10 SUPFAM:SSF48264 GO:GO:0016117 GO:GO:0016705 EMBL:Z97337 EMBL:AY062675 EMBL:BT002582 IPI:IPI00532091 PIR:H71414 RefSeq:NP_193247.2 UniGene:At.27265 ProteinModelPortal:O23365 SMR:O23365 STRING:O23365 PRIDE:O23365 EnsemblPlants:AT4G15110.1 GeneID:827177 KEGG:ath:AT4G15110 GeneFarm:1346 TAIR:At4g15110 HOGENOM:HBG748119 InParanoid:O23365 OMA:ALMESTV PhylomeDB:O23365 ProtClustDB:CLSN2690929 ArrayExpress:O23365 Genevestigator:O23365 GermOnline:AT4G15110 Uniprot:O23365
Root	Isotig08511	0	12	-4.714	0.000297064	TAIR|locus:2157712 - symbol:CEP1 "cysteine endopeptidase 1" species:3702 "Arabidopsis thaliana" [GO:0004197 "cysteine-type endopeptidase activity" evidence=IEA] [GO:0006508 "proteolysis" evidence=IEA;ISS] [GO:0008234 "cysteine-type peptidase activity" evidence=IEA;ISS] InterPro:IPR000668 InterPro:IPR013128 Pfam:PF00112 PRINTS:PR00705 SMART:SM00645 InterPro:IPR000169 GO:GO:0005783 EMBL:CP002688 GenomeReviews:BA000015_GR eggNOG:COG4870 HOGENOM:HBG746690 GO:GO:0004197 GO:GO:0006508 InterPro:IPR013201 PANTHER:PTHR12411 Pfam:PF08246 SMART:SM00848 PROSITE:PS00640 PROSITE:PS00139 PROSITE:PS00639 PROSITE:PS00014 EMBL:AB024031 EMBL:HM367092 EMBL:AY091087 IPI:IPI00516991 RefSeq:NP_568722.1 UniGene:At.7918 HSSP:O65039 ProteinModelPortal:Q9FGR9 SMR:Q9FGR9 MEROPS:C01.A03 PRIDE:Q9FGR9 EnsemblPlants:AT5G50260.1 GeneID:835091 KEGG:ath:AT5G50260 TAIR:At5g50260 InParanoid:Q9FGR9 KO:K01376 OMA:WELYERW PhylomeDB:Q9FGR9 ProtClustDB:CLSN2689970 ArrayExpress:Q9FGR9 Genevestigator:Q9FGR9 Uniprot:Q9FGR9
Root	Isotig08512	0	12	-4.714	0.000297064	TAIR|locus:2152445 - symbol:SAG12 "AT5G45890" species:3702 "Arabidopsis thaliana" [GO:0006508 "proteolysis" evidence=ISS] [GO:0008234 "cysteine-type peptidase activity" evidence=ISS] [GO:0009723 "response to ethylene stimulus" evidence=IEP] [GO:0007568 "aging" evidence=IEP;TAS] [GO:0010150 "leaf senescence" evidence=TAS] [GO:0010282 "senescence-associated vacuole" evidence=IDA] [GO:0009817 "defense response to fungus, incompatible interaction" evidence=IEP] InterPro:IPR000668 InterPro:IPR013128 Pfam:PF00112 PRINTS:PR00705 SMART:SM00645 InterPro:IPR000169 EMBL:CP002688 GO:GO:0004197 GO:GO:0006508 InterPro:IPR013201 PANTHER:PTHR12411 Pfam:PF08246 SMART:SM00848 PROSITE:PS00640 PROSITE:PS00139

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						PROSITE:PS00639 GO:GO:0010150 GO:GO:0009817 EMBL:AB016870 HSSP:O65039 EMBL:AF370131 EMBL:AY040073 IPI:IPI00544181 RefSeq:NP_568651.1 UniGene:At.75256 UniGene:At.7710 ProteinModelPortal:Q9FJ47 SMR:Q9FJ47 IntAct:Q9FJ47 STRING:Q9FJ47 MEROPS:C01.117 PRIDE:Q9FJ47 EnsemblPlants:AT5G45890.1 GeneID:834629 KEGG:ath:AT5G45890 TAIR:At5g45890 InParanoid:Q9FJ47 OMA:NDEQALM PhylomeDB:Q9FJ47 ProtClustDB:CLSN2917735 ArrayExpress:Q9FJ47 Genevestigator:Q9FJ47 GO:GO:0010282 Uniprot:Q9FJ47
Root	Isotig08533	5	31	-2.761	1.77E-06	TAIR|locus:2117939 - symbol:PIP1;5 "AT4G23400" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=ISS] [GO:0015250 "water channel activity" evidence=ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000425 InterPro:IPR012269 InterPro:IPR022357 Pfam:PF00230 PRINTS:PR00783 PROSITE:PS00221 GO:GO:0016021 GO:GO:0005886 GO:GO:0009506 EMBL:CP002687 GenomeReviews:CT486007_GR EMBL:AL161559 GO:GO:0055085 GO:GO:0005215 GO:GO:0006833 EMBL:AL031326 InterPro:IPR023271 Gene3D:G3DSA:1.20.1080.10 SUPFAM:SSF81338 eggNOG:COG0580 HOGENOM:HBG705794 PANTHER:PTHR19139 TIGRFAMs:TIGR00861 KO:K09872 ProtClustDB:CLSN2682869 EMBL:AY059948 EMBL:AY081593 EMBL:AY087945 IPI:IPI00536498 PIR:T05378 RefSeq:NP_194071.1 UniGene:At.2438 ProteinModelPortal:Q8LAA6 SMR:Q8LAA6 IntAct:Q8LAA6 STRING:Q8LAA6 PRIDE:Q8LAA6 EnsemblPlants:AT4G23400.1 GeneID:828439 KEGG:ath:AT4G23400 GeneFarm:4865 TAIR:At4g23400 InParanoid:Q8LAA6 OMA:YDFLLAP PhylomeDB:Q8LAA6 ArrayExpress:Q8LAA6 Genevestigator:Q8LAA6 GermOnline:AT4G23400 Uniprot:Q8LAA6
Root	Isotig08534	5	27	-2.562	1.85E-05	TAIR|locus:2117939 - symbol:PIP1;5 "AT4G23400" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=ISS] [GO:0015250 "water channel activity" evidence=ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000425 InterPro:IPR012269 InterPro:IPR022357 Pfam:PF00230 PRINTS:PR00783 PROSITE:PS00221 GO:GO:0016021 GO:GO:0005886 GO:GO:0009506 EMBL:CP002687 GenomeReviews:CT486007_GR EMBL:AL161559 GO:GO:0055085 GO:GO:0005215 GO:GO:0006833 EMBL:AL031326 InterPro:IPR023271 Gene3D:G3DSA:1.20.1080.10 SUPFAM:SSF81338 eggNOG:COG0580 HOGENOM:HBG705794 PANTHER:PTHR19139 TIGRFAMs:TIGR00861 KO:K09872 ProtClustDB:CLSN2682869 EMBL:AY059948 EMBL:AY081593 EMBL:AY087945 IPI:IPI00536498 PIR:T05378 RefSeq:NP_194071.1 UniGene:At.2438 ProteinModelPortal:Q8LAA6 SMR:Q8LAA6 IntAct:Q8LAA6 STRING:Q8LAA6 PRIDE:Q8LAA6 EnsemblPlants:AT4G23400.1 GeneID:828439 KEGG:ath:AT4G23400 GeneFarm:4865 TAIR:At4g23400 InParanoid:Q8LAA6 OMA:YDFLLAP PhylomeDB:Q8LAA6 ArrayExpress:Q8LAA6 Genevestigator:Q8LAA6 GermOnline:AT4G23400 Uniprot:Q8LAA6
Root	Isotig08539	24	1	4.456	1.32E-06	TAIR|locus:2133945 - symbol:PP2-A1 "AT4G19840" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0030246 "carbohydrate binding" evidence=ISS] [GO:0009625 "response to insect" evidence=IDA] [GO:0043394 "proteoglycan binding" evidence=IDA] EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0009625 EMBL:AL024486 EMBL:AL161551 GO:GO:0043394 HOGENOM:HBG593491 EMBL:AY090355 EMBL:AY122906 EMBL:AY085730 IPI:IPI00545401 PIR:T04765 RefSeq:NP_193719.1 UniGene:At.24681 IntAct:O81865 STRING:O81865 PRIDE:O81865 DNASU:827728 EnsemblPlants:AT4G19840.1 GeneID:827728 KEGG:ath:AT4G19840 TAIR:At4g19840 eggNOG:NOG278951 InParanoid:O81865 OMA:NCFMLFA PhylomeDB:O81865 ProtClustDB:CLSN2915996 ArrayExpress:O81865 Genevestigator:O81865 Uniprot:O81865
Root	Isotig08540	20	1	4.193	1.37E-05	TAIR|locus:2133945 - symbol:PP2-A1 "AT4G19840" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0030246 "carbohydrate binding" evidence=ISS] [GO:0009625 "response to insect" evidence=IDA] [GO:0043394 "proteoglycan binding" evidence=IDA] EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0009625 EMBL:AL024486 EMBL:AL161551 GO:GO:0043394 HOGENOM:HBG593491 EMBL:AY090355 EMBL:AY122906 EMBL:AY085730 IPI:IPI00545401 PIR:T04765 RefSeq:NP_193719.1 UniGene:At.24681 IntAct:O81865 STRING:O81865 PRIDE:O81865 DNASU:827728 EnsemblPlants:AT4G19840.1 GeneID:827728 KEGG:ath:AT4G19840 TAIR:At4g19840 eggNOG:NOG278951 InParanoid:O81865 OMA:NCFMLFA PhylomeDB:O81865 ProtClustDB:CLSN2915996 ArrayExpress:O81865 Genevestigator:O81865 Uniprot:O81865
Root	Isotig08577	19	2	3.119	0.000146225	TAIR|locus:2080585 - symbol:PIP5K4 "AT3G56960" species:3702 "Arabidopsis thaliana" [GO:0016308 "1-phosphatidylinositol-4-phosphate 5-kinase activity" evidence=ISS;IDA] [GO:0005886 "plasma membrane"

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						evidence=IDA] [GO:0010118 "stomatal movement" evidence=IMP] [GO:0006897 "endocytosis" evidence=IMP] [GO:0007164 "establishment of tissue polarity" evidence=IMP] [GO:0009860 "pollen tube growth" evidence=IGI;IMP] [GO:0009827 "plant-type cell wall modification" evidence=IMP] [GO:0009846 "pollen germination" evidence=IGI] [GO:0016324 "apical plasma membrane" evidence=IDA] [GO:0044445 "cytosolic part" evidence=IDA] [GO:0046488 "phosphatidylinositol metabolic process" evidence=IDA] [GO:0090406 "pollen tube" evidence=IDA] InterPro:IPR002498 InterPro:IPR017163 Pfam:PF01504 PIRSF:PIRSF037274 PROSITE:PS51455 GO:GO:0005524 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0016324 GO:GO:0006897 GO:GO:0010118 GO:GO:0009860 GO:GO:0044445 eggNOG:COG4642 InterPro:IPR003409 Pfam:PF02493 SMART:SM00698 EMBL:AL138655 GO:GO:0009846 GO:GO:0009827 InterPro:IPR016034 SMART:SM00330 GO:GO:0090406 GO:GO:0016308 GO:GO:0007164 KO:K00889 InterPro:IPR023610 PANTHER:PTHR23086 HOGENOM:HBG588608 IPI:IPI00523818 PIR:T47756 RefSeq:NP_191255.1 UniGene:At.53961 ProteinModelPortal:Q9M1K2 SMR:Q9M1K2 STRING:Q9M1K2 PRIDE:Q9M1K2 ProMEX:Q9M1K2 EnsemblPlants:AT3G56960.1 GeneID:824863 KEGG:ath:AT3G56960 TAIR:At3g56960 InParanoid:Q9M1K2 OMA:SIQYDPT PhylomeDB:Q9M1K2 ProtClustDB:CLSN2683759 Genevestigator:Q9M1K2 GermOnline:AT3G56960 Uniprot:Q9M1K2
Root	Isotig08603	54	16	1.626	1.54E-05	TAIR|locus:2092492 - symbol:CYSB "AT3G12490" species:3702 "Arabidopsis thaliana" [GO:0004869 "cysteine-type endopeptidase inhibitor activity" evidence=ISS;IDA] [GO:0009628 "response to abiotic stimulus" evidence=IMP] [GO:0050897 "cobalt ion binding" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR000010 Pfam:PF00031 SMART:SM00043 GO:GO:0005829 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005576 GO:GO:0006952 GO:GO:0004869 GO:GO:0050897 EMBL:AP002047 EMBL:AC069474 GO:GO:0009628 InterPro:IPR018073 PROSITE:PS00287 InterPro:IPR020381 ProDom:PD001231 HSSP:P09229 EMBL:AY085950 EMBL:AY065127 EMBL:BT001195 EMBL:AF315737 IPI:IPI00521110 IPI:IPI00657156 RefSeq:NP_566425.1 RefSeq:NP_850570.2 UniGene:At.16910 UniGene:At.48650 ProteinModelPortal:Q8H0X6 SMR:Q8H0X6 STRING:Q8H0X6 PRIDE:Q8H0X6 ProMEX:Q8H0X6 EnsemblPlants:AT3G12490.2 GeneID:820428 KEGG:ath:AT3G12490 TAIR:At3g12490 eggNOG:NOG312503 HOGENOM:HBG317433 InParanoid:Q8H0X6 OMA:FPYELLE PhylomeDB:Q8H0X6 ProtClustDB:CLSN2914970 ArrayExpress:Q8H0X6 Genevestigator:Q8H0X6 Uniprot:Q8H0X6
Root	Isotig08604	53	16	1.599	2.32E-05	TAIR|locus:2092492 - symbol:CYSB "AT3G12490" species:3702 "Arabidopsis thaliana" [GO:0004869 "cysteine-type endopeptidase inhibitor activity" evidence=ISS;IDA] [GO:0009628 "response to abiotic stimulus" evidence=IMP] [GO:0050897 "cobalt ion binding" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR000010 Pfam:PF00031 SMART:SM00043 GO:GO:0005829 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005576 GO:GO:0006952 GO:GO:0004869 GO:GO:0050897 EMBL:AP002047 EMBL:AC069474 GO:GO:0009628 InterPro:IPR018073 PROSITE:PS00287 InterPro:IPR020381 ProDom:PD001231 HSSP:P09229 EMBL:AY085950 EMBL:AY065127 EMBL:BT001195 EMBL:AF315737 IPI:IPI00521110 IPI:IPI00657156 RefSeq:NP_566425.1 RefSeq:NP_850570.2 UniGene:At.16910 UniGene:At.48650 ProteinModelPortal:Q8H0X6 SMR:Q8H0X6 STRING:Q8H0X6 PRIDE:Q8H0X6 ProMEX:Q8H0X6 EnsemblPlants:AT3G12490.2 GeneID:820428 KEGG:ath:AT3G12490 TAIR:At3g12490 eggNOG:NOG312503 HOGENOM:HBG317433 InParanoid:Q8H0X6 OMA:FPYELLE PhylomeDB:Q8H0X6 ProtClustDB:CLSN2914970 ArrayExpress:Q8H0X6 Genevestigator:Q8H0X6 Uniprot:Q8H0X6
Root	Isotig08619	0	11	-4.588	0.000569522	No hit
Root	Isotig08620	0	11	-4.588	0.000569522	ZFIN|ZDB-GENE-050208-453 - symbol:si:dkeyp-34c12.2 "si:dkeyp-34c12.2" species:7955 "Danio rerio" [GO:0007165 "signal transduction" evidence=IEA] Pfam:PF00018 InterPro:IPR002110 InterPro:IPR000159 InterPro:IPR001452 PROSITE:PS50002 PROSITE:PS50088 PROSITE:PS50200 SMART:SM00248 SMART:SM00314 SMART:SM00326 ZFIN:ZDB-GENE-050208-453 GO:GO:0007165 InterPro:IPR020683 Gene3D:G3DSA:1.25.40.20 Pfam:PF12796 SUPFAM:SSF48403 PROSITE:PS50297 SUPFAM:SSF50044 GeneTree:ENSGT00600000084381 EMBL:BX321898 IPI:IPI00998785 Ensembl:ENSDART00000077117 Bgee:F1QLG0 Uniprot:F1QLG0
Root	Isotig08621	0	17	-5.216	1.26E-05	UNIPROTKB|P83304 - symbol:P83304 "Mannose/glucose-specific lectin" species:185447 "Parkia platycephala" [GO:0000771 "agglutination involved in conjugation" evidence=IDA] [GO:0005536 "glucose binding" evidence=IDA] [GO:0005537 "mannose binding" evidence=IDA] [GO:0005575 "cellular_component" evidence=ND] GO:GO:0005537 GO:GO:0005536 InterPro:IPR001229 Gene3D:G3DSA:2.100.10.30 Pfam:PF01419

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						SMART:SM00915 SUPFAM:SSF51101 GO:GO:0000771 PDB:1ZGR PDB:1ZGS PDBsum:1ZGR PDBsum:1ZGS ProteinModelPortal:P83304 SMR:P83304 Uniprot:P83304
Root	Isotig08622	0	17	-5.216	1.26E-05	UNIPROTKB|P83304 - symbol:P83304 "Mannose/glucose-specific lectin" species:185447 "Parkia platycephala" [GO:0000771 "agglutination involved in conjugation" evidence=IDA] [GO:0005536 "glucose binding" evidence=IDA] [GO:0005537 "mannose binding" evidence=IDA] [GO:0005575 "cellular_component" evidence=ND] GO:GO:0005537 GO:GO:0005536 InterPro:IPR001229 Gene3D:G3DSA:2.100.10.30 Pfam:PF01419 SMART:SM00915 SUPFAM:SSF51101 GO:GO:0000771 PDB:1ZGR PDB:1ZGS PDBsum:1ZGR PDBsum:1ZGS ProteinModelPortal:P83304 SMR:P83304 Uniprot:P83304
Root	Isotig08625	14	54	-2.077	9.32E-08	TAIR|locus:2101049 - symbol:CAM7 "calmodulin 7" species:3702 "Arabidopsis thaliana" [GO:0005509 "calcium ion binding" evidence=IEA;ISS] [GO:0005513 "detection of calcium ion" evidence=ISS] [GO:0019722 "calcium-mediated signaling" evidence=IGI] [GO:0005515 "protein binding" evidence=IPI] [GO:0010099 "regulation of photomorphogenesis" evidence=IMP] [GO:0005829 "cytosol" evidence=RCA] InterPro:IPR002048 InterPro:IPR011992 SMART:SM00054 Prosite:PS00018 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005509 GO:GO:0005515 GO:GO:0019722 InterPro:IPR018247 InterPro:IPR018249 Gene3D:G3DSA:1.10.238.10 PROSITE:PS50222 HOGENOM:HBG746798 KO:K02183 ProtClustDB:CLSN2681765 EMBL:AF178073 EMBL:AL162691 EMBL:AY088477 IPI:IPI00533152 PIR:T47417 RefSeq:NP_189967.1 UniGene:At.23208 ProteinModelPortal:P59220 SMR:P59220 IntAct:P59220 STRING:P59220 EnsemblPlants:AT3G43810.1 GeneID:823492 KEGG:ath:AT3G43810 TAIR:At3g43810 InParanoid:P59220 PhylomeDB:P59220 ArrayExpress:P59220 Genevestigator:P59220 GermOnline:AT3G43810 GO:GO:0010099 Uniprot:P59220
Root	Isotig08626	14	51	-1.994	4.31E-07	TAIR|locus:2101049 - symbol:CAM7 "calmodulin 7" species:3702 "Arabidopsis thaliana" [GO:0005509 "calcium ion binding" evidence=IEA;ISS] [GO:0005513 "detection of calcium ion" evidence=ISS] [GO:0019722 "calcium-mediated signaling" evidence=IGI] [GO:0005515 "protein binding" evidence=IPI] [GO:0010099 "regulation of photomorphogenesis" evidence=IMP] [GO:0005829 "cytosol" evidence=RCA] InterPro:IPR002048 InterPro:IPR011992 SMART:SM00054 Prosite:PS00018 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005509 GO:GO:0005515 GO:GO:0019722 InterPro:IPR018247 InterPro:IPR018249 Gene3D:G3DSA:1.10.238.10 PROSITE:PS50222 HOGENOM:HBG746798 KO:K02183 ProtClustDB:CLSN2681765 EMBL:AF178073 EMBL:AL162691 EMBL:AY088477 IPI:IPI00533152 PIR:T47417 RefSeq:NP_189967.1 UniGene:At.23208 ProteinModelPortal:P59220 SMR:P59220 IntAct:P59220 STRING:P59220 EnsemblPlants:AT3G43810.1 GeneID:823492 KEGG:ath:AT3G43810 TAIR:At3g43810 InParanoid:P59220 PhylomeDB:P59220 ArrayExpress:P59220 Genevestigator:P59220 GermOnline:AT3G43810 GO:GO:0010099 Uniprot:P59220
Root	Isotig08627	3	20	-2.866	9.17E-05	TAIR|locus:2055572 - symbol:SPX3 "AT2G45130" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0016036 "cellular response to phosphate starvation" evidence=IEP] [GO:0080040 "positive regulation of cellular response to phosphate starvation" evidence=IMP] EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0016036 InterPro:IPR004331 Pfam:PF03105 PROSITE:PS51382 GO:GO:0080040 EMBL:BT020235 EMBL:BT020499 IPI:IPI00520153 PIR:G84886 RefSeq:NP_182038.1 UniGene:At.50140 EnsemblPlants:AT2G45130.1 GeneID:819120 KEGG:ath:AT2G45130 TAIR:At2g45130 eggNOG:NOG290986 OMA:CGHNDEM PhylomeDB:Q5PP62 ProtClustDB:CLSN2913033 Genevestigator:Q5PP62 Uniprot:Q5PP62
Root	Isotig08635	0	13	-4.829	0.000155955	TAIR|locus:2141762 - symbol:CRK26 "cysteine-rich RLK (RECEPTOR-like protein kinase) 26" species:3702 "Arabidopsis thaliana" [GO:0006468 "protein phosphorylation" evidence=IEA] [GO:0016301 "kinase activity" evidence=ISS] InterPro:IPR000719 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 Pfam:PF00069 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 GO:GO:0016021 GO:GO:0005524 EMBL:CP002687 GenomeReviews:CT486007_GR eggNOG:COG0515 GO:GO:0004872 SUPFAM:SSF56112 GO:GO:0004674 HOGENOM:HBG755340 EMBL:AL161594 EMBL:AL035656 InterPro:IPR002902 Pfam:PF01657 PROSITE:PS51473 EMBL:AK228082 IPI:IPI00538329 IPI:IPI00854312 PIR:T06082 RefSeq:NP_195594.1 UniGene:At.66584 ProteinModelPortal:Q9T0J1 SMR:Q9T0J1 PRIDE:Q9T0J1 EnsemblPlants:AT4G38830.1 GeneID:830038 KEGG:ath:AT4G38830 GeneFarm:218 TAIR:At4g38830 InParanoid:Q9T0J1 OMA:HGQFSFK PhylomeDB:Q9T0J1 ProtClustDB:CLSN2915954 ArrayExpress:Q9T0J1 Genevestigator:Q9T0J1 Uniprot:Q9T0J1
Root	Isotig08636	0	13	-4.829	0.000155955	TAIR|locus:2141762 - symbol:CRK26 "cysteine-rich RLK (RECEPTOR-like protein kinase) 26" species:3702 "Arabidopsis thaliana" [GO:0006468 "protein phosphorylation" evidence=IEA] [GO:0016301 "kinase activity"

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						evidence=ISS] InterPro:IPR000719 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 Pfam:PF00069 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 GO:GO:0016021 GO:GO:0005524 EMBL:CP002687 GenomeReviews:CT486007_GR eggNOG:COG0515 GO:GO:0004872 SUPFAM:SSF56112 GO:GO:0004674 HOGENOM:HBG755340 EMBL:AL161594 EMBL:AL035656 InterPro:IPR002902 Pfam:PF01657 PROSITE:PS51473 EMBL:AK228082 IPI:IPI00538329 IPI:IPI00854312 PIR:T06082 RefSeq:NP_195594.1 UniGene:At.66584 ProteinModelPortal:Q9T0J1 SMR:Q9T0J1 PRIDE:Q9T0J1 EnsemblPlants:AT4G38830.1 GeneID:830038 KEGG:ath:AT4G38830 GeneFarm:218 TAIR:At4g38830 InParanoid:Q9T0J1 OMA:HGQFSFK PhylomeDB:Q9T0J1 ProtClustDB:CLSN2915954 ArrayExpress:Q9T0J1 Genevestigator:Q9T0J1 Uniprot:Q9T0J1
Root	Isotig08647	2	37	-4.338	4.38E-10	No hit
Root	Isotig08648	2	42	-4.521	1.92E-11	No hit
Root	Isotig08651	19	0	5.119	1.05E-05	TAIR|locus:2091762 - symbol:HSFC1 "AT3G24520" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=ISS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0005634 "nucleus" evidence=IEA] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] InterPro:IPR000232 Pfam:PF00447 PRINTS:PR00056 PROSITE:PS00434 SMART:SM00415 GO:GO:0005634 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0006950 GO:GO:0043565 GO:GO:0003700 GO:GO:0006351 InterPro:IPR011991 Gene3D:G3DSA:1.10.10.10 EMBL:AB020746 eggNOG:COG5169 HSSP:P22121 EMBL:AY056111 EMBL:AY072614 IPI:IPI00548593 RefSeq:NP_189095.1 UniGene:At.25607 UniGene:At.73128 ProteinModelPortal:Q9LV52 SMR:Q9LV52 IntAct:Q9LV52 PRIDE:Q9LV52 EnsemblPlants:AT3G24520.1 GeneID:822047 KEGG:ath:AT3G24520 GeneFarm:4086 TAIR:At3g24520 InParanoid:Q9LV52 OMA:NIARRKH PhylomeDB:Q9LV52 ProtClustDB:CLSN2722272 Genevestigator:Q9LV52 InterPro:IPR009938 Pfam:PF07334 Uniprot:Q9LV52
Root	Isotig08652	19	0	5.119	1.05E-05	TAIR|locus:2091762 - symbol:HSFC1 "AT3G24520" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=ISS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0005634 "nucleus" evidence=IEA] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] InterPro:IPR000232 Pfam:PF00447 PRINTS:PR00056 PROSITE:PS00434 SMART:SM00415 GO:GO:0005634 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0006950 GO:GO:0043565 GO:GO:0003700 GO:GO:0006351 InterPro:IPR011991 Gene3D:G3DSA:1.10.10.10 EMBL:AB020746 eggNOG:COG5169 HSSP:P22121 EMBL:AY056111 EMBL:AY072614 IPI:IPI00548593 RefSeq:NP_189095.1 UniGene:At.25607 UniGene:At.73128 ProteinModelPortal:Q9LV52 SMR:Q9LV52 IntAct:Q9LV52 PRIDE:Q9LV52 EnsemblPlants:AT3G24520.1 GeneID:822047 KEGG:ath:AT3G24520 GeneFarm:4086 TAIR:At3g24520 InParanoid:Q9LV52 OMA:NIARRKH PhylomeDB:Q9LV52 ProtClustDB:CLSN2722272 Genevestigator:Q9LV52 InterPro:IPR009938 Pfam:PF07334 Uniprot:Q9LV52
Root	Isotig08653	112	0	7.678	7.03E-25	TAIR|locus:2197823 - symbol:AT1G04560 "AT1G04560" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] Pfam:PF05512 EMBL:CP002684 GenomeReviews:CT485782_GR EMBL:AC002376 EMBL:AF360343 EMBL:AY051080 IPI:IPI00537314 PIR:B86178 RefSeq:NP_563710.1 UniGene:At.10465 PRIDE:O23029 EnsemblPlants:AT1G04560.1 GeneID:839491 KEGG:ath:AT1G04560 TAIR:At1g04560 eggNOG:NOG327574 HOGENOM:HBG593249 InParanoid:O23029 OMA:VAWAITA PhylomeDB:O23029 ProtClustDB:CLSN2687672 ArrayExpress:O23029 Genevestigator:O23029 InterPro:IPR008390 Uniprot:O23029
Root	Isotig08654	108	0	7.626	3.77E-24	TAIR|locus:2197823 - symbol:AT1G04560 "AT1G04560" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] Pfam:PF05512 EMBL:CP002684 GenomeReviews:CT485782_GR EMBL:AC002376 EMBL:AF360343 EMBL:AY051080 IPI:IPI00537314 PIR:B86178 RefSeq:NP_563710.1 UniGene:At.10465 PRIDE:O23029 EnsemblPlants:AT1G04560.1 GeneID:839491 KEGG:ath:AT1G04560 TAIR:At1g04560 eggNOG:NOG327574 HOGENOM:HBG593249 InParanoid:O23029 OMA:VAWAITA PhylomeDB:O23029 ProtClustDB:CLSN2687672 ArrayExpress:O23029 Genevestigator:O23029 InterPro:IPR008390 Uniprot:O23029
Root	Isotig08657	0	14	-4.936	8.24E-05	UNIPROTKB|A8QW53 - symbol:OMT3 "5-pentadecatrienyl resorcinol O-methyltransferase" species:4558 "Sorghum bicolor" [GO:0008171 "O-methyltransferase activity" evidence=IDA] [GO:0008757 "S-adenosylmethionine-dependent methyltransferase activity" evidence=IDA] [GO:0032259 "methylation" evidence=IDA] InterPro:IPR001077 InterPro:IPR012967 InterPro:IPR016461 Pfam:PF00891 Pfam:PF08100 PIRSF:PIRSF005739 InterPro:IPR011991 Gene3D:G3DSA:1.10.10.10 GO:GO:0046983 GO:GO:0008171 GO:GO:0008757 EMBL:EF189708 EMBL:CM000765 RefSeq:XP_002447425.1 UniGene:Sbi.19698 ProteinModelPortal:A8QW53

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EnsemblPlants:Sb06g000820.1 GeneID:8080259 KEGG:sbi:SORBI_06g000820 eggNOG:NOG272168 PhylomeDB:A8QW53 ProtClustDB:CLSN2725062 Uniprot:A8QW53
Root	Isotig08663	4	25	-2.773	1.71E-05	TAIR|locus:2080432 - symbol:AT3G59940 "AT3G59940" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] InterPro:IPR001810 InterPro:IPR006652 Pfam:PF01344 PROSITE:PS50181 SMART:SM00256 SMART:SM00612 GO:GO:0005634 EMBL:CP002686 GenomeReviews:BA000014_GR SUPFAM:SSF81383 InterPro:IPR015916 Gene3D:G3DSA:2.130.10.80 EMBL:AL138647 UniGene:At.1165 UniGene:At.48785 HOGENOM:HBG593750 eggNOG:NOG282025 ProtClustDB:CLSN2685021 EMBL:AY074382 EMBL:AY081325 EMBL:AY091240 EMBL:AY088575 IPI:IPI00534118 PIR:T47818 RefSeq:NP_191553.1 ProteinModelPortal:Q9M1Y1 SMR:Q9M1Y1 IntAct:Q9M1Y1 STRING:Q9M1Y1 PRIDE:Q9M1Y1 EnsemblPlants:AT3G59940.1 GeneID:825164 KEGG:ath:AT3G59940 TAIR:At3g59940 InParanoid:Q9M1Y1 OMA:CFIDSER PhylomeDB:Q9M1Y1 ArrayExpress:Q9M1Y1 Genevestigator:Q9M1Y1 Uniprot:Q9M1Y1
Root	Isotig08664	3	17	-2.631	0.00056383	TAIR|locus:2080432 - symbol:AT3G59940 "AT3G59940" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] InterPro:IPR001810 InterPro:IPR006652 Pfam:PF01344 PROSITE:PS50181 SMART:SM00256 SMART:SM00612 GO:GO:0005634 EMBL:CP002686 GenomeReviews:BA000014_GR SUPFAM:SSF81383 InterPro:IPR015916 Gene3D:G3DSA:2.130.10.80 EMBL:AL138647 UniGene:At.1165 UniGene:At.48785 HOGENOM:HBG593750 eggNOG:NOG282025 ProtClustDB:CLSN2685021 EMBL:AY074382 EMBL:AY081325 EMBL:AY091240 EMBL:AY088575 IPI:IPI00534118 PIR:T47818 RefSeq:NP_191553.1 ProteinModelPortal:Q9M1Y1 SMR:Q9M1Y1 IntAct:Q9M1Y1 STRING:Q9M1Y1 PRIDE:Q9M1Y1 EnsemblPlants:AT3G59940.1 GeneID:825164 KEGG:ath:AT3G59940 TAIR:At3g59940 InParanoid:Q9M1Y1 OMA:CFIDSER PhylomeDB:Q9M1Y1 ArrayExpress:Q9M1Y1 Genevestigator:Q9M1Y1 Uniprot:Q9M1Y1
Root	Isotig08694	12	49	-2.159	1.86E-07	TAIR|locus:2124286 - symbol:CCoAOMT1 "caffeoyl coenzyme A O-methyltransferase 1" species:3702 "Arabidopsis thaliana" [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0009805 "coumarin biosynthetic process" evidence=IMP] [GO:0042409 "caffeoyl-CoA O-methyltransferase activity" evidence=IDA] [GO:0005829 "cytosol" evidence=TAS] InterPro:IPR002935 Pfam:PF01596 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0046686 GO:GO:0046872 EMBL:AL021961 EMBL:AL161584 GO:GO:0009809 GO:GO:0009805 eggNOG:COG4122 HOGENOM:HBG496808 GO:GO:0042409 PANTHER:PTHR10509 OMA:REKTGHH EMBL:AY057554 EMBL:AY062630 EMBL:AY081457 EMBL:AY143979 EMBL:AY088577 IPI:IPI00521545 PIR:T05431 RefSeq:NP_195131.1 UniGene:At.23175 ProteinModelPortal:O49499 SMR:O49499 STRING:O49499 PRIDE:O49499 EnsemblPlants:AT4G34050.1 GeneID:829551 KEGG:ath:AT4G34050 TAIR:At4g34050 InParanoid:O49499 KO:K00588 PhylomeDB:O49499 ProtClustDB:PLN02589 ArrayExpress:O49499 Genevestigator:O49499 Uniprot:O49499
Root	Isotig08703	6	34	-2.631	1.08E-06	TAIR|locus:2090116 - symbol:AT3G15450 "AT3G15450" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] EMBL:CP002686 GenomeReviews:BA000014_GR EMBL:AB022218 EMBL:AC024081 InterPro:IPR024286 Pfam:PF12481 HOGENOM:HBG605462 UniGene:At.48664 UniGene:At.25100 EMBL:AY037223 EMBL:BT000501 IPI:IPI00537203 RefSeq:NP_566513.1 ProteinModelPortal:Q9LE80 IntAct:Q9LE80 STRING:Q9LE80 PRIDE:Q9LE80 ProMEX:Q9LE80 DNASU:820784 EnsemblPlants:AT3G15450.1 GeneID:820784 KEGG:ath:AT3G15450 TAIR:At3g15450 InParanoid:Q9LE80 OMA:EANWALA PhylomeDB:Q9LE80 ProtClustDB:CLSN2917134 Genevestigator:Q9LE80 Uniprot:Q9LE80
Root	Isotig08704	6	35	-2.673	6.02E-07	TAIR|locus:2123994 - symbol:AT4G27450 "AT4G27450" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 EMBL:CP002687 GO:GO:0005634 GO:GO:0005515 EMBL:AF375452 EMBL:AY045885 EMBL:AY091306 EMBL:AY087420 IPI:IPI00539788 RefSeq:NP_567775.1 UniGene:At.25186 UniGene:At.68765 ProteinModelPortal:Q93V62 IntAct:Q93V62 STRING:Q93V62 MEROPS:C44.A04 PRIDE:Q93V62 ProMEX:Q93V62 DNASU:828854 EnsemblPlants:AT4G27450.1 GeneID:828854 KEGG:ath:AT4G27450 TAIR:At4g27450 eggNOG:NOG245574 InParanoid:Q93V62 OMA:VYTRINS PhylomeDB:Q93V62 ProtClustDB:CLSN2917621 Genevestigator:Q93V62 InterPro:IPR024286 Pfam:PF12481 Uniprot:Q93V62
Root	Isotig08707	0	12	-4.714	0.000297064	TAIR|locus:2129116 - symbol:ERF-1 "AT4G17500" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=TAS] [GO:0003700 "sequence-specific DNA binding transcription factor activity"

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						evidence=ISS;TAS] [GO:0005643 "nuclear pore" evidence=ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IDA] [GO:0045893 "positive regulation of transcription, DNA-dependent" evidence=IDA] [GO:0010200 "response to chitin" evidence=IEP] InterPro:IPR001471 InterPro:IPR016177 Pfam:PF00847 PRINTS:PR00367 PROSITE:PS51032 SMART:SM00380 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005634 GO:GO:0006952 GO:GO:0009873 GO:GO:0003677 GO:GO:0003700 GO:GO:0006351 KO:K09286 Gene3D:G3DSA:3.30.730.10 SUPFAM:SSF54171 GO:GO:0010200 EMBL:Z97343 EMBL:AL161546 HOGENOM:HBG749764 EMBL:AY058174 EMBL:AY062533 EMBL:BT002578 EMBL:AB008103 IPI:IPI00518702 PIR:A85196 PIR:T51988 RefSeq:NP_567530.4 UniGene:At.23185 UniGene:At.68141 PDB:1GCC PDB:2GCC PDB:3GCC PDBsum:1GCC PDBsum:2GCC PDBsum:3GCC ProteinModelPortal:O80337 SMR:O80337 STRING:O80337 PRIDE:O80337 EnsemblPlants:AT4G17500.1 GeneID:827464 KEGG:ath:AT4G17500 TAIR:At4g17500 eggNOG:NOG246525 InParanoid:O80337 PhylomeDB:O80337 ProtClustDB:CLSN2715394 ArrayExpress:O80337 Genevestigator:O80337 GermOnline:AT4G17500 Uniprot:O80337
Root	Isotig08708	0	11	-4.588	0.000569522	TAIR|locus:2129116 - symbol:ERF-1 "AT4G17500" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=TAS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS;TAS] [GO:0005643 "nuclear pore" evidence=ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IDA] [GO:0045893 "positive regulation of transcription, DNA-dependent" evidence=IDA] [GO:0010200 "response to chitin" evidence=IEP] InterPro:IPR001471 InterPro:IPR016177 Pfam:PF00847 PRINTS:PR00367 PROSITE:PS51032 SMART:SM00380 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005634 GO:GO:0006952 GO:GO:0009873 GO:GO:0003677 GO:GO:0003700 GO:GO:0006351 KO:K09286 Gene3D:G3DSA:3.30.730.10 SUPFAM:SSF54171 GO:GO:0010200 EMBL:Z97343 EMBL:AL161546 HOGENOM:HBG749764 EMBL:AY058174 EMBL:AY062533 EMBL:BT002578 EMBL:AB008103 IPI:IPI00518702 PIR:A85196 PIR:T51988 RefSeq:NP_567530.4 UniGene:At.23185 UniGene:At.68141 PDB:1GCC PDB:2GCC PDB:3GCC PDBsum:1GCC PDBsum:2GCC PDBsum:3GCC ProteinModelPortal:O80337 SMR:O80337 STRING:O80337 PRIDE:O80337 EnsemblPlants:AT4G17500.1 GeneID:827464 KEGG:ath:AT4G17500 TAIR:At4g17500 eggNOG:NOG246525 InParanoid:O80337 PhylomeDB:O80337 ProtClustDB:CLSN2715394 ArrayExpress:O80337 Genevestigator:O80337 GermOnline:AT4G17500 Uniprot:O80337
Root	Isotig08711	3	28	-3.351	6.51E-07	TAIR|locus:2094977 - symbol:DELTA-TIP "AT3G16240" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=ISS] [GO:0015250 "water channel activity" evidence=ISS;IDA] [GO:0016020 "membrane" evidence=ISS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0015204 "urea transmembrane transporter activity" evidence=IGI] [GO:0015840 "urea transport" evidence=IGI] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0015200 "methylammonium transmembrane transporter activity" evidence=IDA] [GO:0051739 "ammonia transmembrane transporter activity" evidence=IGI] [GO:0005618 "cell wall" evidence=IDA] [GO:0009505 "plant-type cell wall" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0000326 "protein storage vacuole" evidence=IDA] [GO:0042807 "central vacuole" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] [GO:0006833 "water transport" evidence=IDA] [GO:0009705 "plant-type vacuole membrane" evidence=IDA] InterPro:IPR000425 InterPro:IPR012269 InterPro:IPR022357 Pfam:PF00230 PRINTS:PR00783 PROSITE:PS00221 GO:GO:0016021 GO:GO:0005886 GO:GO:0009506 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0009941 EMBL:AB023046 GO:GO:0009705 GO:GO:0009505 GO:GO:0015200 GO:GO:0051739 InterPro:IPR023271 Gene3D:G3DSA:1.20.1080.10 SUPFAM:SSF81338 eggNOG:COG0580 HOGENOM:HBG705794 PANTHER:PTHR19139 TIGRFAMs:TIGR00861 GO:GO:0015250 GO:GO:0000326 UniGene:At.32719 KO:K09873 GO:GO:0042807 EMBL:U39485 EMBL:U39486 EMBL:AY065181 EMBL:AY081622 EMBL:AK229954 EMBL:AY085921 EMBL:Z18064 EMBL:Z29043 EMBL:Z29044 IPI:IPI00524268 RefSeq:NP_188245.1 UniGene:At.23571 UniGene:At.6081 UniGene:At.71329 ProteinModelPortal:Q41951 SMR:Q41951 IntAct:Q41951 STRING:Q41951 PRIDE:Q41951 EnsemblPlants:AT3G16240.1 GeneID:820870 KEGG:ath:AT3G16240 GeneFarm:2255 TAIR:At3g16240 InParanoid:Q41951 OMA:MSGNIAF PhylomeDB:Q41951 ProtClustDB:CLSN2713597 ArrayExpress:Q41951 Genevestigator:Q41951 GermOnline:AT3G16240 Uniprot:Q41951
Root	Isotig08731	0	17	-5.216	1.26E-05	TAIR|locus:2010718 - symbol:NAS4 "AT1G56430" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0030410 "nicotianamine synthase activity" evidence=IGI] [GO:0030418 "nicotianamine biosynthetic process" evidence=IGI] InterPro:IPR004298 Pfam:PF03059 PROSITE:PS51142 EMBL:CP002684 GenomeReviews:CT485782_GR EMBL:AC058785 HOGENOM:HBG594037 KO:K05953

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						ProtClustDB:PLN03075 GO:GO:0030410 GO:GO:0030418 EMBL:AY099758 EMBL:AY128890 IPI:IPI00540066 PIR:B96606 RefSeq:NP_176038.1 UniGene:At.66920 ProteinModelPortal:Q9C7X5 SMR:Q9C7X5 IntAct:Q9C7X5 STRING:Q9C7X5 PRIDE:Q9C7X5 DNASU:842096 EnsemblPlants:AT1G56430.1 GeneID:842096 KEGG:ath:AT1G56430 TAIR:At1g56430 eggNOG:NOG305103 InParanoid:Q9C7X5 OMA:SENIQEM PhylomeDB:Q9C7X5 ArrayExpress:Q9C7X5 Genevestigator:Q9C7X5 GermOnline:AT1G56430 Uniprot:Q9C7X5
Root	Isotig08732	0	15	-5.036	4.38E-05	TAIR|locus:2010718 - symbol:NAS4 "AT1G56430" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0030410 "nicotianamine synthase activity" evidence=IGI] [GO:0030418 "nicotianamine biosynthetic process" evidence=IGI] InterPro:IPR004298 Pfam:PF03059 PROSITE:PS51142 EMBL:CP002684 GenomeReviews:CT485782_GR EMBL:AC058785 HOGENOM:HBG594037 KO:K05953 ProtClustDB:PLN03075 GO:GO:0030410 GO:GO:0030418 EMBL:AY099758 EMBL:AY128890 IPI:IPI00540066 PIR:B96606 RefSeq:NP_176038.1 UniGene:At.66920 ProteinModelPortal:Q9C7X5 SMR:Q9C7X5 IntAct:Q9C7X5 STRING:Q9C7X5 PRIDE:Q9C7X5 DNASU:842096 EnsemblPlants:AT1G56430.1 GeneID:842096 KEGG:ath:AT1G56430 TAIR:At1g56430 eggNOG:NOG305103 InParanoid:Q9C7X5 OMA:SENIQEM PhylomeDB:Q9C7X5 ArrayExpress:Q9C7X5 Genevestigator:Q9C7X5 GermOnline:AT1G56430 Uniprot:Q9C7X5
Root	Isotig08741	0	25	-5.773	1.02E-07	TAIR|locus:2170214 - symbol:AT5G06730 species:3702 "Arabidopsis thaliana" [GO:0004601 "peroxidase activity" evidence=IEA;ISS] [GO:0006979 "response to oxidative stress" evidence=IEA] [GO:0020037 "heme binding" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0005774 "vacuolar membrane" evidence=IDA] InterPro:IPR000823 InterPro:IPR002016 InterPro:IPR010255 InterPro:IPR019793 InterPro:IPR019794 Pfam:PF00141 PRINTS:PR00458 PRINTS:PR00461 PROSITE:PS00435 PROSITE:PS00436 PROSITE:PS50873 GO:GO:0005774 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005576 GO:GO:0020037 GO:GO:0004601 GO:GO:0042744 HOGENOM:HBG597790 SUPFAM:SSF48113 EMBL:AP002032 KO:K00430 eggNOG:NOG310632 ProtClustDB:CLSN2686891 EMBL:AK118827 EMBL:BT008584 EMBL:AY088509 EMBL:Y11794 IPI:IPI00528868 RefSeq:NP_196291.1 UniGene:At.90 ProteinModelPortal:Q9FG34 SMR:Q9FG34 STRING:Q9FG34 PeroxiBase:220 PRIDE:Q9FG34 EnsemblPlants:AT5G06730.1 GeneID:830562 KEGG:ath:AT5G06730 GeneFarm:1908 TAIR:At5g06730 InParanoid:Q9FG34 PhylomeDB:Q9FG34 ArrayExpress:Q9FG34 Genevestigator:Q9FG34 GermOnline:AT5G06730 Uniprot:Q9FG34
Root	Isotig08742	0	24	-5.714	1.84E-07	TAIR|locus:2057180 - symbol:AT2G38380 species:3702 "Arabidopsis thaliana" [GO:0004601 "peroxidase activity" evidence=IEA;ISS] [GO:0020037 "heme binding" evidence=IEA] [GO:0009505 "plant-type cell wall" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0010043 "response to zinc ion" evidence=IEP] InterPro:IPR000823 InterPro:IPR002016 InterPro:IPR010255 InterPro:IPR019793 InterPro:IPR019794 Pfam:PF00141 PRINTS:PR00458 PRINTS:PR00461 PROSITE:PS00435 PROSITE:PS00436 PROSITE:PS50873 GO:GO:0005773 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0005576 GO:GO:0010043 GO:GO:0009651 GO:GO:0020037 GO:GO:0009505 EMBL:AC004683 GO:GO:0004601 GO:GO:0042744 HOGENOM:HBG597790 SUPFAM:SSF48113 KO:K00430 EMBL:M58381 EMBL:AF452388 EMBL:AY059106 EMBL:AY035033 IPI:IPI00538455 PIR:JU0458 PIR:T02507 RefSeq:NP_181372.1 UniGene:At.312 ProteinModelPortal:P24102 SMR:P24102 STRING:P24102 PeroxiBase:115 PRIDE:P24102 ProMEX:P24102 EnsemblPlants:AT2G38380.1 GeneID:818419 KEGG:ath:AT2G38380 GeneFarm:1846 TAIR:At2g38380 eggNOG:euNOG17919 InParanoid:P24102 OMA:FIDAMIR PhylomeDB:P24102 ProtClustDB:CLSN2683115 ArrayExpress:P24102 Genevestigator:P24102 GermOnline:AT2G38380 Uniprot:P24102
Root	Isotig08751	24	92	-2.068	3.64E-12	TAIR|locus:2026616 - symbol:APX1 "AT1G07890" species:3702 "Arabidopsis thaliana" [GO:0016688 "L-ascorbate peroxidase activity" evidence=ISS;IMP;TAS] [GO:0000302 "response to reactive oxygen species" evidence=IMP] [GO:0042744 "hydrogen peroxide catabolic process" evidence=IMP] [GO:0009793 "embryo development ending in seed dormancy" evidence=IMP] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA;TAS] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] [GO:0009408 "response to heat" evidence=IEP] InterPro:IPR002016 InterPro:IPR002207 InterPro:IPR010255 InterPro:IPR019793 InterPro:IPR019794 Pfam:PF00141 PRINTS:PR00458 PRINTS:PR00459 PROSITE:PS00435 PROSITE:PS00436 PROSITE:PS50873 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 GO:GO:0009570 GO:GO:0046686 GO:GO:0005618 GO:GO:0009651 GO:GO:0009793 GO:GO:0009408 GO:GO:0020037 GO:GO:0042744 EMBL:X59600

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EMBL:D14442 EMBL:U63815 EMBL:AC007583 EMBL:AY039879 EMBL:AY056395 EMBL:AY094002 EMBL:AK230096 EMBL:AY086425 IPI:IPI00536287 PIR:D86214 PIR:S20866 RefSeq:NP_001030991.2 RefSeq:NP_001030992.2 RefSeq:NP_001077482.1 RefSeq:NP_001117244.1 RefSeq:NP_172267.1 RefSeq:NP_849607.1 RefSeq:NP_973786.1 UniGene:At.47584 UniGene:At.67008 ProteinModelPortal:Q05431 SMR:Q05431 IntAct:Q05431 STRING:Q05431 PeroxiBase:1890 SWISS-2DPAGE:Q05431 PRIDE:Q05431 ProMEX:Q05431 EnsemblPlants:AT1G07890.1 EnsemblPlants:AT1G07890.2 EnsemblPlants:AT1G07890.3 EnsemblPlants:AT1G07890.4 EnsemblPlants:AT1G07890.5 EnsemblPlants:AT1G07890.7 EnsemblPlants:AT1G07890.8 GeneID:837304 KEGG:ath:AT1G07890 GeneFarm:1942 TAIR:At1g07890 eggNOG:COG0376 HOGENOM:HBG597790 InParanoid:Q05431 KO:K00434 OMA:IAEKNCA PhylomeDB:Q05431 ProtClustDB:PLN02364 ArrayExpress:Q05431 Genevestigator:Q05431 GO:GO:0016688 SUPFAM:SSF48113 Uniprot:Q05431
Root	Isotig08752	19	74	-2.090	3.44E-10	TAIR|locus:2026616 - symbol:APX1 "AT1G07890" species:3702 "Arabidopsis thaliana" [GO:0016688 "L-ascorbate peroxidase activity" evidence=ISS;IMP;TAS] [GO:0000302 "response to reactive oxygen species" evidence=IMP] [GO:0042744 "hydrogen peroxide catabolic process" evidence=IMP] [GO:0009793 "embryo development ending in seed dormancy" evidence=IMP] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA;TAS] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] [GO:0009408 "response to heat" evidence=IEP] InterPro:IPR002016 InterPro:IPR002207 InterPro:IPR010255 InterPro:IPR019793 InterPro:IPR019794 Pfam:PF00141 PRINTS:PR00458 PRINTS:PR00459 PROSITE:PS00435 PROSITE:PS00436 PROSITE:PS50873 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 GO:GO:0009570 GO:GO:0046686 GO:GO:0005618 GO:GO:0009651 GO:GO:0009793 GO:GO:0009408 GO:GO:0020037 GO:GO:0042744 EMBL:X59600 EMBL:D14442 EMBL:U63815 EMBL:AC007583 EMBL:AY039879 EMBL:AY056395 EMBL:AY094002 EMBL:AK230096 EMBL:AY086425 IPI:IPI00536287 PIR:D86214 PIR:S20866 RefSeq:NP_001030991.2 RefSeq:NP_001030992.2 RefSeq:NP_001077482.1 RefSeq:NP_001117244.1 RefSeq:NP_172267.1 RefSeq:NP_849607.1 RefSeq:NP_973786.1 UniGene:At.47584 UniGene:At.67008 ProteinModelPortal:Q05431 SMR:Q05431 IntAct:Q05431 STRING:Q05431 PeroxiBase:1890 SWISS-2DPAGE:Q05431 PRIDE:Q05431 ProMEX:Q05431 EnsemblPlants:AT1G07890.1 EnsemblPlants:AT1G07890.2 EnsemblPlants:AT1G07890.3 EnsemblPlants:AT1G07890.4 EnsemblPlants:AT1G07890.5 EnsemblPlants:AT1G07890.7 EnsemblPlants:AT1G07890.8 GeneID:837304 KEGG:ath:AT1G07890 GeneFarm:1942 TAIR:At1g07890 eggNOG:COG0376 HOGENOM:HBG597790 InParanoid:Q05431 KO:K00434 OMA:IAEKNCA PhylomeDB:Q05431 ProtClustDB:PLN02364 ArrayExpress:Q05431 Genevestigator:Q05431 GO:GO:0016688 SUPFAM:SSF48113 Uniprot:Q05431
Root	Isotig08763	1	13	-3.829	0.000362856	TAIR|locus:2153509 - symbol:AT5G05250 "AT5G05250" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002688 GenomeReviews:BA000015_GR EMBL:AB010692 EMBL:AY054291 IPI:IPI00548957 RefSeq:NP_568152.1 UniGene:At.26381 STRING:Q9FLC9 PRIDE:Q9FLC9 EnsemblPlants:AT5G05250.1 GeneID:830407 KEGG:ath:AT5G05250 TAIR:At5g05250 eggNOG:NOG288610 HOGENOM:HBG595030 InParanoid:Q9FLC9 OMA:MAYAKIG PhylomeDB:Q9FLC9 ProtClustDB:CLSN2917568 Genevestigator:Q9FLC9 Uniprot:Q9FLC9
Root	Isotig08764	0	13	-4.829	0.000155955	TAIR|locus:2153509 - symbol:AT5G05250 "AT5G05250" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002688 GenomeReviews:BA000015_GR EMBL:AB010692 EMBL:AY054291 IPI:IPI00548957 RefSeq:NP_568152.1 UniGene:At.26381 STRING:Q9FLC9 PRIDE:Q9FLC9 EnsemblPlants:AT5G05250.1 GeneID:830407 KEGG:ath:AT5G05250 TAIR:At5g05250 eggNOG:NOG288610 HOGENOM:HBG595030 InParanoid:Q9FLC9 OMA:MAYAKIG PhylomeDB:Q9FLC9 ProtClustDB:CLSN2917568 Genevestigator:Q9FLC9 Uniprot:Q9FLC9
Root	Isotig08775	21	1	4.263	7.63E-06	TAIR|locus:2063130 - symbol:AT2G40390 "AT2G40390" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002685 GenomeReviews:CT485783_GR EMBL:AY649297 IPI:IPI00535270 RefSeq:NP_181570.2 UniGene:At.37058 PRIDE:Q6DR18 EnsemblPlants:AT2G40390.1 GeneID:818632 KEGG:ath:AT2G40390 TAIR:At2g40390 eggNOG:NOG238598 HOGENOM:HBG591957 InParanoid:Q6DR18 OMA:LAITNWI PhylomeDB:Q6DR18 ProtClustDB:CLSN2683474 Genevestigator:Q6DR18 Uniprot:Q6DR18

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig08776	22	0	5.330	1.93E-06	No hit
Root	Isotig08827	16	2	2.871	0.000812389	TAIR|locus:2171417 - symbol:AT5G16550 "AT5G16550" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002688 EMBL:AB005242 UniGene:At.66763 IPI:IPI00527710 RefSeq:NP_568333.1 PRIDE:Q9FFC9 EnsemblPlants:AT5G16550.1 GeneID:831517 KEGG:ath:AT5G16550 TAIR:At5g16550 InParanoid:Q9FFC9 OMA:REVNIES PhylomeDB:Q9FFC9 ProtClustDB:CLSN2689715 Genevestigator:Q9FFC9 Uniprot:Q9FFC9
Root	Isotig08828	16	2	2.871	0.000812389	TAIR|locus:2171417 - symbol:AT5G16550 "AT5G16550" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002688 EMBL:AB005242 UniGene:At.66763 IPI:IPI00527710 RefSeq:NP_568333.1 PRIDE:Q9FFC9 EnsemblPlants:AT5G16550.1 GeneID:831517 KEGG:ath:AT5G16550 TAIR:At5g16550 InParanoid:Q9FFC9 OMA:REVNIES PhylomeDB:Q9FFC9 ProtClustDB:CLSN2689715 Genevestigator:Q9FFC9 Uniprot:Q9FFC9
Root	Isotig08843	1	20	-4.451	3.92E-06	TAIR|locus:2141055 - symbol:MYC4 "AT4G17880" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=ISS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=TAS] [GO:0009718 "anthocyanin biosynthetic process" evidence=IMP] [GO:0045893 "positive regulation of transcription, DNA-dependent" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0006952 "defense response" evidence=IMP] [GO:0043425 "bHLH transcription factor binding" evidence=IPI] InterPro:IPR011598 Pfam:PF00010 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005634 GO:GO:0045893 GO:GO:0006952 GO:GO:0003677 GO:GO:0006351 EMBL:AL161547 EMBL:AL021889 Gene3D:G3DSA:4.10.280.10 SMART:SM00353 SUPFAM:SSF47459 PROSITE:PS50888 InterPro:IPR025610 Pfam:PF14215 GO:GO:0043425 eggNOG:NOG295658 HOGENOM:HBG747745 ProtClustDB:CLSN2686023 GO:GO:0009718 EMBL:AF251689 EMBL:AK221507 IPI:IPI00540927 PIR:T05074 RefSeq:NP_193522.1 UniGene:At.28316 ProteinModelPortal:O49687 SMR:O49687 PRIDE:O49687 EnsemblPlants:AT4G17880.1 GeneID:827511 KEGG:ath:AT4G17880 TAIR:At4g17880 InParanoid:O49687 OMA:SSCERAR PhylomeDB:O49687 ArrayExpress:O49687 Genevestigator:O49687 Uniprot:O49687
Root	Isotig08844	1	22	-4.588	1.10E-06	TAIR|locus:2141055 - symbol:MYC4 "AT4G17880" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=ISS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=TAS] [GO:0009718 "anthocyanin biosynthetic process" evidence=IMP] [GO:0045893 "positive regulation of transcription, DNA-dependent" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0006952 "defense response" evidence=IMP] [GO:0043425 "bHLH transcription factor binding" evidence=IPI] InterPro:IPR011598 Pfam:PF00010 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005634 GO:GO:0045893 GO:GO:0006952 GO:GO:0003677 GO:GO:0006351 EMBL:AL161547 EMBL:AL021889 Gene3D:G3DSA:4.10.280.10 SMART:SM00353 SUPFAM:SSF47459 PROSITE:PS50888 InterPro:IPR025610 Pfam:PF14215 GO:GO:0043425 eggNOG:NOG295658 HOGENOM:HBG747745 ProtClustDB:CLSN2686023 GO:GO:0009718 EMBL:AF251689 EMBL:AK221507 IPI:IPI00540927 PIR:T05074 RefSeq:NP_193522.1 UniGene:At.28316 ProteinModelPortal:O49687 SMR:O49687 PRIDE:O49687 EnsemblPlants:AT4G17880.1 GeneID:827511 KEGG:ath:AT4G17880 TAIR:At4g17880 InParanoid:O49687 OMA:SSCERAR PhylomeDB:O49687 ArrayExpress:O49687 Genevestigator:O49687 Uniprot:O49687
Root	Isotig08857	1	211	-7.850	9.79E-49	TAIR|locus:2116987 - symbol:TIP1;3 "AT4G01470" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=ISS] [GO:0015250 "water channel activity" evidence=ISS;IDA] [GO:0016020 "membrane" evidence=ISS] [GO:0006833 "water transport" evidence=IDA] [GO:0015204 "urea transmembrane transporter activity" evidence=IDA] [GO:0015840 "urea transport" evidence=IDA] InterPro:IPR000425 InterPro:IPR022357 Pfam:PF00230 PRINTS:PR00783 PROSITE:PS00221 GO:GO:0016021 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005774 GO:GO:0006950 InterPro:IPR023271 Gene3D:G3DSA:1.20.1080.10 SUPFAM:SSF81338 HOGENOM:HBG705794 PANTHER:PTHR19139 GO:GO:0015250 EMBL:AF096370 EMBL:AL161492 GO:GO:0015204 KO:K09873 ProtClustDB:PLN00027 EMBL:DQ446793 EMBL:DQ653172 IPI:IPI00524657 PIR:T01947 RefSeq:NP_192056.1 UniGene:At.65315 ProteinModelPortal:O82598 SMR:O82598 STRING:O82598 TCDB:1.A.8.10.6 PRIDE:O82598 EnsemblPlants:AT4G01470.1 GeneID:828051 KEGG:ath:AT4G01470 GeneFarm:4856 TAIR:At4g01470 eggNOG:NOG312454 InParanoid:O82598 OMA:IGSNGHE PhylomeDB:O82598 ArrayExpress:O82598 Genevestigator:O82598 Uniprot:O82598

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig08858	1	204	-7.801	2.22E-47	TAIR|locus:2116987 - symbol:TIP1;3 "AT4G01470" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=ISS] [GO:0015250 "water channel activity" evidence=ISS;IDA] [GO:0016020 "membrane" evidence=ISS] [GO:0006833 "water transport" evidence=IDA] [GO:0015204 "urea transmembrane transporter activity" evidence=IDA] [GO:0015840 "urea transport" evidence=IDA] InterPro:IPR000425 InterPro:IPR022357 Pfam:PF00230 PRINTS:PR00783 PROSITE:PS00221 GO:GO:0016021 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005774 GO:GO:0006950 InterPro:IPR023271 Gene3D:G3DSA:1.20.1080.10 SUPFAM:SSF81338 HOGENOM:HBG705794 PANTHER:PTHR19139 GO:GO:0015250 EMBL:AF096370 EMBL:AL161492 GO:GO:0015204 KO:K09873 ProtClustDB:PLN00027 EMBL:DQ446793 EMBL:DQ653172 IPI:IPI00524657 PIR:T01947 RefSeq:NP_192056.1 UniGene:At.65315 ProteinModelPortal:O82598 SMR:O82598 STRING:O82598 TCDB:1.A.8.10.6 PRIDE:O82598 EnsemblPlants:AT4G01470.1 GeneID:828051 KEGG:ath:AT4G01470 GeneFarm:4856 TAIR:At4g01470 eggNOG:NOG312454 InParanoid:O82598 OMA:IGSNGHE PhylomeDB:O82598 ArrayExpress:O82598 Genevestigator:O82598 Uniprot:O82598
Root	Isotig08877	29	4	2.729	1.12E-05	TAIR|locus:2063104 - symbol:FER4 "AT2G40300" species:3702 "Arabidopsis thaliana" [GO:0006826 "iron ion transport" evidence=IGI;ISS] [GO:0006879 "cellular iron ion homeostasis" evidence=ISS] [GO:0008199 "ferric iron binding" evidence=IEA;ISS] [GO:0016491 "oxidoreductase activity" evidence=IEA] [GO:0046914 "transition metal ion binding" evidence=IEA] [GO:0009507 "chloroplast" evidence=ISS;IDA] [GO:0010039 "response to iron ion" evidence=IEP] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0000302 "response to reactive oxygen species" evidence=IGI] [GO:0009908 "flower development" evidence=IGI] [GO:0015979 "photosynthesis" evidence=IGI] [GO:0048366 "leaf development" evidence=IGI] [GO:0055072 "iron ion homeostasis" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0071214 "cellular response to abiotic stimulus" evidence=IMP] InterPro:IPR001519 InterPro:IPR008331 InterPro:IPR009078 Pfam:PF00210 GO:GO:0005739 GO:GO:0009570 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009941 GO:GO:0006879 EMBL:AF085279 GO:GO:0010039 eggNOG:COG1528 HOGENOM:HBG750128 GO:GO:0008199 GO:GO:0004322 GO:GO:0006826 InterPro:IPR009040 InterPro:IPR012347 Gene3D:G3DSA:1.20.1260.10 PANTHER:PTHR11431 SUPFAM:SSF47240 PROSITE:PS50905 EMBL:AC007020 UniGene:At.27228 InterPro:IPR014034 PROSITE:PS00540 PROSITE:PS00204 KO:K00522 ProtClustDB:CLSN2683400 EMBL:AJ312191 EMBL:AY062795 EMBL:AY081615 IPI:IPI00534160 PIR:G84827 RefSeq:NP_181559.1 UniGene:At.69019 ProteinModelPortal:Q9S756 SMR:Q9S756 STRING:Q9S756 PRIDE:Q9S756 EnsemblPlants:AT2G40300.1 GeneID:818622 KEGG:ath:AT2G40300 TAIR:At2g40300 InParanoid:Q9S756 OMA:AMAYHFD PhylomeDB:Q9S756 ArrayExpress:Q9S756 Genevestigator:Q9S756 GermOnline:AT2G40300 Uniprot:Q9S756
Root	Isotig08883	1	30	-5.036	7.50E-09	TAIR|locus:2084066 - symbol:PPa4 "AT3G53620" species:3702 "Arabidopsis thaliana" [GO:0004427 "inorganic diphosphatase activity" evidence=IDA] [GO:0008152 "metabolic process" evidence=ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA] HAMAP:MF_00209 InterPro:IPR008162 Pfam:PF00719 PROSITE:PS00387 GO:GO:0005829 GO:GO:0046686 EMBL:CP002686 GO:GO:0000287 EMBL:AL132966 GO:GO:0006796 KO:K01507 GO:GO:0004427 Gene3D:G3DSA:3.90.80.10 PANTHER:PTHR10286 SUPFAM:SSF50324 ProtClustDB:PLN02373 OMA:PNDFNVI HSSP:O59570 EMBL:AK226578 IPI:IPI00524492 PIR:T45902 RefSeq:NP_190930.1 UniGene:At.19820 ProteinModelPortal:Q9LFF9 SMR:Q9LFF9 STRING:Q9LFF9 PRIDE:Q9LFF9 EnsemblPlants:AT3G53620.1 GeneID:824530 KEGG:ath:AT3G53620 TAIR:At3g53620 InParanoid:Q9LFF9 PhylomeDB:Q9LFF9 Genevestigator:Q9LFF9 Uniprot:Q9LFF9
Root	Isotig08884	1	25	-4.773	1.66E-07	TAIR|locus:2084066 - symbol:PPa4 "AT3G53620" species:3702 "Arabidopsis thaliana" [GO:0004427 "inorganic diphosphatase activity" evidence=IDA] [GO:0008152 "metabolic process" evidence=ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA] HAMAP:MF_00209 InterPro:IPR008162 Pfam:PF00719 PROSITE:PS00387 GO:GO:0005829 GO:GO:0046686 EMBL:CP002686 GO:GO:0000287 EMBL:AL132966 GO:GO:0006796 KO:K01507 GO:GO:0004427 Gene3D:G3DSA:3.90.80.10 PANTHER:PTHR10286 SUPFAM:SSF50324 ProtClustDB:PLN02373 OMA:PNDFNVI HSSP:O59570 EMBL:AK226578 IPI:IPI00524492 PIR:T45902 RefSeq:NP_190930.1 UniGene:At.19820 ProteinModelPortal:Q9LFF9 SMR:Q9LFF9 STRING:Q9LFF9 PRIDE:Q9LFF9 EnsemblPlants:AT3G53620.1 GeneID:824530 KEGG:ath:AT3G53620 TAIR:At3g53620 InParanoid:Q9LFF9 PhylomeDB:Q9LFF9 Genevestigator:Q9LFF9 Uniprot:Q9LFF9

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig08887	14	1	3.678	0.000484579	No hit
Root	Isotig08888	13	1	3.571	0.000882483	No hit
Root	Isotig08897	0	23	-5.653	3.32E-07	TAIR|locus:2176307 - symbol:CAF1b "AT5G22250" species:3702 "Arabidopsis thaliana" [GO:0004540 "ribonuclease activity" evidence=ISS] [GO:0005634 "nucleus" evidence=IEA] [GO:0009451 "RNA modification" evidence=ISS] [GO:0000289 "nuclear-transcribed mRNA poly(A) tail shortening" evidence=IMP] [GO:0008408 "3'-5' exonuclease activity" evidence=IDA] [GO:0042742 "defense response to bacterium" evidence=IEP] InterPro:IPR006941 InterPro:IPR012337 Pfam:PF04857 GO:GO:0005634 GO:GO:0005737 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0042742 GO:GO:0006355 GO:GO:0046872 GO:GO:0006351 GO:GO:0003723 SUPFAM:SSF53098 eggNOG:COG5228 GO:GO:0004535 HSSP:P39008 HOGENOM:HBG748413 ProtClustDB:CLSN2684465 GO:GO:0000289 EMBL:AB007651 EMBL:AY063985 EMBL:BT001962 IPI:IPI00540783 RefSeq:NP_197617.1 UniGene:At.27479 ProteinModelPortal:Q9FMS6 SMR:Q9FMS6 STRING:Q9FMS6 PRIDE:Q9FMS6 DNASU:832285 EnsemblPlants:AT5G22250.1 GeneID:832285 KEGG:ath:AT5G22250 TAIR:At5g22250 InParanoid:Q9FMS6 OMA:HIMRFCE PhylomeDB:Q9FMS6 ArrayExpress:Q9FMS6 Genevestigator:Q9FMS6 Uniprot:Q9FMS6
Root	Isotig08898	0	24	-5.714	1.84E-07	TAIR|locus:2176307 - symbol:CAF1b "AT5G22250" species:3702 "Arabidopsis thaliana" [GO:0004540 "ribonuclease activity" evidence=ISS] [GO:0005634 "nucleus" evidence=IEA] [GO:0009451 "RNA modification" evidence=ISS] [GO:0000289 "nuclear-transcribed mRNA poly(A) tail shortening" evidence=IMP] [GO:0008408 "3'-5' exonuclease activity" evidence=IDA] [GO:0042742 "defense response to bacterium" evidence=IEP] InterPro:IPR006941 InterPro:IPR012337 Pfam:PF04857 GO:GO:0005634 GO:GO:0005737 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0042742 GO:GO:0006355 GO:GO:0046872 GO:GO:0006351 GO:GO:0003723 SUPFAM:SSF53098 eggNOG:COG5228 GO:GO:0004535 HSSP:P39008 HOGENOM:HBG748413 ProtClustDB:CLSN2684465 GO:GO:0000289 EMBL:AB007651 EMBL:AY063985 EMBL:BT001962 IPI:IPI00540783 RefSeq:NP_197617.1 UniGene:At.27479 ProteinModelPortal:Q9FMS6 SMR:Q9FMS6 STRING:Q9FMS6 PRIDE:Q9FMS6 DNASU:832285 EnsemblPlants:AT5G22250.1 GeneID:832285 KEGG:ath:AT5G22250 TAIR:At5g22250 InParanoid:Q9FMS6 OMA:HIMRFCE PhylomeDB:Q9FMS6 ArrayExpress:Q9FMS6 Genevestigator:Q9FMS6 Uniprot:Q9FMS6
Root	Isotig08904	1	19	-4.377	7.43E-06	TAIR|locus:2079522 - symbol:AT3G62040 species:3702 "Arabidopsis thaliana" [GO:0016787 "hydrolase activity" evidence=IEA;ISS] InterPro:IPR006402 EMBL:CP002686 GenomeReviews:BA000014_GR InterPro:IPR023214 Gene3D:G3DSA:3.40.50.1000 SUPFAM:SSF56784 GO:GO:0016787 eggNOG:COG1011 TIGRFAMs:TIGR01509 EMBL:AL138642 UniGene:At.24742 UniGene:At.48797 InterPro:IPR010237 TIGRFAMs:TIGR01993 EMBL:BT010899 IPI:IPI00520634 PIR:T47996 RefSeq:NP_191763.3 ProteinModelPortal:Q9M262 SMR:Q9M262 PRIDE:Q9M262 EnsemblPlants:AT3G62040.1 GeneID:825377 KEGG:ath:AT3G62040 TAIR:At3g62040 HOGENOM:HBG410732 InParanoid:Q9M262 OMA:HAFNTIC PhylomeDB:Q9M262 ProtClustDB:CLSN2681592 Genevestigator:Q9M262 Uniprot:Q9M262
Root	Isotig08905	0	11	-4.588	0.000569522	TAIR|locus:2170081 - symbol:AT5G50140 "AT5G50140" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] InterPro:IPR002110 PROSITE:PS50088 SMART:SM00248 EMBL:CP002688 GenomeReviews:BA000015_GR InterPro:IPR020683 Gene3D:G3DSA:1.25.40.20 Pfam:PF12796 SUPFAM:SSF48403 PROSITE:PS50297 EMBL:AB026650 HSSP:Q60778 eggNOG:KOG0504 IPI:IPI00530282 RefSeq:NP_199825.1 UniGene:At.55468 ProteinModelPortal:Q9FG97 SMR:Q9FG97 PRIDE:Q9FG97 EnsemblPlants:AT5G50140.1 GeneID:835079 KEGG:ath:AT5G50140 TAIR:At5g50140 HOGENOM:HBG750443 InParanoid:Q9FG97 OMA:ISHAGEM PhylomeDB:Q9FG97 Genevestigator:Q9FG97 Uniprot:Q9FG97
Root	Isotig08913	0	13	-4.829	0.000155955	TAIR|locus:2199297 - symbol:ENDO 2 "AT1G68290" species:3702 "Arabidopsis thaliana" [GO:0003676 "nucleic acid binding" evidence=ISS] [GO:0004519 "endonuclease activity" evidence=ISS] [GO:0006308 "DNA catabolic process" evidence=IEA;ISS] [GO:0000014 "single-stranded DNA specific endodeoxyribonuclease activity" evidence=IDA] [GO:0043765 "T/G mismatch-specific endonuclease activity" evidence=IDA] InterPro:IPR003154 InterPro:IPR008947 Pfam:PF02265 EMBL:CP002684 GO:GO:0003676 EMBL:AC016447 GO:GO:0004519 GO:GO:0006308 Gene3D:G3DSA:1.10.575.10 SUPFAM:SSF48537 HSSP:P24289 ProtClustDB:CLSN2681945 IPI:IPI00543025 PIR:E96706 RefSeq:NP_176996.1 UniGene:At.35544 UniGene:At.43330 ProteinModelPortal:Q9C9G4 SMR:Q9C9G4 PRIDE:Q9C9G4 EnsemblPlants:AT1G68290.1 GeneID:843158 KEGG:ath:AT1G68290 TAIR:At1g68290 InParanoid:Q9C9G4 OMA:AACDWAY PhylomeDB:Q9C9G4 Genevestigator:Q9C9G4 Uniprot:Q9C9G4

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig08925	1	12	-3.714	0.000699736	TAIR|locus:2025421 - symbol:AT1G01490 "AT1G01490" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0030001 "metal ion transport" evidence=IEA] [GO:0046872 "metal ion binding" evidence=IEA;ISS] InterPro:IPR006121 Pfam:PF00403 EMBL:CP002684 GO:GO:0046872 GO:GO:0030001 EMBL:AY063805 EMBL:AY091276 EMBL:Y10084 IPI:IPI00534476 RefSeq:NP_001030928.1 RefSeq:NP_171656.1 UniGene:At.27454 ProteinModelPortal:O03982 PRIDE:O03982 EnsemblPlants:AT1G01490.1 EnsemblPlants:AT1G01490.2 GeneID:839440 KEGG:ath:AT1G01490 TAIR:At1g01490 eggNOG:NOG282717 InParanoid:O03982 OMA:YYAQSIE PhylomeDB:O03982 ProtClustDB:CLSN2912783 ArrayExpress:O03982 Genevestigator:O03982 Uniprot:O03982
Root	Isotig08926	1	12	-3.714	0.000699736	TAIR|locus:2025421 - symbol:AT1G01490 "AT1G01490" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0030001 "metal ion transport" evidence=IEA] [GO:0046872 "metal ion binding" evidence=IEA;ISS] InterPro:IPR006121 Pfam:PF00403 EMBL:CP002684 GO:GO:0046872 GO:GO:0030001 EMBL:AY063805 EMBL:AY091276 EMBL:Y10084 IPI:IPI00534476 RefSeq:NP_001030928.1 RefSeq:NP_171656.1 UniGene:At.27454 ProteinModelPortal:O03982 PRIDE:O03982 EnsemblPlants:AT1G01490.1 EnsemblPlants:AT1G01490.2 GeneID:839440 KEGG:ath:AT1G01490 TAIR:At1g01490 eggNOG:NOG282717 InParanoid:O03982 OMA:YYAQSIE PhylomeDB:O03982 ProtClustDB:CLSN2912783 ArrayExpress:O03982 Genevestigator:O03982 Uniprot:O03982
Root	Isotig08939	105	0	7.585	1.34E-23	TAIR|locus:2061151 - symbol:NRPD1B "AT2G40030" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=ISS] [GO:0003899 "DNA-directed RNA polymerase activity" evidence=ISS] [GO:0005634 "nucleus" evidence=ISS;IDA] [GO:0006351 "transcription, DNA-dependent" evidence=ISS] [GO:0000418 "DNA-directed RNA polymerase IV complex" evidence=IPI] [GO:0006306 "DNA methylation" evidence=IMP] [GO:0000419 "DNA-directed RNA polymerase V complex" evidence=IDA;IPI] [GO:0030880 "RNA polymerase complex" evidence=IPI] [GO:0035194 "posttranscriptional gene silencing by RNA" evidence=IMP] [GO:0005515 "protein binding" evidence=IPI] [GO:0005730 "nucleolus" evidence=IDA] [GO:0016604 "nuclear body" evidence=IDA] [GO:0030422 "production of siRNA involved in RNA interference" evidence=IGI;IMP] InterPro:IPR000722 InterPro:IPR006592 InterPro:IPR007066 InterPro:IPR007080 InterPro:IPR007081 InterPro:IPR015801 Pfam:PF00623 Pfam:PF04983 Pfam:PF04997 Pfam:PF04998 SMART:SM00663 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0005515 GO:GO:0005730 GO:GO:0006355 GO:GO:0003677 GO:GO:0005507 GO:GO:0048038 GO:GO:0009308 Gene3D:G3DSA:3.10.450.40 GO:GO:0030422 GO:GO:0006306 GO:GO:0016604 EMBL:AF002109 GO:GO:0003899 eggNOG:COG0086 GO:GO:0000418 InterPro:IPR021602 Pfam:PF11523 EMBL:AY826516 EMBL:AY927744 EMBL:DQ020656 IPI:IPI00537496 PIR:D84824 PIR:E84824 RefSeq:NP_181532.2 UniGene:At.37106 ProteinModelPortal:Q5D869 SMR:Q5D869 DIP:DIP-48678N IntAct:Q5D869 STRING:Q5D869 PRIDE:Q5D869 EnsemblPlants:AT2G40030.1 GeneID:818591 KEGG:ath:AT2G40030 TAIR:At2g40030 InParanoid:Q5D869 OMA:EGHFGYI PhylomeDB:Q5D869 ProtClustDB:CLSN2681712 ArrayExpress:O04206 Genevestigator:Q5D869 GO:GO:0000419 Uniprot:Q5D869
Root	Isotig08940	104	0	7.571	2.05E-23	TAIR|locus:2061151 - symbol:NRPD1B "AT2G40030" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=ISS] [GO:0003899 "DNA-directed RNA polymerase activity" evidence=ISS] [GO:0005634 "nucleus" evidence=ISS;IDA] [GO:0006351 "transcription, DNA-dependent" evidence=ISS] [GO:0000418 "DNA-directed RNA polymerase IV complex" evidence=IPI] [GO:0006306 "DNA methylation" evidence=IMP] [GO:0000419 "DNA-directed RNA polymerase V complex" evidence=IDA;IPI] [GO:0030880 "RNA polymerase complex" evidence=IPI] [GO:0035194 "posttranscriptional gene silencing by RNA" evidence=IMP] [GO:0005515 "protein binding" evidence=IPI] [GO:0005730 "nucleolus" evidence=IDA] [GO:0016604 "nuclear body" evidence=IDA] [GO:0030422 "production of siRNA involved in RNA interference" evidence=IGI;IMP] InterPro:IPR000722 InterPro:IPR006592 InterPro:IPR007066 InterPro:IPR007080 InterPro:IPR007081 InterPro:IPR015801 Pfam:PF00623 Pfam:PF04983 Pfam:PF04997 Pfam:PF04998 SMART:SM00663 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0005515 GO:GO:0005730 GO:GO:0006355 GO:GO:0003677 GO:GO:0005507 GO:GO:0048038 GO:GO:0009308 Gene3D:G3DSA:3.10.450.40 GO:GO:0030422 GO:GO:0006306 GO:GO:0016604 EMBL:AF002109 GO:GO:0003899 eggNOG:COG0086 GO:GO:0000418 InterPro:IPR021602 Pfam:PF11523 EMBL:AY826516 EMBL:AY927744 EMBL:DQ020656 IPI:IPI00537496 PIR:D84824 PIR:E84824 RefSeq:NP_181532.2 UniGene:At.37106 ProteinModelPortal:Q5D869 SMR:Q5D869 DIP:DIP-48678N IntAct:Q5D869 STRING:Q5D869 PRIDE:Q5D869 EnsemblPlants:AT2G40030.1 GeneID:818591 KEGG:ath:AT2G40030 TAIR:At2g40030 InParanoid:Q5D869 OMA:EGHFGYI PhylomeDB:Q5D869 ProtClustDB:CLSN2681712 ArrayExpress:O04206 Genevestigator:Q5D869 GO:GO:0000419 Uniprot:Q5D869

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig08953	49	1	5.486	1.10E-12	TAIR|locus:2085775 - symbol:ENODL9 "early nodulin-like protein 9" species:3702 "Arabidopsis thaliana" [GO:0005507 "copper ion binding" evidence=IEA;ISS] [GO:0009055 "electron carrier activity" evidence=IEA] [GO:0031225 "anchored to membrane" evidence=TAS] InterPro:IPR003245 Pfam:PF02298 ProDom:PD003122 PROSITE:PS51485 EMBL:CP002686 GO:GO:0009055 GO:GO:0031225 GO:GO:0005507 InterPro:IPR008972 Gene3D:G3DSA:2.60.40.420 SUPFAM:SSF49503 EMBL:AP000410 UniGene:At.48682 UniGene:At.5498 HSSP:P29602 EMBL:BT009716 EMBL:AK228335 IPI:IPI00523618 RefSeq:NP_566665.1 ProteinModelPortal:Q9LJU1 SMR:Q9LJU1 STRING:Q9LJU1 PRIDE:Q9LJU1 EnsemblPlants:AT3G20570.1 GeneID:821604 KEGG:ath:AT3G20570 TAIR:At3g20570 InParanoid:Q9LJU1 OMA:SGNKDNC PhylomeDB:Q9LJU1 ProtClustDB:CLSN2718972 Genevestigator:Q9LJU1 Uniprot:Q9LJU1
Root	Isotig08954	33	0	5.915	5.02E-09	TAIR|locus:2085775 - symbol:ENODL9 "early nodulin-like protein 9" species:3702 "Arabidopsis thaliana" [GO:0005507 "copper ion binding" evidence=IEA;ISS] [GO:0009055 "electron carrier activity" evidence=IEA] [GO:0031225 "anchored to membrane" evidence=TAS] InterPro:IPR003245 Pfam:PF02298 ProDom:PD003122 PROSITE:PS51485 EMBL:CP002686 GO:GO:0009055 GO:GO:0031225 GO:GO:0005507 InterPro:IPR008972 Gene3D:G3DSA:2.60.40.420 SUPFAM:SSF49503 EMBL:AP000410 UniGene:At.48682 UniGene:At.5498 HSSP:P29602 EMBL:BT009716 EMBL:AK228335 IPI:IPI00523618 RefSeq:NP_566665.1 ProteinModelPortal:Q9LJU1 SMR:Q9LJU1 STRING:Q9LJU1 PRIDE:Q9LJU1 EnsemblPlants:AT3G20570.1 GeneID:821604 KEGG:ath:AT3G20570 TAIR:At3g20570 InParanoid:Q9LJU1 OMA:SGNKDNC PhylomeDB:Q9LJU1 ProtClustDB:CLSN2718972 Genevestigator:Q9LJU1 Uniprot:Q9LJU1
Root	Isotig08963	5	25	-2.451	5.85E-05	No hit
Root	Isotig08964	2	23	-3.653	3.09E-06	No hit
Root	Isotig08965	0	13	-4.829	0.000155955	TAIR|locus:2144286 - symbol:AT5G11500 "AT5G11500" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002688 EMBL:AL163815 OMA:CKANSIQ InterPro:IPR008532 Pfam:PF05670 EMBL:AY142650 IPI:IPI00529817 PIR:T48509 RefSeq:NP_196711.1 UniGene:At.22316 UniGene:At.68086 IntAct:Q9LYE1 PRIDE:Q9LYE1 EnsemblPlants:AT5G11500.1 GeneID:831022 KEGG:ath:AT5G11500 TAIR:At5g11500 InParanoid:Q9LYE1 PhylomeDB:Q9LYE1 ProtClustDB:CLSN2686622 Genevestigator:Q9LYE1 Uniprot:Q9LYE1
Root	Isotig08966	0	13	-4.829	0.000155955	TAIR|locus:2144286 - symbol:AT5G11500 "AT5G11500" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002688 EMBL:AL163815 OMA:CKANSIQ InterPro:IPR008532 Pfam:PF05670 EMBL:AY142650 IPI:IPI00529817 PIR:T48509 RefSeq:NP_196711.1 UniGene:At.22316 UniGene:At.68086 IntAct:Q9LYE1 PRIDE:Q9LYE1 EnsemblPlants:AT5G11500.1 GeneID:831022 KEGG:ath:AT5G11500 TAIR:At5g11500 InParanoid:Q9LYE1 PhylomeDB:Q9LYE1 ProtClustDB:CLSN2686622 Genevestigator:Q9LYE1 Uniprot:Q9LYE1
Root	Isotig09011	1	13	-3.829	0.000362856	TAIR|locus:2029491 - symbol:RAP2.4 "AT1G78080" species:3702 "Arabidopsis thaliana" [GO:0006355 "regulation of transcription, DNA-dependent" evidence=ISS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS;IDA;TAS] [GO:0005515 "protein binding" evidence=IPI] [GO:0005634 "nucleus" evidence=IC;IDA] [GO:0006970 "response to osmotic stress" evidence=IEP] [GO:0071472 "cellular response to salt stress" evidence=IEP] [GO:0003677 "DNA binding" evidence=IDA;TAS] [GO:0009414 "response to water deprivation" evidence=IEP;IMP] [GO:0009416 "response to light stimulus" evidence=IEP] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0009873 "ethylene mediated signaling pathway" evidence=IMP] [GO:0010017 "red or far-red light signaling pathway" evidence=IGI] [GO:0009611 "response to wounding" evidence=IEP] [GO:0009736 "cytokinin mediated signaling pathway" evidence=IMP] [GO:0045595 "regulation of cell differentiation" evidence=IMP] [GO:0009409 "response to cold" evidence=IEP] [GO:0043565 "sequence-specific DNA binding" evidence=IDA] InterPro:IPR001471 InterPro:IPR016177 Pfam:PF00847 PRINTS:PR00367 PROSITE:PS51032 SMART:SM00380 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005634 GO:GO:0005515 GO:GO:0009611 GO:GO:0009873 GO:GO:0045595 GO:GO:0043565 GO:GO:0003700 GO:GO:0006351 GO:GO:0009409 GO:GO:0009414 KO:K09286 Gene3D:G3DSA:3.30.730.10 SUPFAM:SSF54171 HSSP:O80337 GO:GO:0009736 GO:GO:0071472 GO:GO:0010017 EMBL:AC009243 HOGENOM:HBG599504 EMBL:AC012680 UniGene:At.25524 EMBL:AF370152 EMBL:AY150468 EMBL:AF003097 IPI:IPI00519366 RefSeq:NP_177931.1 UniGene:At.71798 ProteinModelPortal:Q8H1E4 SMR:Q8H1E4 MINT:MINT-7262714 STRING:Q8H1E4 PRIDE:Q8H1E4 EnsemblPlants:AT1G78080.1 GeneID:844143 KEGG:ath:AT1G78080 TAIR:At1g78080 eggNOG:NOG306355 InParanoid:Q8H1E4 OMA:KLEAICK PhylomeDB:Q8H1E4 ProtClustDB:CLSN2679481 Genevestigator:Q8H1E4 Uniprot:Q8H1E4

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig09012	1	13	-3.829	0.000362856	TAIR|locus:2029491 - symbol:RAP2.4 "AT1G78080" species:3702 "Arabidopsis thaliana" [GO:0006355 "regulation of transcription, DNA-dependent" evidence=ISS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS;IDA;TAS] [GO:0005515 "protein binding" evidence=IPI] [GO:0005634 "nucleus" evidence=IC;IDA] [GO:0006970 "response to osmotic stress" evidence=IEP] [GO:0071472 "cellular response to salt stress" evidence=IEP] [GO:0003677 "DNA binding" evidence=IDA;TAS] [GO:0009414 "response to water deprivation" evidence=IEP;IMP] [GO:0009416 "response to light stimulus" evidence=IEP] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0009873 "ethylene mediated signaling pathway" evidence=IMP] [GO:0010017 "red or far-red light signaling pathway" evidence=IGI] [GO:0009611 "response to wounding" evidence=IEP] [GO:0009736 "cytokinin mediated signaling pathway" evidence=IMP] [GO:0045595 "regulation of cell differentiation" evidence=IMP] [GO:0009409 "response to cold" evidence=IEP] [GO:0043565 "sequence-specific DNA binding" evidence=IDA] InterPro:IPR001471 InterPro:IPR016177 Pfam:PF00847 PRINTS:PR00367 PROSITE:PS51032 SMART:SM00380 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005634 GO:GO:0005515 GO:GO:0009611 GO:GO:0009873 GO:GO:0045595 GO:GO:0043565 GO:GO:0003700 GO:GO:0006351 GO:GO:0009409 GO:GO:0009414 KO:K09286 Gene3D:G3DSA:3.30.730.10 SUPFAM:SSF54171 HSSP:O80337 GO:GO:0009736 GO:GO:0071472 GO:GO:0010017 EMBL:AC009243 HOGENOM:HBG599504 EMBL:AC012680 UniGene:At.25524 EMBL:AF370152 EMBL:AY150468 EMBL:AF003097 IPI:IPI00519366 RefSeq:NP_177931.1 UniGene:At.71798 ProteinModelPortal:Q8H1E4 SMR:Q8H1E4 MINT:MINT-7262714 STRING:Q8H1E4 PRIDE:Q8H1E4 EnsemblPlants:AT1G78080.1 GeneID:844143 KEGG:ath:AT1G78080 TAIR:At1g78080 eggNOG:NOG306355 InParanoid:Q8H1E4 OMA:KLEAICK PhylomeDB:Q8H1E4 ProtClustDB:CLSN2679481 Genevestigator:Q8H1E4 Uniprot:Q8H1E4
Root	Isotig09017	13	0	4.571	0.000344357	TAIR|locus:2013668 - symbol:AT1G29680 "AT1G29680" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0005515 "protein binding" evidence=IPI] EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005515 EMBL:AC068667 UniGene:At.48247 UniGene:At.71163 ProtClustDB:CLSN2682014 InterPro:IPR010686 Pfam:PF06884 HOGENOM:HBG473015 EMBL:BT005255 EMBL:AK118004 IPI:IPI00523169 PIR:B86420 RefSeq:NP_174261.1 IntAct:Q9C7N3 PRIDE:Q9C7N3 DNASU:839845 EnsemblPlants:AT1G29680.1 GeneID:839845 KEGG:ath:AT1G29680 TAIR:At1g29680 eggNOG:NOG295567 InParanoid:Q9C7N3 OMA:AGSTIMQ PhylomeDB:Q9C7N3 Genevestigator:Q9C7N3 Uniprot:Q9C7N3
Root	Isotig09018	13	0	4.571	0.000344357	TAIR|locus:2013668 - symbol:AT1G29680 "AT1G29680" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0005515 "protein binding" evidence=IPI] EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005515 EMBL:AC068667 UniGene:At.48247 UniGene:At.71163 ProtClustDB:CLSN2682014 InterPro:IPR010686 Pfam:PF06884 HOGENOM:HBG473015 EMBL:BT005255 EMBL:AK118004 IPI:IPI00523169 PIR:B86420 RefSeq:NP_174261.1 IntAct:Q9C7N3 PRIDE:Q9C7N3 DNASU:839845 EnsemblPlants:AT1G29680.1 GeneID:839845 KEGG:ath:AT1G29680 TAIR:At1g29680 eggNOG:NOG295567 InParanoid:Q9C7N3 OMA:AGSTIMQ PhylomeDB:Q9C7N3 Genevestigator:Q9C7N3 Uniprot:Q9C7N3
Root	Isotig09031	12	0	4.456	0.000626491	TAIR|locus:2026545 - symbol:AT1G07750 "AT1G07750" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0045735 "nutrient reservoir activity" evidence=ISS] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0008270 "zinc ion binding" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR006044 InterPro:IPR006045 Pfam:PF00190 PRINTS:PR00439 SMART:SM00835 GO:GO:0045735 InterPro:IPR011051 InterPro:IPR014710 Gene3D:G3DSA:2.60.120.10 SUPFAM:SSF51182 EMBL:CP002684 GO:GO:0005829 GO:GO:0009506 GO:GO:0008270 GO:GO:0005507 EMBL:AC007583 EMBL:AF334728 EMBL:AF410308 EMBL:BT001038 IPI:IPI00528478 PIR:A86213 RefSeq:NP_172255.1 UniGene:At.22153 ProteinModelPortal:Q9LQQ3 SMR:Q9LQQ3 PRIDE:Q9LQQ3 EnsemblPlants:AT1G07750.1 GeneID:837290 KEGG:ath:AT1G07750 TAIR:At1g07750 InParanoid:Q9LQQ3 OMA:LETHIKA PhylomeDB:Q9LQQ3 ProtClustDB:CLSN2682742 ArrayExpress:Q9LQQ3 Genevestigator:Q9LQQ3 Uniprot:Q9LQQ3
Root	Isotig09061	53	0	6.599	2.10E-13	No hit
Root	Isotig09062	46	0	6.395	6.55E-12	UNIPROTKB|P06750 - symbol:P06750 "Agglutinin" species:3988 "Ricinus communis" [GO:0005515 "protein binding" evidence=IPI] [GO:0005783 "endoplasmic reticulum" evidence=IDA] InterPro:IPR001574 InterPro:IPR016138 InterPro:IPR016139 InterPro:IPR017988 InterPro:IPR017989 Pfam:PF00161 PRINTS:PR00396 PROSITE:PS00275 GO:GO:0005783 GO:GO:0005515 GO:GO:0006952 GO:GO:0017148 GO:GO:0000166

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0005529 GO:GO:0030598 InterPro:IPR000772 Gene3D:G3DSA:3.40.420.10 Gene3D:G3DSA:4.10.470.10 Pfam:PF00652 SMART:SM00458 SUPFAM:SSF56371 SUPFAM:SSF50370 PROSITE:PS50231 CAZy:CBM13 EMBL:M12089 EMBL:S40368 PIR:A24261 PDB:1RZO PDBsum:1RZO ProteinModelPortal:P06750 SMR:P06750 GlycoSuiteDB:P06750 Uniprot:P06750
Root	Isotig09066	55	2	4.652	1.48E-13	No hit
Root	Isotig09071	0	44	-6.588	2.61E-12	TAIR|locus:2204798 - symbol:MC1 "AT1G02170" species:3702 "Arabidopsis thaliana" [GO:0006508 "proteolysis" evidence=ISS] [GO:0004197 "cysteine-type endopeptidase activity" evidence=IDA] [GO:0043068 "positive regulation of programmed cell death" evidence=IGI;IDA] InterPro:IPR011600 Pfam:PF00656 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0006952 GO:GO:0004197 GO:GO:0006508 GO:GO:0043068 EMBL:U89959 InterPro:IPR005735 Pfam:PF06943 TIGRFAMs:TIGR01053 EMBL:AY219826 EMBL:AY322525 IPI:IPI00531085 RefSeq:NP_171719.2 UniGene:At.10711 UniGene:At.69983 ProteinModelPortal:Q7XJE6 STRING:Q7XJE6 MEROPS:C14.047 PRIDE:Q7XJE6 EnsemblPlants:AT1G02170.1 GeneID:839561 KEGG:ath:AT1G02170 TAIR:At1g02170 eggNOG:NOG68179 HOGENOM:HBG692861 InParanoid:Q7XJE6 OMA:NDAKCMR PhylomeDB:Q7XJE6 Genevestigator:Q7XJE6 Uniprot:Q7XJE6
Root	Isotig09072	0	27	-5.884	3.19E-08	TAIR|locus:2204798 - symbol:MC1 "AT1G02170" species:3702 "Arabidopsis thaliana" [GO:0006508 "proteolysis" evidence=ISS] [GO:0004197 "cysteine-type endopeptidase activity" evidence=IDA] [GO:0043068 "positive regulation of programmed cell death" evidence=IGI;IDA] InterPro:IPR011600 Pfam:PF00656 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0006952 GO:GO:0004197 GO:GO:0006508 GO:GO:0043068 EMBL:U89959 InterPro:IPR005735 Pfam:PF06943 TIGRFAMs:TIGR01053 EMBL:AY219826 EMBL:AY322525 IPI:IPI00531085 RefSeq:NP_171719.2 UniGene:At.10711 UniGene:At.69983 ProteinModelPortal:Q7XJE6 STRING:Q7XJE6 MEROPS:C14.047 PRIDE:Q7XJE6 EnsemblPlants:AT1G02170.1 GeneID:839561 KEGG:ath:AT1G02170 TAIR:At1g02170 eggNOG:NOG68179 HOGENOM:HBG692861 InParanoid:Q7XJE6 OMA:NDAKCMR PhylomeDB:Q7XJE6 Genevestigator:Q7XJE6 Uniprot:Q7XJE6
Root	Isotig09127	0	15	-5.036	4.38E-05	SGD|S000005327 - symbol:AGA1 "Anchorage subunit of a-agglutinin of a-cells" species:4932 "Saccharomyces cerevisiae" [GO:0009277 "fungal-type cell wall" evidence=IDA] [GO:0000752 "agglutination involved in conjugation with cellular fusion" evidence=IMP] [GO:0050839 "cell adhesion molecule binding" evidence=ISS;IMP;TAS] [GO:0031225 "anchored to membrane" evidence=IEA] [GO:0019236 "response to pheromone" evidence=IEA] [GO:0016020 "membrane" evidence=IEA] [GO:0005576 "extracellular region" evidence=IEA] [GO:0005618 "cell wall" evidence=IEA] [GO:0007155 "cell adhesion" evidence=IEA] SGD:S000005327 GO:GO:0005576 GO:GO:0031225 EMBL:BK006947 GO:GO:0050839 EMBL:M60590 EMBL:Z71659 PIR:A41258 RefSeq:NP_014442.1 ProteinModelPortal:P32323 IntAct:P32323 STRING:P32323 EnsemblFungi:YNR044W GeneID:855780 KEGG:sce:YNR044W CYGD:YNR044w eggNOG:NOG12793 GeneTree:ENSGT00650000093537 OMA:YTSTTSY NextBio:980247 ArrayExpress:P32323 Genevestigator:P32323 GermOnline:YNR044W GO:GO:0009277 GO:GO:0000752 Uniprot:P32323
Root	Isotig09128	0	15	-5.036	4.38E-05	DICTYBASE|DDB_G0283391 - symbol:kinX "LISK family protein kinase,protein kinase, TKL group,tyrosine kinase-like protein" species:44689 "Dictyostelium discoideum" [GO:0005575 "cellular_component" evidence=ND] [GO:0004672 "protein kinase activity" evidence=ISS] [GO:0005524 "ATP binding" evidence=ISS] [GO:0006468 "protein phosphorylation" evidence=ISS] InterPro:IPR000719 InterPro:IPR001245 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 Pfam:PF00069 PRINTS:PR00109 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 dictyBase:DDB_G0283391 GO:GO:0005524 GenomeReviews:CM000153_GR eggNOG:COG0515 SUPFAM:SSF56112 GO:GO:0004674 EMBL:AAFI02000055 HSSP:O43318 EMBL:Z37981 PIR:S52076 RefSeq:XP_639097.1 ProteinModelPortal:Q23915 PRIDE:Q23915 EnsemblProtists:DDB0191487 GeneID:8624121 KEGG:ddi:DDB_G0283391 KO:K05743 OMA:PTKVEES PhylomeDB:Q23915 Uniprot:Q23915
Root	Isotig09217	30	7	1.971	0.000234532	TAIR|locus:2041839 - symbol:AT2G15220 "AT2G15220" species:3702 "Arabidopsis thaliana" [GO:0006952 "defense response" evidence=ISS] Pfam:PF04450 EMBL:CP002685 GenomeReviews:CT485783_GR EMBL:AC006298 InterPro:IPR007541 eggNOG:NOG83661 EMBL:AF345341 EMBL:AY090375 IPI:IPI00528646 PIR:D84526 RefSeq:NP_565369.1 UniGene:At.13396 PRIDE:Q9SKL6 EnsemblPlants:AT2G15220.1 GeneID:816011 KEGG:ath:AT2G15220 TAIR:At2g15220 HOGENOM:HBG319630 InParanoid:Q9SKL6 OMA:MENGDGV PhylomeDB:Q9SKL6 ProtClustDB:CLSN2683478 Genevestigator:Q9SKL6 Uniprot:Q9SKL6
Root	Isotig09218	29	7	1.922	0.000375107	TAIR|locus:2041839 - symbol:AT2G15220 "AT2G15220" species:3702 "Arabidopsis thaliana" [GO:0006952 "defense response" evidence=ISS] Pfam:PF04450 EMBL:CP002685 GenomeReviews:CT485783_GR EMBL:AC006298 InterPro:IPR007541 eggNOG:NOG83661 EMBL:AF345341 EMBL:AY090375 IPI:IPI00528646

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						PIR:D84526 RefSeq:NP_565369.1 UniGene:At.13396 PRIDE:Q9SKL6 EnsemblPlants:AT2G15220.1 GeneID:816011 KEGG:ath:AT2G15220 TAIR:At2g15220 HOGENOM:HBG319630 InParanoid:Q9SKL6 OMA:MENGDGV PhylomeDB:Q9SKL6 ProtClustDB:CLSN2683478 Genevestigator:Q9SKL6 Uniprot:Q9SKL6
Root	Isotig09233	2	22	-3.588	5.84E-06	TAIR|locus:2084933 - symbol:IAA16 "indoleacetic acid-induced protein 16" species:3702 "Arabidopsis thaliana" [GO:0005634 "nucleus" evidence=IEA] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0009733 "response to auxin stimulus" evidence=TAS] [GO:0005515 "protein binding" evidence=IPI] InterPro:IPR003311 InterPro:IPR011525 Pfam:PF02309 PROSITE:PS50962 GO:GO:0005634 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0009734 GO:GO:0006355 GO:GO:0006351 GO:GO:0046983 EMBL:AC011437 HOGENOM:HBG750482 eggNOG:NOG281606 EMBL:U49072 EMBL:AF332400 EMBL:AF375420 EMBL:BT000857 EMBL:AY087195 IPI:IPI00530628 RefSeq:NP_187124.1 UniGene:At.24121 IntAct:O24407 STRING:O24407 PRIDE:O24407 DNASU:819633 EnsemblPlants:AT3G04730.1 GeneID:819633 KEGG:ath:AT3G04730 GeneFarm:3175 TAIR:At3g04730 InParanoid:O24407 OMA:FTIGNYG PhylomeDB:O24407 ProtClustDB:CLSN2914703 ArrayExpress:O24407 Genevestigator:O24407 GermOnline:AT3G04730 Uniprot:O24407
Root	Isotig09234	2	22	-3.588	5.84E-06	TAIR|locus:2084933 - symbol:IAA16 "indoleacetic acid-induced protein 16" species:3702 "Arabidopsis thaliana" [GO:0005634 "nucleus" evidence=IEA] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0009733 "response to auxin stimulus" evidence=TAS] [GO:0005515 "protein binding" evidence=IPI] InterPro:IPR003311 InterPro:IPR011525 Pfam:PF02309 PROSITE:PS50962 GO:GO:0005634 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0009734 GO:GO:0006355 GO:GO:0006351 GO:GO:0046983 EMBL:AC011437 HOGENOM:HBG750482 eggNOG:NOG281606 EMBL:U49072 EMBL:AF332400 EMBL:AF375420 EMBL:BT000857 EMBL:AY087195 IPI:IPI00530628 RefSeq:NP_187124.1 UniGene:At.24121 IntAct:O24407 STRING:O24407 PRIDE:O24407 DNASU:819633 EnsemblPlants:AT3G04730.1 GeneID:819633 KEGG:ath:AT3G04730 GeneFarm:3175 TAIR:At3g04730 InParanoid:O24407 OMA:FTIGNYG PhylomeDB:O24407 ProtClustDB:CLSN2914703 ArrayExpress:O24407 Genevestigator:O24407 GermOnline:AT3G04730 Uniprot:O24407
Root	Isotig09239	2	15	-3.036	0.000493759	TAIR|locus:2167101 - symbol:OXS3 "AT5G56550" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0006950 "response to stress" evidence=IMP] [GO:0006979 "response to oxidative stress" evidence=IMP] [GO:0016607 "nuclear speck" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IMP] GO:GO:0046686 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0006979 GO:GO:0016607 EMBL:AB019234 EMBL:AK175485 EMBL:AK176596 IPI:IPI00539472 RefSeq:NP_200466.1 UniGene:At.63908 EnsemblPlants:AT5G56550.1 GeneID:835756 KEGG:ath:AT5G56550 TAIR:At5g56550 eggNOG:NOG283612 InParanoid:Q9LVB9 OMA:LMSHLPI PhylomeDB:Q9LVB9 ProtClustDB:CLSN2916686 Genevestigator:Q9LVB9 Uniprot:Q9LVB9
Root	Isotig09240	2	15	-3.036	0.000493759	TAIR|locus:2167101 - symbol:OXS3 "AT5G56550" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0006950 "response to stress" evidence=IMP] [GO:0006979 "response to oxidative stress" evidence=IMP] [GO:0016607 "nuclear speck" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IMP] GO:GO:0046686 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0006979 GO:GO:0016607 EMBL:AB019234 EMBL:AK175485 EMBL:AK176596 IPI:IPI00539472 RefSeq:NP_200466.1 UniGene:At.63908 EnsemblPlants:AT5G56550.1 GeneID:835756 KEGG:ath:AT5G56550 TAIR:At5g56550 eggNOG:NOG283612 InParanoid:Q9LVB9 OMA:LMSHLPI PhylomeDB:Q9LVB9 ProtClustDB:CLSN2916686 Genevestigator:Q9LVB9 Uniprot:Q9LVB9
Root	Isotig09283	62	0	6.825	2.85E-15	TAIR|locus:2197823 - symbol:AT1G04560 "AT1G04560" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] Pfam:PF05512 EMBL:CP002684 GenomeReviews:CT485782_GR EMBL:AC002376 EMBL:AF360343 EMBL:AY051080 IPI:IPI00537314 PIR:B86178 RefSeq:NP_563710.1 UniGene:At.10465 PRIDE:O23029 EnsemblPlants:AT1G04560.1 GeneID:839491 KEGG:ath:AT1G04560 TAIR:At1g04560 eggNOG:NOG327574 HOGENOM:HBG593249 InParanoid:O23029 OMA:VAWAITA PhylomeDB:O23029 ProtClustDB:CLSN2687672 ArrayExpress:O23029 Genevestigator:O23029 InterPro:IPR008390 Uniprot:O23029
Root	Isotig09284	57	0	6.704	3.06E-14	TAIR|locus:2197823 - symbol:AT1G04560 "AT1G04560" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] Pfam:PF05512 EMBL:CP002684 GenomeReviews:CT485782_GR EMBL:AC002376 EMBL:AF360343 EMBL:AY051080 IPI:IPI00537314 PIR:B86178 RefSeq:NP_563710.1 UniGene:At.10465 PRIDE:O23029

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EnsemblPlants:AT1G04560.1 GeneID:839491 KEGG:ath:AT1G04560 TAIR:At1g04560 eggNOG:NOG327574 HOGENOM:HBG593249 InParanoid:O23029 OMA:VAWAITA PhylomeDB:O23029 ProtClustDB:CLSN2687672 ArrayExpress:O23029 Genevestigator:O23029 InterPro:IPR008390 Uniprot:O23029
Root	Isotig09285	15	0	4.778	0.000105609	UNIPROTKB|Q41050 - symbol:OEP16 "Outer envelope pore protein 16, chloroplastic" species:3888 "Pisum sativum" [GO:0042803 "protein homodimerization activity" evidence=IDA] [GO:0045037 "protein import into chloroplast stroma" evidence=IDA] InterPro:IPR003397 Pfam:PF02466 GO:GO:0016021 GO:GO:0042803 GO:GO:0045037 EMBL:Z73553 PIR:T06471 TCDB:1.B.30.1.1 Uniprot:Q41050
Root	Isotig09286	15	0	4.778	0.000105609	UNIPROTKB|Q41050 - symbol:OEP16 "Outer envelope pore protein 16, chloroplastic" species:3888 "Pisum sativum" [GO:0042803 "protein homodimerization activity" evidence=IDA] [GO:0045037 "protein import into chloroplast stroma" evidence=IDA] InterPro:IPR003397 Pfam:PF02466 GO:GO:0016021 GO:GO:0042803 GO:GO:0045037 EMBL:Z73553 PIR:T06471 TCDB:1.B.30.1.1 Uniprot:Q41050
Root	Isotig09299	15	51	-1.895	1.03E-06	No hit
Root	Isotig09300	27	66	-1.418	6.20E-06	No hit
Root	Isotig09311	18	0	5.041	1.86E-05	TAIR|locus:2093307 - symbol:AT3G15670 "AT3G15670" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0009793 "embryo development ending in seed dormancy" evidence=ISS] [GO:0005634 "nucleus" evidence=IDA] GO:GO:0005634 EMBL:CP002686 EMBL:AB017071 ProtClustDB:CLSN2679745 EMBL:AY040026 EMBL:AY054162 EMBL:AY079410 IPI:IPI00542660 RefSeq:NP_188188.1 UniGene:At.5382 STRING:Q9LW12 PRIDE:Q9LW12 ProMEX:Q9LW12 EnsemblPlants:AT3G15670.1 GeneID:820810 KEGG:ath:AT3G15670 TAIR:At3g15670 InParanoid:Q9LW12 OMA:QYTKETA PhylomeDB:Q9LW12 ArrayExpress:Q9LW12 Genevestigator:Q9LW12 Uniprot:Q9LW12
Root	Isotig09312	16	0	4.871	5.89E-05	TAIR|locus:2093307 - symbol:AT3G15670 "AT3G15670" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0009793 "embryo development ending in seed dormancy" evidence=ISS] [GO:0005634 "nucleus" evidence=IDA] GO:GO:0005634 EMBL:CP002686 EMBL:AB017071 ProtClustDB:CLSN2679745 EMBL:AY040026 EMBL:AY054162 EMBL:AY079410 IPI:IPI00542660 RefSeq:NP_188188.1 UniGene:At.5382 STRING:Q9LW12 PRIDE:Q9LW12 ProMEX:Q9LW12 EnsemblPlants:AT3G15670.1 GeneID:820810 KEGG:ath:AT3G15670 TAIR:At3g15670 InParanoid:Q9LW12 OMA:QYTKETA PhylomeDB:Q9LW12 ArrayExpress:Q9LW12 Genevestigator:Q9LW12 Uniprot:Q9LW12
Root	Isotig09327	18	0	5.041	1.86E-05	TAIR|locus:2197823 - symbol:AT1G04560 "AT1G04560" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] Pfam:PF05512 EMBL:CP002684 GenomeReviews:CT485782_GR EMBL:AC002376 EMBL:AF360343 EMBL:AY051080 IPI:IPI00537314 PIR:B86178 RefSeq:NP_563710.1 UniGene:At.10465 PRIDE:O23029 EnsemblPlants:AT1G04560.1 GeneID:839491 KEGG:ath:AT1G04560 TAIR:At1g04560 eggNOG:NOG327574 HOGENOM:HBG593249 InParanoid:O23029 OMA:VAWAITA PhylomeDB:O23029 ProtClustDB:CLSN2687672 ArrayExpress:O23029 Genevestigator:O23029 InterPro:IPR008390 Uniprot:O23029
Root	Isotig09328	12	0	4.456	0.000626491	TAIR|locus:2197823 - symbol:AT1G04560 "AT1G04560" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] Pfam:PF05512 EMBL:CP002684 GenomeReviews:CT485782_GR EMBL:AC002376 EMBL:AF360343 EMBL:AY051080 IPI:IPI00537314 PIR:B86178 RefSeq:NP_563710.1 UniGene:At.10465 PRIDE:O23029 EnsemblPlants:AT1G04560.1 GeneID:839491 KEGG:ath:AT1G04560 TAIR:At1g04560 eggNOG:NOG327574 HOGENOM:HBG593249 InParanoid:O23029 OMA:VAWAITA PhylomeDB:O23029 ProtClustDB:CLSN2687672 ArrayExpress:O23029 Genevestigator:O23029 InterPro:IPR008390 Uniprot:O23029
Root	Isotig09353	1	13	-3.829	0.000362856	TAIR|locus:2119667 - symbol:NDB3 "AT4G21490" species:3702 "Arabidopsis thaliana" [GO:0003954 "NADH dehydrogenase activity" evidence=ISS] [GO:0055114 "oxidation-reduction process" evidence=IEA] InterPro:IPR001327 InterPro:IPR013027 InterPro:IPR023753 Pfam:PF00070 Pfam:PF07992 PRINTS:PR00368 GenomeReviews:CT486007_GR GO:GO:0050660 GO:GO:0016491 eggNOG:COG1252 EMBL:AL161555 EMBL:AL022603 HOGENOM:HBG319217 IPI:IPI01020302 PIR:T05157 ProteinModelPortal:O65414 SMR:O65414 PRIDE:O65414 TAIR:At4g21490 InParanoid:O65414 PhylomeDB:O65414 ArrayExpress:O65414 Genevestigator:O65414 Uniprot:O65414
Root	Isotig09357	113	0	7.691	4.63E-25	TAIR|locus:2093307 - symbol:AT3G15670 "AT3G15670" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0009793 "embryo development ending in seed dormancy" evidence=ISS] [GO:0005634 "nucleus" evidence=IDA] GO:GO:0005634 EMBL:CP002686 EMBL:AB017071 ProtClustDB:CLSN2679745 EMBL:AY040026 EMBL:AY054162 EMBL:AY079410 IPI:IPI00542660

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						RefSeq:NP_188188.1 UniGene:At.5382 STRING:Q9LW12 PRIDE:Q9LW12 ProMEX:Q9LW12 EnsemblPlants:AT3G15670.1 GeneID:820810 KEGG:ath:AT3G15670 TAIR:At3g15670 InParanoid:Q9LW12 OMA:QYTKETA PhylomeDB:Q9LW12 ArrayExpress:Q9LW12 Genevestigator:Q9LW12 Uniprot:Q9LW12
Root	Isotig09358	105	0	7.585	1.34E-23	TAIR|locus:2093307 - symbol:AT3G15670 "AT3G15670" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0009793 "embryo development ending in seed dormancy" evidence=ISS] [GO:0005634 "nucleus" evidence=IDA] GO:GO:0005634 EMBL:CP002686 EMBL:AB017071 ProtClustDB:CLSN2679745 EMBL:AY040026 EMBL:AY054162 EMBL:AY079410 IPI:IPI00542660 RefSeq:NP_188188.1 UniGene:At.5382 STRING:Q9LW12 PRIDE:Q9LW12 ProMEX:Q9LW12 EnsemblPlants:AT3G15670.1 GeneID:820810 KEGG:ath:AT3G15670 TAIR:At3g15670 InParanoid:Q9LW12 OMA:QYTKETA PhylomeDB:Q9LW12 ArrayExpress:Q9LW12 Genevestigator:Q9LW12 Uniprot:Q9LW12
Root	Isotig09375	0	24	-5.714	1.84E-07	TAIR|locus:2057175 - symbol:PYL4 "AT2G38310" species:3702 "Arabidopsis thaliana" [GO:0005515 "protein binding" evidence=IPI] [GO:0004872 "receptor activity" evidence=IDA] [GO:0009738 "abscisic acid mediated signaling pathway" evidence=IGI;IDA] GO:GO:0005634 GO:GO:0005737 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0042803 GO:GO:0009738 GO:GO:0004872 InterPro:IPR023393 Gene3D:G3DSA:3.30.530.20 EMBL:AC004683 GO:GO:0010427 KO:K14496 InterPro:IPR019587 Pfam:PF10604 HOGENOM:HBG598713 EMBL:AY039586 EMBL:AY054141 EMBL:AY087146 IPI:IPI00527852 PIR:T02514 RefSeq:NP_565887.1 UniGene:At.12775 ProteinModelPortal:O80920 SMR:O80920 DIP:DIP-53474N IntAct:O80920 STRING:O80920 PRIDE:O80920 EnsemblPlants:AT2G38310.1 GeneID:818411 KEGG:ath:AT2G38310 TAIR:At2g38310 eggNOG:NOG268307 InParanoid:O80920 OMA:DERHVIS PhylomeDB:O80920 ProtClustDB:CLSN2917266 ArrayExpress:O80920 Genevestigator:O80920 Uniprot:O80920
Root	Isotig09376	0	23	-5.653	3.32E-07	TAIR|locus:2057175 - symbol:PYL4 "AT2G38310" species:3702 "Arabidopsis thaliana" [GO:0005515 "protein binding" evidence=IPI] [GO:0004872 "receptor activity" evidence=IDA] [GO:0009738 "abscisic acid mediated signaling pathway" evidence=IGI;IDA] GO:GO:0005634 GO:GO:0005737 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0042803 GO:GO:0009738 GO:GO:0004872 InterPro:IPR023393 Gene3D:G3DSA:3.30.530.20 EMBL:AC004683 GO:GO:0010427 KO:K14496 InterPro:IPR019587 Pfam:PF10604 HOGENOM:HBG598713 EMBL:AY039586 EMBL:AY054141 EMBL:AY087146 IPI:IPI00527852 PIR:T02514 RefSeq:NP_565887.1 UniGene:At.12775 ProteinModelPortal:O80920 SMR:O80920 DIP:DIP-53474N IntAct:O80920 STRING:O80920 PRIDE:O80920 EnsemblPlants:AT2G38310.1 GeneID:818411 KEGG:ath:AT2G38310 TAIR:At2g38310 eggNOG:NOG268307 InParanoid:O80920 OMA:DERHVIS PhylomeDB:O80920 ProtClustDB:CLSN2917266 ArrayExpress:O80920 Genevestigator:O80920 Uniprot:O80920
Root	Isotig09381	117	6	4.156	9.43E-26	WB|WBGene00000682 - symbol:col-108 species:6239 "Caenorhabditis elegans" [GO:0042302 "structural constituent of cuticle" evidence=IEA] [GO:0016021 "integral to membrane" evidence=IEA] [GO:0006898 "receptor-mediated endocytosis" evidence=IMP] InterPro:IPR002486 Pfam:PF01484 SMART:SM01088 GO:GO:0006898 InterPro:IPR008160 Pfam:PF01391 HOGENOM:HBG444750 GO:GO:0042302 GeneTree:ENSGT00650000093441 eggNOG:NOG317947 EMBL:FO081611 RefSeq:NP_500133.2 UniGene:Cel.12041 ProteinModelPortal:Q95Y22 PRIDE:Q95Y22 EnsemblMetazoa:Y41D4A.2 GeneID:176985 KEGG:cel:Y41D4A.2 UCSC:Y41D4A.2 CTD:176985 WormBase:Y41D4A.2 InParanoid:Q95Y22 OMA:FREFTEV NextBio:894856 Uniprot:Q95Y22
Root	Isotig09382	99	6	3.915	2.57E-21	No hit
Root	Isotig09387	13	0	4.571	0.000344357	No hit
Root	Isotig09429	1	17	-4.216	2.69E-05	TAIR|locus:2012773 - symbol:ERD9 "AT1G10370" species:3702 "Arabidopsis thaliana" [GO:0004364 "glutathione transferase activity" evidence=ISS;IDA] [GO:0005737 "cytoplasm" evidence=NAS] [GO:0009407 "toxin catabolic process" evidence=TAS] [GO:0009507 "chloroplast" evidence=IDA] [GO:0080167 "response to karrikin" evidence=IEP] [GO:0006749 "glutathione metabolic process" evidence=IMP] [GO:0009704 "de-etiolation" evidence=IMP] [GO:0048527 "lateral root development" evidence=IMP] [GO:0060416 "response to growth hormone stimulus" evidence=IEP] [GO:0009651 "response to salt stress" evidence=IMP] [GO:0080148 "negative regulation of response to water deprivation" evidence=IMP] InterPro:IPR004045 PROSITE:PS50404 InterPro:IPR004046 Pfam:PF00043 EMBL:CP002684 GO:GO:0005829 GO:GO:0009507 GO:GO:0009651 GO:GO:0080167 GO:GO:0048527 GO:GO:0009636 GO:GO:0040008 InterPro:IPR012336 Gene3D:G3DSA:3.40.30.10 SUPFAM:SSF52833 InterPro:IPR010987 Gene3D:G3DSA:1.20.1050.10 SUPFAM:SSF47616 PROSITE:PS50405 GO:GO:0060416 EMBL:AC005489 GO:GO:0006749 InterPro:IPR017933 GO:GO:0004364 GO:GO:0009407 eggNOG:NOG288793 HOGENOM:HBG749301 HSSP:O04941 EMBL:AB039930 EMBL:AF288191 EMBL:BT023743 IPI:IPI00532578 RefSeq:NP_172508.4 UniGene:At.11290 ProteinModelPortal:Q9FUS8

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						SMR:Q9FUS8 PRIDE:Q9FUS8 EnsemblPlants:AT1G10370.1 GeneID:837576 KEGG:ath:AT1G10370 TAIR:At1g10370 InParanoid:Q9FUS8 ProtClustDB:CLSN2679578 Genevestigator:Q9FUS8 GO:GO:0009704 GO:GO:0080148 Uniprot:Q9FUS8
Root	Isotig09430	1	17	-4.216	2.69E-05	TAIR|locus:2012758 - symbol:GSTU18 "AT1G10360" species:3702 "Arabidopsis thaliana" [GO:0004364 "glutathione transferase activity" evidence=ISS] [GO:0005737 "cytoplasm" evidence=NAS] [GO:0009407 "toxin catabolic process" evidence=TAS] InterPro:IPR004045 PROSITE:PS50404 InterPro:IPR004046 Pfam:PF00043 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0009636 InterPro:IPR012336 Gene3D:G3DSA:3.40.30.10 SUPFAM:SSF52833 InterPro:IPR010987 Gene3D:G3DSA:1.20.1050.10 SUPFAM:SSF47616 PROSITE:PS50405 EMBL:AC005489 InterPro:IPR017933 GO:GO:0004364 eggNOG:COG0625 GO:GO:0009407 HOGENOM:HBG749301 HSSP:O04941 ProtClustDB:CLSN2679578 EMBL:AF288190 EMBL:BT000940 EMBL:AK317183 IPI:IPI00517213 RefSeq:NP_172507.1 UniGene:At.11288 ProteinModelPortal:Q9FUS9 SMR:Q9FUS9 IntAct:Q9FUS9 STRING:Q9FUS9 PRIDE:Q9FUS9 EnsemblPlants:AT1G10360.1 GeneID:837575 KEGG:ath:AT1G10360 TAIR:At1g10360 InParanoid:Q9FUS9 OMA:ITIHESA PhylomeDB:Q9FUS9 ArrayExpress:Q9FUS9 Genevestigator:Q9FUS9 Uniprot:Q9FUS9
Root	Isotig09463	29	5	2.407	4.20E-05	No hit
Root	Isotig09464	28	7	1.871	0.000596844	No hit
Root	Isotig09521	50	10	2.193	3.67E-07	TAIR|locus:2081546 - symbol:RPS5A "AT3G11940" species:3702 "Arabidopsis thaliana" [GO:0003735 "structural constituent of ribosome" evidence=ISS] [GO:0005840 "ribosome" evidence=ISS] [GO:0006412 "translation" evidence=ISS] [GO:0022627 "cytosolic small ribosomal subunit" evidence=ISS] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000235 InterPro:IPR005716 InterPro:IPR020606 PIRSF:PIRSF002122 PROSITE:PS00052 Pfam:PF00177 GO:GO:0005886 GO:GO:0009506 GO:GO:0005773 GO:GO:0005618 GO:GO:0009507 EMBL:CP002686 GenomeReviews:BA000014_GR EMBL:AP002040 GO:GO:0006412 GO:GO:0003723 GO:GO:0003735 GO:GO:0022626 EMBL:AC016795 GO:GO:0015935 UniGene:At.24761 eggNOG:COG0049 HOGENOM:HBG297325 KO:K02989 ProtClustDB:CLSN2683972 InterPro:IPR023798 Gene3D:G3DSA:1.10.455.10 PANTHER:PTHR11205 PANTHER:PTHR11205:SF1 SUPFAM:SSF47973 TIGRFAMs:TIGR01028 EMBL:AY045846 EMBL:AY091376 EMBL:AY086938 EMBL:Z18496 IPI:IPI00546269 RefSeq:NP_187800.1 RefSeq:NP_850564.1 ProteinModelPortal:P51427 SMR:P51427 STRING:P51427 PRIDE:P51427 ProMEX:P51427 EnsemblPlants:AT3G11940.1 EnsemblPlants:AT3G11940.2 GeneID:820367 KEGG:ath:AT3G11940 TAIR:At3g11940 InParanoid:P51427 OMA:SVPKAVD PhylomeDB:P51427 Genevestigator:P51427 GermOnline:AT3G11940 Uniprot:P51427
Root	Isotig09522	40	10	1.871	4.07E-05	TAIR|locus:2081546 - symbol:RPS5A "AT3G11940" species:3702 "Arabidopsis thaliana" [GO:0003735 "structural constituent of ribosome" evidence=ISS] [GO:0005840 "ribosome" evidence=ISS] [GO:0006412 "translation" evidence=ISS] [GO:0022627 "cytosolic small ribosomal subunit" evidence=ISS] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000235 InterPro:IPR005716 InterPro:IPR020606 PIRSF:PIRSF002122 PROSITE:PS00052 Pfam:PF00177 GO:GO:0005886 GO:GO:0009506 GO:GO:0005773 GO:GO:0005618 GO:GO:0009507 EMBL:CP002686 GenomeReviews:BA000014_GR EMBL:AP002040 GO:GO:0006412 GO:GO:0003723 GO:GO:0003735 GO:GO:0022626 EMBL:AC016795 GO:GO:0015935 UniGene:At.24761 eggNOG:COG0049 HOGENOM:HBG297325 KO:K02989 ProtClustDB:CLSN2683972 InterPro:IPR023798 Gene3D:G3DSA:1.10.455.10 PANTHER:PTHR11205 PANTHER:PTHR11205:SF1 SUPFAM:SSF47973 TIGRFAMs:TIGR01028 EMBL:AY045846 EMBL:AY091376 EMBL:AY086938 EMBL:Z18496 IPI:IPI00546269 RefSeq:NP_187800.1 RefSeq:NP_850564.1 ProteinModelPortal:P51427 SMR:P51427 STRING:P51427 PRIDE:P51427 ProMEX:P51427 EnsemblPlants:AT3G11940.1 EnsemblPlants:AT3G11940.2 GeneID:820367 KEGG:ath:AT3G11940 TAIR:At3g11940 InParanoid:P51427 OMA:SVPKAVD PhylomeDB:P51427 Genevestigator:P51427 GermOnline:AT3G11940 Uniprot:P51427
Root	Isotig09613	40	12	1.608	0.000223447	TAIR|locus:2130923 - symbol:AT4G17390 species:3702 "Arabidopsis thaliana" [GO:0003735 "structural constituent of ribosome" evidence=IEA;ISS] [GO:0005840 "ribosome" evidence=ISS] [GO:0006412 "translation" evidence=IEA;ISS] [GO:0005730 "nucleolus" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0022625 "cytosolic large ribosomal subunit" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA]

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						[GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR000439 InterPro:IPR012678 InterPro:IPR020925 InterPro:IPR024794 Pfam:PF00827 PROSITE:PS01194 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005730 GO:GO:0016020 GO:GO:0006412 GO:GO:0003735 EMBL:Z97343 EMBL:AL161546 GO:GO:0022625 UniGene:At.20009 SUPFAM:SSF54189 eggNOG:COG1632 HOGENOM:HBG577798 KO:K02877 ProtClustDB:CLSN2685842 Gene3D:G3DSA:3.40.1120.10 PANTHER:PTHR11847 EMBL:AY072118 EMBL:AY122965 EMBL:AY087088 IPI:IPI00546926 PIR:C71443 RefSeq:NP_193470.1 UniGene:At.24376 UniGene:At.71219 ProteinModelPortal:Q8VYF1 SMR:Q8VYF1 STRING:Q8VYF1 PRIDE:Q8VYF1 EnsemblPlants:AT4G17390.1 GeneID:827451 KEGG:ath:AT4G17390 GeneFarm:242 TAIR:At4g17390 InParanoid:Q8VYF1 OMA:AKQGIIV PhylomeDB:Q8VYF1 Genevestigator:Q8VYF1 GermOnline:AT4G17390 Uniprot:Q8VYF1
Root	Isotig09614	43	13	1.597	0.000140286	TAIR|locus:2130923 - symbol:AT4G17390 species:3702 "Arabidopsis thaliana" [GO:0003735 "structural constituent of ribosome" evidence=IEA;ISS] [GO:0005840 "ribosome" evidence=ISS] [GO:0006412 "translation" evidence=IEA;ISS] [GO:0005730 "nucleolus" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0022625 "cytosolic large ribosomal subunit" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR000439 InterPro:IPR012678 InterPro:IPR020925 InterPro:IPR024794 Pfam:PF00827 PROSITE:PS01194 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005730 GO:GO:0016020 GO:GO:0006412 GO:GO:0003735 EMBL:Z97343 EMBL:AL161546 GO:GO:0022625 UniGene:At.20009 SUPFAM:SSF54189 eggNOG:COG1632 HOGENOM:HBG577798 KO:K02877 ProtClustDB:CLSN2685842 Gene3D:G3DSA:3.40.1120.10 PANTHER:PTHR11847 EMBL:AY072118 EMBL:AY122965 EMBL:AY087088 IPI:IPI00546926 PIR:C71443 RefSeq:NP_193470.1 UniGene:At.24376 UniGene:At.71219 ProteinModelPortal:Q8VYF1 SMR:Q8VYF1 STRING:Q8VYF1 PRIDE:Q8VYF1 EnsemblPlants:AT4G17390.1 GeneID:827451 KEGG:ath:AT4G17390 GeneFarm:242 TAIR:At4g17390 InParanoid:Q8VYF1 OMA:AKQGIIV PhylomeDB:Q8VYF1 Genevestigator:Q8VYF1 GermOnline:AT4G17390 Uniprot:Q8VYF1
Root	Isotig09629	9	27	-1.714	0.000905257	TAIR|locus:2007176 - symbol:ELF5A-3 "eukaryotic elongation factor 5A-3" species:3702 "Arabidopsis thaliana" [GO:0003723 "RNA binding" evidence=IEA] [GO:0003743 "translation initiation factor activity" evidence=ISS] [GO:0003746 "translation elongation factor activity" evidence=IEA] [GO:0006413 "translational initiation" evidence=ISS] [GO:0006452 "translational frameshifting" evidence=IEA] [GO:0008612 "peptidyl-lysine modification to hypusine" evidence=IEA] [GO:0043022 "ribosome binding" evidence=IEA] [GO:0045901 "positive regulation of translational elongation" evidence=IEA] [GO:0045905 "positive regulation of translational termination" evidence=IEA] InterPro:IPR001884 InterPro:IPR019769 InterPro:IPR020189 Pfam:PF01287 PIRSF:PIRSF003025 PROSITE:PS00302 Pfam:PF00467 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0043022 GO:GO:0003746 EMBL:AC018364 GO:GO:0003743 EMBL:AC073178 InterPro:IPR012340 Gene3D:G3DSA:2.40.50.140 InterPro:IPR016027 SUPFAM:SSF50249 InterPro:IPR014722 Gene3D:G3DSA:2.30.30.30 GO:GO:0008612 GO:GO:0045901 eggNOG:COG0231 InterPro:IPR008991 SUPFAM:SSF50104 InterPro:IPR005824 HOGENOM:HBG526951 KO:K03263 ProtClustDB:PLN03107 GO:GO:0045905 GO:GO:0006452 PANTHER:PTHR11673 TIGRFAMs:TIGR00037 EMBL:AF372933 EMBL:AY060530 EMBL:AY087040 IPI:IPI00527220 RefSeq:NP_177100.1 UniGene:At.47614 ProteinModelPortal:Q9C505 SMR:Q9C505 STRING:Q9C505 PRIDE:Q9C505 EnsemblPlants:AT1G69410.1 GeneID:843273 KEGG:ath:AT1G69410 TAIR:At1g69410 InParanoid:Q9C505 OMA:CALKEVG PhylomeDB:Q9C505 ArrayExpress:Q9C505 Genevestigator:Q9C505 GermOnline:AT1G69410 Uniprot:Q9C505
Root	Isotig09646	3	19	-2.792	0.000168634	No hit
Root	Isotig09657	36	1	5.041	1.40E-09	TAIR|locus:2171032 - symbol:AT5G46960 species:3702 "Arabidopsis thaliana" [GO:0004857 "enzyme inhibitor activity" evidence=IEA] [GO:0008150 "biological_process" evidence=ND] [GO:0030599 "pectinesterase activity" evidence=IEA] [GO:0046910 "pectinesterase inhibitor activity" evidence=ISS] InterPro:IPR006501 Pfam:PF04043 SMART:SM00856 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0004857 EMBL:AB013394 GO:GO:0030599 Gene3D:G3DSA:1.20.140.40 SUPFAM:SSF101148 TIGRFAMs:TIGR01614 HOGENOM:HBG745715 IPI:IPI00525290 RefSeq:NP_568673.1 UniGene:At.49424 ProteinModelPortal:Q9FJR5 SMR:Q9FJR5 PRIDE:Q9FJR5 EnsemblPlants:AT5G46960.1 GeneID:834742 KEGG:ath:AT5G46960 TAIR:At5g46960 eggNOG:NOG255438 InParanoid:Q9FJR5 OMA:ASHADIG PhylomeDB:Q9FJR5 ProtClustDB:CLSN2917742 Genevestigator:Q9FJR5 Uniprot:Q9FJR5

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig09658	37	0	6.080	6.25E-10	TAIR|locus:2171032 - symbol:AT5G46960 species:3702 "Arabidopsis thaliana" [GO:0004857 "enzyme inhibitor activity" evidence=IEA] [GO:0008150 "biological_process" evidence=ND] [GO:0030599 "pectinesterase activity" evidence=IEA] [GO:0046910 "pectinesterase inhibitor activity" evidence=ISS] InterPro:IPR006501 Pfam:PF04043 SMART:SM00856 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0004857 EMBL:AB013394 GO:GO:0030599 Gene3D:G3DSA:1.20.140.40 SUPFAM:SSF101148 TIGRFAMs:TIGR01614 HOGENOM:HBG745715 IPI:IPI00525290 RefSeq:NP_568673.1 UniGene:At.49424 ProteinModelPortal:Q9FJR5 SMR:Q9FJR5 PRIDE:Q9FJR5 EnsemblPlants:AT5G46960.1 GeneID:834742 KEGG:ath:AT5G46960 TAIR:At5g46960 eggNOG:NOG255438 InParanoid:Q9FJR5 OMA:ASHADIG PhylomeDB:Q9FJR5 ProtClustDB:CLSN2917742 Genevestigator:Q9FJR5 Uniprot:Q9FJR5
Root	Isotig09667	13	0	4.571	0.000344357	TAIR|locus:2127520 - symbol:AT4G22430 "AT4G22430" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] InterPro:IPR001810 Pfam:PF00646 PROSITE:PS50181 GenomeReviews:CT486007_GR SUPFAM:SSF81383 EMBL:AL161557 EMBL:AL033545 EMBL:DQ446861 EMBL:DQ653215 IPI:IPI00759220 PIR:H85256 ProteinModelPortal:Q1PE57 SMR:Q1PE57 TAIR:At4g22430 InParanoid:Q1PE57 ArrayExpress:Q9SUX6 Genevestigator:Q1PE57 Uniprot:Q1PE57
Root	Isotig09697	0	14	-4.936	8.24E-05	TAIR|locus:2118314 - symbol:AT4G29260 species:3702 "Arabidopsis thaliana" [GO:0003993 "acid phosphatase activity" evidence=IEA;ISS] [GO:0008150 "biological_process" evidence=ND] [GO:0005773 "vacuole" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR005519 InterPro:IPR010028 Pfam:PF03767 GO:GO:0005829 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005774 InterPro:IPR023214 Gene3D:G3DSA:3.40.50.1000 SUPFAM:SSF56784 GO:GO:0003993 EMBL:AL161574 HOGENOM:HBG599685 InterPro:IPR014403 PIRSF:PIRSF002674 TIGRFAMs:TIGR01675 eggNOG:NOG41277 ProtClustDB:CLSN2685345 EMBL:AY050945 EMBL:AY091175 IPI:IPI00548735 PIR:T13437 RefSeq:NP_194655.1 UniGene:At.4537 UniGene:At.48918 ProteinModelPortal:Q9M0F5 PRIDE:Q9M0F5 DNASU:829047 EnsemblPlants:AT4G29260.1 GeneID:829047 KEGG:ath:AT4G29260 TAIR:At4g29260 InParanoid:Q9M0F5 OMA:SFDEWVD PhylomeDB:Q9M0F5 Genevestigator:Q9M0F5 Uniprot:Q9M0F5
Root	Isotig09698	0	14	-4.936	8.24E-05	TAIR|locus:2118329 - symbol:AT4G29270 species:3702 "Arabidopsis thaliana" [GO:0003993 "acid phosphatase activity" evidence=IEA;ISS] [GO:0008150 "biological_process" evidence=ND] InterPro:IPR005519 InterPro:IPR010028 Pfam:PF03767 EMBL:CP002687 GenomeReviews:CT486007_GR InterPro:IPR023214 Gene3D:G3DSA:3.40.50.1000 SUPFAM:SSF56784 GO:GO:0003993 EMBL:AL161574 HOGENOM:HBG599685 InterPro:IPR014403 PIRSF:PIRSF002674 TIGRFAMs:TIGR01675 EMBL:AY084437 EMBL:BT004812 EMBL:AK227764 IPI:IPI00538077 PIR:T13440 RefSeq:NP_194656.1 UniGene:At.31944 ProteinModelPortal:Q9M0F4 SMR:Q9M0F4 PRIDE:Q9M0F4 DNASU:829048 EnsemblPlants:AT4G29270.1 GeneID:829048 KEGG:ath:AT4G29270 TAIR:At4g29270 eggNOG:NOG41277 InParanoid:Q9M0F4 OMA:IASYCES PhylomeDB:Q9M0F4 ProtClustDB:CLSN2685345 ArrayExpress:Q9M0F4 Genevestigator:Q9M0F4 Uniprot:Q9M0F4
Root	Isotig09716	2	16	-3.129	0.000262867	TAIR|locus:2177137 - symbol:GLP6 "AT5G39100" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0030145 "manganese ion binding" evidence=IEA] [GO:0045735 "nutrient reservoir activity" evidence=IEA] [GO:0048046 "apoplast" evidence=IEA] InterPro:IPR001929 InterPro:IPR006045 InterPro:IPR019780 Pfam:PF00190 PRINTS:PR00325 PROSITE:PS00725 SMART:SM00835 GO:GO:0045735 InterPro:IPR011051 InterPro:IPR014710 Gene3D:G3DSA:2.60.120.10 SUPFAM:SSF51182 GO:GO:0048046 EMBL:CP002688 GenomeReviews:BA000015_GR EMBL:AB016892 GO:GO:0030145 HOGENOM:HBG744545 EMBL:U75194 IPI:IPI00523561 IPI:IPI01020090 RefSeq:NP_568562.1 UniGene:At.24199 ProteinModelPortal:P92997 GeneID:833903 KEGG:ath:AT5G39100 TAIR:At5g39100 eggNOG:NOG246111 InParanoid:P92997 PhylomeDB:P92997 ArrayExpress:P92997 Genevestigator:P92997 GermOnline:AT5G39100 Uniprot:P92997
Root	Isotig09749	0	20	-5.451	2.00E-06	TAIR|locus:2827077 - symbol:GL22 "germin-like protein subfamily 2 member 2 precursor" species:3702 "Arabidopsis thaliana" [GO:0030145 "manganese ion binding" evidence=IEA] [GO:0045735 "nutrient reservoir activity" evidence=IEA] [GO:0048046 "apoplast" evidence=IEA] InterPro:IPR001929 InterPro:IPR006045 InterPro:IPR019780 Pfam:PF00190 PRINTS:PR00325 PROSITE:PS00725 SMART:SM00835 GO:GO:0045735 InterPro:IPR011051 InterPro:IPR014710 Gene3D:G3DSA:2.60.120.10 SUPFAM:SSF51182 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0048046 GO:GO:0030145 EMBL:AC064879 HOGENOM:HBG744545 EMBL:AK176405 IPI:IPI00540989 PIR:F86153 RefSeq:NP_001077450.1 UniGene:At.27586

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						ProteinModelPortal:Q9FZ27 SMR:Q9FZ27 PRIDE:Q9FZ27 EnsemblPlants:AT1G02335.1 GeneID:3766642 KEGG:ath:AT1G02335 TAIR:At1g02335 eggNOG:NOG39495 PhylomeDB:Q9FZ27 ProtClustDB:CLSN2920119 Genevestigator:Q9FZ27 Uniprot:Q9FZ27
Root	Isotig09750	0	20	-5.451	2.00E-06	TAIR|locus:2827077 - symbol:GL22 "germin-like protein subfamily 2 member 2 precursor" species:3702 "Arabidopsis thaliana" [GO:0030145 "manganese ion binding" evidence=IEA] [GO:0045735 "nutrient reservoir activity" evidence=IEA] [GO:0048046 "apoplast" evidence=IEA] InterPro:IPR001929 InterPro:IPR006045 InterPro:IPR019780 Pfam:PF00190 PRINTS:PR00325 PROSITE:PS00725 SMART:SM00835 GO:GO:0045735 InterPro:IPR011051 InterPro:IPR014710 Gene3D:G3DSA:2.60.120.10 SUPFAM:SSF51182 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0048046 GO:GO:0030145 EMBL:AC064879 HOGENOM:HBG744545 EMBL:AK176405 IPI:IPI00540989 PIR:F86153 RefSeq:NP_001077450.1 UniGene:At.27586 ProteinModelPortal:Q9FZ27 SMR:Q9FZ27 PRIDE:Q9FZ27 EnsemblPlants:AT1G02335.1 GeneID:3766642 KEGG:ath:AT1G02335 TAIR:At1g02335 eggNOG:NOG39495 PhylomeDB:Q9FZ27 ProtClustDB:CLSN2920119 Genevestigator:Q9FZ27 Uniprot:Q9FZ27
Root	Isotig09771	20	0	5.193	5.94E-06	TAIR|locus:2090552 - symbol:AT3G17520 "AT3G17520" species:3702 "Arabidopsis thaliana" [GO:0009793 "embryo development ending in seed dormancy" evidence=ISS] Pfam:PF02987 GenomeReviews:BA000014_GR InterPro:IPR004238 EMBL:BT004128 EMBL:BT020426 IPI:IPI00525902 STRING:Q84W82 PRIDE:Q84W82 TAIR:At3g17520 eggNOG:NOG269272 ArrayExpress:Q84W82 Genevestigator:Q84W82 Uniprot:Q84W82
Root	Isotig09772	20	0	5.193	5.94E-06	TAIR|locus:2090552 - symbol:AT3G17520 "AT3G17520" species:3702 "Arabidopsis thaliana" [GO:0009793 "embryo development ending in seed dormancy" evidence=ISS] Pfam:PF02987 GenomeReviews:BA000014_GR InterPro:IPR004238 EMBL:BT004128 EMBL:BT020426 IPI:IPI00525902 STRING:Q84W82 PRIDE:Q84W82 TAIR:At3g17520 eggNOG:NOG269272 ArrayExpress:Q84W82 Genevestigator:Q84W82 Uniprot:Q84W82
Root	Isotig09777	3	23	-3.068	1.45E-05	TAIR|locus:2078461 - symbol:CCH "copper chaperone" species:3702 "Arabidopsis thaliana" [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0000302 "response to reactive oxygen species" evidence=IGI] [GO:0006827 "high-affinity iron ion transport" evidence=IGI] [GO:0006878 "cellular copper ion homeostasis" evidence=IMP;TAS] [GO:0007568 "aging" evidence=IEP] [GO:0016531 "copper chaperone activity" evidence=ISS] InterPro:IPR006121 Pfam:PF00403 PROSITE:PS50846 GO:GO:0046686 GO:GO:0009507 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0046872 GO:GO:0006878 GO:GO:0009651 SUPFAM:SSF55008 GO:GO:0030001 eggNOG:NOG238748 KO:K07213 HSSP:O00244 HOGENOM:HBG744819 EMBL:AL163763 EMBL:U88711 EMBL:AF361860 EMBL:AY066056 EMBL:AY085657 IPI:IPI00517088 PIR:T47741 RefSeq:NP_191183.1 UniGene:At.24871 ProteinModelPortal:O82089 SMR:O82089 IntAct:O82089 STRING:O82089 PRIDE:O82089 ProMEX:O82089 EnsemblPlants:AT3G56240.1 GeneID:824790 KEGG:ath:AT3G56240 TAIR:At3g56240 InParanoid:O82089 OMA:DIDIKEQ PhylomeDB:O82089 ProtClustDB:CLSN2913444 Genevestigator:O82089 Uniprot:O82089
Root	Isotig09778	3	23	-3.068	1.45E-05	TAIR|locus:2205288 - symbol:ATX1 "homolog of anti-oxidant 1" species:3702 "Arabidopsis thaliana" [GO:0030001 "metal ion transport" evidence=IEA] [GO:0046872 "metal ion binding" evidence=IEA] [GO:0000785 "chromatin" evidence=IDA] InterPro:IPR006121 Pfam:PF00403 PROSITE:PS50846 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0046872 SUPFAM:SSF55008 GO:GO:0030001 GO:GO:0000785 HSSP:O00244 HOGENOM:HBG744819 EMBL:AY039898 EMBL:AY077678 IPI:IPI00524818 RefSeq:NP_564870.1 UniGene:At.57055 ProteinModelPortal:Q94BT9 SMR:Q94BT9 IntAct:Q94BT9 STRING:Q94BT9 PRIDE:Q94BT9 EnsemblPlants:AT1G66240.1 GeneID:842940 KEGG:ath:AT1G66240 TAIR:At1g66240 InParanoid:Q94BT9 OMA:VDIKEQK PhylomeDB:Q94BT9 Genevestigator:Q94BT9 Uniprot:Q94BT9
Root	Isotig09785	42	1	5.263	5.01E-11	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig09786	43	1	5.297	2.89E-11	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component"

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig09789	1	20	-4.451	3.92E-06	TAIR|locus:2081695 - symbol:ATGSTF13 "AT3G62760" species:3702 "Arabidopsis thaliana" [GO:0004364 "glutathione transferase activity" evidence=ISS] [GO:0005737 "cytoplasm" evidence=NAS] [GO:0009407 "toxin catabolic process" evidence=TAS] InterPro:IPR004045 Pfam:PF02798 PROSITE:PS50404 InterPro:IPR004046 Pfam:PF00043 GO:GO:0005829 EMBL:CP002686 GenomeReviews:BA000014_GR EMBL:AL162651 GO:GO:0009636 InterPro:IPR012336 Gene3D:G3DSA:3.40.30.10 SUPFAM:SSF52833 InterPro:IPR010987 Gene3D:G3DSA:1.20.1050.10 SUPFAM:SSF47616 PROSITE:PS50405 InterPro:IPR017933 GO:GO:0004364 eggNOG:COG0625 HOGENOM:HBG753188 GO:GO:0009407 HSSP:Q9ZP62 IPI:IPI00528803 PIR:T48065 RefSeq:NP_191835.1 UniGene:At.54041 ProteinModelPortal:Q9LZI9 SMR:Q9LZI9 PRIDE:Q9LZI9 EnsemblPlants:AT3G62760.1 GeneID:825451 KEGG:ath:AT3G62760 TAIR:At3g62760 InParanoid:Q9LZI9 OMA:KAWWERL PhylomeDB:Q9LZI9 ProtClustDB:CLSN2684163 Genevestigator:Q9LZI9 Uniprot:Q9LZI9
Root	Isotig09790	1	22	-4.588	1.10E-06	TAIR|locus:2081695 - symbol:ATGSTF13 "AT3G62760" species:3702 "Arabidopsis thaliana" [GO:0004364 "glutathione transferase activity" evidence=ISS] [GO:0005737 "cytoplasm" evidence=NAS] [GO:0009407 "toxin catabolic process" evidence=TAS] InterPro:IPR004045 Pfam:PF02798 PROSITE:PS50404 InterPro:IPR004046 Pfam:PF00043 GO:GO:0005829 EMBL:CP002686 GenomeReviews:BA000014_GR EMBL:AL162651 GO:GO:0009636 InterPro:IPR012336 Gene3D:G3DSA:3.40.30.10 SUPFAM:SSF52833 InterPro:IPR010987 Gene3D:G3DSA:1.20.1050.10 SUPFAM:SSF47616 PROSITE:PS50405 InterPro:IPR017933 GO:GO:0004364 eggNOG:COG0625 HOGENOM:HBG753188 GO:GO:0009407 HSSP:Q9ZP62 IPI:IPI00528803 PIR:T48065 RefSeq:NP_191835.1 UniGene:At.54041 ProteinModelPortal:Q9LZI9 SMR:Q9LZI9 PRIDE:Q9LZI9 EnsemblPlants:AT3G62760.1 GeneID:825451 KEGG:ath:AT3G62760 TAIR:At3g62760 InParanoid:Q9LZI9 OMA:KAWWERL PhylomeDB:Q9LZI9 ProtClustDB:CLSN2684163 Genevestigator:Q9LZI9 Uniprot:Q9LZI9
Root	Isotig09799	5	27	-2.562	1.85E-05	TAIR|locus:2167101 - symbol:OXS3 "AT5G56550" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0006950 "response to stress" evidence=IMP] [GO:0006979 "response to oxidative stress" evidence=IMP] [GO:0016607 "nuclear speck" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IMP] GO:GO:0046686 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0006979 GO:GO:0016607 EMBL:AB019234 EMBL:AK175485 EMBL:AK176596 IPI:IPI00539472 RefSeq:NP_200466.1 UniGene:At.63908 EnsemblPlants:AT5G56550.1 GeneID:835756 KEGG:ath:AT5G56550 TAIR:At5g56550 eggNOG:NOG283612 InParanoid:Q9LVB9 OMA:LMSHLPI PhylomeDB:Q9LVB9 ProtClustDB:CLSN2916686 Genevestigator:Q9LVB9 Uniprot:Q9LVB9
Root	Isotig09800	5	27	-2.562	1.85E-05	TAIR|locus:2167101 - symbol:OXS3 "AT5G56550" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0006950 "response to stress" evidence=IMP] [GO:0006979 "response to oxidative stress" evidence=IMP] [GO:0016607 "nuclear speck" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IMP] GO:GO:0046686 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0006979 GO:GO:0016607 EMBL:AB019234 EMBL:AK175485 EMBL:AK176596 IPI:IPI00539472 RefSeq:NP_200466.1 UniGene:At.63908 EnsemblPlants:AT5G56550.1 GeneID:835756 KEGG:ath:AT5G56550 TAIR:At5g56550 eggNOG:NOG283612 InParanoid:Q9LVB9 OMA:LMSHLPI PhylomeDB:Q9LVB9 ProtClustDB:CLSN2916686 Genevestigator:Q9LVB9 Uniprot:Q9LVB9
Root	Isotig09841	1	13	-3.829	0.000362856	TAIR|locus:2201190 - symbol:AT1G23140 "AT1G23140" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0005886 "plasma membrane" evidence=IDA] InterPro:IPR000008 InterPro:IPR008973 Pfam:PF00168 SMART:SM00239 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005886 InterPro:IPR018029 SUPFAM:SSF49562 PROSITE:PS50004 EMBL:AC002311 HSSP:Q9JKS6 EMBL:BT043489 IPI:IPI00533193 PIR:F86365 RefSeq:NP_173727.1 UniGene:At.49306 ProteinModelPortal:O49303 SMR:O49303 PRIDE:O49303 EnsemblPlants:AT1G23140.1 GeneID:838922 KEGG:ath:AT1G23140 TAIR:At1g23140 eggNOG:NOG246634 HOGENOM:HBG319599 InParanoid:O49303 OMA:TRGVENS PhylomeDB:O49303 ProtClustDB:CLSN2914420 Genevestigator:O49303 Uniprot:O49303

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig09842	0	13	-4.829	0.000155955	TAIR|locus:2201190 - symbol:AT1G23140 "AT1G23140" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0005886 "plasma membrane" evidence=IDA] InterPro:IPR000008 InterPro:IPR008973 Pfam:PF00168 SMART:SM00239 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005886 InterPro:IPR018029 SUPFAM:SSF49562 PROSITE:PS50004 EMBL:AC002311 HSSP:Q9JKS6 EMBL:BT043489 IPI:IPI00533193 PIR:F86365 RefSeq:NP_173727.1 UniGene:At.49306 ProteinModelPortal:O49303 SMR:O49303 PRIDE:O49303 EnsemblPlants:AT1G23140.1 GeneID:838922 KEGG:ath:AT1G23140 TAIR:At1g23140 eggNOG:NOG246634 HOGENOM:HBG319599 InParanoid:O49303 OMA:TRGVENS PhylomeDB:O49303 ProtClustDB:CLSN2914420 Genevestigator:O49303 Uniprot:O49303
Root	Isotig09855	1	16	-4.129	5.13E-05	No hit
Root	Isotig09856	0	16	-5.129	2.34E-05	No hit
Root	Isotig09905	1	12	-3.714	0.000699736	TAIR|locus:2060984 - symbol:HIS1-3 "histone H1-3" species:3702 "Arabidopsis thaliana" [GO:0000786 "nucleosome" evidence=IEA;ISS] [GO:0003677 "DNA binding" evidence=ISS] [GO:0005634 "nucleus" evidence=IEA] [GO:0006334 "nucleosome assembly" evidence=ISS] [GO:0009414 "response to water deprivation" evidence=IEP] [GO:0031492 "nucleosomal DNA binding" evidence=ISS] InterPro:IPR005818 InterPro:IPR005819 Pfam:PF00538 PRINTS:PR00624 PROSITE:PS51504 SMART:SM00526 GO:GO:0005634 EMBL:CP002685 GO:GO:0003677 InterPro:IPR011991 Gene3D:G3DSA:1.10.10.10 GO:GO:0009414 GO:GO:0006334 GO:GO:0000786 EMBL:AC006201 KO:K11275 EMBL:U72241 EMBL:U73781 EMBL:AY045797 EMBL:AY079414 EMBL:AY084603 IPI:IPI00539258 PIR:F84559 RefSeq:NP_179396.1 UniGene:At.24439 ProteinModelPortal:P94109 SMR:P94109 STRING:P94109 PRIDE:P94109 EnsemblPlants:AT2G18050.1 GeneID:816317 KEGG:ath:AT2G18050 TAIR:At2g18050 eggNOG:NOG258576 InParanoid:P94109 OMA:TKRTRSS PhylomeDB:P94109 ProtClustDB:CLSN2683930 ArrayExpress:P94109 Genevestigator:P94109 Uniprot:P94109
Root	Isotig09906	1	12	-3.714	0.000699736	TAIR|locus:2060984 - symbol:HIS1-3 "histone H1-3" species:3702 "Arabidopsis thaliana" [GO:0000786 "nucleosome" evidence=IEA;ISS] [GO:0003677 "DNA binding" evidence=ISS] [GO:0005634 "nucleus" evidence=IEA] [GO:0006334 "nucleosome assembly" evidence=ISS] [GO:0009414 "response to water deprivation" evidence=IEP] [GO:0031492 "nucleosomal DNA binding" evidence=ISS] InterPro:IPR005818 InterPro:IPR005819 Pfam:PF00538 PRINTS:PR00624 PROSITE:PS51504 SMART:SM00526 GO:GO:0005634 EMBL:CP002685 GO:GO:0003677 InterPro:IPR011991 Gene3D:G3DSA:1.10.10.10 GO:GO:0009414 GO:GO:0006334 GO:GO:0000786 EMBL:AC006201 KO:K11275 EMBL:U72241 EMBL:U73781 EMBL:AY045797 EMBL:AY079414 EMBL:AY084603 IPI:IPI00539258 PIR:F84559 RefSeq:NP_179396.1 UniGene:At.24439 ProteinModelPortal:P94109 SMR:P94109 STRING:P94109 PRIDE:P94109 EnsemblPlants:AT2G18050.1 GeneID:816317 KEGG:ath:AT2G18050 TAIR:At2g18050 eggNOG:NOG258576 InParanoid:P94109 OMA:TKRTRSS PhylomeDB:P94109 ProtClustDB:CLSN2683930 ArrayExpress:P94109 Genevestigator:P94109 Uniprot:P94109
Root	Isotig09909	0	22	-5.588	6.01E-07	TAIR|locus:2185460 - symbol:CA2 "carbonic anhydrase 2" species:3702 "Arabidopsis thaliana" [GO:0004089 "carbonate dehydratase activity" evidence=IEA;ISS] [GO:0008270 "zinc ion binding" evidence=IEA;ISS] [GO:0015976 "carbon utilization" evidence=ISS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0042742 "defense response to bacterium" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] InterPro:IPR001765 InterPro:IPR015892 Pfam:PF00484 PROSITE:PS00704 PROSITE:PS00705 SMART:SM00947 GO:GO:0005829 GO:GO:0048046 GO:GO:0009570 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0042742 GO:GO:0008270 GO:GO:0031969 GO:GO:0015976 GO:GO:0009535 eggNOG:COG0288 GO:GO:0004089 Gene3D:G3DSA:3.40.1050.10 PANTHER:PTHR11002 SUPFAM:SSF53056 EMBL:L18901 EMBL:AL391149 EMBL:AF324712 EMBL:AF326863 EMBL:AF339686 EMBL:AF428428 EMBL:BT000652 EMBL:BT000663 EMBL:Z26538 IPI:IPI00523587 RefSeq:NP_568303.2 RefSeq:NP_974782.1 UniGene:At.23743 ProteinModelPortal:P42737 SMR:P42737 IntAct:P42737 STRING:P42737 SWISS-2DPAGE:P42737 PRIDE:P42737 ProMEX:P42737 EnsemblPlants:AT5G14740.2 GeneID:831326 KEGG:ath:AT5G14740 TAIR:At5g14740 HOGENOM:HBG711150 InParanoid:P42737 KO:K01673 PhylomeDB:P42737 ProtClustDB:CLSN2915215 ArrayExpress:P42737 Genevestigator:P42737 Uniprot:P42737

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig09910	0	21	-5.521	1.09E-06	TAIR|locus:2016109 - symbol:BCA4 "beta carbonic anhydrase 4" species:3702 "Arabidopsis thaliana" [GO:0004089 "carbonate dehydratase activity" evidence=IEA;ISS] [GO:0008270 "zinc ion binding" evidence=IEA;ISS] [GO:0015976 "carbon utilization" evidence=ISS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0010037 "response to carbon dioxide" evidence=IGI] [GO:0010119 "regulation of stomatal movement" evidence=IGI] InterPro:IPR001765 InterPro:IPR015892 Pfam:PF00484 PROSITE:PS00704 PROSITE:PS00705 SMART:SM00947 EMBL:CP002684 GO:GO:0005886 GO:GO:0010119 GO:GO:0008270 GO:GO:0010037 GO:GO:0009941 GO:GO:0015976 GO:GO:0004089 Gene3D:G3DSA:3.40.1050.10 PANTHER:PTHR11002 SUPFAM:SSF53056 KO:K01673 EMBL:AY034926 EMBL:AY113922 IPI:IPI00523368 RefSeq:NP_177198.1 UniGene:At.10650 HSSP:P17067 ProteinModelPortal:Q94CE4 SMR:Q94CE4 IntAct:Q94CE4 STRING:Q94CE4 PRIDE:Q94CE4 EnsemblPlants:AT1G70410.2 GeneID:843377 KEGG:ath:AT1G70410 TAIR:At1g70410 InParanoid:Q94CE4 OMA:QIQSNDV PhylomeDB:Q94CE4 ProtClustDB:PLN00416 ArrayExpress:Q94CE4 Genevestigator:Q94CE4 Uniprot:Q94CE4
Root	Isotig09975	17	0	4.958	3.30E-05	UNIPROTKB|B6TYV8 - symbol:CNR2 "Cell number regulator 2" species:4577 "Zea mays" [GO:0008285 "negative regulation of cell proliferation" evidence=IMP] GO:GO:0016021 GO:GO:0008285 InterPro:IPR006461 Pfam:PF04749 TIGRFAMs:TIGR01571 EMBL:HM008654 EMBL:EU970173 EMBL:BT068908 RefSeq:NP_001144684.1 UniGene:Zm.7882 EnsemblPlants:GRMZM2G151230_T01 GeneID:100277715 KEGG:zma:100277715 PhylomeDB:B6TYV8 Uniprot:B6TYV8
Root	Isotig09976	16	0	4.871	5.89E-05	UNIPROTKB|B6TYV8 - symbol:CNR2 "Cell number regulator 2" species:4577 "Zea mays" [GO:0008285 "negative regulation of cell proliferation" evidence=IMP] GO:GO:0016021 GO:GO:0008285 InterPro:IPR006461 Pfam:PF04749 TIGRFAMs:TIGR01571 EMBL:HM008654 EMBL:EU970173 EMBL:BT068908 RefSeq:NP_001144684.1 UniGene:Zm.7882 EnsemblPlants:GRMZM2G151230_T01 GeneID:100277715 KEGG:zma:100277715 PhylomeDB:B6TYV8 Uniprot:B6TYV8
Root	Isotig09977	0	18	-5.299	6.77E-06	TAIR|locus:2062525 - symbol:UCC1 "uclacyanin 1" species:3702 "Arabidopsis thaliana" [GO:0005507 "copper ion binding" evidence=IEA;ISS] [GO:0009055 "electron carrier activity" evidence=IEA] [GO:0031225 "anchored to membrane" evidence=TAS] InterPro:IPR000923 InterPro:IPR003245 Pfam:PF02298 ProDom:PD003122 PROSITE:PS00196 PROSITE:PS51485 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009055 GO:GO:0031225 GO:GO:0005507 InterPro:IPR008972 Gene3D:G3DSA:2.60.40.420 SUPFAM:SSF49503 EMBL:AC005700 HOGENOM:HBG748847 EMBL:U76298 IPI:IPI00529571 PIR:D84731 RefSeq:NP_180789.1 UniGene:At.10754 HSSP:P29602 ProteinModelPortal:O82081 SMR:O82081 EnsemblPlants:AT2G32300.1 GeneID:817791 KEGG:ath:AT2G32300 TAIR:At2g32300 eggNOG:NOG247256 InParanoid:O82081 OMA:ATDHTIG PhylomeDB:O82081 ProtClustDB:CLSN2913010 ArrayExpress:O82081 Genevestigator:O82081 Uniprot:O82081
Root	Isotig09978	0	16	-5.129	2.34E-05	TAIR|locus:2062525 - symbol:UCC1 "uclacyanin 1" species:3702 "Arabidopsis thaliana" [GO:0005507 "copper ion binding" evidence=IEA;ISS] [GO:0009055 "electron carrier activity" evidence=IEA] [GO:0031225 "anchored to membrane" evidence=TAS] InterPro:IPR000923 InterPro:IPR003245 Pfam:PF02298 ProDom:PD003122 PROSITE:PS00196 PROSITE:PS51485 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009055 GO:GO:0031225 GO:GO:0005507 InterPro:IPR008972 Gene3D:G3DSA:2.60.40.420 SUPFAM:SSF49503 EMBL:AC005700 HOGENOM:HBG748847 EMBL:U76298 IPI:IPI00529571 PIR:D84731 RefSeq:NP_180789.1 UniGene:At.10754 HSSP:P29602 ProteinModelPortal:O82081 SMR:O82081 EnsemblPlants:AT2G32300.1 GeneID:817791 KEGG:ath:AT2G32300 TAIR:At2g32300 eggNOG:NOG247256 InParanoid:O82081 OMA:ATDHTIG PhylomeDB:O82081 ProtClustDB:CLSN2913010 ArrayExpress:O82081 Genevestigator:O82081 Uniprot:O82081
Root	Isotig10011	16	1	3.871	0.000146741	TAIR|locus:2062561 - symbol:AT2G32280 "AT2G32280" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002685 GenomeReviews:CT485783_GR EMBL:AC005700 UniGene:At.38099 HOGENOM:HBG320297 ProtClustDB:CLSN2683283 InterPro:IPR009606 Pfam:PF06749 EMBL:BT011667 EMBL:AK175644 IPI:IPI00537890 PIR:B84731 RefSeq:NP_180787.1 PRIDE:Q9ZV57 EnsemblPlants:AT2G32280.1 GeneID:817788 KEGG:ath:AT2G32280 TAIR:At2g32280 eggNOG:NOG251887 InParanoid:Q9ZV57 OMA:LQRASPN PhylomeDB:Q9ZV57 ArrayExpress:Q9ZV57 Genevestigator:Q9ZV57 Uniprot:Q9ZV57
Root	Isotig10012	16	1	3.871	0.000146741	TAIR|locus:2062561 - symbol:AT2G32280 "AT2G32280" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002685 GenomeReviews:CT485783_GR EMBL:AC005700 UniGene:At.38099 HOGENOM:HBG320297 ProtClustDB:CLSN2683283 InterPro:IPR009606 Pfam:PF06749 EMBL:BT011667 EMBL:AK175644

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						IPI:IPI00537890 PIR:B84731 RefSeq:NP_180787.1 PRIDE:Q9ZV57 EnsemblPlants:AT2G32280.1 GeneID:817788 KEGG:ath:AT2G32280 TAIR:At2g32280 eggNOG:NOG251887 InParanoid:Q9ZV57 OMA:LQRASPN PhylomeDB:Q9ZV57 ArrayExpress:Q9ZV57 Genevestigator:Q9ZV57 Uniprot:Q9ZV57
Root	Isotig10025	29	1	4.729	7.39E-08	TAIR|locus:2174984 - symbol:AT5G66780 "AT5G66780" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002688 GenomeReviews:BA000015_GR EMBL:AB010700 EMBL:AY048239 EMBL:AY072623 IPI:IPI00539273 RefSeq:NP_201479.1 UniGene:At.6618 PRIDE:Q9FL02 EnsemblPlants:AT5G66780.1 GeneID:836811 KEGG:ath:AT5G66780 TAIR:At5g66780 eggNOG:NOG276454 HOGENOM:HBG748513 OMA:NEIHENH PhylomeDB:Q9FL02 ProtClustDB:CLSN2686878 Genevestigator:Q9FL02 Uniprot:Q9FL02
Root	Isotig10026	29	1	4.729	7.39E-08	TAIR|locus:2174984 - symbol:AT5G66780 "AT5G66780" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002688 GenomeReviews:BA000015_GR EMBL:AB010700 EMBL:AY048239 EMBL:AY072623 IPI:IPI00539273 RefSeq:NP_201479.1 UniGene:At.6618 PRIDE:Q9FL02 EnsemblPlants:AT5G66780.1 GeneID:836811 KEGG:ath:AT5G66780 TAIR:At5g66780 eggNOG:NOG276454 HOGENOM:HBG748513 OMA:NEIHENH PhylomeDB:Q9FL02 ProtClustDB:CLSN2686878 Genevestigator:Q9FL02 Uniprot:Q9FL02
Root	Isotig10037	0	28	-5.936	1.79E-08	TAIR|locus:2091196 - symbol:AT3G19690 "AT3G19690" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005576 "extracellular region" evidence=ISS] [GO:0008150 "biological_process" evidence=ND] InterPro:IPR018244 PROSITE:PS01010 Pfam:PF00188 INTERPRO:IPR001283 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005576 EMBL:AP000417 InterPro:IPR014044 Gene3D:G3DSA:3.40.33.10 PANTHER:PTHR10334 PRINTS:PR00837 SMART:SM00198 SUPFAM:SSF55797 HSSP:P04284 eggNOG:COG2340 HOGENOM:HBG689653 OMA:VEMWYRE EMBL:BT030036 IPI:IPI00548678 PIR:T52399 RefSeq:NP_188603.1 UniGene:At.75495 UniGene:At.8144 ProteinModelPortal:Q9LJM5 SMR:Q9LJM5 STRING:Q9LJM5 EnsemblPlants:AT3G19690.1 GeneID:821506 KEGG:ath:AT3G19690 TAIR:At3g19690 InParanoid:Q9LJM5 PhylomeDB:Q9LJM5 ProtClustDB:CLSN2915437 Genevestigator:Q9LJM5 Uniprot:Q9LJM5
Root	Isotig10038	0	26	-5.829	5.70E-08	TAIR|locus:2091196 - symbol:AT3G19690 "AT3G19690" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005576 "extracellular region" evidence=ISS] [GO:0008150 "biological_process" evidence=ND] InterPro:IPR018244 PROSITE:PS01010 Pfam:PF00188 INTERPRO:IPR001283 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005576 EMBL:AP000417 InterPro:IPR014044 Gene3D:G3DSA:3.40.33.10 PANTHER:PTHR10334 PRINTS:PR00837 SMART:SM00198 SUPFAM:SSF55797 HSSP:P04284 eggNOG:COG2340 HOGENOM:HBG689653 OMA:VEMWYRE EMBL:BT030036 IPI:IPI00548678 PIR:T52399 RefSeq:NP_188603.1 UniGene:At.75495 UniGene:At.8144 ProteinModelPortal:Q9LJM5 SMR:Q9LJM5 STRING:Q9LJM5 EnsemblPlants:AT3G19690.1 GeneID:821506 KEGG:ath:AT3G19690 TAIR:At3g19690 InParanoid:Q9LJM5 PhylomeDB:Q9LJM5 ProtClustDB:CLSN2915437 Genevestigator:Q9LJM5 Uniprot:Q9LJM5
Root	Isotig10087	5	26	-2.507	3.30E-05	No hit
Root	Isotig10088	5	26	-2.507	3.30E-05	No hit
Root	Isotig10127	33	2	3.915	4.43E-08	No hit
Root	Isotig10147	12	0	4.456	0.000626491	UNIPROTKB|Q9FRV1 - symbol:rsca "Basic endochitinase A" species:4550 "Secale cereale" [GO:0004568 "chitinase activity" evidence=IDA] [GO:0005576 "extracellular region" evidence=IC] [GO:0008061 "chitin binding" evidence=IDA] [GO:0016998 "cell wall macromolecule catabolic process" evidence=IDA] [GO:0050832 "defense response to fungus" evidence=IDA] InterPro:IPR000726 InterPro:IPR001002 InterPro:IPR016283 InterPro:IPR018371 Pfam:PF00182 Pfam:PF00187 PIRSF:PIRSF001060 PRINTS:PR00451 ProDom:PD000609 PROSITE:PS00026 PROSITE:PS00773 PROSITE:PS00774 PROSITE:PS50941 SMART:SM00270 GO:GO:0005576 GO:GO:0050832 GO:GO:0031640 CAZy:CBM18 GO:GO:0008061 Gene3D:G3DSA:3.30.60.10 SUPFAM:SSF57016 GO:GO:0004568 GO:GO:0006032 GO:GO:0016998 EMBL:AB051578 PIR:JC2071 ProteinModelPortal:Q9FRV1 SMR:Q9FRV1 CAZy:GH19 Gramene:Q9FRV1 InterPro:IPR023346 SUPFAM:SSF53955 Uniprot:Q9FRV1
Root	Isotig10181	25	2	3.515	4.58E-06	TAIR|locus:505006351 - symbol:MT3 "AT3G15353" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0006878 "cellular copper ion homeostasis" evidence=ISS] EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005507 UniGene:At.1582 EMBL:AP000413 EMBL:AF013959 EMBL:AY074340 EMBL:AY091386 EMBL:AY087213 EMBL:AK229545 IPI:IPI00532414 RefSeq:NP_566509.1 UniGene:At.64998 PRIDE:O22433 EnsemblPlants:AT3G15353.1 GeneID:820771 KEGG:ath:AT3G15353 TAIR:At3g15353 eggNOG:NOG313816

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						HOGENOM:HBG606948 InParanoid:O22433 OMA:ANCKCKC PhylomeDB:O22433 ProtClustDB:CLSN2688402 ArrayExpress:O22433 Genevestigator:O22433 Uniprot:O22433
Root	Isotig10182	26	2	3.571	2.56E-06	TAIR|locus:505006351 - symbol:MT3 "AT3G15353" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0006878 "cellular copper ion homeostasis" evidence=ISS] EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005507 UniGene:At.1582 EMBL:AP000413 EMBL:AF013959 EMBL:AY074340 EMBL:AY091386 EMBL:AY087213 EMBL:AK229545 IPI:IPI00532414 RefSeq:NP_566509.1 UniGene:At.64998 PRIDE:O22433 EnsemblPlants:AT3G15353.1 GeneID:820771 KEGG:ath:AT3G15353 TAIR:At3g15353 eggNOG:NOG313816 HOGENOM:HBG606948 InParanoid:O22433 OMA:ANCKCKC PhylomeDB:O22433 ProtClustDB:CLSN2688402 ArrayExpress:O22433 Genevestigator:O22433 Uniprot:O22433
Root	Isotig10231	16	0	4.871	5.89E-05	No hit
Root	Isotig10232	17	0	4.958	3.30E-05	No hit
Root	Isotig10249	40	0	6.193	1.34E-10	UNIPROTKB|Q41560 - symbol:hsp16.9B "16.9 kDa class I heat shock protein 2" species:4565 "Triticum aestivum" [GO:0051260 "protein homooligomerization" evidence=IDA] Pfam:PF00011 InterPro:IPR002068 GO:GO:0005737 GO:GO:0006950 GO:GO:0051260 InterPro:IPR008978 SUPFAM:SSF49764 PROSITE:PS01031 EMBL:X64618 PIR:S21600 UniGene:Ta.16248 PDB:1GME PDB:2BYU PDB:2H50 PDB:2H53 PDBsum:1GME PDBsum:2BYU PDBsum:2H50 PDBsum:2H53 ProteinModelPortal:Q41560 SMR:Q41560 Gramene:Q41560 Uniprot:Q41560
Root	Isotig10250	40	0	6.193	1.34E-10	UNIPROTKB|Q41560 - symbol:hsp16.9B "16.9 kDa class I heat shock protein 2" species:4565 "Triticum aestivum" [GO:0051260 "protein homooligomerization" evidence=IDA] Pfam:PF00011 InterPro:IPR002068 GO:GO:0005737 GO:GO:0006950 GO:GO:0051260 InterPro:IPR008978 SUPFAM:SSF49764 PROSITE:PS01031 EMBL:X64618 PIR:S21600 UniGene:Ta.16248 PDB:1GME PDB:2BYU PDB:2H50 PDB:2H53 PDBsum:1GME PDBsum:2BYU PDBsum:2H50 PDBsum:2H53 ProteinModelPortal:Q41560 SMR:Q41560 Gramene:Q41560 Uniprot:Q41560
Root	Isotig10277	1	14	-3.936	0.000188601	TAIR|locus:2181808 - symbol:HTA12 "histone H2A 12" species:3702 "Arabidopsis thaliana" [GO:0000786 "nucleosome" evidence=IEA] [GO:0003677 "DNA binding" evidence=IEA;ISS] [GO:0005634 "nucleus" evidence=IEA] [GO:0006334 "nucleosome assembly" evidence=IEA] InterPro:IPR002119 InterPro:IPR007125 InterPro:IPR009072 Pfam:PF00125 PRINTS:PR00620 PROSITE:PS00046 SMART:SM00414 GO:GO:0005634 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0003677 Gene3D:G3DSA:1.10.20.10 SUPFAM:SSF47113 GO:GO:0006334 GO:GO:0000786 EMBL:AL162971 eggNOG:COG5262 HOGENOM:HBG610736 KO:K11251 ProtClustDB:PLN00157 EMBL:AY085515 IPI:IPI00540536 PIR:T48277 RefSeq:NP_195876.1 UniGene:At.26889 ProteinModelPortal:Q9LZ46 SMR:Q9LZ46 STRING:Q9LZ46 PRIDE:Q9LZ46 EnsemblPlants:AT5G02560.1 GeneID:831891 KEGG:ath:AT5G02560 TAIR:At5g02560 InParanoid:Q9LZ46 OMA:ESHHHKS PhylomeDB:Q9LZ46 Genevestigator:Q9LZ46 GermOnline:AT5G02560 Uniprot:Q9LZ46
Root	Isotig10278	1	13	-3.829	0.000362856	TAIR|locus:2181808 - symbol:HTA12 "histone H2A 12" species:3702 "Arabidopsis thaliana" [GO:0000786 "nucleosome" evidence=IEA] [GO:0003677 "DNA binding" evidence=IEA;ISS] [GO:0005634 "nucleus" evidence=IEA] [GO:0006334 "nucleosome assembly" evidence=IEA] InterPro:IPR002119 InterPro:IPR007125 InterPro:IPR009072 Pfam:PF00125 PRINTS:PR00620 PROSITE:PS00046 SMART:SM00414 GO:GO:0005634 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0003677 Gene3D:G3DSA:1.10.20.10 SUPFAM:SSF47113 GO:GO:0006334 GO:GO:0000786 EMBL:AL162971 eggNOG:COG5262 HOGENOM:HBG610736 KO:K11251 ProtClustDB:PLN00157 EMBL:AY085515 IPI:IPI00540536 PIR:T48277 RefSeq:NP_195876.1 UniGene:At.26889 ProteinModelPortal:Q9LZ46 SMR:Q9LZ46 STRING:Q9LZ46 PRIDE:Q9LZ46 EnsemblPlants:AT5G02560.1 GeneID:831891 KEGG:ath:AT5G02560 TAIR:At5g02560 InParanoid:Q9LZ46 OMA:ESHHHKS PhylomeDB:Q9LZ46 Genevestigator:Q9LZ46 GermOnline:AT5G02560 Uniprot:Q9LZ46
Root	Isotig10285	1	12	-3.714	0.000699736	TAIR|locus:2128639 - symbol:LSD1 "AT4G20380" species:3702 "Arabidopsis thaliana" [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=TAS] [GO:0009862 "systemic acquired resistance, salicylic acid mediated signaling pathway" evidence=IEP] [GO:0005515 "protein binding" evidence=IPI] [GO:0002240 "response to molecule of oomycetes origin" evidence=IMP] [GO:0009626 "plant-type hypersensitive response" evidence=IMP] [GO:0001666 "response to hypoxia" evidence=IMP] [GO:0010310 "regulation of hydrogen peroxide metabolic process" evidence=IMP] [GO:0010602 "regulation of 1-aminocyclopropane-1-carboxylate metabolic process" evidence=IMP] [GO:0010618 "aerenchyma formation" evidence=IMP] [GO:0010104 "regulation of ethylene mediated signaling pathway" evidence=IMP] [GO:0043067 "regulation of programmed cell death"

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						evidence=IGI] [GO:0043069 "negative regulation of programmed cell death" evidence=IGI] [GO:0000303 "response to superoxide" evidence=IMP] [GO:0008219 "cell death" evidence=IMP] EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005634 GO:GO:0005737 GO:GO:0006915 GO:GO:0009626 EMBL:AL080253 EMBL:AL161553 HOGENOM:HBG410657 InterPro:IPR005735 Pfam:PF06943 TIGRFAMs:TIGR01053 EMBL:U87833 EMBL:U87834 EMBL:AY080824 EMBL:AY117316 EMBL:AK318980 EMBL:AY087794 IPI:IPI00532559 IPI:IPI00548444 PIR:T10580 RefSeq:NP_001031678.1 RefSeq:NP_001031679.1 RefSeq:NP_001031680.2 RefSeq:NP_001078413.1 RefSeq:NP_567599.3 RefSeq:NP_849548.1 RefSeq:NP_849549.1 UniGene:At.24187 MINT:MINT-3089567 STRING:P94077 PRIDE:P94077 EnsemblPlants:AT4G20380.2 EnsemblPlants:AT4G20380.7 GeneID:827786 KEGG:ath:AT4G20380 TAIR:At4g20380 eggNOG:NOG122705 InParanoid:P94077 OMA:CNTINMV PhylomeDB:P94077 ProtClustDB:CLSN2679959 Genevestigator:P94077 Uniprot:P94077
Root	Isotig10349	12	0	4.456	0.000626491	No hit
Root	Isotig10377	0	35	-6.258	3.45E-10	TAIR|locus:2134966 - symbol:AT4G24130 "AT4G24130" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0005634 "nucleus" evidence=IDA] EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005634 EMBL:AC002343 EMBL:AL161560 EMBL:AL109619 InterPro:IPR007493 Gene3D:G3DSA:2.30.240.10 Pfam:PF04398 SUPFAM:SSF141562 EMBL:BT008528 EMBL:AK118183 IPI:IPI00523393 PIR:T13461 RefSeq:NP_194144.1 UniGene:At.43869 PRIDE:O22978 EnsemblPlants:AT4G24130.1 GeneID:828513 KEGG:ath:AT4G24130 TAIR:At4g24130 eggNOG:NOG301239 HOGENOM:HBG749450 InParanoid:O22978 OMA:TNTRVSY PhylomeDB:O22978 ProtClustDB:CLSN2685388 Genevestigator:O22978 Uniprot:O22978
Root	Isotig10378	0	35	-6.258	3.45E-10	TAIR|locus:2134966 - symbol:AT4G24130 "AT4G24130" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0005634 "nucleus" evidence=IDA] EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005634 EMBL:AC002343 EMBL:AL161560 EMBL:AL109619 InterPro:IPR007493 Gene3D:G3DSA:2.30.240.10 Pfam:PF04398 SUPFAM:SSF141562 EMBL:BT008528 EMBL:AK118183 IPI:IPI00523393 PIR:T13461 RefSeq:NP_194144.1 UniGene:At.43869 PRIDE:O22978 EnsemblPlants:AT4G24130.1 GeneID:828513 KEGG:ath:AT4G24130 TAIR:At4g24130 eggNOG:NOG301239 HOGENOM:HBG749450 InParanoid:O22978 OMA:TNTRVSY PhylomeDB:O22978 ProtClustDB:CLSN2685388 Genevestigator:O22978 Uniprot:O22978
Root	Isotig10381	16	0	4.871	5.89E-05	No hit
Root	Isotig10382	14	0	4.678	0.000190242	No hit
Root	Isotig10389	0	13	-4.829	0.000155955	TAIR|locus:2202265 - symbol:AT1G06330 "AT1G06330" species:3702 "Arabidopsis thaliana" [GO:0005507 "copper ion binding" evidence=ISS] [GO:0005575 "cellular_component" evidence=ND] [GO:0006825 "copper ion transport" evidence=ISS] [GO:0030001 "metal ion transport" evidence=IEA] [GO:0046872 "metal ion binding" evidence=IEA] InterPro:IPR006121 Pfam:PF00403 PROSITE:PS50846 GenomeReviews:CT485782_GR GO:GO:0046872 EMBL:AC068143 SUPFAM:SSF55008 GO:GO:0030001 HOGENOM:HBG746089 eggNOG:NOG278834 IPI:IPI00524778 PIR:A86199 ProteinModelPortal:Q9LMI6 SMR:Q9LMI6 PRIDE:Q9LMI6 TAIR:At1g06330 InParanoid:Q9LMI6 PhylomeDB:Q9LMI6 Genevestigator:Q9LMI6 Uniprot:Q9LMI6
Root	Isotig10390	0	13	-4.829	0.000155955	TAIR|locus:2202265 - symbol:AT1G06330 "AT1G06330" species:3702 "Arabidopsis thaliana" [GO:0005507 "copper ion binding" evidence=ISS] [GO:0005575 "cellular_component" evidence=ND] [GO:0006825 "copper ion transport" evidence=ISS] [GO:0030001 "metal ion transport" evidence=IEA] [GO:0046872 "metal ion binding" evidence=IEA] InterPro:IPR006121 Pfam:PF00403 PROSITE:PS50846 GenomeReviews:CT485782_GR GO:GO:0046872 EMBL:AC068143 SUPFAM:SSF55008 GO:GO:0030001 HOGENOM:HBG746089 eggNOG:NOG278834 IPI:IPI00524778 PIR:A86199 ProteinModelPortal:Q9LMI6 SMR:Q9LMI6 PRIDE:Q9LMI6 TAIR:At1g06330 InParanoid:Q9LMI6 PhylomeDB:Q9LMI6 Genevestigator:Q9LMI6 Uniprot:Q9LMI6
Root	Isotig10447	0	14	-4.936	8.24E-05	TAIR|locus:2168953 - symbol:TIP2;3 "AT5G47450" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=ISS] [GO:0015250 "water channel activity" evidence=ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0009705 "plant-type vacuole membrane" evidence=IDA] [GO:0015200 "methylammonium transmembrane transporter activity" evidence=IDA] [GO:0051739 "ammonia transmembrane transporter activity" evidence=IGI] [GO:0042807 "central vacuole" evidence=IDA] InterPro:IPR000425 InterPro:IPR012269 InterPro:IPR022357 Pfam:PF00230 PRINTS:PR00783 PROSITE:PS00221 GO:GO:0016021 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009705 EMBL:AB025628 GO:GO:0006833 GO:GO:0015200 GO:GO:0051739 InterPro:IPR023271 Gene3D:G3DSA:1.20.1080.10 SUPFAM:SSF81338 eggNOG:COG0580

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						HOGENOM:HBG705794 PANTHER:PTHR19139 TIGRFAMs:TIGR00861 KO:K09873 GO:GO:0042807 ProtClustDB:PLN00166 EMBL:BT011212 EMBL:BT011663 EMBL:AK229341 IPI:IPI00541642 RefSeq:NP_199556.1 UniGene:At.43789 ProteinModelPortal:Q9FGL2 SMR:Q9FGL2 STRING:Q9FGL2 TCDB:1.A.8.10.4 PRIDE:Q9FGL2 EnsemblPlants:AT5G47450.1 GeneID:834794 KEGG:ath:AT5G47450 GeneFarm:4858 TAIR:At5g47450 InParanoid:Q9FGL2 OMA:GHIVACL PhylomeDB:Q9FGL2 ArrayExpress:Q9FGL2 Genevestigator:Q9FGL2 GermOnline:AT5G47450 Uniprot:Q9FGL2
Root	Isotig10459	1	13	-3.829	0.000362856	No hit
Root	Isotig10460	1	13	-3.829	0.000362856	No hit
Root	Isotig10515	39	0	6.156	2.24E-10	UNIPROTKB|A4L7R8 - symbol:Def2 "Defensin-2" species:3349 "Pinus sylvestris" [GO:0005576 "extracellular region" evidence=ISS] [GO:0050832 "defense response to fungus" evidence=ISS] InterPro:IPR003614 InterPro:IPR008176 InterPro:IPR008177 Pfam:PF00304 PRINTS:PR00288 PROSITE:PS00940 SMART:SM00505 GO:GO:0005576 GO:GO:0050832 GO:GO:0031640 EMBL:EF455617 Uniprot:A4L7R8
Root	Isotig10516	42	0	6.263	4.87E-11	UNIPROTKB|A4L7R8 - symbol:Def2 "Defensin-2" species:3349 "Pinus sylvestris" [GO:0005576 "extracellular region" evidence=ISS] [GO:0050832 "defense response to fungus" evidence=ISS] InterPro:IPR003614 InterPro:IPR008176 InterPro:IPR008177 Pfam:PF00304 PRINTS:PR00288 PROSITE:PS00940 SMART:SM00505 GO:GO:0005576 GO:GO:0050832 GO:GO:0031640 EMBL:EF455617 Uniprot:A4L7R8
Root	Isotig10565	15	0	4.778	0.000105609	TAIR|locus:1006230726 - symbol:DSI-1VOC "AT1G07645" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=ISS] [GO:0009628 "response to abiotic stimulus" evidence=IEP] EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0004872 GO:GO:0016301 EMBL:AC007583 HOGENOM:HBG704761 EMBL:AF332448 EMBL:AK118271 IPI:IPI00533753 PIR:D86211 RefSeq:NP_973779.1 UniGene:At.59209 ProteinModelPortal:Q9LQP1 SMR:Q9LQP1 PRIDE:Q9LQP1 EnsemblPlants:AT1G07645.1 GeneID:2745745 KEGG:ath:AT1G07645 TAIR:At1g07645 eggNOG:NOG82103 InParanoid:Q9LQP1 OMA:WGELESG PhylomeDB:Q9LQP1 ProtClustDB:CLSN2681273 Genevestigator:Q9LQP1 Uniprot:Q9LQP1
Root	Isotig10566	14	0	4.678	0.000190242	TAIR|locus:1006230726 - symbol:DSI-1VOC "AT1G07645" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=ISS] [GO:0009628 "response to abiotic stimulus" evidence=IEP] EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0004872 GO:GO:0016301 EMBL:AC007583 HOGENOM:HBG704761 EMBL:AF332448 EMBL:AK118271 IPI:IPI00533753 PIR:D86211 RefSeq:NP_973779.1 UniGene:At.59209 ProteinModelPortal:Q9LQP1 SMR:Q9LQP1 PRIDE:Q9LQP1 EnsemblPlants:AT1G07645.1 GeneID:2745745 KEGG:ath:AT1G07645 TAIR:At1g07645 eggNOG:NOG82103 InParanoid:Q9LQP1 OMA:WGELESG PhylomeDB:Q9LQP1 ProtClustDB:CLSN2681273 Genevestigator:Q9LQP1 Uniprot:Q9LQP1
Root	Isotig10587	0	21	-5.521	1.09E-06	TAIR|locus:505006681 - symbol:DIR1 "AT5G48485" species:3702 "Arabidopsis thaliana" [GO:0006869 "lipid transport" evidence=ISS] [GO:0008289 "lipid binding" evidence=ISS] [GO:0005319 "lipid transporter activity" evidence=ISS] [GO:0009862 "systemic acquired resistance, salicylic acid mediated signaling pathway" evidence=IMP] [GO:0005504 "fatty acid binding" evidence=IDA] [GO:0008270 "zinc ion binding" evidence=IDA] InterPro:IPR013770 GO:GO:0048046 EMBL:CP002688 GenomeReviews:BA000015_GR InterPro:IPR016140 SMART:SM00499 SUPFAM:SSF47699 GO:GO:0008270 GO:GO:0006869 GO:GO:0005504 Gene3D:G3DSA:1.10.110.10 EMBL:AB020745 GO:GO:0009862 EMBL:AF342726 EMBL:AY062857 EMBL:BT006510 EMBL:AY085224 IPI:IPI00525511 RefSeq:NP_568699.1 UniGene:At.27209 PDB:2RKN PDBsum:2RKN ProteinModelPortal:Q8W453 SMR:Q8W453 PRIDE:Q8W453 EnsemblPlants:AT5G48485.1 GeneID:834904 KEGG:ath:AT5G48485 TAIR:At5g48485 eggNOG:NOG297830 InParanoid:Q8W453 OMA:NECKPAV PhylomeDB:Q8W453 ProtClustDB:CLSN2686599 Genevestigator:Q8W453 Pfam:PF14368 Uniprot:Q8W453
Root	Isotig10588	0	20	-5.451	2.00E-06	TAIR|locus:505006681 - symbol:DIR1 "AT5G48485" species:3702 "Arabidopsis thaliana" [GO:0006869 "lipid transport" evidence=ISS] [GO:0008289 "lipid binding" evidence=ISS] [GO:0005319 "lipid transporter activity" evidence=ISS] [GO:0009862 "systemic acquired resistance, salicylic acid mediated signaling pathway" evidence=IMP] [GO:0005504 "fatty acid binding" evidence=IDA] [GO:0008270 "zinc ion binding" evidence=IDA] InterPro:IPR013770 GO:GO:0048046 EMBL:CP002688 GenomeReviews:BA000015_GR InterPro:IPR016140 SMART:SM00499 SUPFAM:SSF47699 GO:GO:0008270 GO:GO:0006869 GO:GO:0005504 Gene3D:G3DSA:1.10.110.10 EMBL:AB020745 GO:GO:0009862 EMBL:AF342726 EMBL:AY062857 EMBL:BT006510 EMBL:AY085224 IPI:IPI00525511 RefSeq:NP_568699.1 UniGene:At.27209 PDB:2RKN PDBsum:2RKN ProteinModelPortal:Q8W453 SMR:Q8W453 PRIDE:Q8W453 EnsemblPlants:AT5G48485.1 GeneID:834904 KEGG:ath:AT5G48485 TAIR:At5g48485 eggNOG:NOG297830 InParanoid:Q8W453

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						OMA:NECKPAV PhylomeDB:Q8W453 ProtClustDB:CLSN2686599 Genevestigator:Q8W453 Pfam:PF14368 Uniprot:Q8W453
Root	Isotig10617	0	16	-5.129	2.34E-05	WB|WBGene00017233 - symbol:F07G11.9 species:6239 "Caenorhabditis elegans" [GO:0008061 "chitin binding" evidence=IEA] [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=IEA] [GO:0005975 "carbohydrate metabolic process" evidence=IEA] [GO:0016998 "cell wall macromolecule catabolic process" evidence=IEA] [GO:0004568 "chitinase activity" evidence=IEA] [GO:0006032 "chitin catabolic process" evidence=IEA] InterPro:IPR001002 InterPro:IPR001223 InterPro:IPR001579 InterPro:IPR002482 InterPro:IPR011583 InterPro:IPR013781 InterPro:IPR018392 Pfam:PF00704 Pfam:PF01476 PROSITE:PS01095 SMART:SM00257 SMART:SM00270 SMART:SM00636 GO:GO:0043169 InterPro:IPR017853 Gene3D:G3DSA:3.20.20.80 SUPFAM:SSF51445 GO:GO:0008061 GO:GO:0004568 GO:GO:0006032 GO:GO:0016998 eggNOG:COG3325 InterPro:IPR010264 Pfam:PF05938 EMBL:FO080517 RefSeq:NP_504862.1 PRIDE:O16237 GeneID:179121 KEGG:cel:F07G11.9 CTD:179121 WormBase:F07G11.9 HOGENOM:HBG386694 Uniprot:O16237
Root	Isotig10618	0	19	-5.377	3.67E-06	WB|WBGene00017233 - symbol:F07G11.9 species:6239 "Caenorhabditis elegans" [GO:0008061 "chitin binding" evidence=IEA] [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=IEA] [GO:0005975 "carbohydrate metabolic process" evidence=IEA] [GO:0016998 "cell wall macromolecule catabolic process" evidence=IEA] [GO:0004568 "chitinase activity" evidence=IEA] [GO:0006032 "chitin catabolic process" evidence=IEA] InterPro:IPR001002 InterPro:IPR001223 InterPro:IPR001579 InterPro:IPR002482 InterPro:IPR011583 InterPro:IPR013781 InterPro:IPR018392 Pfam:PF00704 Pfam:PF01476 PROSITE:PS01095 SMART:SM00257 SMART:SM00270 SMART:SM00636 GO:GO:0043169 InterPro:IPR017853 Gene3D:G3DSA:3.20.20.80 SUPFAM:SSF51445 GO:GO:0008061 GO:GO:0004568 GO:GO:0006032 GO:GO:0016998 eggNOG:COG3325 InterPro:IPR010264 Pfam:PF05938 EMBL:FO080517 RefSeq:NP_504862.1 PRIDE:O16237 GeneID:179121 KEGG:cel:F07G11.9 CTD:179121 WormBase:F07G11.9 HOGENOM:HBG386694 Uniprot:O16237
Root	Isotig10631	1	12	-3.714	0.000699736	TAIR|locus:2172691 - symbol:HTB2 "histone B2" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=IEA;ISS] [GO:0006334 "nucleosome assembly" evidence=IEA] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0005634 "nucleus" evidence=IDA] InterPro:IPR000558 InterPro:IPR007125 InterPro:IPR009072 Pfam:PF00125 PRINTS:PR00621 PROSITE:PS00357 SMART:SM00427 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005515 GO:GO:0005730 GO:GO:0003677 Gene3D:G3DSA:1.10.20.10 SUPFAM:SSF47113 GO:GO:0006334 GO:GO:0000786 HOGENOM:HBG715487 EMBL:AB005243 EMBL:Y07745 IPI:IPI00530497 RefSeq:NP_197679.1 UniGene:At.22477 ProteinModelPortal:Q9FFC0 SMR:Q9FFC0 STRING:Q9FFC0 PRIDE:Q9FFC0 EnsemblPlants:AT5G22880.1 GeneID:832352 KEGG:ath:AT5G22880 TAIR:At5g22880 eggNOG:NOG289161 InParanoid:Q9FFC0 KO:K11252 OMA:IASEGSR PhylomeDB:Q9FFC0 ProtClustDB:CLSN2916201 Genevestigator:Q9FFC0 GermOnline:AT5G22880 PANTHER:PTHR23428 Uniprot:Q9FFC0
Root	Isotig10632	1	12	-3.714	0.000699736	TAIR|locus:2172691 - symbol:HTB2 "histone B2" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=IEA;ISS] [GO:0006334 "nucleosome assembly" evidence=IEA] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0005634 "nucleus" evidence=IDA] InterPro:IPR000558 InterPro:IPR007125 InterPro:IPR009072 Pfam:PF00125 PRINTS:PR00621 PROSITE:PS00357 SMART:SM00427 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005515 GO:GO:0005730 GO:GO:0003677 Gene3D:G3DSA:1.10.20.10 SUPFAM:SSF47113 GO:GO:0006334 GO:GO:0000786 HOGENOM:HBG715487 EMBL:AB005243 EMBL:Y07745 IPI:IPI00530497 RefSeq:NP_197679.1 UniGene:At.22477 ProteinModelPortal:Q9FFC0 SMR:Q9FFC0 STRING:Q9FFC0 PRIDE:Q9FFC0 EnsemblPlants:AT5G22880.1 GeneID:832352 KEGG:ath:AT5G22880 TAIR:At5g22880 eggNOG:NOG289161 InParanoid:Q9FFC0 KO:K11252 OMA:IASEGSR PhylomeDB:Q9FFC0 ProtClustDB:CLSN2916201 Genevestigator:Q9FFC0 GermOnline:AT5G22880 PANTHER:PTHR23428 Uniprot:Q9FFC0
Root	Isotig10963	0	20	-5.451	2.00E-06	No hit
Root	Isotig10964	0	17	-5.216	1.26E-05	No hit
Root	Isotig11106	26	56	-1.236	0.000181219	TAIR|locus:2204700 - symbol:AT1G77460 "AT1G77460" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] InterPro:IPR000225 InterPro:IPR000008 InterPro:IPR008973 InterPro:IPR011989 InterPro:IPR016024 Pfam:PF00168 Pfam:PF00514 PROSITE:PS50176 SMART:SM00185 SMART:SM00239 GO:GO:0005488 SUPFAM:SSF48371

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						Gene3D:G3DSA:1.25.10.10 InterPro:IPR018029 SUPFAM:SSF49562 PROSITE:PS50004 HSSP:Q02248 EMBL:AC010704 IPI:IPI00548388 PIR:H96803 ProteinModelPortal:Q9CAQ9 SMR:Q9CAQ9 PRIDE:Q9CAQ9 TAIR:At1g77460 InParanoid:Q9CAQ9 OMA:VAPSKEC PhylomeDB:Q9CAQ9 Genevestigator:Q9CAQ9 Uniprot:Q9CAQ9
Root	Isotig11117	0	40	-6.451	2.24E-11	TAIR|locus:2025931 - symbol:PEN3 "AT1G59870" species:3702 "Arabidopsis thaliana" [GO:0042626 "ATPase activity, coupled to transmembrane movement of substances" evidence=ISS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009627 "systemic acquired resistance" evidence=IMP] [GO:0009817 "defense response to fungus, incompatible interaction" evidence=IMP] [GO:0006855 "drug transmembrane transport" evidence=ISS] [GO:0031348 "negative regulation of defense response" evidence=IMP] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0015086 "cadmium ion transmembrane transporter activity" evidence=IDA] [GO:0015691 "cadmium ion transport" evidence=IMP] [GO:0016020 "membrane" evidence=IDA] [GO:0042344 "indole glucosinolate catabolic process" evidence=IMP] [GO:0042742 "defense response to bacterium" evidence=IMP] [GO:0052544 "defense response by callose deposition in cell wall" evidence=IMP] [GO:0071366 "cellular response to indolebutyric acid stimulus" evidence=IMP] [GO:0009737 "response to abscisic acid stimulus" evidence=IDA] InterPro:IPR003439 InterPro:IPR003593 InterPro:IPR013525 Pfam:PF00005 Pfam:PF01061 PROSITE:PS00211 PROSITE:PS50893 PROSITE:PS51012 SMART:SM00382 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005739 GO:GO:0005886 GO:GO:0005524 GO:GO:0009737 GO:GO:0005774 GO:GO:0042742 GO:GO:0031348 GO:GO:0009941 eggNOG:COG1131 GO:GO:0016887 HOGENOM:HBG750535 ProtClustDB:PLN03140 InterPro:IPR013581 Pfam:PF08370 EMBL:AC007258 EMBL:AY074515 EMBL:BK001007 IPI:IPI00520351 PIR:H96622 RefSeq:NP_176196.1 UniGene:At.24243 ProteinModelPortal:Q9XIE2 SMR:Q9XIE2 STRING:Q9XIE2 TCDB:3.A.1.205.9 PRIDE:Q9XIE2 ProMEX:Q9XIE2 EnsemblPlants:AT1G59870.1 GeneID:842281 KEGG:ath:AT1G59870 TAIR:At1g59870 InParanoid:Q9XIE2 OMA:FAFCIRT PhylomeDB:Q9XIE2 Genevestigator:Q9XIE2 GermOnline:AT1G59870 GO:GO:0015086 GO:GO:0071366 GO:GO:0052544 GO:GO:0009817 GO:GO:0042344 GO:GO:0009627 Uniprot:Q9XIE2
Root	Isotig11118	28	4	2.678	1.93E-05	UNIPROTKB|Q709C8 - symbol:VPS13C "Vacuolar protein sorting-associated protein 13C" species:9606 "Homo sapiens" [GO:0008104 "protein localization" evidence=IEA] InterPro:IPR009543 Pfam:PF06650 GO:GO:0008104 InterPro:IPR015412 Pfam:PF09333 eggNOG:COG5043 GeneTree:ENSGT00410000025397 HOVERGEN:HBG079736 EMBL:AJ608770 EMBL:AJ608771 EMBL:AJ626860 EMBL:AJ626861 EMBL:AB037842 EMBL:AK000143 EMBL:BC069387 IPI:IPI00412216 IPI:IPI00465428 IPI:IPI00604778 IPI:IPI00797358 RefSeq:NP_001018098.1 RefSeq:NP_060154.3 RefSeq:NP_060550.2 RefSeq:NP_065872.1 UniGene:Hs.511668 ProteinModelPortal:Q709C8 IntAct:Q709C8 STRING:Q709C8 PhosphoSite:Q709C8 DMDM:74712594 PRIDE:Q709C8 Ensembl:ENST00000261517 GeneID:54832 KEGG:hsa:54832 UCSC:uc002agz.1 UCSC:uc002aha.1 UCSC:uc002ahb.1 UCSC:uc002ahc.1 CTD:54832 GeneCards:GC15M062144 H-InvDB:HIX0020938 HGNC:HGNC:23594 HPA:HPA043356 HPA:HPA043507 MIM:608879 neXtProt:NX_Q709C8 PharmGKB:PA134990089 InParanoid:Q709C8 OMA:QPCSLFM PhylomeDB:Q709C8 NextBio:57616 ArrayExpress:Q709C8 Bgee:Q709C8 CleanEx:HS_VPS13C Genevestigator:Q709C8 GermOnline:ENSG00000129003 Uniprot:Q709C8
Root	Isotig11122	28	6	2.093	0.000219123	TAIR|locus:2116900 - symbol:XDH1 "AT4G34890" species:3702 "Arabidopsis thaliana" [GO:0004854 "xanthine dehydrogenase activity" evidence=ISS;IDA] [GO:0006145 "purine base catabolic process" evidence=IMP;TAS] [GO:0006950 "response to stress" evidence=TAS] [GO:0042554 "superoxide anion generation" evidence=IMP] [GO:0046110 "xanthine metabolic process" evidence=IMP] [GO:0000302 "response to reactive oxygen species" evidence=IMP] [GO:0009414 "response to water deprivation" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001041 InterPro:IPR002346 InterPro:IPR002888 InterPro:IPR006058 InterPro:IPR008274 InterPro:IPR016166 InterPro:IPR016167 InterPro:IPR016169 InterPro:IPR016208 Pfam:PF00111 Pfam:PF00941 Pfam:PF01799 Pfam:PF02738 PIRSF:PIRSF000127 PROSITE:PS00197 PROSITE:PS51085 PROSITE:PS51387 InterPro:IPR000674 Pfam:PF01315 GO:GO:0005829 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005506 GO:GO:0009055 GO:GO:0050660 GO:GO:0009414 GO:GO:0000302 GO:GO:0008762 Gene3D:G3DSA:3.30.43.10 SUPFAM:SSF56176 eggNOG:COG4630 GO:GO:0051537 InterPro:IPR012675 InterPro:IPR005107 Gene3D:G3DSA:1.10.150.120 Gene3D:G3DSA:3.30.365.10 Gene3D:G3DSA:3.90.1170.50 Gene3D:G3DSA:3.30.390.50 Gene3D:G3DSA:3.30.465.10 Gene3D:G3DSA:3.10.20.30 Pfam:PF03450

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						SMART:SM01008 SMART:SM01092 SUPFAM:SSF47741 SUPFAM:SSF56003 SUPFAM:SSF54665 SUPFAM:SSF55447 SUPFAM:SSF54292 HOGENOM:HBG386245 GO:GO:0004854 GO:GO:0006145 GO:GO:0042554 KO:K00106 HSSP:P80457 GO:GO:0046110 OMA:SGRAFNY EMBL:AY171562 IPI:IPI00529753 RefSeq:NP_195215.2 UniGene:At.27839 ProteinModelPortal:Q8GUQ8 STRING:Q8GUQ8 PRIDE:Q8GUQ8 ProMEX:Q8GUQ8 EnsemblPlants:AT4G34890.1 GeneID:829641 KEGG:ath:AT4G34890 TAIR:At4g34890 InParanoid:Q8GUQ8 PhylomeDB:Q8GUQ8 ProtClustDB:PLN02906 BRENDA:1.17.1.4 Genevestigator:Q8GUQ8 Uniprot:Q8GUQ8
Root	Isotig11133	58	425	-3.002	5.09E-76	RGD|727924 - symbol:LOC257642 "rRNA promoter binding protein" species:10116 "Rattus norvegicus" [GO:0003690 "double-stranded DNA binding" evidence=IDA] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=IDA] [GO:0008134 "transcription factor binding" evidence=IDA] [GO:0008283 "cell proliferation" evidence=IDA] [GO:0009303 "rRNA transcription" evidence=IDA] RGD:727924 GO:GO:0008134 GO:GO:0008283 GO:GO:0003700 GO:GO:0003690 GO:GO:0009303 EMBL:U77931 IPI:IPI00195015 RefSeq:NP_671477.1 GeneID:257642 KEGG:rno:257642 NextBio:624170 Genevestigator:Q99JC0 Uniprot:Q99JC0
Root	Isotig11161	33	10	1.593	0.000866735	TAIR|locus:2024336 - symbol:CDC5 "AT1G09770" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=ISS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=TAS] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0009870 "defense response signaling pathway, resistance gene-dependent" evidence=IMP] [GO:0010204 "defense response signaling pathway, resistance gene-independent" evidence=IMP] [GO:0042742 "defense response to bacterium" evidence=IMP] [GO:0050832 "defense response to fungus" evidence=IMP] InterPro:IPR001005 InterPro:IPR009057 SMART:SM00717 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005515 GO:GO:0006355 GO:GO:0008380 GO:GO:0007049 GO:GO:0003677 GO:GO:0006397 GO:GO:0045087 GO:GO:0006351 Gene3D:G3DSA:1.10.10.60 SUPFAM:SSF46689 GO:GO:0005681 InterPro:IPR017930 PROSITE:PS51294 eggNOG:COG5147 InterPro:IPR015495 PANTHER:PTHR10641 EMBL:D58424 EMBL:AY519553 EMBL:AC000132 EMBL:AY093057 EMBL:BT008801 EMBL:AK316890 IPI:IPI00542991 PIR:F86231 RefSeq:NP_172448.1 UniGene:At.278 HSSP:P06876 ProteinModelPortal:P92948 SMR:P92948 IntAct:P92948 STRING:P92948 PRIDE:P92948 EnsemblPlants:AT1G09770.1 GeneID:837506 KEGG:ath:AT1G09770 GeneFarm:1651 TAIR:At1g09770 HOGENOM:HBG630413 InParanoid:O04498 KO:K12860 OMA:PRNDYEI PhylomeDB:P92948 ProtClustDB:CLSN2679501 Genevestigator:P92948 InterPro:IPR021786 Pfam:PF11831 Uniprot:P92948
Root	Isotig11163	19	3	2.534	0.000639389	TAIR|locus:2164270 - symbol:UBA 2 "AT5G06460" species:3702 "Arabidopsis thaliana" [GO:0004839 "ubiquitin activating enzyme activity" evidence=ISS;IMP] [GO:0006511 "ubiquitin-dependent protein catabolic process" evidence=TAS] [GO:0005829 "cytosol" evidence=IDA] [GO:0004842 "ubiquitin-protein ligase activity" evidence=IDA] [GO:0005634 "nucleus" evidence=TAS] [GO:0016567 "protein ubiquitination" evidence=IDA] InterPro:IPR000011 InterPro:IPR000127 InterPro:IPR000594 InterPro:IPR016040 Pfam:PF00899 Pfam:PF02134 PRINTS:PR01849 Pfam:PF10585 GO:GO:0005829 GO:GO:0005524 GO:GO:0005634 EMBL:CP002688 GenomeReviews:BA000015_GR Gene3D:G3DSA:3.40.50.720 GO:GO:0004842 eggNOG:COG0476 InterPro:IPR009036 SUPFAM:SSF69572 EMBL:AB006700 HSSP:P12282 GO:GO:0008641 InterPro:IPR023280 InterPro:IPR019572 InterPro:IPR018074 Gene3D:G3DSA:1.10.3240.10 PROSITE:PS00536 PROSITE:PS00865 HOGENOM:HBG356508 KO:K03178 InterPro:IPR018965 InterPro:IPR018075 Pfam:PF09358 SMART:SM00985 TIGRFAMs:TIGR01408 OMA:ANGMAKN ProtClustDB:CLSN2688565 EMBL:U40566 IPI:IPI00540789 RefSeq:NP_568168.1 UniGene:At.27859 UniGene:At.65020 ProteinModelPortal:P92974 SMR:P92974 PRIDE:P92974 EnsemblPlants:AT5G06460.1 GeneID:830534 KEGG:ath:AT5G06460 TAIR:At5g06460 InParanoid:P92974 PhylomeDB:P92974 Genevestigator:P92974 Uniprot:P92974
Root	Isotig11166	0	22	-5.588	6.01E-07	SGD|S000028422 - symbol:TAR1 "Mitochondrial protein potentially involved in respiratory metabolism" species:4932 "Saccharomyces cerevisiae" [GO:0003674 "molecular_function" evidence=ND] [GO:0043457 "regulation of cellular respiration" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IEA;IMP] SGD:S000028422 GO:GO:0005739 EMBL:BK006945 EMBL:U53879 GO:GO:0043457 EMBL:Z73326 EMBL:AF479964 RefSeq:NP_690845.1 ProteinModelPortal:Q8TGM6 STRING:Q8TGM6 EnsemblFungi:YLR154W-C GeneID:1466405 KEGG:sce:YLR154W-C CYGD:YLR154w-c eggNOG:NOG79861 OMA:SCSKEHR OrthoDB:EOG466ZX8 NextBio:967146 Genevestigator:Q8TGM6 GermOnline:YLR154W-C Uniprot:Q8TGM6
Root	Isotig11167	16	2	2.871	0.000812389	TAIR|locus:2043187 - symbol:PUM2 "AT2G29190" species:3702 "Arabidopsis thaliana" [GO:0003723 "RNA binding" evidence=ISS;IDA] [GO:0008150 "biological_process" evidence=ND] [GO:0003729 "mRNA binding"

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						evidence=IPI] [GO:0003730 "mRNA 3'-UTR binding" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001313 InterPro:IPR011989 InterPro:IPR016024 Pfam:PF00806 PROSITE:PS50302 PROSITE:PS50303 SMART:SM00025 GO:GO:0005829 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0006417 SUPFAM:SSF48371 Gene3D:G3DSA:1.25.10.10 GO:GO:0003730 EMBL:AC004561 eggNOG:COG5099 HSSP:Q14671 ProtClustDB:CLSN2717398 InterPro:IPR012940 Pfam:PF07990 EMBL:AY096653 EMBL:AK226635 IPI:IPI00539996 PIR:E84693 RefSeq:NP_001189630.1 RefSeq:NP_180482.1 UniGene:At.28148 UniGene:At.48528 ProteinModelPortal:Q9ZW06 SMR:Q9ZW06 STRING:Q9ZW06 PRIDE:Q9ZW06 ProMEX:Q9ZW06 EnsemblPlants:AT2G29190.1 EnsemblPlants:AT2G29190.2 GeneID:817468 KEGG:ath:AT2G29190 TAIR:At2g29190 InParanoid:Q9ZW06 OMA:ISHIGES PhylomeDB:Q9ZW06 Genevestigator:Q9ZW06 Uniprot:Q9ZW06
Root	Isotig11170	25	0	5.515	3.68E-07	TAIR|locus:2077207 - symbol:AT3G45900 "AT3G45900" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002686 GenomeReviews:BA000014_GR EMBL:BT014753 IPI:IPI00523346 RefSeq:NP_190176.2 UniGene:At.35977 IntAct:Q6IDC0 PRIDE:Q6IDC0 EnsemblPlants:AT3G45900.1 GeneID:823733 KEGG:ath:AT3G45900 TAIR:At3g45900 eggNOG:NOG253158 HOGENOM:HBG317881 InParanoid:Q6IDC0 OMA:RRESPWK PhylomeDB:Q6IDC0 ProtClustDB:CLSN2680890 Genevestigator:Q6IDC0 Uniprot:Q6IDC0
Root	Isotig11171	4	235	-6.005	8.79E-60	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig11178	4	29	-2.987	1.53E-06	TAIR|locus:2207036 - symbol:AT1G72180 "AT1G72180" species:3702 "Arabidopsis thaliana" [GO:0004674 "protein serine/threonine kinase activity" evidence=ISS] [GO:0005524 "ATP binding" evidence=ISS] [GO:0005575 "cellular_component" evidence=ND] [GO:0006468 "protein phosphorylation" evidence=IEA;ISS] [GO:0007169 "transmembrane receptor protein tyrosine kinase signaling pathway" evidence=ISS] [GO:0016301 "kinase activity" evidence=ISS] Pfam:PF00560 InterPro:IPR001611 InterPro:IPR000719 InterPro:IPR008271 InterPro:IPR011009 Pfam:PF00069 PROSITE:PS00108 PROSITE:PS50011 PROSITE:PS51450 GO:GO:0016021 EMBL:CP002684 GO:GO:0005524 GO:GO:0004872 SUPFAM:SSF56112 GO:GO:0004674 EMBL:AC067754 InterPro:IPR013210 Pfam:PF08263 EMBL:FJ708677 IPI:IPI00545271 PIR:C96745 RefSeq:NP_177363.1 UniGene:At.28051 UniGene:At.48363 UniGene:At.74870 ProteinModelPortal:Q9C7T7 SMR:Q9C7T7 PRIDE:Q9C7T7 EnsemblPlants:AT1G72180.1 GeneID:843550 KEGG:ath:AT1G72180 TAIR:At1g72180 InParanoid:Q9C7T7 OMA:FPRFLCQ PhylomeDB:Q9C7T7 ProtClustDB:CLSN2692132 Genevestigator:Q9C7T7 Uniprot:Q9C7T7
Root	Isotig11182	7	36	-2.492	1.13E-06	TAIR|locus:2172457 - symbol:CESA4 "cellulose synthase A4" species:3702 "Arabidopsis thaliana" [GO:0016020 "membrane" evidence=IEA] [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0016759 "cellulose synthase activity" evidence=ISS] [GO:0009834 "secondary cell wall biogenesis" evidence=IMP] [GO:0030244 "cellulose biosynthetic process" evidence=IMP;TAS] [GO:0009863 "salicylic acid mediated signaling pathway" evidence=IGI] [GO:0009867 "jasmonic acid mediated signaling pathway" evidence=IGI] [GO:0009873 "ethylene mediated signaling pathway" evidence=IGI] [GO:0042742 "defense response to bacterium" evidence=IMP] [GO:0050832 "defense response to fungus" evidence=IMP] [GO:0052386 "cell wall thickening" evidence=IMP] [GO:0009832 "plant-type cell wall biogenesis" evidence=TAS] InterPro:IPR005150 Pfam:PF03552 PROSITE:PS50089 Prosite:PS00518 GO:GO:0016021 GO:GO:0005886 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0042742 GO:GO:0050832 GO:GO:0046872 InterPro:IPR013083 Gene3D:G3DSA:3.30.40.10 EMBL:AB006703 GO:GO:0007047 CAZy:GT2 eggNOG:COG1215 GO:GO:0016760 GO:GO:0030244 GO:GO:0009834 HOGENOM:HBG744549 KO:K10999 EMBL:AF458083 EMBL:BT005710 EMBL:BT006111 EMBL:AK228561 IPI:IPI00537913 RefSeq:NP_199216.2 UniGene:At.49129 UniGene:At.71068 ProteinModelPortal:Q84JA6 SMR:Q84JA6 MINT:MINT-6950789 STRING:Q84JA6 PRIDE:Q84JA6 EnsemblPlants:AT5G44030.1 GeneID:834426 KEGG:ath:AT5G44030 GeneFarm:5087 TAIR:At5g44030 InParanoid:Q84JA6 OMA:LLAYCTI PhylomeDB:Q84JA6 ProtClustDB:PLN02915 ArrayExpress:Q84JA6 Genevestigator:Q84JA6 GermOnline:AT5G44030 Uniprot:Q84JA6

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig11194	3	39	-3.829	6.57E-10	TAIR|locus:2155466 - symbol:MMT "AT5G49810" species:3702 "Arabidopsis thaliana" [GO:0008757 "S-adenosylmethionine-dependent methyltransferase activity" evidence=ISS;IMP] [GO:0001887 "selenium compound metabolic process" evidence=IMP] [GO:0046500 "S-adenosylmethionine metabolic process" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR004839 InterPro:IPR015421 InterPro:IPR015422 Pfam:PF00155 GO:GO:0005829 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0030170 InterPro:IPR015424 Gene3D:G3DSA:3.40.640.10 Gene3D:G3DSA:3.90.1150.10 SUPFAM:SSF53383 GO:GO:0016769 GO:GO:0009058 GO:GO:0001887 GO:GO:0046500 EMBL:AF137380 EMBL:AB025612 EMBL:AY094459 EMBL:BT002664 IPI:IPI00522742 PIR:T52306 RefSeq:NP_199792.1 UniGene:At.25276 ProteinModelPortal:Q9LTB2 SMR:Q9LTB2 STRING:Q9LTB2 PRIDE:Q9LTB2 EnsemblPlants:AT5G49810.1 GeneID:835044 KEGG:ath:AT5G49810 GeneFarm:4078 TAIR:At5g49810 eggNOG:NOG269325 HOGENOM:HBG597918 InParanoid:Q9LTB2 KO:K08247 OMA:GGRISHA PhylomeDB:Q9LTB2 ProtClustDB:PLN02672 ArrayExpress:Q9LTB2 Genevestigator:Q9LTB2 GermOnline:AT5G49810 GO:GO:0030732 Uniprot:Q9LTB2
Root	Isotig11198	37	8	2.080	2.32E-05	TAIR|locus:2059258 - symbol:AGO4 "AT2G27040" species:3702 "Arabidopsis thaliana" [GO:0006342 "chromatin silencing" evidence=IMP] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0005719 "nuclear euchromatin" evidence=IDA] [GO:0015030 "Cajal body" evidence=IDA] [GO:0051567 "histone H3-K9 methylation" evidence=IMP] [GO:0006306 "DNA methylation" evidence=IMP] [GO:0010495 "long-distance posttranscriptional gene silencing" evidence=IMP] [GO:0009816 "defense response to bacterium, incompatible interaction" evidence=IMP] [GO:0031048 "chromatin silencing by small RNA" evidence=TAS] [GO:0030422 "production of siRNA involved in RNA interference" evidence=IGI] [GO:0035197 "siRNA binding" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] InterPro:IPR003100 InterPro:IPR003165 InterPro:IPR012337 Pfam:PF02170 Pfam:PF02171 PROSITE:PS50821 PROSITE:PS50822 SMART:SM00950 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0044419 GO:GO:0005515 GO:GO:0006417 GO:GO:0005730 GO:GO:0006351 GO:GO:0030529 GO:GO:0015030 SUPFAM:SSF53098 GO:GO:0031048 HOGENOM:HBG717005 InterPro:IPR014811 Pfam:PF08699 SUPFAM:SSF101690 GO:GO:0035197 GO:GO:0030422 EMBL:AC005623 EMBL:AY035081 EMBL:AY051033 IPI:IPI00540794 PIR:A84668 RefSeq:NP_001189613.1 RefSeq:NP_565633.1 UniGene:At.13165 ProteinModelPortal:Q9ZVD5 SMR:Q9ZVD5 DIP:DIP-53402N IntAct:Q9ZVD5 STRING:Q9ZVD5 PRIDE:Q9ZVD5 EnsemblPlants:AT2G27040.1 EnsemblPlants:AT2G27040.2 GeneID:817246 KEGG:ath:AT2G27040 TAIR:At2g27040 eggNOG:NOG286051 InParanoid:Q93VG2 OMA:NFSARCN PhylomeDB:Q9ZVD5 ProtClustDB:PLN03202 ArrayExpress:Q9ZVD5 Genevestigator:Q9ZVD5 GO:GO:0005719 GO:GO:0009816 GO:GO:0006306 GO:GO:0051567 Uniprot:Q9ZVD5
Root	Isotig11200	32	5	2.549	8.76E-06	TAIR|locus:2012753 - symbol:NFXL1 "NF-X-like 1" species:3702 "Arabidopsis thaliana" [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=IEA;ISS] [GO:0005634 "nucleus" evidence=ISS;IDA] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=ISS] [GO:0008270 "zinc ion binding" evidence=IEA] [GO:0009642 "response to light intensity" evidence=IMP] [GO:0009651 "response to salt stress" evidence=IMP] [GO:0010310 "regulation of hydrogen peroxide metabolic process" evidence=IMP] [GO:0009697 "salicylic acid biosynthetic process" evidence=IMP] [GO:0010188 "response to microbial phytotoxin" evidence=IMP] [GO:0042742 "defense response to bacterium" evidence=IMP] InterPro:IPR001841 InterPro:IPR000967 InterPro:IPR019787 Pfam:PF01422 PROSITE:PS50016 PROSITE:PS50089 PROSITE:PS51061 SMART:SM00184 SMART:SM00438 Prosite:PS00518 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005634 GO:GO:0042742 GO:GO:0003677 GO:GO:0016874 GO:GO:0008270 GO:GO:0003700 GO:GO:0006351 GO:GO:0009651 InterPro:IPR019786 PROSITE:PS01359 eggNOG:NOG12793 GO:GO:0009642 EMBL:AC005489 GO:GO:0009697 GO:GO:0010188 GO:GO:0010310 OMA:ITWASSS IPI:IPI00523119 PIR:D86236 RefSeq:NP_172488.1 UniGene:At.25390 ProteinModelPortal:Q9SY59 STRING:Q9SY59 PRIDE:Q9SY59 EnsemblPlants:AT1G10170.1 GeneID:837555 KEGG:ath:AT1G10170 TAIR:At1g10170 HOGENOM:HBG598263 InParanoid:Q9SY59 PhylomeDB:Q9SY59 ProtClustDB:CLSN2679554 Genevestigator:Q9SY59 Uniprot:Q9SY59
Root	Isotig11204	5	30	-2.714	3.20E-06	TAIR|locus:2196593 - symbol:ABCG40 "AT1G15520" species:3702 "Arabidopsis thaliana" [GO:0042626 "ATPase activity, coupled to transmembrane movement of substances" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0015692 "lead ion transport" evidence=IMP] [GO:0006855 "drug transmembrane transport" evidence=ISS] [GO:0009607 "response to biotic stimulus" evidence=TAS] [GO:0009723 "response to ethylene stimulus" evidence=TAS] [GO:0009751 "response to salicylic acid stimulus" evidence=TAS] [GO:0009753 "response to jasmonic acid stimulus" evidence=TAS] [GO:0010193 "response to ozone" evidence=IEP] [GO:0046865

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						"terpenoid transport" evidence=IDA] [GO:0080168 "abscisic acid transport" evidence=IDA] InterPro:IPR003439 InterPro:IPR003593 InterPro:IPR013525 Pfam:PF00005 Pfam:PF01061 PROSITE:PS00211 PROSITE:PS50893 PROSITE:PS51012 SMART:SM00382 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005886 GO:GO:0005524 GO:GO:0006952 GO:GO:0009753 eggNOG:COG1131 GO:GO:0016887 GO:GO:0080168 HOGENOM:HBG750535 InterPro:IPR013581 Pfam:PF08370 EMBL:AC013453 EMBL:BK001011 IPI:IPI00520750 PIR:A86289 RefSeq:NP_173005.1 UniGene:At.49303 ProteinModelPortal:Q9M9E1 SMR:Q9M9E1 STRING:Q9M9E1 TCDB:3.A.1.205.10 PRIDE:Q9M9E1 EnsemblPlants:AT1G15520.1 GeneID:838122 KEGG:ath:AT1G15520 TAIR:At1g15520 InParanoid:Q9M9E1 OMA:RLFKQYI PhylomeDB:Q9M9E1 ProtClustDB:CLSN2912672 ArrayExpress:Q9M9E1 Genevestigator:Q9M9E1 GermOnline:AT1G15520 GO:GO:0015692 GO:GO:0009607 GO:GO:0009723 GO:GO:0010193 GO:GO:0009751 Uniprot:Q9M9E1
Root	Isotig11209	4	20	-2.451	0.000325095	TAIR|locus:2044717 - symbol:KUP11 "AT2G35060" species:3702 "Arabidopsis thaliana" [GO:0006813 "potassium ion transport" evidence=ISS] [GO:0015079 "potassium ion transmembrane transporter activity" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009555 "pollen development" evidence=IMP] InterPro:IPR003855 Pfam:PF02705 GO:GO:0016021 GO:GO:0005886 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009555 EMBL:AC004238 GO:GO:0015079 eggNOG:COG3158 TIGRFAMs:TIGR00794 ProtClustDB:CLSN2683675 EMBL:AY099600 EMBL:BT002147 IPI:IPI00516522 PIR:T00487 RefSeq:NP_181051.1 UniGene:At.37715 ProteinModelPortal:O64769 PRIDE:O64769 EnsemblPlants:AT2G35060.1 GeneID:818071 KEGG:ath:AT2G35060 TAIR:At2g35060 HOGENOM:HBG606427 InParanoid:O64769 PhylomeDB:O64769 ArrayExpress:O64769 Genevestigator:O64769 Uniprot:O64769
Root	Isotig11210	1	28	-4.936	2.57E-08	TAIR|locus:2031361 - symbol:HMA5 "AT1G63440" species:3702 "Arabidopsis thaliana" [GO:0015662 "ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism" evidence=ISS] [GO:0016020 "membrane" evidence=IEA] [GO:0016021 "integral to membrane" evidence=IEA] [GO:0010273 "detoxification of copper ion" evidence=IMP] [GO:0046688 "response to copper ion" evidence=IMP] InterPro:IPR001757 InterPro:IPR005834 InterPro:IPR006121 InterPro:IPR006122 InterPro:IPR006403 InterPro:IPR006416 InterPro:IPR008250 InterPro:IPR017969 Pfam:PF00122 Pfam:PF00403 Pfam:PF00702 PRINTS:PR00119 PRINTS:PR00942 PROSITE:PS01047 PROSITE:PS50846 InterPro:IPR018303 Prosite:PS00154 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005524 InterPro:IPR023214 Gene3D:G3DSA:3.40.50.1000 SUPFAM:SSF56784 GO:GO:0006754 GO:GO:0005507 InterPro:IPR023300 InterPro:IPR023299 Gene3D:G3DSA:2.70.150.10 Gene3D:G3DSA:3.40.1110.10 TIGRFAMs:TIGR01494 eggNOG:COG2217 HOGENOM:HBG507745 TIGRFAMs:TIGR01525 SUPFAM:SSF55008 KO:K01533 GO:GO:0004008 TIGRFAMs:TIGR00003 EMBL:AC008047 IPI:IPI00548991 PIR:B96660 RefSeq:NP_176533.1 UniGene:At.36129 ProteinModelPortal:Q9SH30 SMR:Q9SH30 IntAct:Q9SH30 STRING:Q9SH30 PRIDE:Q9SH30 EnsemblPlants:AT1G63440.1 GeneID:842650 KEGG:ath:AT1G63440 TAIR:At1g63440 InParanoid:Q9SH30 OMA:CSSTIER PhylomeDB:Q9SH30 ProtClustDB:CLSN2682570 BioCyc:MetaCyc:MONOMER-14503 ArrayExpress:Q9SH30 Genevestigator:Q9SH30 GermOnline:AT1G63440 GO:GO:0010273 Uniprot:Q9SH30
Root	Isotig11218	0	72	-7.299	1.83E-18	TAIR|locus:2029677 - symbol:NIA2 "AT1G37130" species:3702 "Arabidopsis thaliana" [GO:0006809 "nitric oxide biosynthetic process" evidence=IMP] [GO:0005773 "vacuole" evidence=IDA] [GO:0009416 "response to light stimulus" evidence=IMP] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009610 "response to symbiotic fungus" evidence=IEP] [GO:0008940 "nitrate reductase activity" evidence=ISS;IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009703 "nitrate reductase (NADH) activity" evidence=IDA] [GO:0042128 "nitrate assimilation" evidence=IMP] InterPro:IPR000572 InterPro:IPR001199 InterPro:IPR001433 InterPro:IPR001709 InterPro:IPR001834 InterPro:IPR005066 InterPro:IPR008335 InterPro:IPR012137 InterPro:IPR017927 InterPro:IPR017938 InterPro:IPR018506 InterPro:IPR022407 Pfam:PF00173 Pfam:PF00174 Pfam:PF00175 Pfam:PF03404 PIRSF:PIRSF000233 PRINTS:PR00363 PRINTS:PR00371 PRINTS:PR00406 PRINTS:PR00407 PROSITE:PS00191 PROSITE:PS00559 PROSITE:PS50255 PROSITE:PS51384 InterPro:IPR008333 Pfam:PF00970 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0005886 GO:GO:0005773 GO:GO:0009635 GO:GO:0009055 GO:GO:0050660 GO:GO:0020037 GO:GO:0009416 Gene3D:G3DSA:3.10.120.10 SUPFAM:SSF55856 InterPro:IPR014756 SUPFAM:SSF81296 GO:GO:0043546 eggNOG:COG0543 SUPFAM:SSF63380 GO:GO:0006809 GO:GO:0042128 GO:GO:0009610 GO:GO:0030151 KO:K00360 HOGENOM:HBG326850 ProtClustDB:PLN02252 GO:GO:0009703 Gene3D:G3DSA:2.60.40.650 Gene3D:G3DSA:3.90.420.10 SUPFAM:SSF56524 EMBL:J03240 EMBL:AC007505 EMBL:AF367272 EMBL:AF436835 EMBL:AY037183 EMBL:AY039914 EMBL:AY133530 EMBL:AY142568 EMBL:S45385

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EMBL:X13435 IPI:IPI00544857 PIR:A31821 RefSeq:NP_174901.1 UniGene:At.23731 UniGene:At.72953 UniGene:At.74746 UniGene:At.74925 ProteinModelPortal:P11035 SMR:P11035 IntAct:P11035 STRING:P11035 PRIDE:P11035 ProMEX:P11035 EnsemblPlants:AT1G37130.1 GeneID:840630 KEGG:ath:AT1G37130 TAIR:At1g37130 InParanoid:P11035 OMA:RFEHPTQ PhylomeDB:P11035 BRENDA:1.7.1.1 Genevestigator:P11035 GermOnline:AT1G37130 Uniprot:P11035
Root	Isotig11227	16	2	2.871	0.000812389	TAIR|locus:2050982 - symbol:AT2G33570 "AT2G33570" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002685 GenomeReviews:CT485783_GR EMBL:AC002332 InterPro:IPR008166 Pfam:PF01697 eggNOG:NOG314565 EMBL:AY084834 EMBL:AY140059 EMBL:BT008868 IPI:IPI00547928 PIR:B84747 RefSeq:NP_565768.1 UniGene:At.12133 PRIDE:O22807 EnsemblPlants:AT2G33570.1 GeneID:817922 KEGG:ath:AT2G33570 TAIR:At2g33570 HOGENOM:HBG598457 InParanoid:O22807 OMA:YKCEWIS PhylomeDB:O22807 ProtClustDB:CLSN2685738 ArrayExpress:O22807 Genevestigator:O22807 Uniprot:O22807
Root	Isotig11246	7	41	-2.679	6.39E-08	TAIR|locus:2124167 - symbol:IRX1 "AT4G18780" species:3702 "Arabidopsis thaliana" [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0016759 "cellulose synthase activity" evidence=ISS;IMP] [GO:0005886 "plasma membrane" evidence=TAS] [GO:0009834 "secondary cell wall biogenesis" evidence=IMP] [GO:0030244 "cellulose biosynthetic process" evidence=IMP] [GO:0005618 "cell wall" evidence=IDA] [GO:0006970 "response to osmotic stress" evidence=IMP] [GO:0009414 "response to water deprivation" evidence=IMP] [GO:0009863 "salicylic acid mediated signaling pathway" evidence=IGI] [GO:0009867 "jasmonic acid mediated signaling pathway" evidence=IGI] [GO:0009873 "ethylene mediated signaling pathway" evidence=IGI] [GO:0010116 "positive regulation of abscisic acid biosynthetic process" evidence=IGI] [GO:0042742 "defense response to bacterium" evidence=IMP] [GO:0050832 "defense response to fungus" evidence=IMP] [GO:0052386 "cell wall thickening" evidence=IMP] InterPro:IPR005150 Pfam:PF03552 PROSITE:PS50089 Prosite:PS00518 GO:GO:0016021 GO:GO:0005886 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005618 GO:GO:0042742 GO:GO:0050832 GO:GO:0046872 EMBL:AL161549 GO:GO:0009414 GO:GO:0006970 InterPro:IPR013083 Gene3D:G3DSA:3.30.40.10 GO:GO:0007047 CAZy:GT2 eggNOG:COG1215 GO:GO:0016760 GO:GO:0030244 GO:GO:0009834 HOGENOM:HBG744549 KO:K10999 EMBL:AF267742 EMBL:AL035526 EMBL:AY099636 IPI:IPI00540646 PIR:T04870 RefSeq:NP_567564.1 UniGene:At.66621 UniGene:At.68239 ProteinModelPortal:Q8LPK5 SMR:Q8LPK5 MINT:MINT-6950961 STRING:Q8LPK5 PRIDE:Q8LPK5 EnsemblPlants:AT4G18780.1 GeneID:827612 KEGG:ath:AT4G18780 GeneFarm:5091 TAIR:At4g18780 InParanoid:Q8LPK5 OMA:KVFFAFW PhylomeDB:Q8LPK5 ProtClustDB:PLN02195 Genevestigator:Q8LPK5 GermOnline:AT4G18780 GO:GO:0010116 Uniprot:Q8LPK5
Root	Isotig11253	3	19	-2.792	0.000168634	TAIR|locus:2178461 - symbol:GLT1 "AT5G53460" species:3702 "Arabidopsis thaliana" [GO:0042128 "nitrate assimilation" evidence=TAS] [GO:0006537 "glutamate biosynthetic process" evidence=IDA;IMP] [GO:0016040 "glutamate synthase (NADH) activity" evidence=IDA;IMP] [GO:0019676 "ammonia assimilation cycle" evidence=IMP] [GO:0048589 "developmental growth" evidence=IMP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] [GO:0009536 "plastid" evidence=TAS] InterPro:IPR000583 InterPro:IPR002489 InterPro:IPR002932 InterPro:IPR006005 InterPro:IPR006982 InterPro:IPR009051 InterPro:IPR012220 InterPro:IPR012285 InterPro:IPR013785 InterPro:IPR023753 Pfam:PF00310 Pfam:PF01493 Pfam:PF01645 Pfam:PF04898 Pfam:PF07992 PIRSF:PIRSF000187 GO:GO:0009570 GO:GO:0046686 EMBL:CP002688 GenomeReviews:BA000015_GR Gene3D:G3DSA:3.20.20.70 GO:GO:0005506 GO:GO:0050660 EMBL:AB020754 GO:GO:0051538 GO:GO:0006537 GO:GO:0048589 eggNOG:COG0493 Gene3D:G3DSA:1.10.1060.10 GO:GO:0010181 InterPro:IPR017932 PROSITE:PS51278 GO:GO:0019676 SUPFAM:SSF46548 KO:K00264 OMA:WMAARQA GO:GO:0016040 Gene3D:G3DSA:2.160.20.60 SUPFAM:SSF69336 TIGRFAMs:TIGR01317 EMBL:AY099795 EMBL:AK222185 EMBL:AK230382 IPI:IPI00521970 RefSeq:NP_001190529.1 RefSeq:NP_001190530.1 RefSeq:NP_200158.2 UniGene:At.67093 UniGene:At.8951 HSSP:P55038 ProteinModelPortal:Q9LV03 SMR:Q9LV03 STRING:Q9LV03 PRIDE:Q9LV03 EnsemblPlants:AT5G53460.1 EnsemblPlants:AT5G53460.2 EnsemblPlants:AT5G53460.3 GeneID:835427 KEGG:ath:AT5G53460 TAIR:At5g53460 InParanoid:Q9LV03 PhylomeDB:Q9LV03 ProtClustDB:CLSN2683760 BRENDA:1.4.1.14 ArrayExpress:Q8LPH2 Genevestigator:Q9LV03 Uniprot:Q9LV03
Root	Isotig11255	34	5	2.637	3.03E-06	TAIR|locus:2042902 - symbol:FAC1 "AT2G38280" species:3702 "Arabidopsis thaliana" [GO:0003876 "AMP deaminase activity" evidence=IGI;ISS] [GO:0009168 "purine ribonucleoside monophosphate biosynthetic process"

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						evidence=ISS] [GO:0009793 "embryo development ending in seed dormancy" evidence=IMP] [GO:0005792 "microsome" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0043424 "protein histidine kinase binding" evidence=IPI] [GO:0009737 "response to abscisic acid stimulus" evidence=IDA] InterPro:IPR001365 InterPro:IPR006329 InterPro:IPR006650 Pfam:PF00962 PROSITE:PS00485 GO:GO:0005783 GO:GO:0005792 GO:GO:0016021 GO:GO:0005829 GO:GO:0005524 GO:GO:0009737 GO:GO:0005634 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0043424 GO:GO:0046872 GO:GO:0009793 eggNOG:COG1816 HOGENOM:HBG713563 GO:GO:0003876 KO:K01490 GO:GO:0006188 PANTHER:PTHR11359 TIGRFAMs:TIGR01429 EMBL:AC003028 EMBL:AY056301 EMBL:AY133852 EMBL:AK316943 EMBL:AK221552 IPI:IPI00546126 PIR:T01259 RefSeq:NP_565886.1 RefSeq:NP_850294.1 UniGene:At.12466 PDB:2A3L PDBsum:2A3L ProteinModelPortal:O80452 SMR:O80452 IntAct:O80452 STRING:O80452 PRIDE:O80452 EnsemblPlants:AT2G38280.1 EnsemblPlants:AT2G38280.2 GeneID:818408 KEGG:ath:AT2G38280 TAIR:At2g38280 InParanoid:O80452 OMA:TIDPASH PhylomeDB:O80452 ProtClustDB:PLN02768 ArrayExpress:O80452 Genevestigator:O80452 GermOnline:AT2G38280 Uniprot:O80452
Root	Isotig11256	19	3	2.534	0.000639389	TAIR|locus:2091618 - symbol:AT3G22270 "AT3G22270" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] GenomeReviews:BA000014_GR HOGENOM:HBG318375 EMBL:AK228960 IPI:IPI00533404 ProteinModelPortal:Q0WPV0 PRIDE:Q0WPV0 TAIR:At3g22270 eggNOG:NOG323978 InParanoid:Q0WPV0 PhylomeDB:Q0WPV0 Genevestigator:Q0WPV0 Uniprot:Q0WPV0
Root	Isotig11258	1	12	-3.714	0.000699736	TAIR|locus:2091662 - symbol:AT3G14460 species:3702 "Arabidopsis thaliana" [GO:0005524 "ATP binding" evidence=IEA] [GO:0006952 "defense response" evidence=IEA;ISS] Pfam:PF00560 InterPro:IPR001611 InterPro:IPR000767 InterPro:IPR002182 Pfam:PF00931 PRINTS:PR00364 GO:GO:0005524 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0006952 GO:GO:0043531 HOGENOM:HBG749068 EMBL:AB028617 IPI:IPI00537428 RefSeq:NP_188064.1 UniGene:At.65087 ProteinModelPortal:Q9LRR5 SMR:Q9LRR5 PRIDE:Q9LRR5 EnsemblPlants:AT3G14460.1 GeneID:820669 KEGG:ath:AT3G14460 TAIR:At3g14460 eggNOG:NOG295903 InParanoid:Q9LRR5 OMA:AVISARY PhylomeDB:Q9LRR5 ProtClustDB:CLSN2684935 ArrayExpress:Q9LRR5 Genevestigator:Q9LRR5 GermOnline:AT3G14460 Uniprot:Q9LRR5
Root	Isotig11261	48	9	2.286	3.21E-07	TAIR|locus:2205235 - symbol:LOS1 "AT1G56070" species:3702 "Arabidopsis thaliana" [GO:0003746 "translation elongation factor activity" evidence=ISS] [GO:0008135 "translation factor activity, nucleic acid binding" evidence=ISS] [GO:0009409 "response to cold" evidence=IMP] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR000640 InterPro:IPR000795 InterPro:IPR004161 InterPro:IPR005225 InterPro:IPR005517 Pfam:PF00009 Pfam:PF00679 Pfam:PF03144 Pfam:PF03764 PRINTS:PR00315 PROSITE:PS00301 SMART:SM00838 SMART:SM00889 GO:GO:0005525 TIGRFAMs:TIGR00231 EMBL:CP002684 GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 GO:GO:0005774 GO:GO:0009507 GO:GO:0005730 GO:GO:0003924 GO:GO:0005507 GO:GO:0009409 GO:GO:0003746 InterPro:IPR020568 InterPro:IPR014721 Gene3D:G3DSA:3.30.230.10 SUPFAM:SSF54211 InterPro:IPR009000 SUPFAM:SSF50447 InterPro:IPR009022 Gene3D:G3DSA:3.30.70.240 SUPFAM:SSF54980 KO:K03234 OMA:GVMTQTE HSSP:P32324 EMBL:AF367331 EMBL:AY054461 EMBL:BT000661 EMBL:BT000722 EMBL:BT002714 IPI:IPI00517335 RefSeq:NP_849818.1 UniGene:At.47544 ProteinModelPortal:Q9ASR1 SMR:Q9ASR1 STRING:Q9ASR1 PRIDE:Q9ASR1 ProMEX:Q9ASR1 EnsemblPlants:AT1G56070.1 GeneID:842058 KEGG:ath:AT1G56070 TAIR:At1g56070 InParanoid:Q9ASR1 PhylomeDB:Q9ASR1 ProtClustDB:PLN00116 Genevestigator:Q9ASR1 Uniprot:Q9ASR1
Root	Isotig11270	34	90	-1.533	2.23E-08	TAIR|locus:2084756 - symbol:SUS4 "AT3G43190" species:3702 "Arabidopsis thaliana" [GO:0005986 "sucrose biosynthetic process" evidence=ISS] [GO:0008194 "UDP-glycosyltransferase activity" evidence=ISS] [GO:0016157 "sucrose synthase activity" evidence=IGI;ISS;IDA] [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0005773 "vacuole" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR000368 InterPro:IPR001296 InterPro:IPR012820 Pfam:PF00534 Pfam:PF00862 GO:GO:0005829 GO:GO:0005886 GO:GO:0005773 EMBL:CP002686 GO:GO:0009058 CAZy:GT4 EMBL:AL353871 GO:GO:0005985 KO:K00695

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						ProtClustDB:PLN00142 GO:GO:0016157 PANTHER:PTHR12526:SF27 TIGRFAMs:TIGR02470 IPI:IPI00540190 PIR:T49233 RefSeq:NP_566865.2 UniGene:At.1720 ProteinModelPortal:Q9LXL5 SMR:Q9LXL5 STRING:Q9LXL5 PRIDE:Q9LXL5 EnsemblPlants:AT3G43190.1 GeneID:823393 KEGG:ath:AT3G43190 TAIR:At3g43190 InParanoid:Q9LXL5 OMA:KAEEYLM PhylomeDB:Q9LXL5 Genevestigator:Q9LXL5 Uniprot:Q9LXL5
Root	Isotig11271	4	47	-3.684	2.25E-11	TAIR|locus:2206865 - symbol:SUS6 "AT1G73370" species:3702 "Arabidopsis thaliana" [GO:0005986 "sucrose biosynthetic process" evidence=ISS] [GO:0008194 "UDP-glycosyltransferase activity" evidence=ISS] [GO:0016157 "sucrose synthase activity" evidence=ISS;IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0080165 "callose deposition in phloem sieve plate" evidence=IMP] InterPro:IPR000368 InterPro:IPR001296 InterPro:IPR012820 Pfam:PF00534 Pfam:PF00862 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005618 GO:GO:0009058 eggNOG:COG0438 CAZy:GT4 GO:GO:0080165 GO:GO:0005985 EMBL:AC012396 HOGENOM:HBG286768 KO:K00695 ProtClustDB:PLN00142 GO:GO:0016157 PANTHER:PTHR12526:SF27 TIGRFAMs:TIGR02470 IPI:IPI00530921 PIR:C96760 RefSeq:NP_177480.1 UniGene:At.34995 UniGene:At.69495 ProteinModelPortal:Q9FX32 SMR:Q9FX32 STRING:Q9FX32 PRIDE:Q9FX32 EnsemblPlants:AT1G73370.1 GeneID:843672 KEGG:ath:AT1G73370 TAIR:At1g73370 InParanoid:Q9FX32 OMA:DSDAKWK PhylomeDB:Q9FX32 Genevestigator:Q9FX32 Uniprot:Q9FX32
Root	Isotig11278	34	6	2.374	1.09E-05	TAIR|locus:2019667 - symbol:HSP101 "AT1G74310" species:3702 "Arabidopsis thaliana" [GO:0005524 "ATP binding" evidence=ISS] [GO:0016887 "ATPase activity" evidence=ISS] [GO:0009408 "response to heat" evidence=IEP;IGI;IMP] [GO:0043335 "protein unfolding" evidence=IMP] [GO:0009644 "response to high light intensity" evidence=IEP] [GO:0042542 "response to hydrogen peroxide" evidence=IEP] [GO:0005515 "protein binding" evidence=IPI] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] InterPro:IPR001270 InterPro:IPR003593 InterPro:IPR003959 InterPro:IPR004176 InterPro:IPR013093 InterPro:IPR018368 Pfam:PF00004 Pfam:PF02861 Pfam:PF07724 PRINTS:PR00300 PROSITE:PS00870 PROSITE:PS00871 SMART:SM00382 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0005524 GO:GO:0009570 GO:GO:0005634 GO:GO:0005515 GO:GO:0009941 GO:GO:0009408 GO:GO:0009644 GO:GO:0042542 GO:GO:0017111 GO:GO:0043335 eggNOG:COG0542 InterPro:IPR023150 Gene3D:G3DSA:1.10.1780.10 HOGENOM:HBG413133 InterPro:IPR019489 Pfam:PF10431 SMART:SM01086 EMBL:U13949 EMBL:AF218796 EMBL:AC020579 EMBL:AY062596 IPI:IPI00519771 PIR:F96771 RefSeq:NP_565083.1 UniGene:At.48370 UniGene:At.69978 ProteinModelPortal:P42730 SMR:P42730 IntAct:P42730 STRING:P42730 PRIDE:P42730 EnsemblPlants:AT1G74310.1 GeneID:843771 KEGG:ath:AT1G74310 GeneFarm:2733 TAIR:At1g74310 InParanoid:P42730 OMA:EAYEPQF PhylomeDB:P42730 ProtClustDB:CLSN2689194 ArrayExpress:P42730 Genevestigator:P42730 GermOnline:AT1G74310 Uniprot:P42730
Root	Isotig11283	44	138	-1.778	1.39E-14	TAIR|locus:2084756 - symbol:SUS4 "AT3G43190" species:3702 "Arabidopsis thaliana" [GO:0005986 "sucrose biosynthetic process" evidence=ISS] [GO:0008194 "UDP-glycosyltransferase activity" evidence=ISS] [GO:0016157 "sucrose synthase activity" evidence=IGI;ISS;IDA] [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0005773 "vacuole" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR000368 InterPro:IPR001296 InterPro:IPR012820 Pfam:PF00534 Pfam:PF00862 GO:GO:0005829 GO:GO:0005886 GO:GO:0005773 EMBL:CP002686 GO:GO:0009058 CAZy:GT4 EMBL:AL353871 GO:GO:0005985 KO:K00695 ProtClustDB:PLN00142 GO:GO:0016157 PANTHER:PTHR12526:SF27 TIGRFAMs:TIGR02470 IPI:IPI00540190 PIR:T49233 RefSeq:NP_566865.2 UniGene:At.1720 ProteinModelPortal:Q9LXL5 SMR:Q9LXL5 STRING:Q9LXL5 PRIDE:Q9LXL5 EnsemblPlants:AT3G43190.1 GeneID:823393 KEGG:ath:AT3G43190 TAIR:At3g43190 InParanoid:Q9LXL5 OMA:KAEEYLM PhylomeDB:Q9LXL5 Genevestigator:Q9LXL5 Uniprot:Q9LXL5
Root	Isotig11292	6	33	-2.588	1.92E-06	TAIR|locus:2178935 - symbol:IRX3 "AT5G17420" species:3702 "Arabidopsis thaliana" [GO:0016759 "cellulose synthase activity" evidence=ISS;IMP] [GO:0005886 "plasma membrane" evidence=TAS] [GO:0009834 "secondary cell wall biogenesis" evidence=IMP] [GO:0030244 "cellulose biosynthetic process" evidence=IMP] [GO:0010400 "rhamnogalacturonan I side chain metabolic process" evidence=IMP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0052386 "cell wall thickening" evidence=IMP] [GO:0009832 "plant-type cell wall biogenesis" evidence=IMP] InterPro:IPR001841 InterPro:IPR005150 Pfam:PF03552 PROSITE:PS50089 SMART:SM00184 Prosite:PS00518 GO:GO:0016021 GO:GO:0005886 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009507 GO:GO:0008270 InterPro:IPR013083 Gene3D:G3DSA:3.30.40.10 EMBL:AL391142 CAZy:GT2 eggNOG:COG1215 GO:GO:0016760 GO:GO:0030244 GO:GO:0009834 HOGENOM:HBG744549 KO:K10999 EMBL:AF088917

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EMBL:AF091713 EMBL:AY139754 EMBL:BT004543 EMBL:AK220815 IPI:IPI00527128 PIR:T51579 RefSeq:NP_197244.1 UniGene:At.25558 UniGene:At.71017 PDB:1WEO PDBsum:1WEO ProteinModelPortal:Q9SWW6 SMR:Q9SWW6 IntAct:Q9SWW6 MINT:MINT-6950921 STRING:Q9SWW6 PRIDE:Q9SWW6 EnsemblPlants:AT5G17420.1 GeneID:831608 KEGG:ath:AT5G17420 GeneFarm:5090 TAIR:At5g17420 InParanoid:Q9SWW6 OMA:EWGTELG PhylomeDB:Q9SWW6 ProtClustDB:PLN02189 Genevestigator:Q9SWW6 GermOnline:AT5G17420 GO:GO:0010400 Uniprot:Q9SWW6
Root	Isotig11294	1	16	-4.129	5.13E-05	TAIR|locus:2057961 - symbol:ABCB1 "AT2G36910" species:3702 "Arabidopsis thaliana" [GO:0006200 "ATP catabolic process" evidence=IBA] [GO:0010540 "basipetal auxin transport" evidence=IBA] [GO:0010541 "acropetal auxin transport" evidence=IBA] [GO:0016021 "integral to membrane" evidence=IBA] [GO:0042626 "ATPase activity, coupled to transmembrane movement of substances" evidence=ISS;IBA] [GO:0055085 "transmembrane transport" evidence=IBA] [GO:0005516 "calmodulin binding" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0008361 "regulation of cell size" evidence=IMP] [GO:0009637 "response to blue light" evidence=IMP] [GO:0009639 "response to red or far red light" evidence=IMP] [GO:0009640 "photomorphogenesis" evidence=IMP] [GO:0009733 "response to auxin stimulus" evidence=IMP] [GO:0009958 "positive gravitropism" evidence=IGI] [GO:0043481 "anthocyanin accumulation in tissues in response to UV light" evidence=IMP] [GO:0009926 "auxin polar transport" evidence=IMP;TAS] [GO:0010329 "auxin efflux transmembrane transporter activity" evidence=IDA] [GO:0009624 "response to nematode" evidence=IEP] [GO:0048443 "stamen development" evidence=IGI] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR001140 InterPro:IPR003439 InterPro:IPR003593 InterPro:IPR011527 InterPro:IPR017871 Pfam:PF00005 Pfam:PF00664 PROSITE:PS00211 PROSITE:PS50893 SMART:SM00382 GO:GO:0016021 GO:GO:0005886 GO:GO:0009506 GO:GO:0005524 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0005515 GO:GO:0009926 GO:GO:0009624 eggNOG:COG1132 HOGENOM:HBG758042 KO:K05658 GO:GO:0042626 InterPro:IPR017940 SUPFAM:SSF90123 PROSITE:PS50929 GO:GO:0010329 GO:GO:0043481 GO:GO:0009640 GO:GO:0009958 GO:GO:0008361 GO:GO:0009637 GO:GO:0048443 EMBL:X61370 EMBL:AC006922 EMBL:AY140105 IPI:IPI00516477 PIR:A42150 RefSeq:NP_181228.1 UniGene:At.142 ProteinModelPortal:Q9ZR72 SMR:Q9ZR72 IntAct:Q9ZR72 STRING:Q9ZR72 TCDB:2.A.7.12.12 TCDB:3.A.1.201.5 PRIDE:Q9ZR72 EnsemblPlants:AT2G36910.1 GeneID:818265 KEGG:ath:AT2G36910 TAIR:At2g36910 InParanoid:Q9ZR72 OMA:AGRQINK PhylomeDB:Q9ZR72 ProtClustDB:CLSN2683953 Genevestigator:Q9ZR72 GermOnline:AT2G36910 Uniprot:Q9ZR72
Root	Isotig11295	11	30	-1.576	0.000984585	TAIR|locus:2199685 - symbol:GI "AT1G22770" species:3702 "Arabidopsis thaliana" [GO:0009908 "flower development" evidence=TAS] [GO:0005654 "nucleoplasm" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0005634 "nucleus" evidence=IDA] [GO:0042752 "regulation of circadian rhythm" evidence=IMP] [GO:0048578 "positive regulation of long-day photoperiodism, flowering" evidence=IMP] [GO:0009409 "response to cold" evidence=IMP] [GO:0010378 "temperature compensation of the circadian clock" evidence=IMP] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IDA] [GO:0007623 "circadian rhythm" evidence=IDA] [GO:0009637 "response to blue light" evidence=IDA] [GO:0010218 "response to far red light" evidence=IMP] [GO:0080167 "response to karrikin" evidence=IEP] [GO:0042542 "response to hydrogen peroxide" evidence=IMP] EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005654 GO:GO:0005515 GO:GO:0030154 GO:GO:0006355 GO:GO:0007623 GO:GO:0009409 GO:GO:0080167 GO:GO:0009637 GO:GO:0010218 GO:GO:0042542 GO:GO:0009908 GO:GO:0009585 GO:GO:0048578 EMBL:AC003979 GO:GO:0010378 EMBL:AJ133786 EMBL:AF105064 EMBL:AF076686 EMBL:Y12227 IPI:IPI00531066 PIR:T52575 RefSeq:NP_564180.1 UniGene:At.209 IntAct:Q9SQI2 STRING:Q9SQI2 PRIDE:Q9SQI2 EnsemblPlants:AT1G22770.1 GeneID:838883 KEGG:ath:AT1G22770 TAIR:At1g22770 eggNOG:NOG245462 HOGENOM:HBG592018 InParanoid:Q9SQI2 KO:K12124 OMA:LVCPSSE PhylomeDB:Q9SQI2 ProtClustDB:CLSN2687916 ArrayExpress:Q9SQI2 Genevestigator:Q9SQI2 GermOnline:AT1G22770 Uniprot:Q9SQI2
Root	Isotig11297	33	197	-2.707	9.40E-33	TAIR|locus:2084756 - symbol:SUS4 "AT3G43190" species:3702 "Arabidopsis thaliana" [GO:0005986 "sucrose biosynthetic process" evidence=ISS] [GO:0008194 "UDP-glycosyltransferase activity" evidence=ISS] [GO:0016157 "sucrose synthase activity" evidence=IGI;ISS;IDA] [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0005773 "vacuole" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR000368 InterPro:IPR001296 InterPro:IPR012820 Pfam:PF00534 Pfam:PF00862 GO:GO:0005829 GO:GO:0005886

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0005773 EMBL:CP002686 GO:GO:0009058 CAZy:GT4 EMBL:AL353871 GO:GO:0005985 KO:K00695 ProtClustDB:PLN00142 GO:GO:0016157 PANTHER:PTHR12526:SF27 TIGRFAMs:TIGR02470 IPI:IPI00540190 PIR:T49233 RefSeq:NP_566865.2 UniGene:At.1720 ProteinModelPortal:Q9LXL5 SMR:Q9LXL5 STRING:Q9LXL5 PRIDE:Q9LXL5 EnsemblPlants:AT3G43190.1 GeneID:823393 KEGG:ath:AT3G43190 TAIR:At3g43190 InParanoid:Q9LXL5 OMA:KAEEYLM PhylomeDB:Q9LXL5 Genevestigator:Q9LXL5 Uniprot:Q9LXL5
Root	Isotig11306	24	4	2.456	0.000163328	TAIR|locus:2063907 - symbol:P5CS1 "AT2G39800" species:3702 "Arabidopsis thaliana" [GO:0006561 "proline biosynthetic process" evidence=IMP;TAS] [GO:0009414 "response to water deprivation" evidence=IGI;IEP] [GO:0017084 "delta1-pyrroline-5-carboxylate synthetase activity" evidence=ISS] [GO:0016020 "membrane" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0006979 "response to oxidative stress" evidence=IMP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0042538 "hyperosmotic salinity response" evidence=IEP;IMP] [GO:0048364 "root development" evidence=IMP] [GO:0009269 "response to desiccation" evidence=IEP] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] InterPro:IPR000965 InterPro:IPR001048 InterPro:IPR001057 InterPro:IPR005715 InterPro:IPR005766 InterPro:IPR015590 InterPro:IPR016161 InterPro:IPR016162 InterPro:IPR016163 InterPro:IPR019797 InterPro:IPR020593 Pfam:PF00171 Pfam:PF00696 PIRSF:PIRSF036429 PRINTS:PR00474 PROSITE:PS00902 PROSITE:PS01223 GO:GO:0005524 GO:GO:0009507 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0006979 GO:GO:0016020 Gene3D:G3DSA:3.40.309.10 Gene3D:G3DSA:3.40.605.10 SUPFAM:SSF53720 GO:GO:0009414 GO:GO:0048364 GO:GO:0006561 Gene3D:G3DSA:3.40.1160.10 SUPFAM:SSF53633 GO:GO:0042538 GO:GO:0004349 EMBL:AC003000 EMBL:X89414 EMBL:X86777 EMBL:X87330 EMBL:D32138 EMBL:AF424633 EMBL:AY113046 EMBL:AY150430 IPI:IPI00529620 PIR:S66637 PIR:T50685 RefSeq:NP_001189714.1 RefSeq:NP_181510.1 UniGene:At.20482 ProteinModelPortal:P54887 SMR:P54887 IntAct:P54887 STRING:P54887 PRIDE:P54887 EnsemblPlants:AT2G39800.1 EnsemblPlants:AT2G39800.4 GeneID:818566 KEGG:ath:AT2G39800 TAIR:At2g39800 eggNOG:COG0014 HOGENOM:HBG318080 InParanoid:P54887 KO:K12657 OMA:FEARPDC PhylomeDB:P54887 ProtClustDB:PLN02418 Genevestigator:P54887 GermOnline:AT2G39800 GO:GO:0004350 TIGRFAMs:TIGR01092 TIGRFAMs:TIGR00407 TIGRFAMs:TIGR01027 Uniprot:P54887
Root	Isotig11311	13	0	4.571	0.000344357	TAIR|locus:2018264 - symbol:AT1G04390 "AT1G04390" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] InterPro:IPR000210 InterPro:IPR013069 InterPro:IPR016024 Pfam:PF00651 PROSITE:PS50097 GO:GO:0005488 SUPFAM:SSF48371 InterPro:IPR011333 Gene3D:G3DSA:3.30.710.10 SUPFAM:SSF54695 EMBL:AC000104 EMBL:AK228712 IPI:IPI00522893 IPI:IPI01018457 PIR:G86175 ProteinModelPortal:P93820 SMR:P93820 PRIDE:P93820 TAIR:At1g04390 eggNOG:NOG286903 InParanoid:Q0WQI5 Genevestigator:Q0WQI5 Uniprot:P93820
Root	Isotig11320	26	2	3.571	2.56E-06	TAIR|locus:2126296 - symbol:DCAF1 "AT4G31160" species:3702 "Arabidopsis thaliana" [GO:0000166 "nucleotide binding" evidence=ISS] [GO:0005515 "protein binding" evidence=IPI] [GO:0005634 "nucleus" evidence=IDA] [GO:0009793 "embryo development ending in seed dormancy" evidence=IMP] [GO:0009908 "flower development" evidence=IMP] [GO:0010154 "fruit development" evidence=IMP] [GO:0048366 "leaf development" evidence=IMP] [GO:0048367 "shoot development" evidence=IMP] [GO:0048827 "phyllome development" evidence=IMP] [GO:0080008 "CUL4 RING ubiquitin ligase complex" evidence=IPI] InterPro:IPR017986 InterPro:IPR001680 InterPro:IPR006594 InterPro:IPR011989 InterPro:IPR015943 PROSITE:PS50082 PROSITE:PS50294 PROSITE:PS50896 SMART:SM00320 SMART:SM00667 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005634 GO:GO:0005515 Gene3D:G3DSA:1.25.10.10 Gene3D:G3DSA:2.130.10.10 SUPFAM:SSF50978 PROSITE:PS00678 GO:GO:0009793 GO:GO:0048366 GO:GO:0009908 EMBL:AL161578 InterPro:IPR013720 Pfam:PF08513 GO:GO:0080008 EMBL:AL049914 EMBL:AK118434 IPI:IPI00539541 PIR:T10670 RefSeq:NP_194845.4 UniGene:At.19830 ProteinModelPortal:Q9M086 SMR:Q9M086 IntAct:Q9M086 STRING:Q9M086 PRIDE:Q9M086 EnsemblPlants:AT4G31160.1 GeneID:829244 KEGG:ath:AT4G31160 GeneFarm:4077 TAIR:At4g31160 eggNOG:NOG237621 InParanoid:Q9M086 KO:K11789 PhylomeDB:Q9M086 ProtClustDB:CLSN2695281 ArrayExpress:Q9M086 Genevestigator:Q9M086 Uniprot:Q9M086
Root	Isotig11321	8	27	-1.884	0.000397726	TAIR|locus:2016139 - symbol:KUP6 "K+ uptake permease 6" species:3702 "Arabidopsis thaliana" [GO:0006813 "potassium ion transport" evidence=IEA;ISS] [GO:0015079 "potassium ion transmembrane transporter activity" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] InterPro:IPR003855 Pfam:PF02705 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005886 GO:GO:0015079 EMBL:AC003671 eggNOG:COG3158 TIGRFAMs:TIGR00794 HOGENOM:HBG606427 EMBL:AY062542

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EMBL:AY093328 EMBL:AF129482 IPI:IPI00539530 PIR:T01493 RefSeq:NP_177187.2 UniGene:At.27303 ProteinModelPortal:Q8W4I4 IntAct:Q8W4I4 PRIDE:Q8W4I4 EnsemblPlants:AT1G70300.1 GeneID:843366 KEGG:ath:AT1G70300 TAIR:At1g70300 InParanoid:Q8W4I4 OMA:TVHQRVV PhylomeDB:Q8W4I4 ProtClustDB:PLN00149 ArrayExpress:Q8W4I4 Genevestigator:Q8W4I4 GermOnline:AT1G70300 Uniprot:Q8W4I4
Root	Isotig11329	21	1	4.263	7.63E-06	TAIR|locus:2140503 - symbol:EMB1691 "EMBRYO DEFECTIVE 1691" species:3702 "Arabidopsis thaliana" [GO:0003676 "nucleic acid binding" evidence=IEA] [GO:0008168 "methyltransferase activity" evidence=IEA] [GO:0008757 "S-adenosylmethionine-dependent methyltransferase activity" evidence=ISS] [GO:0009793 "embryo development ending in seed dormancy" evidence=NAS] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR002052 InterPro:IPR007757 Pfam:PF05063 PROSITE:PS00092 PROSITE:PS51143 GO:GO:0005829 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0003676 EMBL:AL049481 EMBL:AL161516 GO:GO:0006139 GO:GO:0008168 eggNOG:COG4725 EMBL:AY046016 EMBL:BT000992 IPI:IPI00535180 PIR:T04002 RefSeq:NP_001078365.1 RefSeq:NP_567348.2 UniGene:At.33660 UniGene:At.69911 IntAct:Q94AI4 PRIDE:Q94AI4 EnsemblPlants:AT4G09980.2 GeneID:826589 KEGG:ath:AT4G09980 GeneFarm:4530 TAIR:At4g09980 InParanoid:Q94AI4 OMA:RISEHES PhylomeDB:Q94AI4 ProtClustDB:CLSN2699100 Genevestigator:Q94AI4 GermOnline:AT4G09980 Uniprot:Q94AI4
Root	Isotig11340	0	11	-4.588	0.000569522	TAIR|locus:2091672 - symbol:AT3G14470 species:3702 "Arabidopsis thaliana" [GO:0006952 "defense response" evidence=IEA;ISS] [GO:0005515 "protein binding" evidence=IPI] InterPro:IPR000767 InterPro:IPR002182 Pfam:PF00931 PRINTS:PR00364 GO:GO:0005524 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005515 GO:GO:0006952 GO:GO:0043531 HOGENOM:HBG749068 EMBL:AB028617 IPI:IPI00528279 RefSeq:NP_188065.1 UniGene:At.39233 ProteinModelPortal:Q9LRR4 SMR:Q9LRR4 IntAct:Q9LRR4 STRING:Q9LRR4 PRIDE:Q9LRR4 EnsemblPlants:AT3G14470.1 GeneID:820670 KEGG:ath:AT3G14470 TAIR:At3g14470 eggNOG:NOG280712 InParanoid:Q9LRR4 OMA:FDVFKIT PhylomeDB:Q9LRR4 ProtClustDB:CLSN2915574 ArrayExpress:Q9LRR4 Genevestigator:Q9LRR4 GermOnline:AT3G14470 Uniprot:Q9LRR4
Root	Isotig11342	0	11	-4.588	0.000569522	TAIR|locus:2205430 - symbol:AT1G68940 species:3702 "Arabidopsis thaliana" [GO:0000151 "ubiquitin ligase complex" evidence=IEA] [GO:0004842 "ubiquitin-protein ligase activity" evidence=IEA] [GO:0016567 "protein ubiquitination" evidence=IEA] InterPro:IPR000225 InterPro:IPR003613 InterPro:IPR011989 InterPro:IPR016024 Pfam:PF00514 Pfam:PF04564 PROSITE:PS50176 SMART:SM00185 SMART:SM00504 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005488 SUPFAM:SSF48371 Gene3D:G3DSA:1.25.10.10 InterPro:IPR013083 Gene3D:G3DSA:3.30.40.10 GO:GO:0004842 GO:GO:0000151 EMBL:AC011665 HSSP:Q8VZ40 IPI:IPI00530180 PIR:A96714 RefSeq:NP_177060.3 UniGene:At.52443 ProteinModelPortal:Q9CAA7 SMR:Q9CAA7 PRIDE:Q9CAA7 EnsemblPlants:AT1G68940.1 GeneID:843228 KEGG:ath:AT1G68940 TAIR:At1g68940 eggNOG:NOG294513 HOGENOM:HBG589816 InParanoid:Q9CAA7 OMA:CTLLDDK PhylomeDB:Q9CAA7 ProtClustDB:CLSN2680785 Genevestigator:Q9CAA7 Uniprot:Q9CAA7
Root	Isotig11345	1	21	-4.521	2.07E-06	TAIR|locus:2077607 - symbol:AT3G06880 "AT3G06880" species:3702 "Arabidopsis thaliana" [GO:0000166 "nucleotide binding" evidence=ISS] [GO:0005575 "cellular_component" evidence=ND] InterPro:IPR017986 InterPro:IPR001680 InterPro:IPR015943 Pfam:PF00400 PROSITE:PS50082 PROSITE:PS50294 SMART:SM00320 GenomeReviews:BA000014_GR InterPro:IPR019775 Gene3D:G3DSA:2.130.10.10 SUPFAM:SSF50978 PROSITE:PS00678 EMBL:AC016827 IPI:IPI01019860 ProteinModelPortal:Q9M911 SMR:Q9M911 eggNOG:NOG288723 HOGENOM:HBG318258 InParanoid:Q9M911 OMA:WTGEPYT PhylomeDB:Q9M911 Genevestigator:Q9M911 Uniprot:Q9M911
Root	Isotig11352	1	18	-4.299	1.41E-05	TAIR|locus:2007412 - symbol:AT1G07200 "AT1G07200" species:3702 "Arabidopsis thaliana" [GO:0005524 "ATP binding" evidence=ISS] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0016787 EMBL:AC067971 InterPro:IPR023150 Gene3D:G3DSA:1.10.1780.10 HOGENOM:HBG589559 ProtClustDB:CLSN2688559 IPI:IPI00542322 PIR:B86207 RefSeq:NP_001077474.1 UniGene:At.27670 ProteinModelPortal:Q9LML2 PRIDE:Q9LML2 EnsemblPlants:AT1G07200.2 GeneID:837231 KEGG:ath:AT1G07200 TAIR:At1g07200 PhylomeDB:Q9LML2 Genevestigator:Q9LML2 Uniprot:Q9LML2
Root	Isotig11355	4	19	-2.377	0.000578515	TAIR|locus:2031371 - symbol:AT1G63430 species:3702 "Arabidopsis thaliana" [GO:0004672 "protein kinase activity" evidence=IEA] [GO:0004674 "protein serine/threonine kinase activity" evidence=IEA;ISS] [GO:0005524 "ATP binding" evidence=IEA;ISS] [GO:0006468 "protein phosphorylation" evidence=IEA;ISS] [GO:0007169 "transmembrane receptor protein tyrosine kinase signaling pathway" evidence=ISS] [GO:0005886 "plasma

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						membrane" evidence=IDA] Pfam:PF00560 InterPro:IPR001611 InterPro:IPR000719 InterPro:IPR001245 InterPro:IPR011009 Pfam:PF07714 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005886 GO:GO:0005524 GO:GO:0004872 SUPFAM:SSF56112 GO:GO:0004674 EMBL:AC008047 InterPro:IPR013210 Pfam:PF08263 HOGENOM:HBG749254 EMBL:AK117932 EMBL:FJ708668 IPI:IPI00543834 RefSeq:NP_176532.2 UniGene:At.14999 ProteinModelPortal:C0LGH8 SMR:C0LGH8 PRIDE:C0LGH8 EnsemblPlants:AT1G63430.1 GeneID:842649 KEGG:ath:AT1G63430 GeneFarm:693 TAIR:At1g63430 eggNOG:NOG305556 InParanoid:Q8GY10 OMA:SGRPPYC PhylomeDB:C0LGH8 ProtClustDB:CLSN2686223 Uniprot:C0LGH8
Root	Isotig11365	0	18	-5.299	6.77E-06	TAIR|locus:2100641 - symbol:ABCG19 "AT3G55130" species:3702 "Arabidopsis thaliana" [GO:0042626 "ATPase activity, coupled to transmembrane movement of substances" evidence=ISS] [GO:0005775 "vacuolar lumen" evidence=IDA] [GO:0007034 "vacuolar transport" evidence=IMP] [GO:0042891 "antibiotic transport" evidence=TAS] InterPro:IPR003439 InterPro:IPR003593 InterPro:IPR013525 InterPro:IPR017871 Pfam:PF00005 Pfam:PF01061 PROSITE:PS00211 PROSITE:PS50893 PROSITE:PS51012 SMART:SM00382 GO:GO:0016021 GO:GO:0005524 GO:GO:0005774 EMBL:CP002686 GenomeReviews:BA000014_GR eggNOG:COG1131 GO:GO:0016887 HOGENOM:HBG590889 ProtClustDB:CLSN2685264 EMBL:AL132954 EMBL:AY045932 EMBL:AY079387 IPI:IPI00545207 PIR:T47652 RefSeq:NP_191073.1 UniGene:At.1136 UniGene:At.23809 ProteinModelPortal:Q9M3D6 SMR:Q9M3D6 IntAct:Q9M3D6 PRIDE:Q9M3D6 EnsemblPlants:AT3G55130.1 GeneID:824679 KEGG:ath:AT3G55130 TAIR:At3g55130 InParanoid:Q9M3D6 OMA:NERHIPA PhylomeDB:Q9M3D6 ArrayExpress:Q9M3D6 Genevestigator:Q9M3D6 GermOnline:AT3G55130 GO:GO:0005775 GO:GO:0042891 GO:GO:0007034 Uniprot:Q9M3D6
Root	Isotig11369	3	19	-2.792	0.000168634	TAIR|locus:2043679 - symbol:AT2G45540 "AT2G45540" species:3702 "Arabidopsis thaliana" [GO:0000166 "nucleotide binding" evidence=ISS] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] InterPro:IPR017986 InterPro:IPR001680 InterPro:IPR015943 Pfam:PF00400 PROSITE:PS50082 PROSITE:PS50294 SMART:SM00320 EMBL:CP002685 GenomeReviews:CT485783_GR Gene3D:G3DSA:2.130.10.10 SUPFAM:SSF50978 InterPro:IPR008985 SUPFAM:SSF49899 EMBL:AC003680 eggNOG:NOG236271 InterPro:IPR000409 InterPro:IPR023362 Gene3D:G3DSA:1.10.1540.10 Gene3D:G3DSA:2.30.29.40 Pfam:PF02138 SMART:SM01026 SUPFAM:SSF81837 PROSITE:PS50197 HSSP:Q8NFP9 UniGene:At.48594 IPI:IPI00517715 PIR:T00867 RefSeq:NP_182078.1 ProteinModelPortal:O64634 SMR:O64634 STRING:O64634 PRIDE:O64634 ProMEX:O64634 EnsemblPlants:AT2G45540.1 GeneID:819162 KEGG:ath:AT2G45540 TAIR:At2g45540 HOGENOM:HBG318172 InParanoid:O64634 OMA:VLEDMSD PhylomeDB:O64634 ProtClustDB:CLSN2683358 ArrayExpress:O64634 Genevestigator:O64634 Uniprot:O64634
Root	Isotig11378	1	15	-4.036	9.83E-05	No hit
Root	Isotig11381	18	61	-1.890	9.57E-08	UNIPROTKB|Q06735 - symbol:ATPA "ATP synthase subunit alpha, mitochondrial" species:161934 "Beta vulgaris" [GO:0000275 "mitochondrial proton-transporting ATP synthase complex, catalytic core F(1)" evidence=NAS] [GO:0005739 "mitochondrion" evidence=NAS] [GO:0006754 "ATP biosynthetic process" evidence=NAS] InterPro:IPR000194 InterPro:IPR000793 InterPro:IPR004100 InterPro:IPR005294 InterPro:IPR018118 InterPro:IPR020003 Pfam:PF00006 Pfam:PF00306 Pfam:PF02874 PROSITE:PS00152 GO:GO:0005524 GO:GO:0015991 GO:GO:0000275 GO:GO:0046933 GO:GO:0046961 GO:GO:0015986 InterPro:IPR023366 Gene3D:G3DSA:2.40.30.20 SUPFAM:SSF50615 EMBL:D15065 PIR:S33922 ProteinModelPortal:Q06735 SMR:Q06735 SUPFAM:SSF47917 TIGRFAMs:TIGR00962 Uniprot:Q06735
Root	Isotig11386	19	62	-1.835	1.34E-07	TAIR|locus:2170318 - symbol:ATMS1 "AT5G17920" species:3702 "Arabidopsis thaliana" [GO:0003871 "5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase activity" evidence=ISS] [GO:0005829 "cytosol" evidence=ISS;IDA] [GO:0009086 "methionine biosynthetic process" evidence=ISS] [GO:0008705 "methionine synthase activity" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0005777 "peroxisome" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0010043 "response to zinc ion" evidence=IEP] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR002629 InterPro:IPR006276 InterPro:IPR013215 Pfam:PF01717 Pfam:PF08267 PIRSF:PIRSF000382 GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 GO:GO:0048046 GO:GO:0009570 GO:GO:0046686 GO:GO:0005774 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005777 GO:GO:0010043

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0008270 GO:GO:0005507 GO:GO:0009651 EMBL:AB011480 UniGene:At.24550 EMBL:U97200 EMBL:AF370522 EMBL:AY048201 EMBL:AY056098 EMBL:AY057499 EMBL:AY069876 EMBL:AY070771 EMBL:AY091692 IPI:IPI00522440 RefSeq:NP_001078599.1 RefSeq:NP_197294.1 UniGene:At.22340 UniGene:At.71028 PDB:1U1H PDB:1U1J PDB:1U1U PDB:1U22 PDBsum:1U1H PDBsum:1U1J PDBsum:1U1U PDBsum:1U22 ProteinModelPortal:O50008 SMR:O50008 IntAct:O50008 STRING:O50008 SWISS-2DPAGE:O50008 PRIDE:O50008 ProMEX:O50008 EnsemblPlants:AT5G17920.1 EnsemblPlants:AT5G17920.2 GeneID:831660 KEGG:ath:AT5G17920 TAIR:At5g17920 eggNOG:COG0620 HOGENOM:HBG287495 InParanoid:O50008 KO:K00549 OMA:NIWANDF PhylomeDB:O50008 ProtClustDB:PLN02475 BRENDA:2.1.1.14 Genevestigator:O50008 GermOnline:AT5G17920 GO:GO:0003871 GO:GO:0008705 TIGRFAMs:TIGR01371 Uniprot:O50008
Root	Isotig11387	29	1	4.729	7.39E-08	TAIR|locus:2063907 - symbol:P5CS1 "AT2G39800" species:3702 "Arabidopsis thaliana" [GO:0006561 "proline biosynthetic process" evidence=IMP;TAS] [GO:0009414 "response to water deprivation" evidence=IGI;IEP] [GO:0017084 "delta1-pyrroline-5-carboxylate synthetase activity" evidence=ISS] [GO:0016020 "membrane" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0006979 "response to oxidative stress" evidence=IMP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0042538 "hyperosmotic salinity response" evidence=IEP;IMP] [GO:0048364 "root development" evidence=IMP] [GO:0009269 "response to desiccation" evidence=IEP] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] InterPro:IPR000965 InterPro:IPR001048 InterPro:IPR001057 InterPro:IPR005715 InterPro:IPR005766 InterPro:IPR015590 InterPro:IPR016161 InterPro:IPR016162 InterPro:IPR016163 InterPro:IPR019797 InterPro:IPR020593 Pfam:PF00171 Pfam:PF00696 PIRSF:PIRSF036429 PRINTS:PR00474 PROSITE:PS00902 PROSITE:PS01223 GO:GO:0005524 GO:GO:0009507 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0006979 GO:GO:0016020 Gene3D:G3DSA:3.40.309.10 Gene3D:G3DSA:3.40.605.10 SUPFAM:SSF53720 GO:GO:0009414 GO:GO:0048364 GO:GO:0006561 Gene3D:G3DSA:3.40.1160.10 SUPFAM:SSF53633 GO:GO:0042538 GO:GO:0004349 EMBL:AC003000 EMBL:X89414 EMBL:X86777 EMBL:X87330 EMBL:D32138 EMBL:AF424633 EMBL:AY113046 EMBL:AY150430 IPI:IPI00529620 PIR:S66637 PIR:T50685 RefSeq:NP_001189714.1 RefSeq:NP_181510.1 UniGene:At.20482 ProteinModelPortal:P54887 SMR:P54887 IntAct:P54887 STRING:P54887 PRIDE:P54887 EnsemblPlants:AT2G39800.1 EnsemblPlants:AT2G39800.4 GeneID:818566 KEGG:ath:AT2G39800 TAIR:At2g39800 eggNOG:COG0014 HOGENOM:HBG318080 InParanoid:P54887 KO:K12657 OMA:FEARPDC PhylomeDB:P54887 ProtClustDB:PLN02418 Genevestigator:P54887 GermOnline:AT2G39800 GO:GO:0004350 TIGRFAMs:TIGR01092 TIGRFAMs:TIGR00407 TIGRFAMs:TIGR01027 Uniprot:P54887
Root	Isotig11392	97	44	1.012	6.08E-05	TAIR|locus:2036134 - symbol:AVP1 "AT1G15690" species:3702 "Arabidopsis thaliana" [GO:0009414 "response to water deprivation" evidence=IMP] [GO:0009651 "response to salt stress" evidence=IMP] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009678 "hydrogen-translocating pyrophosphatase activity" evidence=IDA] [GO:0009705 "plant-type vacuole membrane" evidence=IDA] [GO:0010248 "establishment or maintenance of transmembrane electrochemical gradient" evidence=TAS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009926 "auxin polar transport" evidence=IGI] [GO:0010008 "endosome membrane" evidence=IDA] [GO:0000325 "plant-type vacuole" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048366 "leaf development" evidence=IMP] [GO:0005829 "cytosol" evidence=RCA] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR004131 Pfam:PF03030 PIRSF:PIRSF001265 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005739 GO:GO:0005886 GO:GO:0009926 GO:GO:0009941 GO:GO:0009651 GO:GO:0009414 GO:GO:0010008 GO:GO:0009705 GO:GO:0048366 GO:GO:0015992 EMBL:AC034256 UniGene:At.21942 UniGene:At.66944 EMBL:M81892 EMBL:AB015138 EMBL:AY065016 EMBL:AY078953 EMBL:BT002481 EMBL:Z17694 EMBL:Z17695 EMBL:AK221989 IPI:IPI00521876 PIR:A38230 RefSeq:NP_173021.1 UniGene:At.67102 UniGene:At.74973 STRING:P31414 TCDB:3.A.10.1.1 PRIDE:P31414 EnsemblPlants:AT1G15690.1 GeneID:838138 KEGG:ath:AT1G15690 GeneFarm:5159 TAIR:At1g15690 eggNOG:COG3808 InParanoid:P31414 KO:K01507 OMA:MAITSIV PhylomeDB:P31414 ProtClustDB:PLN02255 BRENDA:3.6.1.1 ArrayExpress:P31414 Genevestigator:P31414 GermOnline:AT1G15690 GO:GO:0009678 GO:GO:0004427 GO:GO:0010248 TIGRFAMs:TIGR01104 Uniprot:P31414

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig11401	2	22	-3.588	5.84E-06	TAIR|locus:2140260 - symbol:GA1 "AT4G02780" species:3702 "Arabidopsis thaliana" [GO:0000287 "magnesium ion binding" evidence=IDA] [GO:0009905 "ent-copalyl diphosphate synthase activity" evidence=IMP;IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009686 "gibberellin biosynthetic process" evidence=IMP;IDA] [GO:0009740 "gibberellic acid mediated signaling pathway" evidence=TAS] InterPro:IPR001906 InterPro:IPR005630 Pfam:PF01397 Pfam:PF03936 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0009507 GO:GO:0000287 InterPro:IPR008930 SUPFAM:SSF48239 EMBL:AL161495 InterPro:IPR008949 Gene3D:G3DSA:1.50.30.10 Gene3D:G3DSA:1.10.600.10 SUPFAM:SSF48576 GO:GO:0010333 GO:GO:0009686 EMBL:AC004044 GO:GO:0009740 EMBL:U11034 IPI:IPI00533674 PIR:D85035 RefSeq:NP_192187.1 UniGene:At.355 PDB:3PYA PDB:3PYB PDBsum:3PYA PDBsum:3PYB ProteinModelPortal:Q38802 SMR:Q38802 STRING:Q38802 PRIDE:Q38802 EnsemblPlants:AT4G02780.1 GeneID:828182 KEGG:ath:AT4G02780 GeneFarm:4914 TAIR:At4g02780 eggNOG:NOG14896 HOGENOM:HBG318703 InParanoid:Q38802 KO:K04120 OMA:KLQSQDG PhylomeDB:Q38802 ProtClustDB:PLN02592 BioCyc:ARA:AT4G02780-MONOMER BioCyc:MetaCyc:AT4G02780-MONOMER ArrayExpress:Q38802 Genevestigator:Q38802 GermOnline:AT4G02780 GO:GO:0009905 Uniprot:Q38802
Root	Isotig11404	10	34	-1.895	6.62E-05	TAIR|locus:2039385 - symbol:PIP2;8 "AT2G16850" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=ISS] [GO:0015250 "water channel activity" evidence=ISS] [GO:0016020 "membrane" evidence=ISS;IDA] [GO:0009737 "response to abscisic acid stimulus" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] InterPro:IPR000425 InterPro:IPR012269 InterPro:IPR022357 Pfam:PF00230 PRINTS:PR00783 PROSITE:PS00221 GO:GO:0016021 GO:GO:0005886 GO:GO:0009737 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0005515 GO:GO:0055085 GO:GO:0005215 GO:GO:0006833 EMBL:AC005825 EMBL:AC005167 InterPro:IPR023271 Gene3D:G3DSA:1.20.1080.10 SUPFAM:SSF81338 eggNOG:COG0580 HOGENOM:HBG705794 PANTHER:PTHR19139 TIGRFAMs:TIGR00861 KO:K09872 ProtClustDB:CLSN2683758 EMBL:BT005214 EMBL:AK228097 IPI:IPI00541117 PIR:A84545 RefSeq:NP_179277.1 UniGene:At.27545 ProteinModelPortal:Q9ZVX8 SMR:Q9ZVX8 IntAct:Q9ZVX8 STRING:Q9ZVX8 PRIDE:Q9ZVX8 EnsemblPlants:AT2G16850.1 GeneID:816186 KEGG:ath:AT2G16850 GeneFarm:4872 TAIR:At2g16850 InParanoid:Q9ZVX8 OMA:PRAVAYM PhylomeDB:Q9ZVX8 ArrayExpress:Q9ZVX8 Genevestigator:Q9ZVX8 GermOnline:AT2G16850 Uniprot:Q9ZVX8
Root	Isotig11407	6	46	-3.068	8.71E-10	SGD|S000028422 - symbol:TAR1 "Mitochondrial protein potentially involved in respiratory metabolism" species:4932 "Saccharomyces cerevisiae" [GO:0003674 "molecular_function" evidence=ND] [GO:0043457 "regulation of cellular respiration" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IEA;IMP] SGD:S000028422 GO:GO:0005739 EMBL:BK006945 EMBL:U53879 GO:GO:0043457 EMBL:Z73326 EMBL:AF479964 RefSeq:NP_690845.1 ProteinModelPortal:Q8TGM6 STRING:Q8TGM6 EnsemblFungi:YLR154W-C GeneID:1466405 KEGG:sce:YLR154W-C CYGD:YLR154w-c eggNOG:NOG79861 OMA:SCSKEHR OrthoDB:EOG466ZX8 NextBio:967146 Genevestigator:Q8TGM6 GermOnline:YLR154W-C Uniprot:Q8TGM6
Root	Isotig11439	0	20	-5.451	2.00E-06	TAIR|locus:2201557 - symbol:RGL1 "AT1G66350" species:3702 "Arabidopsis thaliana" [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS;TAS] [GO:0005634 "nucleus" evidence=IDA;TAS] [GO:0009740 "gibberellic acid mediated signaling pathway" evidence=TAS] [GO:0009938 "negative regulation of gibberellic acid mediated signaling pathway" evidence=IMP] [GO:0009651 "response to salt stress" evidence=IGI] [GO:0009723 "response to ethylene stimulus" evidence=IGI] [GO:0009737 "response to abscisic acid stimulus" evidence=IGI] [GO:0042538 "hyperosmotic salinity response" evidence=IGI] [GO:0009739 "response to gibberellin stimulus" evidence=IEP] [GO:2000377 "regulation of reactive oxygen species metabolic process" evidence=IGI] [GO:0009863 "salicylic acid mediated signaling pathway" evidence=IGI] [GO:0009867 "jasmonic acid mediated signaling pathway" evidence=IGI] Pfam:PF03514 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009737 GO:GO:0005634 GO:GO:0030154 GO:GO:0003700 GO:GO:0006351 GO:GO:0009723 GO:GO:0009908 GO:GO:0042538 EMBL:AC020665 GO:GO:0009867 GO:GO:0009863 GO:GO:0009740 GO:GO:2000377 HOGENOM:HBG750217 KO:K14494 GO:GO:0009938 InterPro:IPR021914 InterPro:IPR005202 Pfam:PF12041 PROSITE:PS50985 EMBL:AJ224957 EMBL:AY048749 EMBL:AY070035 EMBL:AY096506 IPI:IPI00518407 PIR:G96688 RefSeq:NP_176809.1 UniGene:At.26400 UniGene:At.75173 ProteinModelPortal:Q9C8Y3 SMR:Q9C8Y3 IntAct:Q9C8Y3 STRING:Q9C8Y3 EnsemblPlants:AT1G66350.1 GeneID:842953 KEGG:ath:AT1G66350 GeneFarm:4239 TAIR:At1g66350 eggNOG:NOG314007 InParanoid:Q9C8Y3 OMA:RTRIESE PhylomeDB:Q9C8Y3 ProtClustDB:CLSN2914366 ArrayExpress:Q9C8Y3 Genevestigator:Q9C8Y3 GermOnline:AT1G66350 Uniprot:Q9C8Y3

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig11447	9	29	-1.817	0.000341695	TAIR|locus:2063197 - symbol:CRK1 "AT2G41140" species:3702 "Arabidopsis thaliana" [GO:0004723 "calcium-dependent protein serine/threonine phosphatase activity" evidence=ISS] [GO:0005509 "calcium ion binding" evidence=ISS] [GO:0006468 "protein phosphorylation" evidence=IEA] [GO:0016301 "kinase activity" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0004683 "calmodulin-dependent protein kinase activity" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] InterPro:IPR000719 InterPro:IPR002290 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR011992 InterPro:IPR017441 Pfam:PF00069 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 SMART:SM00220 GO:GO:0005886 GO:GO:0005524 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0005509 GO:GO:0005515 eggNOG:COG0515 SUPFAM:SSF56112 Gene3D:G3DSA:1.10.238.10 HOGENOM:HBG755340 EMBL:AC004261 HSSP:P49137 GO:GO:0004683 EMBL:AF153351 EMBL:AF435448 IPI:IPI00522531 PIR:T02105 RefSeq:NP_181647.1 UniGene:At.11329 ProteinModelPortal:O80673 SMR:O80673 IntAct:O80673 PRIDE:O80673 EnsemblPlants:AT2G41140.1 GeneID:818713 KEGG:ath:AT2G41140 TAIR:At2g41140 InParanoid:O80673 OMA:GKECEIG PhylomeDB:O80673 ProtClustDB:CLSN2683663 ArrayExpress:O80673 Genevestigator:O80673 Uniprot:O80673
Root	Isotig11456	26	6	1.987	0.000575837	TAIR|locus:2117487 - symbol:AT4G25730 species:3702 "Arabidopsis thaliana" [GO:0003676 "nucleic acid binding" evidence=IEA] [GO:0005634 "nucleus" evidence=IEA] [GO:0006364 "rRNA processing" evidence=IEA] [GO:0008168 "methyltransferase activity" evidence=IEA;ISS] [GO:0031167 "rRNA methylation" evidence=IEA] [GO:0032259 "methylation" evidence=IEA] HAMAP:MF_01547 InterPro:IPR002877 InterPro:IPR012920 InterPro:IPR015507 Pfam:PF01728 Pfam:PF07780 GenomeReviews:CT486007_GR GO:GO:0005634 GO:GO:0003676 GO:GO:0008168 GO:GO:0006364 GO:GO:0001510 eggNOG:COG0293 PANTHER:PTHR10920 InterPro:IPR024576 Pfam:PF11861 HOGENOM:HBG410779 HSSP:P28692 EMBL:AY064128 IPI:IPI00530560 ProteinModelPortal:Q8VZJ4 SMR:Q8VZJ4 STRING:Q8VZJ4 PRIDE:Q8VZJ4 TAIR:At4g25730 InParanoid:Q8VZJ4 PhylomeDB:Q8VZJ4 Genevestigator:Q8VZJ4 Uniprot:Q8VZJ4
Root	Isotig11459	0	27	-5.884	3.19E-08	TAIR|locus:2097258 - symbol:ABCG16 "ATP-binding cassette G16" species:3702 "Arabidopsis thaliana" [GO:0016020 "membrane" evidence=IEA] [GO:0042626 "ATPase activity, coupled to transmembrane movement of substances" evidence=ISS] InterPro:IPR003439 InterPro:IPR003593 InterPro:IPR013525 InterPro:IPR017871 Pfam:PF00005 Pfam:PF01061 PROSITE:PS00211 PROSITE:PS50893 PROSITE:PS51012 SMART:SM00382 GO:GO:0016021 GO:GO:0005524 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0006810 eggNOG:COG1131 GO:GO:0016887 HOGENOM:HBG590889 EMBL:AL132970 EMBL:BX819631 IPI:IPI00541690 PIR:T47648 RefSeq:NP_191069.2 UniGene:At.35054 ProteinModelPortal:Q9M2V7 SMR:Q9M2V7 PRIDE:Q9M2V7 EnsemblPlants:AT3G55090.1 GeneID:824675 KEGG:ath:AT3G55090 TAIR:At3g55090 InParanoid:Q9M2V7 PhylomeDB:Q9M2V7 ProtClustDB:CLSN2683255 Genevestigator:Q9M2V7 GermOnline:AT3G55090 Uniprot:Q9M2V7
Root	Isotig11462	240	119	0.883	1.79E-08	ZFIN|ZDB-GENE-070410-9 - symbol:zgc:158463 "zgc:158463" species:7955 "Danio rerio" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] ZFIN:ZDB-GENE-070410-9 EMBL:BX296557 EMBL:BX537263 EMBL:BC129240 IPI:IPI00837201 RefSeq:NP_001091866.1 RefSeq:XP_003200836.1 UniGene:Dr.155369 Ensembl:ENSDART00000102863 Ensembl:ENSDART00000126982 GeneID:100037361 GeneID:100151188 KEGG:dre:100037361 KEGG:dre:100151188 eggNOG:NOG298153 GeneTree:ENSGT00390000016898 InParanoid:A2VD29 OMA:ACHQHAL OrthoDB:EOG4FJ8BF Bgee:A2VD29 Uniprot:A2VD29
Root	Isotig11472	19	2	3.119	0.000146225	TAIR|locus:2041344 - symbol:AT2G46900 "AT2G46900" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0005829 "cytosol" evidence=IDA] GO:GO:0005829 EMBL:CP002685 EMBL:AC004411 InterPro:IPR006994 PANTHER:PTHR22684 Pfam:PF04910 OMA:HISSEDN EMBL:AY039928 EMBL:AY142575 IPI:IPI00519698 PIR:T02197 RefSeq:NP_566090.1 UniGene:At.12571 IntAct:O80734 STRING:O80734 PRIDE:O80734 EnsemblPlants:AT2G46900.1 GeneID:819303 KEGG:ath:AT2G46900 TAIR:At2g46900 HOGENOM:HBG745700 InParanoid:O80734 PhylomeDB:O80734 ProtClustDB:CLSN2722629 ArrayExpress:O80734 Genevestigator:O80734 Uniprot:O80734
Root	Isotig11473	34	2	3.958	2.49E-08	UNIPROTKB|Q9MZL1 - symbol:Q9MZL1 "Mucin 1" species:9544 "Macaca mulatta" [GO:0005737 "cytoplasm" evidence=IBA] [GO:0009986 "cell surface" evidence=IBA] [GO:0016324 "apical plasma membrane" evidence=IBA] PANTHER:PTHR10006 GO:GO:0005737 GO:GO:0009986 GO:GO:0016324 InterPro:IPR000082 Pfam:PF01390

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						SMART:SM00200 PROSITE:PS50024 eggNOG:NOG77744 HOVERGEN:HBG003075 OrthoDB:EOG4NGGNM InterPro:IPR023217 EMBL:AF176947 STRING:Q9MZL1 InParanoid:Q9MZL1 Uniprot:Q9MZL1
Root	Isotig11476	15	0	4.778	0.000105609	TAIR|locus:2077572 - symbol:RPM1 "AT3G07040" species:3702 "Arabidopsis thaliana" [GO:0006952 "defense response" evidence=ISS;TAS] [GO:0005515 "protein binding" evidence=IPI] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0000166 "nucleotide binding" evidence=ISS] [GO:0009626 "plant-type hypersensitive response" evidence=IDA] Pfam:PF00560 InterPro:IPR001611 InterPro:IPR000767 InterPro:IPR002182 Pfam:PF00931 PRINTS:PR00364 GO:GO:0005886 GO:GO:0005524 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005515 eggNOG:COG4886 GO:GO:0012505 GO:GO:0043531 GO:GO:0009626 EMBL:AC016827 HOGENOM:HBG749068 EMBL:X87851 IPI:IPI00526839 PIR:A57072 RefSeq:NP_187360.1 UniGene:At.40415 ProteinModelPortal:Q39214 SMR:Q39214 STRING:Q39214 PRIDE:Q39214 EnsemblPlants:AT3G07040.1 GeneID:819889 KEGG:ath:AT3G07040 TAIR:At3g07040 InParanoid:Q39214 KO:K13457 OMA:WREISIA PhylomeDB:Q39214 ProtClustDB:CLSN2915520 ArrayExpress:Q39214 Genevestigator:Q39214 Uniprot:Q39214
Root	Isotig11487	0	17	-5.216	1.26E-05	TAIR|locus:2036916 - symbol:AT1G21680 "AT1G21680" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0005773 "vacuole" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0009505 "plant-type cell wall" evidence=IDA] EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005774 GO:GO:0009505 EMBL:AC007727 InterPro:IPR011659 Pfam:PF07676 eggNOG:COG0823 ProtClustDB:CLSN2685543 EMBL:AY046036 EMBL:AY142688 IPI:IPI00537881 PIR:A86350 RefSeq:NP_564147.1 UniGene:At.20376 ProteinModelPortal:Q9XI10 SMR:Q9XI10 STRING:Q9XI10 PRIDE:Q9XI10 EnsemblPlants:AT1G21680.1 GeneID:838770 KEGG:ath:AT1G21680 TAIR:At1g21680 HOGENOM:HBG594070 InParanoid:Q9XI10 OMA:EWIAFAS PhylomeDB:Q9XI10 ArrayExpress:Q9XI10 Genevestigator:Q9XI10 Uniprot:Q9XI10
Root	Isotig11488	2	15	-3.036	0.000493759	TAIR|locus:2173977 - symbol:SVL1 "AT5G55480" species:3702 "Arabidopsis thaliana" [GO:0006071 "glycerol metabolic process" evidence=ISS] [GO:0008081 "phosphoric diester hydrolase activity" evidence=IEA] [GO:0008889 "glycerophosphodiester phosphodiesterase activity" evidence=IEA;ISS] [GO:0031225 "anchored to membrane" evidence=TAS] [GO:0046658 "anchored to plasma membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0010026 "trichome differentiation" evidence=IGI] [GO:0010442 "guard cell morphogenesis" evidence=IGI] [GO:0052541 "plant-type cell wall cellulose metabolic process" evidence=IGI] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR004129 InterPro:IPR017946 Pfam:PF03009 GO:GO:0009506 EMBL:CP002688 GenomeReviews:BA000015_GR Gene3D:G3DSA:3.20.20.190 SUPFAM:SSF51695 GO:GO:0006629 GO:GO:0046658 GO:GO:0006071 EMBL:AB015479 eggNOG:COG0584 GO:GO:0008889 PANTHER:PTHR23344 GO:GO:0010026 EMBL:BT015819 EMBL:BT020207 IPI:IPI00547289 RefSeq:NP_200359.1 UniGene:At.6905 ProteinModelPortal:Q9FJ62 STRING:Q9FJ62 PRIDE:Q9FJ62 EnsemblPlants:AT5G55480.1 GeneID:835641 KEGG:ath:AT5G55480 TAIR:At5g55480 HOGENOM:HBG317152 InParanoid:Q9FJ62 OMA:CTDLAYT PhylomeDB:Q9FJ62 ProtClustDB:CLSN2686985 ArrayExpress:Q9FJ62 Genevestigator:Q9FJ62 GermOnline:AT5G55480 GO:GO:0010442 GO:GO:0052541 Uniprot:Q9FJ62
Root	Isotig11492	1	17	-4.216	2.69E-05	TAIR|locus:2179371 - symbol:FAAH "AT5G64440" species:3702 "Arabidopsis thaliana" [GO:0004040 "amidase activity" evidence=ISS] [GO:0005773 "vacuole" evidence=IDA] [GO:0005783 "endoplasmic reticulum" evidence=IDA] [GO:0047412 "N-(long-chain-acyl)ethanolamine deacylase activity" evidence=IMP] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0042742 "defense response to bacterium" evidence=IMP] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR000120 Pfam:PF01425 GO:GO:0016021 GO:GO:0005886 GO:GO:0005774 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0042742 GO:GO:0005789 GO:GO:0016884 eggNOG:COG0154 InterPro:IPR020556 InterPro:IPR023631 Gene3D:G3DSA:3.90.1300.10 PANTHER:PTHR11895 SUPFAM:SSF75304 PROSITE:PS00571 HSSP:Q8RJN5 EMBL:AF223949 EMBL:AY308736 EMBL:AB025640 EMBL:AY057501 EMBL:AY143870 IPI:IPI00528940 RefSeq:NP_201249.2 UniGene:At.19619 ProteinModelPortal:Q7XJJ7 SMR:Q7XJJ7 STRING:Q7XJJ7 PRIDE:Q93ZI9 EnsemblPlants:AT5G64440.1 GeneID:836565 KEGG:ath:AT5G64440 TAIR:At5g64440 InParanoid:Q7XJJ7 OMA:IKDDIDC PhylomeDB:Q7XJJ7 ProtClustDB:CLSN2694572 Genevestigator:Q7XJJ7 GO:GO:0047412 Uniprot:Q7XJJ7
Root	Isotig11501	15	59	-2.105	1.81E-08	TAIR|locus:2040115 - symbol:AT2G25430 species:3702 "Arabidopsis thaliana" [GO:0005543 "phospholipid binding" evidence=IEA] [GO:0005545 "1-phosphatidylinositol binding" evidence=IEA] [GO:0030276 "clathrin binding" evidence=IEA] [GO:0048268 "clathrin coat assembly" evidence=IEA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] InterPro:IPR011417 InterPro:IPR014712 Pfam:PF07651

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0005886 GO:GO:0005634 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0005794 GO:GO:0005545 GO:GO:0005905 GO:GO:0006897 GO:GO:0030136 GO:GO:0030276 HOGENOM:HBG744562 GO:GO:0030118 GO:GO:0048268 InterPro:IPR008942 InterPro:IPR013809 Gene3D:G3DSA:1.25.40.90 Gene3D:G3DSA:1.20.58.150 SMART:SM00273 SUPFAM:SSF48464 PROSITE:PS50942 EMBL:AC006300 eggNOG:NOG327279 ProtClustDB:CLSN2716947 EMBL:AY139760 EMBL:BT008299 EMBL:AY085092 IPI:IPI00537001 PIR:C84648 RefSeq:NP_565595.1 UniGene:At.20747 ProteinModelPortal:Q8LF20 SMR:Q8LF20 PRIDE:Q8LF20 EnsemblPlants:AT2G25430.1 GeneID:817081 KEGG:ath:AT2G25430 TAIR:At2g25430 InParanoid:Q8LF20 OMA:AFYNWCK PhylomeDB:Q8LF20 ArrayExpress:Q8LF20 Genevestigator:Q8LF20 GermOnline:AT2G25430 Uniprot:Q8LF20
Root	Isotig11515	3	17	-2.631	0.00056383	TAIR|locus:2043268 - symbol:ABCC4 "AT2G47800" species:3702 "Arabidopsis thaliana" [GO:0042626 "ATPase activity, coupled to transmembrane movement of substances" evidence=ISS] [GO:0005773 "vacuole" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA;TAS] [GO:0008517 "folic acid transporter activity" evidence=IGI] [GO:0009414 "response to water deprivation" evidence=IMP] [GO:0010118 "stomatal movement" evidence=IMP] [GO:0009624 "response to nematode" evidence=IEP] [GO:0006855 "drug transmembrane transport" evidence=ISS] [GO:0000325 "plant-type vacuole" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0009611 "response to wounding" evidence=IEP] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR001140 InterPro:IPR003439 InterPro:IPR003593 InterPro:IPR011527 InterPro:IPR017871 Pfam:PF00005 Pfam:PF00664 PROSITE:PS00211 PROSITE:PS50893 SMART:SM00382 GO:GO:0016021 GO:GO:0005886 GO:GO:0009506 GO:GO:0005524 GO:GO:0005774 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009611 GO:GO:0009624 eggNOG:COG1132 HOGENOM:HBG758042 InterPro:IPR017940 SUPFAM:SSF90123 PROSITE:PS50929 GO:GO:0008559 ProtClustDB:CLSN2683725 GO:GO:0000325 GO:GO:0009414 EMBL:AJ002584 EMBL:AF243509 EMBL:AC005309 EMBL:AK226656 EMBL:U96399 IPI:IPI00538325 PIR:F84919 RefSeq:NP_182301.1 UniGene:At.37 ProteinModelPortal:Q7DM58 SMR:Q7DM58 STRING:Q7DM58 PRIDE:Q7DM58 ProMEX:Q7DM58 EnsemblPlants:AT2G47800.1 GeneID:819392 KEGG:ath:AT2G47800 TAIR:At2g47800 InParanoid:Q7DM58 OMA:PSENSSH PhylomeDB:Q7DM58 ArrayExpress:O24525 Genevestigator:Q7DM58 GermOnline:AT2G47800 GO:GO:0008517 GO:GO:0010118 Uniprot:Q7DM58
Root	Isotig11524	3	17	-2.631	0.00056383	TAIR|locus:2205035 - symbol:HEMB1 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004655 "porphobilinogen synthase activity" evidence=IEA;ISS] [GO:0046872 "metal ion binding" evidence=IEA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0006779 "porphyrin-containing compound biosynthetic process" evidence=TAS] InterPro:IPR001731 InterPro:IPR013785 Pfam:PF00490 PRINTS:PR00144 PROSITE:PS00169 SMART:SM01004 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009570 Gene3D:G3DSA:3.20.20.70 GO:GO:0046872 GO:GO:0015995 EMBL:AC013289 GO:GO:0006783 EMBL:AF327428 EMBL:AF361803 EMBL:AY059154 EMBL:AY081254 EMBL:AY113941 EMBL:AY120705 EMBL:AY128711 IPI:IPI00537155 PIR:D96719 RefSeq:NP_001077800.1 RefSeq:NP_177132.1 UniGene:At.10020 UniGene:At.21048 ProteinModelPortal:Q9SFH9 SMR:Q9SFH9 STRING:Q9SFH9 PRIDE:Q9SFH9 ProMEX:Q9SFH9 EnsemblPlants:AT1G69740.1 EnsemblPlants:AT1G69740.2 GeneID:843310 KEGG:ath:AT1G69740 TAIR:At1g69740 eggNOG:COG0113 HOGENOM:HBG285270 InParanoid:Q9SFH9 KO:K01698 OMA:FTSHGHD PhylomeDB:Q9SFH9 ProtClustDB:CLSN2679842 ArrayExpress:Q9SFH9 Genevestigator:Q9SFH9 GermOnline:AT1G69740 GO:GO:0004655 PANTHER:PTHR11458 Uniprot:Q9SFH9
Root	Isotig11531	5	26	-2.507	3.30E-05	TAIR|locus:2013021 - symbol:SERK1 "AT1G71830" species:3702 "Arabidopsis thaliana" [GO:0016301 "kinase activity" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0042802 "identical protein binding" evidence=IPI] [GO:0004675 "transmembrane receptor protein serine/threonine kinase activity" evidence=IDA] [GO:0009793 "embryo development ending in seed dormancy" evidence=IMP] [GO:0005515 "protein binding" evidence=IPI] [GO:0006468 "protein phosphorylation" evidence=IDA] [GO:0046777 "protein autophosphorylation" evidence=TAS] [GO:0009556 "microsporogenesis" evidence=IGI;IMP] [GO:0010152 "pollen maturation" evidence=IMP] [GO:0043234 "protein complex" evidence=IPI] [GO:0009742 "brassinosteroid mediated signaling pathway" evidence=IMP] [GO:0033612 "receptor serine/threonine kinase binding" evidence=IPI] [GO:0007030 "Golgi organization" evidence=IGI] [GO:0010227 "floral organ abscission" evidence=IGI] Pfam:PF00560 InterPro:IPR001611 InterPro:IPR000719 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 Pfam:PF00069 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 GO:GO:0016021 EMBL:CP002684

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GenomeReviews:CT485782_GR GO:GO:0005886 GO:GO:0005524 GO:GO:0009742 GO:GO:0043234 GO:GO:0042802 GO:GO:0005789 eggNOG:COG0515 GO:GO:0004714 SUPFAM:SSF56112 GO:GO:0046777 HOGENOM:HBG755340 GO:GO:0010152 GO:GO:0009793 InterPro:IPR013320 Gene3D:G3DSA:2.60.120.200 GO:GO:0010227 EMBL:AC012654 GO:GO:0007030 GO:GO:0033612 InterPro:IPR013210 Pfam:PF08263 GO:GO:0009556 GO:GO:0004675 EMBL:A67827 EMBL:A67815 EMBL:FJ708676 EMBL:AY048200 EMBL:BT002217 IPI:IPI00541544 PIR:H96740 RefSeq:NP_177328.1 UniGene:At.12027 UniGene:At.72107 ProteinModelPortal:Q94AG2 SMR:Q94AG2 IntAct:Q94AG2 STRING:Q94AG2 EnsemblPlants:AT1G71830.1 GeneID:843513 KEGG:ath:AT1G71830 GeneFarm:518 TAIR:At1g71830 InParanoid:Q94AG2 KO:K13418 OMA:DGFSNKN PhylomeDB:Q94AG2 ProtClustDB:CLSN2914617 Genevestigator:Q94AG2 Uniprot:Q94AG2
Root	Isotig11535	4	26	-2.829	9.39E-06	TAIR|locus:2123693 - symbol:AT4G28300 "AT4G28300" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002687 InterPro:IPR010820 Pfam:PF07223 EMBL:AY063895 EMBL:AY096387 IPI:IPI00533848 RefSeq:NP_194559.2 UniGene:At.24043 UniGene:At.67641 IntAct:Q8VZR8 PRIDE:Q8VZR8 EnsemblPlants:AT4G28300.1 GeneID:828945 KEGG:ath:AT4G28300 TAIR:At4g28300 eggNOG:NOG250925 InParanoid:Q8VZR8 OMA:FNTLLDR PhylomeDB:Q8VZR8 ProtClustDB:CLSN2719561 Genevestigator:Q8VZR8 Uniprot:Q8VZR8
Root	Isotig11555	15	0	4.778	0.000105609	TAIR|locus:2150926 - symbol:FTSH6 "AT5G15250" species:3702 "Arabidopsis thaliana" [GO:0008237 "metallopeptidase activity" evidence=ISS] [GO:0016887 "ATPase activity" evidence=ISS] [GO:0004176 "ATP-dependent peptidase activity" evidence=ISS] [GO:0009507 "chloroplast" evidence=IDA] [GO:0008233 "peptidase activity" evidence=IMP] [GO:0008270 "zinc ion binding" evidence=ISS] [GO:0010304 "PSII associated light-harvesting complex II catabolic process" evidence=IEP] InterPro:IPR000642 InterPro:IPR003593 InterPro:IPR003959 InterPro:IPR003960 InterPro:IPR005936 InterPro:IPR011546 Pfam:PF00004 Pfam:PF01434 Pfam:PF06480 PROSITE:PS00674 SMART:SM00382 GO:GO:0016021 GO:GO:0005524 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0008270 GO:GO:0006508 GO:GO:0004222 GO:GO:0017111 eggNOG:COG0465 TIGRFAMs:TIGR01241 HOGENOM:HBG724153 GO:GO:0009535 EMBL:AL353993 KO:K03798 GO:GO:0010304 ProtClustDB:CLSN2679937 EMBL:DQ446953 IPI:IPI00516735 PIR:T49960 RefSeq:NP_568311.2 UniGene:At.54853 HSSP:O67077 ProteinModelPortal:Q1PDW5 SMR:Q1PDW5 STRING:Q1PDW5 MEROPS:M41.019 PRIDE:Q1PDW5 EnsemblPlants:AT5G15250.1 GeneID:831377 KEGG:ath:AT5G15250 GeneFarm:2511 TAIR:At5g15250 InParanoid:Q1PDW5 PhylomeDB:Q1PDW5 Genevestigator:Q1PDW5 Uniprot:Q1PDW5
Root	Isotig11573	0	12	-4.714	0.000297064	TAIR|locus:2115713 - symbol:ATK5 "AT4G05190" species:3702 "Arabidopsis thaliana" [GO:0003777 "microtubule motor activity" evidence=ISS;IMP] [GO:0005634 "nucleus" evidence=IDA] [GO:0000226 "microtubule cytoskeleton organization" evidence=IMP] [GO:0005876 "spindle microtubule" evidence=IDA] [GO:0051225 "spindle assembly" evidence=IMP] InterPro:IPR001752 InterPro:IPR019821 Pfam:PF00225 PRINTS:PR00380 PROSITE:PS00411 PROSITE:PS50067 SMART:SM00129 GO:GO:0005524 GO:GO:0005634 GO:GO:0051225 GO:GO:0003777 GO:GO:0007018 Gene3D:G3DSA:3.40.850.10 GO:GO:0005876 EMBL:BT010582 EMBL:AK175713 IPI:IPI00517511 ProteinModelPortal:Q6NQ77 SMR:Q6NQ77 STRING:Q6NQ77 PRIDE:Q6NQ77 TAIR:At4g05190 InParanoid:Q6NQ77 PhylomeDB:Q6NQ77 Genevestigator:Q6NQ77 Uniprot:Q6NQ77
Root	Isotig11575	1	16	-4.129	5.13E-05	TAIR|locus:2127666 - symbol:AT4G10540 "AT4G10540" species:3702 "Arabidopsis thaliana" [GO:0004252 "serine-type endopeptidase activity" evidence=IEA;IBA] [GO:0005618 "cell wall" evidence=IBA] [GO:0006508 "proteolysis" evidence=ISS] [GO:0008152 "metabolic process" evidence=IBA] [GO:0042802 "identical protein binding" evidence=IEA] InterPro:IPR000209 InterPro:IPR010259 Pfam:PF00082 Pfam:PF05922 InterPro:IPR003137 Prosite:PS00138 PANTHER:PTHR10795 Pfam:PF02225 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0042802 GO:GO:0006508 GO:GO:0004252 GO:GO:0043086 InterPro:IPR023828 InterPro:IPR015500 Gene3D:G3DSA:3.40.50.200 PRINTS:PR00723 SUPFAM:SSF52743 eggNOG:COG1404 EMBL:AL161517 EMBL:AL049524 HSSP:Q45670 HOGENOM:HBG591621 ProtClustDB:CLSN2688223 IPI:IPI00546289 PIR:T04189 RefSeq:NP_567361.1 UniGene:At.54261 ProteinModelPortal:Q9SZY3 SMR:Q9SZY3 MEROPS:S08.A45 PRIDE:Q9SZY3 EnsemblPlants:AT4G10540.1 GeneID:826646 KEGG:ath:AT4G10540 TAIR:At4g10540 InParanoid:Q9SZY3 OMA:HESFNST PhylomeDB:Q9SZY3 ArrayExpress:Q9SZY3 Genevestigator:Q9SZY3 Uniprot:Q9SZY3
Root	Isotig11580	0	23	-5.653	3.32E-07	TAIR|locus:2119058 - symbol:NRT1.8 "AT4G21680" species:3702 "Arabidopsis thaliana" [GO:0005215 "transporter activity" evidence=ISS] [GO:0006857 "oligopeptide transport" evidence=ISS] [GO:0016020 "membrane"

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0010167 "response to nitrate" evidence=IEP] [GO:0015112 "nitrate transmembrane transporter activity" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] InterPro:IPR000109 Pfam:PF00854 PROSITE:PS01022 PROSITE:PS01023 GO:GO:0016021 GO:GO:0005886 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0046686 GO:GO:0015293 InterPro:IPR016196 SUPFAM:SSF103473 GO:GO:0015112 GO:GO:0042128 EMBL:AL035527 EMBL:AL161555 GO:GO:0010167 UniGene:At.2700 UniGene:At.32611 eggNOG:COG3104 GO:GO:0006857 HOGENOM:HBG605267 EMBL:AK118142 IPI:IPI00537723 PIR:T05843 RefSeq:NP_193899.2 ProteinModelPortal:Q8GXN2 PRIDE:Q8GXN2 EnsemblPlants:AT4G21680.1 GeneID:828255 KEGG:ath:AT4G21680 TAIR:At4g21680 InParanoid:Q8GXN2 OMA:ILILVNQ PhylomeDB:Q8GXN2 ArrayExpress:Q9SVS9 Genevestigator:Q8GXN2 Uniprot:Q8GXN2
Root	Isotig11589	0	18	-5.299	6.77E-06	TAIR|locus:2148171 - symbol:CSLD2 "AT5G16910" species:3702 "Arabidopsis thaliana" [GO:0000271 "polysaccharide biosynthetic process" evidence=ISS] [GO:0009832 "plant-type cell wall biogenesis" evidence=ISS] [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0016759 "cellulose synthase activity" evidence=ISS] [GO:0005794 "Golgi apparatus" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0030173 "integral to Golgi membrane" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0048767 "root hair elongation" evidence=IMP] InterPro:IPR005150 Pfam:PF03552 GO:GO:0005886 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0030173 GO:GO:0009409 GO:GO:0048767 InterPro:IPR013083 Gene3D:G3DSA:3.30.40.10 GO:GO:0007047 CAZy:GT2 eggNOG:COG1215 GO:GO:0016760 GO:GO:0030244 HOGENOM:HBG744549 ProtClustDB:PLN02248 EMBL:AL391141 IPI:IPI00532872 PIR:T51546 RefSeq:NP_197193.1 UniGene:At.20318 ProteinModelPortal:Q9LFL0 SMR:Q9LFL0 PRIDE:Q9LFL0 EnsemblPlants:AT5G16910.1 GeneID:831554 KEGG:ath:AT5G16910 TAIR:At5g16910 InParanoid:Q9LFL0 OMA:WRIKHQN PhylomeDB:Q9LFL0 Genevestigator:Q9LFL0 Uniprot:Q9LFL0
Root	Isotig11602	4	19	-2.377	0.000578515	TAIR|locus:2026674 - symbol:YDA "YODA" species:3702 "Arabidopsis thaliana" [GO:0004672 "protein kinase activity" evidence=IEA] [GO:0004674 "protein serine/threonine kinase activity" evidence=IEA] [GO:0005524 "ATP binding" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0009793 "embryo development ending in seed dormancy" evidence=IMP] [GO:0016301 "kinase activity" evidence=ISS] [GO:0010103 "stomatal complex morphogenesis" evidence=IMP] InterPro:IPR000719 InterPro:IPR002290 InterPro:IPR011009 InterPro:IPR017441 Pfam:PF00069 PROSITE:PS00107 PROSITE:PS50011 SMART:SM00220 EMBL:CP002684 GO:GO:0005524 SUPFAM:SSF56112 GO:GO:0004672 GO:GO:0010103 EMBL:AC011622 HSSP:P00523 EMBL:AY357947 EMBL:AY357948 IPI:IPI00535780 PIR:A96662 RefSeq:NP_176557.1 UniGene:At.21875 ProteinModelPortal:Q9CAD5 SMR:Q9CAD5 STRING:Q9CAD5 PRIDE:Q9CAD5 EnsemblPlants:AT1G63700.1 GeneID:842674 KEGG:ath:AT1G63700 TAIR:At1g63700 InParanoid:Q9CAD5 OMA:PDHLSEE PhylomeDB:Q9CAD5 ProtClustDB:CLSN2682591 Genevestigator:Q9CAD5 Uniprot:Q9CAD5
Root	Isotig11603	1	27	-4.884	4.78E-08	UNIPROTKB|Q70KG3 - symbol:RAFTIN1B "Protein RAFTIN 1B" species:4565 "Triticum aestivum" [GO:0009555 "pollen development" evidence=ISS] [GO:0043668 "exine" evidence=IDA] GO:GO:0009555 InterPro:IPR004873 Pfam:PF03181 PROSITE:PS51277 GO:GO:0043668 EMBL:AJ575664 EMBL:AJ575665 UniGene:Ta.4176 Gramene:Q70KG3 Uniprot:Q70KG3
Root	Isotig11605	20	2	3.193	8.23E-05	TAIR|locus:2077517 - symbol:ADA2A "homolog of yeast ADA2 2A" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=IEA;ISS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0008270 "zinc ion binding" evidence=IEA] [GO:0009409 "response to cold" evidence=IMP] InterPro:IPR000433 InterPro:IPR001005 InterPro:IPR007526 InterPro:IPR009057 Pfam:PF00249 Pfam:PF00569 Pfam:PF04433 PROSITE:PS01357 PROSITE:PS50135 PROSITE:PS50934 SMART:SM00291 SMART:SM00717 GO:GO:0005634 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0006355 GO:GO:0003677 GO:GO:0008270 GO:GO:0006351 GO:GO:0009409 Gene3D:G3DSA:1.10.10.60 SUPFAM:SSF46689 eggNOG:COG5114 HOGENOM:HBG714058 KO:K11314 InterPro:IPR017884 InterPro:IPR016827 PIRSF:PIRSF025024 PROSITE:PS51293 OMA:CNETRIL EMBL:AC013483 EMBL:AC009176 EMBL:AF338769 EMBL:AY040045 EMBL:AF360246 EMBL:BX824819 EMBL:DR751137 EMBL:DR751119 IPI:IPI00530098 IPI:IPI00540890 RefSeq:NP_001078122.2 RefSeq:NP_566317.1 RefSeq:NP_974251.1 UniGene:At.18344 HSSP:O75478 ProteinModelPortal:Q9SFD5 SMR:Q9SFD5 IntAct:Q9SFD5 STRING:Q9SFD5 PRIDE:Q9SFD5 EnsemblPlants:AT3G07740.1 GeneID:819965 KEGG:ath:AT3G07740 TAIR:At3g07740 InParanoid:Q9SFD5 PhylomeDB:Q9SFD5 ProtClustDB:CLSN2688155 ArrayExpress:Q9SFD5 Genevestigator:Q9SFD5 Uniprot:Q9SFD5

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig11624	1	27	-4.884	4.78E-08	TAIR|locus:2023898 - symbol:AT1G13680 species:3702 "Arabidopsis thaliana" [GO:0004629 "phospholipase C activity" evidence=IEA] [GO:0006629 "lipid metabolic process" evidence=IEA] [GO:0008081 "phosphoric diester hydrolase activity" evidence=IEA] [GO:0035556 "intracellular signal transduction" evidence=IEA] InterPro:IPR000909 InterPro:IPR017946 Pfam:PF00388 PROSITE:PS50007 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0035556 EMBL:AC027656 Gene3D:G3DSA:3.20.20.190 SUPFAM:SSF51695 GO:GO:0004629 GO:GO:0006629 HOGENOM:HBG602506 IPI:IPI00531450 PIR:B86270 RefSeq:NP_172824.3 UniGene:At.42015 ProteinModelPortal:Q9LMX9 PRIDE:Q9LMX9 EnsemblPlants:AT1G13680.1 GeneID:837929 KEGG:ath:AT1G13680 TAIR:At1g13680 eggNOG:NOG256598 InParanoid:Q9LMX9 PhylomeDB:Q9LMX9 ProtClustDB:CLSN2684574 Genevestigator:Q9LMX9 Uniprot:Q9LMX9
Root	Isotig11640	0	23	-5.653	3.32E-07	TAIR|locus:2017943 - symbol:ABA3 "AT1G16540" species:3702 "Arabidopsis thaliana" [GO:0006950 "response to stress" evidence=IMP] [GO:0006970 "response to osmotic stress" evidence=IMP] [GO:0009409 "response to cold" evidence=IMP] [GO:0009651 "response to salt stress" evidence=IMP] [GO:0008265 "Mo-molybdopterin cofactor sulfurase activity" evidence=IDA] [GO:0018315 "molybdenum incorporation into molybdenum-molybdopterin complex" evidence=IDA] [GO:0010182 "sugar mediated signaling pathway" evidence=TAS] [GO:0009000 "selenocysteine lyase activity" evidence=IDA] [GO:0009734 "auxin mediated signaling pathway" evidence=IMP] [GO:0009408 "response to heat" evidence=IMP] [GO:0010118 "stomatal movement" evidence=IMP] [GO:0042742 "defense response to bacterium" evidence=IMP] [GO:0045037 "protein import into chloroplast stroma" evidence=IMP] [GO:0009688 "abscisic acid biosynthetic process" evidence=IMP] InterPro:IPR000192 InterPro:IPR005302 InterPro:IPR015421 Pfam:PF00266 Pfam:PF03473 PROSITE:PS51340 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0042742 GO:GO:0030170 InterPro:IPR015424 Gene3D:G3DSA:3.40.640.10 SUPFAM:SSF53383 GO:GO:0009734 GO:GO:0016740 GO:GO:0009409 GO:GO:0009651 GO:GO:0006777 GO:GO:0010118 GO:GO:0009688 GO:GO:0009408 GO:GO:0010182 PROSITE:PS00595 GO:GO:0030151 GO:GO:0045037 GO:GO:0009000 GO:GO:0018315 eggNOG:COG3217 GO:GO:0008265 InterPro:IPR005303 Pfam:PF03476 KO:K15631 OMA:CADRVNT HOGENOM:HBG389264 EMBL:AF325457 EMBL:AY034895 EMBL:AC011808 IPI:IPI00520223 PIR:G86300 RefSeq:NP_564001.1 UniGene:At.18927 ProteinModelPortal:Q9C5X8 STRING:Q9C5X8 PRIDE:Q9C5X8 EnsemblPlants:AT1G16540.1 GeneID:838224 KEGG:ath:AT1G16540 TAIR:At1g16540 InParanoid:Q9C5X8 PhylomeDB:Q9C5X8 ProtClustDB:PLN02724 Genevestigator:Q9C5X8 GermOnline:AT1G16540 Uniprot:Q9C5X8
Root	Isotig11647	2	14	-2.936	0.000925454	TAIR|locus:2181930 - symbol:AT5G11720 species:3702 "Arabidopsis thaliana" [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=IEA;ISS] [GO:0005975 "carbohydrate metabolic process" evidence=IEA] [GO:0005773 "vacuole" evidence=IDA] [GO:0009505 "plant-type cell wall" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] InterPro:IPR000322 InterPro:IPR011013 InterPro:IPR013785 Pfam:PF01055 PROSITE:PS00129 PROSITE:PS00707 GO:GO:0048046 GO:GO:0005773 EMBL:CP002688 Gene3D:G3DSA:3.20.20.70 InterPro:IPR017853 SUPFAM:SSF51445 GO:GO:0005975 GO:GO:0004553 GO:GO:0009505 CAZy:GH31 KO:K01187 GO:GO:0030246 PANTHER:PTHR22762 SUPFAM:SSF74650 EMBL:AL163814 ProtClustDB:CLSN2682302 EMBL:AY053414 EMBL:BT002222 IPI:IPI00538225 PIR:T48531 RefSeq:NP_196733.1 UniGene:At.5116 ProteinModelPortal:Q9LYF8 SMR:Q9LYF8 STRING:Q9LYF8 PRIDE:Q9LYF8 EnsemblPlants:AT5G11720.1 GeneID:831044 KEGG:ath:AT5G11720 TAIR:At5g11720 InParanoid:Q9LYF8 OMA:HGVFLRN PhylomeDB:Q9LYF8 Genevestigator:Q9LYF8 Uniprot:Q9LYF8
Root	Isotig11658	0	15	-5.036	4.38E-05	TAIR|locus:2143104 - symbol:AT5G12010 species:3702 "Arabidopsis thaliana" [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] GO:GO:0005886 GO:GO:0005774 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009507 EMBL:AL163812 eggNOG:NOG243843 EMBL:AY058074 EMBL:BT002297 IPI:IPI00541096 PIR:T48560 RefSeq:NP_196762.1 UniGene:At.5105 IntAct:Q9LYH2 PRIDE:Q9LYH2 EnsemblPlants:AT5G12010.1 GeneID:831074 KEGG:ath:AT5G12010 TAIR:At5g12010 HOGENOM:HBG590752 InParanoid:Q9LYH2 OMA:KEDTALR PhylomeDB:Q9LYH2 ProtClustDB:CLSN2686810 Genevestigator:Q9LYH2 Uniprot:Q9LYH2
Root	Isotig11661	0	17	-5.216	1.26E-05	TAIR|locus:2057873 - symbol:SCPL51 "serine carboxypeptidase-like 51" species:3702 "Arabidopsis thaliana" [GO:0004185 "serine-type carboxypeptidase activity" evidence=IEA;ISS] [GO:0006508 "proteolysis" evidence=IEA;ISS] InterPro:IPR001563 InterPro:IPR018202 Pfam:PF00450 PRINTS:PR00724 PROSITE:PS00131 PROSITE:PS00560 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0005576 GO:GO:0006508

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EMBL:AC006929 GO:GO:0004185 eggNOG:COG2939 PANTHER:PTHR11802 HOGENOM:HBG319189 KO:K09646 EMBL:AF412049 EMBL:BT003041 EMBL:AK175926 EMBL:AK176585 IPI:IPI00538546 IPI:IPI00657446 PIR:E84678 RefSeq:NP_001031434.1 RefSeq:NP_565663.1 UniGene:At.21190 ProteinModelPortal:Q67Y83 MEROPS:S10.017 PRIDE:Q67Y83 EnsemblPlants:AT2G27920.1 GeneID:817336 KEGG:ath:AT2G27920 TAIR:At2g27920 InParanoid:Q67Y83 OMA:GHMAPAD PhylomeDB:Q67Y83 ProtClustDB:CLSN2688493 Genevestigator:Q67Y83 Uniprot:Q67Y83
Root	Isotig11667	12	34	-1.631	0.000323514	TAIR|locus:2154664 - symbol:AT5G53850 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0008152 "metabolic process" evidence=IEA] [GO:0008967 "phosphoglycolate phosphatase activity" evidence=IEA] [GO:0016787 "hydrolase activity" evidence=ISS] [GO:0019509 "L-methionine salvage from methylthioadenosine" evidence=IEA] [GO:0043167 "ion binding" evidence=IEA] [GO:0043874 "acireductone synthase activity" evidence=IEA] [GO:0046570 "methylthioribulose 1-phosphate dehydratase activity" evidence=IEA] [GO:0046872 "metal ion binding" evidence=IEA] [GO:0071267 "L-methionine salvage" evidence=IEA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001303 InterPro:IPR006439 InterPro:IPR010041 InterPro:IPR017714 Pfam:PF00596 SMART:SM01007 GO:GO:0005829 GO:GO:0009570 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0046872 InterPro:IPR023214 Gene3D:G3DSA:3.40.50.1000 SUPFAM:SSF56784 GO:GO:0019509 Gene3D:G3DSA:3.40.225.10 SUPFAM:SSF53639 GO:GO:0008967 EMBL:AB007644 eggNOG:COG4229 KO:K09880 GO:GO:0043874 TIGRFAMs:TIGR01691 TIGRFAMs:TIGR01549 EMBL:BT012606 EMBL:BT015100 EMBL:AK229186 IPI:IPI00545376 RefSeq:NP_974931.1 UniGene:At.1147 UniGene:At.43395 ProteinModelPortal:Q9FN41 SMR:Q9FN41 STRING:Q9FN41 PRIDE:Q9FN41 EnsemblPlants:AT5G53850.2 GeneID:835466 KEGG:ath:AT5G53850 TAIR:At5g53850 InParanoid:Q9FN41 OMA:CAPLFMK PhylomeDB:Q9FN41 ProtClustDB:CLSN2680531 Genevestigator:Q9FN41 GO:GO:0046570 PANTHER:PTHR10640 TIGRFAMs:TIGR03328 Uniprot:Q9FN41
Root	Isotig11670	4	23	-2.653	5.61E-05	TAIR|locus:2009487 - symbol:AT1G22540 "AT1G22540" species:3702 "Arabidopsis thaliana" [GO:0005215 "transporter activity" evidence=ISS] [GO:0006857 "oligopeptide transport" evidence=IEA;ISS] [GO:0016020 "membrane" evidence=IEA;ISS] InterPro:IPR000109 InterPro:IPR018456 Pfam:PF00854 PROSITE:PS01022 PROSITE:PS01023 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005215 InterPro:IPR016196 SUPFAM:SSF103473 EMBL:AC006551 eggNOG:COG3104 GO:GO:0006857 EMBL:AK229285 EMBL:BT033034 IPI:IPI00541328 PIR:F86358 RefSeq:NP_173670.2 UniGene:At.41595 ProteinModelPortal:Q0WP01 PRIDE:Q0WP01 EnsemblPlants:AT1G22540.1 GeneID:838860 KEGG:ath:AT1G22540 TAIR:At1g22540 InParanoid:Q0WP01 OMA:FFCAGVG PhylomeDB:Q0WP01 ProtClustDB:CLSN2918218 Genevestigator:Q0WP01 Uniprot:Q0WP01
Root	Isotig11679	19	2	3.119	0.000146225	TAIR|locus:2025152 - symbol:AT1G75200 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0010181 "FMN binding" evidence=IEA] [GO:0016491 "oxidoreductase activity" evidence=IEA;ISS] [GO:0051536 "iron-sulfur cluster binding" evidence=IEA] InterPro:IPR001094 InterPro:IPR007197 InterPro:IPR008254 Pfam:PF00258 Pfam:PF04055 PRINTS:PR00369 PROSITE:PS50902 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005506 GO:GO:0016491 GO:GO:0051539 GO:GO:0008033 GO:GO:0010181 EMBL:AC025814 HSSP:P29476 KO:K15449 InterPro:IPR013917 Pfam:PF08608 EMBL:AY114005 EMBL:AY080784 IPI:IPI00547363 PIR:C96782 RefSeq:NP_177656.2 UniGene:At.34805 ProteinModelPortal:Q8RXN5 SMR:Q8RXN5 STRING:Q8RXN5 PRIDE:Q8RXN5 EnsemblPlants:AT1G75200.1 GeneID:843857 KEGG:ath:AT1G75200 TAIR:At1g75200 eggNOG:COG0731 HOGENOM:HBG628142 InParanoid:Q8RXN5 OMA:ERREMIT PhylomeDB:Q8RXN5 ProtClustDB:CLSN2690498 ArrayExpress:Q8RXN5 Genevestigator:Q8RXN5 Uniprot:Q8RXN5
Root	Isotig11698	3	18	-2.714	0.000308932	TAIR|locus:2027273 - symbol:AT1G74790 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0008150 "biological_process" evidence=ND] [GO:0031225 "anchored to membrane" evidence=TAS] [GO:0046658 "anchored to plasma membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] InterPro:IPR011041 InterPro:IPR012938 Pfam:PF07995 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005975 InterPro:IPR011042 Gene3D:G3DSA:2.120.10.30 GO:GO:0048038 GO:GO:0046658 EMBL:AC008263 SUPFAM:SSF50952 eggNOG:COG2133 GO:GO:0016901 IPI:IPI00522266 PIR:C96777 RefSeq:NP_177617.2 UniGene:At.43467 ProteinModelPortal:Q9SSG3 SMR:Q9SSG3 PRIDE:Q9SSG3 EnsemblPlants:AT1G74790.1 GeneID:843818 KEGG:ath:AT1G74790 TAIR:At1g74790

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						HOGENOM:HBG688942 InParanoid:Q9SSG3 OMA:YSDFGCC PhylomeDB:Q9SSG3 ProtClustDB:CLSN2687351 ArrayExpress:Q9SSG3 Genevestigator:Q9SSG3 GermOnline:AT1G74790 Uniprot:Q9SSG3
Root	Isotig11699	0	13	-4.829	0.000155955	TAIR|locus:2026177 - symbol:AT1G62660 species:3702 "Arabidopsis thaliana" [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=IEA;ISS] [GO:0071370 "cellular response to gibberellin stimulus" evidence=IEP] [GO:0000325 "plant-type vacuole" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0009617 "response to bacterium" evidence=IEP] InterPro:IPR001362 InterPro:IPR018053 InterPro:IPR021792 Pfam:PF11837 PROSITE:PS00609 SMART:SM00640 EMBL:CP002684 GO:GO:0005975 InterPro:IPR008985 SUPFAM:SSF49899 InterPro:IPR023296 SUPFAM:SSF75005 CAZy:GH32 KO:K01193 GO:GO:0004575 InterPro:IPR013189 InterPro:IPR013148 Pfam:PF08244 Pfam:PF00251 ProtClustDB:CLSN2687777 EMBL:AY048269 EMBL:AY062481 EMBL:AY063904 EMBL:AY114066 EMBL:X99111 IPI:IPI00517592 PIR:S71268 RefSeq:NP_564798.1 UniGene:At.24113 UniGene:At.67066 ProteinModelPortal:Q43348 SMR:Q43348 STRING:Q43348 PRIDE:Q43348 ProMEX:Q43348 EnsemblPlants:AT1G62660.1 GeneID:842563 KEGG:ath:AT1G62660 TAIR:At1g62660 InParanoid:Q43348 OMA:HSIVEGF PhylomeDB:Q43348 ArrayExpress:Q43348 Genevestigator:Q43348 Uniprot:Q43348
Root	Isotig11703	0	17	-5.216	1.26E-05	TAIR|locus:2207056 - symbol:AT1G72300 "AT1G72300" species:3702 "Arabidopsis thaliana" [GO:0004674 "protein serine/threonine kinase activity" evidence=ISS] [GO:0005524 "ATP binding" evidence=ISS] [GO:0005575 "cellular_component" evidence=ND] [GO:0006468 "protein phosphorylation" evidence=ISS] [GO:0007169 "transmembrane receptor protein tyrosine kinase signaling pathway" evidence=ISS] [GO:0001653 "peptide receptor activity" evidence=IMP] [GO:0004888 "transmembrane signaling receptor activity" evidence=IMP] [GO:0009611 "response to wounding" evidence=IGI] Pfam:PF00560 InterPro:IPR001611 InterPro:IPR000719 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 Pfam:PF00069 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 PROSITE:PS51450 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005886 GO:GO:0005524 GO:GO:0009611 eggNOG:COG0515 SUPFAM:SSF56112 GO:GO:0004674 HOGENOM:HBG755340 EMBL:AC067754 GO:GO:0004888 InterPro:IPR013210 Pfam:PF08263 HSSP:P58822 GO:GO:0001653 EMBL:AY080797 EMBL:AY133783 EMBL:AK229165 IPI:IPI00543488 PIR:G96746 RefSeq:NP_177374.1 UniGene:At.35115 ProteinModelPortal:Q9C7S5 SMR:Q9C7S5 PRIDE:Q9C7S5 EnsemblPlants:AT1G72300.1 GeneID:843562 KEGG:ath:AT1G72300 GeneFarm:2505 TAIR:At1g72300 InParanoid:Q9C7S5 OMA:MEKEFKA PhylomeDB:Q9C7S5 ProtClustDB:CLSN2679545 ArrayExpress:Q9C7S5 Genevestigator:Q9C7S5 Uniprot:Q9C7S5
Root	Isotig11717	0	13	-4.829	0.000155955	TAIR|locus:2184158 - symbol:SULTR2;1 "AT5G10180" species:3702 "Arabidopsis thaliana" [GO:0015116 "sulfate transmembrane transporter activity" evidence=IGI;ISS] [GO:0016020 "membrane" evidence=IEA] [GO:0016021 "integral to membrane" evidence=IEA] [GO:0008272 "sulfate transport" evidence=IGI] InterPro:IPR001902 InterPro:IPR011547 InterPro:IPR018045 Pfam:PF00916 PROSITE:PS01130 GO:GO:0016021 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0015293 EMBL:AL356332 GO:GO:0008271 InterPro:IPR002645 Gene3D:G3DSA:3.30.750.24 SUPFAM:SSF52091 PROSITE:PS50801 eggNOG:COG0659 Pfam:PF01740 TIGRFAMs:TIGR00815 HOGENOM:HBG554309 ProtClustDB:CLSN2685981 EMBL:AB003590 EMBL:AB003591 EMBL:AY062546 EMBL:AY093335 IPI:IPI00533684 PIR:T50022 RefSeq:NP_196580.1 UniGene:At.25140 ProteinModelPortal:O04722 SMR:O04722 IntAct:O04722 STRING:O04722 PRIDE:O04722 EnsemblPlants:AT5G10180.1 GeneID:830882 KEGG:ath:AT5G10180 GeneFarm:2356 TAIR:At5g10180 InParanoid:O04722 OMA:ATCAMIA PhylomeDB:O04722 ArrayExpress:O04722 Genevestigator:O04722 GermOnline:AT5G10180 Uniprot:O04722
Root	Isotig11721	2	19	-3.377	3.93E-05	TAIR|locus:2176912 - symbol:PKP-BETA1 "AT5G52920" species:3702 "Arabidopsis thaliana" [GO:0004743 "pyruvate kinase activity" evidence=ISS;IDA] [GO:0006096 "glycolysis" evidence=ISS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0000287 "magnesium ion binding" evidence=IDA] [GO:0010431 "seed maturation" evidence=IMP] [GO:0030955 "potassium ion binding" evidence=IDA] [GO:0006633 "fatty acid biosynthetic process" evidence=IMP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0048316 "seed development" evidence=IMP] [GO:0006629 "lipid metabolic process" evidence=IGI] [GO:0005829 "cytosol" evidence=RCA] InterPro:IPR001697 InterPro:IPR015793 InterPro:IPR015794 InterPro:IPR015806 InterPro:IPR015813 InterPro:IPR018209 Pfam:PF00224 PRINTS:PR01050 PROSITE:PS00110 Pfam:PF02887 GO:GO:0005739 GO:GO:0009570 GO:GO:0046686 EMBL:CP002688 GO:GO:0000287 GO:GO:0006633 EMBL:AB009055 GO:GO:0048316 Gene3D:G3DSA:3.20.20.60 SUPFAM:SSF51621 GO:GO:0006096 GO:GO:0030955 KO:K00873 GO:GO:0004743

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						InterPro:IPR011037 InterPro:IPR015795 Gene3D:G3DSA:2.40.33.10 Gene3D:G3DSA:3.40.1380.20 PANTHER:PTHR11817 SUPFAM:SSF50800 SUPFAM:SSF52935 TIGRFAMs:TIGR01064 HSSP:P14178 ProtClustDB:PLN02623 EMBL:AY084507 IPI:IPI00536297 RefSeq:NP_200104.1 UniGene:At.20836 ProteinModelPortal:Q9FLW9 SMR:Q9FLW9 STRING:Q9FLW9 PRIDE:Q9FLW9 EnsemblPlants:AT5G52920.1 GeneID:835369 KEGG:ath:AT5G52920 TAIR:At5g52920 InParanoid:Q9FLW9 OMA:YQGVCPI PhylomeDB:Q9FLW9 Genevestigator:Q9FLW9 Uniprot:Q9FLW9
Root	Isotig11738	70	0	7.000	6.85E-17	TAIR|locus:2052045 - symbol:NADP-ME1 "AT2G19900" species:3702 "Arabidopsis thaliana" [GO:0004470 "malic enzyme activity" evidence=ISS] [GO:0006108 "malate metabolic process" evidence=ISS;IDA] [GO:0016652 "oxidoreductase activity, acting on NADH or NADPH, NAD or NADP as acceptor" evidence=ISS] [GO:0004473 "malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+) activity" evidence=IDA] [GO:0005829 "cytosol" evidence=NAS] [GO:0051260 "protein homooligomerization" evidence=IDA] InterPro:IPR001891 InterPro:IPR012301 InterPro:IPR012302 InterPro:IPR015884 InterPro:IPR016040 Pfam:PF00390 Pfam:PF03949 PIRSF:PIRSF000106 PRINTS:PR00072 PROSITE:PS00331 SMART:SM00919 GO:GO:0005829 EMBL:CP002685 GenomeReviews:CT485783_GR Gene3D:G3DSA:3.40.50.720 GO:GO:0051287 GO:GO:0046872 GO:GO:0051260 EMBL:AC005169 GO:GO:0006108 eggNOG:COG0281 HOGENOM:HBG289821 GO:GO:0016619 Gene3D:G3DSA:3.40.50.10380 KO:K00029 GO:GO:0004473 HSSP:P40927 OMA:PAFMTEE EMBL:AY062734 EMBL:BT003371 IPI:IPI00545617 PIR:E84582 RefSeq:NP_179580.1 UniGene:At.27251 ProteinModelPortal:O82191 SMR:O82191 IntAct:O82191 STRING:O82191 PRIDE:O82191 EnsemblPlants:AT2G19900.1 GeneID:816509 KEGG:ath:AT2G19900 TAIR:At2g19900 InParanoid:O82191 PhylomeDB:O82191 ProtClustDB:PLN03129 ArrayExpress:O82191 Genevestigator:O82191 Uniprot:O82191
Root	Isotig11740	71	0	7.021	4.32E-17	SGD|S000028422 - symbol:TAR1 "Mitochondrial protein potentially involved in respiratory metabolism" species:4932 "Saccharomyces cerevisiae" [GO:0003674 "molecular_function" evidence=ND] [GO:0043457 "regulation of cellular respiration" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IEA;IMP] SGD:S000028422 GO:GO:0005739 EMBL:BK006945 EMBL:U53879 GO:GO:0043457 EMBL:Z73326 EMBL:AF479964 RefSeq:NP_690845.1 ProteinModelPortal:Q8TGM6 STRING:Q8TGM6 EnsemblFungi:YLR154W-C GeneID:1466405 KEGG:sce:YLR154W-C CYGD:YLR154w-c eggNOG:NOG79861 OMA:SCSKEHR OrthoDB:EOG466ZX8 NextBio:967146 Genevestigator:Q8TGM6 GermOnline:YLR154W-C Uniprot:Q8TGM6
Root	Isotig11747	2	16	-3.129	0.000262867	TAIR|locus:2139614 - symbol:BLH6 "AT4G34610" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] InterPro:IPR001356 InterPro:IPR008422 InterPro:IPR009057 Pfam:PF05920 PROSITE:PS00027 PROSITE:PS50071 SMART:SM00389 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005634 GO:GO:0043565 GO:GO:0003700 GO:GO:0006351 Gene3D:G3DSA:1.10.10.60 SUPFAM:SSF46689 EMBL:AL161585 EMBL:AL023094 InterPro:IPR006563 Pfam:PF07526 SMART:SM00574 HSSP:P55347 HOGENOM:HBG744945 EMBL:BT012291 IPI:IPI00523670 PIR:T05281 RefSeq:NP_001119116.1 RefSeq:NP_195187.1 UniGene:At.50395 UniGene:At.69176 ProteinModelPortal:O65685 SMR:O65685 IntAct:O65685 STRING:O65685 PRIDE:O65685 EnsemblPlants:AT4G34610.1 EnsemblPlants:AT4G34610.2 GeneID:829613 KEGG:ath:AT4G34610 GeneFarm:4052 TAIR:At4g34610 eggNOG:NOG331716 InParanoid:O65685 OMA:EFTENDS PhylomeDB:O65685 ProtClustDB:CLSN2683738 ArrayExpress:O65685 Genevestigator:O65685 Uniprot:O65685
Root	Isotig11751	0	18	-5.299	6.77E-06	TAIR|locus:2134093 - symbol:CCD8 "AT4G32810" species:3702 "Arabidopsis thaliana" [GO:0009507 "chloroplast" evidence=RCA;NAS] [GO:0009733 "response to auxin stimulus" evidence=IMP] [GO:0010223 "secondary shoot formation" evidence=IGI;IMP] [GO:0016702 "oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen" evidence=ISS] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0009850 "auxin metabolic process" evidence=IMP] [GO:0009965 "leaf morphogenesis" evidence=IMP] [GO:0016121 "carotene catabolic process" evidence=IDA] [GO:0016124 "xanthophyll catabolic process" evidence=IDA] [GO:0009926 "auxin polar transport" evidence=IMP] EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0009570 GO:GO:0009733 GO:GO:0009926 GO:GO:0046872 GO:GO:0016702 GO:GO:0009965 GO:GO:0010223 EMBL:AL161582 eggNOG:COG3670 HOGENOM:HBG446903 OMA:ITENYIV InterPro:IPR004294 PANTHER:PTHR10543 Pfam:PF03055 GO:GO:0016121 GO:GO:0016124 EMBL:AY074264 EMBL:AY133732 IPI:IPI00536697 PIR:T10688 RefSeq:NP_195007.2 UniGene:At.31633 ProteinModelPortal:Q8VY26 SMR:Q8VY26 STRING:Q8VY26 PRIDE:Q8VY26 EnsemblPlants:AT4G32810.1

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GeneID:829417 KEGG:ath:AT4G32810 TAIR:At4g32810 InParanoid:Q8VY26 PhylomeDB:Q8VY26 ProtClustDB:CLSN2680232 BioCyc:MetaCyc:AT4G32810-MONOMER Genevestigator:Q8VY26 Uniprot:Q8VY26
Root	Isotig11756	1	12	-3.714	0.000699736	TAIR|locus:2039074 - symbol:JAR1 "AT2G46370" species:3702 "Arabidopsis thaliana" [GO:0009733 "response to auxin stimulus" evidence=ISS] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0009585 "red, far-red light phototransduction" evidence=IMP] [GO:0009640 "photomorphogenesis" evidence=IMP] [GO:0071365 "cellular response to auxin stimulus" evidence=IEP] [GO:0010193 "response to ozone" evidence=IMP] [GO:0010046 "response to mycotoxin" evidence=IMP] [GO:0009861 "jasmonic acid and ethylene-dependent systemic resistance" evidence=IGI] [GO:0009753 "response to jasmonic acid stimulus" evidence=IMP] [GO:0003824 "catalytic activity" evidence=IDA] [GO:0005524 "ATP binding" evidence=ISS] [GO:0005773 "vacuole" evidence=IDA] [GO:0010119 "regulation of stomatal movement" evidence=IMP] [GO:2000377 "regulation of reactive oxygen species metabolic process" evidence=IMP] [GO:0009694 "jasmonic acid metabolic process" evidence=IMP] [GO:0080123 "jasmonate-amino synthetase activity" evidence=IDA] [GO:0010224 "response to UV-B" evidence=IMP] [GO:0031348 "negative regulation of defense response" evidence=IMP] [GO:0019899 "enzyme binding" evidence=IPI] [GO:2000030 "regulation of response to red or far red light" evidence=IMP] [GO:0070566 "adenylyltransferase activity" evidence=IDA] [GO:0009627 "systemic acquired resistance" evidence=IEP] [GO:0009611 "response to wounding" evidence=IEP] [GO:0009864 "induced systemic resistance, jasmonic acid mediated signaling pathway" evidence=IMP] Pfam:PF03321 GO:GO:0005773 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0019899 GO:GO:0031348 GO:GO:0010119 GO:GO:0009640 GO:GO:0009627 GO:GO:0010193 GO:GO:2000030 GO:GO:0009585 GO:GO:0071365 EMBL:AC006526 GO:GO:0010046 GO:GO:0010224 GO:GO:0009861 GO:GO:0009864 GO:GO:0070566 GO:GO:2000377 eggNOG:NOG86848 InterPro:IPR004993 EMBL:AF279129 EMBL:AY050861 EMBL:AY150437 EMBL:AK316746 EMBL:AK319095 EMBL:Z26804 EMBL:AK221189 IPI:IPI00535672 IPI:IPI00846498 IPI:IPI00973655 PIR:A84902 RefSeq:NP_001078069.1 RefSeq:NP_566071.1 RefSeq:NP_850453.1 UniGene:At.13902 ProteinModelPortal:Q9SKE2 STRING:Q9SKE2 PRIDE:Q9SKE2 EnsemblPlants:AT2G46370.1 EnsemblPlants:AT2G46370.2 GeneID:819244 KEGG:ath:AT2G46370 TAIR:At2g46370 InParanoid:Q9LKI2 KO:K14506 OMA:KYVYGIM PhylomeDB:Q9SKE2 ProtClustDB:CLSN2685940 Genevestigator:Q9SKE2 GO:GO:0080123 GO:GO:0009694 Uniprot:Q9SKE2
Root	Isotig11767	1	13	-3.829	0.000362856	TAIR|locus:2034476 - symbol:CYP97A3 "AT1G31800" species:3702 "Arabidopsis thaliana" [GO:0019825 "oxygen binding" evidence=ISS] [GO:0010291 "carotene beta-ring hydroxylase activity" evidence=IMP] [GO:0016117 "carotenoid biosynthetic process" evidence=IMP] [GO:0016123 "xanthophyll biosynthetic process" evidence=IGI] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] InterPro:IPR001128 InterPro:IPR002401 InterPro:IPR017972 Pfam:PF00067 PRINTS:PR00385 PRINTS:PR00463 PROSITE:PS00086 EMBL:CP002684 GO:GO:0009055 EMBL:AC079041 GO:GO:0031969 GO:GO:0020037 Gene3D:G3DSA:1.10.630.10 SUPFAM:SSF48264 GO:GO:0016117 GO:GO:0010291 GO:GO:0016705 HSSP:P14779 UniGene:At.48254 UniGene:At.71094 EMBL:AY056446 EMBL:AY058173 EMBL:AY142017 IPI:IPI00522598 PIR:F86441 RefSeq:NP_564384.1 ProteinModelPortal:Q93VK5 PRIDE:Q93VK5 EnsemblPlants:AT1G31800.1 GeneID:840067 KEGG:ath:AT1G31800 GeneFarm:1344 TAIR:At1g31800 InParanoid:Q93VK5 KO:K15747 OMA:DPSIAKH PhylomeDB:Q93VK5 ProtClustDB:PLN02738 Genevestigator:Q93VK5 Uniprot:Q93VK5
Root	Isotig11771	16	0	4.871	5.89E-05	TAIR|locus:2169749 - symbol:SS1 "starch synthase 1" species:3702 "Arabidopsis thaliana" [GO:0009011 "starch synthase activity" evidence=IEA] [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0009507 "chloroplast" evidence=IDA] [GO:0010021 "amylopectin biosynthetic process" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] InterPro:IPR001296 InterPro:IPR011835 Pfam:PF00534 GO:GO:0009570 EMBL:CP002688 GenomeReviews:BA000015_GR EMBL:AB006701 CAZy:GT5 InterPro:IPR013534 Pfam:PF08323 GO:GO:0009501 eggNOG:COG0297 HOGENOM:HBG596384 KO:K00703 GO:GO:0009011 TIGRFAMs:TIGR02095 OMA:PIVHEIG GO:GO:0010021 EMBL:AY128273 EMBL:AF121673 IPI:IPI00518916 RefSeq:NP_001190378.1 RefSeq:NP_197818.1 UniGene:At.22528 ProteinModelPortal:Q9FNF2 SMR:Q9FNF2 STRING:Q9FNF2 PRIDE:Q9FNF2 EnsemblPlants:AT5G24300.1 EnsemblPlants:AT5G24300.2 GeneID:832497 KEGG:ath:AT5G24300 TAIR:At5g24300 InParanoid:Q9FNF2 PhylomeDB:Q9FNF2 ProtClustDB:CLSN2686324 ArrayExpress:Q9FNF2 Genevestigator:Q9FNF2 GermOnline:AT5G24300 Uniprot:Q9FNF2
Root	Isotig11774	60	1	5.778	3.13E-15	TAIR|locus:2052045 - symbol:NADP-ME1 "AT2G19900" species:3702 "Arabidopsis thaliana" [GO:0004470 "malic enzyme activity" evidence=ISS] [GO:0006108 "malate metabolic process" evidence=ISS;IDA] [GO:0016652

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						"oxidoreductase activity, acting on NADH or NADPH, NAD or NADP as acceptor" evidence=ISS] [GO:0004473 "malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+) activity" evidence=IDA] [GO:0005829 "cytosol" evidence=NAS] [GO:0051260 "protein homooligomerization" evidence=IDA] InterPro:IPR001891 InterPro:IPR012301 InterPro:IPR012302 InterPro:IPR015884 InterPro:IPR016040 Pfam:PF00390 Pfam:PF03949 PIRSF:PIRSF000106 PRINTS:PR00072 PROSITE:PS00331 SMART:SM00919 GO:GO:0005829 EMBL:CP002685 GenomeReviews:CT485783_GR Gene3D:G3DSA:3.40.50.720 GO:GO:0051287 GO:GO:0046872 GO:GO:0051260 EMBL:AC005169 GO:GO:0006108 eggNOG:COG0281 HOGENOM:HBG289821 GO:GO:0016619 Gene3D:G3DSA:3.40.50.10380 KO:K00029 GO:GO:0004473 HSSP:P40927 OMA:PAFMTEE EMBL:AY062734 EMBL:BT003371 IPI:IPI00545617 PIR:E84582 RefSeq:NP_179580.1 UniGene:At.27251 ProteinModelPortal:O82191 SMR:O82191 IntAct:O82191 STRING:O82191 PRIDE:O82191 EnsemblPlants:AT2G19900.1 GeneID:816509 KEGG:ath:AT2G19900 TAIR:At2g19900 InParanoid:O82191 PhylomeDB:O82191 ProtClustDB:PLN03129 ArrayExpress:O82191 Genevestigator:O82191 Uniprot:O82191
Root	Isotig11784	26	2	3.571	2.56E-06	SGD|S000028422 - symbol:TAR1 "Mitochondrial protein potentially involved in respiratory metabolism" species:4932 "Saccharomyces cerevisiae" [GO:0003674 "molecular_function" evidence=ND] [GO:0043457 "regulation of cellular respiration" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IEA;IMP] SGD:S000028422 GO:GO:0005739 EMBL:BK006945 EMBL:U53879 GO:GO:0043457 EMBL:Z73326 EMBL:AF479964 RefSeq:NP_690845.1 ProteinModelPortal:Q8TGM6 STRING:Q8TGM6 EnsemblFungi:YLR154W-C GeneID:1466405 KEGG:sce:YLR154W-C CYGD:YLR154w-c eggNOG:NOG79861 OMA:SCSKEHR OrthoDB:EOG466ZX8 NextBio:967146 Genevestigator:Q8TGM6 GermOnline:YLR154W-C Uniprot:Q8TGM6
Root	Isotig11796	16	0	4.871	5.89E-05	TAIR|locus:2045457 - symbol:HSP70T-2 "heat-shock protein 70T-2" species:3702 "Arabidopsis thaliana" [GO:0005524 "ATP binding" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0006457 "protein folding" evidence=TAS] [GO:0009408 "response to heat" evidence=IEP] [GO:0009644 "response to high light intensity" evidence=IEP] [GO:0042542 "response to hydrogen peroxide" evidence=IEP] InterPro:IPR001023 PRINTS:PR00301 Pfam:PF00012 Prosite:PS00297 Prosite:PS00329 Prosite:PS01036 GO:GO:0005524 EMBL:CP002685 GO:GO:0006950 GO:GO:0009408 GO:GO:0009644 GO:GO:0042542 HSSP:P19120 eggNOG:COG0443 InterPro:IPR018181 InterPro:IPR013126 PANTHER:PTHR19375 EMBL:AC006223 EMBL:AY123990 EMBL:BT001079 EMBL:AY088895 IPI:IPI00520528 PIR:B84729 RefSeq:NP_180771.1 RefSeq:NP_850183.1 UniGene:At.13604 ProteinModelPortal:Q9SKY8 SMR:Q9SKY8 STRING:Q9SKY8 PRIDE:Q9SKY8 EnsemblPlants:AT2G32120.1 EnsemblPlants:AT2G32120.2 GeneID:817771 KEGG:ath:AT2G32120 TAIR:At2g32120 InParanoid:Q9SKY8 OMA:HVLRLMP PhylomeDB:Q9SKY8 ProtClustDB:CLSN2683276 ArrayExpress:Q9SKY8 Genevestigator:Q9SKY8 Uniprot:Q9SKY8
Root	Isotig11798	9	27	-1.714	0.000905257	TAIR|locus:2181422 - symbol:PGLCT "AT5G16150" species:3702 "Arabidopsis thaliana" [GO:0005351 "sugar:hydrogen symporter activity" evidence=ISS] [GO:0015144 "carbohydrate transmembrane transporter activity" evidence=ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0009941 "chloroplast envelope" evidence=IDA] InterPro:IPR003663 InterPro:IPR005828 InterPro:IPR005829 Pfam:PF00083 PRINTS:PR00171 PROSITE:PS00216 PROSITE:PS00217 GO:GO:0016021 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009706 eggNOG:COG0477 InterPro:IPR016196 SUPFAM:SSF103473 GO:GO:0008643 InterPro:IPR020846 PROSITE:PS50850 HOGENOM:HBG744444 GO:GO:0022891 TIGRFAMs:TIGR00879 EMBL:AL391148 EMBL:AY058152 EMBL:AY091052 EMBL:AY117359 EMBL:AF215855 EMBL:AK220813 IPI:IPI00547703 PIR:T51485 RefSeq:NP_568328.1 RefSeq:NP_850828.1 RefSeq:NP_974787.1 UniGene:At.49028 UniGene:At.9990 ProteinModelPortal:Q56ZZ7 IntAct:Q56ZZ7 PRIDE:Q56ZZ7 EnsemblPlants:AT5G16150.1 EnsemblPlants:AT5G16150.2 EnsemblPlants:AT5G16150.3 GeneID:831472 KEGG:ath:AT5G16150 TAIR:At5g16150 InParanoid:Q56ZZ7 OMA:GSVNQLF PhylomeDB:Q56ZZ7 ProtClustDB:CLSN2689710 ArrayExpress:Q93Z41 Genevestigator:Q56ZZ7 Uniprot:Q56ZZ7
Root	Isotig11811	25	1	4.515	7.40E-07	TAIR|locus:2028275 - symbol:AT1G45150 "AT1G45150" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002684 GenomeReviews:CT485782_GR EMBL:BT008320 EMBL:AK227318 IPI:IPI00523041 RefSeq:NP_175129.3 UniGene:At.38729 PRIDE:Q7Y231 EnsemblPlants:AT1G45150.1 GeneID:841083 KEGG:ath:AT1G45150 TAIR:At1g45150 eggNOG:NOG119415 HOGENOM:HBG320113 InParanoid:Q7Y231 OMA:LQYRISP PhylomeDB:Q7Y231 ProtClustDB:CLSN2680742 Genevestigator:Q7Y231 InterPro:IPR025150 Pfam:PF13320 Uniprot:Q7Y231

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig11832	23	3	2.810	7.16E-05	TAIR|locus:505006397 - symbol:ABCF4 "AT3G54540" species:3702 "Arabidopsis thaliana" [GO:0005215 "transporter activity" evidence=ISS] InterPro:IPR003439 InterPro:IPR003593 InterPro:IPR017871 Pfam:PF00005 PROSITE:PS00211 PROSITE:PS50893 SMART:SM00382 GO:GO:0005524 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0006810 GO:GO:0016887 eggNOG:COG0488 EMBL:AL138656 EMBL:AY054525 EMBL:BT008795 EMBL:AK317763 EMBL:AY084906 IPI:IPI00535499 PIR:T47613 RefSeq:NP_567001.1 UniGene:At.1464 UniGene:At.67029 ProteinModelPortal:Q9M1H3 SMR:Q9M1H3 PRIDE:Q9M1H3 EnsemblPlants:AT3G54540.1 GeneID:824619 KEGG:ath:AT3G54540 TAIR:At3g54540 InParanoid:Q9M1H3 KO:K06184 OMA:ISHGRRY PhylomeDB:Q9M1H3 ProtClustDB:CLSN2689163 Genevestigator:Q9M1H3 Uniprot:Q9M1H3
Root	Isotig11859	22	103	-2.356	1.56E-15	SGD|S000028422 - symbol:TAR1 "Mitochondrial protein potentially involved in respiratory metabolism" species:4932 "Saccharomyces cerevisiae" [GO:0003674 "molecular_function" evidence=ND] [GO:0043457 "regulation of cellular respiration" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IEA;IMP] SGD:S000028422 GO:GO:0005739 EMBL:BK006945 EMBL:U53879 GO:GO:0043457 EMBL:Z73326 EMBL:AF479964 RefSeq:NP_690845.1 ProteinModelPortal:Q8TGM6 STRING:Q8TGM6 EnsemblFungi:YLR154W-C GeneID:1466405 KEGG:sce:YLR154W-C CYGD:YLR154w-c eggNOG:NOG79861 OMA:SCSKEHR OrthoDB:EOG466ZX8 NextBio:967146 Genevestigator:Q8TGM6 GermOnline:YLR154W-C Uniprot:Q8TGM6
Root	Isotig11861	0	17	-5.216	1.26E-05	TAIR|locus:2033760 - symbol:PKp3 "AT1G32440" species:3702 "Arabidopsis thaliana" [GO:0004743 "pyruvate kinase activity" evidence=ISS;IDA] [GO:0006096 "glycolysis" evidence=ISS] [GO:0000287 "magnesium ion binding" evidence=IDA] [GO:0006633 "fatty acid biosynthetic process" evidence=IGI] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0030955 "potassium ion binding" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] InterPro:IPR001697 InterPro:IPR015793 InterPro:IPR015794 InterPro:IPR015806 InterPro:IPR015813 InterPro:IPR018209 Pfam:PF00224 PRINTS:PR01050 PROSITE:PS00110 Pfam:PF02887 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009570 GO:GO:0000287 GO:GO:0006633 Gene3D:G3DSA:3.20.20.60 SUPFAM:SSF51621 GO:GO:0006096 GO:GO:0030955 eggNOG:COG0469 HOGENOM:HBG734376 KO:K00873 GO:GO:0004743 InterPro:IPR011037 InterPro:IPR015795 Gene3D:G3DSA:2.40.33.10 Gene3D:G3DSA:3.40.1380.20 PANTHER:PTHR11817 SUPFAM:SSF50800 SUPFAM:SSF52935 TIGRFAMs:TIGR01064 HSSP:P14178 EMBL:AY058121 EMBL:BT001147 IPI:IPI00519857 RefSeq:NP_564402.1 UniGene:At.66798 ProteinModelPortal:Q93Z53 STRING:Q93Z53 PRIDE:Q93Z53 EnsemblPlants:AT1G32440.1 GeneID:840138 KEGG:ath:AT1G32440 TAIR:At1g32440 InParanoid:Q93Z53 OMA:KPSIVAT PhylomeDB:Q93Z53 ProtClustDB:PLN02623 Genevestigator:Q93Z53 Uniprot:Q93Z53
Root	Isotig11863	2	23	-3.653	3.09E-06	TAIR|locus:2175503 - symbol:CPK1 "AT5G04870" species:3702 "Arabidopsis thaliana" [GO:0004683 "calmodulin-dependent protein kinase activity" evidence=ISS] [GO:0006468 "protein phosphorylation" evidence=ISS;IDA] [GO:0016020 "membrane" evidence=NAS] [GO:0016301 "kinase activity" evidence=ISS] [GO:0005777 "peroxisome" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0004674 "protein serine/threonine kinase activity" evidence=IDA] [GO:0046777 "protein autophosphorylation" evidence=IDA] InterPro:IPR000719 InterPro:IPR002048 InterPro:IPR002290 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR011992 InterPro:IPR017441 Pfam:PF00069 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 SMART:SM00054 SMART:SM00220 Prosite:PS00018 Pfam:PF00036 GO:GO:0005524 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005509 GO:GO:0005515 eggNOG:COG0515 SUPFAM:SSF56112 GO:GO:0004674 InterPro:IPR018247 InterPro:IPR018249 Gene3D:G3DSA:1.10.238.10 PROSITE:PS50222 GO:GO:0046777 HOGENOM:HBG755340 BRENDA:2.7.11.1 GO:GO:0005778 InterPro:IPR018248 EMBL:AB008271 EMBL:L14771 EMBL:AK118706 EMBL:BT005932 IPI:IPI00545385 PIR:A49082 RefSeq:NP_196107.1 UniGene:At.293 PDB:2AAO PDBsum:2AAO ProteinModelPortal:Q06850 SMR:Q06850 IntAct:Q06850 STRING:Q06850 PRIDE:Q06850 EnsemblPlants:AT5G04870.1 GeneID:830366 KEGG:ath:AT5G04870 TAIR:At5g04870 InParanoid:Q06850 KO:K13412 OMA:KREILIM PhylomeDB:Q06850 ProtClustDB:CLSN2684030 ArrayExpress:Q06850 Genevestigator:Q06850 GermOnline:AT5G04870 Uniprot:Q06850
Root	Isotig11874	25	79	-1.789	4.97E-09	TAIR|locus:504956338 - symbol:AT5G08680 "AT5G08680" species:3702 "Arabidopsis thaliana" [GO:0046933 "hydrogen ion transporting ATP synthase activity, rotational mechanism" evidence=ISS] [GO:0000275 "mitochondrial proton-transporting ATP synthase complex, catalytic core F(1)" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005753 "mitochondrial proton-transporting ATP

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						synthase complex" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR000194 InterPro:IPR000793 InterPro:IPR003593 InterPro:IPR004100 InterPro:IPR005722 InterPro:IPR018118 InterPro:IPR020003 InterPro:IPR020971 Pfam:PF00006 Pfam:PF00306 Pfam:PF02874 Pfam:PF11421 PROSITE:PS00152 SMART:SM00382 GO:GO:0005524 GO:GO:0046686 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005507 EMBL:AL590346 GO:GO:0015991 GO:GO:0046933 GO:GO:0046961 GO:GO:0015986 GO:GO:0008553 SUPFAM:SSF50615 SUPFAM:SSF47917 HOGENOM:HBG565875 eggNOG:COG0055 KO:K02133 ProtClustDB:CLSN2689552 InterPro:IPR024034 Gene3D:G3DSA:1.10.1140.10 PANTHER:PTHR15184:SF8 TIGRFAMs:TIGR01039 UniGene:At.56834 EMBL:AK117922 EMBL:BT005920 IPI:IPI00517502 RefSeq:NP_680155.1 UniGene:At.45855 ProteinModelPortal:Q9C5A9 SMR:Q9C5A9 IntAct:Q9C5A9 STRING:Q9C5A9 PRIDE:Q9C5A9 EnsemblPlants:AT5G08680.1 GeneID:830769 KEGG:ath:AT5G08680 GeneFarm:2019 TAIR:At5g08680 InParanoid:Q9C5A9 OMA:NGNIVQC PhylomeDB:Q9C5A9 Genevestigator:Q9C5A9 GermOnline:AT5G08680 Uniprot:Q9C5A9
Root	Isotig11877	1	25	-4.773	1.66E-07	TAIR|locus:2037042 - symbol:AT1G53050 species:3702 "Arabidopsis thaliana" [GO:0004672 "protein kinase activity" evidence=IEA] [GO:0004674 "protein serine/threonine kinase activity" evidence=IEA] [GO:0005524 "ATP binding" evidence=IEA] [GO:0006468 "protein phosphorylation" evidence=IEA] [GO:0016301 "kinase activity" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] InterPro:IPR000719 InterPro:IPR002290 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 Pfam:PF00069 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 SMART:SM00220 EMBL:CP002684 GO:GO:0005886 GO:GO:0005524 SUPFAM:SSF56112 GO:GO:0004674 EMBL:AC022520 HSSP:P24941 IPI:IPI00517407 PIR:A96571 RefSeq:NP_175713.1 UniGene:At.16235 ProteinModelPortal:Q9LNN0 SMR:Q9LNN0 PRIDE:Q9LNN0 EnsemblPlants:AT1G53050.1 GeneID:841739 KEGG:ath:AT1G53050 TAIR:At1g53050 InParanoid:Q9LNN0 OMA:GSKGHKI PhylomeDB:Q9LNN0 ProtClustDB:CLSN2679776 Genevestigator:Q9LNN0 Uniprot:Q9LNN0
Root	Isotig11882	20	1	4.193	1.37E-05	SGD|S000028422 - symbol:TAR1 "Mitochondrial protein potentially involved in respiratory metabolism" species:4932 "Saccharomyces cerevisiae" [GO:0003674 "molecular_function" evidence=ND] [GO:0043457 "regulation of cellular respiration" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IEA;IMP] SGD:S000028422 GO:GO:0005739 EMBL:BK006945 EMBL:U53879 GO:GO:0043457 EMBL:Z73326 EMBL:AF479964 RefSeq:NP_690845.1 ProteinModelPortal:Q8TGM6 STRING:Q8TGM6 EnsemblFungi:YLR154W-C GeneID:1466405 KEGG:sce:YLR154W-C CYGD:YLR154w-c eggNOG:NOG79861 OMA:SCSKEHR OrthoDB:EOG466ZX8 NextBio:967146 Genevestigator:Q8TGM6 GermOnline:YLR154W-C Uniprot:Q8TGM6
Root	Isotig11898	4	24	-2.714	3.10E-05	TAIR|locus:2195995 - symbol:STP14 "AT1G77210" species:3702 "Arabidopsis thaliana" [GO:0005351 "sugar:hydrogen symporter activity" evidence=ISS] [GO:0006810 "transport" evidence=IEA] [GO:0015144 "carbohydrate transmembrane transporter activity" evidence=ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0055085 "transmembrane transport" evidence=IEA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005354 "galactose transmembrane transporter activity" evidence=IGI] InterPro:IPR003663 InterPro:IPR005828 InterPro:IPR005829 Pfam:PF00083 PRINTS:PR00171 PROSITE:PS00216 PROSITE:PS00217 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005886 EMBL:AC004260 GO:GO:0015293 eggNOG:COG0477 InterPro:IPR016196 SUPFAM:SSF103473 InterPro:IPR020846 PROSITE:PS50850 HOGENOM:HBG744444 TIGRFAMs:TIGR00879 GO:GO:0005354 EMBL:AJ344334 EMBL:AK119057 EMBL:BT005887 IPI:IPI00519843 PIR:T00450 RefSeq:NP_001185417.1 RefSeq:NP_177845.1 UniGene:At.10767 ProteinModelPortal:Q8GW61 IntAct:Q8GW61 PRIDE:Q8GW61 EnsemblPlants:AT1G77210.1 EnsemblPlants:AT1G77210.2 GeneID:844057 KEGG:ath:AT1G77210 TAIR:At1g77210 InParanoid:Q8GW61 OMA:LEASVEM PhylomeDB:Q8GW61 ProtClustDB:CLSN2682974 Genevestigator:Q8GW61 GermOnline:AT1G77210 Uniprot:Q8GW61
Root	Isotig11904	5	20	-2.129	0.000961902	TAIR|locus:2058754 - symbol:AT2G35710 "AT2G35710" species:3702 "Arabidopsis thaliana" [GO:0009058 "biosynthetic process" evidence=ISS] [GO:0016051 "carbohydrate biosynthetic process" evidence=ISS] [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0016758 "transferase activity, transferring hexosyl groups" evidence=ISS] InterPro:IPR002495 Pfam:PF01501 EMBL:CP002685 GO:GO:0016757 CAZy:GT8 HSSP:P13280 EMBL:AY063949 EMBL:AY096617 IPI:IPI00532801 RefSeq:NP_565817.2 UniGene:At.27134 UniGene:At.68104 ProteinModelPortal:Q8VZP6 STRING:Q8VZP6 PRIDE:Q8VZP6 EnsemblPlants:AT2G35710.1 GeneID:818140 KEGG:ath:AT2G35710 TAIR:At2g35710 InParanoid:Q8VZP6 OMA:AYAFCCA PhylomeDB:Q8VZP6 ProtClustDB:CLSN2681197 Genevestigator:Q8VZP6 Uniprot:Q8VZP6

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig11910	1	16	-4.129	5.13E-05	TAIR|locus:2074755 - symbol:AT3G50170 "AT3G50170" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] InterPro:IPR004158 EMBL:CP002686 EMBL:AL132978 EMBL:AL132976 Pfam:PF03140 IPI:IPI00543335 PIR:T45563 RefSeq:NP_190586.1 UniGene:At.51001 PRIDE:Q9S7S4 EnsemblPlants:AT3G50170.1 GeneID:824179 KEGG:ath:AT3G50170 TAIR:At3g50170 InParanoid:Q9S7S4 OMA:ESSNHIT PhylomeDB:Q9S7S4 ProtClustDB:CLSN2684391 Genevestigator:Q9S7S4 Uniprot:Q9S7S4
Root	Isotig11923	29	4	2.729	1.12E-05	TAIR|locus:2161398 - symbol:DELTA-OAT "AT5G46180" species:3702 "Arabidopsis thaliana" [GO:0004587 "ornithine-oxo-acid transaminase activity" evidence=ISS;IMP] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0006561 "proline biosynthetic process" evidence=IDA;IMP] [GO:0006593 "ornithine catabolic process" evidence=IMP] [GO:0019544 "arginine catabolic process to glutamate" evidence=IMP] [GO:0008270 "zinc ion binding" evidence=IDA] [GO:0042538 "hyperosmotic salinity response" evidence=IDA] InterPro:IPR005814 InterPro:IPR010164 InterPro:IPR015421 InterPro:IPR015422 Pfam:PF00202 PROSITE:PS00600 GO:GO:0005739 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0030170 InterPro:IPR015424 Gene3D:G3DSA:3.40.640.10 Gene3D:G3DSA:3.90.1150.10 SUPFAM:SSF53383 GO:GO:0008270 GO:GO:0006561 HOGENOM:HBG725944 GO:GO:0019544 PANTHER:PTHR11986 EMBL:AB006698 GO:GO:0042538 eggNOG:COG4992 GO:GO:0006593 KO:K00819 GO:GO:0004587 PANTHER:PTHR11986:SF18 TIGRFAMs:TIGR01885 HSSP:P04181 OMA:VWDPEGK EMBL:BT023421 EMBL:BT029160 IPI:IPI00519266 RefSeq:NP_199430.1 UniGene:At.28104 ProteinModelPortal:Q9FNK4 SMR:Q9FNK4 STRING:Q9FNK4 PRIDE:Q9FNK4 EnsemblPlants:AT5G46180.1 GeneID:834660 KEGG:ath:AT5G46180 TAIR:At5g46180 InParanoid:Q9FNK4 PhylomeDB:Q9FNK4 ProtClustDB:PLN02624 Genevestigator:Q9FNK4 Uniprot:Q9FNK4
Root	Isotig11931	3	22	-3.003	2.69E-05	TAIR|locus:2133737 - symbol:CINV2 "AT4G09510" species:3702 "Arabidopsis thaliana" [GO:0004564 "beta-fructofuranosidase activity" evidence=IGI;ISS] [GO:0005829 "cytosol" evidence=NAS] [GO:0005987 "sucrose catabolic process" evidence=IGI] [GO:0048364 "root development" evidence=IGI] InterPro:IPR008928 InterPro:IPR024746 Pfam:PF12899 GO:GO:0005829 EMBL:CP002687 GO:GO:0048364 SUPFAM:SSF48208 GO:GO:0005987 GO:GO:0033926 EMBL:AK176880 IPI:IPI00531622 RefSeq:NP_567347.1 UniGene:At.33690 ProteinModelPortal:Q67XD9 STRING:Q67XD9 CAZy:GH100 PRIDE:Q67XD9 EnsemblPlants:AT4G09510.1 GeneID:826535 KEGG:ath:AT4G09510 TAIR:At4g09510 eggNOG:NOG04872 InParanoid:Q67XD9 OMA:SEMDDFD PhylomeDB:Q67XD9 ProtClustDB:PLN03005 Genevestigator:Q67XD9 GO:GO:0004564 Uniprot:Q67XD9
Root	Isotig11947	16	42	-1.521	0.000145653	TAIR|locus:2008920 - symbol:AT1G12000 "AT1G12000" species:3702 "Arabidopsis thaliana" [GO:0006096 "glycolysis" evidence=ISS] [GO:0010318 "pyrophosphate-dependent phosphofructokinase complex, beta-subunit complex" evidence=ISS] [GO:0047334 "diphosphate-fructose-6-phosphate 1-phosphotransferase activity" evidence=ISS;IMP] [GO:0005618 "cell wall" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0016020 "membrane" evidence=IDA] [GO:0015979 "photosynthesis" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR000023 InterPro:IPR011183 InterPro:IPR013981 Pfam:PF00365 PIRSF:PIRSF005677 EMBL:CP002684 GO:GO:0005524 GO:GO:0046686 GO:GO:0005618 GO:GO:0016020 GO:GO:0006096 GO:GO:0015979 GO:GO:0005945 GO:GO:0003872 InterPro:IPR022953 PRINTS:PR00476 SUPFAM:SSF53784 HSSP:P70826 GO:GO:0047334 Gene3D:G3DSA:1.10.10.480 TIGRFAMs:TIGR02477 EMBL:AY062473 EMBL:AY093260 IPI:IPI00529076 RefSeq:NP_172664.1 UniGene:At.21087 ProteinModelPortal:Q8W4M5 SMR:Q8W4M5 STRING:Q8W4M5 PRIDE:Q8W4M5 EnsemblPlants:AT1G12000.1 GeneID:837752 KEGG:ath:AT1G12000 TAIR:At1g12000 InParanoid:Q8W4M5 KO:K00895 OMA:GNVRVSK PhylomeDB:Q8W4M5 ProtClustDB:PLN02251 ArrayExpress:Q8W4M5 Genevestigator:Q8W4M5 Uniprot:Q8W4M5
Root	Isotig11950	0	32	-6.129	1.84E-09	TAIR|locus:2039954 - symbol:CYP78A6 "cytochrome P450, family 78, subfamily A, polypeptide 6" species:3702 "Arabidopsis thaliana" [GO:0004497 "monooxygenase activity" evidence=IEA] [GO:0005506 "iron ion binding" evidence=IEA] [GO:0009055 "electron carrier activity" evidence=IEA] [GO:0019825 "oxygen binding" evidence=ISS] [GO:0020037 "heme binding" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] InterPro:IPR001128 InterPro:IPR002401 InterPro:IPR017972 Pfam:PF00067 PRINTS:PR00385 PRINTS:PR00463 PROSITE:PS00086 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009055 GO:GO:0004497 eggNOG:COG2124 GO:GO:0020037 Gene3D:G3DSA:1.10.630.10 SUPFAM:SSF48264 EMBL:AC006418 EMBL:AC005819 GO:GO:0016705 HOGENOM:HBG749920 ProtClustDB:CLSN2682843 EMBL:AK226763 IPI:IPI00519585 PIR:F84905 RefSeq:NP_182189.1 UniGene:At.36480 ProteinModelPortal:Q9ZNR0 SMR:Q9ZNR0 PRIDE:Q9ZNR0 EnsemblPlants:AT2G46660.1 GeneID:819278 KEGG:ath:AT2G46660 TAIR:At2g46660

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						InParanoid:Q9ZNR0 OMA:TLAHRRI PhylomeDB:Q9ZNR0 ArrayExpress:Q9ZNR0 Genevestigator:Q9ZNR0 Uniprot:Q9ZNR0
Root	Isotig11952	0	15	-5.036	4.38E-05	TAIR|locus:2091496 - symbol:BGAL1 "AT3G13750" species:3702 "Arabidopsis thaliana" [GO:0004565 "beta-galactosidase activity" evidence=ISS;IDA] [GO:0005975 "carbohydrate metabolic process" evidence=IEA] [GO:0005618 "cell wall" evidence=IDA] [GO:0009505 "plant-type cell wall" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR001944 InterPro:IPR013781 InterPro:IPR019801 Pfam:PF01301 PRINTS:PR00742 PROSITE:PS00435 PROSITE:PS01182 GO:GO:0009506 GO:GO:0048046 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0043169 InterPro:IPR017853 Gene3D:G3DSA:3.20.20.80 SUPFAM:SSF51445 GO:GO:0005975 GO:GO:0005529 EMBL:AP001307 GO:GO:0009505 InterPro:IPR008979 SUPFAM:SSF49785 CAZy:GH35 eggNOG:COG1874 HOGENOM:HBG318019 GO:GO:0004565 PANTHER:PTHR23421 InterPro:IPR000922 Pfam:PF02140 PROSITE:PS50228 EMBL:AJ270297 EMBL:AY093197 EMBL:AK222229 IPI:IPI00516654 RefSeq:NP_187988.1 UniGene:At.21793 UniGene:At.67729 ProteinModelPortal:Q9SCW1 SMR:Q9SCW1 IntAct:Q9SCW1 STRING:Q9SCW1 PRIDE:Q9SCW1 EnsemblPlants:AT3G13750.1 GeneID:820584 KEGG:ath:AT3G13750 GeneFarm:485 TAIR:At3g13750 InParanoid:Q9SCW1 OMA:SWQAYNE PhylomeDB:Q9SCW1 ProtClustDB:CLSN2684807 ArrayExpress:Q8RWC1 Genevestigator:Q9SCW1 Uniprot:Q9SCW1
Root	Isotig11958	5	41	-3.165	4.30E-09	TAIR|locus:2121929 - symbol:PGI1 "AT4G24620" species:3702 "Arabidopsis thaliana" [GO:0004347 "glucose-6-phosphate isomerase activity" evidence=ISS] [GO:0005982 "starch metabolic process" evidence=IMP] [GO:0009536 "plastid" evidence=ISS] [GO:0009911 "positive regulation of flower development" evidence=IMP] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] HAMAP:MF_00473 InterPro:IPR001672 InterPro:IPR018189 Pfam:PF00342 PRINTS:PR00662 PROSITE:PS00174 PROSITE:PS51463 GO:GO:0005829 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0009570 GO:GO:0009941 GO:GO:0006094 GO:GO:0009911 GO:GO:0006096 KO:K01810 GO:GO:0004347 PANTHER:PTHR11469 ProtClustDB:PLN02649 HOGENOM:HBG285902 OMA:RTSITSA GO:GO:0005982 EMBL:BT000953 EMBL:AK227111 IPI:IPI00544886 RefSeq:NP_194193.2 UniGene:At.25158 HSSP:P13376 ProteinModelPortal:Q8H103 STRING:Q8H103 PRIDE:Q8H103 EnsemblPlants:AT4G24620.1 GeneID:828564 KEGG:ath:AT4G24620 TAIR:At4g24620 InParanoid:Q8H103 PhylomeDB:Q8H103 Genevestigator:Q8H103 Uniprot:Q8H103
Root	Isotig11996	7	36	-2.492	1.13E-06	TAIR|locus:2173532 - symbol:COB "AT5G60920" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0009825 "multidimensional cell growth" evidence=IMP] [GO:0009897 "external side of plasma membrane" evidence=ISS] [GO:0031225 "anchored to membrane" evidence=TAS] [GO:0009505 "plant-type cell wall" evidence=IDA] [GO:0010215 "cellulose microfibril organization" evidence=IMP] [GO:0046658 "anchored to plasma membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IMP] [GO:0009930 "longitudinal side of cell surface" evidence=IDA] EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009651 GO:GO:0009505 EMBL:AB008269 GO:GO:0046658 GO:GO:0016328 GO:GO:0009825 InterPro:IPR006918 Pfam:PF04833 ProDom:PD140986 eggNOG:NOG238235 HOGENOM:HBG317196 InterPro:IPR017391 PIRSF:PIRSF038122 EMBL:AF319663 EMBL:AY094402 EMBL:BT001119 EMBL:AY085712 EMBL:AJ006787 IPI:IPI00520003 PIR:T52038 RefSeq:NP_568930.1 UniGene:At.21375 STRING:Q94KT8 PRIDE:Q94KT8 EnsemblPlants:AT5G60920.1 GeneID:836213 KEGG:ath:AT5G60920 GeneFarm:1678 TAIR:At5g60920 InParanoid:Q94KT8 OMA:KIVRPTK PhylomeDB:Q94KT8 ProtClustDB:CLSN2917780 ArrayExpress:Q94KT8 Genevestigator:Q94KT8 GermOnline:AT5G60920 GO:GO:0009930 GO:GO:0010215 Uniprot:Q94KT8
Root	Isotig11998	9	29	-1.817	0.000341695	TAIR|locus:2205235 - symbol:LOS1 "AT1G56070" species:3702 "Arabidopsis thaliana" [GO:0003746 "translation elongation factor activity" evidence=ISS] [GO:0008135 "translation factor activity, nucleic acid binding" evidence=ISS] [GO:0009409 "response to cold" evidence=IMP] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR000640 InterPro:IPR000795 InterPro:IPR004161 InterPro:IPR005225 InterPro:IPR005517 Pfam:PF00009 Pfam:PF00679 Pfam:PF03144 Pfam:PF03764 PRINTS:PR00315 PROSITE:PS00301 SMART:SM00838 SMART:SM00889 GO:GO:0005525 TIGRFAMs:TIGR00231 EMBL:CP002684 GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 GO:GO:0005774 GO:GO:0009507

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0005730 GO:GO:0003924 GO:GO:0005507 GO:GO:0009409 GO:GO:0003746 InterPro:IPR020568 InterPro:IPR014721 Gene3D:G3DSA:3.30.230.10 SUPFAM:SSF54211 InterPro:IPR009000 SUPFAM:SSF50447 InterPro:IPR009022 Gene3D:G3DSA:3.30.70.240 SUPFAM:SSF54980 KO:K03234 OMA:GVMTQTE HSSP:P32324 EMBL:AF367331 EMBL:AY054461 EMBL:BT000661 EMBL:BT000722 EMBL:BT002714 IPI:IPI00517335 RefSeq:NP_849818.1 UniGene:At.47544 ProteinModelPortal:Q9ASR1 SMR:Q9ASR1 STRING:Q9ASR1 PRIDE:Q9ASR1 ProMEX:Q9ASR1 EnsemblPlants:AT1G56070.1 GeneID:842058 KEGG:ath:AT1G56070 TAIR:At1g56070 InParanoid:Q9ASR1 PhylomeDB:Q9ASR1 ProtClustDB:PLN00116 Genevestigator:Q9ASR1 Uniprot:Q9ASR1
Root	Isotig11999	0	14	-4.936	8.24E-05	TAIR|locus:2082078 - symbol:ESK1 "ESKIMO 1" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0009414 "response to water deprivation" evidence=IMP] [GO:0009651 "response to salt stress" evidence=IMP] [GO:0050826 "response to freezing" evidence=IMP] [GO:0009409 "response to cold" evidence=IMP] [GO:0045893 "positive regulation of transcription, DNA-dependent" evidence=IEP] EMBL:CP002686 GO:GO:0045893 GO:GO:0050826 EMBL:AL163832 IPI:IPI00523770 PIR:T49211 RefSeq:NP_191158.1 UniGene:At.43528 STRING:Q9LY46 PRIDE:Q9LY46 EnsemblPlants:AT3G55990.1 GeneID:824765 KEGG:ath:AT3G55990 TAIR:At3g55990 InParanoid:Q9LY46 OMA:WVERNID PhylomeDB:Q9LY46 ProtClustDB:CLSN2688829 Genevestigator:Q9LY46 Uniprot:Q9LY46
Root	Isotig12000	12	51	-2.216	6.44E-08	TAIR|locus:2195503 - symbol:MDAR6 "AT1G63940" species:3702 "Arabidopsis thaliana" [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0009409 "response to cold" evidence=IEP] [GO:0010319 "stromule" evidence=IDA] [GO:0005524 "ATP binding" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] InterPro:IPR001327 InterPro:IPR013027 InterPro:IPR023753 Pfam:PF00070 Pfam:PF07992 PRINTS:PR00368 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005739 GO:GO:0005524 GO:GO:0009570 GO:GO:0046686 GO:GO:0050660 GO:GO:0010319 GO:GO:0009409 eggNOG:COG0446 EMBL:AC010852 HOGENOM:HBG316689 ProtClustDB:CLSN2684894 GO:GO:0016656 EMBL:D84417 EMBL:AY034934 EMBL:AY142572 EMBL:BT000667 IPI:IPI00531614 IPI:IPI00548028 PIR:E96664 RefSeq:NP_564818.1 RefSeq:NP_849839.1 UniGene:At.24374 UniGene:At.72711 ProteinModelPortal:P92947 SMR:P92947 IntAct:P92947 STRING:P92947 PRIDE:P92947 EnsemblPlants:AT1G63940.2 GeneID:842697 KEGG:ath:AT1G63940 TAIR:At1g63940 InParanoid:P92947 OMA:YIGMEVA PhylomeDB:P92947 BRENDA:1.6.5.4 ArrayExpress:P92947 Genevestigator:P92947 Uniprot:P92947
Root	Isotig12001	1	30	-5.036	7.50E-09	UNIPROTKB|Q70KG3 - symbol:RAFTIN1B "Protein RAFTIN 1B" species:4565 "Triticum aestivum" [GO:0009555 "pollen development" evidence=ISS] [GO:0043668 "exine" evidence=IDA] GO:GO:0009555 InterPro:IPR004873 Pfam:PF03181 PROSITE:PS51277 GO:GO:0043668 EMBL:AJ575664 EMBL:AJ575665 UniGene:Ta.4176 Gramene:Q70KG3 Uniprot:Q70KG3
Root	Isotig12004	55	0	6.652	8.00E-14	TAIR|locus:2077793 - symbol:iPGAM2 "AT3G08590" species:3702 "Arabidopsis thaliana" [GO:0046537 "2,3-bisphosphoglycerate-independent phosphoglycerate mutase activity" evidence=IGI;ISS] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0009555 "pollen development" evidence=IGI] [GO:0010118 "stomatal movement" evidence=IGI] InterPro:IPR005995 InterPro:IPR006124 InterPro:IPR011258 InterPro:IPR017849 InterPro:IPR017850 Pfam:PF01676 Pfam:PF06415 PIRSF:PIRSF001492 GO:GO:0005829 GO:GO:0009506 GO:GO:0048046 GO:GO:0046686 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0009555 GO:GO:0010118 GO:GO:0030145 GO:GO:0006096 EMBL:AC012562 Gene3D:G3DSA:3.40.720.10 SUPFAM:SSF53649 eggNOG:COG0696 HOGENOM:HBG613255 KO:K15633 Gene3D:G3DSA:3.40.1450.10 SUPFAM:SSF64158 TIGRFAMs:TIGR01307 ProtClustDB:PLN02538 GO:GO:0046537 EMBL:AY039969 EMBL:AF424615 EMBL:AY113910 IPI:IPI00520882 RefSeq:NP_187471.1 RefSeq:NP_850542.1 UniGene:At.68440 ProteinModelPortal:Q9M9K1 SMR:Q9M9K1 STRING:Q9M9K1 PRIDE:Q9M9K1 EnsemblPlants:AT3G08590.1 EnsemblPlants:AT3G08590.2 GeneID:820006 KEGG:ath:AT3G08590 TAIR:At3g08590 InParanoid:Q9M9K1 OMA:AGRIYAQ PhylomeDB:Q9M9K1 ArrayExpress:Q9M9K1 Genevestigator:Q9M9K1 GermOnline:AT3G08590 Uniprot:Q9M9K1
Root	Isotig12022	63	13	2.148	1.75E-08	TAIR|locus:2131591 - symbol:CAT2 "AT4G35090" species:3702 "Arabidopsis thaliana" [GO:0004096 "catalase activity" evidence=ISS;IMP] [GO:0005777 "peroxisome" evidence=IDA;NAS] [GO:0042744 "hydrogen peroxide catabolic process" evidence=NAS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast"

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						evidence=IDA] [GO:0006995 "cellular response to nitrogen starvation" evidence=IEP] [GO:0009970 "cellular response to sulfate starvation" evidence=IEP] [GO:0016036 "cellular response to phosphate starvation" evidence=IEP] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0010319 "stromule" evidence=IDA] [GO:0006979 "response to oxidative stress" evidence=IMP] [GO:0008219 "cell death" evidence=IMP] [GO:0009648 "photoperiodism" evidence=IMP] [GO:0045454 "cell redox homeostasis" evidence=IMP] [GO:0009416 "response to light stimulus" evidence=IEP] [GO:0005515 "protein binding" evidence=IPI] [GO:0050897 "cobalt ion binding" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] InterPro:IPR002226 InterPro:IPR011614 InterPro:IPR018028 InterPro:IPR020835 InterPro:IPR024708 InterPro:IPR024711 Pfam:PF00199 PIRSF:PIRSF038928 PRINTS:PR00067 PROSITE:PS00437 PROSITE:PS00438 PROSITE:PS51402 SMART:SM01060 InterPro:IPR010582 GO:GO:0005739 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0009507 GO:GO:0005515 GO:GO:0008219 GO:GO:0010319 GO:GO:0009409 GO:GO:0009514 GO:GO:0020037 GO:GO:0050897 EMBL:AL022023 EMBL:AL161586 GO:GO:0016036 GO:GO:0045454 GO:GO:0022626 GO:GO:0006995 GO:GO:0042744 GO:GO:0009970 GO:GO:0004096 eggNOG:COG0753 KO:K03781 Gene3D:G3DSA:2.40.180.10 PANTHER:PTHR11465 Pfam:PF06628 SUPFAM:SSF56634 HOGENOM:HBG339355 ProtClustDB:PLN02609 OMA:DWVYNNT EMBL:X64271 EMBL:X94447 EMBL:AY074301 EMBL:AY113854 IPI:IPI00520641 PIR:T05779 RefSeq:NP_195235.1 UniGene:At.24350 UniGene:At.64718 ProteinModelPortal:P25819 SMR:P25819 IntAct:P25819 STRING:P25819 PeroxiBase:5141 PRIDE:P25819 ProMEX:P25819 EnsemblPlants:AT4G35090.1 GeneID:829661 KEGG:ath:AT4G35090 TAIR:At4g35090 InParanoid:P25819 PhylomeDB:P25819 BioCyc:MetaCyc:AT4G35090-MONOMER ArrayExpress:P25819 Genevestigator:P25819 GO:GO:0009648 Uniprot:P25819
Root	Isotig12025	14	51	-1.994	4.31E-07	TAIR|locus:2017602 - symbol:4CL1 "AT1G51680" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0009411 "response to UV" evidence=IEP] [GO:0009611 "response to wounding" evidence=IEP] [GO:0009620 "response to fungus" evidence=IEP] [GO:0009698 "phenylpropanoid metabolic process" evidence=TAS] [GO:0016207 "4-coumarate-CoA ligase activity" evidence=IDA] InterPro:IPR000873 Pfam:PF00501 Prosite:PS00455 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005524 EMBL:AC025294 GO:GO:0009698 EMBL:U18675 EMBL:AF106084 EMBL:AY376729 EMBL:AY075622 EMBL:AY099747 EMBL:AY133582 IPI:IPI00532346 IPI:IPI00547355 PIR:S57784 RefSeq:NP_175579.1 RefSeq:NP_849793.1 UniGene:At.21694 ProteinModelPortal:Q42524 SMR:Q42524 STRING:Q42524 TCDB:4.C.1.1.7 PRIDE:Q42524 EnsemblPlants:AT1G51680.1 GeneID:841593 KEGG:ath:AT1G51680 TAIR:At1g51680 eggNOG:COG0318 HOGENOM:HBG547964 InParanoid:Q42524 KO:K01904 OMA:ICIRGHQ PhylomeDB:Q42524 ProtClustDB:PLN02246 BioCyc:ARA:AT1G51680-MONOMER BioCyc:MetaCyc:AT1G51680-MONOMER BRENDA:6.2.1.12 ArrayExpress:Q42524 Genevestigator:Q42524 GermOnline:AT1G51680 GO:GO:0016207 InterPro:IPR020845 InterPro:IPR025110 Pfam:PF13193 Uniprot:Q42524
Root	Isotig12035	35	3	3.415	8.27E-08	TAIR|locus:2082787 - symbol:AT3G61490 species:3702 "Arabidopsis thaliana" [GO:0004650 "polygalacturonase activity" evidence=IEA;ISS] [GO:0005975 "carbohydrate metabolic process" evidence=IEA;ISS] InterPro:IPR000743 Pfam:PF00295 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005576 EMBL:AL132962 GO:GO:0005975 CAZy:GH28 eggNOG:COG5434 GO:GO:0004650 InterPro:IPR006626 InterPro:IPR012334 InterPro:IPR011050 Gene3D:G3DSA:2.160.20.10 SMART:SM00710 SUPFAM:SSF51126 GO:GO:0007047 HOGENOM:HBG604585 IPI:IPI00527942 PIR:T47941 RefSeq:NP_001190154.1 RefSeq:NP_191708.1 RefSeq:NP_974473.1 UniGene:At.43625 ProteinModelPortal:Q9M318 SMR:Q9M318 PRIDE:Q9M318 EnsemblPlants:AT3G61490.1 EnsemblPlants:AT3G61490.2 EnsemblPlants:AT3G61490.3 GeneID:825322 KEGG:ath:AT3G61490 TAIR:At3g61490 InParanoid:Q9M318 OMA:CISPYSA PhylomeDB:Q9M318 ProtClustDB:CLSN2915754 Genevestigator:Q9M318 Uniprot:Q9M318
Root	Isotig12060	1	17	-4.216	2.69E-05	TAIR|locus:2033055 - symbol:CRTISO "AT1G06820" species:3702 "Arabidopsis thaliana" [GO:0009507 "chloroplast" evidence=IBA;TAS] [GO:0009662 "etioplast organization" evidence=IMP] [GO:0016117 "carotenoid biosynthetic process" evidence=IGI;TAS] [GO:0046608 "carotenoid isomerase activity" evidence=IGI;IMP] InterPro:IPR014101 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0031969 GO:GO:0016117 EMBL:AC011001 EMBL:BX813870 IPI:IPI00534972 PIR:A86203 RefSeq:NP_172167.2 UniGene:At.47600 UniGene:At.51507 UniGene:At.67219 ProteinModelPortal:Q9M9Y8 SMR:Q9M9Y8 STRING:Q9M9Y8 PRIDE:Q9M9Y8 EnsemblPlants:AT1G06820.1 GeneID:837193 KEGG:ath:AT1G06820 TAIR:At1g06820 eggNOG:COG1233 HOGENOM:HBG284415 InParanoid:Q9M9Y8 KO:K09835 OMA:EEPIYLF PhylomeDB:Q9M9Y8

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						ProtClustDB:CLSN2680687 BioCyc:ARA:AT1G06820-MONOMER BioCyc:MetaCyc:AT1G06820-MONOMER Genevestigator:Q9M9Y8 GermOnline:AT1G06820 GO:GO:0046608 GO:GO:0009662 TIGRFAMs:TIGR02730 Uniprot:Q9M9Y8
Root	Isotig12074	21	4	2.263	0.000779124	UNIPROTKB|Q84S31 - symbol:Q84S31 "Chitinase III" species:29760 "Vitis vinifera" [GO:0004568 "chitinase activity" evidence=IDA] [GO:0006032 "chitin catabolic process" evidence=IDA] [GO:0050832 "defense response to fungus" evidence=IDA] InterPro:IPR001223 InterPro:IPR001579 InterPro:IPR013781 Pfam:PF00704 PROSITE:PS01095 GO:GO:0050832 GO:GO:0043169 InterPro:IPR017853 Gene3D:G3DSA:3.20.20.80 SUPFAM:SSF51445 GO:GO:0004568 GO:GO:0006032 CAZy:GH18 EMBL:AB105374 HSSP:P23472 ProteinModelPortal:Q84S31 SMR:Q84S31 Uniprot:Q84S31
Root	Isotig12081	7	67	-3.388	1.07E-14	UNIPROTKB|A8QW53 - symbol:OMT3 "5-pentadecatrienyl resorcinol O-methyltransferase" species:4558 "Sorghum bicolor" [GO:0008171 "O-methyltransferase activity" evidence=IDA] [GO:0008757 "S-adenosylmethionine-dependent methyltransferase activity" evidence=IDA] [GO:0032259 "methylation" evidence=IDA] InterPro:IPR001077 InterPro:IPR012967 InterPro:IPR016461 Pfam:PF00891 Pfam:PF08100 PIRSF:PIRSF005739 InterPro:IPR011991 Gene3D:G3DSA:1.10.10.10 GO:GO:0046983 GO:GO:0008171 GO:GO:0008757 EMBL:EF189708 EMBL:CM000765 RefSeq:XP_002447425.1 UniGene:Sbi.19698 ProteinModelPortal:A8QW53 EnsemblPlants:Sb06g000820.1 GeneID:8080259 KEGG:sbi:SORBI_06g000820 eggNOG:NOG272168 PhylomeDB:A8QW53 ProtClustDB:CLSN2725062 Uniprot:A8QW53
Root	Isotig12082	16	2	2.871	0.000812389	TAIR|locus:2008828 - symbol:AT1G67570 "AT1G67570" species:3702 "Arabidopsis thaliana" [GO:0005634 "nucleus" evidence=IDA] GenomeReviews:CT485782_GR GO:GO:0005634 eggNOG:NOG304109 InterPro:IPR021924 Pfam:PF12056 EMBL:AY084491 IPI:IPI00542379 TAIR:At1g67570 HOGENOM:HBG746072 InParanoid:Q8LG29 PhylomeDB:Q8LG29 Genevestigator:Q8LG29 Uniprot:Q8LG29
Root	Isotig12089	2	20	-3.451	2.08E-05	TAIR|locus:2062340 - symbol:RWA3 "AT2G34410" species:3702 "Arabidopsis thaliana" [GO:0016413 "O-acetyltransferase activity" evidence=ISS] [GO:0005794 "Golgi apparatus" evidence=IDA] [GO:0009834 "secondary cell wall biogenesis" evidence=IGI] EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0005794 GO:GO:0016740 eggNOG:NOG292587 InterPro:IPR012419 Pfam:PF07779 UniGene:At.66422 UniGene:At.71449 UniGene:At.23647 ProtClustDB:CLSN2689941 UniGene:At.71003 UniGene:At.71384 EMBL:BT015347 EMBL:BT020218 EMBL:AK221547 EMBL:AK228823 EMBL:AK316994 IPI:IPI00541846 RefSeq:NP_001031478.1 RefSeq:NP_180988.3 PRIDE:Q66GQ5 EnsemblPlants:AT2G34410.1 EnsemblPlants:AT2G34410.2 GeneID:818004 KEGG:ath:AT2G34410 TAIR:At2g34410 HOGENOM:HBG316928 InParanoid:Q66GQ5 OMA:IARFAQM PhylomeDB:Q66GQ5 Genevestigator:Q66GQ5 Uniprot:Q66GQ5
Root	Isotig12094	2	19	-3.377	3.93E-05	TAIR|locus:2011236 - symbol:AT1G19110 "AT1G19110" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] InterPro:IPR002035 PROSITE:PS50234 SMART:SM00327 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005886 eggNOG:COG2304 EMBL:AY136389 EMBL:BT000188 IPI:IPI00524765 RefSeq:NP_173345.2 UniGene:At.41760 ProteinModelPortal:Q8L798 PRIDE:Q8L798 EnsemblPlants:AT1G19110.1 GeneID:838494 KEGG:ath:AT1G19110 TAIR:At1g19110 HOGENOM:HBG320497 InParanoid:Q8L798 OMA:DERHICD PhylomeDB:Q8L798 ProtClustDB:CLSN2679572 ArrayExpress:Q8L798 Genevestigator:Q8L798 Uniprot:Q8L798
Root	Isotig12110	14	1	3.678	0.000484579	TAIR|locus:2097925 - symbol:AT3G48060 species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=IEA;ISS] [GO:0005634 "nucleus" evidence=IEA] [GO:0006351 "transcription, DNA-dependent" evidence=IEA] InterPro:IPR001025 InterPro:IPR003617 InterPro:IPR017923 Pfam:PF01426 Pfam:PF08711 PROSITE:PS51038 PROSITE:PS51319 SMART:SM00439 SMART:SM00509 GO:GO:0005634 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0003677 GO:GO:0006351 EMBL:AL049658 Gene3D:G3DSA:1.20.930.10 SUPFAM:SSF47676 HOGENOM:HBG745173 IPI:IPI00534352 PIR:T06677 RefSeq:NP_190389.1 UniGene:At.19774 UniGene:At.48751 ProteinModelPortal:Q9SU69 SMR:Q9SU69 STRING:Q9SU69 PRIDE:Q9SU69 EnsemblPlants:AT3G48060.1 GeneID:823961 KEGG:ath:AT3G48060 TAIR:At3g48060 eggNOG:NOG298939 InParanoid:Q9SU69 OMA:LENIEIM PhylomeDB:Q9SU69 ProtClustDB:CLSN2684022 Genevestigator:Q9SU69 Uniprot:Q9SU69
Root	Isotig12128	28	4	2.678	1.93E-05	TAIR|locus:2024402 - symbol:AT1G09870 species:3702 "Arabidopsis thaliana" [GO:0003993 "acid phosphatase activity" evidence=IEA;ISS] [GO:0008150 "biological_process" evidence=ND] [GO:0005774 "vacuolar membrane" evidence=IDA] InterPro:IPR000560 InterPro:IPR016274 Pfam:PF00328 PIRSF:PIRSF000894 EMBL:CP002684 GO:GO:0005774 GO:GO:0003993 OMA:PVLRFYK EMBL:AY052301 IPI:IPI00546493 PIR:JE0369

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						RefSeq:NP_563856.1 UniGene:At.10235 ProteinModelPortal:Q941B2 PRIDE:Q941B2 EnsemblPlants:AT1G09870.1 GeneID:837519 KEGG:ath:AT1G09870 TAIR:At1g09870 InParanoid:Q941B2 PhylomeDB:Q941B2 ProtClustDB:CLSN2687748 Genevestigator:Q941B2 Uniprot:Q941B2
Root	Isotig12147	11	35	-1.799	9.33E-05	TAIR|locus:2102659 - symbol:AT3G45680 "AT3G45680" species:3702 "Arabidopsis thaliana" [GO:0005215 "transporter activity" evidence=ISS] [GO:0006857 "oligopeptide transport" evidence=ISS] [GO:0016020 "membrane" evidence=IEA;ISS] [GO:0009624 "response to nematode" evidence=IEP] InterPro:IPR000109 InterPro:IPR018456 Pfam:PF00854 PROSITE:PS01022 PROSITE:PS01023 GO:GO:0016021 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0009624 GO:GO:0005215 InterPro:IPR016196 SUPFAM:SSF103473 GO:GO:0042128 EMBL:AL157735 GO:GO:0006857 EMBL:AK117660 IPI:IPI00529935 PIR:T47508 RefSeq:NP_190154.1 UniGene:At.36001 ProteinModelPortal:Q9M175 SMR:Q9M175 PRIDE:Q9M175 EnsemblPlants:AT3G45680.1 GeneID:823710 KEGG:ath:AT3G45680 TAIR:At3g45680 eggNOG:NOG309276 InParanoid:Q9M175 OMA:ACIVIIM PhylomeDB:Q9M175 ProtClustDB:CLSN2915495 Genevestigator:Q9M175 Uniprot:Q9M175
Root	Isotig12151	0	13	-4.829	0.000155955	No hit
Root	Isotig12153	1	13	-3.829	0.000362856	TAIR|locus:2089521 - symbol:CYP72A15 ""cytochrome P450, family 72, subfamily A, polypeptide 15"" species:3702 "Arabidopsis thaliana" [GO:0004497 "monooxygenase activity" evidence=IEA] [GO:0005506 "iron ion binding" evidence=IEA] [GO:0009055 "electron carrier activity" evidence=IEA] [GO:0019825 "oxygen binding" evidence=ISS] [GO:0020037 "heme binding" evidence=IEA] InterPro:IPR001128 InterPro:IPR002401 Pfam:PF00067 PRINTS:PR00385 PRINTS:PR00463 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0009055 GO:GO:0004497 eggNOG:COG2124 GO:GO:0020037 Gene3D:G3DSA:1.10.630.10 SUPFAM:SSF48264 GO:GO:0016705 HSSP:P14779 HOGENOM:HBG715383 EMBL:AB023038 EMBL:AY050827 EMBL:AY096748 IPI:IPI00542070 RefSeq:NP_188087.1 UniGene:At.19957 UniGene:At.23975 ProteinModelPortal:Q9LUC5 SMR:Q9LUC5 STRING:Q9LUC5 PRIDE:Q9LUC5 EnsemblPlants:AT3G14690.1 GeneID:820697 KEGG:ath:AT3G14690 TAIR:At3g14690 InParanoid:Q9LUC5 OMA:TVITIHP PhylomeDB:Q9LUC5 ProtClustDB:CLSN2684942 ArrayExpress:Q9LUC5 Genevestigator:Q9LUC5 Uniprot:Q9LUC5
Root	Isotig12157	64	20	1.549	5.52E-06	TAIR|locus:2131591 - symbol:CAT2 "AT4G35090" species:3702 "Arabidopsis thaliana" [GO:0004096 "catalase activity" evidence=ISS;IMP] [GO:0005777 "peroxisome" evidence=IDA;NAS] [GO:0042744 "hydrogen peroxide catabolic process" evidence=NAS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0006995 "cellular response to nitrogen starvation" evidence=IEP] [GO:0009970 "cellular response to sulfate starvation" evidence=IEP] [GO:0016036 "cellular response to phosphate starvation" evidence=IEP] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0010319 "stromule" evidence=IDA] [GO:0006979 "response to oxidative stress" evidence=IMP] [GO:0008219 "cell death" evidence=IMP] [GO:0009648 "photoperiodism" evidence=IMP] [GO:0045454 "cell redox homeostasis" evidence=IMP] [GO:0009416 "response to light stimulus" evidence=IEP] [GO:0005515 "protein binding" evidence=IPI] [GO:0050897 "cobalt ion binding" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] InterPro:IPR002226 InterPro:IPR011614 InterPro:IPR018028 InterPro:IPR020835 InterPro:IPR024708 InterPro:IPR024711 Pfam:PF00199 PIRSF:PIRSF038928 PRINTS:PR00067 PROSITE:PS00437 PROSITE:PS00438 PROSITE:PS51402 SMART:SM01060 InterPro:IPR010582 GO:GO:0005739 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0009507 GO:GO:0005515 GO:GO:0008219 GO:GO:0010319 GO:GO:0009409 GO:GO:0009514 GO:GO:0020037 GO:GO:0050897 EMBL:AL022023 EMBL:AL161586 GO:GO:0016036 GO:GO:0045454 GO:GO:0022626 GO:GO:0006995 GO:GO:0042744 GO:GO:0009970 GO:GO:0004096 eggNOG:COG0753 KO:K03781 Gene3D:G3DSA:2.40.180.10 PANTHER:PTHR11465 Pfam:PF06628 SUPFAM:SSF56634 HOGENOM:HBG339355 ProtClustDB:PLN02609 OMA:DWVYNNT EMBL:X64271 EMBL:X94447 EMBL:AY074301 EMBL:AY113854 IPI:IPI00520641 PIR:T05779 RefSeq:NP_195235.1 UniGene:At.24350 UniGene:At.64718 ProteinModelPortal:P25819 SMR:P25819 IntAct:P25819 STRING:P25819 PeroxiBase:5141 PRIDE:P25819 ProMEX:P25819 EnsemblPlants:AT4G35090.1 GeneID:829661 KEGG:ath:AT4G35090 TAIR:At4g35090 InParanoid:P25819 PhylomeDB:P25819 BioCyc:MetaCyc:AT4G35090-MONOMER ArrayExpress:P25819 Genevestigator:P25819 GO:GO:0009648 Uniprot:P25819
Root	Isotig12161	13	42	-1.821	1.59E-05	TAIR|locus:3439219 - symbol:TUA6 "AT4G14960" species:3702 "Arabidopsis thaliana" [GO:0005874 "microtubule" evidence=IDA] [GO:0045298 "tubulin complex" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005200 "structural constituent of cytoskeleton" evidence=ISS] [GO:0005730 "nucleolus" evidence=IDA] [GO:0000226

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						"microtubule cytoskeleton organization" evidence=IMP] [GO:0005618 "cell wall" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0071258 "cellular response to gravity" evidence=IMP] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000217 InterPro:IPR002452 InterPro:IPR003008 InterPro:IPR008280 InterPro:IPR017975 InterPro:IPR018316 Pfam:PF00091 Pfam:PF03953 PRINTS:PR01161 PRINTS:PR01162 PROSITE:PS00227 SMART:SM00864 SMART:SM00865 GO:GO:0005525 GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005773 GO:GO:0005618 GO:GO:0005515 GO:GO:0005730 GO:GO:0005198 GO:GO:0003924 GO:GO:0009651 EMBL:AL161540 GO:GO:0000226 GO:GO:0005874 GO:GO:0051258 Gene3D:G3DSA:3.40.50.1440 SUPFAM:SSF52490 GO:GO:0007018 EMBL:Z97337 Gene3D:G3DSA:3.30.1330.20 SUPFAM:SSF55307 GO:GO:0045298 eggNOG:COG5023 GO:GO:0071258 HOGENOM:HBG750007 KO:K07374 InterPro:IPR023123 Gene3D:G3DSA:1.10.287.600 PANTHER:PTHR11588 ProtClustDB:PLN00221 UniGene:At.22368 UniGene:At.48153 EMBL:M84699 EMBL:AY058858 EMBL:AY065347 EMBL:AY079036 EMBL:AY117174 IPI:IPI00520226 PIR:JQ1597 RefSeq:NP_193232.1 ProteinModelPortal:P29511 SMR:P29511 IntAct:P29511 STRING:P29511 PRIDE:P29511 EnsemblPlants:AT4G14960.2 GeneID:827154 KEGG:ath:AT4G14960 TAIR:At4g14960 InParanoid:P29511 OMA:MPSDKAI PhylomeDB:P29511 ArrayExpress:P29511 Genevestigator:P29511 Uniprot:P29511
Root	Isotig12167	16	0	4.871	5.89E-05	ZFIN|ZDB-GENE-030131-4487 - symbol:sec24c "SEC24 family, member C (S. cerevisiae)" species:7955 "Danio rerio" [GO:0030127 "COPII vesicle coat" evidence=IEA] [GO:0006886 "intracellular protein transport" evidence=IEA] [GO:0006888 "ER to Golgi vesicle-mediated transport" evidence=IEA] [GO:0008270 "zinc ion binding" evidence=IEA] [GO:0006810 "transport" evidence=IEA] [GO:0015031 "protein transport" evidence=IEA] InterPro:IPR006895 InterPro:IPR006896 InterPro:IPR006900 Pfam:PF04810 Pfam:PF04811 Pfam:PF04815 ZFIN:ZDB-GENE-030131-4487 GO:GO:0006886 GO:GO:0008270 InterPro:IPR007123 Pfam:PF00626 GO:GO:0006888 GO:GO:0030127 InterPro:IPR012990 Pfam:PF08033 SUPFAM:SSF81811 SUPFAM:SSF82919 GeneTree:ENSGT00590000082962 EMBL:CU469520 EMBL:CU694198 IPI:IPI00972073 Ensembl:ENSDART00000085476 Bgee:F1R9P2 Uniprot:F1R9P2
Root	Isotig12175	0	11	-4.588	0.000569522	TAIR|locus:2127193 - symbol:AT4G23030 "AT4G23030" species:3702 "Arabidopsis thaliana" [GO:0005215 "transporter activity" evidence=ISS] [GO:0006855 "drug transmembrane transport" evidence=IEA] [GO:0015238 "drug transmembrane transporter activity" evidence=IEA] [GO:0015297 "antiporter activity" evidence=IEA] [GO:0055085 "transmembrane transport" evidence=IEA] [GO:0016020 "membrane" evidence=ISS] InterPro:IPR002528 Pfam:PF01554 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0016020 GO:GO:0015238 GO:GO:0015297 EMBL:AL031018 EMBL:AL161558 eggNOG:COG0534 HOGENOM:HBG746942 KO:K03327 PANTHER:PTHR11206 TIGRFAMs:TIGR00797 EMBL:AY082796 IPI:IPI00546793 PIR:T05135 RefSeq:NP_194034.1 UniGene:At.32474 ProteinModelPortal:O82752 SMR:O82752 PRIDE:O82752 EnsemblPlants:AT4G23030.1 GeneID:828402 KEGG:ath:AT4G23030 TAIR:At4g23030 InParanoid:O82752 OMA:GANINLC PhylomeDB:O82752 ProtClustDB:CLSN2685850 ArrayExpress:O82752 Genevestigator:O82752 Uniprot:O82752
Root	Isotig12184	1	16	-4.129	5.13E-05	TAIR|locus:2152445 - symbol:SAG12 "AT5G45890" species:3702 "Arabidopsis thaliana" [GO:0006508 "proteolysis" evidence=ISS] [GO:0008234 "cysteine-type peptidase activity" evidence=ISS] [GO:0009723 "response to ethylene stimulus" evidence=IEP] [GO:0007568 "aging" evidence=IEP;TAS] [GO:0010150 "leaf senescence" evidence=TAS] [GO:0010282 "senescence-associated vacuole" evidence=IDA] [GO:0009817 "defense response to fungus, incompatible interaction" evidence=IEP] InterPro:IPR000668 InterPro:IPR013128 Pfam:PF00112 PRINTS:PR00705 SMART:SM00645 InterPro:IPR000169 EMBL:CP002688 GO:GO:0004197 GO:GO:0006508 InterPro:IPR013201 PANTHER:PTHR12411 Pfam:PF08246 SMART:SM00848 PROSITE:PS00640 PROSITE:PS00139 PROSITE:PS00639 GO:GO:0010150 GO:GO:0009817 EMBL:AB016870 HSSP:O65039 EMBL:AF370131 EMBL:AY040073 IPI:IPI00544181 RefSeq:NP_568651.1 UniGene:At.75256 UniGene:At.7710 ProteinModelPortal:Q9FJ47 SMR:Q9FJ47 IntAct:Q9FJ47 STRING:Q9FJ47 MEROPS:C01.117 PRIDE:Q9FJ47 EnsemblPlants:AT5G45890.1 GeneID:834629 KEGG:ath:AT5G45890 TAIR:At5g45890 InParanoid:Q9FJ47 OMA:NDEQALM PhylomeDB:Q9FJ47 ProtClustDB:CLSN2917735 ArrayExpress:Q9FJ47 Genevestigator:Q9FJ47 GO:GO:0010282 Uniprot:Q9FJ47
Root	Isotig12216	4	19	-2.377	0.000578515	RGD|727924 - symbol:LOC257642 "rRNA promoter binding protein" species:10116 "Rattus norvegicus" [GO:0003690 "double-stranded DNA binding" evidence=IDA] [GO:0003700 "sequence-specific DNA binding

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						transcription factor activity" evidence=IDA] [GO:0008134 "transcription factor binding" evidence=IDA] [GO:0008283 "cell proliferation" evidence=IDA] [GO:0009303 "rRNA transcription" evidence=IDA] RGD:727924 GO:GO:0008134 GO:GO:0008283 GO:GO:0003700 GO:GO:0003690 GO:GO:0009303 EMBL:U77931 IPI:IPI00195015 RefSeq:NP_671477.1 GeneID:257642 KEGG:rno:257642 NextBio:624170 Genevestigator:Q99JC0 Uniprot:Q99JC0
Root	Isotig12217	0	13	-4.829	0.000155955	TAIR|locus:2169434 - symbol:CYP93D1 ""cytochrome P450, family 93, subfamily D, polypeptide 1"" species:3702 "Arabidopsis thaliana" [GO:0004497 "monooxygenase activity" evidence=IEA] [GO:0005506 "iron ion binding" evidence=IEA] [GO:0009055 "electron carrier activity" evidence=IEA] [GO:0019825 "oxygen binding" evidence=ISS] [GO:0020037 "heme binding" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] InterPro:IPR001128 InterPro:IPR002401 InterPro:IPR017972 Pfam:PF00067 PRINTS:PR00385 PRINTS:PR00463 PROSITE:PS00086 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009055 GO:GO:0004497 eggNOG:COG2124 GO:GO:0020037 Gene3D:G3DSA:1.10.630.10 SUPFAM:SSF48264 EMBL:AB010697 GO:GO:0016705 HOGENOM:HBG749920 IPI:IPI00540736 RefSeq:NP_196307.1 UniGene:At.54754 ProteinModelPortal:Q9FL56 SMR:Q9FL56 PRIDE:Q9FL56 EnsemblPlants:AT5G06900.1 GeneID:830580 KEGG:ath:AT5G06900 TAIR:At5g06900 InParanoid:Q9FL56 OMA:DEECAVA PhylomeDB:Q9FL56 ProtClustDB:CLSN2916540 Genevestigator:Q9FL56 Uniprot:Q9FL56
Root	Isotig12220	2	14	-2.936	0.000925454	TAIR|locus:2145643 - symbol:RGLG2 "AT5G14420" species:3702 "Arabidopsis thaliana" [GO:0004842 "ubiquitin-protein ligase activity" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009690 "cytokinin metabolic process" evidence=IGI] [GO:0009850 "auxin metabolic process" evidence=IGI] [GO:0005634 "nucleus" evidence=IDA] [GO:0080148 "negative regulation of response to water deprivation" evidence=IGI] InterPro:IPR001841 InterPro:IPR002035 PROSITE:PS50089 PROSITE:PS50234 SMART:SM00184 SMART:SM00327 Prosite:PS00518 GO:GO:0005886 GO:GO:0005634 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0008270 InterPro:IPR013083 Gene3D:G3DSA:3.30.40.10 GO:GO:0009850 EMBL:AL163817 GO:GO:0004842 InterPro:IPR010734 Pfam:PF07002 GO:GO:0009690 GO:GO:0080148 eggNOG:NOG278119 HOGENOM:HBG746179 EMBL:DQ086862 EMBL:AY099597 EMBL:BT000249 IPI:IPI00535253 PIR:T48615 RefSeq:NP_196946.1 RefSeq:NP_850818.1 RefSeq:NP_974779.1 RefSeq:NP_974780.1 UniGene:At.5177 ProteinModelPortal:Q9LY87 SMR:Q9LY87 STRING:Q9LY87 PRIDE:Q9LY87 EnsemblPlants:AT5G14420.1 EnsemblPlants:AT5G14420.2 EnsemblPlants:AT5G14420.3 EnsemblPlants:AT5G14420.4 GeneID:831293 KEGG:ath:AT5G14420 TAIR:At5g14420 InParanoid:Q9LY87 OMA:EMATTIV PhylomeDB:Q9LY87 ProtClustDB:CLSN2687222 ArrayExpress:Q9LY87 Genevestigator:Q9LY87 Uniprot:Q9LY87
Root	Isotig12227	9	27	-1.714	0.000905257	TAIR|locus:2087755 - symbol:AT3G12860 "AT3G12860" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] InterPro:IPR002687 Pfam:PF01798 EMBL:CP002686 GO:GO:0003676 GO:GO:0030529 EMBL:AB024033 InterPro:IPR012974 InterPro:IPR012976 Pfam:PF08156 Pfam:PF08060 SMART:SM00931 OMA:NHIIQAI HSSP:O28191 IPI:IPI00527919 RefSeq:NP_187892.2 UniGene:At.53283 ProteinModelPortal:Q9LTV0 SMR:Q9LTV0 STRING:Q9LTV0 PRIDE:Q9LTV0 EnsemblPlants:AT3G12860.1 GeneID:820468 KEGG:ath:AT3G12860 TAIR:At3g12860 InParanoid:Q9LTV0 PhylomeDB:Q9LTV0 ProtClustDB:CLSN2682875 Genevestigator:Q9LTV0 Uniprot:Q9LTV0
Root	Isotig12230	0	18	-5.299	6.77E-06	TAIR|locus:2200437 - symbol:NRAMP6 "AT1G15960" species:3702 "Arabidopsis thaliana" [GO:0015103 "inorganic anion transmembrane transporter activity" evidence=ISS] [GO:0016020 "membrane" evidence=IEA] [GO:0030001 "metal ion transport" evidence=ISS;NAS] [GO:0046873 "metal ion transmembrane transporter activity" evidence=ISS;NAS] [GO:0006875 "cellular metal ion homeostasis" evidence=NAS] [GO:0015086 "cadmium ion transmembrane transporter activity" evidence=IDA] [GO:0070574 "cadmium ion transmembrane transport" evidence=IDA] InterPro:IPR001046 Pfam:PF01566 PRINTS:PR00447 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0012505 GO:GO:0015086 EMBL:AC010924 GO:GO:0055072 eggNOG:COG1914 PANTHER:PTHR11706 HOGENOM:HBG312498 TIGRFAMs:TIGR01197 ProtClustDB:CLSN2682113 EMBL:AJ291831 EMBL:AY263397 IPI:IPI00535651 IPI:IPI00992541 PIR:B86294 RefSeq:NP_173048.3 UniGene:At.23016 UniGene:At.72454 ProteinModelPortal:Q9S9N8 SMR:Q9S9N8 EnsemblPlants:AT1G15960.1 GeneID:838166 KEGG:ath:AT1G15960 TAIR:At1g15960 InParanoid:Q9S9N8 OMA:PREDIAN PhylomeDB:Q9S9N8 ArrayExpress:Q9S9N8 Genevestigator:Q9S9N8 GermOnline:AT1G15960 Uniprot:Q9S9N8
Root	Isotig12234	0	15	-5.036	4.38E-05	TAIR|locus:2052357 - symbol:MPK20 "AT2G42880" species:3702 "Arabidopsis thaliana" [GO:0004707 "MAP kinase activity" evidence=ISS] [GO:0007165 "signal transduction" evidence=IC] [GO:0005515 "protein binding"

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						evidence=IPI] InterPro:IPR000719 InterPro:IPR002290 InterPro:IPR003527 InterPro:IPR011009 InterPro:IPR017441 Pfam:PF00069 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS01351 PROSITE:PS50011 SMART:SM00220 GO:GO:0005524 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0005515 eggNOG:COG0515 SUPFAM:SSF56112 HOGENOM:HBG755340 EMBL:AC006931 GO:GO:0004707 EMBL:AF412082 EMBL:BT001021 IPI:IPI00536584 PIR:D84859 RefSeq:NP_565989.1 UniGene:At.14161 ProteinModelPortal:Q9SJG9 SMR:Q9SJG9 IntAct:Q9SJG9 STRING:Q9SJG9 PRIDE:Q9SJG9 EnsemblPlants:AT2G42880.1 GeneID:818888 KEGG:ath:AT2G42880 GeneFarm:849 TAIR:At2g42880 InParanoid:Q9SJG9 OMA:DYINGTE PhylomeDB:Q9SJG9 ProtClustDB:CLSN2917317 ArrayExpress:Q9SJG9 Genevestigator:Q9SJG9 GermOnline:AT2G42880 Uniprot:Q9SJG9
Root	Isotig12236	14	36	-1.492	0.000528966	UNIPROTKB|P00395 - symbol:MT-CO1 "Cytochrome c oxidase subunit 1" species:9606 "Homo sapiens" [GO:0004129 "cytochrome-c oxidase activity" evidence=NAS] [GO:0005515 "protein binding" evidence=IPI] [GO:0005743 "mitochondrial inner membrane" evidence=TAS] [GO:0006123 "mitochondrial electron transport, cytochrome c to oxygen" evidence=NAS] [GO:0006979 "response to oxidative stress" evidence=IEA] [GO:0007568 "aging" evidence=IEA] [GO:0009055 "electron carrier activity" evidence=IEA] [GO:0009060 "aerobic respiration" evidence=IEA] [GO:0016021 "integral to membrane" evidence=IEA] [GO:0020037 "heme binding" evidence=IEA] [GO:0021549 "cerebellum development" evidence=IEA] [GO:0022904 "respiratory electron transport chain" evidence=TAS] [GO:0044281 "small molecule metabolic process" evidence=TAS] [GO:0046688 "response to copper ion" evidence=IEA] [GO:0051602 "response to electrical stimulus" evidence=IEA] [GO:0070469 "respiratory chain" evidence=IEA] Reactome:REACT_111217 InterPro:IPR000883 InterPro:IPR023615 InterPro:IPR023616 Pfam:PF00115 PRINTS:PR01165 PROSITE:PS00077 PROSITE:PS50855 GO:GO:0016021 GO:GO:0005515 GO:GO:0005743 GO:GO:0044281 GO:GO:0009055 GO:GO:0020037 GO:GO:0070469 GO:GO:0009060 GO:GO:0004129 Gene3D:G3DSA:1.20.210.10 PANTHER:PTHR10422 SUPFAM:SSF81442 eggNOG:COG0843 MIM:114500 EMBL:J01415 EMBL:V00662 EMBL:D38112 EMBL:AF346971 EMBL:AF347011 EMBL:AY289076 EMBL:AY289100 EMBL:AY339407 EMBL:AY339408 EMBL:AY339510 EMBL:AY339511 EMBL:AY339512 EMBL:AY339513 EMBL:AY339530 EMBL:AY339531 EMBL:AY339532 EMBL:AY339533 EMBL:AY339534 EMBL:AY339535 EMBL:AY339536 EMBL:AY339537 EMBL:AY339538 EMBL:AY339539 EMBL:AY339540 EMBL:AY339541 EMBL:AY339543 EMBL:AY339581 EMBL:AY339582 EMBL:AY339584 EMBL:AY495147 EMBL:AY495199 EMBL:AY495231 EMBL:AY495232 EMBL:AY495233 EMBL:AY495234 EMBL:AY495235 EMBL:AY495236 EMBL:AY495237 MIM:535000 Orphanet:104 Orphanet:255210 EMBL:AY339402 EMBL:AY339403 EMBL:AY339404 EMBL:AY339405 EMBL:AY339406 EMBL:AY339409 EMBL:AY339410 EMBL:AY339411 EMBL:AY339412 EMBL:AY339421 EMBL:AY339422 EMBL:AY339423 EMBL:AY339424 EMBL:AY339425 EMBL:AY339426 EMBL:AY339427 EMBL:AY339428 EMBL:AY339429 EMBL:AY339430 EMBL:AY339431 EMBL:AY339432 EMBL:AY339433 EMBL:AY339434 EMBL:AY339435 EMBL:AY339436 EMBL:AY339437 EMBL:AY339438 EMBL:AY339439 EMBL:AY339440 EMBL:AY339441 EMBL:AY339442 EMBL:AY339443 EMBL:AY339444 EMBL:AY339445 EMBL:AY339451 EMBL:AY339452 EMBL:AY339453 EMBL:AY339454 EMBL:AY339455 EMBL:AY339456 EMBL:AY339457 EMBL:AY339458 EMBL:AY339459 EMBL:AY339460 EMBL:AY339461 EMBL:AY339462 EMBL:AY339463 EMBL:AY339464 EMBL:AY339465 EMBL:AY339466 EMBL:AY339467 EMBL:AY339468 EMBL:AY339469 EMBL:AY339470 EMBL:AY339471 EMBL:AY339472 EMBL:AY339473 EMBL:AY339474 EMBL:AY339475 EMBL:AY339476 EMBL:AY339477 EMBL:AY339478 EMBL:AY339479 EMBL:AY339480 EMBL:AY339481 EMBL:AY339482 EMBL:AY339483 EMBL:AY339484 EMBL:AY339485 EMBL:AY339486 EMBL:AY339487 EMBL:AY339488 EMBL:AY339489 EMBL:AY339490 EMBL:AY339491 EMBL:AY339492 EMBL:AY339493 EMBL:AY339494 EMBL:AY339495 EMBL:AY339496 EMBL:AY339497 EMBL:AY339498 EMBL:AY339499 EMBL:AY339500 EMBL:AY339501 EMBL:AY339502 EMBL:AY339503 EMBL:AY339504 EMBL:AY339505 EMBL:AY339506 EMBL:AY339507 EMBL:AY339508 EMBL:AY339509 EMBL:AY339515 EMBL:AY339516 EMBL:AY339517 EMBL:AY339518 EMBL:AY339519 EMBL:AY339520 EMBL:AY339521 EMBL:AY339522 EMBL:AY339523 EMBL:AY339524 EMBL:AY339525 EMBL:AY339526 EMBL:AY339527 EMBL:AY339528 EMBL:AY339529 EMBL:AY339542 EMBL:AY339544 EMBL:AY339545 EMBL:AY339546 EMBL:AY339547 EMBL:AY339548 EMBL:AY339549 EMBL:AY339550 EMBL:AY339551 EMBL:AY339552 EMBL:AY339553 EMBL:AY339554 EMBL:AY339555 EMBL:AY339556 EMBL:AY339557 EMBL:AY339558 EMBL:AY339559 EMBL:AY339560 EMBL:AY339563 EMBL:AY339564 EMBL:AY339566 EMBL:AY339567 EMBL:AY339568 EMBL:AY339569 EMBL:AY339570 EMBL:AY339571 EMBL:AY339572 EMBL:AY339573 EMBL:AY339574 EMBL:AY339575 EMBL:AY339576 EMBL:AY339577 EMBL:AY339578 EMBL:AY339579 EMBL:AY339580 EMBL:AY339583 EMBL:AY339585

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EMBL:AY339586 EMBL:AY339587 EMBL:AY339588 EMBL:AY339589 EMBL:AY339590 EMBL:AY339591 EMBL:AY339592 EMBL:AY339593 EMBL:AF346963 EMBL:AF346964 EMBL:AF346965 EMBL:AF346966 EMBL:AF346967 EMBL:AF346970 EMBL:AF346972 EMBL:AF346973 EMBL:AF346974 EMBL:AF346975 EMBL:AF346976 EMBL:AF346977 EMBL:AF346978 EMBL:AF346979 EMBL:AF346980 EMBL:AF346981 EMBL:AF346982 EMBL:AF346983 EMBL:AF346988 EMBL:AF346991 EMBL:AF346993 EMBL:AF346994 EMBL:AF346995 EMBL:AF347000 EMBL:AF347001 EMBL:AF347003 EMBL:AF347004 EMBL:AF347007 EMBL:AF347012 EMBL:AF347013 EMBL:AF347014 EMBL:AF347015 EMBL:AY289051 EMBL:AY289052 EMBL:AY289053 EMBL:AY289056 EMBL:AY289057 EMBL:AY289058 EMBL:AY289059 EMBL:AY289060 EMBL:AY289061 EMBL:AY289062 EMBL:AY289064 EMBL:AY289065 EMBL:AY289066 EMBL:AY289067 EMBL:AY289068 EMBL:AY289069 EMBL:AY289070 EMBL:AY289071 EMBL:AY289073 EMBL:AY289074 EMBL:AY289075 EMBL:AY289077 EMBL:AY289078 EMBL:AY289080 EMBL:AY289081 EMBL:AY289082 EMBL:AY289083 EMBL:AY289084 EMBL:AY289085 EMBL:AY289086 EMBL:AY289088 EMBL:AY289089 EMBL:AY289090 EMBL:AY289092 EMBL:AY289093 EMBL:AY289094 EMBL:AY289095 EMBL:AY289096 EMBL:AY289097 EMBL:AY289098 EMBL:AY289099 EMBL:AY289101 EMBL:AY289102 EMBL:AY495090 EMBL:AY495091 EMBL:AY495092 EMBL:AY495093 EMBL:AY495094 EMBL:AY495095 EMBL:AY495096 EMBL:AY495097 EMBL:AY495098 EMBL:AY495099 EMBL:AY495100 EMBL:AY495101 EMBL:AY495102 EMBL:AY495103 EMBL:AY495104 EMBL:AY495105 EMBL:AY495106 EMBL:AY495107 EMBL:AY495108 EMBL:AY495109 EMBL:AY495110 EMBL:AY495111 EMBL:AY495112 EMBL:AY495113 EMBL:AY495114 EMBL:AY495116 EMBL:AY495117 EMBL:AY495118 EMBL:AY495119 EMBL:AY495120 EMBL:AY495121 EMBL:AY495122 EMBL:AY495124 EMBL:AY495125 EMBL:AY495126 EMBL:AY495127 EMBL:AY495128 EMBL:AY495129 EMBL:AY495130 EMBL:AY495131 EMBL:AY495132 EMBL:AY495133 EMBL:AY495134 EMBL:AY495135 EMBL:AY495136 EMBL:AY495137 EMBL:AY495138 EMBL:AY495139 EMBL:AY495140 EMBL:AY495141 EMBL:AY495142 EMBL:AY495143 EMBL:AY495144 EMBL:AY495145 EMBL:AY495148 EMBL:AY495149 EMBL:AY495150 EMBL:AY495151 EMBL:AY495152 EMBL:AY495153 EMBL:AY495154 EMBL:AY495155 EMBL:AY495156 EMBL:AY495157 EMBL:AY495158 EMBL:AY495159 EMBL:AY495160 EMBL:AY495161 EMBL:AY495162 EMBL:AY495163 EMBL:AY495164 EMBL:AY495165 EMBL:AY495166 EMBL:AY495167 EMBL:AY495168 EMBL:AY495169 EMBL:AY495170 EMBL:AY495171 EMBL:AY495172 EMBL:AY495173 EMBL:AY495174 EMBL:AY495175 EMBL:AY495176 EMBL:AY495177 EMBL:AY495178 EMBL:AY495179 EMBL:AY495180 EMBL:AY495181 EMBL:AY495182 EMBL:AY495183 EMBL:AY495184 EMBL:AY495185 EMBL:AY495186 EMBL:AY495187 EMBL:AY495188 EMBL:AY495189 EMBL:AY495190 EMBL:AY495191 EMBL:AY495192 EMBL:AY495193 EMBL:AY495194 EMBL:AY495195 EMBL:AY495196 EMBL:AY495197 EMBL:AY495198 EMBL:AY495200 EMBL:AY495201 EMBL:AY495202 EMBL:AY495203 EMBL:AY495204 EMBL:AY495205 EMBL:AY495206 EMBL:AY495207 EMBL:AY495208 EMBL:AY495209 EMBL:AY495210 EMBL:AY495211 EMBL:AY495212 EMBL:AY495213 EMBL:AY495214 EMBL:AY495215 EMBL:AY495216 EMBL:AY495217 EMBL:AY495218 EMBL:AY495219 EMBL:AY495220 EMBL:AY495221 EMBL:AY495222 EMBL:AY495223 EMBL:AY495224 EMBL:AY495225 EMBL:AY495228 EMBL:AY495230 EMBL:AY495239 EMBL:AY495240 EMBL:AY495241 EMBL:AY495242 EMBL:AY495243 EMBL:AY495244 EMBL:AY495245 EMBL:AY495246 EMBL:AY495247 EMBL:AY495248 EMBL:AY495249 EMBL:AY495250 EMBL:AY495251 EMBL:AY495252 EMBL:AY495253 EMBL:AY495254 EMBL:AY495255 EMBL:AY495256 EMBL:AY495259 EMBL:AY495261 EMBL:AY495262 EMBL:AY495263 EMBL:AY495264 EMBL:AY495265 EMBL:AY495266 EMBL:AY495267 EMBL:AY495268 EMBL:AY495269 EMBL:AY495270 EMBL:AY495271 EMBL:AY495272 EMBL:AY495273 EMBL:AY495274 EMBL:AY495275 EMBL:AY495277 EMBL:AY495278 EMBL:AY495279 EMBL:AY495280 EMBL:AY495281 EMBL:AY495282 EMBL:AY495284 EMBL:AY495285 EMBL:AY495286 EMBL:AY495287 EMBL:AY495288 EMBL:AY495289 EMBL:AY495290 EMBL:AY495291 EMBL:AY495292 EMBL:AY495293 EMBL:AY495294 EMBL:AY495295 EMBL:AY495297 EMBL:AY495298 EMBL:AY495299 EMBL:AY495301 EMBL:AY495302 EMBL:AY495304 EMBL:AY495305 EMBL:AY495306 EMBL:AY495307 EMBL:AY495308 EMBL:AY495309 EMBL:AY495310 EMBL:AY495311 EMBL:AY495312 EMBL:AY495313 EMBL:AY495314 EMBL:AY495315 EMBL:AY495316 EMBL:AY495317 EMBL:AY495318 EMBL:AY495319 EMBL:AY495320 EMBL:AY495322 EMBL:AY495323 EMBL:AY495324 EMBL:AY495325 EMBL:AY495326 EMBL:AY495327 EMBL:AY495328 EMBL:AY495329 EMBL:AY495330 MIM:220110 Orphanet:254905 GO:GO:0006123 HOVERGEN:HBG003841 OrthoDB:EOG4BG8VW CTD:4512 KO:K02256 GeneTree:ENSGT00390000001518 ProtClustDB:MTH00103 EMBL:AY339514 EMBL:AF346984 EMBL:AF346989 EMBL:AF346990 EMBL:AF346998 EMBL:AF347010 EMBL:AY289055 EMBL:AY289079 EMBL:AY495123

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EMBL:AY495226 EMBL:AY495258 EMBL:AY495276 EMBL:AY495283 EMBL:AY495300 EMBL:AY495303 EMBL:M10546 IPI:IPI00464968 PIR:A00463 RefSeq:YP_003024028.1 ProteinModelPortal:P00395 SMR:P00395 IntAct:P00395 STRING:P00395 TCDB:3.D.4.11.1 PhosphoSite:P00395 DMDM:116977 PRIDE:P00395 Ensembl:ENST00000361624 GeneID:4512 KEGG:hsa:4512 GeneCards:GCMTP005906 H-InvDB:HIX0080302 HGNC:HGNC:7419 HPA:CAB016241 MIM:500008 MIM:516030 MIM:550500 neXtProt:NX_P00395 Orphanet:99845 Orphanet:90641 Orphanet:168609 PharmGKB:PA31225 InParanoid:P00395 PhylomeDB:P00395 BRENDA:1.9.3.1 DrugBank:DB00711 NextBio:17428 Genevestigator:P00395 GermOnline:ENSG00000198804 Uniprot:P00395
Root	Isotig12250	235	316	-0.556	6.66E-06	TAIR|locus:2102420 - symbol:TTN8 "AT3G54670" species:3702 "Arabidopsis thaliana" [GO:0005215 "transporter activity" evidence=ISS] [GO:0005524 "ATP binding" evidence=ISS] [GO:0005634 "nucleus" evidence=ISS] [GO:0007059 "chromosome segregation" evidence=ISS] [GO:0008278 "cohesin complex" evidence=ISS] [GO:0009507 "chloroplast" evidence=IDA] [GO:0007062 "sister chromatid cohesion" evidence=IMP] InterPro:IPR010935 InterPro:IPR024704 Pfam:PF06470 PIRSF:PIRSF005719 SMART:SM00968 InterPro:IPR003395 Pfam:PF02463 GO:GO:0005524 GO:GO:0005634 GO:GO:0009507 GO:GO:0005694 GO:GO:0006281 GO:GO:0006310 GO:GO:0030261 EMBL:AL138650 GO:GO:0007062 SUPFAM:SSF75553 HSSP:Q9X0R4 IPI:IPI00538877 PIR:T47626 ProteinModelPortal:Q9M1T3 SMR:Q9M1T3 STRING:Q9M1T3 PRIDE:Q9M1T3 TAIR:At3g54670 InParanoid:Q9M1T3 PhylomeDB:Q9M1T3 Genevestigator:Q9M1T3 Uniprot:Q9M1T3
Root	Isotig12258	18	2	3.041	0.000259481	TAIR|locus:2127851 - symbol:SHS1 "AT4G32400" species:3702 "Arabidopsis thaliana" [GO:0005215 "transporter activity" evidence=ISS] [GO:0005743 "mitochondrial inner membrane" evidence=ISS] [GO:0006810 "transport" evidence=ISS] [GO:0006839 "mitochondrial transport" evidence=ISS] [GO:0009793 "embryo development ending in seed dormancy" evidence=NAS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009536 "plastid" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0006862 "nucleotide transport" evidence=IGI] [GO:0015215 "nucleotide transmembrane transporter activity" evidence=IGI] [GO:0009941 "chloroplast envelope" evidence=IDA] InterPro:IPR002067 PRINTS:PR00926 Pfam:PF00153 GO:GO:0016021 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005488 GO:GO:0005743 GO:GO:0009941 InterPro:IPR018108 InterPro:IPR023395 Gene3D:G3DSA:1.50.40.10 SUPFAM:SSF103506 PROSITE:PS50920 EMBL:AL161581 EMBL:AL034567 HOGENOM:HBG735918 EMBL:AF372944 EMBL:AY074831 EMBL:AY084938 IPI:IPI00527967 PIR:T05350 RefSeq:NP_194966.1 UniGene:At.2510 ProteinModelPortal:Q9SUV1 SMR:Q9SUV1 STRING:Q9SUV1 PRIDE:Q9SUV1 EnsemblPlants:AT4G32400.1 GeneID:829375 KEGG:ath:AT4G32400 TAIR:At4g32400 eggNOG:NOG266140 InParanoid:Q9SUV1 OMA:VTILEHE PhylomeDB:Q9SUV1 ProtClustDB:CLSN2686034 ArrayExpress:Q9SUV1 Genevestigator:Q9SUV1 GO:GO:0015215 Uniprot:Q9SUV1
Root	Isotig12259	2	18	-3.299	7.42E-05	TAIR|locus:2130504 - symbol:CT-BMY "AT4G17090" species:3702 "Arabidopsis thaliana" [GO:0016161 "beta-amylase activity" evidence=ISS;IDA] [GO:0005983 "starch catabolic process" evidence=IMP;TAS] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0000024 "maltose biosynthetic process" evidence=IMP] BRENDA:3.2.1.2 InterPro:IPR001371 InterPro:IPR001554 InterPro:IPR013781 InterPro:IPR018238 Pfam:PF01373 PRINTS:PR00750 PRINTS:PR00842 PROSITE:PS00506 PROSITE:PS00679 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0009507 GO:GO:0043169 InterPro:IPR017853 Gene3D:G3DSA:3.20.20.80 SUPFAM:SSF51445 GO:GO:0000272 CAZy:GH14 eggNOG:NOG77898 KO:K01177 GO:GO:0016161 EMBL:AJ250341 EMBL:Z97342 EMBL:AL161545 EMBL:AY052315 EMBL:AY061898 EMBL:AY087592 IPI:IPI00524115 PIR:D71439 PIR:H85190 PIR:T52556 RefSeq:NP_567523.1 UniGene:At.22021 UniGene:At.23528 UniGene:At.47944 UniGene:At.67939 HSSP:P10538 ProteinModelPortal:O23553 SMR:O23553 STRING:O23553 PRIDE:O23553 EnsemblPlants:AT4G17090.1 GeneID:827419 KEGG:ath:AT4G17090 TAIR:At4g17090 InParanoid:Q9SMW0 OMA:PHDAGEY PhylomeDB:O23553 ProtClustDB:PLN02803 BioCyc:MetaCyc:AT4G17090-MONOMER Genevestigator:O23553 Uniprot:O23553
Root	Isotig12267	4	21	-2.521	0.000181802	SGD|S000004781 - symbol:EAR1 "Specificity factor required for Rsp5p" species:4932 "Saccharomyces cerevisiae" [GO:0003674 "molecular_function" evidence=ND] [GO:0043328 "protein targeting to vacuole involved in ubiquitin-dependent protein catabolic process via the multivesicular body sorting pathway" evidence=IGI] [GO:0005768 "endosome" evidence=IEA;IDA] [GO:0006810 "transport" evidence=IEA] [GO:0016020 "membrane" evidence=IEA] [GO:0005773 "vacuole" evidence=IEA] [GO:0015031 "protein transport" evidence=IEA] [GO:0016021 "integral to membrane" evidence=IEA] [GO:0005774 "vacuolar membrane" evidence=IEA] [GO:0010008 "endosome membrane" evidence=IEA] InterPro:IPR003877 Pfam:PF00622 SGD:S000004781 GO:GO:0016021 GO:GO:0005774 GO:GO:0010008 EMBL:BK006946 InterPro:IPR008985 SUPFAM:SSF49899 EMBL:Z49808

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EMBL:Z49705 InterPro:IPR001870 InterPro:IPR018355 SMART:SM00449 PROSITE:PS50188 GO:GO:0043328 PIR:S55118 RefSeq:NP_013894.1 ProteinModelPortal:Q03212 IntAct:Q03212 MINT:MINT-4083932 STRING:Q03212 EnsemblFungi:YMR171C GeneID:855207 KEGG:sce:YMR171C CYGD:YMR171c eggNOG:NOG316575 GeneTree:ENSGT00530000067969 HOGENOM:HBG397085 OMA:GRHHHSI OrthoDB:EOG4CZFQQ NextBio:978705 ArrayExpress:Q03212 Genevestigator:Q03212 GermOnline:YMR171C Uniprot:Q03212
Root	Isotig12278	1	14	-3.936	0.000188601	TAIR|locus:2206845 - symbol:AT1G73390 "AT1G73390" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] EMBL:CP002684 GenomeReviews:CT485782_GR InterPro:IPR004328 Gene3D:G3DSA:1.25.40.280 Pfam:PF03097 SMART:SM01041 PROSITE:PS51180 EMBL:AC012396 HOGENOM:HBG316412 ProtClustDB:CLSN2679866 UniGene:At.16891 UniGene:At.34994 EMBL:AY072312 EMBL:BT015943 IPI:IPI00532932 PIR:E96760 RefSeq:NP_177482.1 RefSeq:NP_974137.1 RefSeq:NP_974138.1 ProteinModelPortal:Q9FX34 PRIDE:Q9FX34 EnsemblPlants:AT1G73390.1 EnsemblPlants:AT1G73390.2 EnsemblPlants:AT1G73390.3 GeneID:843674 KEGG:ath:AT1G73390 TAIR:At1g73390 InParanoid:Q9FX34 OMA:EKHRLFV PhylomeDB:Q9FX34 ArrayExpress:Q9FX34 Genevestigator:Q9FX34 Uniprot:Q9FX34
Root	Isotig12292	16	0	4.871	5.89E-05	No hit
Root	Isotig12296	0	17	-5.216	1.26E-05	TAIR|locus:2024685 - symbol:BGLU11 "beta glucosidase 11" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=IEA;ISS] [GO:0005975 "carbohydrate metabolic process" evidence=IEA] [GO:0043169 "cation binding" evidence=IEA] InterPro:IPR001360 InterPro:IPR013781 InterPro:IPR018120 Pfam:PF00232 PRINTS:PR00131 PROSITE:PS00572 PROSITE:PS00653 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0043169 InterPro:IPR017853 Gene3D:G3DSA:3.20.20.80 SUPFAM:SSF51445 GO:GO:0005975 GO:GO:0008422 CAZy:GH1 eggNOG:COG2723 HOGENOM:HBG316462 PANTHER:PTHR10353 EMBL:AC009525 EMBL:AY049274 EMBL:AY062763 EMBL:BT001137 IPI:IPI00536257 IPI:IPI00537900 IPI:IPI00544196 IPI:IPI00890996 IPI:IPI00891207 PIR:G86158 RefSeq:NP_001117217.1 RefSeq:NP_563666.1 RefSeq:NP_849578.5 RefSeq:NP_973745.1 RefSeq:NP_973746.3 UniGene:At.26199 ProteinModelPortal:B3H5Q1 SMR:B3H5Q1 STRING:B3H5Q1 EnsemblPlants:AT1G02850.4 GeneID:839435 KEGG:ath:AT1G02850 TAIR:At1g02850 InParanoid:A8MRZ0 PhylomeDB:B3H5Q1 ProtClustDB:PLN02998 Genevestigator:B3H5Q1 Uniprot:B3H5Q1
Root	Isotig12301	34	7	2.151	3.42E-05	TAIR|locus:2827800 - symbol:ERD7 "AT2G17840" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0009409 "response to cold" evidence=IEP] [GO:0009644 "response to high light intensity" evidence=IEP] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009414 "response to water deprivation" evidence=IEP] GO:GO:0005886 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009409 GO:GO:0009651 GO:GO:0009414 GO:GO:0009644 UniGene:At.19461 UniGene:At.40094 InterPro:IPR009686 Pfam:PF06911 EMBL:AF325067 EMBL:AF428331 EMBL:AY081319 EMBL:BT001230 IPI:IPI00548818 PIR:T00840 RefSeq:NP_179374.1 STRING:O48832 PRIDE:O48832 EnsemblPlants:AT2G17840.1 GeneID:816293 KEGG:ath:AT2G17840 TAIR:At2g17840 eggNOG:NOG243611 HOGENOM:HBG318774 InParanoid:O48832 OMA:MTESVAN PhylomeDB:O48832 ProtClustDB:CLSN2683911 ArrayExpress:O48832 Genevestigator:O48832 Uniprot:O48832
Root	Isotig12302	1	15	-4.036	9.83E-05	TAIR|locus:2176461 - symbol:PHT1;1 "AT5G43350" species:3702 "Arabidopsis thaliana" [GO:0005351 "sugar:hydrogen symporter activity" evidence=ISS] [GO:0015114 "phosphate ion transmembrane transporter activity" evidence=ISS;IMP] [GO:0015144 "carbohydrate transmembrane transporter activity" evidence=ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016036 "cellular response to phosphate starvation" evidence=IEP] [GO:0005315 "inorganic phosphate transmembrane transporter activity" evidence=IDA] [GO:0006817 "phosphate ion transport" evidence=IDA] InterPro:IPR004738 InterPro:IPR005828 Pfam:PF00083 PROSITE:PS00216 PROSITE:PS00217 GO:GO:0016021 GO:GO:0005886 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0015293 GO:GO:0005315 eggNOG:COG0477 InterPro:IPR016196 SUPFAM:SSF103473 EMBL:AB025638 GO:GO:0016036 InterPro:IPR020846 PROSITE:PS50850 HOGENOM:HBG744844 KO:K08176 TIGRFAMs:TIGR00887 EMBL:U62330 EMBL:Y07682 EMBL:D86591 EMBL:D86608 EMBL:AY070432 IPI:IPI00540786 RefSeq:NP_199149.1 UniGene:At.49125 UniGene:At.75359 ProteinModelPortal:Q8VYM2 STRING:Q8VYM2 PRIDE:Q8VYM2 EnsemblPlants:AT5G43350.1 GeneID:834353 KEGG:ath:AT5G43350 GeneFarm:5188 TAIR:At5g43350 InParanoid:Q8VYM2 OMA:GKELMLI

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						PhylomeDB:Q8VYM2 ProtClustDB:CLSN2686812 ArrayExpress:Q8VYM2 Genevestigator:Q8VYM2 GermOnline:AT5G43350 Uniprot:Q8VYM2
Root	Isotig12303	2	19	-3.377	3.93E-05	No hit
Root	Isotig12318	2	16	-3.129	0.000262867	TAIR|locus:2053791 - symbol:AT2G42360 "AT2G42360" species:3702 "Arabidopsis thaliana" [GO:0008270 "zinc ion binding" evidence=ISS] [GO:0004842 "ubiquitin-protein ligase activity" evidence=IDA] [GO:0016567 "protein ubiquitination" evidence=IDA] InterPro:IPR001841 PROSITE:PS50089 SMART:SM00184 Prosite:PS00518 GO:GO:0016021 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0008270 InterPro:IPR013083 Gene3D:G3DSA:3.30.40.10 GO:GO:0004842 HOGENOM:HBG748810 EMBL:AC005956 ProtClustDB:CLSN2683918 EMBL:DQ086853 EMBL:AY074652 EMBL:AK228239 IPI:IPI00531118 PIR:A84853 RefSeq:NP_181765.1 UniGene:At.67220 UniGene:At.70280 UniGene:At.75048 ProteinModelPortal:Q9SLC3 SMR:Q9SLC3 PRIDE:Q9SLC3 EnsemblPlants:AT2G42360.1 GeneID:818837 KEGG:ath:AT2G42360 TAIR:At2g42360 eggNOG:NOG287277 InParanoid:Q9SLC3 OMA:TEVEPRP PhylomeDB:Q9SLC3 ArrayExpress:Q9SLC3 Genevestigator:Q9SLC3 GermOnline:AT2G42360 Uniprot:Q9SLC3
Root	Isotig12334	0	20	-5.451	2.00E-06	TAIR|locus:2183730 - symbol:AT5G10770 "AT5G10770" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=ISS] [GO:0004190 "aspartic-type endopeptidase activity" evidence=IEA] [GO:0006508 "proteolysis" evidence=IEA] InterPro:IPR001461 InterPro:IPR009007 Pfam:PF00026 PRINTS:PR00792 EMBL:CP002688 GO:GO:0006508 GO:GO:0004190 InterPro:IPR021109 SUPFAM:SSF50630 Gene3D:G3DSA:2.40.70.10 PANTHER:PTHR13683 HSSP:P00799 EMBL:AY075656 EMBL:BT001004 IPI:IPI00543783 RefSeq:NP_196638.2 UniGene:At.32336 ProteinModelPortal:Q8S9J6 MEROPS:A01.A15 PRIDE:Q8S9J6 EnsemblPlants:AT5G10770.1 GeneID:830944 KEGG:ath:AT5G10770 TAIR:At5g10770 InParanoid:Q8S9J6 OMA:LEVVYDG PhylomeDB:Q8S9J6 ProtClustDB:CLSN2686424 Genevestigator:Q8S9J6 Uniprot:Q8S9J6
Root	Isotig12342	9	29	-1.817	0.000341695	TAIR|locus:2102072 - symbol:MTO1 "AT3G01120" species:3702 "Arabidopsis thaliana" [GO:0009086 "methionine biosynthetic process" evidence=IMP] [GO:0001887 "selenium compound metabolic process" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0003962 "cystathionine gamma-synthase activity" evidence=ISS;IDA] InterPro:IPR000277 InterPro:IPR015421 InterPro:IPR015422 Pfam:PF01053 PROSITE:PS00868 GO:GO:0009570 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0030170 InterPro:IPR015424 Gene3D:G3DSA:3.40.640.10 Gene3D:G3DSA:3.90.1150.10 SUPFAM:SSF53383 GO:GO:0009086 GO:GO:0001887 EMBL:AC008261 eggNOG:COG0626 HOGENOM:HBG754729 PANTHER:PTHR11808 EMBL:X79707 KO:K01739 GO:GO:0003962 EMBL:X94756 EMBL:U43709 EMBL:U83500 EMBL:AB010888 EMBL:AF039206 EMBL:AY094438 EMBL:AY091062 EMBL:BT002753 IPI:IPI00534631 PIR:S51579 PIR:S71228 RefSeq:NP_186761.1 UniGene:At.20198 ProteinModelPortal:P55217 SMR:P55217 STRING:P55217 PRIDE:P55217 EnsemblPlants:AT3G01120.1 GeneID:821292 KEGG:ath:AT3G01120 TAIR:At3g01120 InParanoid:P55217 OMA:KARRNCS PhylomeDB:P55217 ProtClustDB:CLSN2679254 ArrayExpress:P55217 Genevestigator:P55217 GermOnline:AT3G01120 Uniprot:P55217
Root	Isotig12347	35	87	-1.443	1.48E-07	TAIR|locus:3439219 - symbol:TUA6 "AT4G14960" species:3702 "Arabidopsis thaliana" [GO:0005874 "microtubule" evidence=IDA] [GO:0045298 "tubulin complex" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005200 "structural constituent of cytoskeleton" evidence=ISS] [GO:0005730 "nucleolus" evidence=IDA] [GO:0000226 "microtubule cytoskeleton organization" evidence=IMP] [GO:0005618 "cell wall" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0071258 "cellular response to gravity" evidence=IMP] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000217 InterPro:IPR002452 InterPro:IPR003008 InterPro:IPR008280 InterPro:IPR017975 InterPro:IPR018316 Pfam:PF00091 Pfam:PF03953 PRINTS:PR01161 PRINTS:PR01162 PROSITE:PS00227 SMART:SM00864 SMART:SM00865 GO:GO:0005525 GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005773 GO:GO:0005618 GO:GO:0005515 GO:GO:0005730 GO:GO:0005198 GO:GO:0003924 GO:GO:0009651 EMBL:AL161540 GO:GO:0000226 GO:GO:0005874 GO:GO:0051258 Gene3D:G3DSA:3.40.50.1440 SUPFAM:SSF52490 GO:GO:0007018 EMBL:Z97337 Gene3D:G3DSA:3.30.1330.20 SUPFAM:SSF55307 GO:GO:0045298 eggNOG:COG5023 GO:GO:0071258 HOGENOM:HBG750007 KO:K07374 InterPro:IPR023123 Gene3D:G3DSA:1.10.287.600 PANTHER:PTHR11588 ProtClustDB:PLN00221 UniGene:At.22368 UniGene:At.48153 EMBL:M84699

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EMBL:AY058858 EMBL:AY065347 EMBL:AY079036 EMBL:AY117174 IPI:IPI00520226 PIR:JQ1597 RefSeq:NP_193232.1 ProteinModelPortal:P29511 SMR:P29511 IntAct:P29511 STRING:P29511 PRIDE:P29511 EnsemblPlants:AT4G14960.2 GeneID:827154 KEGG:ath:AT4G14960 TAIR:At4g14960 InParanoid:P29511 OMA:MPSDKAI PhylomeDB:P29511 ArrayExpress:P29511 Genevestigator:P29511 Uniprot:P29511
Root	Isotig12358	1	12	-3.714	0.000699736	TAIR|locus:2093556 - symbol:CYP71B24 ""cytochrome P450, family 71, subfamily B, polypeptide 24"" species:3702 "Arabidopsis thaliana" [GO:0004497 "monooxygenase activity" evidence=IEA] [GO:0005506 "iron ion binding" evidence=IEA] [GO:0009055 "electron carrier activity" evidence=IEA] [GO:0019825 "oxygen binding" evidence=ISS] [GO:0020037 "heme binding" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] InterPro:IPR001128 InterPro:IPR002401 InterPro:IPR017972 Pfam:PF00067 PRINTS:PR00385 PRINTS:PR00463 PROSITE:PS00086 GO:GO:0016021 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0009055 GO:GO:0004497 eggNOG:COG2124 GO:GO:0020037 Gene3D:G3DSA:1.10.630.10 SUPFAM:SSF48264 KO:K00517 GO:GO:0016705 HOGENOM:HBG749920 EMBL:AB024038 ProtClustDB:CLSN2684856 EMBL:AK226798 IPI:IPI00533244 RefSeq:NP_189254.1 UniGene:At.37248 ProteinModelPortal:Q9LTL8 SMR:Q9LTL8 STRING:Q9LTL8 PRIDE:Q9LTL8 EnsemblPlants:AT3G26230.1 GeneID:822224 KEGG:ath:AT3G26230 GeneFarm:1230 TAIR:At3g26230 InParanoid:Q9LTL8 OMA:FICTHPE PhylomeDB:Q9LTL8 ArrayExpress:Q9LTL8 Genevestigator:Q9LTL8 GermOnline:AT3G26230 Uniprot:Q9LTL8
Root	Isotig12374	21	65	-1.759	1.58E-07	ZFIN|ZDB-GENE-070410-9 - symbol:zgc:158463 "zgc:158463" species:7955 "Danio rerio" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] ZFIN:ZDB-GENE-070410-9 EMBL:BX296557 EMBL:BX537263 EMBL:BC129240 IPI:IPI00837201 RefSeq:NP_001091866.1 RefSeq:XP_003200836.1 UniGene:Dr.155369 Ensembl:ENSDART00000102863 Ensembl:ENSDART00000126982 GeneID:100037361 GeneID:100151188 KEGG:dre:100037361 KEGG:dre:100151188 eggNOG:NOG298153 GeneTree:ENSGT00390000016898 InParanoid:A2VD29 OMA:ACHQHAL OrthoDB:EOG4FJ8BF Bgee:A2VD29 Uniprot:A2VD29
Root	Isotig12375	3	30	-3.451	1.87E-07	TAIR|locus:2183154 - symbol:TUA5 "AT5G19780" species:3702 "Arabidopsis thaliana" [GO:0005200 "structural constituent of cytoskeleton" evidence=ISS] [GO:0007017 "microtubule-based process" evidence=TAS] [GO:0045298 "tubulin complex" evidence=ISS] [GO:0005618 "cell wall" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0016020 "membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA;IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000217 InterPro:IPR002452 InterPro:IPR003008 InterPro:IPR008280 InterPro:IPR017975 InterPro:IPR018316 Pfam:PF00091 Pfam:PF03953 PRINTS:PR01161 PRINTS:PR01162 PROSITE:PS00227 SMART:SM00864 SMART:SM00865 GO:GO:0005525 GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 GO:GO:0046686 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005618 GO:GO:0005198 GO:GO:0003924 GO:GO:0005874 GO:GO:0051258 Gene3D:G3DSA:3.40.50.1440 SUPFAM:SSF52490 GO:GO:0007018 Gene3D:G3DSA:3.30.1330.20 SUPFAM:SSF55307 eggNOG:COG5023 EMBL:AF296838 GO:GO:0071258 UniGene:At.49039 HOGENOM:HBG750007 KO:K07374 InterPro:IPR023123 Gene3D:G3DSA:1.10.287.600 ProtClustDB:PLN00221 InterPro:IPR013838 EMBL:M17189 EMBL:M84698 EMBL:AF367301 EMBL:AY040012 EMBL:AY065164 EMBL:AY079366 EMBL:AY143895 EMBL:BT000718 EMBL:BT000719 EMBL:BT001197 IPI:IPI00529143 PIR:A32712 RefSeq:NP_197478.1 RefSeq:NP_197479.1 UniGene:At.23553 ProteinModelPortal:P20363 SMR:P20363 STRING:P20363 PRIDE:P20363 EnsemblPlants:AT5G19770.1 EnsemblPlants:AT5G19780.1 GeneID:832097 GeneID:832098 KEGG:ath:AT5G19770 KEGG:ath:AT5G19780 TAIR:At5g19770 TAIR:At5g19780 InParanoid:P20363 OMA:ISAVREC PhylomeDB:P20363 ArrayExpress:P20363 Genevestigator:P20363 GermOnline:AT5G19770 Uniprot:P20363
Root	Isotig12377	37	8	2.080	2.32E-05	TAIR|locus:2131591 - symbol:CAT2 "AT4G35090" species:3702 "Arabidopsis thaliana" [GO:0004096 "catalase activity" evidence=ISS;IMP] [GO:0005777 "peroxisome" evidence=IDA;NAS] [GO:0042744 "hydrogen peroxide catabolic process" evidence=NAS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0006995 "cellular response to nitrogen starvation" evidence=IEP] [GO:0009970 "cellular response to sulfate starvation" evidence=IEP] [GO:0016036 "cellular response to phosphate starvation" evidence=IEP] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0010319 "stromule" evidence=IDA] [GO:0006979 "response to oxidative stress" evidence=IMP] [GO:0008219 "cell death" evidence=IMP] [GO:0009648 "photoperiodism" evidence=IMP] [GO:0045454 "cell redox homeostasis" evidence=IMP] [GO:0009416 "response to light stimulus" evidence=IEP] [GO:0005515 "protein binding" evidence=IPI] [GO:0050897 "cobalt ion binding" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA]

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						InterPro:IPR002226 InterPro:IPR011614 InterPro:IPR018028 InterPro:IPR020835 InterPro:IPR024708 InterPro:IPR024711 Pfam:PF00199 PIRSF:PIRSF038928 PRINTS:PR00067 PROSITE:PS00437 PROSITE:PS00438 PROSITE:PS51402 SMART:SM01060 InterPro:IPR010582 GO:GO:0005739 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0009507 GO:GO:0005515 GO:GO:0008219 GO:GO:0010319 GO:GO:0009409 GO:GO:0009514 GO:GO:0020037 GO:GO:0050897 EMBL:AL022023 EMBL:AL161586 GO:GO:0016036 GO:GO:0045454 GO:GO:0022626 GO:GO:0006995 GO:GO:0042744 GO:GO:0009970 GO:GO:0004096 eggNOG:COG0753 KO:K03781 Gene3D:G3DSA:2.40.180.10 PANTHER:PTHR11465 Pfam:PF06628 SUPFAM:SSF56634 HOGENOM:HBG339355 ProtClustDB:PLN02609 OMA:DWVYNNT EMBL:X64271 EMBL:X94447 EMBL:AY074301 EMBL:AY113854 IPI:IPI00520641 PIR:T05779 RefSeq:NP_195235.1 UniGene:At.24350 UniGene:At.64718 ProteinModelPortal:P25819 SMR:P25819 IntAct:P25819 STRING:P25819 PeroxiBase:5141 PRIDE:P25819 ProMEX:P25819 EnsemblPlants:AT4G35090.1 GeneID:829661 KEGG:ath:AT4G35090 TAIR:At4g35090 InParanoid:P25819 PhylomeDB:P25819 BioCyc:MetaCyc:AT4G35090-MONOMER ArrayExpress:P25819 Genevestigator:P25819 GO:GO:0009648 Uniprot:P25819
Root	Isotig12401	1	13	-3.829	0.000362856	TAIR|locus:2025396 - symbol:AT1G01540 "AT1G01540" species:3702 "Arabidopsis thaliana" [GO:0016301 "kinase activity" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0004674 "protein serine/threonine kinase activity" evidence=IDA] [GO:0046777 "protein autophosphorylation" evidence=IDA] InterPro:IPR000719 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 Pfam:PF00069 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005886 GO:GO:0005524 EMBL:Y12776 EMBL:AC061957 eggNOG:COG0515 SUPFAM:SSF56112 GO:GO:0004674 GO:GO:0046777 HOGENOM:HBG755340 EMBL:AF332429 EMBL:AF367265 EMBL:AY093964 IPI:IPI00528543 PIR:A86146 RefSeq:NP_171661.1 UniGene:At.24027 ProteinModelPortal:Q3EDL4 SMR:Q3EDL4 PRIDE:Q3EDL4 EnsemblPlants:AT1G01540.2 GeneID:839533 KEGG:ath:AT1G01540 GeneFarm:2081 TAIR:At1g01540 InParanoid:Q3EDL4 OMA:VIGRVRH PhylomeDB:Q3EDL4 ProtClustDB:CLSN2682866 ArrayExpress:O23699 Genevestigator:Q3EDL4 Uniprot:Q3EDL4
Root	Isotig12403	23	0	5.395	1.11E-06	TAIR|locus:2051343 - symbol:DGK5 "diacylglycerol kinase 5" species:3702 "Arabidopsis thaliana" [GO:0004143 "diacylglycerol kinase activity" evidence=IEA;ISS] [GO:0007205 "activation of protein kinase C activity by G-protein coupled receptor protein signaling pathway" evidence=IEA;ISS] InterPro:IPR000756 InterPro:IPR001206 Pfam:PF00609 Pfam:PF00781 PROSITE:PS50146 SMART:SM00045 SMART:SM00046 EMBL:CP002685 GO:GO:0007205 GO:GO:0004143 UniGene:At.46381 UniGene:At.48498 InterPro:IPR016961 PIRSF:PIRSF030829 EMBL:AF360300 EMBL:BT000983 IPI:IPI00530396 RefSeq:NP_001031381.1 RefSeq:NP_850007.1 ProteinModelPortal:Q9C5E5 IntAct:Q9C5E5 PRIDE:Q9C5E5 DNASU:816624 EnsemblPlants:AT2G20900.1 EnsemblPlants:AT2G20900.4 GeneID:816624 KEGG:ath:AT2G20900 TAIR:At2g20900 InParanoid:Q9C5E5 OMA:LATHDCR PhylomeDB:Q9C5E5 ProtClustDB:CLSN2688289 Genevestigator:Q9C5E5 Uniprot:Q9C5E5
Root	Isotig12405	0	21	-5.521	1.09E-06	TAIR|locus:2059708 - symbol:AT2G01900 "AT2G01900" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0016787 "hydrolase activity" evidence=ISS] InterPro:IPR000300 SMART:SM00128 Pfam:PF03372 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0004527 EMBL:AC007069 GO:GO:0004519 InterPro:IPR005135 SUPFAM:SSF56219 GO:GO:0046854 eggNOG:COG5411 HSSP:O43001 HOGENOM:HBG593315 IPI:IPI00541595 PIR:E84430 RefSeq:NP_178299.1 UniGene:At.50064 ProteinModelPortal:Q9SIS4 SMR:Q9SIS4 PRIDE:Q9SIS4 EnsemblPlants:AT2G01900.1 GeneID:814721 KEGG:ath:AT2G01900 TAIR:At2g01900 InParanoid:Q9SIS4 OMA:HDRVILL PhylomeDB:Q9SIS4 ProtClustDB:CLSN2683551 ArrayExpress:Q9SIS4 Genevestigator:Q9SIS4 Uniprot:Q9SIS4
Root	Isotig12407	41	93	-1.311	4.40E-07	TAIR|locus:3439219 - symbol:TUA6 "AT4G14960" species:3702 "Arabidopsis thaliana" [GO:0005874 "microtubule" evidence=IDA] [GO:0045298 "tubulin complex" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005200 "structural constituent of cytoskeleton" evidence=ISS] [GO:0005730 "nucleolus" evidence=IDA] [GO:0000226 "microtubule cytoskeleton organization" evidence=IMP] [GO:0005618 "cell wall" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0071258 "cellular response to gravity" evidence=IMP] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000217 InterPro:IPR002452 InterPro:IPR003008 InterPro:IPR008280 InterPro:IPR017975 InterPro:IPR018316 Pfam:PF00091 Pfam:PF03953 PRINTS:PR01161 PRINTS:PR01162 PROSITE:PS00227 SMART:SM00864 SMART:SM00865 GO:GO:0005525 GO:GO:0005829 GO:GO:0005886 GO:GO:0009506

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005773 GO:GO:0005618 GO:GO:0005515 GO:GO:0005730 GO:GO:0005198 GO:GO:0003924 GO:GO:0009651 EMBL:AL161540 GO:GO:0000226 GO:GO:0005874 GO:GO:0051258 Gene3D:G3DSA:3.40.50.1440 SUPFAM:SSF52490 GO:GO:0007018 EMBL:Z97337 Gene3D:G3DSA:3.30.1330.20 SUPFAM:SSF55307 GO:GO:0045298 eggNOG:COG5023 GO:GO:0071258 HOGENOM:HBG750007 KO:K07374 InterPro:IPR023123 Gene3D:G3DSA:1.10.287.600 PANTHER:PTHR11588 ProtClustDB:PLN00221 UniGene:At.22368 UniGene:At.48153 EMBL:M84699 EMBL:AY058858 EMBL:AY065347 EMBL:AY079036 EMBL:AY117174 IPI:IPI00520226 PIR:JQ1597 RefSeq:NP_193232.1 ProteinModelPortal:P29511 SMR:P29511 IntAct:P29511 STRING:P29511 PRIDE:P29511 EnsemblPlants:AT4G14960.2 GeneID:827154 KEGG:ath:AT4G14960 TAIR:At4g14960 InParanoid:P29511 OMA:MPSDKAI PhylomeDB:P29511 ArrayExpress:P29511 Genevestigator:P29511 Uniprot:P29511
Root	Isotig12431	0	17	-5.216	1.26E-05	TAIR|locus:2158187 - symbol:ARA12 "AT5G67360" species:3702 "Arabidopsis thaliana" [GO:0006508 "proteolysis" evidence=ISS] [GO:0004252 "serine-type endopeptidase activity" evidence=IDA] [GO:0005576 "extracellular region" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0009505 "plant-type cell wall" evidence=IDA] [GO:0010214 "seed coat development" evidence=IMP] [GO:0048359 "mucilage metabolic process involved seed coat development" evidence=IMP] [GO:0080001 "mucilage extrusion from seed coat" evidence=IMP] [GO:0048046 "apoplast" evidence=IDA] InterPro:IPR000209 InterPro:IPR010259 Pfam:PF00082 Pfam:PF05922 InterPro:IPR003137 Prosite:PS00137 Prosite:PS00138 PANTHER:PTHR10795 Pfam:PF02225 GO:GO:0048046 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0042802 GO:GO:0006508 GO:GO:0004252 GO:GO:0009505 GO:GO:0043086 InterPro:IPR023828 InterPro:IPR015500 Gene3D:G3DSA:3.40.50.200 PRINTS:PR00723 SUPFAM:SSF52743 PROSITE:PS00136 eggNOG:COG1404 EMBL:AB007645 GO:GO:0080001 HOGENOM:HBG591621 EMBL:AF065639 EMBL:AF360285 EMBL:AY091773 EMBL:AY142612 EMBL:BT001082 EMBL:X85974 IPI:IPI00548134 PIR:JC7519 PIR:S52770 RefSeq:NP_569048.1 UniGene:At.23238 UniGene:At.67722 UniGene:At.71531 ProteinModelPortal:O65351 SMR:O65351 STRING:O65351 MEROPS:S08.112 PRIDE:O65351 EnsemblPlants:AT5G67360.1 GeneID:836871 KEGG:ath:AT5G67360 GeneFarm:1964 TAIR:At5g67360 InParanoid:O65351 OMA:TYIVHMA PhylomeDB:O65351 ProtClustDB:CLSN2690100 ArrayExpress:O65351 Genevestigator:O65351 GermOnline:AT5G67360 GO:GO:0048359 Uniprot:O65351
Root	Isotig12435	0	15	-5.036	4.38E-05	TAIR|locus:2087368 - symbol:scpl40 "serine carboxypeptidase-like 40" species:3702 "Arabidopsis thaliana" [GO:0004185 "serine-type carboxypeptidase activity" evidence=IEA;ISS] [GO:0006508 "proteolysis" evidence=IEA;ISS] InterPro:IPR001563 InterPro:IPR018202 Pfam:PF00450 PRINTS:PR00724 PROSITE:PS00131 PROSITE:PS00560 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005576 GO:GO:0006508 EMBL:AL163818 GO:GO:0004185 eggNOG:COG2939 PANTHER:PTHR11802 HOGENOM:HBG588032 EMBL:AY087589 EMBL:AK228170 EMBL:BT003126 IPI:IPI00536894 PIR:T49188 RefSeq:NP_191906.1 UniGene:At.33917 UniGene:At.71216 ProteinModelPortal:Q0WRX3 SMR:Q0WRX3 MEROPS:S10.A41 PRIDE:Q0WRX3 EnsemblPlants:AT3G63470.1 GeneID:825522 KEGG:ath:AT3G63470 TAIR:At3g63470 InParanoid:Q0WRX3 OMA:WNNAANV PhylomeDB:Q0WRX3 ProtClustDB:CLSN2914723 Genevestigator:Q0WRX3 Uniprot:Q0WRX3
Root	Isotig12441	15	1	3.778	0.000266457	TAIR|locus:2007943 - symbol:HAB2 "homology to ABI2" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004722 "protein serine/threonine phosphatase activity" evidence=IEA;ISS] [GO:0006470 "protein dephosphorylation" evidence=IEA] InterPro:IPR000222 InterPro:IPR001932 Pfam:PF00481 PROSITE:PS01032 SMART:SM00331 SMART:SM00332 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0006470 GO:GO:0009738 GO:GO:0004722 GO:GO:0046872 EMBL:AC022492 eggNOG:COG0631 Gene3D:G3DSA:3.60.40.10 SUPFAM:SSF81606 GO:GO:0008287 InterPro:IPR015655 PANTHER:PTHR13832 HSSP:P35813 HOGENOM:HBG747569 KO:K14497 EMBL:AK118656 IPI:IPI00532752 RefSeq:NP_173199.2 UniGene:At.41827 ProteinModelPortal:Q9LNP9 SMR:Q9LNP9 DIP:DIP-48989N PRIDE:Q9LNP9 EnsemblPlants:AT1G17550.1 GeneID:838330 KEGG:ath:AT1G17550 TAIR:At1g17550 InParanoid:Q8GWS8 OMA:RRILAWH PhylomeDB:Q9LNP9 ProtClustDB:CLSN2679602 Genevestigator:Q9LNP9 Uniprot:Q9LNP9
Root	Isotig12449	1	12	-3.714	0.000699736	TAIR|locus:2019693 - symbol:ABCG39 "AT1G66950" species:3702 "Arabidopsis thaliana" [GO:0042626 "ATPase activity, coupled to transmembrane movement of substances" evidence=ISS] [GO:0006855 "drug transmembrane transport" evidence=ISS;IMP] [GO:0000302 "response to reactive oxygen species" evidence=IEP] [GO:0005886 "plasma membrane" evidence=IDA] InterPro:IPR003439 InterPro:IPR003593 InterPro:IPR013525 Pfam:PF00005 Pfam:PF01061 PROSITE:PS00211 PROSITE:PS50893 SMART:SM00382 GO:GO:0016021 EMBL:CP002684

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GenomeReviews:CT485782_GR GO:GO:0005886 GO:GO:0005524 eggNOG:COG1131 GO:GO:0016887 HOGENOM:HBG750535 InterPro:IPR013581 Pfam:PF08370 ProtClustDB:CLSN2690483 EMBL:AC007152 EMBL:AC083891 EMBL:BK001010 IPI:IPI00531524 PIR:D96693 RefSeq:NP_176867.2 UniGene:At.35712 ProteinModelPortal:Q7PC84 SMR:Q7PC84 PRIDE:Q7PC84 EnsemblPlants:AT1G66950.1 GeneID:843013 KEGG:ath:AT1G66950 TAIR:At1g66950 InParanoid:Q7PC84 OMA:AKFLWFY PhylomeDB:Q7PC84 ArrayExpress:Q7PC84 Genevestigator:Q7PC84 GermOnline:AT1G66950 GO:GO:0006855 GO:GO:0000302 Uniprot:Q7PC84
Root	Isotig12455	25	2	3.515	4.58E-06	TAIR|locus:2086122 - symbol:AAE7 "AT3G16910" species:3702 "Arabidopsis thaliana" [GO:0016208 "AMP binding" evidence=ISS] [GO:0003987 "acetate-CoA ligase activity" evidence=IDA] [GO:0006083 "acetate metabolic process" evidence=IDA] [GO:0019605 "butyrate metabolic process" evidence=IDA] [GO:0047760 "butyrate-CoA ligase activity" evidence=IDA] [GO:0005777 "peroxisome" evidence=IDA] [GO:0006097 "glyoxylate cycle" evidence=IDA] InterPro:IPR000873 Pfam:PF00501 Prosite:PS00455 EMBL:CP002686 GO:GO:0005777 eggNOG:COG0318 InterPro:IPR025110 Pfam:PF13193 HSSP:P08659 GO:GO:0003824 GO:GO:0047760 GO:GO:0019605 GO:GO:0006097 GO:GO:0006083 GO:GO:0003987 EMBL:AF503766 EMBL:AB026636 EMBL:AY065002 EMBL:AY090269 IPI:IPI00535625 RefSeq:NP_188316.1 UniGene:At.28607 ProteinModelPortal:Q8VZF1 SMR:Q8VZF1 PRIDE:Q9LSQ0 ProMEX:Q8VZF1 EnsemblPlants:AT3G16910.1 GeneID:820946 KEGG:ath:AT3G16910 TAIR:At3g16910 InParanoid:Q8VZF1 OMA:KNPEANK PhylomeDB:Q8VZF1 ProtClustDB:PLN02479 Genevestigator:Q8VZF1 Uniprot:Q8VZF1
Root	Isotig12466	0	17	-5.216	1.26E-05	TAIR|locus:2009175 - symbol:AT1G06650 "AT1G06650" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0016706 "oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors" evidence=ISS] [GO:0005829 "cytosol" evidence=RCA] InterPro:IPR005123 Pfam:PF03171 PROSITE:PS51471 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0046872 EMBL:AC007592 PIR:D86201 HSSP:Q08506 eggNOG:COG3491 HOGENOM:HBG749762 GO:GO:0016706 ProtClustDB:CLSN2682337 EMBL:AY142493 EMBL:AF370322 IPI:IPI00520186 IPI:IPI00524063 RefSeq:NP_172150.1 RefSeq:NP_849602.1 UniGene:At.26217 UniGene:At.42330 ProteinModelPortal:Q8H1S4 SMR:Q8H1S4 PRIDE:Q8H1S4 EnsemblPlants:AT1G06650.2 GeneID:837175 KEGG:ath:AT1G06650 TAIR:At1g06650 InParanoid:Q8H1S4 OMA:ISLEHRV PhylomeDB:Q8H1S4 Genevestigator:Q8H1S4 Uniprot:Q8H1S4
Root	Isotig12471	1	31	-5.083	4.06E-09	TAIR|locus:2202044 - symbol:STP1 "AT1G11260" species:3702 "Arabidopsis thaliana" [GO:0005351 "sugar:hydrogen symporter activity" evidence=ISS] [GO:0006810 "transport" evidence=IEA] [GO:0015144 "carbohydrate transmembrane transporter activity" evidence=ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0055085 "transmembrane transport" evidence=IEA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR003663 InterPro:IPR005828 InterPro:IPR005829 Pfam:PF00083 PRINTS:PR00171 PROSITE:PS00216 PROSITE:PS00217 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005886 GO:GO:0009506 GO:GO:0005634 GO:GO:0005773 GO:GO:0015293 eggNOG:COG0477 InterPro:IPR016196 SUPFAM:SSF103473 GO:GO:0008643 InterPro:IPR020846 PROSITE:PS50850 HOGENOM:HBG744444 GO:GO:0022891 TIGRFAMs:TIGR00879 EMBL:AC007259 EMBL:X55350 EMBL:AY059781 EMBL:AY054249 EMBL:AY133845 EMBL:AY087292 EMBL:AF083803 EMBL:AK221157 IPI:IPI00532110 PIR:E86246 PIR:S12042 RefSeq:NP_172592.1 UniGene:At.24793 UniGene:At.67772 UniGene:At.74867 ProteinModelPortal:P23586 STRING:P23586 TCDB:2.A.1.1.60 PRIDE:P23586 EnsemblPlants:AT1G11260.1 GeneID:837667 KEGG:ath:AT1G11260 TAIR:At1g11260 InParanoid:P23586 OMA:FTCVVAA PhylomeDB:P23586 ProtClustDB:CLSN2681949 ArrayExpress:P23586 Genevestigator:P23586 GermOnline:AT1G11260 Uniprot:P23586
Root	Isotig12490	2	22	-3.588	5.84E-06	TAIR|locus:2165452 - symbol:AOS "AT5G42650" species:3702 "Arabidopsis thaliana" [GO:0009611 "response to wounding" evidence=IEP;IMP] [GO:0009753 "response to jasmonic acid stimulus" evidence=IMP] [GO:0009695 "jasmonic acid biosynthetic process" evidence=IDA;TAS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=ISS;IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0006952 "defense response" evidence=TAS] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0009978 "allene oxide synthase activity" evidence=IDA] [GO:0031407 "oxylipin metabolic process" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009579 "thylakoid"

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						evidence=IDA] [GO:0009620 "response to fungus" evidence=IEP] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0019373 "epoxygenase P450 pathway" evidence=ISS] [GO:0019825 "oxygen binding" evidence=ISS] [GO:0016836 "hydro-lyase activity" evidence=IDA] InterPro:IPR001128 Pfam:PF00067 PROSITE:PS00086 GO:GO:0005739 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0006952 GO:GO:0009753 GO:GO:0009611 GO:GO:0009055 GO:GO:0009695 GO:GO:0009941 GO:GO:0020037 Gene3D:G3DSA:1.10.630.10 SUPFAM:SSF48264 GO:GO:0009620 GO:GO:0009535 GO:GO:0010287 GO:GO:0016705 EMBL:AB007647 EMBL:X92510 EMBL:Y12636 EMBL:AF172727 EMBL:AY062828 EMBL:AY065089 EMBL:AY128733 EMBL:AY128755 IPI:IPI00526231 RefSeq:NP_199079.1 UniGene:At.211 PDB:2RCH PDB:2RCL PDB:2RCM PDB:3CLI PDB:3DSI PDB:3DSJ PDB:3DSK PDBsum:2RCH PDBsum:2RCL PDBsum:2RCM PDBsum:3CLI PDBsum:3DSI PDBsum:3DSJ PDBsum:3DSK ProteinModelPortal:Q96242 SMR:Q96242 IntAct:Q96242 STRING:Q96242 PRIDE:Q96242 EnsemblPlants:AT5G42650.1 GeneID:834273 KEGG:ath:AT5G42650 GeneFarm:1256 TAIR:At5g42650 eggNOG:NOG286560 HOGENOM:HBG593778 InParanoid:Q96242 KO:K01723 OMA:EGEMLFG PhylomeDB:Q96242 ProtClustDB:PLN02648 ArrayExpress:Q96242 Genevestigator:Q96242 GermOnline:AT5G42650 GO:GO:0009978 GO:GO:0047987 Uniprot:Q96242
Root	Isotig12493	0	14	-4.936	8.24E-05	TAIR|locus:2050669 - symbol:AT2G45910 species:3702 "Arabidopsis thaliana" [GO:0000151 "ubiquitin ligase complex" evidence=IEA] [GO:0004672 "protein kinase activity" evidence=IEA] [GO:0004674 "protein serine/threonine kinase activity" evidence=IEA] [GO:0004842 "ubiquitin-protein ligase activity" evidence=IEA] [GO:0005524 "ATP binding" evidence=IEA] [GO:0006468 "protein phosphorylation" evidence=IEA] [GO:0006950 "response to stress" evidence=IEA] [GO:0016301 "kinase activity" evidence=ISS] [GO:0016567 "protein ubiquitination" evidence=IEA] InterPro:IPR000719 InterPro:IPR003613 InterPro:IPR006016 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 Pfam:PF00069 Pfam:PF00582 Pfam:PF04564 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 SMART:SM00504 GO:GO:0005524 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0006950 eggNOG:COG0515 SUPFAM:SSF56112 GO:GO:0004674 HOGENOM:HBG755340 InterPro:IPR013083 Gene3D:G3DSA:3.30.40.10 GO:GO:0004842 InterPro:IPR014729 Gene3D:G3DSA:3.40.50.620 GO:GO:0000151 EMBL:AC004665 HSSP:Q8VZ40 EMBL:BT002512 EMBL:AK227123 IPI:IPI00542046 PIR:T02456 RefSeq:NP_182115.2 UniGene:At.36571 ProteinModelPortal:Q8GUH1 SMR:Q8GUH1 PRIDE:Q8GUH1 EnsemblPlants:AT2G45910.1 GeneID:819199 KEGG:ath:AT2G45910 GeneFarm:1984 TAIR:At2g45910 InParanoid:Q8GUH1 OMA:SQMIPLM PhylomeDB:Q8GUH1 ProtClustDB:CLSN2680270 Genevestigator:Q8GUH1 Uniprot:Q8GUH1
Root	Isotig12509	0	24	-5.714	1.84E-07	TAIR|locus:2061456 - symbol:scpl23 "serine carboxypeptidase-like 23" species:3702 "Arabidopsis thaliana" [GO:0004185 "serine-type carboxypeptidase activity" evidence=IEA;ISS] [GO:0006508 "proteolysis" evidence=IEA;ISS] InterPro:IPR001563 InterPro:IPR018202 Pfam:PF00450 PRINTS:PR00724 PROSITE:PS00131 PROSITE:PS00560 GenomeReviews:CT485783_GR GO:GO:0005576 GO:GO:0006508 GO:GO:0004185 eggNOG:COG2939 PANTHER:PTHR11802 HOGENOM:HBG588032 EMBL:AC005170 HSSP:P08819 IPI:IPI00546396 PIR:E84631 ProteinModelPortal:O82229 SMR:O82229 MEROPS:S10.A30 TAIR:At2g24010 InParanoid:O82229 PhylomeDB:O82229 ArrayExpress:O82229 Genevestigator:O82229 Uniprot:O82229
Root	Isotig12519	0	16	-5.129	2.34E-05	UNIPROTKB|G3N0S8 - symbol:Bt.88669 "Uncharacterized protein" species:9913 "Bos taurus" [GO:0009055 "electron carrier activity" evidence=IEA] [GO:0016712 "oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, reduced flavin or flavoprotein as one donor, and incorporation of one atom of oxygen" evidence=IEA] [GO:0020037 "heme binding" evidence=IEA] InterPro:IPR001128 InterPro:IPR002402 InterPro:IPR008072 InterPro:IPR017972 Pfam:PF00067 PRINTS:PR00385 PRINTS:PR00464 PRINTS:PR01689 PROSITE:PS00086 GO:GO:0009055 GO:GO:0020037 Gene3D:G3DSA:1.10.630.10 SUPFAM:SSF48264 GeneTree:ENSGT00540000069787 GO:GO:0016712 EMBL:DAAA02058295 UniGene:Bt.88669 Ensembl:ENSBTAT00000063483 Uniprot:G3N0S8
Root	Isotig12521	12	36	-1.714	0.0001272	TAIR|locus:2078603 - symbol:SRG3 "AT3G02040" species:3702 "Arabidopsis thaliana" [GO:0006071 "glycerol metabolic process" evidence=ISS] [GO:0008889 "glycerophosphodiester phosphodiesterase activity" evidence=ISS;IDA] [GO:0009536 "plastid" evidence=IDA] [GO:0030643 "cellular phosphate ion homeostasis" evidence=IMP] InterPro:IPR004129 InterPro:IPR017946 Pfam:PF03009 EMBL:CP002686 Gene3D:G3DSA:3.20.20.190 SUPFAM:SSF51695 GO:GO:0006629 EMBL:AC011664 GO:GO:0006071 GO:GO:0009536 GO:GO:0030643 GO:GO:0008889 EMBL:AY072127 EMBL:AY114073 IPI:IPI00531878 RefSeq:NP_566159.1 UniGene:At.20730 UniGene:At.75107 ProteinModelPortal:Q9SGA2 SMR:Q9SGA2

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						PRIDE:Q9SGA2 EnsemblPlants:AT3G02040.1 GeneID:821175 KEGG:ath:AT3G02040 TAIR:At3g02040 InParanoid:Q9SGA2 OMA:AVAFVEF PhylomeDB:Q9SGA2 Genevestigator:Q9SGA2 Uniprot:Q9SGA2
Root	Isotig12535	0	13	-4.829	0.000155955	TAIR|locus:2183730 - symbol:AT5G10770 "AT5G10770" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=ISS] [GO:0004190 "aspartic-type endopeptidase activity" evidence=IEA] [GO:0006508 "proteolysis" evidence=IEA] InterPro:IPR001461 InterPro:IPR009007 Pfam:PF00026 PRINTS:PR00792 EMBL:CP002688 GO:GO:0006508 GO:GO:0004190 InterPro:IPR021109 SUPFAM:SSF50630 Gene3D:G3DSA:2.40.70.10 PANTHER:PTHR13683 HSSP:P00799 EMBL:AY075656 EMBL:BT001004 IPI:IPI00543783 RefSeq:NP_196638.2 UniGene:At.32336 ProteinModelPortal:Q8S9J6 MEROPS:A01.A15 PRIDE:Q8S9J6 EnsemblPlants:AT5G10770.1 GeneID:830944 KEGG:ath:AT5G10770 TAIR:At5g10770 InParanoid:Q8S9J6 OMA:LEVVYDG PhylomeDB:Q8S9J6 ProtClustDB:CLSN2686424 Genevestigator:Q8S9J6 Uniprot:Q8S9J6
Root	Isotig12539	7	24	-1.907	0.000762598	TAIR|locus:2046565 - symbol:PKT3 "AT2G33150" species:3702 "Arabidopsis thaliana" [GO:0019395 "fatty acid oxidation" evidence=TAS] [GO:0003988 "acetyl-CoA C-acyltransferase activity" evidence=ISS;IMP;IDA] [GO:0009611 "response to wounding" evidence=NAS] [GO:0009695 "jasmonic acid biosynthetic process" evidence=NAS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005777 "peroxisome" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] [GO:0009789 "positive regulation of abscisic acid mediated signaling pathway" evidence=IMP] [GO:0006635 "fatty acid beta-oxidation" evidence=TAS] [GO:0010111 "glyoxysome organization" evidence=IMP] InterPro:IPR002155 InterPro:IPR016038 InterPro:IPR016039 InterPro:IPR020610 InterPro:IPR020613 InterPro:IPR020615 InterPro:IPR020616 InterPro:IPR020617 Pfam:PF00108 Pfam:PF02803 PROSITE:PS00098 PROSITE:PS00099 PROSITE:PS00737 GO:GO:0005739 GO:GO:0005774 GO:GO:0009507 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009611 GO:GO:0005730 GO:GO:0009789 GO:GO:0009695 GO:GO:0009514 GO:GO:0006635 eggNOG:COG0183 HOGENOM:HBG370930 Gene3D:G3DSA:3.40.47.10 PANTHER:PTHR18919 SUPFAM:SSF53901 TIGRFAMs:TIGR01930 EMBL:AC002334 GO:GO:0003988 KO:K07513 ProtClustDB:PLN02287 EMBL:AB008854 EMBL:AB008855 EMBL:AY058176 EMBL:AF327529 EMBL:AF349530 EMBL:AY052702 EMBL:AY063720 EMBL:AY087543 EMBL:AK222103 IPI:IPI00546896 PIR:T52110 RefSeq:NP_180873.1 UniGene:At.23661 UniGene:At.72951 PDB:2C7Y PDB:2C7Z PDB:2WU9 PDBsum:2C7Y PDBsum:2C7Z PDBsum:2WU9 ProteinModelPortal:Q56WD9 SMR:Q56WD9 IntAct:Q56WD9 STRING:Q56WD9 PRIDE:Q56WD9 ProMEX:Q56WD9 EnsemblPlants:AT2G33150.1 GeneID:817876 KEGG:ath:AT2G33150 GeneFarm:5069 TAIR:At2g33150 InParanoid:Q56WD9 OMA:AQLGDIC PhylomeDB:Q56WD9 BRENDA:2.3.1.16 ArrayExpress:Q9S7M3 Genevestigator:Q56WD9 GermOnline:AT2G33150 GO:GO:0010111 Uniprot:Q56WD9
Root	Isotig12578	24	103	-2.231	1.23E-14	ZFIN|ZDB-GENE-070410-9 - symbol:zgc:158463 "zgc:158463" species:7955 "Danio rerio" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] ZFIN:ZDB-GENE-070410-9 EMBL:BX296557 EMBL:BX537263 EMBL:BC129240 IPI:IPI00837201 RefSeq:NP_001091866.1 RefSeq:XP_003200836.1 UniGene:Dr.155369 Ensembl:ENSDART00000102863 Ensembl:ENSDART00000126982 GeneID:100037361 GeneID:100151188 KEGG:dre:100037361 KEGG:dre:100151188 eggNOG:NOG298153 GeneTree:ENSGT00390000016898 InParanoid:A2VD29 OMA:ACHQHAL OrthoDB:EOG4FJ8BF Bgee:A2VD29 Uniprot:A2VD29
Root	Isotig12588	15	0	4.778	0.000105609	TAIR|locus:2115050 - symbol:CYP81D3 ""cytochrome P450, family 81, subfamily D, polypeptide 3"" species:3702 "Arabidopsis thaliana" [GO:0004497 "monooxygenase activity" evidence=IEA] [GO:0005506 "iron ion binding" evidence=IEA] [GO:0009055 "electron carrier activity" evidence=IEA] [GO:0019825 "oxygen binding" evidence=ISS] [GO:0020037 "heme binding" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] InterPro:IPR001128 InterPro:IPR002401 InterPro:IPR017972 Pfam:PF00067 PRINTS:PR00385 PRINTS:PR00463 PROSITE:PS00086 GO:GO:0009055 GO:GO:0004497 GO:GO:0020037 Gene3D:G3DSA:1.10.630.10 SUPFAM:SSF48264 GO:GO:0016705 EMBL:AK175373 IPI:IPI00539313 ProteinModelPortal:Q682J4 STRING:Q682J4 PRIDE:Q682J4 TAIR:At4g37340 PhylomeDB:Q682J4 Genevestigator:Q682J4 Uniprot:Q682J4
Root	Isotig12610	34	9	1.789	0.000244108	TAIR|locus:2085770 - symbol:PAP18 "AT3G20500" species:3702 "Arabidopsis thaliana" [GO:0004722 "protein serine/threonine phosphatase activity" evidence=ISS] [GO:0008150 "biological_process" evidence=ND] [GO:0003993 "acid phosphatase activity" evidence=ISS] InterPro:IPR004843 InterPro:IPR008963 InterPro:IPR015914 Pfam:PF00149 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005576

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0046872 GO:GO:0003993 eggNOG:COG1409 EMBL:AP000410 Gene3D:G3DSA:2.60.40.380 SUPFAM:SSF49363 HSSP:P80366 EMBL:AF448725 EMBL:AY062488 EMBL:AY093272 EMBL:AY297742 IPI:IPI00520729 RefSeq:NP_188686.2 UniGene:At.24149 ProteinModelPortal:Q9LJU7 SMR:Q9LJU7 STRING:Q9LJU7 PRIDE:Q9LJU7 EnsemblPlants:AT3G20500.1 GeneID:821596 KEGG:ath:AT3G20500 TAIR:At3g20500 InParanoid:Q9LJU7 OMA:GESTSYS PhylomeDB:Q9LJU7 ProtClustDB:CLSN2690556 ArrayExpress:Q8H6W7 Genevestigator:Q9LJU7 Uniprot:Q9LJU7
Root	Isotig12611	2	26	-3.829	4.59E-07	TAIR|locus:2075532 - symbol:DJ1D "AT3G02720" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0016798 "hydrolase activity, acting on glycosyl bonds" evidence=IEA] InterPro:IPR006286 PROSITE:PS51276 INTERPRO:IPR002818 EMBL:CP002686 GO:GO:0016740 GO:GO:0016798 GO:GO:0006541 EMBL:AC018363 Pfam:PF01965 TIGRFAMs:TIGR01382 EMBL:BT000947 IPI:IPI00522252 RefSeq:NP_186921.1 UniGene:At.20933 PDB:3UK7 PDBsum:3UK7 ProteinModelPortal:Q9M8R4 SMR:Q9M8R4 MEROPS:C56.A01 PRIDE:Q9M8R4 EnsemblPlants:AT3G02720.1 GeneID:820875 KEGG:ath:AT3G02720 TAIR:At3g02720 InParanoid:Q9M8R4 OMA:FLCGDYM PhylomeDB:Q9M8R4 ProtClustDB:CLSN2685107 Genevestigator:Q9M8R4 Uniprot:Q9M8R4
Root	Isotig12614	0	11	-4.588	0.000569522	TAIR|locus:2045228 - symbol:SOBIR1 "AT2G31880" species:3702 "Arabidopsis thaliana" [GO:0004674 "protein serine/threonine kinase activity" evidence=ISS;IDA] [GO:0005524 "ATP binding" evidence=ISS] [GO:0006468 "protein phosphorylation" evidence=ISS] [GO:0007169 "transmembrane receptor protein tyrosine kinase signaling pathway" evidence=ISS] [GO:0016301 "kinase activity" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0010942 "positive regulation of cell death" evidence=IMP] [GO:0031349 "positive regulation of defense response" evidence=IMP] [GO:0004713 "protein tyrosine kinase activity" evidence=IDA] [GO:0060862 "negative regulation of floral organ abscission" evidence=IGI] InterPro:IPR001611 InterPro:IPR000719 InterPro:IPR008271 InterPro:IPR011009 Pfam:PF00069 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 PROSITE:PS51450 GO:GO:0016021 GO:GO:0005886 GO:GO:0005524 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0006952 eggNOG:COG0515 GO:GO:0004714 SUPFAM:SSF56112 GO:GO:0004674 GO:GO:0060862 EMBL:AC006533 GO:GO:0010942 EMBL:AF370596 EMBL:AY058153 EMBL:FJ708707 IPI:IPI00522533 PIR:C84726 RefSeq:NP_180747.1 UniGene:At.13945 UniGene:At.71125 ProteinModelPortal:Q9SKB2 SMR:Q9SKB2 STRING:Q9SKB2 PRIDE:Q9SKB2 EnsemblPlants:AT2G31880.1 GeneID:817746 KEGG:ath:AT2G31880 GeneFarm:2536 TAIR:At2g31880 InParanoid:Q9SKB2 OMA:IIGRGGC PhylomeDB:Q9SKB2 ProtClustDB:CLSN2683270 ArrayExpress:Q9SKB2 Genevestigator:Q9SKB2 GO:GO:0031349 Uniprot:Q9SKB2
Root	Isotig12641	3	30	-3.451	1.87E-07	No hit
Root	Isotig12642	0	25	-5.773	1.02E-07	UNIPROTKB|Q5H873 - symbol:HMT/HLT "13-hydroxylupanine O-tigloyltransferase" species:3870 "Lupinus albus" [GO:0009821 "alkaloid biosynthetic process" evidence=IDA] [GO:0047203 "13-hydroxylupinine O-tigloyltransferase activity" evidence=IDA] InterPro:IPR003480 Pfam:PF02458 InterPro:IPR023213 Gene3D:G3DSA:3.30.559.10 EMBL:AB181292 EMBL:EF381744 ProteinModelPortal:Q5H873 BRENDA:2.3.1.93 GO:GO:0047203 GO:GO:0009821 Uniprot:Q5H873
Root	Isotig12648	62	0	6.825	2.85E-15	TAIR|locus:2151739 - symbol:GSR 1 "glutamine synthase clone R1" species:3702 "Arabidopsis thaliana" [GO:0004356 "glutamate-ammonia ligase activity" evidence=ISS;IDA;IPI] [GO:0005829 "cytosol" evidence=TAS] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0042128 "nitrate assimilation" evidence=TAS] [GO:0005515 "protein binding" evidence=IPI] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR008146 InterPro:IPR008147 InterPro:IPR014746 Pfam:PF00120 Pfam:PF03951 PROSITE:PS00180 PROSITE:PS00181 GO:GO:0005886 GO:GO:0009506 GO:GO:0005524 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005618 GO:GO:0005515 GO:GO:0005507 GO:GO:0022626 GO:GO:0042128 GO:GO:0009399 EMBL:AB018107 EMBL:AF419608 EMBL:AF428386 EMBL:AY079113 EMBL:BT000753 EMBL:AK222005 IPI:IPI00519748 PIR:S18601 RefSeq:NP_198576.1 UniGene:At.7003 ProteinModelPortal:Q56WN1 SMR:Q56WN1 IntAct:Q56WN1 STRING:Q56WN1 PRIDE:Q56WN1 EnsemblPlants:AT5G37600.1 GeneID:833738 KEGG:ath:AT5G37600 TAIR:At5g37600 eggNOG:COG0174 HOGENOM:HBG299709 InParanoid:Q56WN1 KO:K01915 OMA:DPYRVTS PhylomeDB:Q56WN1 ProtClustDB:PLN02284 BRENDA:6.3.1.2 ArrayExpress:Q9FHR0 Genevestigator:Q56WN1 GermOnline:AT5G37600 GO:GO:0004356 GO:GO:0006542 Gene3D:G3DSA:3.30.590.10 Gene3D:G3DSA:3.10.20.70 SUPFAM:SSF54368 Uniprot:Q56WN1

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig12651	0	20	-5.451	2.00E-06	TAIR|locus:2012748 - symbol:AT1G10280 "AT1G10280" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] InterPro:IPR003406 Pfam:PF02485 EMBL:CP002684 GO:GO:0016020 GO:GO:0008375 EMBL:AC005489 UniGene:At.24665 EMBL:BT029295 IPI:IPI00540152 RefSeq:NP_172499.1 UniGene:At.42188 ProteinModelPortal:Q9SY70 PRIDE:Q9SY70 EnsemblPlants:AT1G10280.1 GeneID:837567 KEGG:ath:AT1G10280 TAIR:At1g10280 InParanoid:Q9SY70 OMA:DEPTRYG PhylomeDB:Q9SY70 ProtClustDB:CLSN2679566 Genevestigator:Q9SY70 Uniprot:Q9SY70
Root	Isotig12662	0	17	-5.216	1.26E-05	TAIR|locus:2042947 - symbol:GPAT6 "AT2G38110" species:3702 "Arabidopsis thaliana" [GO:0008152 "metabolic process" evidence=ISS] [GO:0016746 "transferase activity, transferring acyl groups" evidence=ISS] [GO:0003841 "1-acylglycerol-3-phosphate O-acyltransferase activity" evidence=IGI] [GO:0009908 "flower development" evidence=IMP] [GO:0010143 "cutin biosynthetic process" evidence=IMP] InterPro:IPR002123 Pfam:PF01553 SMART:SM00563 GO:GO:0016021 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0008654 GO:GO:0003841 GO:GO:0009908 EMBL:AC003028 GO:GO:0010143 GO:GO:0004366 HOGENOM:HBG590278 KO:K13508 EMBL:AY062721 EMBL:AY114657 IPI:IPI00533394 PIR:T01243 RefSeq:NP_181346.1 UniGene:At.21177 ProteinModelPortal:O80437 STRING:O80437 PRIDE:O80437 EnsemblPlants:AT2G38110.1 GeneID:818389 KEGG:ath:AT2G38110 TAIR:At2g38110 eggNOG:NOG322610 InParanoid:O80437 OMA:GKSPIEV PhylomeDB:O80437 ProtClustDB:PLN02177 ArrayExpress:O80437 Genevestigator:O80437 GermOnline:AT2G38110 Uniprot:O80437
Root	Isotig12665	0	11	-4.588	0.000569522	UNIPROTKB|Q9XHE7 - symbol:CYP71D13 "Cytochrome P450 71D13" species:34256 "Mentha x piperita" [GO:0018674 "(S)-limonene 3-monooxygenase activity" evidence=IDA] [GO:0055114 "oxidation-reduction process" evidence=IDA] InterPro:IPR001128 InterPro:IPR002401 InterPro:IPR017972 Pfam:PF00067 PRINTS:PR00385 PRINTS:PR00463 PROSITE:PS00086 GO:GO:0016021 GO:GO:0005789 GO:GO:0009055 GO:GO:0020037 Gene3D:G3DSA:1.10.630.10 SUPFAM:SSF48264 HSSP:P08684 EMBL:AF124816 ProteinModelPortal:Q9XHE7 BioCyc:MetaCyc:MONOMER-6762 GO:GO:0018674 Uniprot:Q9XHE7
Root	Isotig12672	0	11	-4.588	0.000569522	TAIR|locus:2170224 - symbol:AT5G06740 species:3702 "Arabidopsis thaliana" [GO:0004672 "protein kinase activity" evidence=IEA] [GO:0004674 "protein serine/threonine kinase activity" evidence=IEA] [GO:0005524 "ATP binding" evidence=IEA] [GO:0006468 "protein phosphorylation" evidence=IEA] [GO:0016301 "kinase activity" evidence=ISS] [GO:0030246 "carbohydrate binding" evidence=ISS] InterPro:IPR000719 InterPro:IPR001220 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 Pfam:PF00069 Pfam:PF00139 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 GO:GO:0016021 GO:GO:0005886 GO:GO:0005524 EMBL:CP002688 GenomeReviews:BA000015_GR eggNOG:COG0515 GO:GO:0004872 GO:GO:0005529 SUPFAM:SSF56112 GO:GO:0004674 HOGENOM:HBG755340 InterPro:IPR008985 InterPro:IPR013320 Gene3D:G3DSA:2.60.120.200 SUPFAM:SSF49899 PROSITE:PS00307 EMBL:AP002032 InterPro:IPR019825 HSSP:P05046 IPI:IPI00529565 RefSeq:NP_196292.1 UniGene:At.54751 ProteinModelPortal:Q9FG33 SMR:Q9FG33 PRIDE:Q9FG33 EnsemblPlants:AT5G06740.1 GeneID:830563 KEGG:ath:AT5G06740 GeneFarm:2658 TAIR:At5g06740 InParanoid:Q9FG33 OMA:ELNCVRS PhylomeDB:Q9FG33 ProtClustDB:CLSN2916527 Genevestigator:Q9FG33 Uniprot:Q9FG33
Root	Isotig12683	6	43	-2.970	5.29E-09	TAIR|locus:3439219 - symbol:TUA6 "AT4G14960" species:3702 "Arabidopsis thaliana" [GO:0005874 "microtubule" evidence=IDA] [GO:0045298 "tubulin complex" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005200 "structural constituent of cytoskeleton" evidence=ISS] [GO:0005730 "nucleolus" evidence=IDA] [GO:0000226 "microtubule cytoskeleton organization" evidence=IMP] [GO:0005618 "cell wall" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0071258 "cellular response to gravity" evidence=IMP] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000217 InterPro:IPR002452 InterPro:IPR003008 InterPro:IPR008280 InterPro:IPR017975 InterPro:IPR018316 Pfam:PF00091 Pfam:PF03953 PRINTS:PR01161 PRINTS:PR01162 PROSITE:PS00227 SMART:SM00864 SMART:SM00865 GO:GO:0005525 GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005773 GO:GO:0005618 GO:GO:0005515 GO:GO:0005730 GO:GO:0005198 GO:GO:0003924 GO:GO:0009651 EMBL:AL161540 GO:GO:0000226 GO:GO:0005874 GO:GO:0051258 Gene3D:G3DSA:3.40.50.1440 SUPFAM:SSF52490 GO:GO:0007018 EMBL:Z97337 Gene3D:G3DSA:3.30.1330.20 SUPFAM:SSF55307 GO:GO:0045298 eggNOG:COG5023 GO:GO:0071258 HOGENOM:HBG750007 KO:K07374 InterPro:IPR023123 Gene3D:G3DSA:1.10.287.600

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						PANTHER:PTHR11588 ProtClustDB:PLN00221 UniGene:At.22368 UniGene:At.48153 EMBL:M84699 EMBL:AY058858 EMBL:AY065347 EMBL:AY079036 EMBL:AY117174 IPI:IPI00520226 PIR:JQ1597 RefSeq:NP_193232.1 ProteinModelPortal:P29511 SMR:P29511 IntAct:P29511 STRING:P29511 PRIDE:P29511 EnsemblPlants:AT4G14960.2 GeneID:827154 KEGG:ath:AT4G14960 TAIR:At4g14960 InParanoid:P29511 OMA:MPSDKAI PhylomeDB:P29511 ArrayExpress:P29511 Genevestigator:P29511 Uniprot:P29511
Root	Isotig12696	1	21	-4.521	2.07E-06	TAIR|locus:2154334 - symbol:HCT "AT5G48930" species:3702 "Arabidopsis thaliana" [GO:0016740 "transferase activity" evidence=ISS] [GO:0047172 "shikimate O-hydroxycinnamoyltransferase activity" evidence=IMP] [GO:0047205 "quinate O-hydroxycinnamoyltransferase activity" evidence=IMP] [GO:0009809 "lignin biosynthetic process" evidence=IMP] [GO:0009963 "positive regulation of flavonoid biosynthetic process" evidence=IMP] [GO:0010252 "auxin homeostasis" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR003480 Pfam:PF02458 GO:GO:0005829 EMBL:CP002688 InterPro:IPR023213 Gene3D:G3DSA:3.30.559.10 GO:GO:0016787 EMBL:AB017061 GO:GO:0009809 GO:GO:0010252 EMBL:BT026488 EMBL:AK226213 EMBL:AY084652 IPI:IPI00532885 RefSeq:NP_199704.1 UniGene:At.24445 ProteinModelPortal:Q9FI78 SMR:Q9FI78 IntAct:Q9FI78 STRING:Q9FI78 PRIDE:Q9FI78 DNASU:834951 GeneID:834951 KEGG:ath:AT5G48930 TAIR:At5g48930 InParanoid:Q9FI78 KO:K13065 OMA:INTWSDM PhylomeDB:Q9FI78 ProtClustDB:PLN02663 Genevestigator:Q9FI78 GO:GO:0047205 GO:GO:0047172 GO:GO:0009963 Uniprot:Q9FI78
Root	Isotig12715	2	15	-3.036	0.000493759	TAIR|locus:2009273 - symbol:EMB3003 "AT1G34430" species:3702 "Arabidopsis thaliana" [GO:0004742 "dihydrolipoyllysine-residue acetyltransferase activity" evidence=ISS] [GO:0009793 "embryo development ending in seed dormancy" evidence=NAS] [GO:0016746 "transferase activity, transferring acyl groups" evidence=IEA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] InterPro:IPR001078 InterPro:IPR004167 Pfam:PF00198 Pfam:PF02817 InterPro:IPR000089 Pfam:PF00364 EMBL:CP002684 GO:GO:0005886 InterPro:IPR023213 Gene3D:G3DSA:3.30.559.10 GO:GO:0009941 InterPro:IPR011053 SUPFAM:SSF51230 PROSITE:PS50968 GO:GO:0016746 GO:GO:0022626 EMBL:AC023913 InterPro:IPR003016 PROSITE:PS00189 Gene3D:G3DSA:4.10.320.10 SUPFAM:SSF47005 KO:K00627 HSSP:P10515 EMBL:AY128294 EMBL:BT001042 IPI:IPI00540464 RefSeq:NP_174703.1 UniGene:At.15055 UniGene:At.72010 ProteinModelPortal:Q9C8P0 SMR:Q9C8P0 IntAct:Q9C8P0 STRING:Q9C8P0 PRIDE:Q9C8P0 EnsemblPlants:AT1G34430.1 GeneID:840346 KEGG:ath:AT1G34430 TAIR:At1g34430 InParanoid:Q9C8P0 OMA:FATTHAT PhylomeDB:Q9C8P0 ProtClustDB:CLSN2708031 Genevestigator:Q9C8P0 Uniprot:Q9C8P0
Root	Isotig12718	22	135	-2.746	2.71E-23	TAIR|locus:2009759 - symbol:cICDH "AT1G65930" species:3702 "Arabidopsis thaliana" [GO:0004450 "isocitrate dehydrogenase (NADP+) activity" evidence=ISS;IMP] [GO:0008152 "metabolic process" evidence=ISS] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0048046 "apoplast" evidence=IDA] [GO:0010043 "response to zinc ion" evidence=IEP] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA;NAS] [GO:0006102 "isocitrate metabolic process" evidence=IMP] [GO:0006739 "NADP metabolic process" evidence=IMP] [GO:0042742 "defense response to bacterium" evidence=IMP] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR004790 InterPro:IPR019818 InterPro:IPR024084 Pfam:PF00180 PIRSF:PIRSF000108 PROSITE:PS00470 EMBL:CP002684 GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 GO:GO:0048046 GO:GO:0009570 GO:GO:0046686 GO:GO:0042742 GO:GO:0051287 GO:GO:0010043 GO:GO:0000287 EMBL:AC009513 GO:GO:0005507 GO:GO:0009651 GO:GO:0006099 GO:GO:0006102 Gene3D:G3DSA:3.40.718.10 KO:K00031 GO:GO:0004450 PANTHER:PTHR11822 TIGRFAMs:TIGR00127 OMA:TPDEARM GO:GO:0006739 HSSP:P33198 ProtClustDB:PLN00103 EMBL:AY045631 EMBL:AF419575 EMBL:AY097340 EMBL:BT002400 IPI:IPI00539206 PIR:F96683 RefSeq:NP_176768.1 UniGene:At.24713 ProteinModelPortal:Q9SRZ6 SMR:Q9SRZ6 IntAct:Q9SRZ6 STRING:Q9SRZ6 PRIDE:Q9SRZ6 EnsemblPlants:AT1G65930.1 GeneID:842905 KEGG:ath:AT1G65930 TAIR:At1g65930 InParanoid:Q9SRZ6 PhylomeDB:Q9SRZ6 Genevestigator:Q9SRZ6 Uniprot:Q9SRZ6
Root	Isotig12723	23	50	-1.249	0.000360259	TAIR|locus:2044851 - symbol:LOS2 "AT2G36530" species:3702 "Arabidopsis thaliana" [GO:0004634 "phosphopyruvate hydratase activity" evidence=ISS;IDA] [GO:0003677 "DNA binding" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0009409 "response to cold" evidence=IMP] [GO:0009416 "response to light stimulus" evidence=IMP] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0005740 "mitochondrial envelope" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP]

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						[GO:0005507 "copper ion binding" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000941 InterPro:IPR020809 InterPro:IPR020810 InterPro:IPR020811 Pfam:PF00113 Pfam:PF03952 PIRSF:PIRSF001400 PRINTS:PR00148 PROSITE:PS00164 PANTHER:PTHR11902 GO:GO:0005886 GO:GO:0009506 GO:GO:0009737 GO:GO:0048046 GO:GO:0005634 GO:GO:0046686 GO:GO:0009507 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0006355 GO:GO:0003677 GO:GO:0000287 GO:GO:0006351 GO:GO:0005507 GO:GO:0009409 GO:GO:0009651 EMBL:AC006919 GO:GO:0005740 GO:GO:0009416 GO:GO:0006096 eggNOG:COG0148 HOGENOM:HBG726599 KO:K01689 GO:GO:0000015 GO:GO:0004634 TIGRFAMs:TIGR01060 ProtClustDB:PLN00191 EMBL:X58107 EMBL:AF424603 EMBL:AY054253 EMBL:AY072095 EMBL:AY092986 EMBL:AY150418 IPI:IPI00526310 PIR:JQ1187 RefSeq:NP_181192.1 UniGene:At.24124 UniGene:At.25354 UniGene:At.74012 ProteinModelPortal:P25696 SMR:P25696 STRING:P25696 SWISS-2DPAGE:P25696 PRIDE:P25696 ProMEX:P25696 EnsemblPlants:AT2G36530.1 GeneID:818226 KEGG:ath:AT2G36530 TAIR:At2g36530 InParanoid:P25696 OMA:GELYKNF PhylomeDB:P25696 BioCyc:ARA:AT2G36530-MONOMER BioCyc:MetaCyc:AT2G36530-MONOMER Genevestigator:P25696 GermOnline:AT2G36530 Uniprot:P25696
Root	Isotig12726	22	1	4.330	4.24E-06	TAIR|locus:2013880 - symbol:GSR2 "AT1G66200" species:3702 "Arabidopsis thaliana" [GO:0004356 "glutamate-ammonia ligase activity" evidence=ISS;IDA] [GO:0005829 "cytosol" evidence=IDA;TAS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0042128 "nitrate assimilation" evidence=TAS] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0048046 "apoplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] InterPro:IPR008146 InterPro:IPR008147 InterPro:IPR014746 Pfam:PF00120 Pfam:PF03951 PROSITE:PS00180 PROSITE:PS00181 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005524 GO:GO:0048046 GO:GO:0009570 GO:GO:0005773 EMBL:AC026480 GO:GO:0009941 GO:GO:0005507 GO:GO:0009651 GO:GO:0022626 GO:GO:0042128 GO:GO:0009399 eggNOG:COG0174 HOGENOM:HBG299709 ProtClustDB:PLN02284 GO:GO:0004356 GO:GO:0006542 Gene3D:G3DSA:3.30.590.10 Gene3D:G3DSA:3.10.20.70 SUPFAM:SSF54368 EMBL:AY091101 EMBL:AY122962 EMBL:AY086653 IPI:IPI00532772 PIR:H96686 PIR:S18602 RefSeq:NP_176794.1 UniGene:At.47484 UniGene:At.74857 ProteinModelPortal:Q8LCE1 SMR:Q8LCE1 IntAct:Q8LCE1 STRING:Q8LCE1 PRIDE:Q8LCE1 ProMEX:Q8LCE1 DNASU:842935 EnsemblPlants:AT1G66200.1 GeneID:842935 KEGG:ath:AT1G66200 TAIR:At1g66200 InParanoid:Q8LCE1 OMA:HICVYDP PhylomeDB:Q8LCE1 ArrayExpress:Q9C8C7 Genevestigator:Q8LCE1 Uniprot:Q8LCE1
Root	Isotig12730	14	1	3.678	0.000484579	TAIR|locus:2130634 - symbol:AT4G16440 "AT4G16440" species:3702 "Arabidopsis thaliana" [GO:0008901 "ferredoxin hydrogenase activity" evidence=ISS] [GO:0005829 "cytosol" evidence=IDA] Pfam:PF02906 Pfam:PF02256 GO:GO:0005829 EMBL:CP002687 UniGene:At.33082 UniGene:At.4413 InterPro:IPR009016 InterPro:IPR004108 SUPFAM:SSF53920 InterPro:IPR003149 Gene3D:G3DSA:4.10.260.20 SMART:SM00902 HSSP:P07598 EMBL:AJ320258 IPI:IPI00533761 RefSeq:NP_567496.4 ProteinModelPortal:Q94CL6 SMR:Q94CL6 STRING:Q94CL6 PRIDE:Q94CL6 EnsemblPlants:AT4G16440.1 GeneID:827338 KEGG:ath:AT4G16440 TAIR:At4g16440 InParanoid:Q94CL6 PhylomeDB:Q94CL6 ProtClustDB:CLSN2694296 Genevestigator:Q94CL6 Uniprot:Q94CL6
Root	Isotig12733	0	20	-5.451	2.00E-06	TAIR|locus:2042917 - symbol:AMT2 "AT2G38290" species:3702 "Arabidopsis thaliana" [GO:0008519 "ammonium transmembrane transporter activity" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0015398 "high affinity secondary active ammonium transmembrane transporter activity" evidence=IDA] [GO:0015696 "ammonium transport" evidence=TAS] [GO:0009624 "response to nematode" evidence=IEP] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR001905 InterPro:IPR002229 InterPro:IPR018047 PRINTS:PR00342 PROSITE:PS01219 Pfam:PF00909 GO:GO:0016021 GO:GO:0005886 GO:GO:0009506 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009624 EMBL:AC003028 eggNOG:COG0004 HOGENOM:HBG677626 InterPro:IPR024041 Gene3D:G3DSA:1.10.3430.10 PANTHER:PTHR11730 SUPFAM:SSF111352 TIGRFAMs:TIGR00836 GO:GO:0015398 EMBL:AF182039 EMBL:BT025321 EMBL:AK226212 EMBL:BX819203 IPI:IPI00547072 IPI:IPI00549164 PIR:T01260 RefSeq:NP_181363.1 RefSeq:NP_973634.1 UniGene:At.11996 UniGene:At.70096 ProteinModelPortal:Q9M6N7 SMR:Q9M6N7 STRING:Q9M6N7 TCDB:1.A.11.2.2

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						PRIDE:Q9M6N7 EnsemblPlants:AT2G38290.1 GeneID:818409 KEGG:ath:AT2G38290 GeneFarm:3490 TAIR:At2g38290 InParanoid:Q9M6N7 OMA:IGLRAHE PhylomeDB:Q9M6N7 ProtClustDB:CLSN2912922 ArrayExpress:Q9M6N7 Genevestigator:Q9M6N7 Uniprot:Q9M6N7
Root	Isotig12734	0	11	-4.588	0.000569522	TAIR|locus:2078608 - symbol:AT3G02100 "AT3G02100" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0008152 "metabolic process" evidence=IEA] [GO:0008194 "UDP-glycosyltransferase activity" evidence=ISS] [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] InterPro:IPR002213 Pfam:PF00201 PROSITE:PS00375 EMBL:CP002686 GenomeReviews:BA000014_GR EMBL:AC011664 GO:GO:0016758 CAZy:GT1 PANTHER:PTHR11926 UniGene:At.23364 HOGENOM:HBG746957 IPI:IPI00541030 RefSeq:NP_186859.1 UniGene:At.66468 ProteinModelPortal:Q9SGA8 SMR:Q9SGA8 PRIDE:Q9SGA8 EnsemblPlants:AT3G02100.1 GeneID:820287 KEGG:ath:AT3G02100 GeneFarm:2149 TAIR:At3g02100 eggNOG:NOG273990 InParanoid:Q9SGA8 OMA:TDWLLCN PhylomeDB:Q9SGA8 ProtClustDB:CLSN2915708 Genevestigator:Q9SGA8 Uniprot:Q9SGA8
Root	Isotig12741	72	0	7.041	2.73E-17	TAIR|locus:2179867 - symbol:SAG29 "senescence-associated gene 29" species:3702 "Arabidopsis thaliana" [GO:0016020 "membrane" evidence=IEA;ISS] [GO:0016021 "integral to membrane" evidence=IEA] [GO:0010150 "leaf senescence" evidence=IEP;IMP] [GO:0071446 "cellular response to salicylic acid stimulus" evidence=IEP] [GO:0005887 "integral to plasma membrane" evidence=IDA] [GO:0071215 "cellular response to abscisic acid stimulus" evidence=IEP] [GO:0071470 "cellular response to osmotic stress" evidence=IMP] [GO:0051119 "sugar transmembrane transporter activity" evidence=ISS] InterPro:IPR004316 Pfam:PF03083 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005887 GO:GO:0010150 EMBL:AL391711 GO:GO:0071470 GO:GO:0071215 GO:GO:0071446 GO:GO:0051119 PANTHER:PTHR10791 KO:K15382 eggNOG:NOG308353 EMBL:AY045949 EMBL:AY113934 EMBL:AY087836 EMBL:AF118824 IPI:IPI00530310 RefSeq:NP_196821.1 UniGene:At.46857 TCDB:9.A.58.1.3 EnsemblPlants:AT5G13170.1 GeneID:831156 KEGG:ath:AT5G13170 TAIR:At5g13170 InParanoid:Q9FY94 OMA:WFAYGLF PhylomeDB:Q9FY94 ProtClustDB:CLSN2916510 ArrayExpress:Q9FY94 Genevestigator:Q9FY94 Uniprot:Q9FY94
Root	Isotig12742	27	2	3.626	1.44E-06	TAIR|locus:2122536 - symbol:AT4G39520 "AT4G39520" species:3702 "Arabidopsis thaliana" [GO:0005525 "GTP binding" evidence=ISS;IDA] [GO:0003924 "GTPase activity" evidence=IDA] [GO:0019003 "GDP binding" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR005225 InterPro:IPR006073 InterPro:IPR006074 Pfam:PF01926 PRINTS:PR00326 PROSITE:PS00905 eggNOG:COG1163 OMA:FDVARTG GO:GO:0005525 InterPro:IPR004095 InterPro:IPR012676 Pfam:PF02824 SUPFAM:SSF81271 TIGRFAMs:TIGR00231 GO:GO:0005829 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0003924 EMBL:AL161595 GO:GO:0019003 EMBL:AL078620 ProtClustDB:CLSN2679590 HOGENOM:HBG631304 HSSP:P44681 EMBL:AY035034 IPI:IPI00534664 PIR:T09368 RefSeq:NP_195662.1 UniGene:At.3445 ProteinModelPortal:Q9SVA6 SMR:Q9SVA6 STRING:Q9SVA6 PRIDE:Q9SVA6 EnsemblPlants:AT4G39520.1 GeneID:830106 KEGG:ath:AT4G39520 TAIR:At4g39520 InParanoid:Q9SVA6 PhylomeDB:Q9SVA6 Genevestigator:Q9SVA6 Uniprot:Q9SVA6
Root	Isotig12752	0	13	-4.829	0.000155955	TAIR|locus:2180572 - symbol:GA3 "AT5G25900" species:3702 "Arabidopsis thaliana" [GO:0009707 "chloroplast outer membrane" evidence=IDA] [GO:0005783 "endoplasmic reticulum" evidence=IDA] [GO:0005792 "microsome" evidence=NAS] [GO:0009686 "gibberellin biosynthetic process" evidence=IDA;TAS] [GO:0009740 "gibberellic acid mediated signaling pathway" evidence=TAS] [GO:0010241 "ent-kaurene oxidation to kaurenoic acid" evidence=IMP] [GO:0019825 "oxygen binding" evidence=IMP] InterPro:IPR001128 InterPro:IPR002401 InterPro:IPR017972 Pfam:PF00067 PRINTS:PR00463 PROSITE:PS00086 GO:GO:0005783 GO:GO:0016021 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009055 eggNOG:COG2124 GO:GO:0020037 Gene3D:G3DSA:1.10.630.10 SUPFAM:SSF48264 GO:GO:0009707 EMBL:AF149413 HOGENOM:HBG749920 GO:GO:0009686 GO:GO:0009740 EMBL:AF047719 EMBL:AF047720 EMBL:AF047721 EMBL:AY057671 IPI:IPI00522975 PIR:T51806 RefSeq:NP_197962.1 UniGene:At.10791 ProteinModelPortal:Q93ZB2 SMR:Q93ZB2 STRING:Q93ZB2 PRIDE:Q93ZB2 EnsemblPlants:AT5G25900.1 GeneID:832659 KEGG:ath:AT5G25900 GeneFarm:1435 TAIR:At5g25900 InParanoid:Q93ZB2 KO:K04122 OMA:WETIIET PhylomeDB:Q93ZB2 ProtClustDB:PLN02655 BioCyc:MetaCyc:AT5G25900-MONOMER BRENDA:1.14.13.78 ArrayExpress:Q93ZB2 Genevestigator:Q93ZB2 GermOnline:AT5G25900 GO:GO:0052617 GO:GO:0052616 GO:GO:0052615 GO:GO:0010241 Uniprot:Q93ZB2
Root	Isotig12768	2	25	-3.773	8.67E-07	TAIR|locus:2172214 - symbol:TUB3 "tubulin beta chain 3" species:3702 "Arabidopsis thaliana" [GO:0003924 "GTPase activity" evidence=IEA] [GO:0005198 "structural molecule activity" evidence=IEA;ISS] [GO:0005525 "GTP

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						binding" evidence=IEA] [GO:0045298 "tubulin complex" evidence=TAS] [GO:0005618 "cell wall" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR000217 InterPro:IPR002453 InterPro:IPR003008 InterPro:IPR008280 InterPro:IPR017975 InterPro:IPR018316 Pfam:PF00091 Pfam:PF03953 PRINTS:PR01161 PRINTS:PR01163 PROSITE:PS00227 SMART:SM00864 SMART:SM00865 GO:GO:0005525 GO:GO:0005886 GO:GO:0009506 GO:GO:0046686 GO:GO:0005737 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005618 GO:GO:0005515 GO:GO:0005730 GO:GO:0005198 GO:GO:0003924 GO:GO:0009651 GO:GO:0005874 GO:GO:0051258 Gene3D:G3DSA:3.40.50.1440 SUPFAM:SSF52490 GO:GO:0007018 EMBL:AB009053 EMBL:AB020751 Gene3D:G3DSA:3.30.1330.20 SUPFAM:SSF55307 GO:GO:0045298 eggNOG:COG5023 HOGENOM:HBG750007 InterPro:IPR023123 Gene3D:G3DSA:1.10.287.600 PANTHER:PTHR11588 InterPro:IPR013838 KO:K07375 ProtClustDB:PLN00220 PROSITE:PS00228 OMA:ADEMGEY EMBL:M84700 EMBL:M84701 EMBL:AK117431 EMBL:AY056411 EMBL:AY060550 EMBL:AY062614 EMBL:AY062742 EMBL:AY128785 EMBL:BT002587 EMBL:AY087859 IPI:IPI00525001 PIR:JQ1587 RefSeq:NP_568959.1 RefSeq:NP_568960.1 UniGene:At.24202 UniGene:At.49208 ProteinModelPortal:P29512 SMR:P29512 IntAct:P29512 STRING:P29512 PRIDE:P29512 EnsemblPlants:AT5G62690.1 EnsemblPlants:AT5G62700.1 GeneID:836390 GeneID:836391 KEGG:ath:AT5G62690 KEGG:ath:AT5G62700 TAIR:At5g62690 TAIR:At5g62700 InParanoid:P29512 PhylomeDB:P29512 ArrayExpress:P29512 Genevestigator:P29512 GermOnline:AT5G62690 Uniprot:P29512
Root	Isotig12780	31	9	1.655	0.000908187	TAIR|locus:2198225 - symbol:ATAF1 "AT1G01720" species:3702 "Arabidopsis thaliana" [GO:0007275 "multicellular organismal development" evidence=ISS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0009611 "response to wounding" evidence=IEP] [GO:0009788 "negative regulation of abscisic acid mediated signaling pathway" evidence=IMP] InterPro:IPR003441 Pfam:PF02365 PROSITE:PS51005 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005634 GO:GO:0009611 GO:GO:0006355 GO:GO:0003677 GO:GO:0006351 GO:GO:0009788 EMBL:AC009273 HOGENOM:HBG750044 SUPFAM:SSF101941 EMBL:X74755 EMBL:AF370617 IPI:IPI00547269 PIR:E86148 PIR:S37101 RefSeq:NP_171677.1 UniGene:At.134 UniGene:At.57938 ProteinModelPortal:Q39013 SMR:Q39013 STRING:Q39013 PRIDE:Q39013 EnsemblPlants:AT1G01720.1 GeneID:839265 KEGG:ath:AT1G01720 GeneFarm:4060 TAIR:At1g01720 eggNOG:NOG265262 InParanoid:Q39013 OMA:EIMEEKP PhylomeDB:Q39013 ProtClustDB:CLSN2714451 ArrayExpress:Q39013 Genevestigator:Q39013 GermOnline:AT1G01720 Uniprot:Q39013
Root	Isotig12801	0	13	-4.829	0.000155955	TAIR|locus:2196000 - symbol:EFS "AT1G77300" species:3702 "Arabidopsis thaliana" [GO:0009910 "negative regulation of flower development" evidence=IMP] [GO:0031062 "positive regulation of histone methylation" evidence=IDA] [GO:0042800 "histone methyltransferase activity (H3-K4 specific)" evidence=IDA] [GO:0046975 "histone methyltransferase activity (H3-K36 specific)" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0010223 "secondary shoot formation" evidence=IMP] [GO:0016116 "carotenoid metabolic process" evidence=IMP] [GO:0040029 "regulation of gene expression, epigenetic" evidence=IMP] [GO:0009553 "embryo sac development" evidence=IMP] [GO:0009555 "pollen development" evidence=IMP] [GO:0010452 "histone H3-K36 methylation" evidence=IDA] [GO:0048481 "ovule development" evidence=IMP] [GO:0048653 "anther development" evidence=IMP] [GO:0010363 "regulation of plant-type hypersensitive response" evidence=IMP] [GO:0043067 "regulation of programmed cell death" evidence=IGI] Pfam:PF00856 InterPro:IPR001214 InterPro:IPR006560 InterPro:IPR011124 Pfam:PF07496 PROSITE:PS50280 PROSITE:PS51050 PROSITE:PS51215 SMART:SM00317 SMART:SM00570 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005634 GO:GO:0000775 GO:GO:0008270 EMBL:AC004260 GO:GO:0009555 GO:GO:0048653 GO:GO:0048481 GO:GO:0009910 GO:GO:0009553 eggNOG:COG2940 InterPro:IPR003616 SMART:SM00508 PROSITE:PS50868 GO:GO:0042800 EMBL:DQ340869 EMBL:AK221916 IPI:IPI00542920 IPI:IPI00759360 PIR:T00458 RefSeq:NP_177854.6 UniGene:At.34505 PDB:2L7P PDBsum:2L7P ProteinModelPortal:Q2LAE1 SMR:Q2LAE1 STRING:Q2LAE1 PRIDE:Q2LAE1 GeneID:844066 KEGG:ath:AT1G77300 TAIR:At1g77300 InParanoid:Q2LAE1 PhylomeDB:Q2LAE1 Genevestigator:Q2LAE1 GermOnline:AT1G77300 GO:GO:0016116 GO:GO:0010452 GO:GO:0031062 GO:GO:0040029 GO:GO:0010363 GO:GO:0010223 Uniprot:Q2LAE1
Root	Isotig12815	1	22	-4.588	1.10E-06	TAIR|locus:2148318 - symbol:AtRDUF2 "Arabidopsis thaliana RING and Domain of Unknown Function 1117 2" species:3702 "Arabidopsis thaliana" [GO:0008270 "zinc ion binding" evidence=IEA;ISS] [GO:0010200 "response to chitin" evidence=IEP] InterPro:IPR001841 PROSITE:PS50089 SMART:SM00184 GO:GO:0008270 GO:GO:0010200 EMBL:AB025604 InterPro:IPR013083 Gene3D:G3DSA:3.30.40.10 HSSP:Q9LRB7

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						InterPro:IPR010543 Pfam:PF06547 IPI:IPI00527742 ProteinModelPortal:Q9LTH6 SMR:Q9LTH6 STRING:Q9LTH6 TAIR:At5g59550 InParanoid:Q9LTH6 PhylomeDB:Q9LTH6 Genevestigator:Q9LTH6 Uniprot:Q9LTH6
Root	Isotig12822	17	0	4.958	3.30E-05	UNIPROTKB|B1AKR2 - symbol:TMEM52 "Transmembrane protein 52" species:9606 "Homo sapiens" [GO:0016021 "integral to membrane" evidence=IEA] GO:GO:0016021 EMBL:AL109917 GeneTree:ENSGT00530000063999 UniGene:Hs.123423 HGNC:HGNC:27916 IPI:IPI00607551 ProteinModelPortal:B1AKR2 PRIDE:B1AKR2 Ensembl:ENST00000378598 Bgee:B1AKR2 Uniprot:B1AKR2
Root	Isotig12827	2	18	-3.299	7.42E-05	TAIR|locus:2139084 - symbol:CYP706A4 ""cytochrome P450, family 706, subfamily A, polypeptide 4"" species:3702 "Arabidopsis thaliana" [GO:0004497 "monooxygenase activity" evidence=IEA] [GO:0005506 "iron ion binding" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0009055 "electron carrier activity" evidence=IEA] [GO:0019825 "oxygen binding" evidence=ISS] [GO:0020037 "heme binding" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] InterPro:IPR001128 InterPro:IPR002401 InterPro:IPR017972 Pfam:PF00067 PRINTS:PR00385 PRINTS:PR00463 PROSITE:PS00086 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0009055 GO:GO:0004497 eggNOG:COG2124 GO:GO:0020037 Gene3D:G3DSA:1.10.630.10 SUPFAM:SSF48264 GO:GO:0016705 HOGENOM:HBG749920 EMBL:AL161533 EMBL:AL080318 ProtClustDB:CLSN2685578 EMBL:BT005454 EMBL:AK118782 IPI:IPI00540953 PIR:T48140 RefSeq:NP_192967.1 UniGene:At.23823 ProteinModelPortal:Q9STI1 SMR:Q9STI1 PRIDE:Q9STI1 EnsemblPlants:AT4G12300.1 GeneID:826839 KEGG:ath:AT4G12300 TAIR:At4g12300 InParanoid:Q9STI1 OMA:VRERTRY PhylomeDB:Q9STI1 Genevestigator:Q9STI1 Uniprot:Q9STI1
Root	Isotig12836	0	14	-4.936	8.24E-05	TAIR|locus:2026167 - symbol:KAS III "3-ketoacyl-acyl carrier protein synthase III" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004315 "3-oxoacyl-[acyl-carrier-protein] synthase activity" evidence=IEA;ISS] [GO:0006633 "fatty acid biosynthetic process" evidence=IEA;ISS] [GO:0008152 "metabolic process" evidence=IEA] [GO:0008610 "lipid biosynthetic process" evidence=IEA] [GO:0009507 "chloroplast" evidence=ISS;IDA] [GO:0016747 "transferase activity, transferring acyl groups other than amino-acyl groups" evidence=IEA] [GO:0009570 "chloroplast stroma" evidence=IDA] InterPro:IPR004655 InterPro:IPR013747 InterPro:IPR013751 InterPro:IPR016038 InterPro:IPR016039 Pfam:PF08541 Pfam:PF08545 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009570 GO:GO:0006633 EMBL:AC007190 Gene3D:G3DSA:3.40.47.10 SUPFAM:SSF53901 GO:GO:0004315 EMBL:AC005698 eggNOG:COG0332 HOGENOM:HBG649927 KO:K00648 GO:GO:0033818 TIGRFAMs:TIGR00747 EMBL:L31891 EMBL:Y11689 EMBL:AY063804 EMBL:AY091275 IPI:IPI00539872 RefSeq:NP_001031221.1 RefSeq:NP_176452.1 UniGene:At.386 ProteinModelPortal:P49243 SMR:P49243 STRING:P49243 PRIDE:P49243 EnsemblPlants:AT1G62640.1 EnsemblPlants:AT1G62640.2 GeneID:842561 KEGG:ath:AT1G62640 TAIR:At1g62640 InParanoid:P49243 OMA:FNAKEEA PhylomeDB:P49243 ProtClustDB:PLN02326 ArrayExpress:P49243 Genevestigator:P49243 GermOnline:AT1G62640 Uniprot:P49243
Root	Isotig12845	1	19	-4.377	7.43E-06	TAIR|locus:2127776 - symbol:CESA1 "AT4G32410" species:3702 "Arabidopsis thaliana" [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0016759 "cellulose synthase activity" evidence=ISS] [GO:0009832 "plant-type cell wall biogenesis" evidence=TAS] [GO:0030244 "cellulose biosynthetic process" evidence=IMP;TAS] [GO:0009833 "primary cell wall biogenesis" evidence=IMP] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] [GO:0042538 "hyperosmotic salinity response" evidence=IMP] InterPro:IPR001841 InterPro:IPR005150 Pfam:PF03552 PROSITE:PS50089 SMART:SM00184 Prosite:PS00518 GO:GO:0016021 GO:GO:0005886 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005794 GO:GO:0008270 InterPro:IPR013083 Gene3D:G3DSA:3.30.40.10 GO:GO:0007047 EMBL:AL161581 EMBL:AL034567 CAZy:GT2 GO:GO:0042538 eggNOG:COG1215 GO:GO:0016760 GO:GO:0030244 EMBL:AF027172 EMBL:BT008654 EMBL:AK222115 EMBL:AK226243 IPI:IPI00536785 PIR:T05351 RefSeq:NP_194967.1 UniGene:At.21246 ProteinModelPortal:O48946 SMR:O48946 DIP:DIP-59354N STRING:O48946 PRIDE:O48946 EnsemblPlants:AT4G32410.1 GeneID:829376 KEGG:ath:AT4G32410 GeneFarm:5084 TAIR:At4g32410 HOGENOM:HBG744549 InParanoid:O48946 KO:K10999 OMA:DIENEFN PhylomeDB:O48946 ProtClustDB:PLN02400 Genevestigator:O48946 GermOnline:AT4G32410 GO:GO:0009833 Uniprot:O48946
Root	Isotig12849	7	24	-1.907	0.000762598	TAIR|locus:2089070 - symbol:MTO3 "AT3G17390" species:3702 "Arabidopsis thaliana" [GO:0004478 "methionine adenosyltransferase activity" evidence=ISS] [GO:0006556 "S-adenosylmethionine biosynthetic process" evidence=ISS] [GO:0006555 "methionine metabolic process" evidence=IMP] [GO:0009809 "lignin biosynthetic process" evidence=IMP] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						"membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR002133 InterPro:IPR022628 InterPro:IPR022629 InterPro:IPR022630 InterPro:IPR022631 InterPro:IPR022636 Pfam:PF00438 Pfam:PF02772 Pfam:PF02773 PIRSF:PIRSF000497 PROSITE:PS00376 PROSITE:PS00377 GO:GO:0005886 GO:GO:0009506 GO:GO:0005524 GO:GO:0005737 GO:GO:0005618 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005730 GO:GO:0006555 GO:GO:0046872 GO:GO:0009409 GO:GO:0009809 GO:GO:0006730 EMBL:AB022216 KO:K00789 GO:GO:0006556 HOGENOM:HBG443662 ProtClustDB:PLN02243 GO:GO:0004478 PANTHER:PTHR11964 SUPFAM:SSF55973 TIGRFAMs:TIGR01034 OMA:FHDAFIE HSSP:P13444 EMBL:AY037214 EMBL:AY120708 EMBL:BT000712 EMBL:BT002665 EMBL:AK230129 EMBL:AY087184 IPI:IPI00536966 RefSeq:NP_188365.1 UniGene:At.5781 UniGene:At.70071 ProteinModelPortal:Q9LUT2 SMR:Q9LUT2 STRING:Q9LUT2 PRIDE:Q9LUT2 EnsemblPlants:AT3G17390.1 GeneID:821003 KEGG:ath:AT3G17390 TAIR:At3g17390 InParanoid:Q9LUT2 PhylomeDB:Q9LUT2 ArrayExpress:Q9LUT2 Genevestigator:Q9LUT2 Uniprot:Q9LUT2
Root	Isotig12867	32	153	-2.386	1.25E-22	TAIR|locus:2117939 - symbol:PIP1;5 "AT4G23400" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=ISS] [GO:0015250 "water channel activity" evidence=ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000425 InterPro:IPR012269 InterPro:IPR022357 Pfam:PF00230 PRINTS:PR00783 PROSITE:PS00221 GO:GO:0016021 GO:GO:0005886 GO:GO:0009506 EMBL:CP002687 GenomeReviews:CT486007_GR EMBL:AL161559 GO:GO:0055085 GO:GO:0005215 GO:GO:0006833 EMBL:AL031326 InterPro:IPR023271 Gene3D:G3DSA:1.20.1080.10 SUPFAM:SSF81338 eggNOG:COG0580 HOGENOM:HBG705794 PANTHER:PTHR19139 TIGRFAMs:TIGR00861 KO:K09872 ProtClustDB:CLSN2682869 EMBL:AY059948 EMBL:AY081593 EMBL:AY087945 IPI:IPI00536498 PIR:T05378 RefSeq:NP_194071.1 UniGene:At.2438 ProteinModelPortal:Q8LAA6 SMR:Q8LAA6 IntAct:Q8LAA6 STRING:Q8LAA6 PRIDE:Q8LAA6 EnsemblPlants:AT4G23400.1 GeneID:828439 KEGG:ath:AT4G23400 GeneFarm:4865 TAIR:At4g23400 InParanoid:Q8LAA6 OMA:YDFLLAP PhylomeDB:Q8LAA6 ArrayExpress:Q8LAA6 Genevestigator:Q8LAA6 GermOnline:AT4G23400 Uniprot:Q8LAA6
Root	Isotig12868	5	24	-2.392	0.000103464	TAIR|locus:2156927 - symbol:HIPP27 "heavy metal associated isoprenylated plant protein 27" species:3702 "Arabidopsis thaliana" [GO:0030001 "metal ion transport" evidence=IEA] [GO:0046872 "metal ion binding" evidence=IEA;ISS] [GO:0005886 "plasma membrane" evidence=IDA] InterPro:IPR006121 Pfam:PF00403 PROSITE:PS50846 GO:GO:0005886 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0046872 SUPFAM:SSF55008 GO:GO:0030001 HOGENOM:HBG746089 EMBL:AK175898 EMBL:AK176006 IPI:IPI00525836 RefSeq:NP_201412.2 UniGene:At.28881 ProteinModelPortal:Q67ZW1 SMR:Q67ZW1 IntAct:Q67ZW1 PRIDE:Q67ZW1 DNASU:836743 EnsemblPlants:AT5G66110.1 GeneID:836743 KEGG:ath:AT5G66110 TAIR:At5g66110 eggNOG:NOG252302 InParanoid:Q67ZW1 OMA:VVPHPYA PhylomeDB:Q67ZW1 ProtClustDB:CLSN2918890 ArrayExpress:Q67ZW1 Genevestigator:Q67ZW1 Uniprot:Q67ZW1
Root	Isotig12883	16	0	4.871	5.89E-05	TAIR|locus:2044851 - symbol:LOS2 "AT2G36530" species:3702 "Arabidopsis thaliana" [GO:0004634 "phosphopyruvate hydratase activity" evidence=ISS;IDA] [GO:0003677 "DNA binding" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0009409 "response to cold" evidence=IMP] [GO:0009416 "response to light stimulus" evidence=IMP] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0005740 "mitochondrial envelope" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000941 InterPro:IPR020809 InterPro:IPR020810 InterPro:IPR020811 Pfam:PF00113 Pfam:PF03952 PIRSF:PIRSF001400 PRINTS:PR00148 PROSITE:PS00164 PANTHER:PTHR11902 GO:GO:0005886 GO:GO:0009506 GO:GO:0009737 GO:GO:0048046 GO:GO:0005634 GO:GO:0046686 GO:GO:0009507 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0006355 GO:GO:0003677 GO:GO:0000287 GO:GO:0006351 GO:GO:0005507 GO:GO:0009409 GO:GO:0009651 EMBL:AC006919 GO:GO:0005740 GO:GO:0009416 GO:GO:0006096 eggNOG:COG0148 HOGENOM:HBG726599 KO:K01689 GO:GO:0000015 GO:GO:0004634 TIGRFAMs:TIGR01060 ProtClustDB:PLN00191 EMBL:X58107 EMBL:AF424603 EMBL:AY054253 EMBL:AY072095 EMBL:AY092986 EMBL:AY150418 IPI:IPI00526310 PIR:JQ1187

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						RefSeq:NP_181192.1 UniGene:At.24124 UniGene:At.25354 UniGene:At.74012 ProteinModelPortal:P25696 SMR:P25696 STRING:P25696 SWISS-2DPAGE:P25696 PRIDE:P25696 ProMEX:P25696 EnsemblPlants:AT2G36530.1 GeneID:818226 KEGG:ath:AT2G36530 TAIR:At2g36530 InParanoid:P25696 OMA:GELYKNF PhylomeDB:P25696 BioCyc:ARA:AT2G36530-MONOMER BioCyc:MetaCyc:AT2G36530-MONOMER Genevestigator:P25696 GermOnline:AT2G36530 Uniprot:P25696
Root	Isotig12896	1	18	-4.299	1.41E-05	TAIR|locus:2092757 - symbol:AT3G18170 "AT3G18170" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=IEA] InterPro:IPR007657 Pfam:PF04577 CAZy:GT61 GO:GO:0016757 EMBL:AB020749 IPI:IPI00527317 PRIDE:Q9LV23 TAIR:At3g18170 InParanoid:Q9LV23 PhylomeDB:Q9LV23 Genevestigator:Q9LV23 Uniprot:Q9LV23
Root	Isotig12917	2	14	-2.936	0.000925454	TAIR|locus:2076676 - symbol:LPAT2 "AT3G57650" species:3702 "Arabidopsis thaliana" [GO:0003841 "1-acylglycerol-3-phosphate O-acyltransferase activity" evidence=ISS;IDA] [GO:0008152 "metabolic process" evidence=IEA;ISS] [GO:0005783 "endoplasmic reticulum" evidence=IDA] InterPro:IPR002123 Pfam:PF01553 SMART:SM00563 GO:GO:0016021 GO:GO:0007275 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005789 GO:GO:0008654 GO:GO:0003841 EMBL:AL049660 eggNOG:COG0204 BRENDA:2.3.1.51 EMBL:AY084461 IPI:IPI00528234 PIR:T06755 RefSeq:NP_567052.1 UniGene:At.34815 STRING:Q8LG50 PRIDE:Q8LG50 EnsemblPlants:AT3G57650.1 GeneID:824934 KEGG:ath:AT3G57650 TAIR:At3g57650 HOGENOM:HBG320199 InParanoid:Q8LG50 KO:K13523 OMA:INFIQLC PhylomeDB:Q8LG50 Genevestigator:Q8LG50 GermOnline:AT3G57650 Uniprot:Q8LG50
Root	Isotig12918	1	18	-4.299	1.41E-05	UNIPROTKB|P29717 - symbol:XOG1 "Glucan 1,3-beta-glucosidase" species:237561 "Candida albicans SC5314" [GO:0004338 "glucan exo-1,3-beta-glucosidase activity" evidence=IMP;IDA] [GO:0005576 "extracellular region" evidence=IDA] [GO:0006073 "cellular glucan metabolic process" evidence=IMP] [GO:0009986 "cell surface" evidence=IDA] [GO:0031505 "fungal-type cell wall organization" evidence=IMP] [GO:0031589 "cell-substrate adhesion" evidence=IDA] [GO:0050839 "cell adhesion molecule binding" evidence=IDA] InterPro:IPR001547 InterPro:IPR013781 InterPro:IPR018087 Pfam:PF00150 PROSITE:PS00659 GO:GO:0005576 EMBL:AACQ01000015 GO:GO:0009986 GO:GO:0043169 InterPro:IPR017853 Gene3D:G3DSA:3.20.20.80 SUPFAM:SSF51445 CAZy:GH5 GO:GO:0031505 GO:GO:0050839 GO:GO:0031589 EMBL:AL033497 KO:K01210 GO:GO:0004338 eggNOG:COG2730 GO:GO:0006073 EMBL:X56556 PIR:A47702 PIR:T52149 RefSeq:XP_721488.1 PDB:1CZ1 PDB:1EQC PDB:1EQP PDB:2PB1 PDB:2PBO PDB:2PC8 PDB:2PF0 PDB:3N9K PDB:3O6A PDBsum:1CZ1 PDBsum:1EQC PDBsum:1EQP PDBsum:2PB1 PDBsum:2PBO PDBsum:2PC8 PDBsum:2PF0 PDBsum:3N9K PDBsum:3O6A ProteinModelPortal:P29717 SMR:P29717 STRING:P29717 GeneID:3636837 KEGG:cal:CaO19.2990 PhylomeDB:P29717 PMAP-CutDB:P29717 Uniprot:P29717
Root	Isotig12919	21	0	5.263	3.38E-06	TAIR|locus:2079286 - symbol:AT3G26430 "AT3G26430" species:3702 "Arabidopsis thaliana" [GO:0004091 "carboxylesterase activity" evidence=ISS] [GO:0006629 "lipid metabolic process" evidence=IEA] [GO:0016788 "hydrolase activity, acting on ester bonds" evidence=IEA] InterPro:IPR001087 Pfam:PF00657 PROSITE:PS01098 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005576 GO:GO:0016042 GO:GO:0016788 HOGENOM:HBG749527 EMBL:AP001298 EMBL:AY062535 EMBL:AY093315 IPI:IPI00519679 RefSeq:NP_189274.1 UniGene:At.48707 ProteinModelPortal:Q9LIN2 PRIDE:Q9LIN2 EnsemblPlants:AT3G26430.1 GeneID:822247 KEGG:ath:AT3G26430 TAIR:At3g26430 eggNOG:NOG317989 InParanoid:Q9LIN2 OMA:HNTAPLG PhylomeDB:Q9LIN2 ProtClustDB:CLSN2915536 Genevestigator:Q9LIN2 Uniprot:Q9LIN2
Root	Isotig12924	1	13	-3.829	0.000362856	TAIR|locus:2151376 - symbol:AT5G17540 "AT5G17540" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0016747 "transferase activity, transferring acyl groups other than amino-acyl groups" evidence=IEA] InterPro:IPR003480 Pfam:PF02458 EMBL:CP002688 GenomeReviews:BA000015_GR InterPro:IPR023213 Gene3D:G3DSA:3.30.559.10 GO:GO:0016747 EMBL:AL391151 eggNOG:NOG323053 HOGENOM:HBG599319 UniGene:At.27444 EMBL:BT033140 IPI:IPI00526367 PIR:T51458 RefSeq:NP_197256.1 UniGene:At.31533 ProteinModelPortal:Q9LF70 SMR:Q9LF70 PRIDE:Q9LF70 EnsemblPlants:AT5G17540.1 GeneID:831620 KEGG:ath:AT5G17540 TAIR:At5g17540 InParanoid:Q9LF70 OMA:HREYDEM PhylomeDB:Q9LF70 ProtClustDB:CLSN2914884 Genevestigator:Q9LF70 Uniprot:Q9LF70
Root	Isotig12956	0	12	-4.714	0.000297064	TAIR|locus:2141201 - symbol:CRK29 "AT4G21410" species:3702 "Arabidopsis thaliana" [GO:0016301 "kinase activity" evidence=ISS] [GO:0005773 "vacuole" evidence=IDA] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] [GO:0005886 "plasma membrane" evidence=IDA] InterPro:IPR000719 InterPro:IPR008271

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						InterPro:IPR011009 InterPro:IPR017441 Pfam:PF00069 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 GO:GO:0016021 GO:GO:0005886 GO:GO:0005524 GO:GO:0009737 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005773 eggNOG:COG0515 GO:GO:0004872 SUPFAM:SSF56112 GO:GO:0004674 HOGENOM:HBG755340 EMBL:AL161555 EMBL:AL022603 EMBL:AL031187 InterPro:IPR002902 Pfam:PF01657 PROSITE:PS51473 ProtClustDB:CLSN2685554 EMBL:AY074844 IPI:IPI00516505 PIR:T05149 RefSeq:NP_193872.2 UniGene:At.43984 ProteinModelPortal:Q8S9L6 SMR:Q8S9L6 PRIDE:Q8S9L6 EnsemblPlants:AT4G21410.1 GeneID:827893 KEGG:ath:AT4G21410 GeneFarm:237 TAIR:At4g21410 InParanoid:Q8S9L6 OMA:ISANRDD PhylomeDB:Q8S9L6 ArrayExpress:O65406 Genevestigator:Q8S9L6 Uniprot:Q8S9L6
Root	Isotig12965	0	14	-4.936	8.24E-05	TAIR|locus:2064681 - symbol:MOD1 "AT2G05990" species:3702 "Arabidopsis thaliana" [GO:0016491 "oxidoreductase activity" evidence=ISS] [GO:0005835 "fatty acid synthase complex" evidence=TAS] [GO:0006633 "fatty acid biosynthetic process" evidence=IMP] [GO:0016631 "enoyl-[acyl-carrier-protein] reductase activity" evidence=IMP] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0004318 "enoyl-[acyl-carrier-protein] reductase (NADH) activity" evidence=ISS] [GO:0005507 "copper ion binding" evidence=IDA] InterPro:IPR016040 InterPro:IPR002347 GO:GO:0009570 EMBL:CP002685 GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 GO:GO:0009941 GO:GO:0006633 GO:GO:0005507 PRINTS:PR00081 GO:GO:0009579 GO:GO:0016631 GO:GO:0005835 KO:K00208 OMA:MGVANNR EMBL:AC005970 EMBL:AY056192 EMBL:AY113962 IPI:IPI00527352 PIR:H84473 RefSeq:NP_565331.1 RefSeq:NP_849940.1 UniGene:At.23842 HSSP:P80030 ProteinModelPortal:Q9SLA8 SMR:Q9SLA8 STRING:Q9SLA8 PRIDE:Q9SLA8 ProMEX:Q9SLA8 EnsemblPlants:AT2G05990.1 EnsemblPlants:AT2G05990.2 GeneID:815152 KEGG:ath:AT2G05990 TAIR:At2g05990 InParanoid:Q9SLA8 PhylomeDB:Q9SLA8 ProtClustDB:PLN02730 ArrayExpress:Q9SLA8 Genevestigator:Q9SLA8 Uniprot:Q9SLA8
Root	Isotig12967	0	19	-5.377	3.67E-06	TAIR|locus:2142434 - symbol:AT5G10560 "AT5G10560" species:3702 "Arabidopsis thaliana" [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=ISS] [GO:0005975 "carbohydrate metabolic process" evidence=IEA] [GO:0009044 "xylan 1,4-beta-xylosidase activity" evidence=TAS] [GO:0005773 "vacuole" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] InterPro:IPR001764 InterPro:IPR002772 Pfam:PF00933 Pfam:PF01915 PROSITE:PS00775 GO:GO:0005774 EMBL:CP002688 GenomeReviews:BA000015_GR EMBL:AL353995 InterPro:IPR017853 SUPFAM:SSF51445 GO:GO:0005975 GO:GO:0005578 GO:GO:0009044 eggNOG:COG1472 Gene3D:G3DSA:3.40.50.1700 Gene3D:G3DSA:3.20.20.300 SUPFAM:SSF52279 CAZy:GH3 EMBL:AY057483 EMBL:AK117237 IPI:IPI00531020 PIR:T49983 RefSeq:NP_196618.1 UniGene:At.1811 ProteinModelPortal:Q9LXA8 STRING:Q9LXA8 PRIDE:Q9LXA8 EnsemblPlants:AT5G10560.1 GeneID:830921 KEGG:ath:AT5G10560 TAIR:At5g10560 InParanoid:Q9LXA8 OMA:LSACCKH PhylomeDB:Q9LXA8 ProtClustDB:PLN03080 Genevestigator:Q9LXA8 Uniprot:Q9LXA8
Root	Isotig12980	15	1	3.778	0.000266457	TAIR|locus:2160972 - symbol:ERF1-1 "AT5G47880" species:3702 "Arabidopsis thaliana" [GO:0003747 "translation release factor activity" evidence=IGI;ISS] [GO:0006415 "translational termination" evidence=IGI;ISS] InterPro:IPR004403 InterPro:IPR005140 InterPro:IPR005141 InterPro:IPR005142 Pfam:PF03465 Pfam:PF03463 Pfam:PF03464 GO:GO:0005737 EMBL:CP002688 GenomeReviews:BA000015_GR EMBL:AB016886 EMBL:U40217 IPI:IPI00545707 RefSeq:NP_001032029.1 RefSeq:NP_199599.1 UniGene:At.22135 ProteinModelPortal:Q39097 SMR:Q39097 STRING:Q39097 PRIDE:Q39097 EnsemblPlants:AT5G47880.1 EnsemblPlants:AT5G47880.2 GeneID:834839 KEGG:ath:AT5G47880 TAIR:At5g47880 eggNOG:COG1503 HOGENOM:HBG497188 InParanoid:Q39097 KO:K03265 OMA:QEANTEN PhylomeDB:Q39097 ProtClustDB:CLSN2682479 ArrayExpress:Q39097 Genevestigator:Q39097 GermOnline:AT5G47880 GO:GO:0016149 InterPro:IPR024049 Gene3D:G3DSA:3.30.960.10 PANTHER:PTHR10113 SUPFAM:SSF55481 TIGRFAMs:TIGR03676 Uniprot:Q39097
Root	Isotig12991	1	19	-4.377	7.43E-06	TAIR|locus:2164506 - symbol:UPM1 "AT5G40850" species:3702 "Arabidopsis thaliana" [GO:0004851 "uroporphyrin-III C-methyltransferase activity" evidence=ISS;IDA] [GO:0006779 "porphyrin-containing compound biosynthetic process" evidence=ISS] [GO:0009507 "chloroplast" evidence=IDA] [GO:0019354 "siroheme biosynthetic process" evidence=IDA] InterPro:IPR000878 InterPro:IPR003043 InterPro:IPR006366 InterPro:IPR014776 InterPro:IPR014777 Pfam:PF00590 PROSITE:PS00839 PROSITE:PS00840 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009507 EMBL:AB011477 GO:GO:0043115 Gene3D:G3DSA:3.40.1010.10 SUPFAM:SSF53790 eggNOG:COG0007 HOGENOM:HBG730212 GO:GO:0004851

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0019354 Gene3D:G3DSA:3.30.950.10 TIGRFAMs:TIGR01469 UniGene:At.20285 EMBL:L47479 EMBL:AY058093 EMBL:AF462833 EMBL:AY079029 EMBL:AY142030 IPI:IPI00524626 RefSeq:NP_198901.1 HSSP:P25924 ProteinModelPortal:Q42606 SMR:Q42606 STRING:Q42606 PRIDE:Q42606 EnsemblPlants:AT5G40850.1 GeneID:834085 KEGG:ath:AT5G40850 TAIR:At5g40850 InParanoid:Q42606 OMA:ADSLNWF PhylomeDB:Q42606 ProtClustDB:PLN02625 Genevestigator:Q42606 InterPro:IPR012383 PIRSF:PIRSF036478 Uniprot:Q42606
Root	Isotig13004	13	0	4.571	0.000344357	TAIR|locus:2037853 - symbol:AT1G15330 "AT1G15330" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0003006 "developmental process involved in reproduction" evidence=IMP] [GO:0009553 "embryo sac development" evidence=IMP] [GO:0009555 "pollen development" evidence=IMP] [GO:0010183 "pollen tube guidance" evidence=IMP] [GO:0048443 "stamen development" evidence=IMP] InterPro:IPR000644 Pfam:PF00571 PROSITE:PS51371 SMART:SM00116 EMBL:CP002684 GO:GO:0048443 GO:GO:0009555 EMBL:AC007591 GO:GO:0009553 GO:GO:0010183 EMBL:BT023415 EMBL:AK229160 EMBL:BT026513 IPI:IPI00545829 PIR:F86287 RefSeq:NP_172985.1 UniGene:At.11420 ProteinModelPortal:Q9XI37 SMR:Q9XI37 PRIDE:Q9XI37 ProMEX:Q9XI37 GeneID:838102 KEGG:ath:AT1G15330 TAIR:At1g15330 eggNOG:NOG272438 HOGENOM:HBG750533 InParanoid:Q9XI37 OMA:VRKHYIG PhylomeDB:Q9XI37 ProtClustDB:CLSN2679465 Genevestigator:Q9XI37 Uniprot:Q9XI37
Root	Isotig13013	0	15	-5.036	4.38E-05	TAIR|locus:2157042 - symbol:AT5G49760 "AT5G49760" species:3702 "Arabidopsis thaliana" [GO:0016301 "kinase activity" evidence=ISS] [GO:0005773 "vacuole" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] Pfam:PF00560 InterPro:IPR001611 InterPro:IPR000719 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 Pfam:PF00069 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 PROSITE:PS51450 GO:GO:0016021 GO:GO:0005886 GO:GO:0005524 GO:GO:0005773 EMBL:CP002688 GenomeReviews:BA000015_GR eggNOG:COG0515 GO:GO:0004872 SUPFAM:SSF56112 GO:GO:0004674 HSSP:P36897 InterPro:IPR013210 Pfam:PF08263 HOGENOM:HBG316990 ProtClustDB:CLSN2686993 EMBL:BT006486 EMBL:FJ708797 EMBL:AK117123 IPI:IPI00519776 RefSeq:NP_199787.2 UniGene:At.7125 ProteinModelPortal:Q8GZ99 SMR:Q8GZ99 IntAct:Q8GZ99 PRIDE:Q8GZ99 EnsemblPlants:AT5G49760.1 GeneID:835039 KEGG:ath:AT5G49760 TAIR:At5g49760 InParanoid:Q8GZ99 OMA:IENIMQL PhylomeDB:Q8GZ99 Genevestigator:Q8GZ99 Uniprot:Q8GZ99
Root	Isotig13015	6	53	-3.272	1.24E-11	TAIR|locus:2078603 - symbol:SRG3 "AT3G02040" species:3702 "Arabidopsis thaliana" [GO:0006071 "glycerol metabolic process" evidence=ISS] [GO:0008889 "glycerophosphodiester phosphodiesterase activity" evidence=ISS;IDA] [GO:0009536 "plastid" evidence=IDA] [GO:0030643 "cellular phosphate ion homeostasis" evidence=IMP] InterPro:IPR004129 InterPro:IPR017946 Pfam:PF03009 EMBL:CP002686 Gene3D:G3DSA:3.20.20.190 SUPFAM:SSF51695 GO:GO:0006629 EMBL:AC011664 GO:GO:0006071 GO:GO:0009536 GO:GO:0030643 GO:GO:0008889 EMBL:AY072127 EMBL:AY114073 IPI:IPI00531878 RefSeq:NP_566159.1 UniGene:At.20730 UniGene:At.75107 ProteinModelPortal:Q9SGA2 SMR:Q9SGA2 PRIDE:Q9SGA2 EnsemblPlants:AT3G02040.1 GeneID:821175 KEGG:ath:AT3G02040 TAIR:At3g02040 InParanoid:Q9SGA2 OMA:AVAFVEF PhylomeDB:Q9SGA2 Genevestigator:Q9SGA2 Uniprot:Q9SGA2
Root	Isotig13018	15	87	-2.665	3.99E-15	TAIR|locus:2053275 - symbol:UXS6 "UDP-XYL synthase 6" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA;ISS] [GO:0008152 "metabolic process" evidence=IEA] [GO:0009225 "nucleotide-sugar metabolic process" evidence=ISS] [GO:0044237 "cellular metabolic process" evidence=IEA] [GO:0050662 "coenzyme binding" evidence=IEA] [GO:0005886 "plasma membrane" evidence=IDA] InterPro:IPR001509 InterPro:IPR016040 Pfam:PF01370 GO:GO:0005886 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 HOGENOM:HBG755066 GO:GO:0003824 GO:GO:0044237 GO:GO:0050662 EMBL:AC005727 HSSP:P27830 ProtClustDB:CLSN2683686 EMBL:AY099703 EMBL:AY128899 IPI:IPI00536112 PIR:F84688 RefSeq:NP_001077972.1 RefSeq:NP_180443.1 RefSeq:NP_973555.1 UniGene:At.38572 ProteinModelPortal:Q9ZV36 SMR:Q9ZV36 STRING:Q9ZV36 PRIDE:Q9ZV36 EnsemblPlants:AT2G28760.1 EnsemblPlants:AT2G28760.2 EnsemblPlants:AT2G28760.3 GeneID:817426 KEGG:ath:AT2G28760 TAIR:At2g28760 InParanoid:Q9ZV36 OMA:KLMQNEK PhylomeDB:Q9ZV36 ArrayExpress:Q9ZV36 Genevestigator:Q9ZV36 Uniprot:Q9ZV36
Root	Isotig13035	1	13	-3.829	0.000362856	TAIR|locus:2074964 - symbol:AT3G09690 "AT3G09690" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0016787 "hydrolase activity" evidence=ISS] EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0016787 EMBL:AC016661

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						eggNOG:NOG282915 HOGENOM:HBG593976 ProtClustDB:CLSN2685157 UniGene:At.40057 EMBL:BT011759 EMBL:AK226307 IPI:IPI00523811 RefSeq:NP_001030665.1 RefSeq:NP_187580.1 ProteinModelPortal:Q9SF34 SMR:Q9SF34 IntAct:Q9SF34 MEROPS:S33.A30 PRIDE:Q9SF34 EnsemblPlants:AT3G09690.1 EnsemblPlants:AT3G09690.2 GeneID:820126 KEGG:ath:AT3G09690 TAIR:At3g09690 InParanoid:Q9SF34 OMA:EGHFSYF PhylomeDB:Q9SF34 Genevestigator:Q9SF34 Uniprot:Q9SF34
Root	Isotig13048	5	36	-2.977	8.93E-08	TAIR|locus:2122063 - symbol:CPK5 "calmodulin-domain protein kinase 5" species:3702 "Arabidopsis thaliana" [GO:0004672 "protein kinase activity" evidence=IEA] [GO:0004674 "protein serine/threonine kinase activity" evidence=IEA] [GO:0004683 "calmodulin-dependent protein kinase activity" evidence=ISS] [GO:0005509 "calcium ion binding" evidence=IEA] [GO:0005524 "ATP binding" evidence=IEA] [GO:0006468 "protein phosphorylation" evidence=ISS] [GO:0016301 "kinase activity" evidence=ISS] [GO:0016020 "membrane" evidence=TAS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009737 "response to abscisic acid stimulus" evidence=IDA] InterPro:IPR000719 InterPro:IPR002048 InterPro:IPR002290 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR011992 InterPro:IPR017441 Pfam:PF00069 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 SMART:SM00054 SMART:SM00220 Prosite:PS00018 Pfam:PF00036 GO:GO:0005829 GO:GO:0005886 GO:GO:0005524 GO:GO:0009737 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005509 eggNOG:COG0515 SUPFAM:SSF56112 GO:GO:0004674 InterPro:IPR018247 InterPro:IPR018249 Gene3D:G3DSA:1.10.238.10 PROSITE:PS50222 HOGENOM:HBG755340 InterPro:IPR018248 EMBL:AL161587 EMBL:AL022604 KO:K13412 HSSP:Q06850 EMBL:U31834 EMBL:AK227104 IPI:IPI00524740 PIR:T06126 RefSeq:NP_195257.1 UniGene:At.21676 ProteinModelPortal:Q38871 SMR:Q38871 STRING:Q38871 PRIDE:Q38871 EnsemblPlants:AT4G35310.1 GeneID:829685 KEGG:ath:AT4G35310 TAIR:At4g35310 InParanoid:Q38871 OMA:NIRDIYT PhylomeDB:Q38871 ProtClustDB:CLSN2916179 ArrayExpress:Q38871 Genevestigator:Q38871 Uniprot:Q38871
Root	Isotig13082	16	0	4.871	5.89E-05	UNIPROTKB|G4NEG1 - symbol:MGG_17531 "Putative uncharacterized protein" species:242507 "Magnaporthe oryzae 70-15" [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] InterPro:IPR000210 InterPro:IPR013069 Pfam:PF00651 PROSITE:PS50097 EMBL:CM001235 InterPro:IPR011333 Gene3D:G3DSA:3.30.710.10 SUPFAM:SSF54695 RefSeq:XP_369129.1 GeneID:2674298 Uniprot:G4NEG1
Root	Isotig13091	21	2	3.263	4.62E-05	TAIR|locus:2163503 - symbol:AT5G45360 "AT5G45360" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] InterPro:IPR001810 PROSITE:PS50181 SMART:SM00256 EMBL:CP002688 GenomeReviews:BA000015_GR SUPFAM:SSF81383 EMBL:AB018113 EMBL:BT002873 EMBL:BT004395 EMBL:BT005876 EMBL:AK227481 EMBL:AY087595 IPI:IPI00522962 IPI:IPI00845143 RefSeq:NP_568643.1 UniGene:At.21436 UniGene:At.48851 ProteinModelPortal:Q9FHK0 SMR:Q9FHK0 IntAct:Q9FHK0 STRING:Q9FHK0 PRIDE:Q9FHK0 EnsemblPlants:AT5G45360.1 GeneID:834572 KEGG:ath:AT5G45360 TAIR:At5g45360 eggNOG:NOG277275 HOGENOM:HBG607597 InParanoid:Q9FHK0 OMA:AWKKLYI PhylomeDB:Q9FHK0 ProtClustDB:CLSN2689932 ArrayExpress:Q9FHK0 Genevestigator:Q9FHK0 InterPro:IPR004289 Pfam:PF03048 Uniprot:Q9FHK0
Root	Isotig13113	0	16	-5.129	2.34E-05	TAIR|locus:2183730 - symbol:AT5G10770 "AT5G10770" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=ISS] [GO:0004190 "aspartic-type endopeptidase activity" evidence=IEA] [GO:0006508 "proteolysis" evidence=IEA] InterPro:IPR001461 InterPro:IPR009007 Pfam:PF00026 PRINTS:PR00792 EMBL:CP002688 GO:GO:0006508 GO:GO:0004190 InterPro:IPR021109 SUPFAM:SSF50630 Gene3D:G3DSA:2.40.70.10 PANTHER:PTHR13683 HSSP:P00799 EMBL:AY075656 EMBL:BT001004 IPI:IPI00543783 RefSeq:NP_196638.2 UniGene:At.32336 ProteinModelPortal:Q8S9J6 MEROPS:A01.A15 PRIDE:Q8S9J6 EnsemblPlants:AT5G10770.1 GeneID:830944 KEGG:ath:AT5G10770 TAIR:At5g10770 InParanoid:Q8S9J6 OMA:LEVVYDG PhylomeDB:Q8S9J6 ProtClustDB:CLSN2686424 Genevestigator:Q8S9J6 Uniprot:Q8S9J6
Root	Isotig13116	0	47	-6.684	5.35E-13	TAIR|locus:2136002 - symbol:AT4G24340 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA;ISS] [GO:0009116 "nucleoside metabolic process" evidence=IEA;ISS] InterPro:IPR000845 Pfam:PF01048 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0003824 eggNOG:COG0775 GO:GO:0009116 InterPro:IPR018017 PANTHER:PTHR21234 EMBL:BT005314 EMBL:AK119074 IPI:IPI00543031 RefSeq:NP_567699.1 UniGene:At.3464 ProteinModelPortal:Q8GW53 PRIDE:Q8GW53 EnsemblPlants:AT4G24340.1 GeneID:828537 KEGG:ath:AT4G24340 TAIR:At4g24340 HOGENOM:HBG744986 InParanoid:Q8GW53 OMA:TEEDAFL PhylomeDB:Q8GW53 ProtClustDB:CLSN2689584 Genevestigator:Q8GW53 Uniprot:Q8GW53

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig13128	1	17	-4.216	2.69E-05	TAIR|locus:2063125 - symbol:TBL33 "AT2G40320" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] eggNOG:NOG29130 EMBL:BT004282 IPI:IPI00518171 PRIDE:Q84W34 TAIR:At2g40320 InParanoid:Q84W34 PhylomeDB:Q84W34 Genevestigator:Q84W34 Uniprot:Q84W34
Root	Isotig13163	1	121	-7.048	2.03E-30	TAIR|locus:2204798 - symbol:MC1 "AT1G02170" species:3702 "Arabidopsis thaliana" [GO:0006508 "proteolysis" evidence=ISS] [GO:0004197 "cysteine-type endopeptidase activity" evidence=IDA] [GO:0043068 "positive regulation of programmed cell death" evidence=IGI;IDA] InterPro:IPR011600 Pfam:PF00656 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0006952 GO:GO:0004197 GO:GO:0006508 GO:GO:0043068 EMBL:U89959 InterPro:IPR005735 Pfam:PF06943 TIGRFAMs:TIGR01053 EMBL:AY219826 EMBL:AY322525 IPI:IPI00531085 RefSeq:NP_171719.2 UniGene:At.10711 UniGene:At.69983 ProteinModelPortal:Q7XJE6 STRING:Q7XJE6 MEROPS:C14.047 PRIDE:Q7XJE6 EnsemblPlants:AT1G02170.1 GeneID:839561 KEGG:ath:AT1G02170 TAIR:At1g02170 eggNOG:NOG68179 HOGENOM:HBG692861 InParanoid:Q7XJE6 OMA:NDAKCMR PhylomeDB:Q7XJE6 Genevestigator:Q7XJE6 Uniprot:Q7XJE6
Root	Isotig13171	2	15	-3.036	0.000493759	No hit
Root	Isotig13186	14	1	3.678	0.000484579	TAIR|locus:2090709 - symbol:AT3G19310 species:3702 "Arabidopsis thaliana" [GO:0004629 "phospholipase C activity" evidence=IEA] [GO:0006629 "lipid metabolic process" evidence=IEA] [GO:0008081 "phosphoric diester hydrolase activity" evidence=IEA] [GO:0035556 "intracellular signal transduction" evidence=IEA] InterPro:IPR000909 InterPro:IPR017946 PROSITE:PS50007 EMBL:CP002686 GO:GO:0035556 Gene3D:G3DSA:3.20.20.190 SUPFAM:SSF51695 GO:GO:0004629 GO:GO:0006629 GO:GO:0016301 EMBL:AB025624 IPI:IPI00521862 RefSeq:NP_188562.1 UniGene:At.38419 ProteinModelPortal:Q9LT86 PRIDE:Q9LT86 EnsemblPlants:AT3G19310.1 GeneID:821465 KEGG:ath:AT3G19310 TAIR:At3g19310 InParanoid:Q9LT86 OMA:VDVANGH PhylomeDB:Q9LT86 ProtClustDB:CLSN2915371 Genevestigator:Q9LT86 Uniprot:Q9LT86
Root	Isotig13213	24	0	5.456	6.37E-07	No hit
Root	Isotig13215	71	10	2.699	8.39E-12	No hit
Root	Isotig13226	0	13	-4.829	0.000155955	TAIR|locus:2099580 - symbol:ASN1 "AT3G47340" species:3702 "Arabidopsis thaliana" [GO:0009063 "cellular amino acid catabolic process" evidence=TAS] [GO:0043617 "cellular response to sucrose starvation" evidence=IEP] [GO:0009744 "response to sucrose stimulus" evidence=IEP] [GO:0009749 "response to glucose stimulus" evidence=IEP] [GO:0009750 "response to fructose stimulus" evidence=IEP] [GO:0009646 "response to absence of light" evidence=TAS] [GO:0004066 "asparagine synthase (glutamine-hydrolyzing) activity" evidence=ISS] InterPro:IPR001962 InterPro:IPR006426 Pfam:PF00733 PIRSF:PIRSF001589 GO:GO:0005524 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0009750 GO:GO:0009749 GO:GO:0009744 GO:GO:0009646 GO:GO:0009063 InterPro:IPR014729 Gene3D:G3DSA:3.40.50.620 GO:GO:0006529 eggNOG:COG0367 HOGENOM:HBG752912 KO:K01953 GO:GO:0004066 GO:GO:0006541 InterPro:IPR017932 TIGRFAMs:TIGR01536 PROSITE:PS51278 MEROPS:C44.974 OMA:IGTTHHE EMBL:L29083 EMBL:AL096860 EMBL:AF419557 EMBL:AY072214 EMBL:AY096592 IPI:IPI00541909 PIR:T12989 RefSeq:NP_190318.1 UniGene:At.20782 ProteinModelPortal:P49078 SMR:P49078 STRING:P49078 PRIDE:P49078 EnsemblPlants:AT3G47340.1 GeneID:823888 KEGG:ath:AT3G47340 TAIR:At3g47340 InParanoid:P49078 PhylomeDB:P49078 ProtClustDB:PLN02549 ArrayExpress:P49078 Genevestigator:P49078 GO:GO:0043617 Uniprot:P49078
Root	Isotig13227	12	39	-1.829	3.01E-05	UNIPROTKB|P93508 - symbol:P93508 "Calreticulin" species:3988 "Ricinus communis" [GO:0005788 "endoplasmic reticulum lumen" evidence=IDA] InterPro:IPR001580 InterPro:IPR009033 InterPro:IPR009169 InterPro:IPR018124 Pfam:PF00262 PIRSF:PIRSF002356 PRINTS:PR00626 PROSITE:PS00803 PROSITE:PS00804 PROSITE:PS00805 GO:GO:0005509 GO:GO:0006457 GO:GO:0005529 GO:GO:0051082 InterPro:IPR008985 InterPro:IPR013320 Gene3D:G3DSA:2.60.120.200 SUPFAM:SSF49899 GO:GO:0005788 PROSITE:PS00014 PANTHER:PTHR11073 SUPFAM:SSF63887 KO:K08057 EMBL:U74631 EMBL:U74630 PIR:T10172 RefSeq:XP_002512501.1 ProteinModelPortal:P93508 SMR:P93508 GeneID:8269812 KEGG:rcu:RCOM_1434770 PhylomeDB:P93508 ProtClustDB:CLSN2719690 Uniprot:P93508
Root	Isotig13246	20	1	4.193	1.37E-05	TAIR|locus:2118041 - symbol:AT4G12130 species:3702 "Arabidopsis thaliana" [GO:0004047 "aminomethyltransferase activity" evidence=IEA;ISS] [GO:0005737 "cytoplasm" evidence=IEA] [GO:0006546 "glycine catabolic process" evidence=IEA] InterPro:IPR006222 Pfam:PF01571 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005737 eggNOG:COG0354 KO:K06980 InterPro:IPR017703 TIGRFAMs:TIGR03317 HOGENOM:HBG700628 GO:GO:0004047 GO:GO:0006546 InterPro:IPR013977

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						Pfam:PF08669 OMA:MDRLHGV EMBL:AY139983 EMBL:BT008478 IPI:IPI00536251 RefSeq:NP_192950.2 UniGene:At.33503 ProteinModelPortal:Q8L733 PRIDE:Q8L733 EnsemblPlants:AT4G12130.1 GeneID:826821 KEGG:ath:AT4G12130 TAIR:At4g12130 InParanoid:Q8L733 PhylomeDB:Q8L733 ProtClustDB:CLSN2681601 Genevestigator:Q8L733 Uniprot:Q8L733
Root	Isotig13256	0	19	-5.377	3.67E-06	TAIR|locus:2097993 - symbol:AT3G62160 "AT3G62160" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0016740 "transferase activity" evidence=ISS] [GO:0016747 "transferase activity, transferring acyl groups other than amino-acyl groups" evidence=IEA] InterPro:IPR003480 Pfam:PF02458 EMBL:CP002686 GenomeReviews:BA000014_GR InterPro:IPR023213 Gene3D:G3DSA:3.30.559.10 GO:GO:0016747 EMBL:AL138651 HOGENOM:HBG599319 EMBL:BT020224 EMBL:BT020438 IPI:IPI00527765 PIR:T48008 RefSeq:NP_191775.1 UniGene:At.34171 ProteinModelPortal:Q9M1Q8 PRIDE:Q9M1Q8 EnsemblPlants:AT3G62160.1 GeneID:825389 KEGG:ath:AT3G62160 TAIR:At3g62160 eggNOG:NOG284877 InParanoid:Q9M1Q8 OMA:GFVMGLR PhylomeDB:Q9M1Q8 ProtClustDB:CLSN2684119 Genevestigator:Q9M1Q8 Uniprot:Q9M1Q8
Root	Isotig13297	0	14	-4.936	8.24E-05	TAIR|locus:2206400 - symbol:ALIS5 "AT1G79450" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0016020 "membrane" evidence=ISS] [GO:0009543 "chloroplast thylakoid lumen" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] InterPro:IPR005045 Pfam:PF03381 PIRSF:PIRSF015840 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005886 GO:GO:0000139 GO:GO:0005789 GO:GO:0031902 eggNOG:COG5035 HOGENOM:HBG525157 PANTHER:PTHR10926 EMBL:AC007202 EMBL:AY088777 EMBL:BX816946 IPI:IPI00522484 IPI:IPI00546489 PIR:F96825 RefSeq:NP_565210.1 RefSeq:NP_974175.1 UniGene:At.34111 STRING:Q8L8W0 PRIDE:Q8L8W0 EnsemblPlants:AT1G79450.1 GeneID:844283 KEGG:ath:AT1G79450 TAIR:At1g79450 InParanoid:Q8L8W0 OMA:NTSADIP PhylomeDB:Q8L8W0 ProtClustDB:CLSN2917495 Genevestigator:Q8L8W0 Uniprot:Q8L8W0
Root	Isotig13303	16	2	2.871	0.000812389	TAIR|locus:504956461 - symbol:AT5G22090 "AT5G22090" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009507 EMBL:AL589883 InterPro:IPR021410 Pfam:PF11250 EMBL:AK118109 EMBL:BT026355 IPI:IPI00541705 RefSeq:NP_001190360.1 RefSeq:NP_680195.2 UniGene:At.23491 PRIDE:Q0V865 EnsemblPlants:AT5G22090.1 EnsemblPlants:AT5G22090.2 GeneID:832270 KEGG:ath:AT5G22090 TAIR:At5g22090 eggNOG:NOG271129 HOGENOM:HBG749111 InParanoid:Q0V865 OMA:STNTESF PhylomeDB:Q0V865 ProtClustDB:CLSN2680152 Genevestigator:Q0V865 Uniprot:Q0V865
Root	Isotig13335	16	0	4.871	5.89E-05	TAIR|locus:2141816 - symbol:AT4G38810 species:3702 "Arabidopsis thaliana" [GO:0005509 "calcium ion binding" evidence=IEA;ISS] [GO:0005575 "cellular_component" evidence=ND] InterPro:IPR002048 InterPro:IPR011992 SMART:SM00054 Prosite:PS00018 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005509 InterPro:IPR018247 InterPro:IPR018249 Gene3D:G3DSA:1.10.238.10 PROSITE:PS50222 EMBL:AL161594 EMBL:AL035656 EMBL:AY056249 IPI:IPI00516483 PIR:T06080 RefSeq:NP_195592.1 UniGene:At.21986 ProteinModelPortal:Q9T0I9 SMR:Q9T0I9 PRIDE:Q9T0I9 EnsemblPlants:AT4G38810.2 GeneID:830036 KEGG:ath:AT4G38810 TAIR:At4g38810 HOGENOM:HBG318825 InParanoid:Q9T0I9 OMA:VAHSENT PhylomeDB:Q9T0I9 ProtClustDB:CLSN2685638 Genevestigator:Q9T0I9 Uniprot:Q9T0I9
Root	Isotig13361	1	16	-4.129	5.13E-05	TAIR|locus:2166523 - symbol:AT5G51920 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0008152 "metabolic process" evidence=IEA] [GO:0030170 "pyridoxal phosphate binding" evidence=IEA] InterPro:IPR000192 InterPro:IPR015421 Pfam:PF00266 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0030170 InterPro:IPR015424 Gene3D:G3DSA:3.40.640.10 SUPFAM:SSF53383 GO:GO:0003824 EMBL:AB015478 eggNOG:COG0520 EMBL:AB025623 HOGENOM:HBG601423 EMBL:AY735719 EMBL:AY924857 IPI:IPI00530533 RefSeq:NP_200005.1 UniGene:At.64285 ProteinModelPortal:Q9FGL6 PRIDE:Q9FGL6 EnsemblPlants:AT5G51920.1 GeneID:835267 KEGG:ath:AT5G51920 TAIR:At5g51920 InParanoid:Q9FGL6 OMA:NFSGVQH PhylomeDB:Q9FGL6 ProtClustDB:CLSN2916839 Genevestigator:Q9FGL6 Uniprot:Q9FGL6
Root	Isotig13377	1	185	-7.660	1.20E-43	TAIR|locus:2204798 - symbol:MC1 "AT1G02170" species:3702 "Arabidopsis thaliana" [GO:0006508 "proteolysis" evidence=ISS] [GO:0004197 "cysteine-type endopeptidase activity" evidence=IDA] [GO:0043068 "positive regulation of programmed cell death" evidence=IGI;IDA] InterPro:IPR011600 Pfam:PF00656 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0006952 GO:GO:0004197 GO:GO:0006508 GO:GO:0043068 EMBL:U89959 InterPro:IPR005735 Pfam:PF06943 TIGRFAMs:TIGR01053 EMBL:AY219826 EMBL:AY322525 IPI:IPI00531085 RefSeq:NP_171719.2 UniGene:At.10711 UniGene:At.69983 ProteinModelPortal:Q7XJE6

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
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Root	Isotig13380	0	14	-4.936	8.24E-05	TAIR|locus:505006103 - symbol:AT1G05805 "AT1G05805" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=ISS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=TAS] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR011598 Pfam:PF00010 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0005634 GO:GO:0006355 GO:GO:0003677 GO:GO:0006351 Gene3D:G3DSA:4.10.280.10 SMART:SM00353 SUPFAM:SSF47459 PROSITE:PS50888 EMBL:AC009999 HOGENOM:HBG592906 EMBL:BT000954 EMBL:AY086106 IPI:IPI00516925 PIR:F86192 RefSeq:NP_563749.1 UniGene:At.11933 ProteinModelPortal:Q8H102 SMR:Q8H102 IntAct:Q8H102 STRING:Q8H102 PRIDE:Q8H102 EnsemblPlants:AT1G05805.1 GeneID:837090 KEGG:ath:AT1G05805 TAIR:At1g05805 eggNOG:NOG249421 InParanoid:Q8H102 OMA:NEVNETP PhylomeDB:Q8H102 ProtClustDB:CLSN2687697 ArrayExpress:Q8H102 Genevestigator:Q8H102 Uniprot:Q8H102
Root	Isotig13386	2	16	-3.129	0.000262867	TAIR|locus:2044631 - symbol:AT2G15760 "AT2G15760" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0005516 "calmodulin binding" evidence=TAS] [GO:0005886 "plasma membrane" evidence=IDA] GO:GO:0005886 EMBL:CP002685 GenomeReviews:CT485783_GR EMBL:AC006248 EMBL:AC006438 ProtClustDB:CLSN2714519 InterPro:IPR012442 Pfam:PF07816 EMBL:AF345343 EMBL:AY088268 EMBL:BT026445 IPI:IPI00519889 PIR:A84533 RefSeq:NP_565379.1 UniGene:At.13860 STRING:Q9ZQD8 PRIDE:Q9ZQD8 EnsemblPlants:AT2G15760.1 GeneID:816070 KEGG:ath:AT2G15760 TAIR:At2g15760 eggNOG:NOG292804 HOGENOM:HBG745254 InParanoid:Q9ZQD8 OMA:SAHEMHY PhylomeDB:Q9ZQD8 ArrayExpress:Q9ZQD8 Genevestigator:Q9ZQD8 Uniprot:Q9ZQD8
Root	Isotig13404	0	87	-7.572	1.49E-21	TAIR|locus:2204798 - symbol:MC1 "AT1G02170" species:3702 "Arabidopsis thaliana" [GO:0006508 "proteolysis" evidence=ISS] [GO:0004197 "cysteine-type endopeptidase activity" evidence=IDA] [GO:0043068 "positive regulation of programmed cell death" evidence=IGI;IDA] InterPro:IPR011600 Pfam:PF00656 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0006952 GO:GO:0004197 GO:GO:0006508 GO:GO:0043068 EMBL:U89959 InterPro:IPR005735 Pfam:PF06943 TIGRFAMs:TIGR01053 EMBL:AY219826 EMBL:AY322525 IPI:IPI00531085 RefSeq:NP_171719.2 UniGene:At.10711 UniGene:At.69983 ProteinModelPortal:Q7XJE6 STRING:Q7XJE6 MEROPS:C14.047 PRIDE:Q7XJE6 EnsemblPlants:AT1G02170.1 GeneID:839561 KEGG:ath:AT1G02170 TAIR:At1g02170 eggNOG:NOG68179 HOGENOM:HBG692861 InParanoid:Q7XJE6 OMA:NDAKCMR PhylomeDB:Q7XJE6 Genevestigator:Q7XJE6 Uniprot:Q7XJE6
Root	Isotig13448	1	35	-5.258	3.57E-10	TAIR|locus:2204798 - symbol:MC1 "AT1G02170" species:3702 "Arabidopsis thaliana" [GO:0006508 "proteolysis" evidence=ISS] [GO:0004197 "cysteine-type endopeptidase activity" evidence=IDA] [GO:0043068 "positive regulation of programmed cell death" evidence=IGI;IDA] InterPro:IPR011600 Pfam:PF00656 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0006952 GO:GO:0004197 GO:GO:0006508 GO:GO:0043068 EMBL:U89959 InterPro:IPR005735 Pfam:PF06943 TIGRFAMs:TIGR01053 EMBL:AY219826 EMBL:AY322525 IPI:IPI00531085 RefSeq:NP_171719.2 UniGene:At.10711 UniGene:At.69983 ProteinModelPortal:Q7XJE6 STRING:Q7XJE6 MEROPS:C14.047 PRIDE:Q7XJE6 EnsemblPlants:AT1G02170.1 GeneID:839561 KEGG:ath:AT1G02170 TAIR:At1g02170 eggNOG:NOG68179 HOGENOM:HBG692861 InParanoid:Q7XJE6 OMA:NDAKCMR PhylomeDB:Q7XJE6 Genevestigator:Q7XJE6 Uniprot:Q7XJE6
Root	Isotig13466	5	36	-2.977	8.93E-08	TAIR|locus:2119251 - symbol:AT4G33420 species:3702 "Arabidopsis thaliana" [GO:0004601 "peroxidase activity" evidence=IEA;ISS] [GO:0006979 "response to oxidative stress" evidence=IEA] [GO:0020037 "heme binding" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] InterPro:IPR000823 InterPro:IPR002016 InterPro:IPR010255 InterPro:IPR019793 InterPro:IPR019794 Pfam:PF00141 PRINTS:PR00458 PRINTS:PR00461 PROSITE:PS00435 PROSITE:PS00436 PROSITE:PS50873 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005576 GO:GO:0006979 EMBL:AL161583 EMBL:AL035678 GO:GO:0020037 GO:GO:0004601 HOGENOM:HBG597790 SUPFAM:SSF48113 KO:K00430 EMBL:AF451951 EMBL:BT044614 IPI:IPI00539387 PIR:T05993 RefSeq:NP_567919.1 UniGene:At.28650 ProteinModelPortal:Q9SZB9 SMR:Q9SZB9 STRING:Q9SZB9 PeroxiBase:213 PRIDE:Q9SZB9 EnsemblPlants:AT4G33420.1 GeneID:829479 KEGG:ath:AT4G33420 GeneFarm:1879 TAIR:At4g33420 eggNOG:NOG276365 InParanoid:Q9SZB9 ProtClustDB:CLSN2689733 Genevestigator:Q9SZB9 GermOnline:AT4G33420 Uniprot:Q9SZB9

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<tr><th>Tissue</th><th>Identification</th><th># of reads (stress)</th><th># of reads (control)</th><th>Fold Change</th><th>p-value</th><th>Description</th></tr>
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<tr><td>Root</td><td>Isotig13487</td><td>5</td><td>142</td><td>-4.957</td><td>4.10E-36</td><td>TAIR|locus:2204798 - symbol:MC1 "AT1G02170" species:3702 "Arabidopsis thaliana" [GO:0006508 "proteolysis" evidence=ISS] [GO:0004197 "cysteine-type endopeptidase activity" evidence=IDA] [GO:0043068 "positive regulation of programmed cell death" evidence=IGI;IDA] InterPro:IPR011600 Pfam:PF00656 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0006952 GO:GO:0004197 GO:GO:0006508 GO:GO:0043068 EMBL:U89959 InterPro:IPR005735 Pfam:PF06943 TIGRFAMs:TIGR01053 EMBL:AY219826 EMBL:AY322525 IPI:IPI00531085 RefSeq:NP_171719.2 UniGene:At.10711 UniGene:At.69983 ProteinModelPortal:Q7XJE6 STRING:Q7XJE6 MEROPS:C14.047 PRIDE:Q7XJE6 EnsemblPlants:AT1G02170.1 GeneID:839561 KEGG:ath:AT1G02170 TAIR:At1g02170 eggNOG:NOG68179 HOGENOM:HBG692861 InParanoid:Q7XJE6 OMA:NDAKCMR PhylomeDB:Q7XJE6 Genevestigator:Q7XJE6 Uniprot:Q7XJE6</td></tr>
<tr><td>Root</td><td>Isotig13498</td><td>2</td><td>14</td><td>-2.936</td><td>0.000925454</td><td>TAIR|locus:2128043 - symbol:STY17 "AT4G35780" species:3702 "Arabidopsis thaliana" [GO:0004672 "protein kinase activity" evidence=ISS] [GO:0004712 "protein serine/threonine/tyrosine kinase activity" evidence=ISS] [GO:0005829 "cytosol" evidence=IDA] [GO:0009658 "chloroplast organization" evidence=IGI] InterPro:IPR000719 InterPro:IPR001245 InterPro:IPR002912 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR020635 Pfam:PF01842 Pfam:PF07714 PRINTS:PR00109 PROSITE:PS00108 PROSITE:PS50011 SMART:SM00219 GO:GO:0005829 GO:GO:0005524 EMBL:CP002687 SUPFAM:SSF56112 GO:GO:0004674 GO:GO:0016597 GO:GO:0004713 HSSP:P41240 ProtClustDB:CLSN2683904 EMBL:AY093017 EMBL:AY128938 IPI:IPI00540362 RefSeq:NP_195303.2 UniGene:At.31384 ProteinModelPortal:Q8RWL6 SMR:Q8RWL6 IntAct:Q8RWL6 PRIDE:Q8RWL6 EnsemblPlants:AT4G35780.1 GeneID:829731 KEGG:ath:AT4G35780 TAIR:At4g35780 InParanoid:Q8RWL6 OMA:LHKHKGV PhylomeDB:Q8RWL6 Genevestigator:Q8RWL6 Uniprot:Q8RWL6</td></tr>
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Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
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Root	Isotig13522	0	12	-4.714	0.000297064	TAIR|locus:2092070 - symbol:LTA2 "AT3G25860" species:3702 "Arabidopsis thaliana" [GO:0004742 "dihydrolipoyllysine-residue acetyltransferase activity" evidence=ISS;IDA] [GO:0008152 "metabolic process" evidence=ISS] [GO:0006086 "acetyl-CoA biosynthetic process from pyruvate" evidence=TAS] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] InterPro:IPR001078 InterPro:IPR004167 Pfam:PF00198 Pfam:PF02817 InterPro:IPR000089 Pfam:PF00364 GO:GO:0009570 EMBL:CP002686 GO:GO:0016020 InterPro:IPR023213 Gene3D:G3DSA:3.30.559.10 GO:GO:0009941 InterPro:IPR011053 SUPFAM:SSF51230 PROSITE:PS50968 GO:GO:0009534 GO:GO:0022626 GO:GO:0006086 InterPro:IPR003016 PROSITE:PS00189 Gene3D:G3DSA:4.10.320.10 SUPFAM:SSF47005 HSSP:P07016 GO:GO:0004742 ProtClustDB:CLSN2708031 EMBL:AF066079 EMBL:AY037262 EMBL:BT002343 IPI:IPI00549147 RefSeq:NP_189215.1 UniGene:At.23227 ProteinModelPortal:Q9SQI8 SMR:Q9SQI8 IntAct:Q9SQI8 STRING:Q9SQI8 PRIDE:Q9SQI8 EnsemblPlants:AT3G25860.1 GeneID:822181 KEGG:ath:AT3G25860 TAIR:At3g25860 InParanoid:Q9SQI8 OMA:QKWKELV PhylomeDB:Q9SQI8 Genevestigator:Q9SQI8 Uniprot:Q9SQI8
Root	Isotig13529	1	16	-4.129	5.13E-05	UNIPROTKB|Q8W2B7 - symbol:Bx8 "DIMBOA UDP-glucosyltransferase BX8" species:4577 "Zea mays" [GO:0008152 "metabolic process" evidence=IDA] [GO:0046527 "glucosyltransferase activity" evidence=IDA] InterPro:IPR002213 Pfam:PF00201 PROSITE:PS00375 CAZy:GT1 GO:GO:0046527 PANTHER:PTHR11926 EMBL:AF331854 ProteinModelPortal:Q8W2B7 PRIDE:Q8W2B7 Gramene:Q8W2B7 MaizeGDB:9021865 Uniprot:Q8W2B7
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Root	Isotig13541	1	15	-4.036	9.83E-05	TAIR|locus:2083850 - symbol:PHF1 "AT3G52190" species:3702 "Arabidopsis thaliana" [GO:0000166 "nucleotide binding" evidence=ISS] [GO:0005783 "endoplasmic reticulum" evidence=IDA] [GO:0006817 "phosphate ion transport" evidence=IMP] [GO:0006888 "ER to Golgi vesicle-mediated transport" evidence=IMP] [GO:0016036 "cellular response to phosphate starvation" evidence=IEP] [GO:0005886 "plasma membrane" evidence=IDA] InterPro:IPR017986 InterPro:IPR001680 InterPro:IPR015943 Pfam:PF00400 PROSITE:PS50082 PROSITE:PS50294 SMART:SM00320 GO:GO:0016021 GO:GO:0005886 EMBL:CP002686 GenomeReviews:BA000014_GR Gene3D:G3DSA:2.130.10.10 SUPFAM:SSF50978 PROSITE:PS00678 GO:GO:0005789 GO:GO:0015031 GO:GO:0006888 GO:GO:0016036 EMBL:AL049711 GO:GO:0006817 EMBL:AK117697 IPI:IPI00543117 PIR:T49098 RefSeq:NP_566961.1 UniGene:At.20633 ProteinModelPortal:Q8GYE0 SMR:Q8GYE0 PRIDE:Q8GYE0 EnsemblPlants:AT3G52190.1 GeneID:824384 KEGG:ath:AT3G52190 GeneFarm:3702 TAIR:At3g52190 eggNOG:KOG0771 HOGENOM:HBG318009 InParanoid:Q8GYE0 OMA:ADWKEWQ PhylomeDB:Q8GYE0 ProtClustDB:CLSN2917420 Genevestigator:Q8GYE0 GermOnline:AT3G52190 Uniprot:Q8GYE0
Root	Isotig13555	6	28	-2.351	3.31E-05	TAIR|locus:2161845 - symbol:AT5G56140 "AT5G56140" species:3702 "Arabidopsis thaliana" [GO:0003676 "nucleic acid binding" evidence=ISS] [GO:0003723 "RNA binding" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] InterPro:IPR004087 PROSITE:PS50084 SMART:SM00322 GO:GO:0005634 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0003723 EMBL:AB011476 eggNOG:COG5176 HSSP:Q32NN2 EMBL:AY080852 EMBL:BT000873 IPI:IPI00544767

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						RefSeq:NP_200425.1 UniGene:At.29404 ProteinModelPortal:Q9FKT4 SMR:Q9FKT4 PRIDE:Q9FKT4 EnsemblPlants:AT5G56140.1 GeneID:835713 KEGG:ath:AT5G56140 TAIR:At5g56140 HOGENOM:HBG319392 InParanoid:Q9FKT4 OMA:PMEETHD PhylomeDB:Q9FKT4 ProtClustDB:CLSN2916672 Genevestigator:Q9FKT4 Uniprot:Q9FKT4
Root	Isotig13574	0	12	-4.714	0.000297064	TAIR|locus:2124529 - symbol:DSEL "AT4G18550" species:3702 "Arabidopsis thaliana" [GO:0004806 "triglyceride lipase activity" evidence=ISS] [GO:0005575 "cellular_component" evidence=ND] [GO:0006629 "lipid metabolic process" evidence=ISS] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0008970 "phosphatidylcholine 1-acylhydrolase activity" evidence=IDA] [GO:0010187 "negative regulation of seed germination" evidence=IMP] [GO:0019915 "lipid storage" evidence=IMP] [GO:0046340 "diacylglycerol catabolic process" evidence=IDA] [GO:0047372 "acylglycerol lipase activity" evidence=IDA] [GO:0052651 "monoacylglycerol catabolic process" evidence=IDA] InterPro:IPR002921 Pfam:PF01764 PROSITE:PS00120 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005737 GO:GO:0004806 GO:GO:0047372 GO:GO:0010187 GO:GO:0019915 EMBL:AL161548 GO:GO:0046340 EMBL:AL021710 GO:GO:0052651 EMBL:BT030056 EMBL:AK118061 IPI:IPI00541564 PIR:T04551 RefSeq:NP_193590.1 UniGene:At.32892 ProteinModelPortal:O49523 EnsemblPlants:AT4G18550.1 GeneID:827587 KEGG:ath:AT4G18550 TAIR:At4g18550 eggNOG:NOG253202 HOGENOM:HBG745631 InParanoid:O49523 OMA:KESNWMG PhylomeDB:O49523 ProtClustDB:PLN02571 BioCyc:MetaCyc:AT4G18550-MONOMER ArrayExpress:O49523 Genevestigator:O49523 GO:GO:0008970 Uniprot:O49523
Root	Isotig13580	0	15	-5.036	4.38E-05	UNIPROTKB|A8QW53 - symbol:OMT3 "5-pentadecatrienyl resorcinol O-methyltransferase" species:4558 "Sorghum bicolor" [GO:0008171 "O-methyltransferase activity" evidence=IDA] [GO:0008757 "S-adenosylmethionine-dependent methyltransferase activity" evidence=IDA] [GO:0032259 "methylation" evidence=IDA] InterPro:IPR001077 InterPro:IPR012967 InterPro:IPR016461 Pfam:PF00891 Pfam:PF08100 PIRSF:PIRSF005739 InterPro:IPR011991 Gene3D:G3DSA:1.10.10.10 GO:GO:0046983 GO:GO:0008171 GO:GO:0008757 EMBL:EF189708 EMBL:CM000765 RefSeq:XP_002447425.1 UniGene:Sbi.19698 ProteinModelPortal:A8QW53 EnsemblPlants:Sb06g000820.1 GeneID:8080259 KEGG:sbi:SORBI_06g000820 eggNOG:NOG272168 PhylomeDB:A8QW53 ProtClustDB:CLSN2725062 Uniprot:A8QW53
Root	Isotig13595	5	22	-2.266	0.000318925	TAIR|locus:2204660 - symbol:AT1G77670 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0008483 "transaminase activity" evidence=ISS] [GO:0009058 "biosynthetic process" evidence=IEA] [GO:0016769 "transferase activity, transferring nitrogenous groups" evidence=IEA] [GO:0016847 "1-aminocyclopropane-1-carboxylate synthase activity" evidence=IEA] [GO:0030170 "pyridoxal phosphate binding" evidence=IEA] InterPro:IPR001176 InterPro:IPR004839 InterPro:IPR015421 InterPro:IPR015422 Pfam:PF00155 PRINTS:PR00753 EMBL:CP002684 GO:GO:0016847 GO:GO:0030170 InterPro:IPR015424 Gene3D:G3DSA:3.40.640.10 Gene3D:G3DSA:3.90.1150.10 SUPFAM:SSF53383 GO:GO:0008483 EMBL:AC010704 OMA:HICFAVE HSSP:Q56232 EMBL:BT028918 IPI:IPI00521321 PIR:D96806 RefSeq:NP_177890.1 UniGene:At.24928 ProteinModelPortal:Q9CAP1 SMR:Q9CAP1 STRING:Q9CAP1 PRIDE:Q9CAP1 EnsemblPlants:AT1G77670.1 GeneID:844103 KEGG:ath:AT1G77670 TAIR:At1g77670 InParanoid:Q9CAP1 PhylomeDB:Q9CAP1 ProtClustDB:PLN00175 Genevestigator:Q9CAP1 Uniprot:Q9CAP1
Root	Isotig13599	10	37	-2.016	1.44E-05	UNIPROTKB|Q6VMW0 - symbol:OMT2 "8-hydroxyquercetin 8-O-methyltransferase" species:34256 "Mentha x piperita" [GO:0009812 "flavonoid metabolic process" evidence=IDA] [GO:0030761 "8-hydroxyquercitin 8-O-methyltransferase activity" evidence=IDA] [GO:0032259 "methylation" evidence=IDA] InterPro:IPR001077 InterPro:IPR012967 InterPro:IPR016461 Pfam:PF00891 Pfam:PF08100 PIRSF:PIRSF005739 InterPro:IPR011991 Gene3D:G3DSA:1.10.10.10 GO:GO:0046983 GO:GO:0008171 GO:GO:0009812 EMBL:AY337459 ProteinModelPortal:Q6VMW0 BRENDA:2.1.1.88 GO:GO:0030761 Uniprot:Q6VMW0
Root	Isotig13608	1	13	-3.829	0.000362856	TAIR|locus:2020638 - symbol:LGT8 "AT1G70090" species:3702 "Arabidopsis thaliana" [GO:0016051 "carbohydrate biosynthetic process" evidence=ISS] [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0016758 "transferase activity, transferring hexosyl groups" evidence=ISS] [GO:0047262 "polygalacturonate 4-alpha-galacturonosyltransferase activity" evidence=ISS] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR002495 Pfam:PF01501 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0000139 GO:GO:0007047 GO:GO:0016757 EMBL:AC002062 CAZy:GT8 HOGENOM:HBG594866 eggNOG:COG1442 ProtClustDB:CLSN2682378 EMBL:AF370264 EMBL:AY063081 IPI:IPI00528533 PIR:F96723 RefSeq:NP_001117576.1 RefSeq:NP_564983.1 UniGene:At.20996 UniGene:At.74177 ProteinModelPortal:O04536 PRIDE:O04536 EnsemblPlants:AT1G70090.1 EnsemblPlants:AT1G70090.2 GeneID:843345

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						KEGG:ath:AT1G70090 TAIR:At1g70090 InParanoid:O04536 OMA:FARFYMP PhylomeDB:O04536 ArrayExpress:O04536 Genevestigator:O04536 Uniprot:O04536
Root	Isotig13612	1	14	-3.936	0.000188601	TAIR|locus:2171544 - symbol:NUDT8 "nudix hydrolase homolog 8" species:3702 "Arabidopsis thaliana" [GO:0016787 "hydrolase activity" evidence=IEA;ISS] [GO:0005829 "cytosol" evidence=RCA] [GO:0009611 "response to wounding" evidence=IEP] InterPro:IPR000086 InterPro:IPR015797 InterPro:IPR020084 Pfam:PF00293 PROSITE:PS00893 PROSITE:PS51462 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009611 GO:GO:0046872 Gene3D:G3DSA:3.90.79.10 SUPFAM:SSF55811 GO:GO:0016787 EMBL:AB018117 HOGENOM:HBG593794 InterPro:IPR003293 PRINTS:PR01356 eggNOG:NOG137117 EMBL:AY125502 EMBL:BT000563 EMBL:AY087784 IPI:IPI00519383 RefSeq:NP_568680.1 UniGene:At.29907 ProteinModelPortal:Q8L7W2 SMR:Q8L7W2 PRIDE:Q8L7W2 EnsemblPlants:AT5G47240.1 GeneID:834771 KEGG:ath:AT5G47240 TAIR:At5g47240 InParanoid:Q8L7W2 OMA:HAHNVAF PhylomeDB:Q8L7W2 ProtClustDB:CLSN2917743 Genevestigator:Q8L7W2 GermOnline:AT5G47240 Uniprot:Q8L7W2
Root	Isotig13624	0	11	-4.588	0.000569522	TAIR|locus:2056886 - symbol:FT1 "AT2G03220" species:3702 "Arabidopsis thaliana" [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0008417 "fucosyltransferase activity" evidence=ISS;TAS] [GO:0009832 "plant-type cell wall biogenesis" evidence=TAS] [GO:0009969 "xyloglucan biosynthetic process" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR004938 Pfam:PF03254 GO:GO:0016021 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0032580 GO:GO:0007047 EMBL:AC005313 GO:GO:0008107 GO:GO:0042546 CAZy:GT37 HOGENOM:HBG319216 KO:K13681 EMBL:AF154111 EMBL:AY139993 EMBL:BT002477 EMBL:BT003401 IPI:IPI00530227 PIR:T02704 RefSeq:NP_178421.1 UniGene:At.20298 IntAct:Q9SWH5 STRING:Q9SWH5 PRIDE:Q9SWH5 EnsemblPlants:AT2G03220.1 GeneID:814851 KEGG:ath:AT2G03220 TAIR:At2g03220 eggNOG:NOG240652 InParanoid:Q9SWH5 OMA:APDPPCR PhylomeDB:Q9SWH5 ProtClustDB:CLSN2913257 BioCyc:MetaCyc:MONOMER-13997 ArrayExpress:Q9SWH5 Genevestigator:Q9SWH5 GermOnline:AT2G03220 GO:GO:0009969 Uniprot:Q9SWH5
Root	Isotig13632	32	245	-3.066	1.94E-45	UNIPROTKB|Q6VMW0 - symbol:OMT2 "8-hydroxyquercetin 8-O-methyltransferase" species:34256 "Mentha x piperita" [GO:0009812 "flavonoid metabolic process" evidence=IDA] [GO:0030761 "8-hydroxyquercitin 8-O-methyltransferase activity" evidence=IDA] [GO:0032259 "methylation" evidence=IDA] InterPro:IPR001077 InterPro:IPR012967 InterPro:IPR016461 Pfam:PF00891 Pfam:PF08100 PIRSF:PIRSF005739 InterPro:IPR011991 Gene3D:G3DSA:1.10.10.10 GO:GO:0046983 GO:GO:0008171 GO:GO:0009812 EMBL:AY337459 ProteinModelPortal:Q6VMW0 BRENDA:2.1.1.88 GO:GO:0030761 Uniprot:Q6VMW0
Root	Isotig13639	1	12	-3.714	0.000699736	TAIR|locus:2205677 - symbol:FRUCT5 "AT1G55120" species:3702 "Arabidopsis thaliana" [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=ISS] [GO:0005975 "carbohydrate metabolic process" evidence=IEA] [GO:0031219 "levanase activity" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] InterPro:IPR001362 InterPro:IPR018053 PROSITE:PS00609 SMART:SM00640 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0048046 GO:GO:0005773 GO:GO:0005618 InterPro:IPR008985 SUPFAM:SSF49899 InterPro:IPR023296 Gene3D:G3DSA:2.115.10.20 SUPFAM:SSF75005 EMBL:AC073944 CAZy:GH32 eggNOG:COG1621 HOGENOM:HBG317462 InterPro:IPR013189 InterPro:IPR013148 Pfam:PF08244 Pfam:PF00251 EMBL:AB029310 EMBL:AK176675 IPI:IPI00548648 PIR:G96592 RefSeq:NP_564676.1 UniGene:At.458 ProteinModelPortal:Q67XZ3 SMR:Q67XZ3 PRIDE:Q67XZ3 EnsemblPlants:AT1G55120.1 GeneID:841955 KEGG:ath:AT1G55120 TAIR:At1g55120 InParanoid:Q67XZ3 OMA:HSIVESY PhylomeDB:Q67XZ3 ProtClustDB:CLSN2688819 ArrayExpress:Q67XZ3 Genevestigator:Q67XZ3 GO:GO:0051669 Uniprot:Q67XZ3
Root	Isotig13679	24	2	3.456	8.16E-06	TAIR|locus:2141385 - symbol:SAM-2 "AT4G01850" species:3702 "Arabidopsis thaliana" [GO:0004478 "methionine adenosyltransferase activity" evidence=ISS] [GO:0006556 "S-adenosylmethionine biosynthetic process" evidence=ISS] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0071281 "cellular response to iron ion" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA;RCA] [GO:0070062 "extracellular vesicular exosome" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR002133 InterPro:IPR022628 InterPro:IPR022629 InterPro:IPR022630 InterPro:IPR022631 InterPro:IPR022636 Pfam:PF00438 Pfam:PF02772 Pfam:PF02773 PIRSF:PIRSF000497 PROSITE:PS00376 PROSITE:PS00377 GO:GO:0005829 GO:GO:0009506 GO:GO:0005524 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005618 GO:GO:0071281 GO:GO:0005730 GO:GO:0005507 EMBL:AC007138 EMBL:AL161493 GO:GO:0070062 GO:GO:0006730 KO:K00789 GO:GO:0006556 UniGene:At.24731 eggNOG:COG0192 HOGENOM:HBG443662 ProtClustDB:PLN02243 GO:GO:0004478 PANTHER:PTHR11964 SUPFAM:SSF55973 TIGRFAMs:TIGR01034 EMBL:M33217 EMBL:AY072327

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EMBL:AY094454 EMBL:BT000575 EMBL:Z33778 EMBL:Z29136 IPI:IPI00529348 PIR:JQ0410 RefSeq:NP_001078345.1 RefSeq:NP_192094.1 UniGene:At.24433 UniGene:At.71920 ProteinModelPortal:P17562 SMR:P17562 STRING:P17562 PRIDE:P17562 ProMEX:P17562 EnsemblPlants:AT4G01850.1 EnsemblPlants:AT4G01850.2 GeneID:826987 KEGG:ath:AT4G01850 TAIR:At4g01850 InParanoid:P17562 OMA:ATIDYEK PhylomeDB:P17562 ArrayExpress:P17562 Genevestigator:P17562 GermOnline:AT4G01850 Uniprot:P17562
Root	Isotig13683	7	25	-1.965	0.000455586	TAIR|locus:2013880 - symbol:GSR2 "AT1G66200" species:3702 "Arabidopsis thaliana" [GO:0004356 "glutamate-ammonia ligase activity" evidence=ISS;IDA] [GO:0005829 "cytosol" evidence=IDA;TAS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0042128 "nitrate assimilation" evidence=TAS] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0048046 "apoplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] InterPro:IPR008146 InterPro:IPR008147 InterPro:IPR014746 Pfam:PF00120 Pfam:PF03951 PROSITE:PS00180 PROSITE:PS00181 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005524 GO:GO:0048046 GO:GO:0009570 GO:GO:0005773 EMBL:AC026480 GO:GO:0009941 GO:GO:0005507 GO:GO:0009651 GO:GO:0022626 GO:GO:0042128 GO:GO:0009399 eggNOG:COG0174 HOGENOM:HBG299709 ProtClustDB:PLN02284 GO:GO:0004356 GO:GO:0006542 Gene3D:G3DSA:3.30.590.10 Gene3D:G3DSA:3.10.20.70 SUPFAM:SSF54368 EMBL:AY091101 EMBL:AY122962 EMBL:AY086653 IPI:IPI00532772 PIR:H96686 PIR:S18602 RefSeq:NP_176794.1 UniGene:At.47484 UniGene:At.74857 ProteinModelPortal:Q8LCE1 SMR:Q8LCE1 IntAct:Q8LCE1 STRING:Q8LCE1 PRIDE:Q8LCE1 ProMEX:Q8LCE1 DNASU:842935 EnsemblPlants:AT1G66200.1 GeneID:842935 KEGG:ath:AT1G66200 TAIR:At1g66200 InParanoid:Q8LCE1 OMA:HICVYDP PhylomeDB:Q8LCE1 ArrayExpress:Q9C8C7 Genevestigator:Q8LCE1 Uniprot:Q8LCE1
Root	Isotig13719	18	2	3.041	0.000259481	TAIR|locus:2027549 - symbol:GolS2 "AT1G56600" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0016051 "carbohydrate biosynthetic process" evidence=ISS] [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0016758 "transferase activity, transferring hexosyl groups" evidence=ISS] [GO:0006012 "galactose metabolic process" evidence=IDA] [GO:0006979 "response to oxidative stress" evidence=IEP] [GO:0009409 "response to cold" evidence=IMP] [GO:0009651 "response to salt stress" evidence=IMP] [GO:0047216 "inositol 3-alpha-galactosyltransferase activity" evidence=IDA] [GO:0009414 "response to water deprivation" evidence=IEP] InterPro:IPR002495 Pfam:PF01501 EMBL:CP002684 GO:GO:0006979 GO:GO:0009409 GO:GO:0009651 GO:GO:0009414 GO:GO:0006012 EMBL:AC009323 CAZy:GT8 OMA:DSQDAAN ProtClustDB:PLN00176 GO:GO:0047216 EMBL:AY050410 EMBL:AY058238 EMBL:AB062849 IPI:IPI00517274 PIR:G96607 RefSeq:NP_176053.1 UniGene:At.19795 ProteinModelPortal:Q9FXB2 SMR:Q9FXB2 STRING:Q9FXB2 PRIDE:Q9FXB2 EnsemblPlants:AT1G56600.1 GeneID:842114 KEGG:ath:AT1G56600 TAIR:At1g56600 InParanoid:Q9FXB2 PhylomeDB:Q9FXB2 Genevestigator:Q9FXB2 Uniprot:Q9FXB2
Root	Isotig13746	2	15	-3.036	0.000493759	TAIR|locus:2150441 - symbol:GME "AT5G28840" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=ISS] [GO:0009225 "nucleotide-sugar metabolic process" evidence=ISS] [GO:0047918 "GDP-mannose 3,5-epimerase activity" evidence=ISS;IDA] [GO:0019853 "L-ascorbic acid biosynthetic process" evidence=TAS] [GO:0051287 "NAD binding" evidence=TAS] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001509 InterPro:IPR016040 Pfam:PF01370 GO:GO:0005829 EMBL:CP002688 GenomeReviews:BA000015_GR eggNOG:COG0451 Gene3D:G3DSA:3.40.50.720 GO:GO:0051287 HOGENOM:HBG755066 GO:GO:0019853 EMBL:AF272706 EMBL:AY057660 EMBL:AY057694 EMBL:AY116953 IPI:IPI00536932 RefSeq:NP_001190417.1 RefSeq:NP_198236.1 UniGene:At.21733 PDB:2C54 PDB:2C59 PDB:2C5A PDB:2C5E PDBsum:2C54 PDBsum:2C59 PDBsum:2C5A PDBsum:2C5E ProteinModelPortal:Q93VR3 SMR:Q93VR3 STRING:Q93VR3 PRIDE:Q93VR3 EnsemblPlants:AT5G28840.1 EnsemblPlants:AT5G28840.2 GeneID:833002 KEGG:ath:AT5G28840 TAIR:At5g28840 InParanoid:Q93VR3 KO:K10046 OMA:IDDCVEG PhylomeDB:Q93VR3 ProtClustDB:PLN02695 BioCyc:ARA:AT5G28840-MONOMER BioCyc:MetaCyc:AT5G28840-MONOMER Genevestigator:Q93VR3 GermOnline:AT5G28840 GO:GO:0047918 Uniprot:Q93VR3
Root	Isotig13801	4	37	-3.338	1.13E-08	TAIR|locus:2044856 - symbol:AT2G36460 "AT2G36460" species:3702 "Arabidopsis thaliana" [GO:0006098 "pentose-phosphate shunt" evidence=TAS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0016020 "membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0005507 "copper ion binding"

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000741 InterPro:IPR013785 Pfam:PF00274 PROSITE:PS00158 GO:GO:0005829 GO:GO:0005739 GO:GO:0005886 GO:GO:0009506 GO:GO:0046686 EMBL:CP002685 GenomeReviews:CT485783_GR Gene3D:G3DSA:3.20.20.70 GO:GO:0005507 GO:GO:0009651 EMBL:AC006919 GO:GO:0006096 HOGENOM:HBG559178 KO:K01623 GO:GO:0004332 PANTHER:PTHR11627 ProtClustDB:PLN02455 HSSP:P00883 EMBL:AY034897 EMBL:AY063044 EMBL:AY085114 EMBL:AK226842 IPI:IPI00536892 PIR:A84781 RefSeq:NP_181187.1 UniGene:At.23119 ProteinModelPortal:Q9SJQ9 SMR:Q9SJQ9 IntAct:Q9SJQ9 STRING:Q9SJQ9 PRIDE:Q9SJQ9 ProMEX:Q9SJQ9 EnsemblPlants:AT2G36460.1 GeneID:818220 KEGG:ath:AT2G36460 TAIR:At2g36460 InParanoid:Q9SJQ9 OMA:CAQVTEA PhylomeDB:Q9SJQ9 ArrayExpress:Q9SJQ9 Genevestigator:Q9SJQ9 Uniprot:Q9SJQ9
Root	Isotig13807	6	38	-2.792	1.04E-07	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig13811	0	19	-5.377	3.67E-06	TAIR|locus:2196496 - symbol:UGT85A5 "UDP-glucosyl transferase 85A5" species:3702 "Arabidopsis thaliana" [GO:0008152 "metabolic process" evidence=IEA] [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0015020 "glucuronosyltransferase activity" evidence=ISS] InterPro:IPR002213 Pfam:PF00201 PROSITE:PS00375 EMBL:AC068562 EMBL:CP002684 GO:GO:0016758 CAZy:GT1 PANTHER:PTHR11926 HOGENOM:HBG746957 eggNOG:NOG326467 EMBL:AY765462 EMBL:AY039897 EMBL:AY077671 EMBL:AK230378 IPI:IPI00522085 IPI:IPI00530831 PIR:F86356 RefSeq:NP_564170.1 RefSeq:NP_973885.1 UniGene:At.15676 ProteinModelPortal:Q9LMF0 SMR:Q9LMF0 PRIDE:Q9LMF0 EnsemblPlants:AT1G22370.2 GeneID:838844 KEGG:ath:AT1G22370 TAIR:At1g22370 InParanoid:Q9LMF0 OMA:MWREEME PhylomeDB:Q9LMF0 Genevestigator:Q9LMF0 Uniprot:Q9LMF0
Root	Isotig13831	0	22	-5.588	6.01E-07	TAIR|locus:2202476 - symbol:PDH-E1 BETA "AT1G30120" species:3702 "Arabidopsis thaliana" [GO:0004739 "pyruvate dehydrogenase (acetyl-transferring) activity" evidence=ISS;TAS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA;TAS] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0006633 "fatty acid biosynthetic process" evidence=TAS] [GO:0010240 "plastid pyruvate dehydrogenase complex" evidence=TAS] InterPro:IPR005476 InterPro:IPR009014 InterPro:IPR015941 Pfam:PF02780 InterPro:IPR005475 Pfam:PF02779 EMBL:CP002684 GO:GO:0009570 GO:GO:0009941 GO:GO:0006633 SMART:SM00861 GO:GO:0004739 Gene3D:G3DSA:3.40.50.920 SUPFAM:SSF52922 EMBL:AC074176 KO:K00162 HSSP:Q8ZUR7 ProtClustDB:CLSN2682059 EMBL:AF361583 EMBL:AY093988 EMBL:AK221898 IPI:IPI00533851 PIR:C86425 RefSeq:NP_174304.1 UniGene:At.10483 UniGene:At.70613 ProteinModelPortal:Q9C6Z3 SMR:Q9C6Z3 IntAct:Q9C6Z3 STRING:Q9C6Z3 PRIDE:Q9C6Z3 EnsemblPlants:AT1G30120.1 GeneID:839891 KEGG:ath:AT1G30120 TAIR:At1g30120 InParanoid:Q9C6Z3 OMA:SIRKTHR PhylomeDB:Q9C6Z3 Genevestigator:Q9C6Z3 GO:GO:0010240 Uniprot:Q9C6Z3
Root	Isotig13834	13	34	-1.516	0.00065265	TAIR|locus:2044856 - symbol:AT2G36460 "AT2G36460" species:3702 "Arabidopsis thaliana" [GO:0006098 "pentose-phosphate shunt" evidence=TAS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0016020 "membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000741 InterPro:IPR013785 Pfam:PF00274 PROSITE:PS00158 GO:GO:0005829 GO:GO:0005739 GO:GO:0005886 GO:GO:0009506 GO:GO:0046686 EMBL:CP002685 GenomeReviews:CT485783_GR Gene3D:G3DSA:3.20.20.70 GO:GO:0005507 GO:GO:0009651 EMBL:AC006919 GO:GO:0006096 HOGENOM:HBG559178 KO:K01623 GO:GO:0004332 PANTHER:PTHR11627 ProtClustDB:PLN02455 HSSP:P00883 EMBL:AY034897 EMBL:AY063044 EMBL:AY085114 EMBL:AK226842 IPI:IPI00536892 PIR:A84781 RefSeq:NP_181187.1 UniGene:At.23119 ProteinModelPortal:Q9SJQ9 SMR:Q9SJQ9 IntAct:Q9SJQ9 STRING:Q9SJQ9 PRIDE:Q9SJQ9 ProMEX:Q9SJQ9 EnsemblPlants:AT2G36460.1 GeneID:818220

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						KEGG:ath:AT2G36460 TAIR:At2g36460 InParanoid:Q9SJQ9 OMA:CAQVTEA PhylomeDB:Q9SJQ9 ArrayExpress:Q9SJQ9 Genevestigator:Q9SJQ9 Uniprot:Q9SJQ9
Root	Isotig13841	13	1	3.571	0.000882483	No hit
Root	Isotig13843	17	73	-2.231	8.32E-11	TAIR|locus:2143171 - symbol:RGP2 "reversibly glycosylated polypeptide 2" species:3702 "Arabidopsis thaliana" [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0005829 "cytosol" evidence=RCA] [GO:0033356 "UDP-L-arabinose metabolic process" evidence=IMP] [GO:0052691 "UDP-arabinopyranose mutase activity" evidence=IDA] [GO:0016020 "membrane" evidence=ISS] InterPro:IPR004901 Pfam:PF03214 PIRSF:PIRSF016429 GO:GO:0046686 EMBL:CP002688 GO:GO:0005618 GO:GO:0005515 GO:GO:0005794 GO:GO:0030054 GO:GO:0009651 GO:GO:0009555 GO:GO:0007047 GO:GO:0022626 GO:GO:0030244 EMBL:AL391144 GO:GO:0008466 CAZy:GT75 eggNOG:NOG82578 KO:K13379 ProtClustDB:PLN03180 GO:GO:0052691 GO:GO:0033356 EMBL:AF013628 EMBL:AY039846 EMBL:AY120691 EMBL:AY087476 IPI:IPI00520967 PIR:T51394 RefSeq:NP_197069.1 UniGene:At.24638 IntAct:Q9LFW1 STRING:Q9LFW1 PRIDE:Q9LFW1 GeneID:831419 KEGG:ath:AT5G15650 TAIR:At5g15650 HOGENOM:HBG317372 InParanoid:Q9LFW1 OMA:KCYLELA PhylomeDB:Q9LFW1 Genevestigator:Q9LFW1 GO:GO:0071669 Uniprot:Q9LFW1
Root	Isotig13875	13	0	4.571	0.000344357	TAIR|locus:2135932 - symbol:VEP1 "AT4G24220" species:3702 "Arabidopsis thaliana" [GO:0009611 "response to wounding" evidence=IEP] [GO:0010051 "xylem and phloem pattern formation" evidence=IMP] [GO:0008202 "steroid metabolic process" evidence=IDA] [GO:0035671 "enone reductase activity" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR016040 GO:GO:0005829 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0009611 GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 GO:GO:0008202 EMBL:AL078637 EMBL:AL161561 UniGene:At.32364 UniGene:At.71005 GO:GO:0010051 GO:GO:0035671 HOGENOM:HBG353845 ProtClustDB:CLSN2685402 EMBL:AY062451 EMBL:AY087323 EMBL:BT008479 EMBL:EF579963 IPI:IPI00524911 PIR:T09885 RefSeq:NP_194153.1 ProteinModelPortal:Q9STX2 SMR:Q9STX2 PRIDE:Q9STX2 EnsemblPlants:AT4G24220.1 GeneID:828523 KEGG:ath:AT4G24220 TAIR:At4g24220 InParanoid:Q9STX2 OMA:GLKHYLG PhylomeDB:Q9STX2 ArrayExpress:Q9STX2 Genevestigator:Q9STX2 Uniprot:Q9STX2
Root	Isotig13891	1	12	-3.714	0.000699736	TAIR|locus:2076451 - symbol:PP2A-4 "AT3G58500" species:3702 "Arabidopsis thaliana" [GO:0005634 "nucleus" evidence=IDA] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0000159 "protein phosphatase type 2A complex" evidence=TAS] [GO:0006470 "protein dephosphorylation" evidence=TAS] [GO:0004722 "protein serine/threonine phosphatase activity" evidence=ISS] InterPro:IPR004843 InterPro:IPR006186 Pfam:PF00149 PRINTS:PR00114 PROSITE:PS00125 SMART:SM00156 GO:GO:0005829 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0000159 GO:GO:0005730 GO:GO:0006470 GO:GO:0046872 GO:GO:0004721 eggNOG:COG0639 EMBL:AL137082 HOGENOM:HBG716770 KO:K04382 EMBL:U08047 EMBL:U60136 EMBL:AY057604 EMBL:AY056222 EMBL:AY113023 IPI:IPI00528567 PIR:S52660 RefSeq:NP_567066.1 UniGene:At.25267 ProteinModelPortal:P48578 SMR:P48578 IntAct:P48578 STRING:P48578 PRIDE:P48578 EnsemblPlants:AT3G58500.1 GeneID:825019 KEGG:ath:AT3G58500 TAIR:At3g58500 InParanoid:P48578 OMA:IMEVDEQ PhylomeDB:P48578 ProtClustDB:CLSN2688889 Genevestigator:P48578 Uniprot:P48578
Root	Isotig13893	103	3	4.973	1.55E-24	No hit
Root	Isotig13911	0	13	-4.829	0.000155955	TAIR|locus:2168758 - symbol:GPDHp "AT5G40610" species:3702 "Arabidopsis thaliana" [GO:0004367 "glycerol-3-phosphate dehydrogenase [NAD+] activity" evidence=ISS;IDA] [GO:0006072 "glycerol-3-phosphate metabolic process" evidence=ISS] [GO:0009331 "glycerol-3-phosphate dehydrogenase complex" evidence=ISS] [GO:0009507 "chloroplast" evidence=IDA] [GO:0046167 "glycerol-3-phosphate biosynthetic process" evidence=IDA] InterPro:IPR006109 InterPro:IPR006168 InterPro:IPR008927 InterPro:IPR011128 InterPro:IPR013328 InterPro:IPR016040 InterPro:IPR017751 Pfam:PF01210 Pfam:PF07479 PIRSF:PIRSF000114 PRINTS:PR00077 PROSITE:PS00957 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009507 GO:GO:0042803 Gene3D:G3DSA:3.40.50.720 GO:GO:0051287 Gene3D:G3DSA:1.10.1040.10 SUPFAM:SSF48179 EMBL:AB009052 GO:GO:0009331 HSSP:Q8N1B0 eggNOG:COG0240 HOGENOM:HBG586392 KO:K00006 OMA:KIFCKGQ GO:GO:0004367 GO:GO:0046168 PANTHER:PTHR11728 TIGRFAMs:TIGR03376 EMBL:AJ242602 EMBL:BT000967 EMBL:AY080863 IPI:IPI00538973 RefSeq:NP_198877.1 UniGene:At.695 ProteinModelPortal:Q9SCX9 SMR:Q9SCX9 STRING:Q9SCX9 PRIDE:Q9SCX9 EnsemblPlants:AT5G40610.1

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GeneID:834060 KEGG:ath:AT5G40610 TAIR:At5g40610 InParanoid:Q9SCX9 PhylomeDB:Q9SCX9 ProtClustDB:CLSN2686185 Genevestigator:Q9SCX9 Uniprot:Q9SCX9
Root	Isotig13917	1	18	-4.299	1.41E-05	TAIR|locus:2152385 - symbol:AT5G45910 "AT5G45910" species:3702 "Arabidopsis thaliana" [GO:0004091 "carboxylesterase activity" evidence=ISS] [GO:0006629 "lipid metabolic process" evidence=IEA] [GO:0016788 "hydrolase activity, acting on ester bonds" evidence=IEA] InterPro:IPR001087 Pfam:PF00657 PROSITE:PS01098 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005576 GO:GO:0016042 GO:GO:0016788 EMBL:AB016870 EMBL:AY085579 IPI:IPI00544452 RefSeq:NP_199403.1 UniGene:At.29987 ProteinModelPortal:Q9FJ45 PRIDE:Q9FJ45 EnsemblPlants:AT5G45910.1 GeneID:834631 KEGG:ath:AT5G45910 TAIR:At5g45910 eggNOG:NOG290843 InParanoid:Q9FJ45 OMA:SARCGHI PhylomeDB:Q9FJ45 ProtClustDB:CLSN2715809 Genevestigator:Q9FJ45 Uniprot:Q9FJ45
Root	Isotig13922	7	33	-2.366	6.09E-06	TAIR|locus:2064950 - symbol:AT2G39040 species:3702 "Arabidopsis thaliana" [GO:0004601 "peroxidase activity" evidence=IEA;ISS] [GO:0006979 "response to oxidative stress" evidence=IEA] [GO:0020037 "heme binding" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] InterPro:IPR000823 InterPro:IPR002016 InterPro:IPR010255 InterPro:IPR019793 Pfam:PF00141 PRINTS:PR00458 PRINTS:PR00461 PROSITE:PS00435 PROSITE:PS00436 PROSITE:PS50873 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0005576 GO:GO:0020037 GO:GO:0004601 EMBL:AC005770 GO:GO:0042744 HOGENOM:HBG597790 SUPFAM:SSF48113 KO:K00430 EMBL:BT026452 IPI:IPI00540929 PIR:D84812 RefSeq:NP_181437.1 UniGene:At.37216 ProteinModelPortal:Q9ZV04 SMR:Q9ZV04 STRING:Q9ZV04 PeroxiBase:117 PRIDE:Q9ZV04 EnsemblPlants:AT2G39040.1 GeneID:818490 KEGG:ath:AT2G39040 GeneFarm:1849 TAIR:At2g39040 eggNOG:NOG276728 InParanoid:Q9ZV04 OMA:PSAGANF PhylomeDB:Q9ZV04 ProtClustDB:CLSN2912987 Genevestigator:Q9ZV04 GermOnline:AT2G39040 Uniprot:Q9ZV04
Root	Isotig13925	4	24	-2.714	3.10E-05	TAIR|locus:2031103 - symbol:FBP "AT1G43670" species:3702 "Arabidopsis thaliana" [GO:0006000 "fructose metabolic process" evidence=ISS] [GO:0042132 "fructose 1,6-bisphosphate 1-phosphatase activity" evidence=ISS;IDA] [GO:0005986 "sucrose biosynthetic process" evidence=IMP] [GO:0005983 "starch catabolic process" evidence=IMP] [GO:0015979 "photosynthesis" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0009737 "response to abscisic acid stimulus" evidence=IMP] [GO:0009750 "response to fructose stimulus" evidence=IMP] [GO:0030388 "fructose 1,6-bisphosphate metabolic process" evidence=IDA] InterPro:IPR000146 InterPro:IPR020548 Pfam:PF00316 PIRSF:PIRSF000904 PRINTS:PR00115 PROSITE:PS00124 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0009737 GO:GO:0005634 GO:GO:0046872 GO:GO:0009750 GO:GO:0005983 GO:GO:0030388 GO:GO:0015979 UniGene:At.23691 GO:GO:0042132 eggNOG:COG0158 HOGENOM:HBG731261 KO:K03841 PANTHER:PTHR11556 OMA:YGSATMV EMBL:AC009526 EMBL:BT000470 EMBL:BT008732 IPI:IPI00520560 PIR:H96499 RefSeq:NP_175032.1 UniGene:At.12074 ProteinModelPortal:Q9MA79 SMR:Q9MA79 IntAct:Q9MA79 STRING:Q9MA79 PRIDE:Q9MA79 EnsemblPlants:AT1G43670.1 GeneID:840953 KEGG:ath:AT1G43670 TAIR:At1g43670 InParanoid:Q9MA79 PhylomeDB:Q9MA79 ProtClustDB:PLN02262 BioCyc:ARA:AT1G43670-MONOMER BioCyc:MetaCyc:AT1G43670-MONOMER ArrayExpress:Q9MA79 Genevestigator:Q9MA79 GermOnline:AT1G43670 GO:GO:0005986 Uniprot:Q9MA79
Root	Isotig13944	7	28	-2.129	9.37E-05	TAIR|locus:2178128 - symbol:ACT7 "AT5G09810" species:3702 "Arabidopsis thaliana" [GO:0007010 "cytoskeleton organization" evidence=TAS] [GO:0009733 "response to auxin stimulus" evidence=IEP] [GO:0009845 "seed germination" evidence=IMP] [GO:0048364 "root development" evidence=IMP] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0010053 "root epidermal cell differentiation" evidence=IMP] [GO:0048767 "root hair elongation" evidence=IMP] [GO:0051301 "cell division" evidence=IMP] [GO:0005515 "protein binding" evidence=IPI] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005200 "structural constituent of cytoskeleton" evidence=ISS] [GO:0005856 "cytoskeleton" evidence=ISS] [GO:0009416 "response to light stimulus" evidence=IEP] [GO:0009611 "response to wounding" evidence=IEP] InterPro:IPR004001 PROSITE:PS00406 PROSITE:PS00432 InterPro:IPR004000 GO:GO:0005829 GO:GO:0005739 GO:GO:0005886 GO:GO:0009506 GO:GO:0005524 GO:GO:0009570 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005618 GO:GO:0005515 GO:GO:0009733 GO:GO:0009611 GO:GO:0005730 GO:GO:0005856 GO:GO:0051301 GO:GO:0009941 EMBL:AB016893 GO:GO:0048767 GO:GO:0009845 GO:GO:0009416

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						HOGENOM:HBG559892 PANTHER:PTHR11937 Pfam:PF00022 PRINTS:PR00190 SMART:SM00268 KO:K10355 InterPro:IPR020902 PROSITE:PS01132 ProtClustDB:CLSN2682469 UniGene:At.23346 EMBL:U37281 EMBL:U27811 EMBL:AY062702 EMBL:AY063980 EMBL:AY096397 EMBL:AY114679 EMBL:AY120779 IPI:IPI00524611 PIR:S68107 RefSeq:NP_196543.1 UniGene:At.23605 UniGene:At.24396 ProteinModelPortal:P53492 SMR:P53492 IntAct:P53492 STRING:P53492 PRIDE:P53492 ProMEX:P53492 EnsemblPlants:AT5G09810.1 GeneID:830841 KEGG:ath:AT5G09810 TAIR:At5g09810 InParanoid:P53492 OMA:NSICVIL PhylomeDB:P53492 ArrayExpress:P53492 Genevestigator:P53492 GermOnline:AT5G09810 Uniprot:P53492
Root	Isotig13987	4	25	-2.773	1.71E-05	UNIPROTKB|Q84N28 - symbol:OMT1 "Flavone O-methyltransferase 1" species:4565 "Triticum aestivum" [GO:0009611 "response to wounding" evidence=IDA] [GO:0009723 "response to ethylene stimulus" evidence=IDA] [GO:0009751 "response to salicylic acid stimulus" evidence=IDA] [GO:0042542 "response to hydrogen peroxide" evidence=IDA] InterPro:IPR001077 InterPro:IPR012967 InterPro:IPR016461 Pfam:PF00891 Pfam:PF08100 PIRSF:PIRSF005739 GO:GO:0009611 InterPro:IPR011991 Gene3D:G3DSA:1.10.10.10 GO:GO:0009723 GO:GO:0009751 GO:GO:0046983 GO:GO:0042542 GO:GO:0008171 GO:GO:0009813 EMBL:AY226581 UniGene:Ta.336 HSSP:P28002 ProteinModelPortal:Q84N28 SMR:Q84N28 Gramene:Q84N28 Uniprot:Q84N28
Root	Isotig14007	13	0	4.571	0.000344357	TAIR|locus:2012612 - symbol:SAC52 "AT1G14320" species:3702 "Arabidopsis thaliana" [GO:0003735 "structural constituent of ribosome" evidence=ISS] [GO:0006412 "translation" evidence=ISS;TAS] [GO:0015934 "large ribosomal subunit" evidence=ISS] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005730 "nucleolus" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0022625 "cytosolic large ribosomal subunit" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0005840 "ribosome" evidence=IPI] [GO:0071493 "cellular response to UV-B" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR001197 InterPro:IPR016180 InterPro:IPR018255 Pfam:PF00252 PIRSF:PIRSF005590 PROSITE:PS01257 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005774 GO:GO:0009507 GO:GO:0005515 GO:GO:0006952 GO:GO:0005730 GO:GO:0006412 GO:GO:0003735 EMBL:AC012188 GO:GO:0071493 GO:GO:0022625 eggNOG:COG0197 EMBL:AF428286 EMBL:AF428470 EMBL:AY045866 EMBL:AY113989 EMBL:BT000679 IPI:IPI00538015 PIR:E86277 RefSeq:NP_563945.2 UniGene:At.20914 ProteinModelPortal:Q93VT9 SMR:Q93VT9 STRING:Q93VT9 PRIDE:Q93VT9 EnsemblPlants:AT1G14320.1 GeneID:837993 KEGG:ath:AT1G14320 GeneFarm:164 TAIR:At1g14320 HOGENOM:HBG512729 InParanoid:Q93VT9 KO:K02866 OMA:ICANKYV PhylomeDB:Q93VT9 ProtClustDB:CLSN2682855 ArrayExpress:Q93VT9 Genevestigator:Q93VT9 GermOnline:AT1G14320 SUPFAM:SSF54686 TIGRFAMs:TIGR00279 Uniprot:Q93VT9
Root	Isotig14023	26	85	-1.838	6.41E-10	TAIR|locus:2130419 - symbol:OASA1 "AT4G14880" species:3702 "Arabidopsis thaliana" [GO:0004124 "cysteine synthase activity" evidence=IGI;IDA] [GO:0005829 "cytosol" evidence=ISS;IDA] [GO:0006535 "cysteine biosynthetic process from serine" evidence=TAS] [GO:0046686 "response to cadmium ion" evidence=IEP;IMP;IDA] [GO:0007568 "aging" evidence=IMP] [GO:0005634 "nucleus" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005777 "peroxisome" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0019344 "cysteine biosynthetic process" evidence=IMP] [GO:0048046 "apoplast" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0009570 "chloroplast stroma" evidence=IDA] InterPro:IPR001216 InterPro:IPR001926 InterPro:IPR005856 InterPro:IPR005859 Pfam:PF00291 PROSITE:PS00901 GO:GO:0005829 GO:GO:0005886 EMBL:CP002687 GO:GO:0048046 GO:GO:0009570 GO:GO:0005634 GO:GO:0046686 GO:GO:0005774 GO:GO:0005515 GO:GO:0030170 SUPFAM:SSF53686 GO:GO:0005777 GO:GO:0007568 GO:GO:0016740 EMBL:AL161540 EMBL:Z97337 eggNOG:COG0031 GO:GO:0006535 UniGene:At.34389 GO:GO:0004124 EMBL:X80376 EMBL:X84097 EMBL:AJ272027 EMBL:AY045825 EMBL:BT025878 IPI:IPI00519731 PIR:A71412 PIR:S48694 RefSeq:NP_001190732.1 RefSeq:NP_001190733.1 RefSeq:NP_193224.1 RefSeq:NP_849386.1 UniGene:At.30 PDB:1Z7W PDB:1Z7Y PDB:2ISQ PDBsum:1Z7W PDBsum:1Z7Y PDBsum:2ISQ ProteinModelPortal:P47998 SMR:P47998 IntAct:P47998 STRING:P47998 PRIDE:P47998 EnsemblPlants:AT4G14880.1 EnsemblPlants:AT4G14880.2 EnsemblPlants:AT4G14880.3 EnsemblPlants:AT4G14880.4 GeneID:827145 KEGG:ath:AT4G14880 TAIR:At4g14880 InParanoid:P47998 KO:K01738 OMA:SCGERYM PhylomeDB:P47998 ProtClustDB:PLN02565 ArrayExpress:P47998 Genevestigator:P47998 GermOnline:AT4G14880 TIGRFAMs:TIGR01139 TIGRFAMs:TIGR01136 Uniprot:P47998

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig14029	0	12	-4.714	0.000297064	TAIR|locus:2148398 - symbol:ZIP2 "AT5G59520" species:3702 "Arabidopsis thaliana" [GO:0005385 "zinc ion transmembrane transporter activity" evidence=ISS;TAS] [GO:0006829 "zinc ion transport" evidence=ISS;TAS] [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0005375 "copper ion transmembrane transporter activity" evidence=IGI] [GO:0005886 "plasma membrane" evidence=IDA] InterPro:IPR003689 Pfam:PF02535 GO:GO:0016021 GO:GO:0005886 EMBL:CP002688 GenomeReviews:BA000015_GR EMBL:AB025604 GO:GO:0006829 GO:GO:0005375 KO:K14709 eggNOG:NOG84653 OMA:AIMATIM HOGENOM:HBG317175 ProtClustDB:CLSN2686468 EMBL:AF033536 IPI:IPI00548997 PIR:T52184 RefSeq:NP_200760.1 UniGene:At.23375 STRING:Q9LTH9 PRIDE:Q9LTH9 EnsemblPlants:AT5G59520.1 GeneID:836071 KEGG:ath:AT5G59520 GeneFarm:2373 TAIR:At5g59520 InParanoid:Q9LTH9 PhylomeDB:Q9LTH9 ArrayExpress:Q9LTH9 Genevestigator:Q9LTH9 GermOnline:AT5G59520 Uniprot:Q9LTH9
Root	Isotig14051	6	28	-2.351	3.31E-05	UNIPROTKB|Q6VMW0 - symbol:OMT2 "8-hydroxyquercetin 8-O-methyltransferase" species:34256 "Mentha x piperita" [GO:0009812 "flavonoid metabolic process" evidence=IDA] [GO:0030761 "8-hydroxyquercitin 8-O-methyltransferase activity" evidence=IDA] [GO:0032259 "methylation" evidence=IDA] InterPro:IPR001077 InterPro:IPR012967 InterPro:IPR016461 Pfam:PF00891 Pfam:PF08100 PIRSF:PIRSF005739 InterPro:IPR011991 Gene3D:G3DSA:1.10.10.10 GO:GO:0046983 GO:GO:0008171 GO:GO:0009812 EMBL:AY337459 ProteinModelPortal:Q6VMW0 BRENDA:2.1.1.88 GO:GO:0030761 Uniprot:Q6VMW0
Root	Isotig14059	9	30	-1.866	0.000207951	TAIR|locus:2013001 - symbol:AT1G71695 species:3702 "Arabidopsis thaliana" [GO:0004601 "peroxidase activity" evidence=IEA;ISS] [GO:0006979 "response to oxidative stress" evidence=IEA] [GO:0020037 "heme binding" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0009505 "plant-type cell wall" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000823 InterPro:IPR002016 InterPro:IPR010255 InterPro:IPR019793 InterPro:IPR019794 Pfam:PF00141 PRINTS:PR00458 PRINTS:PR00461 PROSITE:PS00435 PROSITE:PS00436 PROSITE:PS50873 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009506 GO:GO:0005773 GO:GO:0005576 GO:GO:0016020 GO:GO:0020037 GO:GO:0009505 EMBL:AC012654 EMBL:AC016163 GO:GO:0004601 GO:GO:0042744 HOGENOM:HBG597790 SUPFAM:SSF48113 KO:K00430 EMBL:X98318 EMBL:X98773 EMBL:AF334732 EMBL:BT000715 EMBL:AY087964 IPI:IPI00538176 PIR:A96739 RefSeq:NP_177313.1 UniGene:At.67041 UniGene:At.94 ProteinModelPortal:Q96520 SMR:Q96520 STRING:Q96520 PeroxiBase:93 PRIDE:Q96520 EnsemblPlants:AT1G71695.1 GeneID:843498 KEGG:ath:AT1G71695 GeneFarm:1474 TAIR:At1g71695 eggNOG:NOG252730 InParanoid:Q96520 OMA:NCSARNT PhylomeDB:Q96520 ProtClustDB:CLSN2679267 ArrayExpress:Q96520 Genevestigator:Q96520 GermOnline:AT1G71695 Uniprot:Q96520
Root	Isotig14065	1	17	-4.216	2.69E-05	TAIR|locus:2204798 - symbol:MC1 "AT1G02170" species:3702 "Arabidopsis thaliana" [GO:0006508 "proteolysis" evidence=ISS] [GO:0004197 "cysteine-type endopeptidase activity" evidence=IDA] [GO:0043068 "positive regulation of programmed cell death" evidence=IGI;IDA] InterPro:IPR011600 Pfam:PF00656 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0006952 GO:GO:0004197 GO:GO:0006508 GO:GO:0043068 EMBL:U89959 InterPro:IPR005735 Pfam:PF06943 TIGRFAMs:TIGR01053 EMBL:AY219826 EMBL:AY322525 IPI:IPI00531085 RefSeq:NP_171719.2 UniGene:At.10711 UniGene:At.69983 ProteinModelPortal:Q7XJE6 STRING:Q7XJE6 MEROPS:C14.047 PRIDE:Q7XJE6 EnsemblPlants:AT1G02170.1 GeneID:839561 KEGG:ath:AT1G02170 TAIR:At1g02170 eggNOG:NOG68179 HOGENOM:HBG692861 InParanoid:Q7XJE6 OMA:NDAKCMR PhylomeDB:Q7XJE6 Genevestigator:Q7XJE6 Uniprot:Q7XJE6
Root	Isotig14070	5	43	-3.233	1.27E-09	No hit
Root	Isotig14073	1	12	-3.714	0.000699736	UNIPROTKB|E2R0W8 - symbol:GDF5 "Uncharacterized protein" species:9615 "Canis lupus familiaris" [GO:0005576 "extracellular region" evidence=IEA] [GO:0008083 "growth factor activity" evidence=IEA] [GO:0040007 "growth" evidence=IEA] InterPro:IPR001111 InterPro:IPR001839 InterPro:IPR017948 Pfam:PF00019 Pfam:PF00688 PROSITE:PS00250 PROSITE:PS51362 SMART:SM00204 PANTHER:PTHR11848 GO:GO:0040007 GO:GO:0005576 GO:GO:0008083 InterPro:IPR015615 CTD:8200 GeneTree:ENSGT00650000093347 KO:K04664 OMA:PITPHEY RefSeq:XP_542974.1 ProteinModelPortal:E2R0W8 Ensembl:ENSCAFT00000012802 GeneID:485850 KEGG:cfa:485850 PhylomeDB:E2R0W8 Uniprot:E2R0W8
Root	Isotig14103	2	18	-3.299	7.42E-05	TAIR|locus:2183612 - symbol:AT5G36250 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004722 "protein serine/threonine phosphatase activity" evidence=ISS] [GO:0005634 "nucleus" evidence=IDA] InterPro:IPR001932 Pfam:PF00481 PROSITE:PS01032 SMART:SM00331 SMART:SM00332

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0005634 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0046872 GO:GO:0004721 eggNOG:COG0631 Gene3D:G3DSA:3.60.40.10 SUPFAM:SSF81606 EMBL:AB026661 InterPro:IPR015655 PANTHER:PTHR13832 ProtClustDB:CLSN2685212 EMBL:AY061752 EMBL:AY113035 IPI:IPI00538708 RefSeq:NP_198474.1 UniGene:At.27370 ProteinModelPortal:Q9FG61 SMR:Q9FG61 IntAct:Q9FG61 PRIDE:Q9FG61 EnsemblPlants:AT5G36250.1 GeneID:833622 KEGG:ath:AT5G36250 TAIR:At5g36250 InParanoid:Q9FG61 OMA:GHIVAKR PhylomeDB:Q9FG61 Genevestigator:Q9FG61 Uniprot:Q9FG61
Root	Isotig14104	1	16	-4.129	5.13E-05	No hit
Root	Isotig14109	12	0	4.456	0.000626491	TAIR|locus:2170528 - symbol:SIP1 "AT5G40390" species:3702 "Arabidopsis thaliana" [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=ISS] [GO:0005986 "sucrose biosynthetic process" evidence=IMP] [GO:0010325 "raffinose family oligosaccharide biosynthetic process" evidence=IMP] [GO:0019593 "mannitol biosynthetic process" evidence=IMP] [GO:0047274 "galactinol-sucrose galactosyltransferase activity" evidence=ISS] [GO:0009507 "chloroplast" evidence=IDA] [GO:0006979 "response to oxidative stress" evidence=IEP] [GO:0009414 "response to water deprivation" evidence=IEP] [GO:0009737 "response to abscisic acid stimulus" evidence=IDA] InterPro:IPR013785 GO:GO:0009737 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009507 GO:GO:0006979 Gene3D:G3DSA:3.20.20.70 InterPro:IPR017853 SUPFAM:SSF51445 GO:GO:0009414 CAZy:GH36 InterPro:IPR008811 Pfam:PF05691 EMBL:AB006702 HOGENOM:HBG611539 KO:K06617 GO:GO:0047274 EMBL:AY062781 EMBL:AY081645 IPI:IPI00530152 RefSeq:NP_198855.1 UniGene:At.8441 ProteinModelPortal:Q9FND9 STRING:Q9FND9 PRIDE:Q9FND9 EnsemblPlants:AT5G40390.1 GeneID:834037 KEGG:ath:AT5G40390 TAIR:At5g40390 eggNOG:NOG287560 InParanoid:Q9FND9 OMA:ETRRNQC PhylomeDB:Q9FND9 ProtClustDB:PLN02711 Uniprot:Q9FND9
Root	Isotig14110	0	24	-5.714	1.84E-07	TAIR|locus:2130329 - symbol:AT4G16260 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=IEA;ISS] [GO:0043169 "cation binding" evidence=IEA] [GO:0005618 "cell wall" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0009817 "defense response to fungus, incompatible interaction" evidence=IDA] InterPro:IPR000490 InterPro:IPR013781 Pfam:PF00332 PROSITE:PS00587 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005774 GO:GO:0005618 GO:GO:0043169 InterPro:IPR017853 Gene3D:G3DSA:3.20.20.80 SUPFAM:SSF51445 GO:GO:0005975 GO:GO:0004553 GO:GO:0009651 GO:GO:0009817 CAZy:GH17 HSSP:P15737 EMBL:AY064130 EMBL:AY143867 IPI:IPI00944240 RefSeq:NP_193361.4 UniGene:At.22570 ProteinModelPortal:Q8VZJ2 SMR:Q8VZJ2 PRIDE:Q8VZJ2 EnsemblPlants:AT4G16260.1 GeneID:827320 KEGG:ath:AT4G16260 TAIR:At4g16260 PhylomeDB:Q8VZJ2 ProtClustDB:CLSN2927419 Genevestigator:Q8VZJ2 Uniprot:Q8VZJ2
Root	Isotig14119	2	19	-3.377	3.93E-05	TAIR|locus:2059708 - symbol:AT2G01900 "AT2G01900" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0016787 "hydrolase activity" evidence=ISS] InterPro:IPR000300 SMART:SM00128 Pfam:PF03372 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0004527 EMBL:AC007069 GO:GO:0004519 InterPro:IPR005135 SUPFAM:SSF56219 GO:GO:0046854 eggNOG:COG5411 HSSP:O43001 HOGENOM:HBG593315 IPI:IPI00541595 PIR:E84430 RefSeq:NP_178299.1 UniGene:At.50064 ProteinModelPortal:Q9SIS4 SMR:Q9SIS4 PRIDE:Q9SIS4 EnsemblPlants:AT2G01900.1 GeneID:814721 KEGG:ath:AT2G01900 TAIR:At2g01900 InParanoid:Q9SIS4 OMA:HDRVILL PhylomeDB:Q9SIS4 ProtClustDB:CLSN2683551 ArrayExpress:Q9SIS4 Genevestigator:Q9SIS4 Uniprot:Q9SIS4
Root	Isotig14140	3	22	-3.003	2.69E-05	TAIR|locus:2094598 - symbol:IAA7 "AT3G23050" species:3702 "Arabidopsis thaliana" [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0005515 "protein binding" evidence=IPI] [GO:0009733 "response to auxin stimulus" evidence=TAS] [GO:0005634 "nucleus" evidence=IDA] [GO:0009611 "response to wounding" evidence=IEP] [GO:0009753 "response to jasmonic acid stimulus" evidence=IEP] [GO:0009630 "gravitropism" evidence=IMP] [GO:0009414 "response to water deprivation" evidence=IMP] InterPro:IPR003311 InterPro:IPR011525 Pfam:PF02309 PROSITE:PS50962 GO:GO:0005634 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0009753 GO:GO:0009611 GO:GO:0009734 GO:GO:0006355 GO:GO:0006351 GO:GO:0009414 GO:GO:0009630 GO:GO:0046983 EMBL:AB026655 HOGENOM:HBG750482 KO:K14484 eggNOG:NOG281606 EMBL:U18409 EMBL:AF332395 EMBL:AY054651 EMBL:AY072461 EMBL:AY087765 IPI:IPI00517741 PIR:S58494 RefSeq:NP_188945.1 UniGene:At.22260 UniGene:At.67783 PDB:2P1N PDB:2P1O PDB:2P1Q PDBsum:2P1N PDBsum:2P1O PDBsum:2P1Q DIP:DIP-33345N IntAct:Q38825 STRING:Q38825 PRIDE:Q38825 DNASU:821879 EnsemblPlants:AT3G23050.1 GeneID:821879

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						KEGG:ath:AT3G23050 GeneFarm:3154 TAIR:At3g23050 InParanoid:Q38825 OMA:NESKLMN PhylomeDB:Q38825 ProtClustDB:CLSN2684190 ArrayExpress:Q38825 Genevestigator:Q38825 Uniprot:Q38825
Root	Isotig14155	2	17	-3.216	0.000139706	TAIR|locus:2013001 - symbol:AT1G71695 species:3702 "Arabidopsis thaliana" [GO:0004601 "peroxidase activity" evidence=IEA;ISS] [GO:0006979 "response to oxidative stress" evidence=IEA] [GO:0020037 "heme binding" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0009505 "plant-type cell wall" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000823 InterPro:IPR002016 InterPro:IPR010255 InterPro:IPR019793 InterPro:IPR019794 Pfam:PF00141 PRINTS:PR00458 PRINTS:PR00461 PROSITE:PS00435 PROSITE:PS00436 PROSITE:PS50873 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009506 GO:GO:0005773 GO:GO:0005576 GO:GO:0016020 GO:GO:0020037 GO:GO:0009505 EMBL:AC012654 EMBL:AC016163 GO:GO:0004601 GO:GO:0042744 HOGENOM:HBG597790 SUPFAM:SSF48113 KO:K00430 EMBL:X98318 EMBL:X98773 EMBL:AF334732 EMBL:BT000715 EMBL:AY087964 IPI:IPI00538176 PIR:A96739 RefSeq:NP_177313.1 UniGene:At.67041 UniGene:At.94 ProteinModelPortal:Q96520 SMR:Q96520 STRING:Q96520 PeroxiBase:93 PRIDE:Q96520 EnsemblPlants:AT1G71695.1 GeneID:843498 KEGG:ath:AT1G71695 GeneFarm:1474 TAIR:At1g71695 eggNOG:NOG252730 InParanoid:Q96520 OMA:NCSARNT PhylomeDB:Q96520 ProtClustDB:CLSN2679267 ArrayExpress:Q96520 Genevestigator:Q96520 GermOnline:AT1G71695 Uniprot:Q96520
Root	Isotig14157	1	17	-4.216	2.69E-05	TAIR|locus:2047380 - symbol:AT2G24800 species:3702 "Arabidopsis thaliana" [GO:0004601 "peroxidase activity" evidence=IEA;ISS] [GO:0006979 "response to oxidative stress" evidence=IEA] [GO:0020037 "heme binding" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] InterPro:IPR000823 InterPro:IPR002016 InterPro:IPR010255 InterPro:IPR019793 Pfam:PF00141 PRINTS:PR00458 PRINTS:PR00461 PROSITE:PS00435 PROSITE:PS00436 PROSITE:PS50873 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0005576 GO:GO:0020037 EMBL:AC006585 GO:GO:0004601 GO:GO:0042744 eggNOG:COG0376 HOGENOM:HBG597790 SUPFAM:SSF48113 KO:K00430 IPI:IPI00531914 PIR:F84640 RefSeq:NP_180053.1 UniGene:At.52898 ProteinModelPortal:Q9SK52 SMR:Q9SK52 STRING:Q9SK52 PeroxiBase:99 PRIDE:Q9SK52 EnsemblPlants:AT2G24800.1 GeneID:817017 KEGG:ath:AT2G24800 GeneFarm:1842 TAIR:At2g24800 InParanoid:Q9SK52 OMA:HCSAFSD PhylomeDB:Q9SK52 ProtClustDB:CLSN2912945 ArrayExpress:Q9SK52 Genevestigator:Q9SK52 GermOnline:AT2G24800 Uniprot:Q9SK52
Root	Isotig14170	49	16	1.486	0.000115562	TAIR|locus:2090975 - symbol:RAP2.2 "AT3G14230" species:3702 "Arabidopsis thaliana" [GO:0006355 "regulation of transcription, DNA-dependent" evidence=ISS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS;TAS] [GO:0001666 "response to hypoxia" evidence=IMP] [GO:0010468 "regulation of gene expression" evidence=IEP] [GO:0003677 "DNA binding" evidence=TAS] [GO:0005634 "nucleus" evidence=IC] InterPro:IPR001471 InterPro:IPR016177 Pfam:PF00847 PRINTS:PR00367 PROSITE:PS51032 SMART:SM00380 GO:GO:0005634 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0009873 GO:GO:0003677 GO:GO:0001666 GO:GO:0003700 GO:GO:0006351 KO:K09286 Gene3D:G3DSA:3.30.730.10 SUPFAM:SSF54171 HSSP:O80337 EMBL:AB022220 HOGENOM:HBG595502 ProtClustDB:CLSN2682146 EMBL:AY054539 EMBL:BT000374 EMBL:AY085580 EMBL:AF003095 IPI:IPI00519633 IPI:IPI00544839 RefSeq:NP_566482.1 RefSeq:NP_850582.1 UniGene:At.25146 ProteinModelPortal:Q9LUM4 SMR:Q9LUM4 STRING:Q9LUM4 EnsemblPlants:AT3G14230.1 GeneID:820643 KEGG:ath:AT3G14230 TAIR:At3g14230 eggNOG:NOG250271 InParanoid:Q9LUM4 OMA:SAFDCED PhylomeDB:Q9LUM4 ArrayExpress:Q9LUM4 Genevestigator:Q9LUM4 Uniprot:Q9LUM4
Root	Isotig14202	0	20	-5.451	2.00E-06	TAIR|locus:2101135 - symbol:BT2 "AT3G48360" species:3702 "Arabidopsis thaliana" [GO:0006355 "regulation of transcription, DNA-dependent" evidence=TAS] [GO:0005515 "protein binding" evidence=IPI] [GO:0005516 "calmodulin binding" evidence=IDA] [GO:0009611 "response to wounding" evidence=IEP] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] [GO:0009751 "response to salicylic acid stimulus" evidence=IEP] [GO:0042542 "response to hydrogen peroxide" evidence=IEP] [GO:0009734 "auxin mediated signaling pathway" evidence=IMP] [GO:0051973 "positive regulation of telomerase activity" evidence=IGI;IPI] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0009553 "embryo sac development" evidence=IGI] [GO:0009555 "pollen development" evidence=IGI] [GO:0009733 "response to auxin stimulus" evidence=IEP] [GO:0007623 "circadian rhythm" evidence=IEP] [GO:0009409 "response to cold" evidence=IEP] [GO:0009738 "abscisic acid mediated signaling pathway" evidence=IMP] [GO:0009743 "response to carbohydrate stimulus" evidence=IEP] [GO:0009753 "response to

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						jasmonic acid stimulus" evidence=IEP] [GO:0010167 "response to nitrate" evidence=IEP] [GO:0010182 "sugar mediated signaling pathway" evidence=IMP] [GO:0080134 "regulation of response to stress" evidence=IMP] InterPro:IPR000197 InterPro:IPR000210 InterPro:IPR013069 Pfam:PF00651 Pfam:PF02135 PROSITE:PS50097 PROSITE:PS50134 SMART:SM00225 GO:GO:0005634 GO:GO:0005737 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0009753 GO:GO:0009611 GO:GO:0009738 GO:GO:0009734 GO:GO:0006355 GO:GO:0007623 GO:GO:0008270 GO:GO:0009409 GO:GO:0009651 GO:GO:0005516 GO:GO:0009555 GO:GO:0009751 GO:GO:0010182 InterPro:IPR011333 Gene3D:G3DSA:3.30.710.10 SUPFAM:SSF54695 GO:GO:0051973 GO:GO:0042542 GO:GO:0009553 GO:GO:0003712 GO:GO:0010167 KO:K00517 eggNOG:NOG287613 ProtClustDB:CLSN2687065 GO:GO:0004402 Gene3D:G3DSA:1.20.1020.10 SUPFAM:SSF57933 EMBL:AY316675 EMBL:AL049659 EMBL:AY040015 EMBL:AY079408 EMBL:BT000678 EMBL:AK226596 IPI:IPI00536189 PIR:T06706 RefSeq:NP_566902.1 UniGene:At.21922 UniGene:At.67255 ProteinModelPortal:Q94BN0 SMR:Q94BN0 IntAct:Q94BN0 STRING:Q94BN0 PRIDE:Q94BN0 EnsemblPlants:AT3G48360.1 GeneID:823994 KEGG:ath:AT3G48360 TAIR:At3g48360 InParanoid:Q94BN0 OMA:RMWQLLR PhylomeDB:Q94BN0 Genevestigator:Q94BN0 GO:GO:0080134 Uniprot:Q94BN0
Root	Isotig14239	26	4	2.571	5.65E-05	TAIR|locus:2138121 - symbol:UGE2 "AT4G23920" species:3702 "Arabidopsis thaliana" [GO:0003978 "UDP-glucose 4-epimerase activity" evidence=IGI;IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0046983 "protein dimerization activity" evidence=IPI] [GO:0042546 "cell wall biogenesis" evidence=IMP] InterPro:IPR001509 InterPro:IPR005886 InterPro:IPR016040 Pfam:PF01370 GO:GO:0005829 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 HOGENOM:HBG755066 GO:GO:0046983 GO:GO:0050662 eggNOG:COG1087 GO:GO:0003978 GO:GO:0006012 InterPro:IPR025308 PANTHER:PTHR10366:SF39 Pfam:PF13950 TIGRFAMs:TIGR01179 EMBL:AL078468 EMBL:AL161560 KO:K01784 GO:GO:0042546 ProtClustDB:PLN02240 EMBL:BT008539 IPI:IPI00516246 PIR:T08911 RefSeq:NP_194123.1 UniGene:At.3390 ProteinModelPortal:Q9T0A7 SMR:Q9T0A7 IntAct:Q9T0A7 STRING:Q9T0A7 PRIDE:Q9T0A7 EnsemblPlants:AT4G23920.1 GeneID:828492 KEGG:ath:AT4G23920 TAIR:At4g23920 InParanoid:Q9T0A7 OMA:SAINPYG PhylomeDB:Q9T0A7 ArrayExpress:Q9T0A7 Genevestigator:Q9T0A7 GermOnline:AT4G23920 Uniprot:Q9T0A7
Root	Isotig14243	10	34	-1.895	6.62E-05	TAIR|locus:2141176 - symbol:B120 species:3702 "Arabidopsis thaliana" [GO:0004672 "protein kinase activity" evidence=IEA;ISS] [GO:0004674 "protein serine/threonine kinase activity" evidence=IEA] [GO:0005524 "ATP binding" evidence=IEA] [GO:0006468 "protein phosphorylation" evidence=IEA] [GO:0048544 "recognition of pollen" evidence=IEA] [GO:0005886 "plasma membrane" evidence=IDA] InterPro:IPR000719 InterPro:IPR000858 InterPro:IPR001245 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR024171 Pfam:PF00954 Pfam:PF07714 PIRSF:PIRSF000641 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 PROSITE:PS50026 InterPro:IPR001480 GO:GO:0016021 GO:GO:0005524 EMBL:CP002687 GenomeReviews:CT486007_GR eggNOG:COG0515 GO:GO:0004872 GO:GO:0005529 SUPFAM:SSF56112 GO:GO:0004674 HOGENOM:HBG755340 GO:GO:0005516 PROSITE:PS00022 PROSITE:PS01186 EMBL:AL161555 EMBL:EF637083 EMBL:AL022603 EMBL:AL031187 EMBL:AK229175 IPI:IPI00537448 PIR:T05181 RefSeq:NP_193870.1 UniGene:At.32633 HSSP:Q38784 ProteinModelPortal:O81906 SMR:O81906 STRING:O81906 PRIDE:O81906 EnsemblPlants:AT4G21390.1 GeneID:827891 KEGG:ath:AT4G21390 GeneFarm:77 TAIR:At4g21390 InParanoid:O81906 OMA:WRSGQWN PhylomeDB:O81906 ProtClustDB:CLSN2682023 ArrayExpress:O81906 Genevestigator:O81906 GO:GO:0044459 GO:GO:0048544 InterPro:IPR013227 InterPro:IPR003609 Gene3D:G3DSA:2.90.10.10 Pfam:PF01453 Pfam:PF08276 SMART:SM00108 SMART:SM00473 SUPFAM:SSF51110 PROSITE:PS50927 PROSITE:PS50948 Uniprot:O81906
Root	Isotig14257	9	77	-3.226	4.80E-16	TAIR|locus:2117939 - symbol:PIP1;5 "AT4G23400" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=ISS] [GO:0015250 "water channel activity" evidence=ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000425 InterPro:IPR012269 InterPro:IPR022357 Pfam:PF00230 PRINTS:PR00783 PROSITE:PS00221 GO:GO:0016021 GO:GO:0005886 GO:GO:0009506 EMBL:CP002687 GenomeReviews:CT486007_GR EMBL:AL161559 GO:GO:0055085 GO:GO:0005215 GO:GO:0006833 EMBL:AL031326 InterPro:IPR023271 Gene3D:G3DSA:1.20.1080.10 SUPFAM:SSF81338 eggNOG:COG0580 HOGENOM:HBG705794 PANTHER:PTHR19139 TIGRFAMs:TIGR00861 KO:K09872 ProtClustDB:CLSN2682869 EMBL:AY059948 EMBL:AY081593 EMBL:AY087945 IPI:IPI00536498 PIR:T05378 RefSeq:NP_194071.1 UniGene:At.2438 ProteinModelPortal:Q8LAA6 SMR:Q8LAA6 IntAct:Q8LAA6 STRING:Q8LAA6 PRIDE:Q8LAA6

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EnsemblPlants:AT4G23400.1 GeneID:828439 KEGG:ath:AT4G23400 GeneFarm:4865 TAIR:At4g23400 InParanoid:Q8LAA6 OMA:YDFLLAP PhylomeDB:Q8LAA6 ArrayExpress:Q8LAA6 Genevestigator:Q8LAA6 GermOnline:AT4G23400 Uniprot:Q8LAA6
Root	Isotig14262	12	0	4.456	0.000626491	TAIR|locus:2141070 - symbol:AT4G17900 "AT4G17900" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] EMBL:CP002687 GenomeReviews:CT486007_GR HOGENOM:HBG747962 InterPro:IPR006734 Pfam:PF04640 EMBL:BT029385 EMBL:AK227244 IPI:IPI00529939 RefSeq:NP_193524.2 UniGene:At.2047 STRING:Q0WUB8 PRIDE:Q0WUB8 EnsemblPlants:AT4G17900.1 GeneID:827514 KEGG:ath:AT4G17900 TAIR:At4g17900 InParanoid:Q0WUB8 OMA:NRWPPWL PhylomeDB:Q0WUB8 ProtClustDB:CLSN2918589 Genevestigator:Q0WUB8 Uniprot:Q0WUB8
Root	Isotig14264	0	42	-6.521	7.61E-12	TAIR|locus:2082543 - symbol:BGL2 "AT3G57260" species:3702 "Arabidopsis thaliana" [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=ISS] [GO:0009627 "systemic acquired resistance" evidence=IEP;NAS] [GO:0004338 "glucan exo-1,3-beta-glucosidase activity" evidence=ISS] [GO:0005773 "vacuole" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0048046 "apoplast" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0008810 "cellulase activity" evidence=TAS] InterPro:IPR000490 InterPro:IPR013781 Pfam:PF00332 PROSITE:PS00587 GO:GO:0048046 GO:GO:0005773 GO:GO:0005618 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005515 GO:GO:0043169 InterPro:IPR017853 Gene3D:G3DSA:3.20.20.80 SUPFAM:SSF51445 GO:GO:0005975 GO:GO:0009409 GO:GO:0009627 EMBL:AL137080 CAZy:GH17 GO:GO:0042973 GO:GO:0008810 HOGENOM:HBG605194 EMBL:M90509 EMBL:M58462 EMBL:AY099668 EMBL:AY128847 EMBL:AY086134 IPI:IPI00547460 PIR:JQ1694 PIR:T45804 RefSeq:NP_191285.1 UniGene:At.22313 ProteinModelPortal:P33157 SMR:P33157 IntAct:P33157 STRING:P33157 PRIDE:P33157 EnsemblPlants:AT3G57260.1 GeneID:824893 KEGG:ath:AT3G57260 TAIR:At3g57260 eggNOG:NOG268889 InParanoid:P33157 OMA:VENAKTY PhylomeDB:P33157 ProtClustDB:CLSN2915357 ArrayExpress:P33157 Genevestigator:P33157 GermOnline:AT3G57260 Uniprot:P33157
Root	Isotig14283	1	12	-3.714	0.000699736	TAIR|locus:2182860 - symbol:XBAT33 "AT5G07270" species:3702 "Arabidopsis thaliana" [GO:0004842 "ubiquitin-protein ligase activity" evidence=IDA] [GO:0016567 "protein ubiquitination" evidence=IDA] InterPro:IPR001841 InterPro:IPR002110 PROSITE:PS50088 PROSITE:PS50089 SMART:SM00184 SMART:SM00248 Prosite:PS00518 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0008270 eggNOG:COG0666 InterPro:IPR020683 Gene3D:G3DSA:1.25.40.20 Pfam:PF12796 SUPFAM:SSF48403 PROSITE:PS50297 EMBL:AL163652 InterPro:IPR013083 Gene3D:G3DSA:3.30.40.10 GO:GO:0004842 InterPro:IPR017907 EMBL:DQ086846 EMBL:BT029297 IPI:IPI00525189 PIR:T48498 RefSeq:NP_196344.2 UniGene:At.43358 ProteinModelPortal:Q4FE45 SMR:Q4FE45 PRIDE:Q4FE45 EnsemblPlants:AT5G07270.1 GeneID:830618 KEGG:ath:AT5G07270 TAIR:At5g07270 InParanoid:Q4FE45 OMA:VRCALYL PhylomeDB:Q4FE45 ProtClustDB:CLSN2681033 Genevestigator:Q4FE45 Uniprot:Q4FE45
Root	Isotig14289	0	12	-4.714	0.000297064	TAIR|locus:2057981 - symbol:PAL1 "PHE ammonia lyase 1" species:3702 "Arabidopsis thaliana" [GO:0005737 "cytoplasm" evidence=IEA] [GO:0009699 "phenylpropanoid biosynthetic process" evidence=TAS] [GO:0045548 "phenylalanine ammonia-lyase activity" evidence=ISS;IDA;TAS] [GO:0006979 "response to oxidative stress" evidence=IEP] [GO:0080167 "response to karrikin" evidence=IEP] [GO:0009555 "pollen development" evidence=IMP] [GO:0009819 "drought recovery" evidence=IMP] [GO:0010224 "response to UV-B" evidence=IMP] [GO:0046244 "salicylic acid catabolic process" evidence=IMP] [GO:0046274 "lignin catabolic process" evidence=IMP] [GO:0006952 "defense response" evidence=TAS] [GO:0009611 "response to wounding" evidence=TAS] InterPro:IPR001106 InterPro:IPR005922 InterPro:IPR008948 InterPro:IPR022313 Pfam:PF00221 PROSITE:PS00488 GO:GO:0005737 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0006979 GO:GO:0009058 GO:GO:0080167 EMBL:AC006922 GO:GO:0009555 SUPFAM:SSF48557 GO:GO:0006559 InterPro:IPR024083 Gene3D:G3DSA:1.10.275.10 GO:GO:0010224 eggNOG:COG2986 GO:GO:0046274 EMBL:L33677 EMBL:AY303128 EMBL:AY045919 EMBL:AY079363 EMBL:BT003330 EMBL:X62747 IPI:IPI00519512 PIR:G84787 PIR:S52990 RefSeq:NP_181241.1 UniGene:At.21614 UniGene:At.22705 ProteinModelPortal:P35510 SMR:P35510 IntAct:P35510 STRING:P35510 PRIDE:P35510 EnsemblPlants:AT2G37040.1 GeneID:818280 KEGG:ath:AT2G37040 TAIR:At2g37040 HOGENOM:HBG318028 InParanoid:P35510 KO:K10775 OMA:QRGADFL PhylomeDB:P35510 ProtClustDB:PLN02457 BRENDA:4.3.1.24 Genevestigator:P35510 GermOnline:AT2G37040 GO:GO:0045548 GO:GO:0009819 GO:GO:0046244 InterPro:IPR023144 Gene3D:G3DSA:1.10.274.20 TIGRFAMs:TIGR01226 Uniprot:P35510

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig14309	11	75	-2.898	2.59E-14	TAIR|locus:2075236 - symbol:MYB48 "AT3G46130" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=ISS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=ISS;TAS] [GO:0009751 "response to salicylic acid stimulus" evidence=IEP] [GO:0005634 "nucleus" evidence=IDA] InterPro:IPR001005 InterPro:IPR009057 Pfam:PF00249 SMART:SM00717 GO:GO:0005634 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0006355 GO:GO:0003677 GO:GO:0006351 GO:GO:0009751 Gene3D:G3DSA:1.10.10.60 SUPFAM:SSF46689 InterPro:IPR017930 PROSITE:PS51294 eggNOG:COG5147 InterPro:IPR015495 PANTHER:PTHR10641 EMBL:AL355775 HOGENOM:HBG750380 EMBL:AF272733 EMBL:AY519594 EMBL:DQ075255 EMBL:DQ075256 EMBL:DQ075257 EMBL:AK176475 IPI:IPI00528378 IPI:IPI00656574 IPI:IPI00759334 IPI:IPI00759367 PIR:T49254 RefSeq:NP_001030816.1 RefSeq:NP_001078249.1 RefSeq:NP_190199.1 UniGene:At.1475 UniGene:At.72744 ProteinModelPortal:Q9LX82 SMR:Q9LX82 STRING:Q9LX82 EnsemblPlants:AT3G46130.1 GeneID:823756 KEGG:ath:AT3G46130 GeneFarm:1132 TAIR:At3g46130 InParanoid:Q9LX82 OMA:REIDHSA PhylomeDB:Q9LX82 ProtClustDB:CLSN2684805 Genevestigator:Q9LX82 GermOnline:AT3G46130 Uniprot:Q9LX82
Root	Isotig14326	0	12	-4.714	0.000297064	TAIR|locus:2123056 - symbol:CRK32 "cysteine-rich RLK (RECEPTOR-like protein kinase) 32" species:3702 "Arabidopsis thaliana" [GO:0006468 "protein phosphorylation" evidence=IEA] [GO:0016301 "kinase activity" evidence=ISS] InterPro:IPR000719 InterPro:IPR001245 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 Pfam:PF07714 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 GO:GO:0016021 GO:GO:0005524 EMBL:CP002687 GenomeReviews:CT486007_GR eggNOG:COG0515 GO:GO:0004872 SUPFAM:SSF56112 GO:GO:0004674 HOGENOM:HBG755340 EMBL:AL161532 EMBL:AL050399 InterPro:IPR002902 Pfam:PF01657 PROSITE:PS51473 ProtClustDB:CLSN2685318 IPI:IPI00520282 PIR:T10568 RefSeq:NP_192887.1 UniGene:At.54276 ProteinModelPortal:Q9LDS6 SMR:Q9LDS6 PRIDE:Q9LDS6 EnsemblPlants:AT4G11480.1 GeneID:826753 KEGG:ath:AT4G11480 GeneFarm:209 TAIR:At4g11480 InParanoid:Q9LDS6 OMA:IGSARIY PhylomeDB:Q9LDS6 ArrayExpress:Q9LDS6 Genevestigator:Q9LDS6 Uniprot:Q9LDS6
Root	Isotig14331	13	1	3.571	0.000882483	TAIR|locus:2010911 - symbol:AT1G64890 "AT1G64890" species:3702 "Arabidopsis thaliana" [GO:0005215 "transporter activity" evidence=ISS] [GO:0006810 "transport" evidence=ISS] [GO:0016020 "membrane" evidence=ISS] Pfam:PF03092 EMBL:CP002684 InterPro:IPR016196 SUPFAM:SSF103473 EMBL:AC006193 InterPro:IPR004324 EMBL:BT002319 IPI:IPI00542815 PIR:C96672 RefSeq:NP_564843.1 UniGene:At.14815 UniGene:At.71486 ProteinModelPortal:Q9XIQ7 TCDB:2.A.71.3.1 PRIDE:Q9XIQ7 EnsemblPlants:AT1G64890.1 GeneID:842797 KEGG:ath:AT1G64890 TAIR:At1g64890 InParanoid:Q9XIQ7 OMA:QAISWLA PhylomeDB:Q9XIQ7 ProtClustDB:CLSN2689026 Genevestigator:Q9XIQ7 Uniprot:Q9XIQ7
Root	Isotig14342	0	14	-4.936	8.24E-05	TAIR|locus:2102539 - symbol:WRKY70 "AT3G56400" species:3702 "Arabidopsis thaliana" [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS;IMP] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=ISS] [GO:0009753 "response to jasmonic acid stimulus" evidence=IMP] [GO:0009862 "systemic acquired resistance, salicylic acid mediated signaling pathway" evidence=IMP] [GO:0009864 "induced systemic resistance, jasmonic acid mediated signaling pathway" evidence=IMP] [GO:0042742 "defense response to bacterium" evidence=IMP] [GO:0045892 "negative regulation of transcription, DNA-dependent" evidence=IMP] [GO:0050832 "defense response to fungus" evidence=IMP] [GO:0031347 "regulation of defense response" evidence=IMP] [GO:0010200 "response to chitin" evidence=IEP] [GO:0005515 "protein binding" evidence=IPI] [GO:0009751 "response to salicylic acid stimulus" evidence=IEP] [GO:1900056 "negative regulation of leaf senescence" evidence=IGI] InterPro:IPR003657 Pfam:PF03106 PROSITE:PS50811 SMART:SM00774 GO:GO:0005634 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0045892 GO:GO:0050832 GO:GO:0043565 GO:GO:0003700 GO:GO:0006351 GO:GO:0010200 EMBL:AL163972 GO:GO:0009862 GO:GO:0009864 Gene3D:G3DSA:2.20.25.80 SUPFAM:SSF118290 HOGENOM:HBG318091 EMBL:AF421157 EMBL:AY039933 EMBL:AY142566 EMBL:AY087389 IPI:IPI00521165 PIR:T49041 RefSeq:NP_191199.1 UniGene:At.5242 ProteinModelPortal:Q9LY00 SMR:Q9LY00 IntAct:Q9LY00 STRING:Q9LY00 EnsemblPlants:AT3G56400.1 GeneID:824807 KEGG:ath:AT3G56400 TAIR:At3g56400 eggNOG:NOG282461 InParanoid:Q9LY00 OMA:NASCDND PhylomeDB:Q9LY00 ProtClustDB:CLSN2683639 ArrayExpress:Q9LY00 Genevestigator:Q9LY00 GermOnline:AT3G56400 Uniprot:Q9LY00
Root	Isotig14346	1	17	-4.216	2.69E-05	TAIR|locus:2020768 - symbol:AT1G03610 "AT1G03610" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002684

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						InterPro:IPR008507 Pfam:PF05623 ProtClustDB:CLSN2679850 EMBL:AY084969 IPI:IPI00518195 PIR:T00899 RefSeq:NP_563688.1 UniGene:At.42535 EnsemblPlants:AT1G03610.1 GeneID:838961 KEGG:ath:AT1G03610 TAIR:At1g03610 eggNOG:NOG267091 InParanoid:Q8LF98 OMA:ESEDGEC PhylomeDB:Q8LF98 Genevestigator:Q8LF98 Uniprot:Q8LF98
Root	Isotig14349	1	21	-4.521	2.07E-06	TAIR|locus:2161423 - symbol:APE2 "AT5G46110" species:3702 "Arabidopsis thaliana" [GO:0015297 "antiporter activity" evidence=ISS] [GO:0015120 "phosphoglycerate transmembrane transporter activity" evidence=IDA] [GO:0015713 "phosphoglycerate transport" evidence=IDA] [GO:0015717 "triose phosphate transport" evidence=IMP] [GO:0035436 "triose phosphate transmembrane transport" evidence=IDA] [GO:0071917 "triose-phosphate transmembrane transporter activity" evidence=IMP;IDA] [GO:0009643 "photosynthetic acclimation" evidence=IMP] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] InterPro:IPR004696 Pfam:PF03151 GO:GO:0016021 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0031969 EMBL:AB006698 InterPro:IPR004853 KO:K15283 GO:GO:0015120 GO:GO:0071917 TIGRFAMs:TIGR00817 GO:GO:0009643 UniGene:At.26418 EMBL:AF097648 EMBL:AY037211 EMBL:AY050811 EMBL:AY056790 EMBL:AY091414 EMBL:BT002683 EMBL:AY087499 EMBL:AK222032 IPI:IPI00846992 PIR:T51692 RefSeq:NP_851138.1 UniGene:At.25255 IntAct:Q9ZSR7 STRING:Q9ZSR7 PRIDE:Q9ZSR7 EnsemblPlants:AT5G46110.1 GeneID:834652 KEGG:ath:AT5G46110 TAIR:At5g46110 eggNOG:NOG265656 InParanoid:Q9ZSR7 OMA:AASQFIM ProtClustDB:CLSN2680450 ArrayExpress:Q9ZSR7 Genevestigator:Q9ZSR7 Uniprot:Q9ZSR7
Root	Isotig14363	0	16	-5.129	2.34E-05	TAIR|locus:2093227 - symbol:PLDALPHA1 "AT3G15730" species:3702 "Arabidopsis thaliana" [GO:0004630 "phospholipase D activity" evidence=ISS;IDA;IMP] [GO:0005634 "nucleus" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0030136 "clathrin-coated vesicle" evidence=IDA] [GO:0006631 "fatty acid metabolic process" evidence=IMP;TAS] [GO:0005515 "protein binding" evidence=IPI] [GO:0009507 "chloroplast" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0009789 "positive regulation of abscisic acid mediated signaling pathway" evidence=IMP] [GO:0010119 "regulation of stomatal movement" evidence=IMP] [GO:0009845 "seed germination" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005546 "phosphatidylinositol-4,5-bisphosphate binding" evidence=IDA] InterPro:IPR000008 InterPro:IPR001736 InterPro:IPR008973 InterPro:IPR011402 Pfam:PF00168 Pfam:PF00614 PIRSF:PIRSF036470 PROSITE:PS50035 SMART:SM00155 SMART:SM00239 GO:GO:0005829 GO:GO:0005739 GO:GO:0005886 GO:GO:0009506 GO:GO:0005634 GO:GO:0005773 GO:GO:0046686 GO:GO:0009507 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005509 GO:GO:0005515 GO:GO:0009738 GO:GO:0009873 GO:GO:0009789 GO:GO:0010119 GO:GO:0046470 GO:GO:0016042 GO:GO:0006631 GO:GO:0030136 GO:GO:0009845 SUPFAM:SSF49562 PROSITE:PS50004 GO:GO:0005546 EMBL:AB017071 eggNOG:COG1502 InterPro:IPR015679 PANTHER:PTHR18896 GO:GO:0070290 GO:GO:0004630 KO:K01115 EMBL:U36381 EMBL:AF428278 IPI:IPI00527854 RefSeq:NP_188194.1 UniGene:At.23882 ProteinModelPortal:Q38882 SMR:Q38882 IntAct:Q38882 STRING:Q38882 PRIDE:Q38882 DNASU:820816 EnsemblPlants:AT3G15730.1 GeneID:820816 KEGG:ath:AT3G15730 TAIR:At3g15730 HOGENOM:HBG748198 InParanoid:Q38882 OMA:KLQYFDV PhylomeDB:Q38882 ProtClustDB:PLN02270 ArrayExpress:Q38882 Genevestigator:Q38882 GermOnline:AT3G15730 InterPro:IPR024632 Pfam:PF12357 Uniprot:Q38882
Root	Isotig14370	0	16	-5.129	2.34E-05	TAIR|locus:2119251 - symbol:AT4G33420 species:3702 "Arabidopsis thaliana" [GO:0004601 "peroxidase activity" evidence=IEA;ISS] [GO:0006979 "response to oxidative stress" evidence=IEA] [GO:0020037 "heme binding" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] InterPro:IPR000823 InterPro:IPR002016 InterPro:IPR010255 InterPro:IPR019793 InterPro:IPR019794 Pfam:PF00141 PRINTS:PR00458 PRINTS:PR00461 PROSITE:PS00435 PROSITE:PS00436 PROSITE:PS50873 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005576 GO:GO:0006979 EMBL:AL161583 EMBL:AL035678 GO:GO:0020037 GO:GO:0004601 HOGENOM:HBG597790 SUPFAM:SSF48113 KO:K00430 EMBL:AF451951 EMBL:BT044614 IPI:IPI00539387 PIR:T05993 RefSeq:NP_567919.1 UniGene:At.28650 ProteinModelPortal:Q9SZB9 SMR:Q9SZB9 STRING:Q9SZB9 PeroxiBase:213 PRIDE:Q9SZB9 EnsemblPlants:AT4G33420.1 GeneID:829479 KEGG:ath:AT4G33420 GeneFarm:1879 TAIR:At4g33420 eggNOG:NOG276365 InParanoid:Q9SZB9 ProtClustDB:CLSN2689733 Genevestigator:Q9SZB9 GermOnline:AT4G33420 Uniprot:Q9SZB9

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig14381	4	42	-3.521	5.08E-10	TAIR|locus:2147645 - symbol:AT5G19890 species:3702 "Arabidopsis thaliana" [GO:0004601 "peroxidase activity" evidence=IEA;ISS] [GO:0006979 "response to oxidative stress" evidence=IEA] [GO:0020037 "heme binding" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] InterPro:IPR000823 InterPro:IPR002016 InterPro:IPR010255 InterPro:IPR019793 InterPro:IPR019794 Pfam:PF00141 PRINTS:PR00458 PRINTS:PR00461 PROSITE:PS00435 PROSITE:PS00436 PROSITE:PS50873 GO:GO:0005634 GO:GO:0005737 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005576 GO:GO:0020037 GO:GO:0004601 GO:GO:0042744 HOGENOM:HBG597790 SUPFAM:SSF48113 DrugBank:DB00143 EMBL:AF296836 KO:K00430 EMBL:X98453 EMBL:AY123985 EMBL:BT000582 EMBL:AY088025 IPI:IPI00527390 RefSeq:NP_568385.1 UniGene:At.143 PDB:1QGJ PDBsum:1QGJ ProteinModelPortal:Q39034 SMR:Q39034 STRING:Q39034 PeroxiBase:225 PRIDE:Q39034 EnsemblPlants:AT5G19890.1 GeneID:832111 KEGG:ath:AT5G19890 GeneFarm:1914 TAIR:At5g19890 eggNOG:NOG317070 InParanoid:Q39034 OMA:PNINSAR PhylomeDB:Q39034 ProtClustDB:CLSN2689805 ArrayExpress:Q39034 Genevestigator:Q39034 GermOnline:AT5G19890 Uniprot:Q39034
Root	Isotig14384	31	136	-2.262	3.90E-19	TAIR|locus:2117939 - symbol:PIP1;5 "AT4G23400" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=ISS] [GO:0015250 "water channel activity" evidence=ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000425 InterPro:IPR012269 InterPro:IPR022357 Pfam:PF00230 PRINTS:PR00783 PROSITE:PS00221 GO:GO:0016021 GO:GO:0005886 GO:GO:0009506 EMBL:CP002687 GenomeReviews:CT486007_GR EMBL:AL161559 GO:GO:0055085 GO:GO:0005215 GO:GO:0006833 EMBL:AL031326 InterPro:IPR023271 Gene3D:G3DSA:1.20.1080.10 SUPFAM:SSF81338 eggNOG:COG0580 HOGENOM:HBG705794 PANTHER:PTHR19139 TIGRFAMs:TIGR00861 KO:K09872 ProtClustDB:CLSN2682869 EMBL:AY059948 EMBL:AY081593 EMBL:AY087945 IPI:IPI00536498 PIR:T05378 RefSeq:NP_194071.1 UniGene:At.2438 ProteinModelPortal:Q8LAA6 SMR:Q8LAA6 IntAct:Q8LAA6 STRING:Q8LAA6 PRIDE:Q8LAA6 EnsemblPlants:AT4G23400.1 GeneID:828439 KEGG:ath:AT4G23400 GeneFarm:4865 TAIR:At4g23400 InParanoid:Q8LAA6 OMA:YDFLLAP PhylomeDB:Q8LAA6 ArrayExpress:Q8LAA6 Genevestigator:Q8LAA6 GermOnline:AT4G23400 Uniprot:Q8LAA6
Root	Isotig14386	18	0	5.041	1.86E-05	No hit
Root	Isotig14392	30	79	-1.526	1.78E-07	TAIR|locus:2176441 - symbol:c-NAD-MDH2 "cytosolic-NAD-dependent malate dehydrogenase 2" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0005975 "carbohydrate metabolic process" evidence=IEA] [GO:0006096 "glycolysis" evidence=IEA] [GO:0006108 "malate metabolic process" evidence=IEA] [GO:0008152 "metabolic process" evidence=IEA] [GO:0016491 "oxidoreductase activity" evidence=IEA] [GO:0016615 "malate dehydrogenase activity" evidence=IEA;ISS] [GO:0016616 "oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor" evidence=IEA] [GO:0030060 "L-malate dehydrogenase activity" evidence=IEA] [GO:0044262 "cellular carbohydrate metabolic process" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR001236 InterPro:IPR001252 InterPro:IPR001557 InterPro:IPR010945 InterPro:IPR011274 InterPro:IPR015955 InterPro:IPR016040 InterPro:IPR022383 Pfam:PF00056 Pfam:PF02866 PIRSF:PIRSF000102 PROSITE:PS00068 GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 EMBL:AB025638 GO:GO:0006099 GO:GO:0044262 Gene3D:G3DSA:3.90.110.10 SUPFAM:SSF56327 GO:GO:0006108 eggNOG:COG0039 PANTHER:PTHR23382 HOGENOM:HBG289884 KO:K00025 OMA:FPVQIKD GO:GO:0030060 TIGRFAMs:TIGR01759 TIGRFAMs:TIGR01758 ProtClustDB:PLN00135 EMBL:AY072137 EMBL:AY091220 IPI:IPI00543463 RefSeq:NP_199147.1 UniGene:At.27775 ProteinModelPortal:P57106 SMR:P57106 STRING:P57106 PRIDE:P57106 EnsemblPlants:AT5G43330.1 GeneID:834351 KEGG:ath:AT5G43330 TAIR:At5g43330 InParanoid:P57106 PhylomeDB:P57106 ArrayExpress:P57106 Genevestigator:P57106 GermOnline:AT5G43330 Uniprot:P57106
Root	Isotig14395	14	1	3.678	0.000484579	No hit
Root	Isotig14413	3	23	-3.068	1.45E-05	TAIR|locus:2065058 - symbol:CZF1 "AT2G40140" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=TAS] [GO:0009409 "response

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						to cold" evidence=IEP] [GO:0050832 "defense response to fungus" evidence=IMP] [GO:0010200 "response to chitin" evidence=IEP] InterPro:IPR002110 InterPro:IPR000571 Pfam:PF00642 PROSITE:PS50088 PROSITE:PS50103 SMART:SM00248 SMART:SM00356 GO:GO:0005634 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0006355 GO:GO:0050832 GO:GO:0003677 GO:GO:0008270 InterPro:IPR020683 Gene3D:G3DSA:1.25.40.20 SUPFAM:SSF48403 PROSITE:PS50297 GO:GO:0009409 EMBL:AF085279 GO:GO:0010200 eggNOG:NOG69137 EMBL:AY093016 EMBL:AY128937 IPI:IPI00522137 PIR:G84825 RefSeq:NP_001031517.1 RefSeq:NP_181543.1 UniGene:At.27663 ProteinModelPortal:Q9XEE6 SMR:Q9XEE6 STRING:Q9XEE6 PRIDE:Q9XEE6 EnsemblPlants:AT2G40140.1 EnsemblPlants:AT2G40140.2 GeneID:818605 KEGG:ath:AT2G40140 TAIR:At2g40140 HOGENOM:HBG594924 InParanoid:Q9XEE6 OMA:ANTISMM PhylomeDB:Q9XEE6 ProtClustDB:CLSN2683392 ArrayExpress:Q9XEE6 Genevestigator:Q9XEE6 Uniprot:Q9XEE6
Root	Isotig14427	3	20	-2.866	9.17E-05	TAIR|locus:2024021 - symbol:AT1G24360 species:3702 "Arabidopsis thaliana" [GO:0006633 "fatty acid biosynthetic process" evidence=IEA] [GO:0008152 "metabolic process" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0004316 "3-oxoacyl-[acyl-carrier-protein] reductase (NADPH) activity" evidence=ISS] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] InterPro:IPR002198 InterPro:IPR011284 InterPro:IPR016040 InterPro:IPR020904 Pfam:PF00106 PIRSF:PIRSF000126 PRINTS:PR00080 PROSITE:PS00061 InterPro:IPR002347 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009570 Gene3D:G3DSA:3.40.50.720 GO:GO:0051287 GO:GO:0009941 GO:GO:0006633 GO:GO:0005507 eggNOG:COG1028 HOGENOM:HBG750976 PRINTS:PR00081 EMBL:AC000103 EMBL:AC002396 KO:K00059 GO:GO:0004316 TIGRFAMs:TIGR01830 EMBL:X64464 EMBL:AF324985 EMBL:AY059816 EMBL:AY081491 IPI:IPI00543619 PIR:A86378 PIR:S22416 PIR:T00667 RefSeq:NP_564216.1 UniGene:At.4 UniGene:At.67665 ProteinModelPortal:P33207 SMR:P33207 STRING:P33207 PRIDE:P33207 EnsemblPlants:AT1G24360.1 GeneID:839053 KEGG:ath:AT1G24360 TAIR:At1g24360 InParanoid:P33207 OMA:STDMTES PhylomeDB:P33207 ProtClustDB:CLSN2718402 BioCyc:MetaCyc:AT1G24360-MONOMER ArrayExpress:P33207 Genevestigator:P33207 GermOnline:AT1G24360 Uniprot:P33207
Root	Isotig14442	6	38	-2.792	1.04E-07	TAIR|locus:2147645 - symbol:AT5G19890 species:3702 "Arabidopsis thaliana" [GO:0004601 "peroxidase activity" evidence=IEA;ISS] [GO:0006979 "response to oxidative stress" evidence=IEA] [GO:0020037 "heme binding" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] InterPro:IPR000823 InterPro:IPR002016 InterPro:IPR010255 InterPro:IPR019793 InterPro:IPR019794 Pfam:PF00141 PRINTS:PR00458 PRINTS:PR00461 PROSITE:PS00435 PROSITE:PS00436 PROSITE:PS50873 GO:GO:0005634 GO:GO:0005737 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005576 GO:GO:0020037 GO:GO:0004601 GO:GO:0042744 HOGENOM:HBG597790 SUPFAM:SSF48113 DrugBank:DB00143 EMBL:AF296836 KO:K00430 EMBL:X98453 EMBL:AY123985 EMBL:BT000582 EMBL:AY088025 IPI:IPI00527390 RefSeq:NP_568385.1 UniGene:At.143 PDB:1QGJ PDBsum:1QGJ ProteinModelPortal:Q39034 SMR:Q39034 STRING:Q39034 PeroxiBase:225 PRIDE:Q39034 EnsemblPlants:AT5G19890.1 GeneID:832111 KEGG:ath:AT5G19890 GeneFarm:1914 TAIR:At5g19890 eggNOG:NOG317070 InParanoid:Q39034 OMA:PNINSAR PhylomeDB:Q39034 ProtClustDB:CLSN2689805 ArrayExpress:Q39034 Genevestigator:Q39034 GermOnline:AT5G19890 Uniprot:Q39034
Root	Isotig14443	44	9	2.161	2.29E-06	TAIR|locus:2128238 - symbol:BTI2 "AT4G11220" species:3702 "Arabidopsis thaliana" [GO:0005783 "endoplasmic reticulum" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005789 "endoplasmic reticulum membrane" evidence=IDA] [GO:0071458 "integral to cytosolic side of endoplasmic reticulum membrane" evidence=IDA] [GO:0071782 "endoplasmic reticulum tubular network" evidence=IDA] [GO:0071786 "endoplasmic reticulum tubular network organization" evidence=IMP] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR003388 Pfam:PF02453 PROSITE:PS50845 GO:GO:0005886 EMBL:CP002687 GenomeReviews:CT486007_GR EMBL:AL096882 EMBL:AL161531 GO:GO:0071458 PANTHER:PTHR10994 GO:GO:0071786 GO:GO:0071782 eggNOG:NOG303514 ProtClustDB:CLSN2685988 EMBL:AY034901 EMBL:AY048273 EMBL:AY057606 EMBL:BT002368 EMBL:AY086294 IPI:IPI00525362 PIR:T13013 RefSeq:NP_192861.1 UniGene:At.3649 ProteinModelPortal:Q9SUT9 SMR:Q9SUT9 IntAct:Q9SUT9 STRING:Q9SUT9 PRIDE:Q9SUT9 EnsemblPlants:AT4G11220.1 GeneID:826724 KEGG:ath:AT4G11220

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						TAIR:At4g11220 HOGENOM:HBG596795 InParanoid:Q9SUT9 OMA:HEESSPN PhylomeDB:Q9SUT9 Genevestigator:Q9SUT9 Uniprot:Q9SUT9
Root	Isotig14449	13	1	3.571	0.000882483	TAIR|locus:2129755 - symbol:SDG2 "AT4G15180" species:3702 "Arabidopsis thaliana" [GO:0009791 "post-embryonic development" evidence=IMP] [GO:0010228 "vegetative to reproductive phase transition of meristem" evidence=IMP] [GO:0042800 "histone methyltransferase activity (H3-K4 specific)" evidence=IDA] [GO:0048440 "carpel development" evidence=IMP] [GO:0048443 "stamen development" evidence=IMP] Pfam:PF00856 InterPro:IPR001214 InterPro:IPR003169 PROSITE:PS50280 SMART:SM00317 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005634 EMBL:Z97338 GO:GO:0048443 EMBL:AL161540 GO:GO:0010228 GO:GO:0048440 eggNOG:COG2940 GO:GO:0042800 EMBL:AK226725 IPI:IPI00523932 PIR:G71415 RefSeq:NP_193253.4 UniGene:At.21894 UniGene:At.263 ProteinModelPortal:O23372 SMR:O23372 STRING:O23372 PRIDE:O23372 ProMEX:O23372 EnsemblPlants:AT4G15180.1 GeneID:827183 KEGG:ath:AT4G15180 TAIR:At4g15180 HOGENOM:HBG318382 PhylomeDB:O23372 ProtClustDB:CLSN2708518 ArrayExpress:O23372 Genevestigator:O23372 GermOnline:AT4G15180 SUPFAM:SSF55277 Uniprot:O23372
Root	Isotig14456	0	11	-4.588	0.000569522	TAIR|locus:2051008 - symbol:AT2G33590 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0009809 "lignin biosynthetic process" evidence=ISS] [GO:0016621 "cinnamoyl-CoA reductase activity" evidence=ISS] [GO:0050662 "coenzyme binding" evidence=IEA] [GO:0046686 "response to cadmium ion" evidence=IEP] InterPro:IPR001509 InterPro:IPR016040 Pfam:PF01370 GO:GO:0046686 EMBL:CP002685 GenomeReviews:CT485783_GR eggNOG:COG0451 GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 HOGENOM:HBG755066 GO:GO:0003824 GO:GO:0044237 GO:GO:0050662 EMBL:AC002332 EMBL:AY120714 EMBL:AY084584 EMBL:BT000055 IPI:IPI00536249 PIR:D84747 RefSeq:NP_180917.1 UniGene:At.19951 ProteinModelPortal:O22809 SMR:O22809 STRING:O22809 PRIDE:O22809 EnsemblPlants:AT2G33590.1 GeneID:817925 KEGG:ath:AT2G33590 TAIR:At2g33590 InParanoid:O22809 OMA:CLAKTRA PhylomeDB:O22809 ProtClustDB:CLSN2683499 ArrayExpress:O22809 Genevestigator:O22809 Uniprot:O22809
Root	Isotig14467	0	32	-6.129	1.84E-09	UNIPROTKB|Q84N28 - symbol:OMT1 "Flavone O-methyltransferase 1" species:4565 "Triticum aestivum" [GO:0009611 "response to wounding" evidence=IDA] [GO:0009723 "response to ethylene stimulus" evidence=IDA] [GO:0009751 "response to salicylic acid stimulus" evidence=IDA] [GO:0042542 "response to hydrogen peroxide" evidence=IDA] InterPro:IPR001077 InterPro:IPR012967 InterPro:IPR016461 Pfam:PF00891 Pfam:PF08100 PIRSF:PIRSF005739 GO:GO:0009611 InterPro:IPR011991 Gene3D:G3DSA:1.10.10.10 GO:GO:0009723 GO:GO:0009751 GO:GO:0046983 GO:GO:0042542 GO:GO:0008171 GO:GO:0009813 EMBL:AY226581 UniGene:Ta.336 HSSP:P28002 ProteinModelPortal:Q84N28 SMR:Q84N28 Gramene:Q84N28 Uniprot:Q84N28
Root	Isotig14497	1	18	-4.299	1.41E-05	TAIR|locus:2018753 - symbol:AT1G28600 "AT1G28600" species:3702 "Arabidopsis thaliana" [GO:0004091 "carboxylesterase activity" evidence=ISS] [GO:0006629 "lipid metabolic process" evidence=IEA] [GO:0016788 "hydrolase activity, acting on ester bonds" evidence=IEA] [GO:0005618 "cell wall" evidence=IDA] InterPro:IPR001087 Pfam:PF00657 PROSITE:PS01098 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005618 GO:GO:0005576 GO:GO:0016042 GO:GO:0016788 eggNOG:COG3240 EMBL:AC007508 ProtClustDB:CLSN2679644 EMBL:AF385739 EMBL:AY133675 EMBL:AY087645 IPI:IPI00539035 IPI:IPI00657542 RefSeq:NP_001031103.1 RefSeq:NP_174182.1 UniGene:At.16399 ProteinModelPortal:Q94F40 PRIDE:Q94F40 EnsemblPlants:AT1G28600.1 GeneID:839760 KEGG:ath:AT1G28600 TAIR:At1g28600 InParanoid:Q94F40 OMA:RFIANTW PhylomeDB:Q94F40 Genevestigator:Q94F40 Uniprot:Q94F40
Root	Isotig14519	0	11	-4.588	0.000569522	TAIR|locus:2052851 - symbol:ASP1 "AT2G30970" species:3702 "Arabidopsis thaliana" [GO:0005739 "mitochondrion" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0004069 "L-aspartate:2-oxoglutarate aminotransferase activity" evidence=IDA] InterPro:IPR000796 InterPro:IPR004838 InterPro:IPR004839 InterPro:IPR015421 Pfam:PF00155 PRINTS:PR00799 PROSITE:PS00105 GO:GO:0046686 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0004069 GO:GO:0030170 InterPro:IPR015424 Gene3D:G3DSA:3.40.640.10 SUPFAM:SSF53383 GO:GO:0005759 GO:GO:0006103 GO:GO:0009058 GO:GO:0006536 EMBL:U15026 EMBL:AC004669 EMBL:AY059912 EMBL:AY128806 IPI:IPI00539251 PIR:H84714 RefSeq:NP_001118421.1 RefSeq:NP_180654.1 UniGene:At.513 ProteinModelPortal:P46643 SMR:P46643 STRING:P46643 PRIDE:P46643 EnsemblPlants:AT2G30970.1 EnsemblPlants:AT2G30970.2 GeneID:817648 KEGG:ath:AT2G30970 GeneFarm:4377 TAIR:At2g30970 eggNOG:COG1448 HOGENOM:HBG446828 InParanoid:P46643 KO:K14455 OMA:AYRDDNT PhylomeDB:P46643

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						ProtClustDB:PLN02397 ArrayExpress:P46643 Genevestigator:P46643 GermOnline:AT2G30970 GO:GO:0005507 GO:GO:0080130 GO:GO:0006531 PANTHER:PTHR11879 Uniprot:P46643
Root	Isotig14527	4	32	-3.129	2.46E-07	TAIR|locus:2176441 - symbol:c-NAD-MDH2 "cytosolic-NAD-dependent malate dehydrogenase 2" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0005975 "carbohydrate metabolic process" evidence=IEA] [GO:0006096 "glycolysis" evidence=IEA] [GO:0006108 "malate metabolic process" evidence=IEA] [GO:0008152 "metabolic process" evidence=IEA] [GO:0016491 "oxidoreductase activity" evidence=IEA] [GO:0016615 "malate dehydrogenase activity" evidence=IEA;ISS] [GO:0016616 "oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor" evidence=IEA] [GO:0030060 "L-malate dehydrogenase activity" evidence=IEA] [GO:0044262 "cellular carbohydrate metabolic process" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR001236 InterPro:IPR001252 InterPro:IPR001557 InterPro:IPR010945 InterPro:IPR011274 InterPro:IPR015955 InterPro:IPR016040 InterPro:IPR022383 Pfam:PF00056 Pfam:PF02866 PIRSF:PIRSF000102 PROSITE:PS00068 GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 EMBL:AB025638 GO:GO:0006099 GO:GO:0044262 Gene3D:G3DSA:3.90.110.10 SUPFAM:SSF56327 GO:GO:0006108 eggNOG:COG0039 PANTHER:PTHR23382 HOGENOM:HBG289884 KO:K00025 OMA:FPVQIKD GO:GO:0030060 TIGRFAMs:TIGR01759 TIGRFAMs:TIGR01758 ProtClustDB:PLN00135 EMBL:AY072137 EMBL:AY091220 IPI:IPI00543463 RefSeq:NP_199147.1 UniGene:At.27775 ProteinModelPortal:P57106 SMR:P57106 STRING:P57106 PRIDE:P57106 EnsemblPlants:AT5G43330.1 GeneID:834351 KEGG:ath:AT5G43330 TAIR:At5g43330 InParanoid:P57106 PhylomeDB:P57106 ArrayExpress:P57106 Genevestigator:P57106 GermOnline:AT5G43330 Uniprot:P57106
Root	Isotig14594	0	24	-5.714	1.84E-07	TAIR|locus:2153529 - symbol:PRX52 "AT5G05340" species:3702 "Arabidopsis thaliana" [GO:0004601 "peroxidase activity" evidence=ISS] [GO:0006979 "response to oxidative stress" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0005618 "cell wall" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0005829 "cytosol" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR000823 InterPro:IPR002016 InterPro:IPR010255 InterPro:IPR019793 InterPro:IPR019794 Pfam:PF00141 PRINTS:PR00458 PRINTS:PR00461 PROSITE:PS00435 PROSITE:PS00436 PROSITE:PS50873 GO:GO:0005829 GO:GO:0048046 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005618 GO:GO:0005515 GO:GO:0020037 GO:GO:0004601 GO:GO:0042744 HOGENOM:HBG597790 SUPFAM:SSF48113 EMBL:AB010692 KO:K00430 EMBL:AY065270 IPI:IPI00527468 RefSeq:NP_196153.1 UniGene:At.28537 ProteinModelPortal:Q9FLC0 SMR:Q9FLC0 IntAct:Q9FLC0 STRING:Q9FLC0 PeroxiBase:218 PRIDE:Q9FLC0 EnsemblPlants:AT5G05340.1 GeneID:830416 KEGG:ath:AT5G05340 GeneFarm:1905 TAIR:At5g05340 eggNOG:NOG298084 InParanoid:Q9FLC0 OMA:TNFRARI PhylomeDB:Q9FLC0 ProtClustDB:CLSN2916362 ArrayExpress:Q9FLC0 Genevestigator:Q9FLC0 GermOnline:AT5G05340 Uniprot:Q9FLC0
Root	Isotig14615	7	26	-2.022	0.00027047	TAIR|locus:2174433 - symbol:AT5G57850 "AT5G57850" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=ISS] [GO:0008153 "para-aminobenzoic acid biosynthetic process" evidence=IDA] [GO:0008696 "4-amino-4-deoxychorismate lyase activity" evidence=IGI] [GO:0009507 "chloroplast" evidence=IDA] [GO:0046654 "tetrahydrofolate biosynthetic process" evidence=IGI] [GO:0009570 "chloroplast stroma" evidence=IDA] InterPro:IPR001544 Pfam:PF01063 PROSITE:PS00770 GO:GO:0009570 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0008483 GO:GO:0046654 EMBL:AB013396 eggNOG:COG0115 KO:K00826 PANTHER:PTHR11825 SUPFAM:SSF56752 EMBL:AY099783 EMBL:AY128874 IPI:IPI00547510 RefSeq:NP_200593.2 UniGene:At.7653 ProteinModelPortal:Q8L493 SMR:Q8L493 STRING:Q8L493 PRIDE:Q8L493 EnsemblPlants:AT5G57850.1 GeneID:835895 KEGG:ath:AT5G57850 TAIR:At5g57850 HOGENOM:HBG746950 InParanoid:Q8L493 OMA:PGDFQLS PhylomeDB:Q8L493 ProtClustDB:PLN02845 BioCyc:MetaCyc:AT5G57850-MONOMER ArrayExpress:Q8L493 Genevestigator:Q8L493 GermOnline:AT5G57850 GO:GO:0008696 GO:GO:0008153 Uniprot:Q8L493
Root	Isotig14618	0	13	-4.829	0.000155955	TAIR|locus:2040287 - symbol:BHLH100 "AT2G41240" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=ISS] [GO:0005634 "nucleus" evidence=IEA] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=TAS] [GO:0009414 "response to water deprivation" evidence=IEP] InterPro:IPR015660

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						InterPro:IPR011598 Pfam:PF00010 PANTHER:PTHR13935 GO:GO:0005634 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0006355 GO:GO:0003677 GO:GO:0006351 GO:GO:0009414 Gene3D:G3DSA:4.10.280.10 SMART:SM00353 SUPFAM:SSF47459 PROSITE:PS50888 EMBL:AC005662 HSSP:P61244 EMBL:AY074635 EMBL:AF488626 IPI:IPI00522524 IPI:IPI00548751 PIR:E84839 RefSeq:NP_181657.1 RefSeq:NP_850349.1 UniGene:At.37027 ProteinModelPortal:Q9ZVB5 SMR:Q9ZVB5 EnsemblPlants:AT2G41240.1 GeneID:818723 KEGG:ath:AT2G41240 TAIR:At2g41240 eggNOG:NOG256140 HOGENOM:HBG591891 InParanoid:Q9ZVB5 OMA:HNASERE PhylomeDB:Q9ZVB5 ProtClustDB:CLSN2683761 Genevestigator:Q9ZVB5 Uniprot:Q9ZVB5
Root	Isotig14626	5	66	-3.851	8.29E-16	TAIR|locus:2084031 - symbol:PIP2A "AT3G53420" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=ISS] [GO:0015250 "water channel activity" evidence=ISS;IDA] [GO:0016020 "membrane" evidence=ISS;IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA;TAS] [GO:0005773 "vacuole" evidence=IDA] [GO:0009414 "response to water deprivation" evidence=IEP] [GO:0080170 "hydrogen peroxide transmembrane transport" evidence=IDA] [GO:0031625 "ubiquitin protein ligase binding" evidence=IPI] [GO:0009737 "response to abscisic acid stimulus" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0006833 "water transport" evidence=IDA] InterPro:IPR000425 InterPro:IPR012269 InterPro:IPR022357 Pfam:PF00230 PRINTS:PR00783 PROSITE:PS00221 GO:GO:0016021 GO:GO:0005886 GO:GO:0009506 GO:GO:0009737 GO:GO:0005773 GO:GO:0009507 EMBL:CP002686 GenomeReviews:BA000014_GR EMBL:AL132966 GO:GO:0009414 GO:GO:0031625 InterPro:IPR023271 Gene3D:G3DSA:1.20.1080.10 SUPFAM:SSF81338 eggNOG:COG0580 HOGENOM:HBG705794 PANTHER:PTHR19139 TIGRFAMs:TIGR00861 GO:GO:0015250 GO:GO:0080170 KO:K09872 EMBL:X75883 EMBL:AY039579 EMBL:AY044327 EMBL:AY056085 EMBL:AF428426 EMBL:AY072374 EMBL:AY087854 IPI:IPI00532482 PIR:S44084 RefSeq:NP_001030851.1 RefSeq:NP_190910.1 UniGene:At.47609 ProteinModelPortal:P43286 SMR:P43286 MINT:MINT-6951259 STRING:P43286 TCDB:1.A.8.11.4 PRIDE:P43286 ProMEX:P43286 EnsemblPlants:AT3G53420.1 EnsemblPlants:AT3G53420.2 GeneID:824510 KEGG:ath:AT3G53420 GeneFarm:4866 TAIR:At3g53420 InParanoid:P43286 OMA:VFMAITI PhylomeDB:P43286 ProtClustDB:CLSN2683965 ArrayExpress:P43286 Genevestigator:P43286 GermOnline:AT3G53420 Uniprot:P43286
Root	Isotig14636	3	17	-2.631	0.00056383	TAIR|locus:2180617 - symbol:AT5G25930 species:3702 "Arabidopsis thaliana" [GO:0006468 "protein phosphorylation" evidence=IEA] [GO:0016301 "kinase activity" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] Pfam:PF00560 InterPro:IPR001611 InterPro:IPR000719 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 Pfam:PF00069 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 GO:GO:0016021 GO:GO:0005886 GO:GO:0005524 EMBL:CP002688 GO:GO:0004872 SUPFAM:SSF56112 GO:GO:0004674 HOGENOM:HBG755340 InterPro:IPR013320 Gene3D:G3DSA:2.60.120.200 KO:K00924 EMBL:AF149413 InterPro:IPR013210 Pfam:PF08263 EMBL:BT004058 EMBL:FJ708783 IPI:IPI00529952 RefSeq:NP_197965.1 UniGene:At.30881 UniGene:At.66768 ProteinModelPortal:Q9XGZ2 SMR:Q9XGZ2 STRING:Q9XGZ2 PRIDE:Q9XGZ2 EnsemblPlants:AT5G25930.1 GeneID:832662 KEGG:ath:AT5G25930 TAIR:At5g25930 InParanoid:Q9XGZ2 OMA:NIREENV PhylomeDB:Q9XGZ2 ProtClustDB:CLSN2916431 ArrayExpress:Q9XGZ2 Genevestigator:Q9XGZ2 Uniprot:Q9XGZ2
Root	Isotig14641	0	13	-4.829	0.000155955	TAIR|locus:2119251 - symbol:AT4G33420 species:3702 "Arabidopsis thaliana" [GO:0004601 "peroxidase activity" evidence=IEA;ISS] [GO:0006979 "response to oxidative stress" evidence=IEA] [GO:0020037 "heme binding" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] InterPro:IPR000823 InterPro:IPR002016 InterPro:IPR010255 InterPro:IPR019793 InterPro:IPR019794 Pfam:PF00141 PRINTS:PR00458 PRINTS:PR00461 PROSITE:PS00435 PROSITE:PS00436 PROSITE:PS50873 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005576 GO:GO:0006979 EMBL:AL161583 EMBL:AL035678 GO:GO:0020037 GO:GO:0004601 HOGENOM:HBG597790 SUPFAM:SSF48113 KO:K00430 EMBL:AF451951 EMBL:BT044614 IPI:IPI00539387 PIR:T05993 RefSeq:NP_567919.1 UniGene:At.28650 ProteinModelPortal:Q9SZB9 SMR:Q9SZB9 STRING:Q9SZB9 PeroxiBase:213 PRIDE:Q9SZB9 EnsemblPlants:AT4G33420.1 GeneID:829479 KEGG:ath:AT4G33420 GeneFarm:1879 TAIR:At4g33420 eggNOG:NOG276365 InParanoid:Q9SZB9 ProtClustDB:CLSN2689733 Genevestigator:Q9SZB9 GermOnline:AT4G33420 Uniprot:Q9SZB9
Root	Isotig14660	73	0	7.061	1.73E-17	ZFIN|ZDB-GENE-030131-576 - symbol:clk4a "CDC-like kinase 4a" species:7955 "Danio rerio" [GO:0004672 "protein kinase activity" evidence=IEA] [GO:0005524 "ATP binding" evidence=IEA] [GO:0006468 "protein

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						phosphorylation" evidence=IEA] [GO:0016772 "transferase activity, transferring phosphorus-containing groups" evidence=IEA] [GO:0004674 "protein serine/threonine kinase activity" evidence=IEA] [GO:0000166 "nucleotide binding" evidence=IEA] InterPro:IPR000719 InterPro:IPR002290 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 Pfam:PF00069 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 SMART:SM00220 ZFIN:ZDB-GENE-030131-576 GO:GO:0005524 SUPFAM:SSF56112 GO:GO:0004674 GeneTree:ENSGT00580000081366 EMBL:CABZ01078974 EMBL:FP102782 IPI:IPI00999108 Ensembl:ENSDART00000126279 Bgee:E7F7P1 Uniprot:E7F7P1
Root	Isotig14705	0	16	-5.129	2.34E-05	TAIR|locus:2207210 - symbol:RCI3 "AT1G05260" species:3702 "Arabidopsis thaliana" [GO:0004601 "peroxidase activity" evidence=ISS;IDA] [GO:0005783 "endoplasmic reticulum" evidence=ISS] [GO:0009269 "response to desiccation" evidence=IMP] [GO:0009409 "response to cold" evidence=IEP] [GO:0042538 "hyperosmotic salinity response" evidence=IMP] InterPro:IPR000823 InterPro:IPR002016 InterPro:IPR010255 InterPro:IPR019793 InterPro:IPR019794 Pfam:PF00141 PRINTS:PR00458 PRINTS:PR00461 PROSITE:PS00435 PROSITE:PS00436 PROSITE:PS50873 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005576 GO:GO:0009409 GO:GO:0020037 GO:GO:0004601 GO:GO:0009269 GO:GO:0042744 HOGENOM:HBG597790 SUPFAM:SSF48113 GO:GO:0042538 EMBL:AC000098 KO:K00430 eggNOG:NOG242082 ProtClustDB:CLSN2681995 EMBL:U97684 EMBL:BT004817 EMBL:AY084678 IPI:IPI00521040 PIR:B86187 RefSeq:NP_172018.1 UniGene:At.23986 ProteinModelPortal:O23044 SMR:O23044 IntAct:O23044 STRING:O23044 PeroxiBase:79 PRIDE:O23044 EnsemblPlants:AT1G05260.1 GeneID:837028 KEGG:ath:AT1G05260 GeneFarm:1833 TAIR:At1g05260 InParanoid:O23044 OMA:ANIPPPT PhylomeDB:O23044 ArrayExpress:O23044 Genevestigator:O23044 GermOnline:AT1G05260 Uniprot:O23044
Root	Isotig14720	31	0	5.825	1.45E-08	TAIR|locus:2077081 - symbol:AT3G22490 "AT3G22490" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0009793 "embryo development ending in seed dormancy" evidence=ISS] Pfam:PF04927 EMBL:CP002686 EMBL:AP000731 UniGene:At.64534 InterPro:IPR007011 ProtClustDB:CLSN2684142 EMBL:BT002907 EMBL:BT004425 IPI:IPI00543172 RefSeq:NP_188888.1 PRIDE:Q9LJ97 EnsemblPlants:AT3G22490.1 GeneID:821820 KEGG:ath:AT3G22490 TAIR:At3g22490 InParanoid:Q9LJ97 OMA:QTAGNKP PhylomeDB:Q9LJ97 ArrayExpress:Q9LJ97 Genevestigator:Q9LJ97 Uniprot:Q9LJ97
Root	Isotig14736	0	14	-4.936	8.24E-05	No hit
Root	Isotig14737	1	16	-4.129	5.13E-05	TAIR|locus:2094942 - symbol:AT3G16350 "AT3G16350" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=ISS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=TAS] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0009723 "response to ethylene stimulus" evidence=IEP] [GO:0009733 "response to auxin stimulus" evidence=IEP] [GO:0009739 "response to gibberellin stimulus" evidence=IEP] [GO:0009753 "response to jasmonic acid stimulus" evidence=IEP] [GO:0046686 "response to cadmium ion" evidence=IEP] InterPro:IPR001005 InterPro:IPR001878 InterPro:IPR009057 Pfam:PF00249 SMART:SM00343 SMART:SM00717 GO:GO:0005634 GO:GO:0046686 EMBL:CP002686 GO:GO:0009733 GO:GO:0009753 GO:GO:0006355 GO:GO:0003677 GO:GO:0008270 GO:GO:0009651 GO:GO:0009723 Gene3D:G3DSA:1.10.10.60 SUPFAM:SSF46689 GO:GO:0009739 Gene3D:G3DSA:4.10.60.10 InterPro:IPR017930 InterPro:IPR006447 TIGRFAMs:TIGR01557 PROSITE:PS51294 EMBL:BT005832 IPI:IPI00535787 RefSeq:NP_188256.1 UniGene:At.47678 ProteinModelPortal:Q84TG2 SMR:Q84TG2 PRIDE:Q84TG2 EnsemblPlants:AT3G16350.1 GeneID:820882 KEGG:ath:AT3G16350 TAIR:At3g16350 InParanoid:Q84TG2 OMA:GMATRHE PhylomeDB:Q84TG2 ProtClustDB:CLSN2913348 Genevestigator:Q84TG2 Uniprot:Q84TG2
Root	Isotig14741	3	43	-3.970	5.33E-11	TAIR|locus:2170698 - symbol:HIR1 "HYPERSENSITIVE-INDUCED RESPONSE PROTEIN 1" species:3702 "Arabidopsis thaliana" [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0043424 "protein histidine kinase binding" evidence=IPI] [GO:0005829 "cytosol" evidence=RCA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR001972 InterPro:IPR001107 Pfam:PF01145 GO:GO:0005886 GO:GO:0009506 GO:GO:0005774 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0043424 EMBL:AB009053 eggNOG:COG0330 PANTHER:PTHR10264 SMART:SM00244 EMBL:AY062850 EMBL:AY114572 EMBL:AY086631 IPI:IPI00546529 RefSeq:NP_201080.1 UniGene:At.71021 ProteinModelPortal:Q9FM19 SMR:Q9FM19 IntAct:Q9FM19 PRIDE:Q9FM19 EnsemblPlants:AT5G62740.1 GeneID:836395 KEGG:ath:AT5G62740 TAIR:At5g62740

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						HOGENOM:HBG519201 InParanoid:Q9FM19 OMA:KANDAYY PhylomeDB:Q9FM19 ProtClustDB:CLSN2682581 ArrayExpress:Q9FM19 Genevestigator:Q9FM19 Uniprot:Q9FM19
Root	Isotig14782	18	43	-1.385	0.000339352	TAIR|locus:2081695 - symbol:ATGSTF13 "AT3G62760" species:3702 "Arabidopsis thaliana" [GO:0004364 "glutathione transferase activity" evidence=ISS] [GO:0005737 "cytoplasm" evidence=NAS] [GO:0009407 "toxin catabolic process" evidence=TAS] InterPro:IPR004045 Pfam:PF02798 PROSITE:PS50404 InterPro:IPR004046 Pfam:PF00043 GO:GO:0005829 EMBL:CP002686 GenomeReviews:BA000014_GR EMBL:AL162651 GO:GO:0009636 InterPro:IPR012336 Gene3D:G3DSA:3.40.30.10 SUPFAM:SSF52833 InterPro:IPR010987 Gene3D:G3DSA:1.20.1050.10 SUPFAM:SSF47616 PROSITE:PS50405 InterPro:IPR017933 GO:GO:0004364 eggNOG:COG0625 HOGENOM:HBG753188 GO:GO:0009407 HSSP:Q9ZP62 IPI:IPI00528803 PIR:T48065 RefSeq:NP_191835.1 UniGene:At.54041 ProteinModelPortal:Q9LZI9 SMR:Q9LZI9 PRIDE:Q9LZI9 EnsemblPlants:AT3G62760.1 GeneID:825451 KEGG:ath:AT3G62760 TAIR:At3g62760 InParanoid:Q9LZI9 OMA:KAWWERL PhylomeDB:Q9LZI9 ProtClustDB:CLSN2684163 Genevestigator:Q9LZI9 Uniprot:Q9LZI9
Root	Isotig14793	0	20	-5.451	2.00E-06	TAIR|locus:2148186 - symbol:AT5G17000 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0008270 "zinc ion binding" evidence=IEA] [GO:0016491 "oxidoreductase activity" evidence=IEA] [GO:0006979 "response to oxidative stress" evidence=IEP] InterPro:IPR002085 InterPro:IPR013149 InterPro:IPR016040 Pfam:PF00107 EMBL:CP002688 GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 GO:GO:0008270 GO:GO:0016491 InterPro:IPR011032 PANTHER:PTHR11695 SUPFAM:SSF50129 KO:K08070 ProtClustDB:CLSN2682646 EMBL:AY058070 EMBL:AY150406 IPI:IPI00519373 RefSeq:NP_197202.2 UniGene:At.9911 ProteinModelPortal:Q93Z72 SMR:Q93Z72 STRING:Q93Z72 PRIDE:Q93Z72 DNASU:831563 EnsemblPlants:AT5G17000.1 GeneID:831563 KEGG:ath:AT5G17000 TAIR:At5g17000 InParanoid:Q93Z72 OMA:YMEDISE PhylomeDB:Q93Z72 Genevestigator:Q93Z72 Uniprot:Q93Z72
Root	Isotig14803	2	14	-2.936	0.000925454	TAIR|locus:2194829 - symbol:AT1G44770 "AT1G44770" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002684 GenomeReviews:CT485782_GR EMBL:BT003128 EMBL:AK228160 IPI:IPI00527519 RefSeq:NP_175098.1 UniGene:At.25472 PRIDE:Q84WK2 EnsemblPlants:AT1G44770.1 GeneID:841041 KEGG:ath:AT1G44770 TAIR:At1g44770 HOGENOM:HBG320109 InParanoid:Q84WK2 OMA:AKGVHAT PhylomeDB:Q84WK2 ProtClustDB:CLSN2679861 Genevestigator:Q84WK2 Uniprot:Q84WK2
Root	Isotig14807	28	56	-1.129	0.000494096	TAIR|locus:2081695 - symbol:ATGSTF13 "AT3G62760" species:3702 "Arabidopsis thaliana" [GO:0004364 "glutathione transferase activity" evidence=ISS] [GO:0005737 "cytoplasm" evidence=NAS] [GO:0009407 "toxin catabolic process" evidence=TAS] InterPro:IPR004045 Pfam:PF02798 PROSITE:PS50404 InterPro:IPR004046 Pfam:PF00043 GO:GO:0005829 EMBL:CP002686 GenomeReviews:BA000014_GR EMBL:AL162651 GO:GO:0009636 InterPro:IPR012336 Gene3D:G3DSA:3.40.30.10 SUPFAM:SSF52833 InterPro:IPR010987 Gene3D:G3DSA:1.20.1050.10 SUPFAM:SSF47616 PROSITE:PS50405 InterPro:IPR017933 GO:GO:0004364 eggNOG:COG0625 HOGENOM:HBG753188 GO:GO:0009407 HSSP:Q9ZP62 IPI:IPI00528803 PIR:T48065 RefSeq:NP_191835.1 UniGene:At.54041 ProteinModelPortal:Q9LZI9 SMR:Q9LZI9 PRIDE:Q9LZI9 EnsemblPlants:AT3G62760.1 GeneID:825451 KEGG:ath:AT3G62760 TAIR:At3g62760 InParanoid:Q9LZI9 OMA:KAWWERL PhylomeDB:Q9LZI9 ProtClustDB:CLSN2684163 Genevestigator:Q9LZI9 Uniprot:Q9LZI9
Root	Isotig14818	5	21	-2.199	0.000555521	TAIR|locus:2063746 - symbol:AT2G03500 "AT2G03500" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=ISS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=TAS] InterPro:IPR001005 InterPro:IPR008207 InterPro:IPR009057 Pfam:PF00249 GO:GO:0005634 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0006355 GO:GO:0003677 Gene3D:G3DSA:1.10.10.60 SUPFAM:SSF46689 GO:GO:0004871 GO:GO:0000160 Gene3D:G3DSA:1.20.120.160 HSSP:O49397 InterPro:IPR017930 InterPro:IPR006447 TIGRFAMs:TIGR01557 PROSITE:PS51294 EMBL:AC006284 HOGENOM:HBG599741 EMBL:AY060559 EMBL:AY133630 EMBL:AK221662 IPI:IPI00544167 PIR:B84449 RefSeq:NP_027544.1 UniGene:At.27373 ProteinModelPortal:Q9ZQ85 SMR:Q9ZQ85 IntAct:Q9ZQ85 PRIDE:Q9ZQ85 EnsemblPlants:AT2G03500.1 GeneID:814878 KEGG:ath:AT2G03500 TAIR:At2g03500 eggNOG:NOG301728 InParanoid:Q9ZQ85 OMA:QSYSMLL PhylomeDB:Q9ZQ85 ProtClustDB:CLSN2687945 ArrayExpress:Q9ZQ85 Genevestigator:Q9ZQ85 Uniprot:Q9ZQ85
Root	Isotig14854	54	6	3.041	2.50E-10	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
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Root	Isotig14868	0	18	-5.299	6.77E-06	TAIR|locus:2195733 - symbol:BAN "AT1G61720" species:3702 "Arabidopsis thaliana" [GO:0033729 "anthocyanidin reductase activity" evidence=IDA] [GO:0009964 "negative regulation of flavonoid biosynthetic process" evidence=IMP] [GO:0016491 "oxidoreductase activity" evidence=ISS] InterPro:IPR001509 InterPro:IPR016040 Pfam:PF01370 EMBL:CP002684 GenomeReviews:CT485782_GR eggNOG:COG0451 GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 HOGENOM:HBG755066 GO:GO:0050662 EMBL:AF092912 EMBL:AC005882 EMBL:DQ446384 EMBL:AK175960 IPI:IPI00523362 PIR:H96642 RefSeq:NP_176365.1 UniGene:At.11057 ProteinModelPortal:Q9SEV0 SMR:Q9SEV0 STRING:Q9SEV0 PRIDE:Q9SEV0 EnsemblPlants:AT1G61720.1 GeneID:842469 KEGG:ath:AT1G61720 TAIR:At1g61720 InParanoid:Q9SEV0 KO:K08695 OMA:ICCAYNT PhylomeDB:Q9SEV0 ProtClustDB:PLN00198 Genevestigator:Q9SEV0 GO:GO:0033729 GO:GO:0009813 GO:GO:0009964 Uniprot:Q9SEV0
Root	Isotig14875	1	12	-3.714	0.000699736	TAIR|locus:2129181 - symbol:PLA-I{beta]2 "AT4G16820" species:3702 "Arabidopsis thaliana" [GO:0004806 "triglyceride lipase activity" evidence=ISS;IDA] [GO:0006629 "lipid metabolic process" evidence=IEA;ISS] [GO:0008970 "phosphatidylcholine 1-acylhydrolase activity" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0047714 "galactolipase activity" evidence=IDA] InterPro:IPR002921 Pfam:PF01764 PROSITE:PS00120 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0009507 GO:GO:0016042 GO:GO:0004806 EMBL:Z97342 EMBL:AL161545 HOGENOM:HBG745631 GO:GO:0008970 GO:GO:0047714 IPI:IPI00531771 IPI:IPI01019984 PIR:E71435 RefSeq:NP_567515.1 UniGene:At.54366 ProteinModelPortal:O23522 PRIDE:O23522 GeneID:827388 KEGG:ath:AT4G16820 TAIR:At4g16820 eggNOG:NOG303389 InParanoid:O23522 PhylomeDB:O23522 ArrayExpress:O23522 Genevestigator:O23522 Uniprot:O23522
Root	Isotig14879	0	15	-5.036	4.38E-05	TAIR|locus:2152445 - symbol:SAG12 "AT5G45890" species:3702 "Arabidopsis thaliana" [GO:0006508 "proteolysis" evidence=ISS] [GO:0008234 "cysteine-type peptidase activity" evidence=ISS] [GO:0009723 "response to ethylene stimulus" evidence=IEP] [GO:0007568 "aging" evidence=IEP;TAS] [GO:0010150 "leaf senescence" evidence=TAS] [GO:0010282 "senescence-associated vacuole" evidence=IDA] [GO:0009817 "defense response to fungus, incompatible interaction" evidence=IEP] InterPro:IPR000668 InterPro:IPR013128 Pfam:PF00112 PRINTS:PR00705 SMART:SM00645 InterPro:IPR000169 EMBL:CP002688 GO:GO:0004197 GO:GO:0006508 InterPro:IPR013201 PANTHER:PTHR12411 Pfam:PF08246 SMART:SM00848 PROSITE:PS00640 PROSITE:PS00139 PROSITE:PS00639 GO:GO:0010150 GO:GO:0009817 EMBL:AB016870 HSSP:O65039 EMBL:AF370131 EMBL:AY040073 IPI:IPI00544181 RefSeq:NP_568651.1 UniGene:At.75256 UniGene:At.7710 ProteinModelPortal:Q9FJ47 SMR:Q9FJ47 IntAct:Q9FJ47 STRING:Q9FJ47 MEROPS:C01.117 PRIDE:Q9FJ47 EnsemblPlants:AT5G45890.1 GeneID:834629 KEGG:ath:AT5G45890 TAIR:At5g45890 InParanoid:Q9FJ47 OMA:NDEQALM PhylomeDB:Q9FJ47 ProtClustDB:CLSN2917735 ArrayExpress:Q9FJ47 Genevestigator:Q9FJ47 GO:GO:0010282 Uniprot:Q9FJ47
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Root	Isotig14910	1	14	-3.936	0.000188601	TAIR|locus:2154925 - symbol:AT5G66390 species:3702 "Arabidopsis thaliana" [GO:0004601 "peroxidase activity" evidence=IEA;ISS] [GO:0006979 "response to oxidative stress" evidence=IEA] [GO:0020037 "heme binding" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] InterPro:IPR000823 InterPro:IPR002016 InterPro:IPR010255 InterPro:IPR019793 Pfam:PF00141 PRINTS:PR00458 PRINTS:PR00461 PROSITE:PS00435 PROSITE:PS00436 PROSITE:PS50873 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005576

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Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
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Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						KEGG:ath:AT1G05260 GeneFarm:1833 TAIR:At1g05260 InParanoid:O23044 OMA:ANIPPPT PhylomeDB:O23044 ArrayExpress:O23044 Genevestigator:O23044 GermOnline:AT1G05260 Uniprot:O23044
Root	Isotig15052	14	0	4.678	0.000190242	TAIR|locus:2118929 - symbol:OST1 "AT4G33950" species:3702 "Arabidopsis thaliana" [GO:0016301 "kinase activity" evidence=ISS;IDA] [GO:0009414 "response to water deprivation" evidence=IGI;IMP] [GO:0009737 "response to abscisic acid stimulus" evidence=IDA;IMP] [GO:0010119 "regulation of stomatal movement" evidence=IMP] [GO:0004672 "protein kinase activity" evidence=IDA;TAS] [GO:0009931 "calcium-dependent protein serine/threonine kinase activity" evidence=ISS] [GO:0009738 "abscisic acid mediated signaling pathway" evidence=TAS] [GO:2000377 "regulation of reactive oxygen species metabolic process" evidence=IMP] [GO:0006970 "response to osmotic stress" evidence=IGI;IDA] [GO:0009651 "response to salt stress" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0010118 "stomatal movement" evidence=IMP] [GO:0042742 "defense response to bacterium" evidence=IMP] [GO:0005829 "cytosol" evidence=RCA;IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0005985 "sucrose metabolic process" evidence=IMP] [GO:0006636 "unsaturated fatty acid biosynthetic process" evidence=IMP] [GO:0019432 "triglyceride biosynthetic process" evidence=IMP] [GO:0040007 "growth" evidence=IMP] [GO:0048366 "leaf development" evidence=IMP] InterPro:IPR000719 InterPro:IPR002290 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 Pfam:PF00069 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 SMART:SM00220 GO:GO:0005829 GO:GO:0005524 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005634 GO:GO:0040007 GO:GO:0042742 GO:GO:0009738 GO:GO:0010119 eggNOG:COG0515 SUPFAM:SSF56112 GO:GO:0004674 HOGENOM:HBG755340 GO:GO:0009651 GO:GO:0009414 GO:GO:0010118 GO:GO:0019432 GO:GO:0048366 GO:GO:0006636 EMBL:AL031032 EMBL:AL161584 GO:GO:0019903 GO:GO:0010359 GO:GO:0005985 GO:GO:2000377 KO:K14498 EMBL:AJ316009 EMBL:AY054624 EMBL:AY081538 IPI:IPI00547757 IPI:IPI00900499 PIR:T05223 RefSeq:NP_567945.1 UniGene:At.2399 PDB:3UC4 PDB:3UDB PDB:3ZUT PDB:3ZUU PDBsum:3UC4 PDBsum:3UDB PDBsum:3ZUT PDBsum:3ZUU ProteinModelPortal:Q940H6 SMR:Q940H6 DIP:DIP-36705N IntAct:Q940H6 MINT:MINT-7260107 STRING:Q940H6 PRIDE:Q940H6 EnsemblPlants:AT4G33950.1 GeneID:829541 KEGG:ath:AT4G33950 TAIR:At4g33950 InParanoid:Q940H6 OMA:QYEEPEQ PhylomeDB:Q940H6 ProtClustDB:CLSN2917660 Genevestigator:Q940H6 Uniprot:Q940H6
Root	Isotig15115	1	13	-3.829	0.000362856	TAIR|locus:2064222 - symbol:ANNAT4 "AT2G38750" species:3702 "Arabidopsis thaliana" [GO:0005509 "calcium ion binding" evidence=ISS;NAS] [GO:0005544 "calcium-dependent phospholipid binding" evidence=ISS] [GO:0009986 "cell surface" evidence=NAS] [GO:0006970 "response to osmotic stress" evidence=IMP] [GO:0009737 "response to abscisic acid stimulus" evidence=IMP] [GO:0009408 "response to heat" evidence=IEP] [GO:0009409 "response to cold" evidence=IEP] [GO:0009414 "response to water deprivation" evidence=IEP] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR001464 InterPro:IPR018502 Pfam:PF00191 PRINTS:PR00196 PROSITE:PS00223 SMART:SM00335 GO:GO:0009506 GO:GO:0009737 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0005509 GO:GO:0009409 GO:GO:0009651 GO:GO:0009414 GO:GO:0009408 EMBL:AC005499 GO:GO:0005544 Gene3D:G3DSA:1.10.220.10 PANTHER:PTHR10502 SUPFAM:SSF47874 HOGENOM:HBG745057 InterPro:IPR009118 PANTHER:PTHR10502:SF10 EMBL:AF188363 EMBL:AY087194 EMBL:AY042835 EMBL:AY081483 IPI:IPI00524217 PIR:H84808 RefSeq:NP_181409.1 UniGene:At.20551 ProteinModelPortal:Q9ZVJ6 SMR:Q9ZVJ6 IntAct:Q9ZVJ6 STRING:Q9ZVJ6 PRIDE:Q9ZVJ6 EnsemblPlants:AT2G38750.1 GeneID:818457 KEGG:ath:AT2G38750 GeneFarm:1475 TAIR:At2g38750 eggNOG:NOG260459 InParanoid:Q9ZVJ6 OMA:MWAMHPW PhylomeDB:Q9ZVJ6 ProtClustDB:CLSN2912982 ArrayExpress:Q9ZVJ6 Genevestigator:Q9ZVJ6 Uniprot:Q9ZVJ6
Root	Isotig15145	28	57	-1.155	0.000345522	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig15156	17	1	3.958	8.09E-05	TAIR|locus:2031402 - symbol:AAP3 "AT1G77380" species:3702 "Arabidopsis thaliana" [GO:0015171 "amino acid transmembrane transporter activity" evidence=ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0015802 "basic

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						amino acid transport" evidence=IDA] GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005886 GO:GO:0031965 eggNOG:NOG126188 GO:GO:0015293 InterPro:IPR013057 Pfam:PF01490 HOGENOM:HBG319901 EMBL:X77499 EMBL:AC078898 EMBL:AY099788 EMBL:AY128905 EMBL:AY085581 IPI:IPI00521673 PIR:H96802 RefSeq:NP_177862.1 UniGene:At.5381 ProteinModelPortal:Q39134 IntAct:Q39134 TCDB:2.A.18.2.3 EnsemblPlants:AT1G77380.1 GeneID:844074 KEGG:ath:AT1G77380 TAIR:At1g77380 InParanoid:Q39134 OMA:IEKQASI PhylomeDB:Q39134 ProtClustDB:CLSN2912854 ArrayExpress:Q39134 GO:GO:0015802 Uniprot:Q39134
Root	Isotig15176	7	41	-2.679	6.39E-08	RGD|727924 - symbol:LOC257642 "rRNA promoter binding protein" species:10116 "Rattus norvegicus" [GO:0003690 "double-stranded DNA binding" evidence=IDA] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=IDA] [GO:0008134 "transcription factor binding" evidence=IDA] [GO:0008283 "cell proliferation" evidence=IDA] [GO:0009303 "rRNA transcription" evidence=IDA] RGD:727924 GO:GO:0008134 GO:GO:0008283 GO:GO:0003700 GO:GO:0003690 GO:GO:0009303 EMBL:U77931 IPI:IPI00195015 RefSeq:NP_671477.1 GeneID:257642 KEGG:rno:257642 NextBio:624170 Genevestigator:Q99JC0 Uniprot:Q99JC0
Root	Isotig15181	16	1	3.871	0.000146741	TAIR|locus:2129136 - symbol:HB-2 "AT4G16780" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=ISS] [GO:0005634 "nucleus" evidence=ISS;IDA] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=ISS] [GO:0008283 "cell proliferation" evidence=IMP] [GO:0009733 "response to auxin stimulus" evidence=IMP] [GO:0009826 "unidimensional cell growth" evidence=IMP] [GO:0045892 "negative regulation of transcription, DNA-dependent" evidence=IDA] [GO:0048364 "root development" evidence=IMP] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0009735 "response to cytokinin stimulus" evidence=IEP] [GO:0009641 "shade avoidance" evidence=IEP] [GO:0010017 "red or far-red light signaling pathway" evidence=IEP] [GO:0010218 "response to far red light" evidence=IEP] [GO:0042803 "protein homodimerization activity" evidence=IDA] [GO:0043565 "sequence-specific DNA binding" evidence=IDA] [GO:0010016 "shoot morphogenesis" evidence=IMP] InterPro:IPR000047 InterPro:IPR001356 InterPro:IPR003106 InterPro:IPR006712 InterPro:IPR009057 InterPro:IPR017970 Pfam:PF00046 Pfam:PF02183 Pfam:PF04618 PRINTS:PR00031 PROSITE:PS00027 PROSITE:PS50071 SMART:SM00340 SMART:SM00389 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005634 GO:GO:0045892 GO:GO:0042803 GO:GO:0009735 GO:GO:0009733 GO:GO:0008283 GO:GO:0003700 GO:GO:0006351 GO:GO:0010218 GO:GO:0048364 Gene3D:G3DSA:1.10.10.60 SUPFAM:SSF46689 GO:GO:0009826 EMBL:AL161544 GO:GO:0009585 GO:GO:0000976 KO:K09338 GO:GO:0009641 EMBL:Z97342 EMBL:M90394 EMBL:Z19602 EMBL:X68145 EMBL:X68146 EMBL:AF375453 EMBL:AY081747 EMBL:EF193551 EMBL:EF193552 EMBL:EF193553 EMBL:EF193554 EMBL:EF193555 EMBL:EF193556 EMBL:EF193557 EMBL:EF193558 EMBL:EF193559 EMBL:EF193560 EMBL:EF193561 EMBL:EF193562 EMBL:EF193563 EMBL:EF193564 EMBL:EF193565 EMBL:AY174653 EMBL:AY174654 EMBL:AY174655 EMBL:AY174656 IPI:IPI00517186 PIR:S31424 RefSeq:NP_193411.1 UniGene:At.24419 UniGene:At.74809 ProteinModelPortal:Q05466 SMR:Q05466 IntAct:Q05466 STRING:Q05466 PRIDE:Q05466 EnsemblPlants:AT4G16780.1 GeneID:827384 KEGG:ath:AT4G16780 GeneFarm:3977 TAIR:At4g16780 eggNOG:NOG150160 InParanoid:Q05466 PhylomeDB:Q05466 ProtClustDB:CLSN2685845 ArrayExpress:Q05466 Genevestigator:Q05466 GermOnline:AT4G16780 GO:GO:0010016 Uniprot:Q05466
Root	Isotig15195	0	25	-5.773	1.02E-07	TAIR|locus:2114540 - symbol:SWEET11 "AT3G48740" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0016020 "membrane" evidence=IEA;ISS] [GO:0016021 "integral to membrane" evidence=IEA] [GO:0005887 "integral to plasma membrane" evidence=ISS] [GO:0051119 "sugar transmembrane transporter activity" evidence=ISS] InterPro:IPR004316 Pfam:PF03083 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005887 EMBL:AL133315 GO:GO:0051119 PANTHER:PTHR10791 HOGENOM:HBG745285 KO:K15382 eggNOG:NOG308353 OMA:NTENTWA EMBL:AF361825 EMBL:AF419559 EMBL:AY070412 EMBL:AY078041 EMBL:AY096594 IPI:IPI00530568 PIR:T46218 RefSeq:NP_190443.1 UniGene:At.27455 IntAct:Q9SMM5 PRIDE:Q9SMM5 ProMEX:Q9SMM5 EnsemblPlants:AT3G48740.1 GeneID:824035 KEGG:ath:AT3G48740 TAIR:At3g48740 InParanoid:Q9SMM5 PhylomeDB:Q9SMM5 ProtClustDB:CLSN2684213 ArrayExpress:Q9SMM5 Genevestigator:Q9SMM5 Uniprot:Q9SMM5
Root	Isotig15198	1	29	-4.987	1.39E-08	No hit
Root	Isotig15253	0	11	-4.588	0.000569522	TAIR|locus:2181778 - symbol:AT5G02540 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0008152 "metabolic process" evidence=IEA] [GO:0016491 "oxidoreductase activity" evidence=IEA;ISS] [GO:0055114 "oxidation-reduction process" evidence=IEA] InterPro:IPR002198

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						InterPro:IPR016040 Pfam:PF00106 PRINTS:PR00080 InterPro:IPR002347 GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 GO:GO:0016491 PRINTS:PR00081 EMBL:AY093050 EMBL:BT000303 IPI:IPI00547295 ProteinModelPortal:Q8RWJ2 TAIR:At5g02540 InParanoid:Q8RWJ2 PhylomeDB:Q8RWJ2 ArrayExpress:Q8RWJ2 Genevestigator:Q8RWJ2 Uniprot:Q8RWJ2
Root	Isotig15278	0	13	-4.829	0.000155955	TAIR|locus:2030086 - symbol:OPR1 "AT1G76680" species:3702 "Arabidopsis thaliana" [GO:0010150 "leaf senescence" evidence=TAS] [GO:0009611 "response to wounding" evidence=IEP] [GO:0009695 "jasmonic acid biosynthetic process" evidence=TAS] [GO:0006629 "lipid metabolic process" evidence=TAS] [GO:0009751 "response to salicylic acid stimulus" evidence=IEP] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0016629 "12-oxophytodienoate reductase activity" evidence=ISS;IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0031407 "oxylipin metabolic process" evidence=IDA] InterPro:IPR001155 InterPro:IPR013785 Pfam:PF00724 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0046686 GO:GO:0009611 Gene3D:G3DSA:3.20.20.70 GO:GO:0009751 GO:GO:0031408 GO:GO:0010181 EMBL:AC010718 eggNOG:COG1902 HOGENOM:HBG583461 EMBL:Y10617 EMBL:U92460 EMBL:AY074874 EMBL:BT020365 EMBL:AY087801 IPI:IPI00548191 PIR:B96795 RefSeq:NP_177794.1 UniGene:At.11155 UniGene:At.67448 UniGene:At.73001 PDB:1VJI PDB:2Q3R PDBsum:1VJI PDBsum:2Q3R ProteinModelPortal:Q8LAH7 SMR:Q8LAH7 IntAct:Q8LAH7 STRING:Q8LAH7 PRIDE:Q8LAH7 EnsemblPlants:AT1G76680.1 GeneID:844001 KEGG:ath:AT1G76680 GeneFarm:4901 TAIR:At1g76680 InParanoid:Q8LAH7 KO:K05894 PhylomeDB:Q8LAH7 ProtClustDB:CLSN2682783 Genevestigator:Q8LAH7 GO:GO:0016629 Uniprot:Q8LAH7
Root	Isotig15284	0	30	-6.036	5.71E-09	TAIR|locus:2153529 - symbol:PRX52 "AT5G05340" species:3702 "Arabidopsis thaliana" [GO:0004601 "peroxidase activity" evidence=ISS] [GO:0006979 "response to oxidative stress" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0005618 "cell wall" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0005829 "cytosol" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR000823 InterPro:IPR002016 InterPro:IPR010255 InterPro:IPR019793 InterPro:IPR019794 Pfam:PF00141 PRINTS:PR00458 PRINTS:PR00461 PROSITE:PS00435 PROSITE:PS00436 PROSITE:PS50873 GO:GO:0005829 GO:GO:0048046 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005618 GO:GO:0005515 GO:GO:0020037 GO:GO:0004601 GO:GO:0042744 HOGENOM:HBG597790 SUPFAM:SSF48113 EMBL:AB010692 KO:K00430 EMBL:AY065270 IPI:IPI00527468 RefSeq:NP_196153.1 UniGene:At.28537 ProteinModelPortal:Q9FLC0 SMR:Q9FLC0 IntAct:Q9FLC0 STRING:Q9FLC0 PeroxiBase:218 PRIDE:Q9FLC0 EnsemblPlants:AT5G05340.1 GeneID:830416 KEGG:ath:AT5G05340 GeneFarm:1905 TAIR:At5g05340 eggNOG:NOG298084 InParanoid:Q9FLC0 OMA:TNFRARI PhylomeDB:Q9FLC0 ProtClustDB:CLSN2916362 ArrayExpress:Q9FLC0 Genevestigator:Q9FLC0 GermOnline:AT5G05340 Uniprot:Q9FLC0
Root	Isotig15301	7	55	-3.103	1.58E-11	TAIR|locus:2123994 - symbol:AT4G27450 "AT4G27450" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 EMBL:CP002687 GO:GO:0005634 GO:GO:0005515 EMBL:AF375452 EMBL:AY045885 EMBL:AY091306 EMBL:AY087420 IPI:IPI00539788 RefSeq:NP_567775.1 UniGene:At.25186 UniGene:At.68765 ProteinModelPortal:Q93V62 IntAct:Q93V62 STRING:Q93V62 MEROPS:C44.A04 PRIDE:Q93V62 ProMEX:Q93V62 DNASU:828854 EnsemblPlants:AT4G27450.1 GeneID:828854 KEGG:ath:AT4G27450 TAIR:At4g27450 eggNOG:NOG245574 InParanoid:Q93V62 OMA:VYTRINS PhylomeDB:Q93V62 ProtClustDB:CLSN2917621 Genevestigator:Q93V62 InterPro:IPR024286 Pfam:PF12481 Uniprot:Q93V62
Root	Isotig15312	0	13	-4.829	0.000155955	TAIR|locus:2065058 - symbol:CZF1 "AT2G40140" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=TAS] [GO:0009409 "response to cold" evidence=IEP] [GO:0050832 "defense response to fungus" evidence=IMP] [GO:0010200 "response to chitin" evidence=IEP] InterPro:IPR002110 InterPro:IPR000571 Pfam:PF00642 PROSITE:PS50088 PROSITE:PS50103 SMART:SM00248 SMART:SM00356 GO:GO:0005634 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0006355 GO:GO:0050832 GO:GO:0003677 GO:GO:0008270 InterPro:IPR020683 Gene3D:G3DSA:1.25.40.20 SUPFAM:SSF48403 PROSITE:PS50297 GO:GO:0009409 EMBL:AF085279 GO:GO:0010200 eggNOG:NOG69137 EMBL:AY093016 EMBL:AY128937 IPI:IPI00522137 PIR:G84825 RefSeq:NP_001031517.1 RefSeq:NP_181543.1 UniGene:At.27663 ProteinModelPortal:Q9XEE6

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						SMR:Q9XEE6 STRING:Q9XEE6 PRIDE:Q9XEE6 EnsemblPlants:AT2G40140.1 EnsemblPlants:AT2G40140.2 GeneID:818605 KEGG:ath:AT2G40140 TAIR:At2g40140 HOGENOM:HBG594924 InParanoid:Q9XEE6 OMA:ANTISMM PhylomeDB:Q9XEE6 ProtClustDB:CLSN2683392 ArrayExpress:Q9XEE6 Genevestigator:Q9XEE6 Uniprot:Q9XEE6
Root	Isotig15316	1	13	-3.829	0.000362856	TAIR|locus:2119976 - symbol:PAP2 "AT4G29080" species:3702 "Arabidopsis thaliana" [GO:0005622 "intracellular" evidence=ISS] [GO:0005634 "nucleus" evidence=IEA] [GO:0006417 "regulation of translation" evidence=ISS] [GO:0009733 "response to auxin stimulus" evidence=ISS;TAS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] InterPro:IPR003311 InterPro:IPR011525 Pfam:PF02309 PROSITE:PS50962 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005634 GO:GO:0009734 GO:GO:0006355 GO:GO:0006351 GO:GO:0046983 EMBL:AL078470 EMBL:AL161574 HOGENOM:HBG750482 EMBL:AF087936 EMBL:AJ458326 EMBL:AF332402 EMBL:AY053404 EMBL:AY133516 IPI:IPI00539897 PIR:T08963 RefSeq:NP_194637.1 UniGene:At.3406 IntAct:Q9ZSY8 STRING:Q9ZSY8 PRIDE:Q9ZSY8 EnsemblPlants:AT4G29080.1 GeneID:829029 KEGG:ath:AT4G29080 GeneFarm:3186 TAIR:At4g29080 eggNOG:NOG266390 InParanoid:Q9ZSY8 OMA:FRKNSMA PhylomeDB:Q9ZSY8 ProtClustDB:CLSN2916037 ArrayExpress:Q9ZSY8 Genevestigator:Q9ZSY8 GermOnline:AT4G29080 Uniprot:Q9ZSY8
Root	Isotig15334	0	13	-4.829	0.000155955	TAIR|locus:2152385 - symbol:AT5G45910 "AT5G45910" species:3702 "Arabidopsis thaliana" [GO:0004091 "carboxylesterase activity" evidence=ISS] [GO:0006629 "lipid metabolic process" evidence=IEA] [GO:0016788 "hydrolase activity, acting on ester bonds" evidence=IEA] InterPro:IPR001087 Pfam:PF00657 PROSITE:PS01098 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005576 GO:GO:0016042 GO:GO:0016788 EMBL:AB016870 EMBL:AY085579 IPI:IPI00544452 RefSeq:NP_199403.1 UniGene:At.29987 ProteinModelPortal:Q9FJ45 PRIDE:Q9FJ45 EnsemblPlants:AT5G45910.1 GeneID:834631 KEGG:ath:AT5G45910 TAIR:At5g45910 eggNOG:NOG290843 InParanoid:Q9FJ45 OMA:SARCGHI PhylomeDB:Q9FJ45 ProtClustDB:CLSN2715809 Genevestigator:Q9FJ45 Uniprot:Q9FJ45
Root	Isotig15372	1	14	-3.936	0.000188601	TAIR|locus:2015616 - symbol:ACR11 "ACT domain repeats 11" species:3702 "Arabidopsis thaliana" [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0010319 "stromule" evidence=IDA] [GO:0009416 "response to light stimulus" evidence=IEP] [GO:0009744 "response to sucrose stimulus" evidence=IEP] EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009570 GO:GO:0009941 GO:GO:0010319 GO:GO:0009409 GO:GO:0009744 GO:GO:0009416 GO:GO:0009535 EMBL:AC051629 GO:GO:0016779 UniGene:At.19280 UniGene:At.16052 UniGene:At.24697 EMBL:AF386988 EMBL:BT006317 EMBL:JF797176 IPI:IPI00517825 PIR:B86304 RefSeq:NP_564010.1 ProteinModelPortal:Q9FZ47 SMR:Q9FZ47 STRING:Q9FZ47 PRIDE:Q9FZ47 ProMEX:Q9FZ47 EnsemblPlants:AT1G16880.1 GeneID:838259 KEGG:ath:AT1G16880 TAIR:At1g16880 eggNOG:NOG288292 HOGENOM:HBG589584 InParanoid:Q9FZ47 OMA:ATIVEIT PhylomeDB:Q9FZ47 ProtClustDB:CLSN2687834 Genevestigator:Q9FZ47 Uniprot:Q9FZ47
Root	Isotig15375	4	59	-4.012	1.25E-14	TAIR|locus:2126026 - symbol:PIP1;4 "AT4G00430" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=ISS] [GO:0015250 "water channel activity" evidence=ISS] [GO:0016020 "membrane" evidence=ISS;IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009414 "response to water deprivation" evidence=IEP] InterPro:IPR000425 InterPro:IPR012269 InterPro:IPR022357 Pfam:PF00230 PRINTS:PR00783 PROSITE:PS00221 GO:GO:0016021 GO:GO:0005886 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0055085 GO:GO:0009414 GO:GO:0005215 GO:GO:0006833 EMBL:AF013293 EMBL:AF195115 EMBL:AL161471 InterPro:IPR023271 Gene3D:G3DSA:1.20.1080.10 SUPFAM:SSF81338 eggNOG:COG0580 HOGENOM:HBG705794 PANTHER:PTHR19139 TIGRFAMs:TIGR00861 OMA:ITHNFKD KO:K09872 ProtClustDB:CLSN2682869 UniGene:At.20518 UniGene:At.20892 EMBL:D26609 EMBL:D85192 EMBL:AY099825 EMBL:AY120785 EMBL:BT000330 EMBL:BT006313 IPI:IPI00521990 PIR:T01528 RefSeq:NP_567178.1 ProteinModelPortal:Q39196 SMR:Q39196 IntAct:Q39196 STRING:Q39196 PRIDE:Q39196 EnsemblPlants:AT4G00430.1 GeneID:827956 KEGG:ath:AT4G00430 GeneFarm:2265 TAIR:At4g00430 InParanoid:Q39196 PhylomeDB:Q39196 ArrayExpress:Q39196 Genevestigator:Q39196 Uniprot:Q39196
Root	Isotig15379	260	0	8.893	4.38E-49	No hit
Root	Isotig15401	19	1	4.119	2.48E-05	TAIR|locus:2043142 - symbol:HAI3 "highly ABA-induced PP2C gene 3" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004722 "protein serine/threonine phosphatase activity" evidence=IEA;ISS] [GO:0006470 "protein dephosphorylation" evidence=IEA] [GO:0008287 "protein serine/threonine

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						phosphatase complex" evidence=IEA] InterPro:IPR000222 InterPro:IPR001932 Pfam:PF00481 PROSITE:PS01032 SMART:SM00331 SMART:SM00332 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0006470 GO:GO:0004722 GO:GO:0046872 eggNOG:COG0631 Gene3D:G3DSA:3.60.40.10 SUPFAM:SSF81606 EMBL:AC004561 GO:GO:0008287 InterPro:IPR015655 PANTHER:PTHR13832 HSSP:P35813 HOGENOM:HBG747569 KO:K14497 ProtClustDB:CLSN2682567 EMBL:DQ056553 EMBL:BT022047 EMBL:BT023483 IPI:IPI00536276 PIR:F84695 RefSeq:NP_180499.1 UniGene:At.50109 ProteinModelPortal:Q9ZW21 SMR:Q9ZW21 DIP:DIP-48991N IntAct:Q9ZW21 PRIDE:Q9ZW21 EnsemblPlants:AT2G29380.1 GeneID:817487 KEGG:ath:AT2G29380 TAIR:At2g29380 InParanoid:Q9ZW21 OMA:CRNGKPV PhylomeDB:Q9ZW21 ArrayExpress:Q9ZW21 Genevestigator:Q9ZW21 Uniprot:Q9ZW21
Root	Isotig15412	3	36	-3.714	4.33E-09	No hit
Root	Isotig15458	0	14	-4.936	8.24E-05	UNIPROTKB|Q9FRV1 - symbol:rsca "Basic endochitinase A" species:4550 "Secale cereale" [GO:0004568 "chitinase activity" evidence=IDA] [GO:0005576 "extracellular region" evidence=IC] [GO:0008061 "chitin binding" evidence=IDA] [GO:0016998 "cell wall macromolecule catabolic process" evidence=IDA] [GO:0050832 "defense response to fungus" evidence=IDA] InterPro:IPR000726 InterPro:IPR001002 InterPro:IPR016283 InterPro:IPR018371 Pfam:PF00182 Pfam:PF00187 PIRSF:PIRSF001060 PRINTS:PR00451 ProDom:PD000609 PROSITE:PS00026 PROSITE:PS00773 PROSITE:PS00774 PROSITE:PS50941 SMART:SM00270 GO:GO:0005576 GO:GO:0050832 GO:GO:0031640 CAZy:CBM18 GO:GO:0008061 Gene3D:G3DSA:3.30.60.10 SUPFAM:SSF57016 GO:GO:0004568 GO:GO:0006032 GO:GO:0016998 EMBL:AB051578 PIR:JC2071 ProteinModelPortal:Q9FRV1 SMR:Q9FRV1 CAZy:GH19 Gramene:Q9FRV1 InterPro:IPR023346 SUPFAM:SSF53955 Uniprot:Q9FRV1
Root	Isotig15507	158	2	6.175	2.51E-37	No hit
Root	Isotig15520	21	0	5.263	3.38E-06	No hit
Root	Isotig15550	0	11	-4.588	0.000569522	TAIR|locus:2081670 - symbol:GATL7 "AT3G62660" species:3702 "Arabidopsis thaliana" [GO:0016051 "carbohydrate biosynthetic process" evidence=ISS] [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0016758 "transferase activity, transferring hexosyl groups" evidence=ISS] [GO:0047262 "polygalacturonate 4-alpha-galacturonosyltransferase activity" evidence=ISS] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR002495 Pfam:PF01501 GO:GO:0016021 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0000139 EMBL:AL162651 GO:GO:0007047 GO:GO:0016757 CAZy:GT8 HOGENOM:HBG594866 ProtClustDB:CLSN2679375 EMBL:AY072114 EMBL:AY096607 EMBL:BT000748 IPI:IPI00526289 PIR:T48055 RefSeq:NP_191825.2 UniGene:At.4823 UniGene:At.74115 ProteinModelPortal:Q8VYF4 PRIDE:Q8VYF4 EnsemblPlants:AT3G62660.1 GeneID:825440 KEGG:ath:AT3G62660 TAIR:At3g62660 eggNOG:NOG302075 InParanoid:Q8VYF4 OMA:WMEIQKS PhylomeDB:Q8VYF4 ArrayExpress:Q8VYF4 Genevestigator:Q8VYF4 Uniprot:Q8VYF4
Root	Isotig15567	5	38	-3.055	2.67E-08	MGI|MGI:2444070 - symbol:Nlrc3 "NLR family, CARD domain containing 3" species:10090 "Mus musculus" [GO:0005737 "cytoplasm" evidence=ISO;ISS] [GO:0005524 "ATP binding" evidence=IEA] [GO:0000166 "nucleotide binding" evidence=IEA] [GO:0007249 "I-kappaB kinase/NF-kappaB cascade" evidence=ISO;ISS] [GO:0032088 "negative regulation of NF-kappaB transcription factor activity" evidence=ISO;ISS] [GO:0042110 "T cell activation" evidence=ISS] [GO:0003674 "molecular_function" evidence=ND] MGI:MGI:2444070 GO:GO:0005524 GO:GO:0005737 GO:GO:0042110 GO:GO:0032088 GO:GO:0007249 InterPro:IPR007111 PROSITE:PS50837 GeneTree:ENSGT00650000093077 eggNOG:NOG69209 HOVERGEN:HBG055285 EMBL:AK220314 EMBL:AK079766 EMBL:AK084199 EMBL:AK171971 EMBL:BC130223 IPI:IPI00652368 IPI:IPI00671345 IPI:IPI00677124 IPI:IPI00678735 IPI:IPI00828619 UniGene:Mm.215994 ProteinModelPortal:Q5DU56 SMR:Q5DU56 PhosphoSite:Q5DU56 PRIDE:Q5DU56 Ensembl:ENSMUST00000163478 UCSC:uc007xzc.1 UCSC:uc007xzd.1 UCSC:uc007xze.1 OrthoDB:EOG4BZN26 Bgee:Q5DU56 CleanEx:MM_NLRC3 Genevestigator:Q5DU56 Uniprot:Q5DU56
Root	Isotig15580	0	16	-5.129	2.34E-05	TAIR|locus:2159098 - symbol:TT4 "AT5G13930" species:3702 "Arabidopsis thaliana" [GO:0005515 "protein binding" evidence=IPI] [GO:0009926 "auxin polar transport" evidence=IMP] [GO:0005783 "endoplasmic reticulum" evidence=IDA] [GO:0009705 "plant-type vacuole membrane" evidence=IDA] [GO:0010224 "response to UV-B" evidence=IMP] [GO:0005634 "nucleus" evidence=IDA] [GO:0031540 "regulation of anthocyanin biosynthetic process" evidence=IEP] [GO:0009611 "response to wounding" evidence=IEP] [GO:0009753 "response to jasmonic acid stimulus" evidence=IEP] [GO:0009629 "response to gravity" evidence=IMP] [GO:0009733 "response to auxin stimulus" evidence=IEP] [GO:0009813 "flavonoid biosynthetic process" evidence=ISS;IMP] [GO:0009715 "chalcone

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						biosynthetic process" evidence=IMP] [GO:0016210 "naringenin-chalcone synthase activity" evidence=IMP] [GO:0006979 "response to oxidative stress" evidence=IEP] InterPro:IPR001099 InterPro:IPR011141 InterPro:IPR012328 InterPro:IPR016038 InterPro:IPR016039 InterPro:IPR018088 Pfam:PF00195 Pfam:PF02797 PIRSF:PIRSF000451 PROSITE:PS00441 GO:GO:0005783 GO:GO:0005634 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005515 GO:GO:0009733 GO:GO:0009753 GO:GO:0006979 GO:GO:0009611 GO:GO:0009926 GO:GO:0009705 GO:GO:0009629 EMBL:AB005230 GO:GO:0031540 Gene3D:G3DSA:3.40.47.10 SUPFAM:SSF53901 GO:GO:0009813 GO:GO:0010224 GO:GO:0016210 EMBL:M20308 EMBL:S80554 EMBL:Y18602 EMBL:Y18603 EMBL:AF112086 EMBL:AY044331 EMBL:AY054278 EMBL:AY058155 EMBL:AY090376 EMBL:AY087778 EMBL:BT000596 EMBL:Z17650 EMBL:Z17649 IPI:IPI00545547 PIR:A27721 RefSeq:NP_196897.1 UniGene:At.297 UniGene:At.69414 UniGene:At.71936 ProteinModelPortal:P13114 SMR:P13114 IntAct:P13114 STRING:P13114 PRIDE:P13114 EnsemblPlants:AT5G13930.1 GeneID:831241 KEGG:ath:AT5G13930 TAIR:At5g13930 eggNOG:COG3424 HOGENOM:HBG588210 InParanoid:P13114 KO:K00660 OMA:CTGIMIP PhylomeDB:P13114 ProtClustDB:CLSN2916621 BioCyc:MetaCyc:AT5G13930-MONOMER BRENDA:2.3.1.74 Genevestigator:P13114 Uniprot:P13114
Root	Isotig15586	13	0	4.571	0.000344357	No hit
Root	Isotig15605	0	27	-5.884	3.19E-08	TAIR|locus:2152445 - symbol:SAG12 "AT5G45890" species:3702 "Arabidopsis thaliana" [GO:0006508 "proteolysis" evidence=ISS] [GO:0008234 "cysteine-type peptidase activity" evidence=ISS] [GO:0009723 "response to ethylene stimulus" evidence=IEP] [GO:0007568 "aging" evidence=IEP;TAS] [GO:0010150 "leaf senescence" evidence=TAS] [GO:0010282 "senescence-associated vacuole" evidence=IDA] [GO:0009817 "defense response to fungus, incompatible interaction" evidence=IEP] InterPro:IPR000668 InterPro:IPR013128 Pfam:PF00112 PRINTS:PR00705 SMART:SM00645 InterPro:IPR000169 EMBL:CP002688 GO:GO:0004197 GO:GO:0006508 InterPro:IPR013201 PANTHER:PTHR12411 Pfam:PF08246 SMART:SM00848 PROSITE:PS00640 PROSITE:PS00139 PROSITE:PS00639 GO:GO:0010150 GO:GO:0009817 EMBL:AB016870 HSSP:O65039 EMBL:AF370131 EMBL:AY040073 IPI:IPI00544181 RefSeq:NP_568651.1 UniGene:At.75256 UniGene:At.7710 ProteinModelPortal:Q9FJ47 SMR:Q9FJ47 IntAct:Q9FJ47 STRING:Q9FJ47 MEROPS:C01.117 PRIDE:Q9FJ47 EnsemblPlants:AT5G45890.1 GeneID:834629 KEGG:ath:AT5G45890 TAIR:At5g45890 InParanoid:Q9FJ47 OMA:NDEQALM PhylomeDB:Q9FJ47 ProtClustDB:CLSN2917735 ArrayExpress:Q9FJ47 Genevestigator:Q9FJ47 GO:GO:0010282 Uniprot:Q9FJ47
Root	Isotig15612	14	1	3.678	0.000484579	RGD|727924 - symbol:LOC257642 "rRNA promoter binding protein" species:10116 "Rattus norvegicus" [GO:0003690 "double-stranded DNA binding" evidence=IDA] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=IDA] [GO:0008134 "transcription factor binding" evidence=IDA] [GO:0008283 "cell proliferation" evidence=IDA] [GO:0009303 "rRNA transcription" evidence=IDA] RGD:727924 GO:GO:0008134 GO:GO:0008283 GO:GO:0003700 GO:GO:0003690 GO:GO:0009303 EMBL:U77931 IPI:IPI00195015 RefSeq:NP_671477.1 GeneID:257642 KEGG:rno:257642 NextBio:624170 Genevestigator:Q99JC0 Uniprot:Q99JC0
Root	Isotig15618	15	40	-1.544	0.00017868	TAIR|locus:2057906 - symbol:GAMMA-TIP "AT2G36830" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=ISS] [GO:0009740 "gibberellic acid mediated signaling pathway" evidence=TAS] [GO:0015250 "water channel activity" evidence=ISS;IDA] [GO:0016020 "membrane" evidence=ISS] [GO:0009705 "plant-type vacuole membrane" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0015204 "urea transmembrane transporter activity" evidence=IGI] [GO:0015840 "urea transport" evidence=IGI] [GO:0005773 "vacuole" evidence=IDA] [GO:0080170 "hydrogen peroxide transmembrane transport" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0000326 "protein storage vacuole" evidence=IDA] [GO:0042807 "central vacuole" evidence=IDA] [GO:0006833 "water transport" evidence=IDA] InterPro:IPR000425 InterPro:IPR022357 Pfam:PF00230 PRINTS:PR00783 PROSITE:PS00221 GO:GO:0016021 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009941 EMBL:AC006922 GO:GO:0009705 InterPro:IPR023271 Gene3D:G3DSA:1.20.1080.10 SUPFAM:SSF81338 eggNOG:COG0580 HOGENOM:HBG705794 PANTHER:PTHR19139 GO:GO:0015250 GO:GO:0000326 GO:GO:0015204 GO:GO:0080170 EMBL:X54854 EMBL:X63552 EMBL:M84344 EMBL:X72581 EMBL:AF370172 EMBL:AY059134 EMBL:AY087558 EMBL:Z18124 EMBL:Z18771 EMBL:Z26215 IPI:IPI00531328 PIR:S13718 PIR:S22202 RefSeq:NP_181221.1 UniGene:At.25221 UniGene:At.43252 UniGene:At.67051 ProteinModelPortal:P25818 SMR:P25818 IntAct:P25818 STRING:P25818 TCDB:1.A.8.10.3 PRIDE:P25818 EnsemblPlants:AT2G36830.1 GeneID:818255 KEGG:ath:AT2G36830 GeneFarm:4855 TAIR:At2g36830 InParanoid:P25818 KO:K09873 OMA:INTTHEQ PhylomeDB:P25818

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						ProtClustDB:PLN00027 ArrayExpress:P25818 Genevestigator:P25818 GermOnline:AT2G36830 GO:GO:0042807 Uniprot:P25818
Root	Isotig15627	0	11	-4.588	0.000569522	TAIR|locus:2060550 - symbol:AT2G41480 species:3702 "Arabidopsis thaliana" [GO:0004601 "peroxidase activity" evidence=IEA;ISS] [GO:0006979 "response to oxidative stress" evidence=IEA] [GO:0020037 "heme binding" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] InterPro:IPR000823 InterPro:IPR002016 InterPro:IPR010255 InterPro:IPR019793 InterPro:IPR019794 Pfam:PF00141 PRINTS:PR00458 PRINTS:PR00461 PROSITE:PS00435 PROSITE:PS00436 PROSITE:PS50873 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0005576 GO:GO:0020037 GO:GO:0004601 GO:GO:0042744 HOGENOM:HBG597790 SUPFAM:SSF48113 EMBL:AC004625 EMBL:AY139994 EMBL:BT008727 IPI:IPI00538575 PIR:T02443 UniGene:At.42826 ProteinModelPortal:O80822 SMR:O80822 STRING:O80822 PeroxiBase:118 PRIDE:O80822 EnsemblPlants:AT2G41480.1 GeneFarm:1851 TAIR:At2g41480 eggNOG:NOG250431 InParanoid:O80822 OMA:GNSDPTI PhylomeDB:O80822 ArrayExpress:O80822 Genevestigator:O80822 GermOnline:AT2G41480 Uniprot:O80822
Root	Isotig15643	33	8	1.915	0.000152977	No hit
Root	Isotig15707	5	24	-2.392	0.000103464	TAIR|locus:2123994 - symbol:AT4G27450 "AT4G27450" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 EMBL:CP002687 GO:GO:0005634 GO:GO:0005515 EMBL:AF375452 EMBL:AY045885 EMBL:AY091306 EMBL:AY087420 IPI:IPI00539788 RefSeq:NP_567775.1 UniGene:At.25186 UniGene:At.68765 ProteinModelPortal:Q93V62 IntAct:Q93V62 STRING:Q93V62 MEROPS:C44.A04 PRIDE:Q93V62 ProMEX:Q93V62 DNASU:828854 EnsemblPlants:AT4G27450.1 GeneID:828854 KEGG:ath:AT4G27450 TAIR:At4g27450 eggNOG:NOG245574 InParanoid:Q93V62 OMA:VYTRINS PhylomeDB:Q93V62 ProtClustDB:CLSN2917621 Genevestigator:Q93V62 InterPro:IPR024286 Pfam:PF12481 Uniprot:Q93V62
Root	Isotig15719	2	17	-3.216	0.000139706	TAIR|locus:2032060 - symbol:GRF2 "AT1G78300" species:3702 "Arabidopsis thaliana" [GO:0045309 "protein phosphorylated amino acid binding" evidence=TAS] [GO:0005773 "vacuole" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009742 "brassinosteroid mediated signaling pathway" evidence=IPI] [GO:0005829 "cytosol" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR000308 PIRSF:PIRSF000868 PRINTS:PR00305 EMBL:CP002684 GenomeReviews:CT485782_GR eggNOG:COG5040 HOGENOM:HBG611720 GO:GO:0005829 GO:GO:0005886 GO:GO:0019904 GO:GO:0009742 InterPro:IPR023409 InterPro:IPR023410 Gene3D:G3DSA:1.20.190.20 PANTHER:PTHR18860 Pfam:PF00244 SMART:SM00101 SUPFAM:SSF48445 PROSITE:PS00796 PROSITE:PS00797 EMBL:M96855 EMBL:U09376 EMBL:AC013430 EMBL:AF462807 EMBL:AY077667 EMBL:AY086467 IPI:IPI00517524 PIR:A47237 RefSeq:NP_565176.1 UniGene:At.23337 ProteinModelPortal:Q01525 SMR:Q01525 IntAct:Q01525 STRING:Q01525 PRIDE:Q01525 EnsemblPlants:AT1G78300.1 GeneID:844165 KEGG:ath:AT1G78300 TAIR:At1g78300 InParanoid:Q01525 OMA:DEIKEAP PhylomeDB:Q01525 ProtClustDB:CLSN2917484 ArrayExpress:Q01525 Genevestigator:Q01525 GermOnline:AT1G78300 GO:GO:0005774 Uniprot:Q01525
Root	Isotig15792	0	30	-6.036	5.71E-09	TAIR|locus:2082543 - symbol:BGL2 "AT3G57260" species:3702 "Arabidopsis thaliana" [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=ISS] [GO:0009627 "systemic acquired resistance" evidence=IEP;NAS] [GO:0004338 "glucan exo-1,3-beta-glucosidase activity" evidence=ISS] [GO:0005773 "vacuole" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0048046 "apoplast" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0008810 "cellulase activity" evidence=TAS] InterPro:IPR000490 InterPro:IPR013781 Pfam:PF00332 PROSITE:PS00587 GO:GO:0048046 GO:GO:0005773 GO:GO:0005618 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005515 GO:GO:0043169 InterPro:IPR017853 Gene3D:G3DSA:3.20.20.80 SUPFAM:SSF51445 GO:GO:0005975 GO:GO:0009409 GO:GO:0009627 EMBL:AL137080 CAZy:GH17 GO:GO:0042973 GO:GO:0008810 HOGENOM:HBG605194 EMBL:M90509 EMBL:M58462 EMBL:AY099668 EMBL:AY128847 EMBL:AY086134 IPI:IPI00547460 PIR:JQ1694 PIR:T45804 RefSeq:NP_191285.1 UniGene:At.22313 ProteinModelPortal:P33157 SMR:P33157 IntAct:P33157 STRING:P33157 PRIDE:P33157 EnsemblPlants:AT3G57260.1 GeneID:824893 KEGG:ath:AT3G57260 TAIR:At3g57260 eggNOG:NOG268889

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						InParanoid:P33157 OMA:VENAKTY PhylomeDB:P33157 ProtClustDB:CLSN2915357 ArrayExpress:P33157 Genevestigator:P33157 GermOnline:AT3G57260 Uniprot:P33157
Root	Isotig15795	18	41	-1.317	0.00076488	TAIR|locus:2026616 - symbol:APX1 "AT1G07890" species:3702 "Arabidopsis thaliana" [GO:0016688 "L-ascorbate peroxidase activity" evidence=ISS;IMP;TAS] [GO:0000302 "response to reactive oxygen species" evidence=IMP] [GO:0042744 "hydrogen peroxide catabolic process" evidence=IMP] [GO:0009793 "embryo development ending in seed dormancy" evidence=IMP] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA;TAS] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] [GO:0009408 "response to heat" evidence=IEP] InterPro:IPR002016 InterPro:IPR002207 InterPro:IPR010255 InterPro:IPR019793 InterPro:IPR019794 Pfam:PF00141 PRINTS:PR00458 PRINTS:PR00459 PROSITE:PS00435 PROSITE:PS00436 PROSITE:PS50873 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 GO:GO:0009570 GO:GO:0046686 GO:GO:0005618 GO:GO:0009651 GO:GO:0009793 GO:GO:0009408 GO:GO:0020037 GO:GO:0042744 EMBL:X59600 EMBL:D14442 EMBL:U63815 EMBL:AC007583 EMBL:AY039879 EMBL:AY056395 EMBL:AY094002 EMBL:AK230096 EMBL:AY086425 IPI:IPI00536287 PIR:D86214 PIR:S20866 RefSeq:NP_001030991.2 RefSeq:NP_001030992.2 RefSeq:NP_001077482.1 RefSeq:NP_001117244.1 RefSeq:NP_172267.1 RefSeq:NP_849607.1 RefSeq:NP_973786.1 UniGene:At.47584 UniGene:At.67008 ProteinModelPortal:Q05431 SMR:Q05431 IntAct:Q05431 STRING:Q05431 PeroxiBase:1890 SWISS-2DPAGE:Q05431 PRIDE:Q05431 ProMEX:Q05431 EnsemblPlants:AT1G07890.1 EnsemblPlants:AT1G07890.2 EnsemblPlants:AT1G07890.3 EnsemblPlants:AT1G07890.4 EnsemblPlants:AT1G07890.5 EnsemblPlants:AT1G07890.7 EnsemblPlants:AT1G07890.8 GeneID:837304 KEGG:ath:AT1G07890 GeneFarm:1942 TAIR:At1g07890 eggNOG:COG0376 HOGENOM:HBG597790 InParanoid:Q05431 KO:K00434 OMA:IAEKNCA PhylomeDB:Q05431 ProtClustDB:PLN02364 ArrayExpress:Q05431 Genevestigator:Q05431 GO:GO:0016688 SUPFAM:SSF48113 Uniprot:Q05431
Root	Isotig15811	0	15	-5.036	4.38E-05	TAIR|locus:2080938 - symbol:AT3G51000 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004301 "epoxide hydrolase activity" evidence=ISS] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR000639 PRINTS:PR00412 GO:GO:0005829 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0016787 eggNOG:COG0596 HOGENOM:HBG748003 EMBL:AL132980 MEROPS:S33.971 HSSP:O31243 EMBL:AF372961 EMBL:AY074835 IPI:IPI00523692 PIR:T45731 RefSeq:NP_190669.1 UniGene:At.849 ProteinModelPortal:Q9SD45 SMR:Q9SD45 IntAct:Q9SD45 STRING:Q9SD45 PRIDE:Q9SD45 EnsemblPlants:AT3G51000.1 GeneID:824264 KEGG:ath:AT3G51000 TAIR:At3g51000 InParanoid:Q9SD45 OMA:GHHFIQQ PhylomeDB:Q9SD45 ProtClustDB:CLSN2684580 Genevestigator:Q9SD45 Uniprot:Q9SD45
Root	Isotig15817	2	16	-3.129	0.000262867	TAIR|locus:2144246 - symbol:AT5G11460 "AT5G11460" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002688 GenomeReviews:BA000015_GR EMBL:AL163815 InterPro:IPR007650 Pfam:PF04570 HOGENOM:HBG591183 EMBL:BT014982 EMBL:BT026508 IPI:IPI00538137 PIR:T48505 RefSeq:NP_196707.1 UniGene:At.50451 PRIDE:Q9LYE4 EnsemblPlants:AT5G11460.1 GeneID:831017 KEGG:ath:AT5G11460 TAIR:At5g11460 eggNOG:NOG319746 InParanoid:Q9LYE4 OMA:SECRSKE PhylomeDB:Q9LYE4 ProtClustDB:CLSN2916357 Genevestigator:Q9LYE4 Uniprot:Q9LYE4
Root	Isotig15838	31	0	5.825	1.45E-08	TAIR|locus:2179867 - symbol:SAG29 "senescence-associated gene 29" species:3702 "Arabidopsis thaliana" [GO:0016020 "membrane" evidence=IEA;ISS] [GO:0016021 "integral to membrane" evidence=IEA] [GO:0010150 "leaf senescence" evidence=IEP;IMP] [GO:0071446 "cellular response to salicylic acid stimulus" evidence=IEP] [GO:0005887 "integral to plasma membrane" evidence=IDA] [GO:0071215 "cellular response to abscisic acid stimulus" evidence=IEP] [GO:0071470 "cellular response to osmotic stress" evidence=IMP] [GO:0051119 "sugar transmembrane transporter activity" evidence=ISS] InterPro:IPR004316 Pfam:PF03083 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005887 GO:GO:0010150 EMBL:AL391711 GO:GO:0071470 GO:GO:0071215 GO:GO:0071446 GO:GO:0051119 PANTHER:PTHR10791 KO:K15382 eggNOG:NOG308353 EMBL:AY045949 EMBL:AY113934 EMBL:AY087836 EMBL:AF118824 IPI:IPI00530310 RefSeq:NP_196821.1 UniGene:At.46857 TCDB:9.A.58.1.3 EnsemblPlants:AT5G13170.1 GeneID:831156 KEGG:ath:AT5G13170 TAIR:At5g13170 InParanoid:Q9FY94 OMA:WFAYGLF PhylomeDB:Q9FY94 ProtClustDB:CLSN2916510 ArrayExpress:Q9FY94 Genevestigator:Q9FY94 Uniprot:Q9FY94

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig15849	15	0	4.778	0.000105609	MGI|MGI:2444070 - symbol:Nlrc3 "NLR family, CARD domain containing 3" species:10090 "Mus musculus" [GO:0005737 "cytoplasm" evidence=ISO;ISS] [GO:0005524 "ATP binding" evidence=IEA] [GO:0000166 "nucleotide binding" evidence=IEA] [GO:0007249 "I-kappaB kinase/NF-kappaB cascade" evidence=ISO;ISS] [GO:0032088 "negative regulation of NF-kappaB transcription factor activity" evidence=ISO;ISS] [GO:0042110 "T cell activation" evidence=ISS] [GO:0003674 "molecular_function" evidence=ND] MGI:MGI:2444070 GO:GO:0005524 GO:GO:0005737 GO:GO:0042110 GO:GO:0032088 GO:GO:0007249 InterPro:IPR007111 PROSITE:PS50837 GeneTree:ENSGT00650000093077 eggNOG:NOG69209 HOVERGEN:HBG055285 EMBL:AK220314 EMBL:AK079766 EMBL:AK084199 EMBL:AK171971 EMBL:BC130223 IPI:IPI00652368 IPI:IPI00671345 IPI:IPI00677124 IPI:IPI00678735 IPI:IPI00828619 UniGene:Mm.215994 ProteinModelPortal:Q5DU56 SMR:Q5DU56 PhosphoSite:Q5DU56 PRIDE:Q5DU56 Ensembl:ENSMUST00000163478 UCSC:uc007xzc.1 UCSC:uc007xzd.1 UCSC:uc007xze.1 OrthoDB:EOG4BZN26 Bgee:Q5DU56 CleanEx:MM_NLRC3 Genevestigator:Q5DU56 Uniprot:Q5DU56
Root	Isotig15850	0	15	-5.036	4.38E-05	No hit
Root	Isotig15904	0	18	-5.299	6.77E-06	TAIR|locus:2194007 - symbol:ERF73 "AT1G72360" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=ISS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS;TAS] [GO:0005634 "nucleus" evidence=ISS;IDA] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=ISS;IDA] [GO:0034059 "response to anoxia" evidence=IGI] [GO:0009873 "ethylene mediated signaling pathway" evidence=IMP;TAS] [GO:0071369 "cellular response to ethylene stimulus" evidence=IMP] [GO:0071456 "cellular response to hypoxia" evidence=IEP] InterPro:IPR001471 InterPro:IPR016177 Pfam:PF00847 PRINTS:PR00367 PROSITE:PS51032 SMART:SM00380 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005634 GO:GO:0009873 GO:GO:0003677 GO:GO:0071456 GO:GO:0003700 GO:GO:0006351 Gene3D:G3DSA:3.30.730.10 SUPFAM:SSF54171 HSSP:O80337 EMBL:AC016529 GO:GO:0034059 EMBL:BT002063 EMBL:BT006259 IPI:IPI00846814 PIR:E96747 RefSeq:NP_001077812.1 RefSeq:NP_177380.2 UniGene:At.35111 UniGene:At.68119 ProteinModelPortal:Q8H0T5 SMR:Q8H0T5 IntAct:Q8H0T5 PRIDE:Q8H0T5 EnsemblPlants:AT1G72360.1 GeneID:843568 KEGG:ath:AT1G72360 TAIR:At1g72360 eggNOG:NOG321379 HOGENOM:HBG595502 OMA:KKHEPND PhylomeDB:Q8H0T5 ProtClustDB:CLSN2680644 ArrayExpress:Q8H0T5 Genevestigator:Q8H0T5 Uniprot:Q8H0T5
Root	Isotig15995	0	15	-5.036	4.38E-05	TAIR|locus:2153529 - symbol:PRX52 "AT5G05340" species:3702 "Arabidopsis thaliana" [GO:0004601 "peroxidase activity" evidence=ISS] [GO:0006979 "response to oxidative stress" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0005618 "cell wall" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0005829 "cytosol" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR000823 InterPro:IPR002016 InterPro:IPR010255 InterPro:IPR019793 InterPro:IPR019794 Pfam:PF00141 PRINTS:PR00458 PRINTS:PR00461 PROSITE:PS00435 PROSITE:PS00436 PROSITE:PS50873 GO:GO:0005829 GO:GO:0048046 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005618 GO:GO:0005515 GO:GO:0020037 GO:GO:0004601 GO:GO:0042744 HOGENOM:HBG597790 SUPFAM:SSF48113 EMBL:AB010692 KO:K00430 EMBL:AY065270 IPI:IPI00527468 RefSeq:NP_196153.1 UniGene:At.28537 ProteinModelPortal:Q9FLC0 SMR:Q9FLC0 IntAct:Q9FLC0 STRING:Q9FLC0 PeroxiBase:218 PRIDE:Q9FLC0 EnsemblPlants:AT5G05340.1 GeneID:830416 KEGG:ath:AT5G05340 GeneFarm:1905 TAIR:At5g05340 eggNOG:NOG298084 InParanoid:Q9FLC0 OMA:TNFRARI PhylomeDB:Q9FLC0 ProtClustDB:CLSN2916362 ArrayExpress:Q9FLC0 Genevestigator:Q9FLC0 GermOnline:AT5G05340 Uniprot:Q9FLC0
Root	Isotig15997	3	18	-2.714	0.000308932	No hit
Root	Isotig16004	40	0	6.193	1.34E-10	No hit
Root	Isotig16006	18	0	5.041	1.86E-05	TAIR|locus:2012612 - symbol:SAC52 "AT1G14320" species:3702 "Arabidopsis thaliana" [GO:0003735 "structural constituent of ribosome" evidence=ISS] [GO:0006412 "translation" evidence=ISS;TAS] [GO:0015934 "large ribosomal subunit" evidence=ISS] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005730 "nucleolus" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0022625 "cytosolic large ribosomal subunit" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0005840 "ribosome" evidence=IPI] [GO:0071493 "cellular response to UV-B" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR001197 InterPro:IPR016180 InterPro:IPR018255 Pfam:PF00252 PIRSF:PIRSF005590 PROSITE:PS01257 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005774 GO:GO:0009507

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0005515 GO:GO:0006952 GO:GO:0005730 GO:GO:0006412 GO:GO:0003735 EMBL:AC012188 GO:GO:0071493 GO:GO:0022625 eggNOG:COG0197 EMBL:AF428286 EMBL:AF428470 EMBL:AY045866 EMBL:AY113989 EMBL:BT000679 IPI:IPI00538015 PIR:E86277 RefSeq:NP_563945.2 UniGene:At.20914 ProteinModelPortal:Q93VT9 SMR:Q93VT9 STRING:Q93VT9 PRIDE:Q93VT9 EnsemblPlants:AT1G14320.1 GeneID:837993 KEGG:ath:AT1G14320 GeneFarm:164 TAIR:At1g14320 HOGENOM:HBG512729 InParanoid:Q93VT9 KO:K02866 OMA:ICANKYV PhylomeDB:Q93VT9 ProtClustDB:CLSN2682855 ArrayExpress:Q93VT9 Genevestigator:Q93VT9 GermOnline:AT1G14320 SUPFAM:SSF54686 TIGRFAMs:TIGR00279 Uniprot:Q93VT9
Root	Isotig16008	0	11	-4.588	0.000569522	TAIR|locus:2035686 - symbol:AT1G55200 species:3702 "Arabidopsis thaliana" [GO:0004672 "protein kinase activity" evidence=IEA] [GO:0004713 "protein tyrosine kinase activity" evidence=IEA] [GO:0005524 "ATP binding" evidence=IEA] [GO:0006468 "protein phosphorylation" evidence=IEA] [GO:0016301 "kinase activity" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] InterPro:IPR000719 InterPro:IPR001245 InterPro:IPR008266 InterPro:IPR011009 Pfam:PF07714 PROSITE:PS00109 PROSITE:PS50011 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005886 GO:GO:0005524 eggNOG:COG0515 SUPFAM:SSF56112 HSSP:P36897 EMBL:AC027034 GO:GO:0004713 InterPro:IPR014729 Gene3D:G3DSA:3.40.50.620 UniGene:At.66851 ProtClustDB:CLSN2684799 EMBL:AY063963 EMBL:AY096404 IPI:IPI00534365 PIR:G96593 RefSeq:NP_175916.1 UniGene:At.27126 ProteinModelPortal:Q9C890 SMR:Q9C890 PRIDE:Q9C890 EnsemblPlants:AT1G55200.1 GeneID:841963 KEGG:ath:AT1G55200 TAIR:At1g55200 HOGENOM:HBG320272 InParanoid:Q9C890 OMA:PWISEYL PhylomeDB:Q9C890 ArrayExpress:Q9C890 Genevestigator:Q9C890 Uniprot:Q9C890
Root	Isotig16027	6	50	-3.188	7.71E-11	TAIR|locus:2084031 - symbol:PIP2A "AT3G53420" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=ISS] [GO:0015250 "water channel activity" evidence=ISS;IDA] [GO:0016020 "membrane" evidence=ISS;IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA;TAS] [GO:0005773 "vacuole" evidence=IDA] [GO:0009414 "response to water deprivation" evidence=IEP] [GO:0080170 "hydrogen peroxide transmembrane transport" evidence=IDA] [GO:0031625 "ubiquitin protein ligase binding" evidence=IPI] [GO:0009737 "response to abscisic acid stimulus" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0006833 "water transport" evidence=IDA] InterPro:IPR000425 InterPro:IPR012269 InterPro:IPR022357 Pfam:PF00230 PRINTS:PR00783 PROSITE:PS00221 GO:GO:0016021 GO:GO:0005886 GO:GO:0009506 GO:GO:0009737 GO:GO:0005773 GO:GO:0009507 EMBL:CP002686 GenomeReviews:BA000014_GR EMBL:AL132966 GO:GO:0009414 GO:GO:0031625 InterPro:IPR023271 Gene3D:G3DSA:1.20.1080.10 SUPFAM:SSF81338 eggNOG:COG0580 HOGENOM:HBG705794 PANTHER:PTHR19139 TIGRFAMs:TIGR00861 GO:GO:0015250 GO:GO:0080170 KO:K09872 EMBL:X75883 EMBL:AY039579 EMBL:AY044327 EMBL:AY056085 EMBL:AF428426 EMBL:AY072374 EMBL:AY087854 IPI:IPI00532482 PIR:S44084 RefSeq:NP_001030851.1 RefSeq:NP_190910.1 UniGene:At.47609 ProteinModelPortal:P43286 SMR:P43286 MINT:MINT-6951259 STRING:P43286 TCDB:1.A.8.11.4 PRIDE:P43286 ProMEX:P43286 EnsemblPlants:AT3G53420.1 EnsemblPlants:AT3G53420.2 GeneID:824510 KEGG:ath:AT3G53420 GeneFarm:4866 TAIR:At3g53420 InParanoid:P43286 OMA:VFMAITI PhylomeDB:P43286 ProtClustDB:CLSN2683965 ArrayExpress:P43286 Genevestigator:P43286 GermOnline:AT3G53420 Uniprot:P43286
Root	Isotig16038	0	11	-4.588	0.000569522	SGD|S000028422 - symbol:TAR1 "Mitochondrial protein potentially involved in respiratory metabolism" species:4932 "Saccharomyces cerevisiae" [GO:0003674 "molecular_function" evidence=ND] [GO:0043457 "regulation of cellular respiration" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IEA;IMP] SGD:S000028422 GO:GO:0005739 EMBL:BK006945 EMBL:U53879 GO:GO:0043457 EMBL:Z73326 EMBL:AF479964 RefSeq:NP_690845.1 ProteinModelPortal:Q8TGM6 STRING:Q8TGM6 EnsemblFungi:YLR154W-C GeneID:1466405 KEGG:sce:YLR154W-C CYGD:YLR154w-c eggNOG:NOG79861 OMA:SCSKEHR OrthoDB:EOG466ZX8 NextBio:967146 Genevestigator:Q8TGM6 GermOnline:YLR154W-C Uniprot:Q8TGM6
Root	Isotig16050	3	21	-2.936	4.98E-05	TAIR|locus:2094977 - symbol:DELTA-TIP "AT3G16240" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=ISS] [GO:0015250 "water channel activity" evidence=ISS;IDA] [GO:0016020 "membrane" evidence=ISS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0015204 "urea transmembrane transporter activity" evidence=IGI] [GO:0015840 "urea transport" evidence=IGI] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0015200 "methylammonium transmembrane transporter activity" evidence=IDA] [GO:0051739 "ammonia transmembrane

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						transporter activity" evidence=IGI] [GO:0005618 "cell wall" evidence=IDA] [GO:0009505 "plant-type cell wall" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0000326 "protein storage vacuole" evidence=IDA] [GO:0042807 "central vacuole" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] [GO:0006833 "water transport" evidence=IDA] [GO:0009705 "plant-type vacuole membrane" evidence=IDA] InterPro:IPR000425 InterPro:IPR012269 InterPro:IPR022357 Pfam:PF00230 PRINTS:PR00783 PROSITE:PS00221 GO:GO:0016021 GO:GO:0005886 GO:GO:0009506 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0009941 EMBL:AB023046 GO:GO:0009705 GO:GO:0009505 GO:GO:0015200 GO:GO:0051739 InterPro:IPR023271 Gene3D:G3DSA:1.20.1080.10 SUPFAM:SSF81338 eggNOG:COG0580 HOGENOM:HBG705794 PANTHER:PTHR19139 TIGRFAMs:TIGR00861 GO:GO:0015250 GO:GO:0000326 UniGene:At.32719 KO:K09873 GO:GO:0042807 EMBL:U39485 EMBL:U39486 EMBL:AY065181 EMBL:AY081622 EMBL:AK229954 EMBL:AY085921 EMBL:Z18064 EMBL:Z29043 EMBL:Z29044 IPI:IPI00524268 RefSeq:NP_188245.1 UniGene:At.23571 UniGene:At.6081 UniGene:At.71329 ProteinModelPortal:Q41951 SMR:Q41951 IntAct:Q41951 STRING:Q41951 PRIDE:Q41951 EnsemblPlants:AT3G16240.1 GeneID:820870 KEGG:ath:AT3G16240 GeneFarm:2255 TAIR:At3g16240 InParanoid:Q41951 OMA:MSGNIAF PhylomeDB:Q41951 ProtClustDB:CLSN2713597 ArrayExpress:Q41951 Genevestigator:Q41951 GermOnline:AT3G16240 Uniprot:Q41951
Root	Isotig16063	0	12	-4.714	0.000297064	TAIR|locus:2082543 - symbol:BGL2 "AT3G57260" species:3702 "Arabidopsis thaliana" [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=ISS] [GO:0009627 "systemic acquired resistance" evidence=IEP;NAS] [GO:0004338 "glucan exo-1,3-beta-glucosidase activity" evidence=ISS] [GO:0005773 "vacuole" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0048046 "apoplast" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0008810 "cellulase activity" evidence=TAS] InterPro:IPR000490 InterPro:IPR013781 Pfam:PF00332 PROSITE:PS00587 GO:GO:0048046 GO:GO:0005773 GO:GO:0005618 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005515 GO:GO:0043169 InterPro:IPR017853 Gene3D:G3DSA:3.20.20.80 SUPFAM:SSF51445 GO:GO:0005975 GO:GO:0009409 GO:GO:0009627 EMBL:AL137080 CAZy:GH17 GO:GO:0042973 GO:GO:0008810 HOGENOM:HBG605194 EMBL:M90509 EMBL:M58462 EMBL:AY099668 EMBL:AY128847 EMBL:AY086134 IPI:IPI00547460 PIR:JQ1694 PIR:T45804 RefSeq:NP_191285.1 UniGene:At.22313 ProteinModelPortal:P33157 SMR:P33157 IntAct:P33157 STRING:P33157 PRIDE:P33157 EnsemblPlants:AT3G57260.1 GeneID:824893 KEGG:ath:AT3G57260 TAIR:At3g57260 eggNOG:NOG268889 InParanoid:P33157 OMA:VENAKTY PhylomeDB:P33157 ProtClustDB:CLSN2915357 ArrayExpress:P33157 Genevestigator:P33157 GermOnline:AT3G57260 Uniprot:P33157
Root	Isotig16078	28	78	-1.607	7.14E-08	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig16134	33	0	5.915	5.02E-09	UNIPROTKB|A8CVF3 - symbol:DHN1 "Dehydrin DHN1" species:82927 "Avicennia marina" [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0010555 "response to mannitol stimulus" evidence=IEP] [GO:0042631 "cellular response to water deprivation" evidence=IEP] [GO:0071472 "cellular response to salt stress" evidence=IEP] [GO:0071482 "cellular response to light stimulus" evidence=IEP] InterPro:IPR000167 Pfam:PF00257 PROSITE:PS00315 PROSITE:PS00823 GO:GO:0005634 GO:GO:0005737 GO:GO:0071472 GO:GO:0042631 GO:GO:0010555 EMBL:EU121850 EMBL:EU121851 GO:GO:0071482 Uniprot:A8CVF3
Root	Isotig16149	2	16	-3.129	0.000262867	TAIR|locus:2827916 - symbol:ARAC1 "Arabidopsis RAC-like 1" species:3702 "Arabidopsis thaliana" [GO:0005525 "GTP binding" evidence=IEA;ISS] [GO:0009738 "abscisic acid mediated signaling pathway" evidence=TAS] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0005819 "spindle" evidence=IDA] [GO:0009524 "phragmoplast" evidence=IDA] [GO:0009734 "auxin mediated signaling pathway" evidence=IMP] InterPro:IPR001806 InterPro:IPR003578 InterPro:IPR005225 Pfam:PF00071 PRINTS:PR00449 PROSITE:PS51420 SMART:SM00174 GO:GO:0005525 TIGRFAMs:TIGR00231 GO:GO:0005634 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009738 GO:GO:0009734 GO:GO:0016020 GO:GO:0005819

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0007264 eggNOG:COG1100 HOGENOM:HBG745225 GO:GO:0009524 KO:K07975 ProtClustDB:CLSN2682707 EMBL:U64919 EMBL:U41295 EMBL:AF115466 EMBL:AY093046 EMBL:BT000393 IPI:IPI00525208 PIR:T08857 RefSeq:NP_001077910.1 RefSeq:NP_179371.1 UniGene:At.23460 ProteinModelPortal:Q38902 SMR:Q38902 DIP:DIP-29819N STRING:Q38902 PRIDE:Q38902 EnsemblPlants:AT2G17800.1 EnsemblPlants:AT2G17800.2 GeneID:816290 KEGG:ath:AT2G17800 GeneFarm:4159 TAIR:At2g17800 InParanoid:Q38902 OMA:SSMANDI PhylomeDB:Q38902 ArrayExpress:Q38902 Genevestigator:Q38902 GermOnline:AT2G17800 Uniprot:Q38902
Root	Isotig16244	0	11	-4.588	0.000569522	TAIR|locus:1006230719 - symbol:AT1G13635 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA;ISS] [GO:0005575 "cellular_component" evidence=ND] [GO:0006281 "DNA repair" evidence=IEA] [GO:0006284 "base-excision repair" evidence=IEA] [GO:0008725 "DNA-3-methyladenine glycosylase activity" evidence=IEA] InterPro:IPR005019 InterPro:IPR011257 Pfam:PF03352 GenomeReviews:CT485782_GR eggNOG:COG2818 HOGENOM:HBG747469 GO:GO:0008725 GO:GO:0006284 Gene3D:G3DSA:1.10.340.30 SUPFAM:SSF48150 EMBL:AC027656 HSSP:P05100 IPI:IPI00521326 PIR:E86269 ProteinModelPortal:Q9LMY4 SMR:Q9LMY4 TAIR:At1g13635 InParanoid:Q9LMY4 PhylomeDB:Q9LMY4 Genevestigator:Q9LMY4 Uniprot:Q9LMY4
Root	Isotig16276	1	16	-4.129	5.13E-05	TAIR|locus:2030091 - symbol:AT1G76800 "AT1G76800" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0071281 "cellular response to iron ion" evidence=IEP] [GO:0071369 "cellular response to ethylene stimulus" evidence=IEP] [GO:0071732 "cellular response to nitric oxide" evidence=IEP] [GO:0010039 "response to iron ion" evidence=IEP] Pfam:PF01988 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005774 GO:GO:0071281 GO:GO:0006811 GO:GO:0071732 EMBL:AC010718 GO:GO:0055072 GO:GO:0071369 eggNOG:COG1814 HOGENOM:HBG748253 InterPro:IPR008217 ProtClustDB:CLSN2682939 EMBL:BT014942 EMBL:BT015634 IPI:IPI00523449 PIR:F96796 RefSeq:NP_177806.1 UniGene:At.34609 STRING:Q9SRD3 PRIDE:Q9SRD3 GeneID:844014 KEGG:ath:AT1G76800 TAIR:At1g76800 InParanoid:Q9SRD3 OMA:LMVFGWL PhylomeDB:Q9SRD3 Genevestigator:Q9SRD3 Uniprot:Q9SRD3
Root	Isotig16298	1	12	-3.714	0.000699736	TAIR|locus:2009031 - symbol:AT1G34060 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0016846 "carbon-sulfur lyase activity" evidence=IEA;ISS] [GO:0030170 "pyridoxal phosphate binding" evidence=IEA] InterPro:IPR006947 InterPro:IPR006948 InterPro:IPR015421 InterPro:IPR015422 Pfam:PF04863 Pfam:PF04864 GO:GO:0016021 EMBL:CP002684 GO:GO:0030170 InterPro:IPR015424 Gene3D:G3DSA:3.40.640.10 Gene3D:G3DSA:3.90.1150.10 SUPFAM:SSF53383 GO:GO:0008483 GO:GO:0016846 EMBL:AC015446 Gene3D:G3DSA:2.10.25.30 HSSP:Q01594 eggNOG:NOG290378 ProtClustDB:CLSN2679564 EMBL:AY058162 IPI:IPI00536735 PIR:E86464 RefSeq:NP_564435.1 UniGene:At.26614 ProteinModelPortal:Q93Z38 SMR:Q93Z38 PRIDE:Q93Z38 GeneID:840303 KEGG:ath:AT1G34060 TAIR:At1g34060 InParanoid:Q9FX14 Genevestigator:Q93Z38 Uniprot:Q93Z38
Root	Isotig16364	1	61	-6.060	1.00E-16	TAIR|locus:2116987 - symbol:TIP1;3 "AT4G01470" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=ISS] [GO:0015250 "water channel activity" evidence=ISS;IDA] [GO:0016020 "membrane" evidence=ISS] [GO:0006833 "water transport" evidence=IDA] [GO:0015204 "urea transmembrane transporter activity" evidence=IDA] [GO:0015840 "urea transport" evidence=IDA] InterPro:IPR000425 InterPro:IPR022357 Pfam:PF00230 PRINTS:PR00783 PROSITE:PS00221 GO:GO:0016021 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005774 GO:GO:0006950 InterPro:IPR023271 Gene3D:G3DSA:1.20.1080.10 SUPFAM:SSF81338 HOGENOM:HBG705794 PANTHER:PTHR19139 GO:GO:0015250 EMBL:AF096370 EMBL:AL161492 GO:GO:0015204 KO:K09873 ProtClustDB:PLN00027 EMBL:DQ446793 EMBL:DQ653172 IPI:IPI00524657 PIR:T01947 RefSeq:NP_192056.1 UniGene:At.65315 ProteinModelPortal:O82598 SMR:O82598 STRING:O82598 TCDB:1.A.8.10.6 PRIDE:O82598 EnsemblPlants:AT4G01470.1 GeneID:828051 KEGG:ath:AT4G01470 GeneFarm:4856 TAIR:At4g01470 eggNOG:NOG312454 InParanoid:O82598 OMA:IGSNGHE PhylomeDB:O82598 ArrayExpress:O82598 Genevestigator:O82598 Uniprot:O82598
Root	Isotig16375	2	39	-4.414	1.25E-10	TAIR|locus:2084031 - symbol:PIP2A "AT3G53420" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=ISS] [GO:0015250 "water channel activity" evidence=ISS;IDA] [GO:0016020 "membrane" evidence=ISS;IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA;TAS] [GO:0005773 "vacuole" evidence=IDA] [GO:0009414 "response to water deprivation" evidence=IEP] [GO:0080170 "hydrogen peroxide transmembrane transport" evidence=IDA] [GO:0031625 "ubiquitin

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						protein ligase binding" evidence=IPI] [GO:0009737 "response to abscisic acid stimulus" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0006833 "water transport" evidence=IDA] InterPro:IPR000425 InterPro:IPR012269 InterPro:IPR022357 Pfam:PF00230 PRINTS:PR00783 PROSITE:PS00221 GO:GO:0016021 GO:GO:0005886 GO:GO:0009506 GO:GO:0009737 GO:GO:0005773 GO:GO:0009507 EMBL:CP002686 GenomeReviews:BA000014_GR EMBL:AL132966 GO:GO:0009414 GO:GO:0031625 InterPro:IPR023271 Gene3D:G3DSA:1.20.1080.10 SUPFAM:SSF81338 eggNOG:COG0580 HOGENOM:HBG705794 PANTHER:PTHR19139 TIGRFAMs:TIGR00861 GO:GO:0015250 GO:GO:0080170 KO:K09872 EMBL:X75883 EMBL:AY039579 EMBL:AY044327 EMBL:AY056085 EMBL:AF428426 EMBL:AY072374 EMBL:AY087854 IPI:IPI00532482 PIR:S44084 RefSeq:NP_001030851.1 RefSeq:NP_190910.1 UniGene:At.47609 ProteinModelPortal:P43286 SMR:P43286 MINT:MINT-6951259 STRING:P43286 TCDB:1.A.8.11.4 PRIDE:P43286 ProMEX:P43286 EnsemblPlants:AT3G53420.1 EnsemblPlants:AT3G53420.2 GeneID:824510 KEGG:ath:AT3G53420 GeneFarm:4866 TAIR:At3g53420 InParanoid:P43286 OMA:VFMAITI PhylomeDB:P43286 ProtClustDB:CLSN2683965 ArrayExpress:P43286 Genevestigator:P43286 GermOnline:AT3G53420 Uniprot:P43286
Root	Isotig16376	112	0	7.678	7.03E-25	TAIR|locus:2093307 - symbol:AT3G15670 "AT3G15670" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0009793 "embryo development ending in seed dormancy" evidence=ISS] [GO:0005634 "nucleus" evidence=IDA] GO:GO:0005634 EMBL:CP002686 EMBL:AB017071 ProtClustDB:CLSN2679745 EMBL:AY040026 EMBL:AY054162 EMBL:AY079410 IPI:IPI00542660 RefSeq:NP_188188.1 UniGene:At.5382 STRING:Q9LW12 PRIDE:Q9LW12 ProMEX:Q9LW12 EnsemblPlants:AT3G15670.1 GeneID:820810 KEGG:ath:AT3G15670 TAIR:At3g15670 InParanoid:Q9LW12 OMA:QYTKETA PhylomeDB:Q9LW12 ArrayExpress:Q9LW12 Genevestigator:Q9LW12 Uniprot:Q9LW12
Root	Isotig16377	27	1	4.626	2.33E-07	TAIR|locus:2171417 - symbol:AT5G16550 "AT5G16550" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002688 EMBL:AB005242 UniGene:At.66763 IPI:IPI00527710 RefSeq:NP_568333.1 PRIDE:Q9FFC9 EnsemblPlants:AT5G16550.1 GeneID:831517 KEGG:ath:AT5G16550 TAIR:At5g16550 InParanoid:Q9FFC9 OMA:REVNIES PhylomeDB:Q9FFC9 ProtClustDB:CLSN2689715 Genevestigator:Q9FFC9 Uniprot:Q9FFC9
Root	Isotig16410	2	14	-2.936	0.000925454	No hit
Root	Isotig16430	44	4	3.330	2.70E-09	UNIPROTKB|Q9AVB0 - symbol:Q9AVB0 "Lectin-B" species:3527 "Phytolacca americana" [GO:0008061 "chitin binding" evidence=ISS] [GO:0045840 "positive regulation of mitosis" evidence=IDA] InterPro:IPR001002 InterPro:IPR018371 Pfam:PF00187 PRINTS:PR00451 ProDom:PD000609 PROSITE:PS00026 PROSITE:PS50941 SMART:SM00270 GO:GO:0051781 GO:GO:0005529 GO:GO:0045840 CAZy:CBM18 GO:GO:0008061 Gene3D:G3DSA:3.30.60.10 SUPFAM:SSF57016 EMBL:AB059241 PIR:JC5559 ProteinModelPortal:Q9AVB0 SMR:Q9AVB0 Uniprot:Q9AVB0
Root	Isotig16451	1	20	-4.451	3.92E-06	No hit
Root	Isotig16495	50	6	2.930	2.24E-09	TAIR|locus:2151326 - symbol:GSTL3 "Glutathione transferase L3" species:3702 "Arabidopsis thaliana" [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR004045 PROSITE:PS50404 GO:GO:0005829 GO:GO:0046686 EMBL:CP002688 GO:GO:0009636 InterPro:IPR012336 Gene3D:G3DSA:3.40.30.10 SUPFAM:SSF52833 InterPro:IPR010987 Gene3D:G3DSA:1.20.1050.10 SUPFAM:SSF47616 PROSITE:PS50405 EMBL:AL162973 InterPro:IPR017933 GO:GO:0004364 eggNOG:COG0625 HSSP:O65032 ProtClustDB:CLSN2687366 EMBL:AY140069 EMBL:BT002166 EMBL:AK227162 EMBL:AY085126 IPI:IPI00535440 PIR:T48300 RefSeq:NP_195899.1 UniGene:At.33363 ProteinModelPortal:Q9LZ06 SMR:Q9LZ06 STRING:Q9LZ06 PRIDE:Q9LZ06 EnsemblPlants:AT5G02790.1 GeneID:831798 KEGG:ath:AT5G02790 TAIR:At5g02790 InParanoid:Q9LZ06 OMA:IPFVERF PhylomeDB:Q9LZ06 Genevestigator:Q9LZ06 Uniprot:Q9LZ06
Root	Isotig16533	0	12	-4.714	0.000297064	TAIR|locus:2041399 - symbol:CYP709B2 ""cytochrome P450, family 709, subfamily B, polypeptide 2"" species:3702 "Arabidopsis thaliana" [GO:0004497 "monooxygenase activity" evidence=IEA] [GO:0005506 "iron ion binding" evidence=IEA] [GO:0009055 "electron carrier activity" evidence=IEA] [GO:0019825 "oxygen binding" evidence=ISS] [GO:0020037 "heme binding" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] InterPro:IPR001128 InterPro:IPR002401 InterPro:IPR017972 Pfam:PF00067 PRINTS:PR00385 PRINTS:PR00463 PROSITE:PS00086 GenomeReviews:CT485783_GR GO:GO:0009055 GO:GO:0004497 EMBL:AC004411 eggNOG:COG2124 GO:GO:0020037 Gene3D:G3DSA:1.10.630.10 SUPFAM:SSF48264 GO:GO:0016705 HSSP:P14779 HOGENOM:HBG715383 EMBL:BT011625 EMBL:BT014808 IPI:IPI00524075 PIR:T02192

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						ProteinModelPortal:O80729 SMR:O80729 PRIDE:O80729 TAIR:At2g46950 InParanoid:O80729 PhylomeDB:O80729 ArrayExpress:O80729 Genevestigator:O80729 Uniprot:O80729
Root	Isotig16625	8	26	-1.829	0.00065698	TAIR|locus:2009655 - symbol:ERF8 "AT1G53170" species:3702 "Arabidopsis thaliana" [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS;TAS] [GO:0003677 "DNA binding" evidence=TAS] [GO:0005634 "nucleus" evidence=IC] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=TAS] [GO:0009873 "ethylene mediated signaling pathway" evidence=TAS] InterPro:IPR001471 InterPro:IPR016177 Pfam:PF00847 PRINTS:PR00367 PROSITE:PS51032 SMART:SM00380 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005634 GO:GO:0009873 GO:GO:0003677 GO:GO:0003700 GO:GO:0006351 EMBL:AC008007 Gene3D:G3DSA:3.30.730.10 SUPFAM:SSF54171 HOGENOM:HBG744062 ProtClustDB:CLSN2679790 EMBL:AB036884 EMBL:AK117541 EMBL:BT005401 IPI:IPI00546471 PIR:D96572 RefSeq:NP_175725.1 UniGene:At.4604 ProteinModelPortal:Q9MAI5 SMR:Q9MAI5 IntAct:Q9MAI5 PRIDE:Q9MAI5 EnsemblPlants:AT1G53170.1 GeneID:841751 KEGG:ath:AT1G53170 TAIR:At1g53170 eggNOG:NOG271218 InParanoid:Q9MAI5 OMA:HESNAAK PhylomeDB:Q9MAI5 ArrayExpress:Q9MAI5 Genevestigator:Q9MAI5 GermOnline:AT1G53170 Uniprot:Q9MAI5
Root	Isotig16645	1	16	-4.129	5.13E-05	TAIR|locus:2061171 - symbol:WLIM2a "AT2G39900" species:3702 "Arabidopsis thaliana" [GO:0051015 "actin filament binding" evidence=IDA] [GO:0051017 "actin filament bundle assembly" evidence=IDA] Pfam:PF00412 InterPro:IPR001841 InterPro:IPR001781 PROSITE:PS00478 PROSITE:PS50023 SMART:SM00132 SMART:SM00184 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0008270 GO:GO:0051015 GO:GO:0051017 Gene3D:G3DSA:2.10.110.10 EMBL:AF002109 HOGENOM:HBG403138 eggNOG:NOG294681 HSSP:P32965 EMBL:AY094448 EMBL:AY122901 IPI:IPI00520072 PIR:G84822 RefSeq:NP_181519.1 UniGene:At.42956 ProteinModelPortal:O04193 SMR:O04193 IntAct:O04193 STRING:O04193 PRIDE:O04193 EnsemblPlants:AT2G39900.1 GeneID:818577 KEGG:ath:AT2G39900 TAIR:At2g39900 InParanoid:O04193 OMA:HLIKCAS PhylomeDB:O04193 ProtClustDB:CLSN2683380 ArrayExpress:O04193 Genevestigator:O04193 Uniprot:O04193
Root	Isotig16670	0	22	-5.588	6.01E-07	TAIR|locus:2055572 - symbol:SPX3 "AT2G45130" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0016036 "cellular response to phosphate starvation" evidence=IEP] [GO:0080040 "positive regulation of cellular response to phosphate starvation" evidence=IMP] EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0016036 InterPro:IPR004331 Pfam:PF03105 PROSITE:PS51382 GO:GO:0080040 EMBL:BT020235 EMBL:BT020499 IPI:IPI00520153 PIR:G84886 RefSeq:NP_182038.1 UniGene:At.50140 EnsemblPlants:AT2G45130.1 GeneID:819120 KEGG:ath:AT2G45130 TAIR:At2g45130 eggNOG:NOG290986 OMA:CGHNDEM PhylomeDB:Q5PP62 ProtClustDB:CLSN2913033 Genevestigator:Q5PP62 Uniprot:Q5PP62
Root	Isotig16677	33	4	2.915	1.26E-06	UNIPROTKB|P06750 - symbol:P06750 "Agglutinin" species:3988 "Ricinus communis" [GO:0005515 "protein binding" evidence=IPI] [GO:0005783 "endoplasmic reticulum" evidence=IDA] InterPro:IPR001574 InterPro:IPR016138 InterPro:IPR016139 InterPro:IPR017988 InterPro:IPR017989 Pfam:PF00161 PRINTS:PR00396 PROSITE:PS00275 GO:GO:0005783 GO:GO:0005515 GO:GO:0006952 GO:GO:0017148 GO:GO:0000166 GO:GO:0005529 GO:GO:0030598 InterPro:IPR000772 Gene3D:G3DSA:3.40.420.10 Gene3D:G3DSA:4.10.470.10 Pfam:PF00652 SMART:SM00458 SUPFAM:SSF56371 SUPFAM:SSF50370 PROSITE:PS50231 CAZy:CBM13 EMBL:M12089 EMBL:S40368 PIR:A24261 PDB:1RZO PDBsum:1RZO ProteinModelPortal:P06750 SMR:P06750 GlycoSuiteDB:P06750 Uniprot:P06750
Root	Isotig16718	1	15	-4.036	9.83E-05	TAIR|locus:2079522 - symbol:AT3G62040 species:3702 "Arabidopsis thaliana" [GO:0016787 "hydrolase activity" evidence=IEA;ISS] InterPro:IPR006402 EMBL:CP002686 GenomeReviews:BA000014_GR InterPro:IPR023214 Gene3D:G3DSA:3.40.50.1000 SUPFAM:SSF56784 GO:GO:0016787 eggNOG:COG1011 TIGRFAMs:TIGR01509 EMBL:AL138642 UniGene:At.24742 UniGene:At.48797 InterPro:IPR010237 TIGRFAMs:TIGR01993 EMBL:BT010899 IPI:IPI00520634 PIR:T47996 RefSeq:NP_191763.3 ProteinModelPortal:Q9M262 SMR:Q9M262 PRIDE:Q9M262 EnsemblPlants:AT3G62040.1 GeneID:825377 KEGG:ath:AT3G62040 TAIR:At3g62040 HOGENOM:HBG410732 InParanoid:Q9M262 OMA:HAFNTIC PhylomeDB:Q9M262 ProtClustDB:CLSN2681592 Genevestigator:Q9M262 Uniprot:Q9M262
Root	Isotig16756	0	11	-4.588	0.000569522	TAIR|locus:2020312 - symbol:GSTU25 "AT1G17180" species:3702 "Arabidopsis thaliana" [GO:0004364 "glutathione transferase activity" evidence=ISS] [GO:0005737 "cytoplasm" evidence=NAS] [GO:0009407 "toxin catabolic process" evidence=TAS] InterPro:IPR004045 PROSITE:PS50404 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0009636 InterPro:IPR012336

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						Gene3D:G3DSA:3.40.30.10 SUPFAM:SSF52833 InterPro:IPR010987 Gene3D:G3DSA:1.20.1050.10 SUPFAM:SSF47616 PROSITE:PS50405 EMBL:AC007651 InterPro:IPR017933 GO:GO:0004364 eggNOG:COG0625 HSSP:O65032 GO:GO:0009407 HOGENOM:HBG749301 EMBL:AK118907 EMBL:BT005643 IPI:IPI00519758 PIR:H86307 RefSeq:NP_173161.1 UniGene:At.41849 ProteinModelPortal:Q9SHH7 SMR:Q9SHH7 IntAct:Q9SHH7 STRING:Q9SHH7 PRIDE:Q9SHH7 EnsemblPlants:AT1G17180.1 GeneID:838289 KEGG:ath:AT1G17180 TAIR:At1g17180 InParanoid:Q9SHH7 OMA:EHEAGKK PhylomeDB:Q9SHH7 ProtClustDB:CLSN2681880 ArrayExpress:Q9SHH7 Genevestigator:Q9SHH7 Uniprot:Q9SHH7
Root	Isotig16758	2	14	-2.936	0.000925454	TAIR|locus:2102926 - symbol:AT3G30390 "AT3G30390" species:3702 "Arabidopsis thaliana" [GO:0006865 "amino acid transport" evidence=ISS] [GO:0015171 "amino acid transmembrane transporter activity" evidence=ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0005773 "vacuole" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] GO:GO:0016021 GO:GO:0005774 EMBL:CP002686 InterPro:IPR013057 Pfam:PF01490 HOGENOM:HBG601878 EMBL:AY052201 EMBL:AF428287 EMBL:AP001314 IPI:IPI00520585 RefSeq:NP_001030795.1 RefSeq:NP_566854.1 UniGene:At.21575 ProteinModelPortal:Q9LI61 STRING:Q9LI61 PRIDE:Q9LI61 EnsemblPlants:AT3G30390.1 EnsemblPlants:AT3G30390.2 GeneID:822740 KEGG:ath:AT3G30390 TAIR:At3g30390 InParanoid:Q9LI61 OMA:AFICHYN PhylomeDB:Q9LI61 ProtClustDB:CLSN2687270 Genevestigator:Q9LI61 Uniprot:Q9LI61
Root	Isotig16765	13	40	-1.750	4.15E-05	TAIR|locus:2099906 - symbol:TPI "AT3G55440" species:3702 "Arabidopsis thaliana" [GO:0004807 "triose-phosphate isomerase activity" evidence=ISS;IDA] [GO:0005829 "cytosol" evidence=ISS;IDA] [GO:0008152 "metabolic process" evidence=ISS] [GO:0006096 "glycolysis" evidence=IC] [GO:0044262 "cellular carbohydrate metabolic process" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0010043 "response to zinc ion" evidence=IEP] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR000652 InterPro:IPR013785 InterPro:IPR020861 InterPro:IPR022896 Pfam:PF00121 PROSITE:PS00171 PROSITE:PS51440 GO:GO:0005829 GO:GO:0005739 GO:GO:0005886 GO:GO:0009506 GO:GO:0048046 GO:GO:0009570 GO:GO:0046686 GO:GO:0005774 GO:GO:0005618 EMBL:CP002686 GenomeReviews:BA000014_GR Gene3D:G3DSA:3.20.20.70 GO:GO:0010043 GO:GO:0006098 GO:GO:0005507 GO:GO:0006094 GO:GO:0009651 GO:GO:0006096 EMBL:AL132975 eggNOG:COG0149 HOGENOM:HBG708281 KO:K01803 GO:GO:0004807 PANTHER:PTHR21139 SUPFAM:SSF51351 TIGRFAMs:TIGR00419 EMBL:U02949 EMBL:AF375426 EMBL:AY074822 IPI:IPI00549121 PIR:T47683 PIR:T50646 RefSeq:NP_191104.1 UniGene:At.24563 UniGene:At.31873 ProteinModelPortal:P48491 SMR:P48491 IntAct:P48491 STRING:P48491 SWISS-2DPAGE:P48491 World-2DPAGE:0003:P48491 PRIDE:P48491 ProMEX:P48491 EnsemblPlants:AT3G55440.1 GeneID:824710 KEGG:ath:AT3G55440 TAIR:At3g55440 InParanoid:P48491 OMA:ISGQWPR PhylomeDB:P48491 ProtClustDB:PLN02561 BioCyc:ARA:AT3G55440-MONOMER BioCyc:MetaCyc:AT3G55440-MONOMER ArrayExpress:P48491 Genevestigator:P48491 GermOnline:AT3G55440 Uniprot:P48491
Root	Isotig16776	130	0	7.893	4.24E-28	No hit
Root	Isotig16782	70	28	1.193	9.92E-05	TAIR|locus:2012773 - symbol:ERD9 "AT1G10370" species:3702 "Arabidopsis thaliana" [GO:0004364 "glutathione transferase activity" evidence=ISS;IDA] [GO:0005737 "cytoplasm" evidence=NAS] [GO:0009407 "toxin catabolic process" evidence=TAS] [GO:0009507 "chloroplast" evidence=IDA] [GO:0080167 "response to karrikin" evidence=IEP] [GO:0006749 "glutathione metabolic process" evidence=IMP] [GO:0009704 "de-etiolation" evidence=IMP] [GO:0048527 "lateral root development" evidence=IMP] [GO:0060416 "response to growth hormone stimulus" evidence=IEP] [GO:0009651 "response to salt stress" evidence=IMP] [GO:0080148 "negative regulation of response to water deprivation" evidence=IMP] InterPro:IPR004045 PROSITE:PS50404 InterPro:IPR004046 Pfam:PF00043 EMBL:CP002684 GO:GO:0005829 GO:GO:0009507 GO:GO:0009651 GO:GO:0080167 GO:GO:0048527 GO:GO:0009636 GO:GO:0040008 InterPro:IPR012336 Gene3D:G3DSA:3.40.30.10 SUPFAM:SSF52833 InterPro:IPR010987 Gene3D:G3DSA:1.20.1050.10 SUPFAM:SSF47616 PROSITE:PS50405 GO:GO:0060416 EMBL:AC005489 GO:GO:0006749 InterPro:IPR017933 GO:GO:0004364 GO:GO:0009407 eggNOG:NOG288793 HOGENOM:HBG749301 HSSP:O04941 EMBL:AB039930 EMBL:AF288191 EMBL:BT023743 IPI:IPI00532578 RefSeq:NP_172508.4 UniGene:At.11290 ProteinModelPortal:Q9FUS8

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						SMR:Q9FUS8 PRIDE:Q9FUS8 EnsemblPlants:AT1G10370.1 GeneID:837576 KEGG:ath:AT1G10370 TAIR:At1g10370 InParanoid:Q9FUS8 ProtClustDB:CLSN2679578 Genevestigator:Q9FUS8 GO:GO:0009704 GO:GO:0080148 Uniprot:Q9FUS8
Root	Isotig16819	15	1	3.778	0.000266457	TAIR|locus:2102112 - symbol:AT3G01170 species:3702 "Arabidopsis thaliana" [GO:0003735 "structural constituent of ribosome" evidence=IEA] [GO:0005622 "intracellular" evidence=IEA] [GO:0005840 "ribosome" evidence=IEA] [GO:0006412 "translation" evidence=IEA] InterPro:IPR008195 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0006412 GO:GO:0003735 GO:GO:0005840 PANTHER:PTHR10759 EMBL:BT012180 EMBL:AK175253 EMBL:AK229300 IPI:IPI00537822 RefSeq:NP_566133.1 UniGene:At.21822 EnsemblPlants:AT3G01170.1 GeneID:820469 KEGG:ath:AT3G01170 TAIR:At3g01170 eggNOG:NOG296377 HOGENOM:HBG748828 InParanoid:Q6NLZ8 OMA:IAVITAC PhylomeDB:Q6NLZ8 ProtClustDB:CLSN2687961 ArrayExpress:Q6NLZ8 Genevestigator:Q6NLZ8 Uniprot:Q6NLZ8
Root	Isotig16866	2	21	-3.521	1.10E-05	TAIR|locus:2166806 - symbol:AT5G23370 "AT5G23370" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] Pfam:PF02893 EMBL:CP002688 GenomeReviews:BA000015_GR InterPro:IPR004182 SMART:SM00568 EMBL:AB007648 HOGENOM:HBG745499 ProtClustDB:CLSN2686137 IPI:IPI00523352 RefSeq:NP_197728.1 UniGene:At.65542 EnsemblPlants:AT5G23370.1 GeneID:832401 KEGG:ath:AT5G23370 TAIR:At5g23370 eggNOG:NOG264012 InParanoid:Q9FMW4 OMA:ARILQMG PhylomeDB:Q9FMW4 Genevestigator:Q9FMW4 Uniprot:Q9FMW4
Root	Isotig16907	2	39	-4.414	1.25E-10	TAIR|locus:2158247 - symbol:LBD37 "AT5G67420" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0006807 "nitrogen compound metabolic process" evidence=IMP] [GO:0060776 "simple leaf morphogenesis" evidence=IMP] EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0006807 EMBL:AB007645 InterPro:IPR004883 Pfam:PF03195 PROSITE:PS50891 EMBL:AF447894 EMBL:AB473872 EMBL:AY087998 EMBL:BT024477 IPI:IPI00519656 RefSeq:NP_201543.1 UniGene:At.27456 EnsemblPlants:AT5G67420.1 GeneID:836878 KEGG:ath:AT5G67420 TAIR:At5g67420 eggNOG:NOG269376 HOGENOM:HBG748035 InParanoid:Q9FN11 OMA:QWIETAD PhylomeDB:Q9FN11 ProtClustDB:CLSN2715396 ArrayExpress:Q9FN11 Genevestigator:Q9FN11 GermOnline:AT5G67420 GO:GO:0060776 Uniprot:Q9FN11
Root	Isotig16909	8	34	-2.216	1.01E-05	TAIR|locus:2027615 - symbol:AT1G56700 "AT1G56700" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0006508 "proteolysis" evidence=IEA;ISS] InterPro:IPR000816 Pfam:PF01470 PIRSF:PIRSF015592 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0006508 EMBL:AC009323 InterPro:IPR016125 Gene3D:G3DSA:3.40.630.20 PANTHER:PTHR23402 SUPFAM:SSF53182 ProtClustDB:CLSN2688884 EMBL:AY086107 EMBL:BT005858 EMBL:AK227509 IPI:IPI00519337 PIR:H96608 RefSeq:NP_001077729.1 RefSeq:NP_564721.1 UniGene:At.26992 HSSP:O07883 ProteinModelPortal:Q9FXC0 SMR:Q9FXC0 STRING:Q9FXC0 MEROPS:C15.A02 PRIDE:Q9FXC0 EnsemblPlants:AT1G56700.1 EnsemblPlants:AT1G56700.2 GeneID:842126 KEGG:ath:AT1G56700 TAIR:At1g56700 HOGENOM:HBG594240 InParanoid:Q9FXC0 OMA:SSIAERE PhylomeDB:Q9FXC0 Genevestigator:Q9FXC0 Uniprot:Q9FXC0
Root	Isotig16933	6	22	-2.003	0.00086822	TAIR|locus:2092339 - symbol:ERF7 "AT3G20310" species:3702 "Arabidopsis thaliana" [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS;TAS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=TAS] [GO:0003677 "DNA binding" evidence=TAS] [GO:0005634 "nucleus" evidence=IC;IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0009414 "response to water deprivation" evidence=IMP] [GO:0009737 "response to abscisic acid stimulus" evidence=IMP] [GO:0043565 "sequence-specific DNA binding" evidence=IDA] [GO:0045892 "negative regulation of transcription, DNA-dependent" evidence=IDA] [GO:0009873 "ethylene mediated signaling pathway" evidence=TAS] InterPro:IPR001471 InterPro:IPR016177 Pfam:PF00847 PRINTS:PR00367 PROSITE:PS51032 SMART:SM00380 GO:GO:0009737 GO:GO:0005634 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0045892 GO:GO:0005515 GO:GO:0006952 GO:GO:0009873 GO:GO:0043565 GO:GO:0003700 GO:GO:0006351 GO:GO:0009414 KO:K09286 Gene3D:G3DSA:3.30.730.10 SUPFAM:SSF54171 EMBL:AB024036 HOGENOM:HBG744062 ProtClustDB:CLSN2682907 EMBL:AB032201 EMBL:AY037254 EMBL:AY094001 EMBL:AY085023 EMBL:AK228460 IPI:IPI00537654 RefSeq:NP_188666.1 UniGene:At.20161 ProteinModelPortal:Q9LDE4 SMR:Q9LDE4 IntAct:Q9LDE4 STRING:Q9LDE4 PRIDE:Q9LDE4 EnsemblPlants:AT3G20310.1 GeneID:821575 KEGG:ath:AT3G20310 TAIR:At3g20310 eggNOG:NOG322216 InParanoid:Q9LDE4 OMA:VAPEDCH PhylomeDB:Q9LDE4 ArrayExpress:Q9LDE4 Genevestigator:Q9LDE4 GermOnline:AT3G20310 Uniprot:Q9LDE4

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig16935	17	2	2.958	0.000459627	TAIR|locus:2015413 - symbol:AT1G47480 "AT1G47480" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0008152 "metabolic process" evidence=IEA] [GO:0016787 "hydrolase activity" evidence=IEA] InterPro:IPR002168 InterPro:IPR013094 Pfam:PF07859 PROSITE:PS01173 PROSITE:PS01174 EMBL:CP002684 GenomeReviews:CT485782_GR eggNOG:COG0657 GO:GO:0004091 EMBL:AC007519 GO:GO:0080030 GO:GO:0080032 GO:GO:0080031 EMBL:AY084535 IPI:IPI00541562 PIR:A96515 RefSeq:NP_564507.1 UniGene:At.43200 ProteinModelPortal:Q9SX78 SMR:Q9SX78 PRIDE:Q9SX78 EnsemblPlants:AT1G47480.1 GeneID:841155 KEGG:ath:AT1G47480 TAIR:At1g47480 InParanoid:Q9SX78 OMA:INEPWIN PhylomeDB:Q9SX78 ProtClustDB:CLSN2917173 Genevestigator:Q9SX78 Uniprot:Q9SX78
Root	Isotig16954	1	13	-3.829	0.000362856	TAIR|locus:2196496 - symbol:UGT85A5 "UDP-glucosyl transferase 85A5" species:3702 "Arabidopsis thaliana" [GO:0008152 "metabolic process" evidence=IEA] [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0015020 "glucuronosyltransferase activity" evidence=ISS] InterPro:IPR002213 Pfam:PF00201 PROSITE:PS00375 EMBL:AC068562 EMBL:CP002684 GO:GO:0016758 CAZy:GT1 PANTHER:PTHR11926 HOGENOM:HBG746957 eggNOG:NOG326467 EMBL:AY765462 EMBL:AY039897 EMBL:AY077671 EMBL:AK230378 IPI:IPI00522085 IPI:IPI00530831 PIR:F86356 RefSeq:NP_564170.1 RefSeq:NP_973885.1 UniGene:At.15676 ProteinModelPortal:Q9LMF0 SMR:Q9LMF0 PRIDE:Q9LMF0 EnsemblPlants:AT1G22370.2 GeneID:838844 KEGG:ath:AT1G22370 TAIR:At1g22370 InParanoid:Q9LMF0 OMA:MWREEME PhylomeDB:Q9LMF0 Genevestigator:Q9LMF0 Uniprot:Q9LMF0
Root	Isotig16990	0	12	-4.714	0.000297064	TAIR|locus:2018149 - symbol:ABA2 "AT1G52340" species:3702 "Arabidopsis thaliana" [GO:0016491 "oxidoreductase activity" evidence=ISS] [GO:0010301 "xanthoxin dehydrogenase activity" evidence=IDA] [GO:0004022 "alcohol dehydrogenase (NAD) activity" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0010182 "sugar mediated signaling pathway" evidence=TAS] [GO:0009408 "response to heat" evidence=IMP] [GO:0009414 "response to water deprivation" evidence=IMP] [GO:0010115 "regulation of abscisic acid biosynthetic process" evidence=IMP] [GO:0009750 "response to fructose stimulus" evidence=IMP] [GO:0009688 "abscisic acid biosynthetic process" evidence=IMP] [GO:0006561 "proline biosynthetic process" evidence=IMP] InterPro:IPR002198 InterPro:IPR016040 PRINTS:PR00080 PROSITE:PS00061 InterPro:IPR002347 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 GO:GO:0009414 EMBL:AC037424 EMBL:BT003412 EMBL:AY099603 EMBL:AY082344 EMBL:AY082345 IPI:IPI00534478 PIR:F96563 RefSeq:NP_175644.1 UniGene:At.37618 UniGene:At.66802 HSSP:P69167 ProteinModelPortal:Q9C826 SMR:Q9C826 IntAct:Q9C826 STRING:Q9C826 PRIDE:Q9C826 EnsemblPlants:AT1G52340.1 GeneID:841665 KEGG:ath:AT1G52340 TAIR:At1g52340 eggNOG:COG1028 HOGENOM:HBG750976 InParanoid:Q9C826 KO:K09841 OMA:ISGDNLM PhylomeDB:Q9C826 ProtClustDB:PLN02253 BioCyc:ARA:AT1G52340-MONOMER BioCyc:MetaCyc:AT1G52340-MONOMER ArrayExpress:Q9C826 Genevestigator:Q9C826 GO:GO:0010301 GO:GO:0009688 GO:GO:0006561 GO:GO:0010115 GO:GO:0009750 GO:GO:0009408 GO:GO:0010182 PRINTS:PR00081 Uniprot:Q9C826
Root	Isotig17029	3	17	-2.631	0.00056383	TAIR|locus:2089070 - symbol:MTO3 "AT3G17390" species:3702 "Arabidopsis thaliana" [GO:0004478 "methionine adenosyltransferase activity" evidence=ISS] [GO:0006556 "S-adenosylmethionine biosynthetic process" evidence=ISS] [GO:0006555 "methionine metabolic process" evidence=IMP] [GO:0009809 "lignin biosynthetic process" evidence=IMP] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR002133 InterPro:IPR022628 InterPro:IPR022629 InterPro:IPR022630 InterPro:IPR022631 InterPro:IPR022636 Pfam:PF00438 Pfam:PF02772 Pfam:PF02773 PIRSF:PIRSF000497 PROSITE:PS00376 PROSITE:PS00377 GO:GO:0005886 GO:GO:0009506 GO:GO:0005524 GO:GO:0005737 GO:GO:0005618 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005730 GO:GO:0006555 GO:GO:0046872 GO:GO:0009409 GO:GO:0009809 GO:GO:0006730 EMBL:AB022216 KO:K00789 GO:GO:0006556 HOGENOM:HBG443662 ProtClustDB:PLN02243 GO:GO:0004478 PANTHER:PTHR11964 SUPFAM:SSF55973 TIGRFAMs:TIGR01034 OMA:FHDAFIE HSSP:P13444 EMBL:AY037214 EMBL:AY120708 EMBL:BT000712 EMBL:BT002665 EMBL:AK230129 EMBL:AY087184 IPI:IPI00536966 RefSeq:NP_188365.1 UniGene:At.5781 UniGene:At.70071 ProteinModelPortal:Q9LUT2 SMR:Q9LUT2 STRING:Q9LUT2 PRIDE:Q9LUT2 EnsemblPlants:AT3G17390.1 GeneID:821003 KEGG:ath:AT3G17390 TAIR:At3g17390 InParanoid:Q9LUT2 PhylomeDB:Q9LUT2 ArrayExpress:Q9LUT2 Genevestigator:Q9LUT2 Uniprot:Q9LUT2

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig17057	0	15	-5.036	4.38E-05	TAIR|locus:2058641 - symbol:DEAR3 "AT2G23340" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=ISS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0005634 "nucleus" evidence=ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA;ISS] InterPro:IPR001471 InterPro:IPR016177 Pfam:PF00847 PRINTS:PR00367 PROSITE:PS51032 SMART:SM00380 GO:GO:0005634 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009873 GO:GO:0003677 GO:GO:0003700 GO:GO:0006351 Gene3D:G3DSA:3.30.730.10 SUPFAM:SSF54171 HSSP:O80337 EMBL:AC002391 HOGENOM:HBG749764 EMBL:AK118495 EMBL:BT003741 IPI:IPI00528876 PIR:T00498 RefSeq:NP_179915.1 UniGene:At.43320 ProteinModelPortal:O22174 SMR:O22174 EnsemblPlants:AT2G23340.1 GeneID:816866 KEGG:ath:AT2G23340 TAIR:At2g23340 eggNOG:NOG273209 InParanoid:O22174 OMA:LPDPENS PhylomeDB:O22174 ProtClustDB:CLSN2683886 ArrayExpress:O22174 Genevestigator:O22174 Uniprot:O22174
Root	Isotig17100	0	11	-4.588	0.000569522	TAIR|locus:505006716 - symbol:AT5G65205 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008152 "metabolic process" evidence=IEA] [GO:0016491 "oxidoreductase activity" evidence=IEA;ISS] [GO:0055114 "oxidation-reduction process" evidence=IEA] InterPro:IPR002198 InterPro:IPR016040 InterPro:IPR020904 Pfam:PF00106 PIRSF:PIRSF000126 PRINTS:PR00080 PROSITE:PS00061 InterPro:IPR002347 EMBL:CP002688 GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 GO:GO:0016491 PRINTS:PR00081 HSSP:P14061 OMA:KQCFEVN ProtClustDB:CLSN2690087 EMBL:AF424590 EMBL:AY098984 IPI:IPI00519227 RefSeq:NP_569008.1 UniGene:At.26303 ProteinModelPortal:Q944R2 SMR:Q944R2 PRIDE:Q944R2 EnsemblPlants:AT5G65205.1 GeneID:836644 KEGG:ath:AT5G65205 TAIR:At5g65205 InParanoid:Q944R2 PhylomeDB:Q944R2 Genevestigator:Q944R2 Uniprot:Q944R2
Root	Isotig17156	1	17	-4.216	2.69E-05	TAIR|locus:2168912 - symbol:AAP6 "AT5G49630" species:3702 "Arabidopsis thaliana" [GO:0015171 "amino acid transmembrane transporter activity" evidence=ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0015172 "acidic amino acid transmembrane transporter activity" evidence=IDA] [GO:0015175 "neutral amino acid transmembrane transporter activity" evidence=IDA] [GO:0015810 "aspartate transport" evidence=IDA] [GO:0015827 "tryptophan transport" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] GO:GO:0016021 GO:GO:0005886 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0015175 GO:GO:0015827 GO:GO:0015293 InterPro:IPR013057 Pfam:PF01490 HOGENOM:HBG319901 GO:GO:0015172 EMBL:X95736 EMBL:AB025627 EMBL:AK229102 IPI:IPI00517925 PIR:T50691 RefSeq:NP_199774.1 UniGene:At.163 ProteinModelPortal:P92934 TCDB:2.A.18.2.4 EnsemblPlants:AT5G49630.1 GeneID:835025 KEGG:ath:AT5G49630 TAIR:At5g49630 eggNOG:NOG265519 InParanoid:P92934 OMA:FAYAYST PhylomeDB:P92934 ProtClustDB:CLSN2686986 GO:GO:0015810 Uniprot:P92934
Root	Isotig17168	13	0	4.571	0.000344357	No hit
Root	Isotig17213	0	16	-5.129	2.34E-05	TAIR|locus:2180429 - symbol:AT5G20700 "AT5G20700" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] EMBL:CP002688 GenomeReviews:BA000015_GR InterPro:IPR007650 Pfam:PF04570 HOGENOM:HBG744231 EMBL:BT008340 EMBL:AK117339 IPI:IPI00544176 RefSeq:NP_197570.1 UniGene:At.43800 PRIDE:Q8GYX2 EnsemblPlants:AT5G20700.1 GeneID:832193 KEGG:ath:AT5G20700 TAIR:At5g20700 eggNOG:NOG294340 InParanoid:Q8GYX2 OMA:INDDRRE PhylomeDB:Q8GYX2 ProtClustDB:CLSN2916807 Genevestigator:Q8GYX2 Uniprot:Q8GYX2
Root	Isotig17365	4	36	-3.299	2.10E-08	TAIR|locus:2101217 - symbol:SAP5 "AT3G12630" species:3702 "Arabidopsis thaliana" [GO:0004842 "ubiquitin-protein ligase activity" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0009414 "response to water deprivation" evidence=IMP] [GO:0016567 "protein ubiquitination" evidence=IDA] [GO:0051865 "protein autoubiquitination" evidence=IDA] InterPro:IPR000058 InterPro:IPR002653 Pfam:PF01428 Pfam:PF01754 PROSITE:PS51036 PROSITE:PS51039 SMART:SM00154 GO:GO:0005634 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0003677 GO:GO:0008270 GO:GO:0009414 GO:GO:0004842 EMBL:AC069474 GO:GO:0051865 EMBL:AP002044 HSSP:O88878 HOGENOM:HBG747225 Gene3D:G3DSA:4.10.1110.10 EMBL:BT009714 EMBL:AK228330 EMBL:AY084755 IPI:IPI00525375 RefSeq:NP_566429.1 UniGene:At.27888 UniGene:At.64490 UniGene:At.69245 ProteinModelPortal:Q9LHJ8 SMR:Q9LHJ8 IntAct:Q9LHJ8 STRING:Q9LHJ8 PRIDE:Q9LHJ8 EnsemblPlants:AT3G12630.1 GeneID:820443 KEGG:ath:AT3G12630 TAIR:At3g12630 eggNOG:NOG309723 InParanoid:Q9LHJ8 OMA:SYDYKTA PhylomeDB:Q9LHJ8 ProtClustDB:CLSN2688310 Genevestigator:Q9LHJ8 Uniprot:Q9LHJ8

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig17449	9	33	-2.003	4.53E-05	TAIR|locus:2101217 - symbol:SAP5 "AT3G12630" species:3702 "Arabidopsis thaliana" [GO:0004842 "ubiquitin-protein ligase activity" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0009414 "response to water deprivation" evidence=IMP] [GO:0016567 "protein ubiquitination" evidence=IDA] [GO:0051865 "protein autoubiquitination" evidence=IDA] InterPro:IPR000058 InterPro:IPR002653 Pfam:PF01428 Pfam:PF01754 PROSITE:PS51036 PROSITE:PS51039 SMART:SM00154 GO:GO:0005634 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0003677 GO:GO:0008270 GO:GO:0009414 GO:GO:0004842 EMBL:AC069474 GO:GO:0051865 EMBL:AP002044 HSSP:O88878 HOGENOM:HBG747225 Gene3D:G3DSA:4.10.1110.10 EMBL:BT009714 EMBL:AK228330 EMBL:AY084755 IPI:IPI00525375 RefSeq:NP_566429.1 UniGene:At.27888 UniGene:At.64490 UniGene:At.69245 ProteinModelPortal:Q9LHJ8 SMR:Q9LHJ8 IntAct:Q9LHJ8 STRING:Q9LHJ8 PRIDE:Q9LHJ8 EnsemblPlants:AT3G12630.1 GeneID:820443 KEGG:ath:AT3G12630 TAIR:At3g12630 eggNOG:NOG309723 InParanoid:Q9LHJ8 OMA:SYDYKTA PhylomeDB:Q9LHJ8 ProtClustDB:CLSN2688310 Genevestigator:Q9LHJ8 Uniprot:Q9LHJ8
Root	Isotig17482	1	12	-3.714	0.000699736	TAIR|locus:2018521 - symbol:EXPB2 "expansin B2" species:3702 "Arabidopsis thaliana" [GO:0005576 "extracellular region" evidence=IEA] [GO:0009826 "unidimensional cell growth" evidence=ISS;NAS] [GO:0009828 "plant-type cell wall loosening" evidence=ISS;NAS] [GO:0009831 "plant-type cell wall modification involved in multidimensional cell growth" evidence=ISS] InterPro:IPR005795 InterPro:IPR007118 PRINTS:PR00829 PRINTS:PR01225 Pfam:PF01357 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005618 GO:GO:0005576 GO:GO:0016020 GO:GO:0009826 GO:GO:0019953 EMBL:AC001229 EMBL:AC007234 InterPro:IPR014733 InterPro:IPR009009 InterPro:IPR007112 Gene3D:G3DSA:2.40.40.10 Pfam:PF03330 SMART:SM00837 SUPFAM:SSF50685 PROSITE:PS50842 HOGENOM:HBG605129 InterPro:IPR007117 Gene3D:G3DSA:2.60.40.760 SUPFAM:SSF49590 PROSITE:PS50843 GO:GO:0009828 IPI:IPI00521534 PIR:F96681 RefSeq:NP_564860.3 UniGene:At.52384 ProteinModelPortal:Q9SHY6 SMR:Q9SHY6 PRIDE:Q9SHY6 EnsemblPlants:AT1G65680.1 GeneID:842879 KEGG:ath:AT1G65680 TAIR:At1g65680 eggNOG:NOG271185 InParanoid:Q9SHY6 OMA:DSGSNPY PhylomeDB:Q9SHY6 ProtClustDB:CLSN2681539 ArrayExpress:Q9SHY6 Genevestigator:Q9SHY6 GermOnline:AT1G65680 Uniprot:Q9SHY6
Root	Isotig17484	212	0	8.599	1.04E-41	No hit
Root	Isotig17498	3	22	-3.003	2.69E-05	TAIR|locus:2027615 - symbol:AT1G56700 "AT1G56700" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0006508 "proteolysis" evidence=IEA;ISS] InterPro:IPR000816 Pfam:PF01470 PIRSF:PIRSF015592 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0006508 EMBL:AC009323 InterPro:IPR016125 Gene3D:G3DSA:3.40.630.20 PANTHER:PTHR23402 SUPFAM:SSF53182 ProtClustDB:CLSN2688884 EMBL:AY086107 EMBL:BT005858 EMBL:AK227509 IPI:IPI00519337 PIR:H96608 RefSeq:NP_001077729.1 RefSeq:NP_564721.1 UniGene:At.26992 HSSP:O07883 ProteinModelPortal:Q9FXC0 SMR:Q9FXC0 STRING:Q9FXC0 MEROPS:C15.A02 PRIDE:Q9FXC0 EnsemblPlants:AT1G56700.1 EnsemblPlants:AT1G56700.2 GeneID:842126 KEGG:ath:AT1G56700 TAIR:At1g56700 HOGENOM:HBG594240 InParanoid:Q9FXC0 OMA:SSIAERE PhylomeDB:Q9FXC0 Genevestigator:Q9FXC0 Uniprot:Q9FXC0
Root	Isotig17510	4	20	-2.451	0.000325095	TAIR|locus:2124286 - symbol:CCoAOMT1 "caffeoyl coenzyme A O-methyltransferase 1" species:3702 "Arabidopsis thaliana" [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0009805 "coumarin biosynthetic process" evidence=IMP] [GO:0042409 "caffeoyl-CoA O-methyltransferase activity" evidence=IDA] [GO:0005829 "cytosol" evidence=TAS] InterPro:IPR002935 Pfam:PF01596 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0046686 GO:GO:0046872 EMBL:AL021961 EMBL:AL161584 GO:GO:0009809 GO:GO:0009805 eggNOG:COG4122 HOGENOM:HBG496808 GO:GO:0042409 PANTHER:PTHR10509 OMA:REKTGHH EMBL:AY057554 EMBL:AY062630 EMBL:AY081457 EMBL:AY143979 EMBL:AY088577 IPI:IPI00521545 PIR:T05431 RefSeq:NP_195131.1 UniGene:At.23175 ProteinModelPortal:O49499 SMR:O49499 STRING:O49499 PRIDE:O49499 EnsemblPlants:AT4G34050.1 GeneID:829551 KEGG:ath:AT4G34050 TAIR:At4g34050 InParanoid:O49499 KO:K00588 PhylomeDB:O49499 ProtClustDB:PLN02589 ArrayExpress:O49499 Genevestigator:O49499 Uniprot:O49499
Root	Isotig17521	0	20	-5.451	2.00E-06	TAIR|locus:2177724 - symbol:AT5G65030 "AT5G65030" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002688 GenomeReviews:BA000015_GR EMBL:AB019236 UniGene:At.20837 EMBL:BT029499 IPI:IPI00548443 RefSeq:NP_201308.1 UniGene:At.66744 ProteinModelPortal:Q9LV76 PRIDE:Q9LV76 EnsemblPlants:AT5G65030.1 GeneID:836627 KEGG:ath:AT5G65030

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						TAIR:At5g65030 eggNOG:NOG255009 HOGENOM:HBG175356 InParanoid:Q9LV76 OMA:IEVNTRE PhylomeDB:Q9LV76 ProtClustDB:CLSN2686374 Genevestigator:Q9LV76 Uniprot:Q9LV76
Root	Isotig17551	1	33	-5.173	1.20E-09	TAIR|locus:2056755 - symbol:RNS1 "AT2G02990" species:3702 "Arabidopsis thaliana" [GO:0004521 "endoribonuclease activity" evidence=ISS] [GO:0009611 "response to wounding" evidence=IEP] [GO:0009867 "jasmonic acid mediated signaling pathway" evidence=IEP] [GO:0005618 "cell wall" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0004540 "ribonuclease activity" evidence=IDA] [GO:0007568 "aging" evidence=IEP] [GO:0016036 "cellular response to phosphate starvation" evidence=IEP] [GO:0005576 "extracellular region" evidence=IDA] [GO:0009718 "anthocyanin biosynthetic process" evidence=IMP] InterPro:IPR001568 InterPro:IPR018188 Pfam:PF00445 PROSITE:PS00530 PROSITE:PS00531 EMBL:AC004138 GO:GO:0005886 GO:GO:0005618 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0005576 GO:GO:0009611 GO:GO:0003723 GO:GO:0016036 GO:GO:0009718 GO:GO:0033897 Gene3D:G3DSA:3.90.730.10 PANTHER:PTHR11240 SUPFAM:SSF55895 EMBL:U05206 EMBL:AY072413 EMBL:AY114710 EMBL:DQ446504 EMBL:DQ652992 EMBL:AY086747 EMBL:Z27289 EMBL:Z27290 IPI:IPI00525841 PIR:A84443 RefSeq:NP_178399.1 UniGene:At.10792 ProteinModelPortal:P42813 SMR:P42813 IntAct:P42813 STRING:P42813 PRIDE:P42813 EnsemblPlants:AT2G02990.1 GeneID:814828 KEGG:ath:AT2G02990 TAIR:At2g02990 eggNOG:NOG285082 HOGENOM:HBG747499 InParanoid:P42813 OMA:LIECPVF PhylomeDB:P42813 ProtClustDB:CLSN2913210 ArrayExpress:P42813 Genevestigator:P42813 GermOnline:AT2G02990 Uniprot:P42813
Root	Isotig17555	2	17	-3.216	0.000139706	TAIR|locus:2094736 - symbol:GLTP3 "GLYCOLIPID TRANSFER PROTEIN 3" species:3702 "Arabidopsis thaliana" [GO:0005737 "cytoplasm" evidence=IEA] [GO:0017089 "glycolipid transporter activity" evidence=IEA] [GO:0046836 "glycolipid transport" evidence=IEA] [GO:0051861 "glycolipid binding" evidence=IEA] InterPro:IPR014830 Pfam:PF08718 GO:GO:0005737 EMBL:CP002686 EMBL:AB023045 GO:GO:0051861 GO:GO:0017089 Gene3D:G3DSA:1.10.3520.10 SUPFAM:SSF110004 IPI:IPI00938705 UniGene:At.38091 ProteinModelPortal:Q9LU33 SMR:Q9LU33 EnsemblPlants:AT3G21260.3 TAIR:At3g21260 PhylomeDB:Q9LU33 Genevestigator:Q9LU33 Uniprot:Q9LU33
Root	Isotig17558	31	8	1.825	0.000382406	TAIR|locus:2042087 - symbol:PGY1 "PIGGYBACK1" species:3702 "Arabidopsis thaliana" [GO:0003723 "RNA binding" evidence=IEA] [GO:0003735 "structural constituent of ribosome" evidence=IEA;ISS] [GO:0006412 "translation" evidence=ISS] [GO:0015934 "large ribosomal subunit" evidence=ISS] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0022625 "cytosolic large ribosomal subunit" evidence=IDA] [GO:0009955 "adaxial/abaxial pattern specification" evidence=IGI] [GO:0048569 "post-embryonic organ development" evidence=IGI] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR002143 InterPro:IPR016094 InterPro:IPR016095 InterPro:IPR023674 Pfam:PF00687 PIRSF:PIRSF002155 Prosite:PS01199 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0006412 GO:GO:0003723 GO:GO:0003735 EMBL:AC006232 EMBL:AC005824 SUPFAM:SSF56808 GO:GO:0022625 GO:GO:0048569 eggNOG:COG0081 HOGENOM:HBG316566 KO:K02865 ProtClustDB:CLSN2687446 InterPro:IPR023673 Gene3D:G3DSA:3.30.190.20 Gene3D:G3DSA:3.40.50.790 EMBL:AF360146 EMBL:AY056371 EMBL:AY081263 EMBL:BT006262 EMBL:Z27264 IPI:IPI00541952 PIR:A84674 RefSeq:NP_565654.1 RefSeq:NP_850104.1 UniGene:At.19006 ProteinModelPortal:P59230 SMR:P59230 STRING:P59230 PRIDE:P59230 EnsemblPlants:AT2G27530.1 EnsemblPlants:AT2G27530.2 GeneID:817299 KEGG:ath:AT2G27530 GeneFarm:212 TAIR:At2g27530 InParanoid:P59230 OMA:KATMSPP PhylomeDB:P59230 ArrayExpress:P59230 Genevestigator:P59230 GermOnline:AT2G27530 GO:GO:0009955 Uniprot:P59230
Root	Isotig17571	34	0	5.958	2.97E-09	TAIR|locus:2183329 - symbol:AT5G07330 "AT5G07330" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002688 GenomeReviews:BA000015_GR EMBL:AL163912 HOGENOM:HBG746117 ProtClustDB:CLSN2687068 EMBL:BT010400 EMBL:AK118558 IPI:IPI00533921 PIR:T49872 RefSeq:NP_196350.1 UniGene:At.32734 PRIDE:Q9LY27 EnsemblPlants:AT5G07330.1 GeneID:830624 KEGG:ath:AT5G07330 TAIR:At5g07330 eggNOG:NOG262444 InParanoid:Q9LY27 OMA:HIHEFES PhylomeDB:Q9LY27 Genevestigator:Q9LY27 Uniprot:Q9LY27
Root	Isotig17606	39	0	6.156	2.24E-10	TAIR|locus:2077081 - symbol:AT3G22490 "AT3G22490" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0009793 "embryo development ending in seed dormancy" evidence=ISS] Pfam:PF04927 EMBL:CP002686 EMBL:AP000731 UniGene:At.64534 InterPro:IPR007011 ProtClustDB:CLSN2684142 EMBL:BT002907 EMBL:BT004425

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						IPI:IPI00543172 RefSeq:NP_188888.1 PRIDE:Q9LJ97 EnsemblPlants:AT3G22490.1 GeneID:821820 KEGG:ath:AT3G22490 TAIR:At3g22490 InParanoid:Q9LJ97 OMA:QTAGNKP PhylomeDB:Q9LJ97 ArrayExpress:Q9LJ97 Genevestigator:Q9LJ97 Uniprot:Q9LJ97
Root	Isotig17610	0	11	-4.588	0.000569522	TAIR|locus:2115949 - symbol:AT4G05460 "AT4G05460" species:3702 "Arabidopsis thaliana" [GO:0004842 "ubiquitin-protein ligase activity" evidence=ISS] [GO:0006511 "ubiquitin-dependent protein catabolic process" evidence=TAS] Pfam:PF00560 InterPro:IPR001611 InterPro:IPR001810 PROSITE:PS50181 SMART:SM00256 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005634 EMBL:AL161503 HOGENOM:HBG588423 EMBL:BT003081 EMBL:AY087774 EMBL:AK227360 IPI:IPI00546408 PIR:F85068 RefSeq:NP_567294.1 UniGene:At.48830 UniGene:At.66629 ProteinModelPortal:Q9M0U9 SMR:Q9M0U9 IntAct:Q9M0U9 STRING:Q9M0U9 PRIDE:Q9M0U9 EnsemblPlants:AT4G05460.1 GeneID:825896 KEGG:ath:AT4G05460 TAIR:At4g05460 eggNOG:NOG251781 InParanoid:Q9M0U9 OMA:IDMHNLG PhylomeDB:Q9M0U9 ProtClustDB:CLSN2917517 ArrayExpress:Q9M0U9 Genevestigator:Q9M0U9 Uniprot:Q9M0U9
Root	Isotig17712	2	25	-3.773	8.67E-07	TAIR|locus:2081091 - symbol:AT3G06390 "AT3G06390" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] GO:GO:0016021 GO:GO:0005886 EMBL:CP002686 GenomeReviews:BA000014_GR EMBL:AC011623 InterPro:IPR006702 InterPro:IPR006459 Pfam:PF04535 TIGRFAMs:TIGR01569 EMBL:BT003953 EMBL:BT005725 IPI:IPI00528355 RefSeq:NP_187290.1 UniGene:At.27805 STRING:Q9SQU2 PRIDE:Q9SQU2 EnsemblPlants:AT3G06390.1 GeneID:819813 KEGG:ath:AT3G06390 TAIR:At3g06390 eggNOG:NOG329326 HOGENOM:HBG749703 InParanoid:Q9SQU2 OMA:NDSPAFI PhylomeDB:Q9SQU2 ProtClustDB:CLSN2696701 ArrayExpress:Q9SQU2 Genevestigator:Q9SQU2 Uniprot:Q9SQU2
Root	Isotig17764	0	12	-4.714	0.000297064	TAIR|locus:2129885 - symbol:NF-YB3 ""nuclear factor Y, subunit B3"" species:3702 "Arabidopsis thaliana" [GO:0005622 "intracellular" evidence=IEA] [GO:0005634 "nucleus" evidence=IEA] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] InterPro:IPR003956 InterPro:IPR003957 InterPro:IPR003958 InterPro:IPR009072 Pfam:PF00808 PRINTS:PR00615 PROSITE:PS00685 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005634 GO:GO:0006355 GO:GO:0043565 GO:GO:0006351 Gene3D:G3DSA:1.10.20.10 SUPFAM:SSF47113 EMBL:Z97336 EMBL:AL161539 eggNOG:COG2036 OMA:REDDNDE HOGENOM:HBG748799 PANTHER:PTHR11064:SF9 EMBL:AK117818 EMBL:BT003684 IPI:IPI00516812 PIR:G71407 RefSeq:NP_193190.1 UniGene:At.33269 ProteinModelPortal:O23310 SMR:O23310 IntAct:O23310 STRING:O23310 PRIDE:O23310 EnsemblPlants:AT4G14540.1 GeneID:827101 KEGG:ath:AT4G14540 GeneFarm:5133 TAIR:At4g14540 InParanoid:O23310 PhylomeDB:O23310 ProtClustDB:CLSN2685335 ArrayExpress:O23310 Genevestigator:O23310 GermOnline:AT4G14540 Uniprot:O23310
Root	Isotig17833	295	0	9.076	2.98E-54	No hit
Root	Isotig17915	0	16	-5.129	2.34E-05	TAIR|locus:2162361 - symbol:AT5G42500 "AT5G42500" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0006952 "defense response" evidence=ISS] Pfam:PF03018 EMBL:CP002688 GenomeReviews:BA000015_GR EMBL:AB016888 InterPro:IPR004265 HOGENOM:HBG605442 ProtClustDB:CLSN2686597 eggNOG:NOG235510 EMBL:AY093095 EMBL:BT008442 IPI:IPI00528213 RefSeq:NP_199065.1 UniGene:At.30167 PRIDE:Q9FIG7 EnsemblPlants:AT5G42500.1 GeneID:834257 KEGG:ath:AT5G42500 TAIR:At5g42500 InParanoid:Q9FIG7 OMA:NFGVIMI PhylomeDB:Q9FIG7 ArrayExpress:Q9FIG7 Genevestigator:Q9FIG7 Uniprot:Q9FIG7
Root	Isotig17918	29	7	1.922	0.000375107	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig18016	14	51	-1.994	4.31E-07	TAIR|locus:2081695 - symbol:ATGSTF13 "AT3G62760" species:3702 "Arabidopsis thaliana" [GO:0004364 "glutathione transferase activity" evidence=ISS] [GO:0005737 "cytoplasm" evidence=NAS] [GO:0009407 "toxin catabolic process" evidence=TAS] InterPro:IPR004045 Pfam:PF02798 PROSITE:PS50404 InterPro:IPR004046

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						Pfam:PF00043 GO:GO:0005829 EMBL:CP002686 GenomeReviews:BA000014_GR EMBL:AL162651 GO:GO:0009636 InterPro:IPR012336 Gene3D:G3DSA:3.40.30.10 SUPFAM:SSF52833 InterPro:IPR010987 Gene3D:G3DSA:1.20.1050.10 SUPFAM:SSF47616 PROSITE:PS50405 InterPro:IPR017933 GO:GO:0004364 eggNOG:COG0625 HOGENOM:HBG753188 GO:GO:0009407 HSSP:Q9ZP62 IPI:IPI00528803 PIR:T48065 RefSeq:NP_191835.1 UniGene:At.54041 ProteinModelPortal:Q9LZI9 SMR:Q9LZI9 PRIDE:Q9LZI9 EnsemblPlants:AT3G62760.1 GeneID:825451 KEGG:ath:AT3G62760 TAIR:At3g62760 InParanoid:Q9LZI9 OMA:KAWWERL PhylomeDB:Q9LZI9 ProtClustDB:CLSN2684163 Genevestigator:Q9LZI9 Uniprot:Q9LZI9
Root	Isotig18030	81	0	7.211	4.65E-19	TAIR|locus:2139777 - symbol:OSM34 "AT4G11650" species:3702 "Arabidopsis thaliana" [GO:0051707 "response to other organism" evidence=ISS] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0009817 "defense response to fungus, incompatible interaction" evidence=IDA] [GO:0009816 "defense response to bacterium, incompatible interaction" evidence=ISS] Pfam:PF00314 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0009651 GO:GO:0009817 EMBL:AL161532 EMBL:AL049500 EMBL:X89008 IPI:IPI00528920 PIR:T04212 RefSeq:NP_192902.1 UniGene:At.25216 ProteinModelPortal:P50700 SMR:P50700 STRING:P50700 PRIDE:P50700 EnsemblPlants:AT4G11650.1 GeneID:826770 KEGG:ath:AT4G11650 TAIR:At4g11650 eggNOG:NOG304630 HOGENOM:HBG748210 InParanoid:P50700 OMA:RVVFCPR PhylomeDB:P50700 ProtClustDB:CLSN2915891 ArrayExpress:P50700 Genevestigator:P50700 GermOnline:AT4G11650 InterPro:IPR001938 InterPro:IPR017949 Gene3D:G3DSA:2.60.110.10 PIRSF:PIRSF002703 PRINTS:PR00347 SMART:SM00205 SUPFAM:SSF49870 PROSITE:PS00316 PROSITE:PS51367 Uniprot:P50700
Root	Isotig18066	40	0	6.193	1.34E-10	TAIR|locus:2116762 - symbol:AT4G31830 "AT4G31830" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002687 GenomeReviews:CT486007_GR EMBL:AL161579 EMBL:AL049607 EMBL:BT010813 EMBL:BT011290 IPI:IPI00539008 PIR:T06305 RefSeq:NP_194911.1 UniGene:At.31710 IntAct:Q9SZ50 PRIDE:Q9SZ50 EnsemblPlants:AT4G31830.1 GeneID:829312 KEGG:ath:AT4G31830 TAIR:At4g31830 eggNOG:NOG287408 HOGENOM:HBG748438 InParanoid:Q9SZ50 OMA:THKMSPE PhylomeDB:Q9SZ50 ProtClustDB:CLSN2685982 ArrayExpress:Q9SZ50 Genevestigator:Q9SZ50 Uniprot:Q9SZ50
Root	Isotig18120	275	0	8.974	2.55E-51	No hit
Root	Isotig18162	107	1	6.612	1.83E-25	No hit
Root	Isotig18208	440	0	9.652	3.01E-74	No hit
Root	Isotig18239	23	0	5.395	1.11E-06	TAIR|locus:2116762 - symbol:AT4G31830 "AT4G31830" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002687 GenomeReviews:CT486007_GR EMBL:AL161579 EMBL:AL049607 EMBL:BT010813 EMBL:BT011290 IPI:IPI00539008 PIR:T06305 RefSeq:NP_194911.1 UniGene:At.31710 IntAct:Q9SZ50 PRIDE:Q9SZ50 EnsemblPlants:AT4G31830.1 GeneID:829312 KEGG:ath:AT4G31830 TAIR:At4g31830 eggNOG:NOG287408 HOGENOM:HBG748438 InParanoid:Q9SZ50 OMA:THKMSPE PhylomeDB:Q9SZ50 ProtClustDB:CLSN2685982 ArrayExpress:Q9SZ50 Genevestigator:Q9SZ50 Uniprot:Q9SZ50
Root	Isotig18262	68	20	1.637	1.09E-06	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig18278	33	0	5.915	5.02E-09	TAIR|locus:2090552 - symbol:AT3G17520 "AT3G17520" species:3702 "Arabidopsis thaliana" [GO:0009793 "embryo development ending in seed dormancy" evidence=ISS] Pfam:PF02987 GenomeReviews:BA000014_GR InterPro:IPR004238 EMBL:BT004128 EMBL:BT020426 IPI:IPI00525902 STRING:Q84W82 PRIDE:Q84W82 TAIR:At3g17520 eggNOG:NOG269272 ArrayExpress:Q84W82 Genevestigator:Q84W82 Uniprot:Q84W82
Root	Isotig18313	0	12	-4.714	0.000297064	TAIR|locus:2012773 - symbol:ERD9 "AT1G10370" species:3702 "Arabidopsis thaliana" [GO:0004364 "glutathione transferase activity" evidence=ISS;IDA] [GO:0005737 "cytoplasm" evidence=NAS] [GO:0009407 "toxin catabolic process" evidence=TAS] [GO:0009507 "chloroplast" evidence=IDA] [GO:0080167 "response to karrikin"

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						evidence=IEP] [GO:0006749 "glutathione metabolic process" evidence=IMP] [GO:0009704 "de-etiolation" evidence=IMP] [GO:0048527 "lateral root development" evidence=IMP] [GO:0060416 "response to growth hormone stimulus" evidence=IEP] [GO:0009651 "response to salt stress" evidence=IMP] [GO:0080148 "negative regulation of response to water deprivation" evidence=IMP] InterPro:IPR004045 PROSITE:PS50404 InterPro:IPR004046 Pfam:PF00043 EMBL:CP002684 GO:GO:0005829 GO:GO:0009507 GO:GO:0009651 GO:GO:0080167 GO:GO:0048527 GO:GO:0009636 GO:GO:0040008 InterPro:IPR012336 Gene3D:G3DSA:3.40.30.10 SUPFAM:SSF52833 InterPro:IPR010987 Gene3D:G3DSA:1.20.1050.10 SUPFAM:SSF47616 PROSITE:PS50405 GO:GO:0060416 EMBL:AC005489 GO:GO:0006749 InterPro:IPR017933 GO:GO:0004364 GO:GO:0009407 eggNOG:NOG288793 HOGENOM:HBG749301 HSSP:O04941 EMBL:AB039930 EMBL:AF288191 EMBL:BT023743 IPI:IPI00532578 RefSeq:NP_172508.4 UniGene:At.11290 ProteinModelPortal:Q9FUS8 SMR:Q9FUS8 PRIDE:Q9FUS8 EnsemblPlants:AT1G10370.1 GeneID:837576 KEGG:ath:AT1G10370 TAIR:At1g10370 InParanoid:Q9FUS8 ProtClustDB:CLSN2679578 Genevestigator:Q9FUS8 GO:GO:0009704 GO:GO:0080148 Uniprot:Q9FUS8
Root	Isotig18340	2	14	-2.936	0.000925454	UNIPROTKB|P26969 - symbol:GDCSP "Glycine dehydrogenase [decarboxylating], mitochondrial" species:3888 "Pisum sativum" [GO:0005960 "glycine cleavage complex" evidence=IDA] InterPro:IPR003437 InterPro:IPR015421 InterPro:IPR020580 InterPro:IPR020581 Pfam:PF02347 GO:GO:0005739 GO:GO:0030170 InterPro:IPR015424 Gene3D:G3DSA:3.40.640.10 SUPFAM:SSF53383 GO:GO:0006544 GO:GO:0005960 GO:GO:0004375 PANTHER:PTHR11773 TIGRFAMs:TIGR00461 EMBL:X59773 EMBL:X54377 PIR:A42109 ProteinModelPortal:P26969 IntAct:P26969 PRIDE:P26969 Uniprot:P26969
Root	Isotig18353	71	0	7.021	4.32E-17	TAIR|locus:2174984 - symbol:AT5G66780 "AT5G66780" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002688 GenomeReviews:BA000015_GR EMBL:AB010700 EMBL:AY048239 EMBL:AY072623 IPI:IPI00539273 RefSeq:NP_201479.1 UniGene:At.6618 PRIDE:Q9FL02 EnsemblPlants:AT5G66780.1 GeneID:836811 KEGG:ath:AT5G66780 TAIR:At5g66780 eggNOG:NOG276454 HOGENOM:HBG748513 OMA:NEIHENH PhylomeDB:Q9FL02 ProtClustDB:CLSN2686878 Genevestigator:Q9FL02 Uniprot:Q9FL02
Root	Isotig18356	0	27	-5.884	3.19E-08	No hit
Root	Isotig18365	239	0	8.772	6.67E-46	No hit
Root	Isotig18380	0	11	-4.588	0.000569522	TAIR|locus:2171258 - symbol:AT5G58490 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0008152 "metabolic process" evidence=IEA] [GO:0009809 "lignin biosynthetic process" evidence=ISS] [GO:0016621 "cinnamoyl-CoA reductase activity" evidence=ISS] [GO:0044237 "cellular metabolic process" evidence=IEA] [GO:0050662 "coenzyme binding" evidence=IEA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001509 InterPro:IPR016040 Pfam:PF01370 GO:GO:0005829 EMBL:CP002688 GenomeReviews:BA000015_GR eggNOG:COG0451 GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 HOGENOM:HBG755066 GO:GO:0003824 GO:GO:0044237 GO:GO:0050662 EMBL:AB025632 EMBL:AY086975 EMBL:BT002742 IPI:IPI00534797 RefSeq:NP_200657.1 UniGene:At.28374 ProteinModelPortal:Q9FGH3 SMR:Q9FGH3 STRING:Q9FGH3 PRIDE:Q9FGH3 EnsemblPlants:AT5G58490.1 GeneID:835962 KEGG:ath:AT5G58490 TAIR:At5g58490 InParanoid:Q9FGH3 OMA:NSKARDV PhylomeDB:Q9FGH3 ProtClustDB:CLSN2686256 ArrayExpress:Q9FGH3 Genevestigator:Q9FGH3 Uniprot:Q9FGH3
Root	Isotig18425	63	0	6.848	1.78E-15	TAIR|locus:2174984 - symbol:AT5G66780 "AT5G66780" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002688 GenomeReviews:BA000015_GR EMBL:AB010700 EMBL:AY048239 EMBL:AY072623 IPI:IPI00539273 RefSeq:NP_201479.1 UniGene:At.6618 PRIDE:Q9FL02 EnsemblPlants:AT5G66780.1 GeneID:836811 KEGG:ath:AT5G66780 TAIR:At5g66780 eggNOG:NOG276454 HOGENOM:HBG748513 OMA:NEIHENH PhylomeDB:Q9FL02 ProtClustDB:CLSN2686878 Genevestigator:Q9FL02 Uniprot:Q9FL02
Root	Isotig18434	0	15	-5.036	4.38E-05	No hit
Root	Isotig18459	1	16	-4.129	5.13E-05	TAIR|locus:2141385 - symbol:SAM-2 "AT4G01850" species:3702 "Arabidopsis thaliana" [GO:0004478 "methionine adenosyltransferase activity" evidence=ISS] [GO:0006556 "S-adenosylmethionine biosynthetic process" evidence=ISS] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0071281 "cellular response to iron ion" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA;RCA] [GO:0070062 "extracellular vesicular exosome" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR002133 InterPro:IPR022628 InterPro:IPR022629 InterPro:IPR022630 InterPro:IPR022631 InterPro:IPR022636 Pfam:PF00438 Pfam:PF02772 Pfam:PF02773 PIRSF:PIRSF000497

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						PROSITE:PS00376 PROSITE:PS00377 GO:GO:0005829 GO:GO:0009506 GO:GO:0005524 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005618 GO:GO:0071281 GO:GO:0005730 GO:GO:0005507 EMBL:AC007138 EMBL:AL161493 GO:GO:0070062 GO:GO:0006730 KO:K00789 GO:GO:0006556 UniGene:At.24731 eggNOG:COG0192 HOGENOM:HBG443662 ProtClustDB:PLN02243 GO:GO:0004478 PANTHER:PTHR11964 SUPFAM:SSF55973 TIGRFAMs:TIGR01034 EMBL:M33217 EMBL:AY072327 EMBL:AY094454 EMBL:BT000575 EMBL:Z33778 EMBL:Z29136 IPI:IPI00529348 PIR:JQ0410 RefSeq:NP_001078345.1 RefSeq:NP_192094.1 UniGene:At.24433 UniGene:At.71920 ProteinModelPortal:P17562 SMR:P17562 STRING:P17562 PRIDE:P17562 ProMEX:P17562 EnsemblPlants:AT4G01850.1 EnsemblPlants:AT4G01850.2 GeneID:826987 KEGG:ath:AT4G01850 TAIR:At4g01850 InParanoid:P17562 OMA:ATIDYEK PhylomeDB:P17562 ArrayExpress:P17562 Genevestigator:P17562 GermOnline:AT4G01850 Uniprot:P17562
Root	Isotig18464	0	15	-5.036	4.38E-05	TAIR|locus:2175846 - symbol:AT5G60680 "AT5G60680" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002688 EMBL:AB005246 InterPro:IPR007608 Pfam:PF04520 EMBL:AY063871 EMBL:AY091231 IPI:IPI00538611 RefSeq:NP_200876.1 UniGene:At.7237 STRING:Q9FF51 PRIDE:Q9FF51 EnsemblPlants:AT5G60680.1 GeneID:836189 KEGG:ath:AT5G60680 TAIR:At5g60680 InParanoid:Q9FF51 OMA:RSIEDND PhylomeDB:Q9FF51 ProtClustDB:CLSN2916410 ArrayExpress:Q9FF51 Genevestigator:Q9FF51 Uniprot:Q9FF51
Root	Isotig18492	112	41	1.321	9.70E-08	TAIR|locus:2064965 - symbol:EULS3 "AT2G39050" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0030246 "carbohydrate binding" evidence=IDA] GO:GO:0005634 GO:GO:0005737 EMBL:CP002685 GenomeReviews:CT485783_GR InterPro:IPR000772 SUPFAM:SSF50370 PROSITE:PS50231 GO:GO:0030246 EMBL:AC005770 Pfam:PF14200 EMBL:AF411801 EMBL:AY093795 EMBL:AY087909 IPI:IPI00536641 PIR:E84812 RefSeq:NP_565899.1 UniGene:At.22599 ProteinModelPortal:Q945P1 SMR:Q945P1 PRIDE:Q945P1 EnsemblPlants:AT2G39050.1 GeneID:818491 KEGG:ath:AT2G39050 TAIR:At2g39050 eggNOG:NOG254161 HOGENOM:HBG750017 InParanoid:Q945P1 OMA:GYRTIRM PhylomeDB:Q945P1 ProtClustDB:CLSN2681741 ArrayExpress:Q945P1 Genevestigator:Q945P1 Uniprot:Q945P1
Root	Isotig18510	0	11	-4.588	0.000569522	UNIPROTKB|G4MV90 - symbol:MGG_01722 "Adenylyl cyclase-associated protein" species:242507 "Magnaporthe oryzae 70-15" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] InterPro:IPR001837 InterPro:IPR006599 InterPro:IPR013912 InterPro:IPR013992 InterPro:IPR016098 InterPro:IPR018106 Pfam:PF01213 Pfam:PF08603 PROSITE:PS01088 SMART:SM00673 GO:GO:0003779 GO:GO:0007010 GO:GO:0000902 EMBL:CM001232 InterPro:IPR017901 Gene3D:G3DSA:2.160.20.70 PANTHER:PTHR10652 SUPFAM:SSF101278 SUPFAM:SSF69340 PROSITE:PS51329 Uniprot:G4MV90
Root	Isotig18546	8	28	-1.936	0.000239276	TAIR|locus:2147304 - symbol:FQR1 "AT5G54500" species:3702 "Arabidopsis thaliana" [GO:0009733 "response to auxin stimulus" evidence=IEP] [GO:0010181 "FMN binding" evidence=IDA] [GO:0016655 "oxidoreductase activity, acting on NADH or NADPH, quinone or similar compound as acceptor" evidence=IDA] [GO:0055114 "oxidation-reduction process" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] InterPro:IPR008254 InterPro:IPR010089 PROSITE:PS50902 Pfam:PF03358 GO:GO:0005886 GO:GO:0005774 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0045892 GO:GO:0009733 GO:GO:0016655 GO:GO:0010181 EMBL:AB026634 HOGENOM:HBG686708 InterPro:IPR005025 TIGRFAMs:TIGR01755 ProtClustDB:CLSN2685577 EMBL:AY120735 EMBL:BT002194 IPI:IPI00529112 RefSeq:NP_200261.1 UniGene:At.43051 ProteinModelPortal:Q9LSQ5 SMR:Q9LSQ5 STRING:Q9LSQ5 ANU-2DPAGE:Q9LSQ5 PRIDE:Q9LSQ5 EnsemblPlants:AT5G54500.1 GeneID:835538 KEGG:ath:AT5G54500 TAIR:At5g54500 InParanoid:Q9LSQ5 OMA:YSHAFPL PhylomeDB:Q9LSQ5 ArrayExpress:Q9LSQ5 Genevestigator:Q9LSQ5 Uniprot:Q9LSQ5
Root	Isotig18592	17	0	4.958	3.30E-05	TAIR|locus:2093307 - symbol:AT3G15670 "AT3G15670" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0009793 "embryo development ending in seed dormancy" evidence=ISS] [GO:0005634 "nucleus" evidence=IDA] GO:GO:0005634 EMBL:CP002686 EMBL:AB017071 ProtClustDB:CLSN2679745 EMBL:AY040026 EMBL:AY054162 EMBL:AY079410 IPI:IPI00542660 RefSeq:NP_188188.1 UniGene:At.5382 STRING:Q9LW12 PRIDE:Q9LW12 ProMEX:Q9LW12 EnsemblPlants:AT3G15670.1 GeneID:820810 KEGG:ath:AT3G15670 TAIR:At3g15670 InParanoid:Q9LW12 OMA:QYTKETA PhylomeDB:Q9LW12 ArrayExpress:Q9LW12 Genevestigator:Q9LW12 Uniprot:Q9LW12

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig18603	12	37	-1.753	7.91E-05	TAIR|locus:2147304 - symbol:FQR1 "AT5G54500" species:3702 "Arabidopsis thaliana" [GO:0009733 "response to auxin stimulus" evidence=IEP] [GO:0010181 "FMN binding" evidence=IDA] [GO:0016655 "oxidoreductase activity, acting on NADH or NADPH, quinone or similar compound as acceptor" evidence=IDA] [GO:0055114 "oxidation-reduction process" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] InterPro:IPR008254 InterPro:IPR010089 PROSITE:PS50902 Pfam:PF03358 GO:GO:0005886 GO:GO:0005774 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0045892 GO:GO:0009733 GO:GO:0016655 GO:GO:0010181 EMBL:AB026634 HOGENOM:HBG686708 InterPro:IPR005025 TIGRFAMs:TIGR01755 ProtClustDB:CLSN2685577 EMBL:AY120735 EMBL:BT002194 IPI:IPI00529112 RefSeq:NP_200261.1 UniGene:At.43051 ProteinModelPortal:Q9LSQ5 SMR:Q9LSQ5 STRING:Q9LSQ5 ANU-2DPAGE:Q9LSQ5 PRIDE:Q9LSQ5 EnsemblPlants:AT5G54500.1 GeneID:835538 KEGG:ath:AT5G54500 TAIR:At5g54500 InParanoid:Q9LSQ5 OMA:YSHAFPL PhylomeDB:Q9LSQ5 ArrayExpress:Q9LSQ5 Genevestigator:Q9LSQ5 Uniprot:Q9LSQ5
Root	Isotig18606	62	0	6.825	2.85E-15	TAIR|locus:2132090 - symbol:ISU1 "AT4G22220" species:3702 "Arabidopsis thaliana" [GO:0016226 "iron-sulfur cluster assembly" evidence=IGI;ISS] [GO:0005198 "structural molecule activity" evidence=ISS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] InterPro:IPR002871 InterPro:IPR011339 Pfam:PF01592 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005506 GO:GO:0005759 GO:GO:0016226 EMBL:AL161556 GO:GO:0051537 EMBL:AL021712 eggNOG:COG0822 HOGENOM:HBG584215 OMA:SSMVTEM TIGRFAMs:TIGR01999 EMBL:AJ866966 EMBL:AF361579 EMBL:AY081721 EMBL:AY088584 IPI:IPI00516740 PIR:T04903 RefSeq:NP_193953.1 UniGene:At.43669 HSSP:Q57074 ProteinModelPortal:O49627 SMR:O49627 IntAct:O49627 STRING:O49627 PRIDE:O49627 EnsemblPlants:AT4G22220.1 GeneID:828316 KEGG:ath:AT4G22220 TAIR:At4g22220 InParanoid:O49627 PhylomeDB:O49627 ProtClustDB:CLSN2684974 ArrayExpress:O49627 Genevestigator:O49627 Uniprot:O49627
Root	Isotig18667	4	26	-2.829	9.39E-06	ZFIN|ZDB-GENE-070410-9 - symbol:zgc:158463 "zgc:158463" species:7955 "Danio rerio" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] ZFIN:ZDB-GENE-070410-9 EMBL:BX296557 EMBL:BX537263 EMBL:BC129240 IPI:IPI00837201 RefSeq:NP_001091866.1 RefSeq:XP_003200836.1 UniGene:Dr.155369 Ensembl:ENSDART00000102863 Ensembl:ENSDART00000126982 GeneID:100037361 GeneID:100151188 KEGG:dre:100037361 KEGG:dre:100151188 eggNOG:NOG298153 GeneTree:ENSGT00390000016898 InParanoid:A2VD29 OMA:ACHQHAL OrthoDB:EOG4FJ8BF Bgee:A2VD29 Uniprot:A2VD29
Root	Isotig18673	17	2	2.958	0.000459627	FB|FBgn0052133 - symbol:ptip species:7227 "Drosophila melanogaster" [GO:0008134 "transcription factor binding" evidence=ISS] [GO:0005622 "intracellular" evidence=IEA] [GO:0007448 "anterior/posterior pattern specification, imaginal disc" evidence=IMP] [GO:0016571 "histone methylation" evidence=IMP] [GO:0009880 "embryonic pattern specification" evidence=IMP] [GO:0002805 "regulation of antimicrobial peptide biosynthetic process" evidence=IMP] InterPro:IPR001357 Pfam:PF00533 PROSITE:PS50172 SMART:SM00292 EMBL:AE014296 GO:GO:0005622 SUPFAM:SSF52113 GO:GO:0009880 GO:GO:0002805 eggNOG:NOG310206 GO:GO:0016571 GO:GO:0007448 GeneTree:ENSGT00600000084454 KO:K14972 RefSeq:NP_729947.2 UniGene:Dm.24000 ProteinModelPortal:Q9VUB7 SMR:Q9VUB7 IntAct:Q9VUB7 MINT:MINT-1742539 STRING:Q9VUB7 EnsemblMetazoa:FBtr0075784 GeneID:39552 KEGG:dme:Dmel_CG32133 UCSC:CG32133-RA CTD:39552 FlyBase:FBgn0052133 InParanoid:Q9VUB7 OMA:QRHVINT OrthoDB:EOG41G1K5 PhylomeDB:Q9VUB7 NextBio:814237 ArrayExpress:Q9VUB7 Bgee:Q9VUB7 Uniprot:Q9VUB7
Root	Isotig18678	40	0	6.193	1.34E-10	TAIR|locus:2093307 - symbol:AT3G15670 "AT3G15670" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0009793 "embryo development ending in seed dormancy" evidence=ISS] [GO:0005634 "nucleus" evidence=IDA] GO:GO:0005634 EMBL:CP002686 EMBL:AB017071 ProtClustDB:CLSN2679745 EMBL:AY040026 EMBL:AY054162 EMBL:AY079410 IPI:IPI00542660 RefSeq:NP_188188.1 UniGene:At.5382 STRING:Q9LW12 PRIDE:Q9LW12 ProMEX:Q9LW12 EnsemblPlants:AT3G15670.1 GeneID:820810 KEGG:ath:AT3G15670 TAIR:At3g15670 InParanoid:Q9LW12 OMA:QYTKETA PhylomeDB:Q9LW12 ArrayExpress:Q9LW12 Genevestigator:Q9LW12 Uniprot:Q9LW12
Root	Isotig18688	25	3	2.930	2.36E-05	TAIR|locus:2044641 - symbol:COR413-PM1 "AT2G15970" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005886 "plasma membrane" evidence=ISS] [GO:0009631 "cold acclimation" evidence=IEP] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] [GO:0042631 "cellular response to water deprivation" evidence=IEP] [GO:0005773 "vacuole" evidence=IDA] GO:GO:0009737

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0005773 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0042631 GO:GO:0009631 EMBL:AC006438 UniGene:At.22305 HOGENOM:HBG595418 ProtClustDB:CLSN2717102 InterPro:IPR008892 Pfam:PF05562 eggNOG:NOG267474 EMBL:AF283004 EMBL:AY093767 EMBL:AY088558 EMBL:AY143813 EMBL:AB044404 IPI:IPI00547690 PIR:C84535 RefSeq:NP_179196.1 UniGene:At.24347 STRING:Q9XIM7 PRIDE:Q9XIM7 EnsemblPlants:AT2G15970.1 GeneID:816092 KEGG:ath:AT2G15970 TAIR:At2g15970 InParanoid:Q9XIM7 OMA:GTTFLEW PhylomeDB:Q9XIM7 ArrayExpress:Q9XIM7 Genevestigator:Q9XIM7 Uniprot:Q9XIM7
Root	Isotig18697	34	0	5.958	2.97E-09	TAIR|locus:2139777 - symbol:OSM34 "AT4G11650" species:3702 "Arabidopsis thaliana" [GO:0051707 "response to other organism" evidence=ISS] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0009817 "defense response to fungus, incompatible interaction" evidence=IDA] [GO:0009816 "defense response to bacterium, incompatible interaction" evidence=ISS] Pfam:PF00314 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0009651 GO:GO:0009817 EMBL:AL161532 EMBL:AL049500 EMBL:X89008 IPI:IPI00528920 PIR:T04212 RefSeq:NP_192902.1 UniGene:At.25216 ProteinModelPortal:P50700 SMR:P50700 STRING:P50700 PRIDE:P50700 EnsemblPlants:AT4G11650.1 GeneID:826770 KEGG:ath:AT4G11650 TAIR:At4g11650 eggNOG:NOG304630 HOGENOM:HBG748210 InParanoid:P50700 OMA:RVVFCPR PhylomeDB:P50700 ProtClustDB:CLSN2915891 ArrayExpress:P50700 Genevestigator:P50700 GermOnline:AT4G11650 InterPro:IPR001938 InterPro:IPR017949 Gene3D:G3DSA:2.60.110.10 PIRSF:PIRSF002703 PRINTS:PR00347 SMART:SM00205 SUPFAM:SSF49870 PROSITE:PS00316 PROSITE:PS51367 Uniprot:P50700
Root	Isotig18701	2	27	-3.884	2.43E-07	TAIR|locus:2012773 - symbol:ERD9 "AT1G10370" species:3702 "Arabidopsis thaliana" [GO:0004364 "glutathione transferase activity" evidence=ISS;IDA] [GO:0005737 "cytoplasm" evidence=NAS] [GO:0009407 "toxin catabolic process" evidence=TAS] [GO:0009507 "chloroplast" evidence=IDA] [GO:0080167 "response to karrikin" evidence=IEP] [GO:0006749 "glutathione metabolic process" evidence=IMP] [GO:0009704 "de-etiolation" evidence=IMP] [GO:0048527 "lateral root development" evidence=IMP] [GO:0060416 "response to growth hormone stimulus" evidence=IEP] [GO:0009651 "response to salt stress" evidence=IMP] [GO:0080148 "negative regulation of response to water deprivation" evidence=IMP] InterPro:IPR004045 PROSITE:PS50404 InterPro:IPR004046 Pfam:PF00043 EMBL:CP002684 GO:GO:0005829 GO:GO:0009507 GO:GO:0009651 GO:GO:0080167 GO:GO:0048527 GO:GO:0009636 GO:GO:0040008 InterPro:IPR012336 Gene3D:G3DSA:3.40.30.10 SUPFAM:SSF52833 InterPro:IPR010987 Gene3D:G3DSA:1.20.1050.10 SUPFAM:SSF47616 PROSITE:PS50405 GO:GO:0060416 EMBL:AC005489 GO:GO:0006749 InterPro:IPR017933 GO:GO:0004364 GO:GO:0009407 eggNOG:NOG288793 HOGENOM:HBG749301 HSSP:O04941 EMBL:AB039930 EMBL:AF288191 EMBL:BT023743 IPI:IPI00532578 RefSeq:NP_172508.4 UniGene:At.11290 ProteinModelPortal:Q9FUS8 SMR:Q9FUS8 PRIDE:Q9FUS8 EnsemblPlants:AT1G10370.1 GeneID:837576 KEGG:ath:AT1G10370 TAIR:At1g10370 InParanoid:Q9FUS8 ProtClustDB:CLSN2679578 Genevestigator:Q9FUS8 GO:GO:0009704 GO:GO:0080148 Uniprot:Q9FUS8
Root	Isotig18718	49	0	6.486	1.48E-12	TAIR|locus:2043358 - symbol:TSPO "AT2G47770" species:3702 "Arabidopsis thaliana" [GO:0005783 "endoplasmic reticulum" evidence=IDA] [GO:0005795 "Golgi stack" evidence=IDA] [GO:0006970 "response to osmotic stress" evidence=IEP] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] [GO:0016020 "membrane" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] [GO:0006778 "porphyrin-containing compound metabolic process" evidence=IMP] [GO:0020037 "heme binding" evidence=IDA] InterPro:IPR004307 Pfam:PF03073 PIRSF:PIRSF005859 GO:GO:0005783 GO:GO:0016021 GO:GO:0009737 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0005795 GO:GO:0009651 EMBL:AC005309 GO:GO:0020037 GO:GO:0006778 PANTHER:PTHR10057 EMBL:AF428356 EMBL:AY045981 EMBL:AY079391 IPI:IPI00544586 PIR:C84919 RefSeq:NP_566110.1 UniGene:At.23206 IntAct:O82245 STRING:O82245 PRIDE:O82245 EnsemblPlants:AT2G47770.1 GeneID:819389 KEGG:ath:AT2G47770 TAIR:At2g47770 eggNOG:NOG296779 HOGENOM:HBG749672 InParanoid:O82245 OMA:SSSWIPP PhylomeDB:O82245 ProtClustDB:CLSN2688990 ArrayExpress:O82245 Genevestigator:O82245 Uniprot:O82245
Root	Isotig18723	84	4	4.263	3.52E-19	TAIR|locus:2064965 - symbol:EULS3 "AT2G39050" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0030246 "carbohydrate binding" evidence=IDA] GO:GO:0005634 GO:GO:0005737 EMBL:CP002685 GenomeReviews:CT485783_GR InterPro:IPR000772 SUPFAM:SSF50370 PROSITE:PS50231 GO:GO:0030246 EMBL:AC005770 Pfam:PF14200 EMBL:AF411801 EMBL:AY093795 EMBL:AY087909 IPI:IPI00536641 PIR:E84812 RefSeq:NP_565899.1 UniGene:At.22599 ProteinModelPortal:Q945P1 SMR:Q945P1

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						PRIDE:Q945P1 EnsemblPlants:AT2G39050.1 GeneID:818491 KEGG:ath:AT2G39050 TAIR:At2g39050 eggNOG:NOG254161 HOGENOM:HBG750017 InParanoid:Q945P1 OMA:GYRTIRM PhylomeDB:Q945P1 ProtClustDB:CLSN2681741 ArrayExpress:Q945P1 Genevestigator:Q945P1 Uniprot:Q945P1
Root	Isotig18731	168	27	2.508	5.77E-24	TAIR|locus:2064965 - symbol:EULS3 "AT2G39050" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0030246 "carbohydrate binding" evidence=IDA] GO:GO:0005634 GO:GO:0005737 EMBL:CP002685 GenomeReviews:CT485783_GR InterPro:IPR000772 SUPFAM:SSF50370 PROSITE:PS50231 GO:GO:0030246 EMBL:AC005770 Pfam:PF14200 EMBL:AF411801 EMBL:AY093795 EMBL:AY087909 IPI:IPI00536641 PIR:E84812 RefSeq:NP_565899.1 UniGene:At.22599 ProteinModelPortal:Q945P1 SMR:Q945P1 PRIDE:Q945P1 EnsemblPlants:AT2G39050.1 GeneID:818491 KEGG:ath:AT2G39050 TAIR:At2g39050 eggNOG:NOG254161 HOGENOM:HBG750017 InParanoid:Q945P1 OMA:GYRTIRM PhylomeDB:Q945P1 ProtClustDB:CLSN2681741 ArrayExpress:Q945P1 Genevestigator:Q945P1 Uniprot:Q945P1
Root	Isotig18756	67	3	4.352	9.28E-16	TAIR|locus:2119003 - symbol:AT4G21620 "AT4G21620" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002687 GenomeReviews:CT486007_GR EMBL:AL035527 EMBL:AL161555 UniGene:At.44911 EMBL:AF360336 EMBL:AY051071 EMBL:AY058136 EMBL:AY085743 EMBL:AK226947 IPI:IPI00547700 PIR:T05837 RefSeq:NP_193893.1 IntAct:Q9SVT5 PRIDE:Q9SVT5 EnsemblPlants:AT4G21620.1 GeneID:828249 KEGG:ath:AT4G21620 TAIR:At4g21620 eggNOG:NOG325948 InParanoid:Q9SVT5 OMA:CKKKCIA ProtClustDB:CLSN2915919 Genevestigator:Q9SVT5 Uniprot:Q9SVT5
Root	Isotig18768	0	15	-5.036	4.38E-05	TAIR|locus:2153529 - symbol:PRX52 "AT5G05340" species:3702 "Arabidopsis thaliana" [GO:0004601 "peroxidase activity" evidence=ISS] [GO:0006979 "response to oxidative stress" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0005618 "cell wall" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0005829 "cytosol" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR000823 InterPro:IPR002016 InterPro:IPR010255 InterPro:IPR019793 InterPro:IPR019794 Pfam:PF00141 PRINTS:PR00458 PRINTS:PR00461 PROSITE:PS00435 PROSITE:PS00436 PROSITE:PS50873 GO:GO:0005829 GO:GO:0048046 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005618 GO:GO:0005515 GO:GO:0020037 GO:GO:0004601 GO:GO:0042744 HOGENOM:HBG597790 SUPFAM:SSF48113 EMBL:AB010692 KO:K00430 EMBL:AY065270 IPI:IPI00527468 RefSeq:NP_196153.1 UniGene:At.28537 ProteinModelPortal:Q9FLC0 SMR:Q9FLC0 IntAct:Q9FLC0 STRING:Q9FLC0 PeroxiBase:218 PRIDE:Q9FLC0 EnsemblPlants:AT5G05340.1 GeneID:830416 KEGG:ath:AT5G05340 GeneFarm:1905 TAIR:At5g05340 eggNOG:NOG298084 InParanoid:Q9FLC0 OMA:TNFRARI PhylomeDB:Q9FLC0 ProtClustDB:CLSN2916362 ArrayExpress:Q9FLC0 Genevestigator:Q9FLC0 GermOnline:AT5G05340 Uniprot:Q9FLC0
Root	Isotig18822	51	0	6.543	5.57E-13	TAIR|locus:2132090 - symbol:ISU1 "AT4G22220" species:3702 "Arabidopsis thaliana" [GO:0016226 "iron-sulfur cluster assembly" evidence=IGI;ISS] [GO:0005198 "structural molecule activity" evidence=ISS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] InterPro:IPR002871 InterPro:IPR011339 Pfam:PF01592 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005506 GO:GO:0005759 GO:GO:0016226 EMBL:AL161556 GO:GO:0051537 EMBL:AL021712 eggNOG:COG0822 HOGENOM:HBG584215 OMA:SSMVTEM TIGRFAMs:TIGR01999 EMBL:AJ866966 EMBL:AF361579 EMBL:AY081721 EMBL:AY088584 IPI:IPI00516740 PIR:T04903 RefSeq:NP_193953.1 UniGene:At.43669 HSSP:Q57074 ProteinModelPortal:O49627 SMR:O49627 IntAct:O49627 STRING:O49627 PRIDE:O49627 EnsemblPlants:AT4G22220.1 GeneID:828316 KEGG:ath:AT4G22220 TAIR:At4g22220 InParanoid:O49627 PhylomeDB:O49627 ProtClustDB:CLSN2684974 ArrayExpress:O49627 Genevestigator:O49627 Uniprot:O49627
Root	Isotig18847	49	17	1.398	0.000229772	UNIPROTKB|F1S5P1 - symbol:COL17A1 "Uncharacterized protein" species:9823 "Sus scrofa" [GO:0030056 "hemidesmosome" evidence=IEA] [GO:0031581 "hemidesmosome assembly" evidence=IEA] InterPro:IPR008160 Pfam:PF01391 GeneTree:ENSGT00650000093297 OMA:GDMGSQG EMBL:CT737413 EMBL:CT737145 Ensembl:ENSSSCT00000011603 Uniprot:F1S5P1
Root	Isotig18911	0	28	-5.936	1.79E-08	DICTYBASE|DDB_G0276937 - symbol:expl5 "expansin-like protein" species:44689 "Dictyostelium discoideum" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] dictyBase:DDB_G0276937 Pfam:PF01357 GO:GO:0005576 GenomeReviews:CM000151_GR EMBL:AAFI02000019 InterPro:IPR014733 InterPro:IPR009009 InterPro:IPR007112 Gene3D:G3DSA:2.40.40.10 Pfam:PF03330 SMART:SM00837 SUPFAM:SSF50685

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						PROSITE:PS50842 InterPro:IPR007117 Gene3D:G3DSA:2.60.40.760 SUPFAM:SSF49590 eggNOG:NOG119598 HSSP:P43213 HOGENOM:HBG077223 ProtClustDB:CLSZ2430666 RefSeq:XP_642827.1 ProteinModelPortal:Q86AV4 EnsemblProtists:DDB0231627 GeneID:8620690 KEGG:ddi:DDB_G0276937 InParanoid:Q86AV4 OMA:WISMARN Uniprot:Q86AV4
Root	Isotig18912	36	81	-1.299	2.86E-06	TAIR|locus:2047097 - symbol:AT2G21130 species:3702 "Arabidopsis thaliana" [GO:0003755 "peptidyl-prolyl cis-trans isomerase activity" evidence=IEA;ISS] [GO:0006457 "protein folding" evidence=IEA;ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR002130 InterPro:IPR020892 InterPro:IPR024936 Pfam:PF00160 PIRSF:PIRSF001467 PRINTS:PR00153 PROSITE:PS00170 PROSITE:PS50072 GO:GO:0005829 GO:GO:0005886 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0006457 GO:GO:0042277 eggNOG:COG0652 HOGENOM:HBG610621 KO:K01802 ProtClustDB:CLSN2683570 GO:GO:0003755 Gene3D:G3DSA:2.40.100.10 SUPFAM:SSF50891 EMBL:AF020434 EMBL:AC006264 EMBL:AY087454 IPI:IPI00537930 PIR:E84597 PIR:T50772 RefSeq:NP_179709.1 UniGene:At.10399 ProteinModelPortal:Q9SKQ0 SMR:Q9SKQ0 STRING:Q9SKQ0 PRIDE:Q9SKQ0 ProMEX:Q9SKQ0 EnsemblPlants:AT2G21130.1 GeneID:816648 KEGG:ath:AT2G21130 TAIR:At2g21130 InParanoid:Q9SKQ0 OMA:HPKVFFD PhylomeDB:Q9SKQ0 ArrayExpress:Q9SKQ0 Genevestigator:Q9SKQ0 GermOnline:AT2G21130 Uniprot:Q9SKQ0
Root	Isotig18913	51	15	1.637	2.43E-05	TAIR|locus:2196646 - symbol:PGY2 "PIGGYBACK2" species:3702 "Arabidopsis thaliana" [GO:0003735 "structural constituent of ribosome" evidence=IEA;ISS] [GO:0006412 "translation" evidence=ISS] [GO:0015934 "large ribosomal subunit" evidence=ISS] [GO:0019843 "rRNA binding" evidence=IEA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0022625 "cytosolic large ribosomal subunit" evidence=IDA] [GO:0009955 "adaxial/abaxial pattern specification" evidence=IGI] [GO:0005829 "cytosol" evidence=RCA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR000702 InterPro:IPR002359 InterPro:IPR020040 Pfam:PF00347 PIRSF:PIRSF002162 PROSITE:PS00700 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005886 GO:GO:0009506 GO:GO:0005774 GO:GO:0005730 GO:GO:0006412 GO:GO:0009941 GO:GO:0003735 GO:GO:0019843 GO:GO:0022625 EMBL:AC021045 UniGene:At.23014 GO:GO:0009955 eggNOG:COG0097 HOGENOM:HBG606796 Gene3D:G3DSA:3.90.930.12 PANTHER:PTHR11655 SUPFAM:SSF56053 EMBL:X91958 EMBL:AF324688 EMBL:AF326873 EMBL:AF339694 EMBL:AF375419 EMBL:AY039593 EMBL:AY054156 EMBL:AY058051 EMBL:AY072446 EMBL:AY128910 EMBL:Z17727 EMBL:Z17728 IPI:IPI00545250 PIR:F86455 PIR:S71255 RefSeq:NP_564417.1 RefSeq:NP_564418.1 UniGene:At.22864 UniGene:At.68560 UniGene:At.7385 ProteinModelPortal:P49209 SMR:P49209 IntAct:P49209 STRING:P49209 PRIDE:P49209 EnsemblPlants:AT1G33120.1 EnsemblPlants:AT1G33140.1 GeneID:840208 GeneID:840211 KEGG:ath:AT1G33120 KEGG:ath:AT1G33140 GeneFarm:416 GeneFarm:420 TAIR:At1g33120 TAIR:At1g33140 InParanoid:P49209 KO:K02940 OMA:RDTRIFQ PhylomeDB:P49209 ProtClustDB:CLSN2685696 ArrayExpress:P49209 Genevestigator:P49209 GermOnline:AT1G33120 Uniprot:P49209
Root	Isotig18952	0	13	-4.829	0.000155955	TAIR|locus:2092950 - symbol:AT3G20980 "AT3G20980" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] GenomeReviews:BA000014_GR EMBL:AP000604 eggNOG:KOG0017 IPI:IPI01020495 PRIDE:Q9LJD3 TAIR:At3g20980 InParanoid:Q9LJD3 PhylomeDB:Q9LJD3 Genevestigator:Q9LJD3 Uniprot:Q9LJD3
Root	Isotig18980	16	0	4.871	5.89E-05	TAIR|locus:504955645 - symbol:PIMT1 "protein-l-isoaspartate methyltransferase 1" species:3702 "Arabidopsis thaliana" [GO:0004719 "protein-L-isoaspartate (D-aspartate) O-methyltransferase activity" evidence=IEA;ISS] [GO:0006464 "protein modification process" evidence=ISS] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0007568 "aging" evidence=IMP] [GO:0009651 "response to salt stress" evidence=IMP] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] [GO:0009845 "seed germination" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR000682 Pfam:PF01135 PROSITE:PS01279 GO:GO:0005829 GO:GO:0009737 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0007568 GO:GO:0009651 GO:GO:0009845 EMBL:AL049659 UniGene:At.3161 UniGene:At.70492 eggNOG:COG2518 GO:GO:0004719 PANTHER:PTHR11579 EMBL:U31288 EMBL:BT029372 IPI:IPI00518020 PIR:T06709 RefSeq:NP_680112.2 RefSeq:NP_851013.2 ProteinModelPortal:Q42539 SMR:Q42539 STRING:Q42539 PRIDE:Q42539 EnsemblPlants:AT3G48330.1 EnsemblPlants:AT3G48330.2 GeneID:823991 KEGG:ath:AT3G48330

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						TAIR:At3g48330 HOGENOM:HBG699907 InParanoid:Q42539 PhylomeDB:Q42539 ProtClustDB:CLSN2708507 Genevestigator:Q42539 TIGRFAMs:TIGR00080 Uniprot:Q42539
Root	Isotig19014	12	0	4.456	0.000626491	No hit
Root	Isotig19034	0	12	-4.714	0.000297064	TAIR|locus:2057175 - symbol:PYL4 "AT2G38310" species:3702 "Arabidopsis thaliana" [GO:0005515 "protein binding" evidence=IPI] [GO:0004872 "receptor activity" evidence=IDA] [GO:0009738 "abscisic acid mediated signaling pathway" evidence=IGI;IDA] GO:GO:0005634 GO:GO:0005737 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0042803 GO:GO:0009738 GO:GO:0004872 InterPro:IPR023393 Gene3D:G3DSA:3.30.530.20 EMBL:AC004683 GO:GO:0010427 KO:K14496 InterPro:IPR019587 Pfam:PF10604 HOGENOM:HBG598713 EMBL:AY039586 EMBL:AY054141 EMBL:AY087146 IPI:IPI00527852 PIR:T02514 RefSeq:NP_565887.1 UniGene:At.12775 ProteinModelPortal:O80920 SMR:O80920 DIP:DIP-53474N IntAct:O80920 STRING:O80920 PRIDE:O80920 EnsemblPlants:AT2G38310.1 GeneID:818411 KEGG:ath:AT2G38310 TAIR:At2g38310 eggNOG:NOG268307 InParanoid:O80920 OMA:DERHVIS PhylomeDB:O80920 ProtClustDB:CLSN2917266 ArrayExpress:O80920 Genevestigator:O80920 Uniprot:O80920
Root	Isotig19084	122	38	1.554	3.22E-10	No hit
Root	Isotig19089	3	18	-2.714	0.000308932	TAIR|locus:2016477 - symbol:AT1G19530 "AT1G19530" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0009061 "anaerobic respiration" evidence=IEP;IMP] EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009061 EMBL:AF370213 EMBL:AY056353 EMBL:AY087914 IPI:IPI00522726 RefSeq:NP_564090.1 UniGene:At.20370 IntAct:Q93WK6 STRING:Q93WK6 PRIDE:Q93WK6 DNASU:838540 EnsemblPlants:AT1G19530.1 GeneID:838540 KEGG:ath:AT1G19530 TAIR:At1g19530 eggNOG:NOG250070 HOGENOM:HBG746605 InParanoid:Q93WK6 OMA:NWAFLNE PhylomeDB:Q93WK6 ProtClustDB:CLSN2917023 ArrayExpress:Q93WK6 Genevestigator:Q93WK6 Uniprot:Q93WK6
Root	Isotig19220	23	0	5.395	1.11E-06	TAIR|locus:2043358 - symbol:TSPO "AT2G47770" species:3702 "Arabidopsis thaliana" [GO:0005783 "endoplasmic reticulum" evidence=IDA] [GO:0005795 "Golgi stack" evidence=IDA] [GO:0006970 "response to osmotic stress" evidence=IEP] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] [GO:0016020 "membrane" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] [GO:0006778 "porphyrin-containing compound metabolic process" evidence=IMP] [GO:0020037 "heme binding" evidence=IDA] InterPro:IPR004307 Pfam:PF03073 PIRSF:PIRSF005859 GO:GO:0005783 GO:GO:0016021 GO:GO:0009737 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0005795 GO:GO:0009651 EMBL:AC005309 GO:GO:0020037 GO:GO:0006778 PANTHER:PTHR10057 EMBL:AF428356 EMBL:AY045981 EMBL:AY079391 IPI:IPI00544586 PIR:C84919 RefSeq:NP_566110.1 UniGene:At.23206 IntAct:O82245 STRING:O82245 PRIDE:O82245 EnsemblPlants:AT2G47770.1 GeneID:819389 KEGG:ath:AT2G47770 TAIR:At2g47770 eggNOG:NOG296779 HOGENOM:HBG749672 InParanoid:O82245 OMA:SSSWIPP PhylomeDB:O82245 ProtClustDB:CLSN2688990 ArrayExpress:O82245 Genevestigator:O82245 Uniprot:O82245
Root	Isotig19304	15	0	4.778	0.000105609	TAIR|locus:2012320 - symbol:GolS3 "AT1G09350" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0016051 "carbohydrate biosynthetic process" evidence=ISS] [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0016758 "transferase activity, transferring hexosyl groups" evidence=ISS] [GO:0006979 "response to oxidative stress" evidence=IEP] [GO:0009409 "response to cold" evidence=IEP] InterPro:IPR002495 Pfam:PF01501 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0006979 GO:GO:0009409 EMBL:AC003970 GO:GO:0016757 CAZy:GT8 HSSP:P13280 HOGENOM:HBG316599 ProtClustDB:PLN00176 eggNOG:NOG303574 EMBL:AF370546 EMBL:AY081452 EMBL:AB062850 IPI:IPI00519127 PIR:F86226 RefSeq:NP_172406.1 UniGene:At.15716 UniGene:At.67798 ProteinModelPortal:O80518 SMR:O80518 STRING:O80518 PRIDE:O80518 EnsemblPlants:AT1G09350.1 GeneID:837457 KEGG:ath:AT1G09350 TAIR:At1g09350 InParanoid:O80518 OMA:KMLVEKW PhylomeDB:O80518 ArrayExpress:O80518 Genevestigator:O80518 Uniprot:O80518
Root	Isotig19306	4	22	-2.588	0.000101225	TAIR|locus:2093247 - symbol:AT3G15630 "AT3G15630" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002686 GenomeReviews:BA000014_GR EMBL:AB017071 EMBL:AY052241 EMBL:AY060508 IPI:IPI00533188 RefSeq:NP_566521.1 UniGene:At.20536 STRING:Q9LW16 EnsemblPlants:AT3G15630.1 GeneID:820805 KEGG:ath:AT3G15630 TAIR:At3g15630 eggNOG:NOG293987 HOGENOM:HBG597979 InParanoid:Q9LW16 OMA:TIISCSA PhylomeDB:Q9LW16 ProtClustDB:CLSN2688413 Genevestigator:Q9LW16 Uniprot:Q9LW16

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig19352	1	16	-4.129	5.13E-05	TAIR|locus:2012773 - symbol:ERD9 "AT1G10370" species:3702 "Arabidopsis thaliana" [GO:0004364 "glutathione transferase activity" evidence=ISS;IDA] [GO:0005737 "cytoplasm" evidence=NAS] [GO:0009407 "toxin catabolic process" evidence=TAS] [GO:0009507 "chloroplast" evidence=IDA] [GO:0080167 "response to karrikin" evidence=IEP] [GO:0006749 "glutathione metabolic process" evidence=IMP] [GO:0009704 "de-etiolation" evidence=IMP] [GO:0048527 "lateral root development" evidence=IMP] [GO:0060416 "response to growth hormone stimulus" evidence=IEP] [GO:0009651 "response to salt stress" evidence=IMP] [GO:0080148 "negative regulation of response to water deprivation" evidence=IMP] InterPro:IPR004045 PROSITE:PS50404 InterPro:IPR004046 Pfam:PF00043 EMBL:CP002684 GO:GO:0005829 GO:GO:0009507 GO:GO:0009651 GO:GO:0080167 GO:GO:0048527 GO:GO:0009636 GO:GO:0040008 InterPro:IPR012336 Gene3D:G3DSA:3.40.30.10 SUPFAM:SSF52833 InterPro:IPR010987 Gene3D:G3DSA:1.20.1050.10 SUPFAM:SSF47616 PROSITE:PS50405 GO:GO:0060416 EMBL:AC005489 GO:GO:0006749 InterPro:IPR017933 GO:GO:0004364 GO:GO:0009407 eggNOG:NOG288793 HOGENOM:HBG749301 HSSP:O04941 EMBL:AB039930 EMBL:AF288191 EMBL:BT023743 IPI:IPI00532578 RefSeq:NP_172508.4 UniGene:At.11290 ProteinModelPortal:Q9FUS8 SMR:Q9FUS8 PRIDE:Q9FUS8 EnsemblPlants:AT1G10370.1 GeneID:837576 KEGG:ath:AT1G10370 TAIR:At1g10370 InParanoid:Q9FUS8 ProtClustDB:CLSN2679578 Genevestigator:Q9FUS8 GO:GO:0009704 GO:GO:0080148 Uniprot:Q9FUS8
Root	Isotig19392	102	40	1.222	1.69E-06	No hit
Root	Isotig19425	0	24	-5.714	1.84E-07	TAIR|locus:2162366 - symbol:AT5G42510 "AT5G42510" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0006952 "defense response" evidence=ISS] Pfam:PF03018 EMBL:CP002688 GenomeReviews:BA000015_GR EMBL:AB016888 InterPro:IPR004265 HOGENOM:HBG605442 ProtClustDB:CLSN2686597 EMBL:BT030625 IPI:IPI00537223 RefSeq:NP_199066.1 UniGene:At.65624 PRIDE:Q9FIG6 EnsemblPlants:AT5G42510.1 GeneID:834258 KEGG:ath:AT5G42510 TAIR:At5g42510 eggNOG:NOG235510 InParanoid:Q9FIG6 OMA:GMVAMID PhylomeDB:Q9FIG6 Genevestigator:Q9FIG6 Uniprot:Q9FIG6
Root	Isotig19439	26	0	5.571	2.13E-07	No hit
Root	Isotig19471	6	27	-2.299	5.77E-05	TAIR|locus:2083715 - symbol:AT3G52100 species:3702 "Arabidopsis thaliana" [GO:0008270 "zinc ion binding" evidence=IEA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR001841 InterPro:IPR001965 InterPro:IPR019787 PROSITE:PS50016 PROSITE:PS50089 SMART:SM00184 SMART:SM00249 InterPro:IPR011011 GO:GO:0009506 GenomeReviews:BA000014_GR GO:GO:0008270 InterPro:IPR013083 Gene3D:G3DSA:3.30.40.10 SUPFAM:SSF57903 InterPro:IPR019786 PROSITE:PS01359 eggNOG:NOG12793 EMBL:AL049711 HOGENOM:HBG589189 IPI:IPI01020590 PIR:T49089 ProteinModelPortal:Q9SUZ5 SMR:Q9SUZ5 PRIDE:Q9SUZ5 TAIR:At3g52100 InParanoid:Q9SUZ5 PhylomeDB:Q9SUZ5 Genevestigator:Q9SUZ5 Uniprot:Q9SUZ5
Root	Isotig19499	0	11	-4.588	0.000569522	TAIR|locus:2089526 - symbol:CYP72A7 ""cytochrome P450, family 72, subfamily A, polypeptide 7"" species:3702 "Arabidopsis thaliana" [GO:0004497 "monooxygenase activity" evidence=IEA] [GO:0005506 "iron ion binding" evidence=IEA] [GO:0009055 "electron carrier activity" evidence=IEA] [GO:0019825 "oxygen binding" evidence=ISS] [GO:0020037 "heme binding" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0005783 "endoplasmic reticulum" evidence=IDA] InterPro:IPR001128 InterPro:IPR002401 InterPro:IPR017972 Pfam:PF00067 PRINTS:PR00385 PRINTS:PR00463 PROSITE:PS00086 GO:GO:0005783 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0009055 GO:GO:0004497 eggNOG:COG2124 GO:GO:0020037 Gene3D:G3DSA:1.10.630.10 SUPFAM:SSF48264 GO:GO:0016705 HSSP:P14779 HOGENOM:HBG715383 EMBL:AB023038 ProtClustDB:CLSN2684942 EMBL:AY072303 EMBL:BT003388 IPI:IPI00536730 RefSeq:NP_188079.1 UniGene:At.43876 ProteinModelPortal:Q9LUD3 SMR:Q9LUD3 PRIDE:Q9LUD3 EnsemblPlants:AT3G14610.1 GeneID:820689 KEGG:ath:AT3G14610 TAIR:At3g14610 InParanoid:Q9LUD3 OMA:WASHRRI PhylomeDB:Q9LUD3 ArrayExpress:Q9LUD3 Genevestigator:Q9LUD3 Uniprot:Q9LUD3
Root	Isotig19512	0	13	-4.829	0.000155955	TAIR|locus:2089915 - symbol:DMP1 "AT3G21520" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0005783 "endoplasmic reticulum" evidence=IDA] [GO:0009705 "plant-type vacuole membrane" evidence=IDA] GO:GO:0005783 EMBL:CP002686 GenomeReviews:BA000014_GR EMBL:AB019232 GO:GO:0009705 HOGENOM:HBG591658 InterPro:IPR007770 Pfam:PF05078 UniGene:At.50211 UniGene:At.66548 EMBL:AY080599 EMBL:AY114034 IPI:IPI00537148 RefSeq:NP_188789.2 PRIDE:Q9LVF4 EnsemblPlants:AT3G21520.1 GeneID:821706

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						KEGG:ath:AT3G21520 TAIR:At3g21520 eggNOG:NOG242170 InParanoid:Q9LVF4 OMA:ANTASCF PhylomeDB:Q9LVF4 ProtClustDB:CLSN2917949 ArrayExpress:Q9LVF4 Genevestigator:Q9LVF4 Uniprot:Q9LVF4
Root	Isotig19565	35	0	6.000	1.76E-09	TAIR|locus:2171032 - symbol:AT5G46960 species:3702 "Arabidopsis thaliana" [GO:0004857 "enzyme inhibitor activity" evidence=IEA] [GO:0008150 "biological_process" evidence=ND] [GO:0030599 "pectinesterase activity" evidence=IEA] [GO:0046910 "pectinesterase inhibitor activity" evidence=ISS] InterPro:IPR006501 Pfam:PF04043 SMART:SM00856 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0004857 EMBL:AB013394 GO:GO:0030599 Gene3D:G3DSA:1.20.140.40 SUPFAM:SSF101148 TIGRFAMs:TIGR01614 HOGENOM:HBG745715 IPI:IPI00525290 RefSeq:NP_568673.1 UniGene:At.49424 ProteinModelPortal:Q9FJR5 SMR:Q9FJR5 PRIDE:Q9FJR5 EnsemblPlants:AT5G46960.1 GeneID:834742 KEGG:ath:AT5G46960 TAIR:At5g46960 eggNOG:NOG255438 InParanoid:Q9FJR5 OMA:ASHADIG PhylomeDB:Q9FJR5 ProtClustDB:CLSN2917742 Genevestigator:Q9FJR5 Uniprot:Q9FJR5
Root	Isotig19678	0	19	-5.377	3.67E-06	No hit
Root	Isotig19692	0	15	-5.036	4.38E-05	No hit
Root	Isotig19702	0	26	-5.829	5.70E-08	UNIPROTKB|P83304 - symbol:P83304 "Mannose/glucose-specific lectin" species:185447 "Parkia platycephala" [GO:0000771 "agglutination involved in conjugation" evidence=IDA] [GO:0005536 "glucose binding" evidence=IDA] [GO:0005537 "mannose binding" evidence=IDA] [GO:0005575 "cellular_component" evidence=ND] GO:GO:0005537 GO:GO:0005536 InterPro:IPR001229 Gene3D:G3DSA:2.100.10.30 Pfam:PF01419 SMART:SM00915 SUPFAM:SSF51101 GO:GO:0000771 PDB:1ZGR PDB:1ZGS PDBsum:1ZGR PDBsum:1ZGS ProteinModelPortal:P83304 SMR:P83304 Uniprot:P83304
Root	Isotig19731	2	20	-3.451	2.08E-05	No hit
Root	Isotig19735	95	24	1.856	3.19E-10	TAIR|locus:2129795 - symbol:DI21 "AT4G15910" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0009790 "embryo development" evidence=ISS] [GO:0009414 "response to water deprivation" evidence=IEP] [GO:0009737 "response to abscisic acid stimulus" evidence=IGI] InterPro:IPR004926 Pfam:PF03242 GO:GO:0009737 EMBL:CP002687 GO:GO:0009414 EMBL:BT003165 EMBL:X78585 IPI:IPI00529996 PIR:S51479 RefSeq:NP_193326.4 UniGene:At.48862 STRING:Q39084 EnsemblPlants:AT4G15910.1 GeneID:827273 KEGG:ath:AT4G15910 TAIR:At4g15910 PhylomeDB:Q39084 ProtClustDB:CLSN2927415 Genevestigator:Q39084 Uniprot:Q39084
Root	Isotig19798	14	0	4.678	0.000190242	TAIR|locus:2158735 - symbol:AT5G44310 "AT5G44310" species:3702 "Arabidopsis thaliana" [GO:0009793 "embryo development ending in seed dormancy" evidence=ISS] EMBL:CP002688 EMBL:AB011475 IPI:IPI00522827 RefSeq:NP_199244.1 UniGene:At.43190 PRIDE:Q9FKV7 EnsemblPlants:AT5G44310.2 GeneID:834454 KEGG:ath:AT5G44310 TAIR:At5g44310 InParanoid:Q9FKV7 OMA:NEGASRA ProtClustDB:CLSN2687244 Genevestigator:Q9FKV7 Uniprot:Q9FKV7
Root	Isotig19815	1	52	-5.829	1.64E-14	TAIR|locus:2131749 - symbol:AT4G27270 species:3702 "Arabidopsis thaliana" [GO:0010181 "FMN binding" evidence=IEA] [GO:0016491 "oxidoreductase activity" evidence=IEA] [GO:0045892 "negative regulation of transcription, DNA-dependent" evidence=IEA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR008254 InterPro:IPR010089 PROSITE:PS50902 Pfam:PF03358 GO:GO:0005886 GO:GO:0009506 EMBL:CP002687 GO:GO:0045892 GO:GO:0016491 GO:GO:0010181 InterPro:IPR005025 TIGRFAMs:TIGR01755 ProtClustDB:CLSN2685577 EMBL:BT010514 EMBL:AK221196 IPI:IPI00538320 RefSeq:NP_194457.2 UniGene:At.32111 UniGene:At.45 ProteinModelPortal:Q6NQE2 SMR:Q6NQE2 IntAct:Q6NQE2 STRING:Q6NQE2 PRIDE:Q6NQE2 DNASU:828835 EnsemblPlants:AT4G27270.1 GeneID:828835 KEGG:ath:AT4G27270 TAIR:At4g27270 InParanoid:Q6NQE2 OMA:MYHWGAI PhylomeDB:Q6NQE2 Genevestigator:Q6NQE2 Uniprot:Q6NQE2
Root	Isotig19892	158	0	8.175	6.39E-33	No hit
Root	Isotig19917	215	0	8.619	3.50E-42	UNIPROTKB|A8CVF3 - symbol:DHN1 "Dehydrin DHN1" species:82927 "Avicennia marina" [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0010555 "response to mannitol stimulus" evidence=IEP] [GO:0042631 "cellular response to water deprivation" evidence=IEP] [GO:0071472 "cellular response to salt stress" evidence=IEP] [GO:0071482 "cellular response to light stimulus" evidence=IEP] InterPro:IPR000167 Pfam:PF00257 PROSITE:PS00315 PROSITE:PS00823 GO:GO:0005634 GO:GO:0005737 GO:GO:0071472 GO:GO:0042631 GO:GO:0010555 EMBL:EU121850 EMBL:EU121851 GO:GO:0071482 Uniprot:A8CVF3
Root	Isotig19949	58	0	6.729	1.90E-14	TAIR|locus:2132090 - symbol:ISU1 "AT4G22220" species:3702 "Arabidopsis thaliana" [GO:0016226 "iron-sulfur cluster assembly" evidence=IGI;ISS] [GO:0005198 "structural molecule activity" evidence=ISS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] InterPro:IPR002871 InterPro:IPR011339

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						Pfam:PF01592 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005506 GO:GO:0005759 GO:GO:0016226 EMBL:AL161556 GO:GO:0051537 EMBL:AL021712 eggNOG:COG0822 HOGENOM:HBG584215 OMA:SSMVTEM TIGRFAMs:TIGR01999 EMBL:AJ866966 EMBL:AF361579 EMBL:AY081721 EMBL:AY088584 IPI:IPI00516740 PIR:T04903 RefSeq:NP_193953.1 UniGene:At.43669 HSSP:Q57074 ProteinModelPortal:O49627 SMR:O49627 IntAct:O49627 STRING:O49627 PRIDE:O49627 EnsemblPlants:AT4G22220.1 GeneID:828316 KEGG:ath:AT4G22220 TAIR:At4g22220 InParanoid:O49627 PhylomeDB:O49627 ProtClustDB:CLSN2684974 ArrayExpress:O49627 Genevestigator:O49627 Uniprot:O49627
Root	Isotig19962	1	16	-4.129	5.13E-05	TAIR|locus:2152420 - symbol:PYL11 "AT5G45860" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] GO:GO:0005634 GO:GO:0005737 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0042803 GO:GO:0009738 GO:GO:0004872 InterPro:IPR023393 Gene3D:G3DSA:3.30.530.20 EMBL:AB016870 GO:GO:0010427 KO:K14496 InterPro:IPR019587 Pfam:PF10604 IPI:IPI00544403 RefSeq:NP_199398.1 UniGene:At.65641 ProteinModelPortal:Q9FJ50 SMR:Q9FJ50 IntAct:Q9FJ50 PRIDE:Q9FJ50 EnsemblPlants:AT5G45860.1 GeneID:834626 KEGG:ath:AT5G45860 TAIR:At5g45860 eggNOG:NOG256798 HOGENOM:HBG598713 InParanoid:Q9FJ50 OMA:QTIDAPL PhylomeDB:Q9FJ50 ProtClustDB:CLSN2685444 Genevestigator:Q9FJ50 Uniprot:Q9FJ50
Root	Isotig19965	0	11	-4.588	0.000569522	TAIR|locus:2162361 - symbol:AT5G42500 "AT5G42500" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0006952 "defense response" evidence=ISS] Pfam:PF03018 EMBL:CP002688 GenomeReviews:BA000015_GR EMBL:AB016888 InterPro:IPR004265 HOGENOM:HBG605442 ProtClustDB:CLSN2686597 eggNOG:NOG235510 EMBL:AY093095 EMBL:BT008442 IPI:IPI00528213 RefSeq:NP_199065.1 UniGene:At.30167 PRIDE:Q9FIG7 EnsemblPlants:AT5G42500.1 GeneID:834257 KEGG:ath:AT5G42500 TAIR:At5g42500 InParanoid:Q9FIG7 OMA:NFGVIMI PhylomeDB:Q9FIG7 ArrayExpress:Q9FIG7 Genevestigator:Q9FIG7 Uniprot:Q9FIG7
Root	Isotig20003	21	0	5.263	3.38E-06	TAIR|locus:2198175 - symbol:ADF11 "actin depolymerizing factor 11" species:3702 "Arabidopsis thaliana" [GO:0003779 "actin binding" evidence=IEA] [GO:0005622 "intracellular" evidence=IEA;ISS] [GO:0008150 "biological_process" evidence=ND] InterPro:IPR002108 Pfam:PF00241 PROSITE:PS51263 SMART:SM00102 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0003779 GO:GO:0005622 EMBL:AC009273 EMBL:AY072410 EMBL:BT001250 EMBL:AY088305 IPI:IPI00533839 PIR:A86149 RefSeq:NP_171680.1 UniGene:At.43294 ProteinModelPortal:Q9LQ81 SMR:Q9LQ81 STRING:Q9LQ81 PRIDE:Q9LQ81 EnsemblPlants:AT1G01750.1 GeneID:839281 KEGG:ath:AT1G01750 TAIR:At1g01750 eggNOG:NOG303866 HOGENOM:HBG628477 InParanoid:Q9LQ81 OMA:IVFKINE PhylomeDB:Q9LQ81 ProtClustDB:CLSN2682878 ArrayExpress:Q9LQ81 Genevestigator:Q9LQ81 GermOnline:AT1G01750 Uniprot:Q9LQ81
Root	Isotig20115	5	25	-2.451	5.85E-05	No hit
Root	Isotig20310	16	0	4.871	5.89E-05	UNIPROTKB|Q66GS9 - symbol:CEP135 "Centrosomal protein of 135 kDa" species:9606 "Homo sapiens" [GO:0000086 "G2/M transition of mitotic cell cycle" evidence=TAS] [GO:0000278 "mitotic cell cycle" evidence=TAS] [GO:0005813 "centrosome" evidence=IDA] [GO:0005814 "centriole" evidence=IDA] [GO:0005829 "cytosol" evidence=TAS] [GO:0007099 "centriole replication" evidence=IMP] [GO:0008022 "protein C-terminus binding" evidence=IPI] [GO:0010457 "centriole-centriole cohesion" evidence=IMP] GO:GO:0005829 GO:GO:0008022 Reactome:REACT_115566 GO:GO:0000086 GO:GO:0005814 GO:GO:0007099 EMBL:AK023683 EMBL:AC118280 EMBL:AC110611 EMBL:AC092627 EMBL:BC012003 EMBL:BC136535 EMBL:BC136536 EMBL:AB014535 EMBL:BK005586 IPI:IPI00017423 IPI:IPI00550987 RefSeq:NP_079285.2 UniGene:Hs.518767 ProteinModelPortal:Q66GS9 IntAct:Q66GS9 MINT:MINT-1200560 STRING:Q66GS9 PhosphoSite:Q66GS9 DMDM:296434460 PRIDE:Q66GS9 Ensembl:ENST00000257287 GeneID:9662 KEGG:hsa:9662 UCSC:uc003hbh.1 UCSC:uc003hbj.1 CTD:9662 GeneCards:GC04P056815 H-InvDB:HIX0019826 HGNC:HGNC:29086 MIM:611423 neXtProt:NX_Q66GS9 PharmGKB:PA128394551 eggNOG:NOG149145 GeneTree:ENSGT00530000063949 HOGENOM:HBG714586 HOVERGEN:HBG081318 InParanoid:Q66GS9 OMA:NEQLQRS OrthoDB:EOG49P9XN PhylomeDB:Q66GS9 NextBio:36283 ArrayExpress:Q58F25 Bgee:Q66GS9 CleanEx:HS_CEP135 Genevestigator:Q66GS9 GermOnline:ENSG00000174799 GO:GO:0010457 Uniprot:Q66GS9
Root	Isotig20329	0	24	-5.714	1.84E-07	TAIR|locus:2131749 - symbol:AT4G27270 species:3702 "Arabidopsis thaliana" [GO:0010181 "FMN binding" evidence=IEA] [GO:0016491 "oxidoreductase activity" evidence=IEA] [GO:0045892 "negative regulation of transcription, DNA-dependent" evidence=IEA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR008254 InterPro:IPR010089 PROSITE:PS50902 Pfam:PF03358

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0005886 GO:GO:0009506 EMBL:CP002687 GO:GO:0045892 GO:GO:0016491 GO:GO:0010181 InterPro:IPR005025 TIGRFAMs:TIGR01755 ProtClustDB:CLSN2685577 EMBL:BT010514 EMBL:AK221196 IPI:IPI00538320 RefSeq:NP_194457.2 UniGene:At.32111 UniGene:At.45 ProteinModelPortal:Q6NQE2 SMR:Q6NQE2 IntAct:Q6NQE2 STRING:Q6NQE2 PRIDE:Q6NQE2 DNASU:828835 EnsemblPlants:AT4G27270.1 GeneID:828835 KEGG:ath:AT4G27270 TAIR:At4g27270 InParanoid:Q6NQE2 OMA:MYHWGAI PhylomeDB:Q6NQE2 Genevestigator:Q6NQE2 Uniprot:Q6NQE2
Root	Isotig20335	35	0	6.000	1.76E-09	UNIPROTKB|G4MW14 - symbol:MGG_08940 "Putative uncharacterized protein" species:242507 "Magnaporthe oryzae 70-15" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CM001232 RefSeq:XP_364095.2 GeneID:2679926 Uniprot:G4MW14
Root	Isotig20461	0	12	-4.714	0.000297064	TAIR|locus:2117293 - symbol:AT4G25030 "AT4G25030" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002687 GenomeReviews:CT486007_GR EMBL:AL161562 EMBL:AL035523 EMBL:AY085639 EMBL:BT024736 EMBL:AK228468 EMBL:AK317301 IPI:IPI00530773 PIR:T05524 RefSeq:NP_194233.1 RefSeq:NP_974613.1 UniGene:At.22641 STRING:Q9SW23 PRIDE:Q9SW23 EnsemblPlants:AT4G25030.1 EnsemblPlants:AT4G25030.2 GeneID:828606 KEGG:ath:AT4G25030 TAIR:At4g25030 eggNOG:NOG312033 HOGENOM:HBG598338 InParanoid:Q9SW23 OMA:WREHTEK PhylomeDB:Q9SW23 ProtClustDB:CLSN2915960 ArrayExpress:Q9SW23 Genevestigator:Q9SW23 Uniprot:Q9SW23
Root	Isotig20475	2	18	-3.299	7.42E-05	TAIR|locus:2087002 - symbol:AT3G29000 species:3702 "Arabidopsis thaliana" [GO:0005509 "calcium ion binding" evidence=IEA;ISS] [GO:0008150 "biological_process" evidence=ND] InterPro:IPR001751 InterPro:IPR002048 InterPro:IPR011992 PROSITE:PS00303 SMART:SM00054 Prosite:PS00018 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005509 InterPro:IPR018247 InterPro:IPR018249 Gene3D:G3DSA:1.10.238.10 PROSITE:PS50222 EMBL:AB025615 HSSP:P02588 EMBL:BX823042 IPI:IPI00530829 RefSeq:NP_189542.1 UniGene:At.50235 ProteinModelPortal:Q9MBG5 SMR:Q9MBG5 DNASU:822540 EnsemblPlants:AT3G29000.1 GeneID:822540 KEGG:ath:AT3G29000 TAIR:At3g29000 eggNOG:NOG325283 HOGENOM:HBG185667 InParanoid:Q9MBG5 OMA:NCLVMIR PhylomeDB:Q9MBG5 ProtClustDB:CLSN2684089 Genevestigator:Q9MBG5 Uniprot:Q9MBG5
Root	Isotig20485	60	0	6.778	7.33E-15	TAIR|locus:2025346 - symbol:LEA14 "AT1G01470" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0009269 "response to desiccation" evidence=ISS] [GO:0009793 "embryo development ending in seed dormancy" evidence=ISS] [GO:0009644 "response to high light intensity" evidence=IEP] [GO:0009611 "response to wounding" evidence=IEP] [GO:0050832 "defense response to fungus" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR013990 SMART:SM00769 InterPro:IPR004864 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 InterPro:IPR013783 Gene3D:G3DSA:2.60.40.10 EMBL:Y12776 EMBL:AC061957 GO:GO:0009611 GO:GO:0050832 GO:GO:0009644 GO:GO:0009269 EMBL:Y10085 EMBL:AY074855 EMBL:BT015111 EMBL:Z37258 IPI:IPI00525938 PIR:D86145 RefSeq:NP_171654.1 UniGene:At.25113 PDB:1XO8 PDBsum:1XO8 ProteinModelPortal:O03983 SMR:O03983 IntAct:O03983 STRING:O03983 PRIDE:O03983 DNASU:837071 EnsemblPlants:AT1G01470.1 GeneID:837071 KEGG:ath:AT1G01470 TAIR:At1g01470 eggNOG:NOG271766 HOGENOM:HBG320411 InParanoid:O03983 OMA:YSHSIPI PhylomeDB:O03983 ProtClustDB:CLSN2682861 Genevestigator:O03983 GermOnline:AT1G01470 Pfam:PF03168 Uniprot:O03983
Root	Isotig20487	0	20	-5.451	2.00E-06	TAIR|locus:2177724 - symbol:AT5G65030 "AT5G65030" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002688 GenomeReviews:BA000015_GR EMBL:AB019236 UniGene:At.20837 EMBL:BT029499 IPI:IPI00548443 RefSeq:NP_201308.1 UniGene:At.66744 ProteinModelPortal:Q9LV76 PRIDE:Q9LV76 EnsemblPlants:AT5G65030.1 GeneID:836627 KEGG:ath:AT5G65030 TAIR:At5g65030 eggNOG:NOG255009 HOGENOM:HBG175356 InParanoid:Q9LV76 OMA:IEVNTRE PhylomeDB:Q9LV76 ProtClustDB:CLSN2686374 Genevestigator:Q9LV76 Uniprot:Q9LV76
Root	Isotig20490	83	0	7.246	1.90E-19	No hit
Root	Isotig20736	33	0	5.915	5.02E-09	TAIR|locus:2183329 - symbol:AT5G07330 "AT5G07330" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002688 GenomeReviews:BA000015_GR EMBL:AL163912 HOGENOM:HBG746117 ProtClustDB:CLSN2687068

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EMBL:BT010400 EMBL:AK118558 IPI:IPI00533921 PIR:T49872 RefSeq:NP_196350.1 UniGene:At.32734 PRIDE:Q9LY27 EnsemblPlants:AT5G07330.1 GeneID:830624 KEGG:ath:AT5G07330 TAIR:At5g07330 eggNOG:NOG262444 InParanoid:Q9LY27 OMA:HIHEFES PhylomeDB:Q9LY27 Genevestigator:Q9LY27 Uniprot:Q9LY27
Root	Isotig20875	0	12	-4.714	0.000297064	TAIR|locus:2201148 - symbol:AT1G21890 species:3702 "Arabidopsis thaliana" [GO:0016020 "membrane" evidence=IEA;ISS] InterPro:IPR000620 Pfam:PF00892 GO:GO:0016020 EMBL:AY065236 EMBL:AY133841 IPI:IPI00544852 PRIDE:Q8VZ54 TAIR:At1g21890 eggNOG:NOG260625 InParanoid:Q8VZ54 PhylomeDB:Q8VZ54 ArrayExpress:Q8VZ54 Genevestigator:Q8VZ54 Uniprot:Q8VZ54
Root	Isotig20943	29	3	3.144	2.49E-06	TAIR|locus:2116762 - symbol:AT4G31830 "AT4G31830" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002687 GenomeReviews:CT486007_GR EMBL:AL161579 EMBL:AL049607 EMBL:BT010813 EMBL:BT011290 IPI:IPI00539008 PIR:T06305 RefSeq:NP_194911.1 UniGene:At.31710 IntAct:Q9SZ50 PRIDE:Q9SZ50 EnsemblPlants:AT4G31830.1 GeneID:829312 KEGG:ath:AT4G31830 TAIR:At4g31830 eggNOG:NOG287408 HOGENOM:HBG748438 InParanoid:Q9SZ50 OMA:THKMSPE PhylomeDB:Q9SZ50 ProtClustDB:CLSN2685982 ArrayExpress:Q9SZ50 Genevestigator:Q9SZ50 Uniprot:Q9SZ50
Root	Isotig20946	0	11	-4.588	0.000569522	TAIR|locus:2160932 - symbol:AT5G47920 "AT5G47920" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002688 GenomeReviews:BA000015_GR EMBL:AB016886 InterPro:IPR008480 Pfam:PF05553 EMBL:AK117194 IPI:IPI00522408 RefSeq:NP_199603.1 UniGene:At.29873 UniGene:At.67834 PRIDE:Q9FII9 EnsemblPlants:AT5G47920.1 GeneID:834843 KEGG:ath:AT5G47920 TAIR:At5g47920 eggNOG:NOG236215 HOGENOM:HBG592596 InParanoid:Q9FII9 OMA:SISNKIH PhylomeDB:Q9FII9 ProtClustDB:CLSN2916328 Genevestigator:Q9FII9 Uniprot:Q9FII9
Root	Isotig20962	28	97	-1.922	1.03E-11	No hit
Root	Isotig20969	14	0	4.678	0.000190242	TAIR|locus:2174984 - symbol:AT5G66780 "AT5G66780" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002688 GenomeReviews:BA000015_GR EMBL:AB010700 EMBL:AY048239 EMBL:AY072623 IPI:IPI00539273 RefSeq:NP_201479.1 UniGene:At.6618 PRIDE:Q9FL02 EnsemblPlants:AT5G66780.1 GeneID:836811 KEGG:ath:AT5G66780 TAIR:At5g66780 eggNOG:NOG276454 HOGENOM:HBG748513 OMA:NEIHENH PhylomeDB:Q9FL02 ProtClustDB:CLSN2686878 Genevestigator:Q9FL02 Uniprot:Q9FL02
Root	Isotig20981	19	1	4.119	2.48E-05	No hit
Root	Isotig20984	28	0	5.678	7.19E-08	MGI|MGI:2141921 - symbol:Zfp575 "zinc finger protein 575" species:10090 "Mus musculus" [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0005634 "nucleus" evidence=IEA] [GO:0046872 "metal ion binding" evidence=IEA] [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0003677 "DNA binding" evidence=IEA] [GO:0008270 "zinc ion binding" evidence=IEA] [GO:0003676 "nucleic acid binding" evidence=IEA] [GO:0005622 "intracellular" evidence=IEA] [GO:0008150 "biological_process" evidence=ND] Pfam:PF00096 InterPro:IPR007087 InterPro:IPR013087 InterPro:IPR015880 PROSITE:PS00028 PROSITE:PS50157 SMART:SM00355 MGI:MGI:2141921 GO:GO:0005634 GO:GO:0006355 GO:GO:0003677 GO:GO:0008270 GO:GO:0006351 Gene3D:G3DSA:3.30.160.60 HOVERGEN:HBG018163 HOGENOM:HBG717200 GeneTree:ENSGT00650000093236 eggNOG:NOG262756 OrthoDB:EOG4S4PH3 EMBL:AK159025 IPI:IPI00756203 RefSeq:NP_001028377.1 UniGene:Mm.20117 ProteinModelPortal:Q3TXZ1 SMR:Q3TXZ1 PRIDE:Q3TXZ1 Ensembl:ENSMUST00000094705 GeneID:101544 KEGG:mmu:101544 CTD:101544 InParanoid:Q3TXZ1 OMA:HRCSSCN NextBio:355008 ArrayExpress:Q3TXZ1 Bgee:Q3TXZ1 CleanEx:MM_ZFP575 Genevestigator:Q3TXZ1 GermOnline:ENSMUSG00000066721 Uniprot:Q3TXZ1
Root	Isotig20997	17	0	4.958	3.30E-05	No hit
Root	Isotig21018	25	1	4.515	7.40E-07	TAIR|locus:2091196 - symbol:AT3G19690 "AT3G19690" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005576 "extracellular region" evidence=ISS] [GO:0008150 "biological_process" evidence=ND] InterPro:IPR018244 PROSITE:PS01010 Pfam:PF00188 INTERPRO:IPR001283 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005576 EMBL:AP000417 InterPro:IPR014044 Gene3D:G3DSA:3.40.33.10 PANTHER:PTHR10334 PRINTS:PR00837 SMART:SM00198 SUPFAM:SSF55797 HSSP:P04284 eggNOG:COG2340 HOGENOM:HBG689653 OMA:VEMWYRE EMBL:BT030036 IPI:IPI00548678 PIR:T52399 RefSeq:NP_188603.1 UniGene:At.75495 UniGene:At.8144 ProteinModelPortal:Q9LJM5 SMR:Q9LJM5

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						STRING:Q9LJM5 EnsemblPlants:AT3G19690.1 GeneID:821506 KEGG:ath:AT3G19690 TAIR:At3g19690 InParanoid:Q9LJM5 PhylomeDB:Q9LJM5 ProtClustDB:CLSN2915437 Genevestigator:Q9LJM5 Uniprot:Q9LJM5
Root	Isotig21029	1	30	-5.036	7.50E-09	No hit
Root	Isotig21044	4	22	-2.588	0.000101225	TAIR|locus:2057407 - symbol:PYL2 "AT2G26040" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0005515 "protein binding" evidence=IPI] [GO:0009738 "abscisic acid mediated signaling pathway" evidence=IGI;IDA] [GO:0004872 "receptor activity" evidence=IDA] [GO:0042803 "protein homodimerization activity" evidence=IDA] GO:GO:0005634 GO:GO:0005737 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0042803 GO:GO:0009738 GO:GO:0004872 InterPro:IPR023393 Gene3D:G3DSA:3.30.530.20 EMBL:AC004747 GO:GO:0010427 PDB:3KB3 PDB:3NMT PDBsum:3KB3 PDBsum:3NMT PDB:3NMV PDBsum:3NMV KO:K14496 InterPro:IPR019587 Pfam:PF10604 HOGENOM:HBG598713 IPI:IPI00546194 PIR:T02619 RefSeq:NP_180174.1 UniGene:At.66246 PDB:3KAZ PDB:3KB0 PDB:3KDH PDB:3KDI PDB:3KL1 PDB:3NJ0 PDB:3NJ1 PDB:3NMH PDB:3NMP PDB:3NR4 PDB:3NS2 PDBsum:3KAZ PDBsum:3KB0 PDBsum:3KDH PDBsum:3KDI PDBsum:3KL1 PDBsum:3NJ0 PDBsum:3NJ1 PDBsum:3NMH PDBsum:3NMP PDBsum:3NR4 PDBsum:3NS2 ProteinModelPortal:O80992 SMR:O80992 DIP:DIP-48582N IntAct:O80992 STRING:O80992 PRIDE:O80992 EnsemblPlants:AT2G26040.1 GeneID:817145 KEGG:ath:AT2G26040 TAIR:At2g26040 eggNOG:NOG299178 InParanoid:O80992 OMA:IPEGNTE PhylomeDB:O80992 ProtClustDB:CLSN2683286 ArrayExpress:O80992 Genevestigator:O80992 Uniprot:O80992
Root	Isotig21073	27	2	3.626	1.44E-06	ZFIN|ZDB-GENE-070410-9 - symbol:zgc:158463 "zgc:158463" species:7955 "Danio rerio" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] ZFIN:ZDB-GENE-070410-9 EMBL:BX296557 EMBL:BX537263 EMBL:BC129240 IPI:IPI00837201 RefSeq:NP_001091866.1 RefSeq:XP_003200836.1 UniGene:Dr.155369 Ensembl:ENSDART00000102863 Ensembl:ENSDART00000126982 GeneID:100037361 GeneID:100151188 KEGG:dre:100037361 KEGG:dre:100151188 eggNOG:NOG298153 GeneTree:ENSGT00390000016898 InParanoid:A2VD29 OMA:ACHQHAL OrthoDB:EOG4FJ8BF Bgee:A2VD29 Uniprot:A2VD29
Root	Isotig21089	14	65	-2.344	2.73E-10	TAIR|locus:2153619 - symbol:AT5G05960 "AT5G05960" species:3702 "Arabidopsis thaliana" [GO:0006869 "lipid transport" evidence=ISS] [GO:0008289 "lipid binding" evidence=ISS] InterPro:IPR013770 EMBL:CP002688 InterPro:IPR016140 SMART:SM00499 SUPFAM:SSF47699 GO:GO:0006869 Gene3D:G3DSA:1.10.110.10 Pfam:PF14368 UniGene:At.43072 UniGene:At.66777 EMBL:AY086919 EMBL:BT024550 IPI:IPI00526394 RefSeq:NP_568160.1 ProteinModelPortal:Q8LBY9 SMR:Q8LBY9 STRING:Q8LBY9 EnsemblPlants:AT5G05960.1 GeneID:830481 KEGG:ath:AT5G05960 TAIR:At5g05960 eggNOG:NOG262474 InParanoid:Q8LBY9 OMA:KLAPCAM PhylomeDB:Q8LBY9 ProtClustDB:CLSN2917576 Genevestigator:Q8LBY9 Uniprot:Q8LBY9
Root	Isotig21090	1	13	-3.829	0.000362856	TAIR|locus:2156937 - symbol:STR16 "AT5G66040" species:3702 "Arabidopsis thaliana" [GO:0007568 "aging" evidence=ISS] [GO:0004792 "thiosulfate sulfurtransferase activity" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] PROSITE:PS00683 Pfam:PF00581 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009507 EMBL:AB011474 InterPro:IPR001763 Gene3D:G3DSA:3.40.250.10 SMART:SM00450 SUPFAM:SSF52821 PROSITE:PS50206 eggNOG:COG0607 HOGENOM:HBG743107 GO:GO:0004792 EMBL:X89036 EMBL:AY049302 EMBL:BT000864 EMBL:AY084763 IPI:IPI00531957 PIR:S58275 RefSeq:NP_851278.1 UniGene:At.23333 PDB:1TQ1 PDBsum:1TQ1 ProteinModelPortal:Q39129 SMR:Q39129 STRING:Q39129 PRIDE:Q39129 EnsemblPlants:AT5G66040.1 GeneID:836734 KEGG:ath:AT5G66040 GeneFarm:4731 TAIR:At5g66040 InParanoid:Q39129 OMA:ELCSAGF PhylomeDB:Q39129 BRENDA:2.8.1.1 ArrayExpress:Q39129 Genevestigator:Q39129 Uniprot:Q39129
Root	Isotig21093	15	0	4.778	0.000105609	TAIR|locus:2206629 - symbol:AtLEA4-1 "AT1G32560" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0009793 "embryo development ending in seed dormancy" evidence=ISS] [GO:0006970 "response to osmotic stress" evidence=IMP] [GO:0009414 "response to water deprivation" evidence=IMP] [GO:0048316 "seed development" evidence=IMP] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR005513 Pfam:PF03760 ProDom:PD005538 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009506 GO:GO:0009790 GO:GO:0009414 GO:GO:0006970 GO:GO:0048316 EMBL:AC055769 EMBL:AY063826 EMBL:AY096424 EMBL:X89505 IPI:IPI00545826 PIR:S71249 RefSeq:NP_174534.1 UniGene:At.5386 STRING:Q39138 PRIDE:Q39138 EnsemblPlants:AT1G32560.1 GeneID:840150 KEGG:ath:AT1G32560 TAIR:At1g32560 eggNOG:NOG312967 InParanoid:Q39138 OMA:HAEDKLM PhylomeDB:Q39138 ProtClustDB:CLSN2720625 ArrayExpress:Q39138 Genevestigator:Q39138 Uniprot:Q39138
Root	Isotig21098	6	61	-3.475	9.12E-14	No hit

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig21109	25	67	-1.551	1.14E-06	TAIR|locus:2057584 - symbol:AT2G33830 "AT2G33830" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] EMBL:CP002685 EMBL:AF361846 EMBL:AY066049 EMBL:AB050786 IPI:IPI00545289 PIR:B84750 RefSeq:NP_850220.1 UniGene:At.25108 STRING:P93017 PRIDE:P93017 EnsemblPlants:AT2G33830.2 GeneID:817950 KEGG:ath:AT2G33830 TAIR:At2g33830 eggNOG:NOG238346 InParanoid:P93017 OMA:HPGSNIA PhylomeDB:P93017 ProtClustDB:CLSN2687243 Genevestigator:P93017 InterPro:IPR008406 Pfam:PF05564 Uniprot:P93017
Root	Isotig21131	3	41	-3.902	1.87E-10	TAIR|locus:2152420 - symbol:PYL11 "AT5G45860" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] GO:GO:0005634 GO:GO:0005737 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0042803 GO:GO:0009738 GO:GO:0004872 InterPro:IPR023393 Gene3D:G3DSA:3.30.530.20 EMBL:AB016870 GO:GO:0010427 KO:K14496 InterPro:IPR019587 Pfam:PF10604 IPI:IPI00544403 RefSeq:NP_199398.1 UniGene:At.65641 ProteinModelPortal:Q9FJ50 SMR:Q9FJ50 IntAct:Q9FJ50 PRIDE:Q9FJ50 EnsemblPlants:AT5G45860.1 GeneID:834626 KEGG:ath:AT5G45860 TAIR:At5g45860 eggNOG:NOG256798 HOGENOM:HBG598713 InParanoid:Q9FJ50 OMA:QTIDAPL PhylomeDB:Q9FJ50 ProtClustDB:CLSN2685444 Genevestigator:Q9FJ50 Uniprot:Q9FJ50
Root	Isotig21141	0	16	-5.129	2.34E-05	No hit
Root	Isotig21301	38	2	4.119	2.46E-09	No hit
Root	Isotig21322	13	0	4.571	0.000344357	No hit
Root	Isotig21330	35	11	1.541	0.000816539	TAIR|locus:2020088 - symbol:AT1G54290 species:3702 "Arabidopsis thaliana" [GO:0003743 "translation initiation factor activity" evidence=IEA;ISS] [GO:0006412 "translation" evidence=IEA] [GO:0006413 "translational initiation" evidence=IEA;ISS] InterPro:IPR001950 InterPro:IPR005874 Pfam:PF01253 PIRSF:PIRSF004499 PROSITE:PS50296 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0006417 EMBL:AC005287 GO:GO:0003743 eggNOG:COG0023 SUPFAM:SSF55159 HOGENOM:HBG522548 KO:K03113 OMA:QNLKTFD TIGRFAMs:TIGR01160 ProtClustDB:CLSN2682406 EMBL:AF372910 EMBL:BT000649 IPI:IPI00530446 PIR:D96584 RefSeq:NP_175831.1 UniGene:At.20055 ProteinModelPortal:Q94JV4 SMR:Q94JV4 IntAct:Q94JV4 STRING:Q94JV4 PRIDE:Q94JV4 EnsemblPlants:AT1G54290.1 GeneID:841870 KEGG:ath:AT1G54290 TAIR:At1g54290 InParanoid:Q94JV4 PhylomeDB:Q94JV4 ArrayExpress:Q94JV4 Genevestigator:Q94JV4 GermOnline:AT1G54290 Uniprot:Q94JV4
Root	Isotig21401	56	0	6.678	4.94E-14	No hit
Root	Isotig21409	86	1	6.297	5.25E-21	ZFIN|ZDB-GENE-070410-9 - symbol:zgc:158463 "zgc:158463" species:7955 "Danio rerio" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] ZFIN:ZDB-GENE-070410-9 EMBL:BX296557 EMBL:BX537263 EMBL:BC129240 IPI:IPI00837201 RefSeq:NP_001091866.1 RefSeq:XP_003200836.1 UniGene:Dr.155369 Ensembl:ENSDART00000102863 Ensembl:ENSDART00000126982 GeneID:100037361 GeneID:100151188 KEGG:dre:100037361 KEGG:dre:100151188 eggNOG:NOG298153 GeneTree:ENSGT00390000016898 InParanoid:A2VD29 OMA:ACHQHAL OrthoDB:EOG4FJ8BF Bgee:A2VD29 Uniprot:A2VD29
Root	Isotig21421	13	0	4.571	0.000344357	TAIR|locus:2183329 - symbol:AT5G07330 "AT5G07330" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002688 GenomeReviews:BA000015_GR EMBL:AL163912 HOGENOM:HBG746117 ProtClustDB:CLSN2687068 EMBL:BT010400 EMBL:AK118558 IPI:IPI00533921 PIR:T49872 RefSeq:NP_196350.1 UniGene:At.32734 PRIDE:Q9LY27 EnsemblPlants:AT5G07330.1 GeneID:830624 KEGG:ath:AT5G07330 TAIR:At5g07330 eggNOG:NOG262444 InParanoid:Q9LY27 OMA:HIHEFES PhylomeDB:Q9LY27 Genevestigator:Q9LY27 Uniprot:Q9LY27
Root	Isotig21436	33	78	-1.370	1.71E-06	TAIR|locus:2057584 - symbol:AT2G33830 "AT2G33830" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] EMBL:CP002685 EMBL:AF361846 EMBL:AY066049 EMBL:AB050786 IPI:IPI00545289 PIR:B84750 RefSeq:NP_850220.1 UniGene:At.25108 STRING:P93017 PRIDE:P93017 EnsemblPlants:AT2G33830.2 GeneID:817950 KEGG:ath:AT2G33830 TAIR:At2g33830 eggNOG:NOG238346 InParanoid:P93017 OMA:HPGSNIA PhylomeDB:P93017 ProtClustDB:CLSN2687243 Genevestigator:P93017 InterPro:IPR008406 Pfam:PF05564 Uniprot:P93017
Root	Isotig21457	29	6	2.144	0.000134201	TAIR|locus:2062933 - symbol:AT2G46140 "AT2G46140" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0009269 "response to desiccation" evidence=IEA;ISS] [GO:0009793 "embryo development ending in seed dormancy" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA]

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						[GO:0005829 "cytosol" evidence=IDA] InterPro:IPR013990 SMART:SM00769 InterPro:IPR004864 GO:GO:0005829 GO:GO:0005886 EMBL:CP002685 GenomeReviews:CT485783_GR InterPro:IPR013783 Gene3D:G3DSA:2.60.40.10 EMBL:AC005397 GO:GO:0009269 HOGENOM:HBG320411 ProtClustDB:CLSN2682861 Pfam:PF03168 EMBL:BT005673 EMBL:BT004206 EMBL:AY086763 IPI:IPI00531665 PIR:B84899 RefSeq:NP_182137.1 UniGene:At.36550 PDB:1YYC PDBsum:1YYC ProteinModelPortal:O82355 SMR:O82355 PRIDE:O82355 DNASU:819221 EnsemblPlants:AT2G46140.1 GeneID:819221 KEGG:ath:AT2G46140 TAIR:At2g46140 eggNOG:NOG292167 InParanoid:O82355 OMA:DIDYQLD PhylomeDB:O82355 ArrayExpress:O82355 Genevestigator:O82355 GermOnline:AT2G46140 Uniprot:O82355
Root	Isotig21513	0	11	-4.588	0.000569522	TAIR|locus:2145683 - symbol:AT5G14360 "AT5G14360" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] InterPro:IPR000626 Pfam:PF00240 SMART:SM00213 EMBL:CP002688 GenomeReviews:BA000015_GR EMBL:AL163817 InterPro:IPR019955 PROSITE:PS50053 HOGENOM:HBG592878 EMBL:BT012122 EMBL:BT012376 IPI:IPI00545760 PIR:T48609 RefSeq:NP_196940.1 UniGene:At.50454 ProteinModelPortal:Q9LY93 SMR:Q9LY93 EnsemblPlants:AT5G14360.1 GeneID:831287 KEGG:ath:AT5G14360 TAIR:At5g14360 eggNOG:NOG238171 InParanoid:Q9LY93 OMA:PCRTISV PhylomeDB:Q9LY93 ProtClustDB:CLSN2916708 Genevestigator:Q9LY93 Uniprot:Q9LY93
Root	Isotig21581	236	5	5.432	6.04E-55	TAIR|locus:2153619 - symbol:AT5G05960 "AT5G05960" species:3702 "Arabidopsis thaliana" [GO:0006869 "lipid transport" evidence=ISS] [GO:0008289 "lipid binding" evidence=ISS] InterPro:IPR013770 EMBL:CP002688 InterPro:IPR016140 SMART:SM00499 SUPFAM:SSF47699 GO:GO:0006869 Gene3D:G3DSA:1.10.110.10 Pfam:PF14368 UniGene:At.43072 UniGene:At.66777 EMBL:AY086919 EMBL:BT024550 IPI:IPI00526394 RefSeq:NP_568160.1 ProteinModelPortal:Q8LBY9 SMR:Q8LBY9 STRING:Q8LBY9 EnsemblPlants:AT5G05960.1 GeneID:830481 KEGG:ath:AT5G05960 TAIR:At5g05960 eggNOG:NOG262474 InParanoid:Q8LBY9 OMA:KLAPCAM PhylomeDB:Q8LBY9 ProtClustDB:CLSN2917576 Genevestigator:Q8LBY9 Uniprot:Q8LBY9
Root	Isotig21599	1	16	-4.129	5.13E-05	No hit
Root	Isotig21616	18	0	5.041	1.86E-05	No hit
Root	Isotig21659	26	0	5.571	2.13E-07	TAIR|locus:2100123 - symbol:AT3G10020 "AT3G10020" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0006979 "response to oxidative stress" evidence=IMP] [GO:0009061 "anaerobic respiration" evidence=IEP;IMP] EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0006979 GO:GO:0009061 EMBL:AC010927 UniGene:At.24905 EMBL:AY048222 EMBL:AY052262 EMBL:AY054173 EMBL:AY091708 EMBL:AY088481 IPI:IPI00529555 RefSeq:NP_566365.1 UniGene:At.23159 IntAct:Q9SR67 STRING:Q9SR67 PRIDE:Q9SR67 EnsemblPlants:AT3G10020.1 GeneID:820163 KEGG:ath:AT3G10020 TAIR:At3g10020 HOGENOM:HBG749915 InParanoid:Q9SR67 OMA:GKYTWEG PhylomeDB:Q9SR67 ProtClustDB:CLSN2688230 Genevestigator:Q9SR67 Uniprot:Q9SR67
Root	Isotig21701	79	7	3.367	1.17E-15	TAIR|locus:2119003 - symbol:AT4G21620 "AT4G21620" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002687 GenomeReviews:CT486007_GR EMBL:AL035527 EMBL:AL161555 UniGene:At.44911 EMBL:AF360336 EMBL:AY051071 EMBL:AY058136 EMBL:AY085743 EMBL:AK226947 IPI:IPI00547700 PIR:T05837 RefSeq:NP_193893.1 IntAct:Q9SVT5 PRIDE:Q9SVT5 EnsemblPlants:AT4G21620.1 GeneID:828249 KEGG:ath:AT4G21620 TAIR:At4g21620 eggNOG:NOG325948 InParanoid:Q9SVT5 OMA:CKKKCIA ProtClustDB:CLSN2915919 Genevestigator:Q9SVT5 Uniprot:Q9SVT5
Root	Isotig21721	7	27	-2.077	0.000159635	RGD|727924 - symbol:LOC257642 "rRNA promoter binding protein" species:10116 "Rattus norvegicus" [GO:0003690 "double-stranded DNA binding" evidence=IDA] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=IDA] [GO:0008134 "transcription factor binding" evidence=IDA] [GO:0008283 "cell proliferation" evidence=IDA] [GO:0009303 "rRNA transcription" evidence=IDA] RGD:727924 GO:GO:0008134 GO:GO:0008283 GO:GO:0003700 GO:GO:0003690 GO:GO:0009303 EMBL:U77931 IPI:IPI00195015 RefSeq:NP_671477.1 GeneID:257642 KEGG:rno:257642 NextBio:624170 Genevestigator:Q99JC0 Uniprot:Q99JC0
Root	Isotig21748	25	0	5.515	3.68E-07	No hit
Root	Isotig21801	27	4	2.626	3.31E-05	TAIR|locus:2119003 - symbol:AT4G21620 "AT4G21620" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002687 GenomeReviews:CT486007_GR EMBL:AL035527 EMBL:AL161555 UniGene:At.44911 EMBL:AF360336 EMBL:AY051071 EMBL:AY058136 EMBL:AY085743 EMBL:AK226947 IPI:IPI00547700 PIR:T05837

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						RefSeq:NP_193893.1 IntAct:Q9SVT5 PRIDE:Q9SVT5 EnsemblPlants:AT4G21620.1 GeneID:828249 KEGG:ath:AT4G21620 TAIR:At4g21620 eggNOG:NOG325948 InParanoid:Q9SVT5 OMA:CKKKCIA ProtClustDB:CLSN2915919 Genevestigator:Q9SVT5 Uniprot:Q9SVT5
Root	Isotig21898	14	1	3.678	0.000484579	TAIR|locus:4515102981 - symbol:AT2G41475 "AT2G41475" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR001024 GO:GO:0009506 EMBL:CP002685 InterPro:IPR008976 Gene3D:G3DSA:2.60.60.20 SUPFAM:SSF49723 EMBL:AK175164 EMBL:AK175615 EMBL:AK175765 EMBL:AK221826 EMBL:AK221888 EMBL:AK228257 IPI:IPI00521526 RefSeq:NP_001118501.1 UniGene:At.43627 ProteinModelPortal:Q681K2 SMR:Q681K2 PRIDE:Q681K2 EnsemblPlants:AT2G41475.1 GeneID:6240499 KEGG:ath:AT2G41475 TAIR:At2g41475 PhylomeDB:Q681K2 ProtClustDB:CLSN2925507 Genevestigator:Q681K2 InterPro:IPR010417 Pfam:PF06232 Uniprot:Q681K2
Root	Isotig21944	305	0	9.124	1.06E-55	UNIPROTKB|A8CVF3 - symbol:DHN1 "Dehydrin DHN1" species:82927 "Avicennia marina" [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0010555 "response to mannitol stimulus" evidence=IEP] [GO:0042631 "cellular response to water deprivation" evidence=IEP] [GO:0071472 "cellular response to salt stress" evidence=IEP] [GO:0071482 "cellular response to light stimulus" evidence=IEP] InterPro:IPR000167 Pfam:PF00257 PROSITE:PS00315 PROSITE:PS00823 GO:GO:0005634 GO:GO:0005737 GO:GO:0071472 GO:GO:0042631 GO:GO:0010555 EMBL:EU121850 EMBL:EU121851 GO:GO:0071482 Uniprot:A8CVF3
Root	Isotig21945	0	34	-6.216	6.02E-10	TAIR|locus:2134178 - symbol:AT4G33720 "AT4G33720" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005576 "extracellular region" evidence=IEA;ISS] [GO:0008150 "biological_process" evidence=ND] InterPro:IPR018244 PROSITE:PS01009 PROSITE:PS01010 Pfam:PF00188 INTERPRO:IPR001283 EMBL:CP002687 GO:GO:0005576 EMBL:AL031394 EMBL:AL161584 InterPro:IPR014044 Gene3D:G3DSA:3.40.33.10 PANTHER:PTHR10334 PRINTS:PR00837 SMART:SM00198 SUPFAM:SSF55797 HSSP:P04284 InterPro:IPR002413 PRINTS:PR00838 eggNOG:COG2340 EMBL:AF324705 EMBL:AF327419 EMBL:AF339699 EMBL:AY039577 EMBL:AY088337 EMBL:AY129483 IPI:IPI00531736 PIR:T04989 RefSeq:NP_195098.1 UniGene:At.25142 ProteinModelPortal:O81888 SMR:O81888 STRING:O81888 PRIDE:O81888 EnsemblPlants:AT4G33720.1 GeneID:829514 KEGG:ath:AT4G33720 TAIR:At4g33720 InParanoid:O81888 OMA:NRARAEV PhylomeDB:O81888 ProtClustDB:CLSN2915982 Genevestigator:O81888 Uniprot:O81888
Root	Isotig21957	1	14	-3.936	0.000188601	No hit
Root	Isotig21972	0	13	-4.829	0.000155955	TAIR|locus:2018566 - symbol:AT1G65820 "AT1G65820" species:3702 "Arabidopsis thaliana" [GO:0002540 "leukotriene production involved in inflammatory response" evidence=IBA] [GO:0004364 "glutathione transferase activity" evidence=ISS] [GO:0004602 "glutathione peroxidase activity" evidence=IBA] [GO:0005792 "microsome" evidence=IBA] [GO:0019370 "leukotriene biosynthetic process" evidence=IBA] [GO:0055114 "oxidation-reduction process" evidence=IBA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005783 "endoplasmic reticulum" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] GO:GO:0005783 GenomeReviews:CT485782_GR GO:GO:0005773 GO:GO:0016020 InterPro:IPR023352 InterPro:IPR001129 Gene3D:G3DSA:1.20.120.550 Pfam:PF01124 EMBL:AC007234 IPI:IPI01020050 ProteinModelPortal:Q9SHX5 SMR:Q9SHX5 PRIDE:Q9SHX5 TAIR:At1g65820 PhylomeDB:Q9SHX5 Genevestigator:Q9SHX5 Uniprot:Q9SHX5
Root	Isotig22112	17	2	2.958	0.000459627	TAIR|locus:505006307 - symbol:AT2G38905 "AT2G38905" species:3702 "Arabidopsis thaliana" [GO:0009409 "response to cold" evidence=ISS] [GO:0016021 "integral to membrane" evidence=IEA] [GO:0042538 "hyperosmotic salinity response" evidence=ISS] InterPro:IPR000612 Pfam:PF01679 PROSITE:PS01309 GO:GO:0016021 EMBL:CP002685 GenomeReviews:CT485783_GR EMBL:AC005770 HOGENOM:HBG741476 PANTHER:PTHR21659 ProtClustDB:CLSN2688798 EMBL:AY052231 EMBL:AY060504 IPI:IPI00533167 RefSeq:NP_565897.1 UniGene:At.26429 EnsemblPlants:AT2G38905.1 GeneID:818475 KEGG:ath:AT2G38905 TAIR:At2g38905 eggNOG:NOG331170 InParanoid:Q941D7 OMA:WINIILC PhylomeDB:Q941D7 ArrayExpress:Q941D7 Genevestigator:Q941D7 Uniprot:Q941D7
Root	Isotig22183	0	25	-5.773	1.02E-07	TAIR|locus:2134178 - symbol:AT4G33720 "AT4G33720" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005576 "extracellular region" evidence=IEA;ISS] [GO:0008150 "biological_process" evidence=ND] InterPro:IPR018244 PROSITE:PS01009 PROSITE:PS01010 Pfam:PF00188 INTERPRO:IPR001283 EMBL:CP002687 GO:GO:0005576 EMBL:AL031394 EMBL:AL161584 InterPro:IPR014044 Gene3D:G3DSA:3.40.33.10 PANTHER:PTHR10334 PRINTS:PR00837 SMART:SM00198 SUPFAM:SSF55797

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						HSSP:P04284 InterPro:IPR002413 PRINTS:PR00838 eggNOG:COG2340 EMBL:AF324705 EMBL:AF327419 EMBL:AF339699 EMBL:AY039577 EMBL:AY088337 EMBL:AY129483 IPI:IPI00531736 PIR:T04989 RefSeq:NP_195098.1 UniGene:At.25142 ProteinModelPortal:O81888 SMR:O81888 STRING:O81888 PRIDE:O81888 EnsemblPlants:AT4G33720.1 GeneID:829514 KEGG:ath:AT4G33720 TAIR:At4g33720 InParanoid:O81888 OMA:NRARAEV PhylomeDB:O81888 ProtClustDB:CLSN2915982 Genevestigator:O81888 Uniprot:O81888
Root	Isotig22204	0	18	-5.299	6.77E-06	TAIR|locus:2168758 - symbol:GPDHp "AT5G40610" species:3702 "Arabidopsis thaliana" [GO:0004367 "glycerol-3-phosphate dehydrogenase [NAD+] activity" evidence=ISS;IDA] [GO:0006072 "glycerol-3-phosphate metabolic process" evidence=ISS] [GO:0009331 "glycerol-3-phosphate dehydrogenase complex" evidence=ISS] [GO:0009507 "chloroplast" evidence=IDA] [GO:0046167 "glycerol-3-phosphate biosynthetic process" evidence=IDA] InterPro:IPR006109 InterPro:IPR006168 InterPro:IPR008927 InterPro:IPR011128 InterPro:IPR013328 InterPro:IPR016040 InterPro:IPR017751 Pfam:PF01210 Pfam:PF07479 PIRSF:PIRSF000114 PRINTS:PR00077 PROSITE:PS00957 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009507 GO:GO:0042803 Gene3D:G3DSA:3.40.50.720 GO:GO:0051287 Gene3D:G3DSA:1.10.1040.10 SUPFAM:SSF48179 EMBL:AB009052 GO:GO:0009331 HSSP:Q8N1B0 eggNOG:COG0240 HOGENOM:HBG586392 KO:K00006 OMA:KIFCKGQ GO:GO:0004367 GO:GO:0046168 PANTHER:PTHR11728 TIGRFAMs:TIGR03376 EMBL:AJ242602 EMBL:BT000967 EMBL:AY080863 IPI:IPI00538973 RefSeq:NP_198877.1 UniGene:At.695 ProteinModelPortal:Q9SCX9 SMR:Q9SCX9 STRING:Q9SCX9 PRIDE:Q9SCX9 EnsemblPlants:AT5G40610.1 GeneID:834060 KEGG:ath:AT5G40610 TAIR:At5g40610 InParanoid:Q9SCX9 PhylomeDB:Q9SCX9 ProtClustDB:CLSN2686185 Genevestigator:Q9SCX9 Uniprot:Q9SCX9
Root	Isotig22422	29	0	5.729	4.20E-08	UNIPROTKB|A8CVF3 - symbol:DHN1 "Dehydrin DHN1" species:82927 "Avicennia marina" [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0010555 "response to mannitol stimulus" evidence=IEP] [GO:0042631 "cellular response to water deprivation" evidence=IEP] [GO:0071472 "cellular response to salt stress" evidence=IEP] [GO:0071482 "cellular response to light stimulus" evidence=IEP] InterPro:IPR000167 Pfam:PF00257 PROSITE:PS00315 PROSITE:PS00823 GO:GO:0005634 GO:GO:0005737 GO:GO:0071472 GO:GO:0042631 GO:GO:0010555 EMBL:EU121850 EMBL:EU121851 GO:GO:0071482 Uniprot:A8CVF3
Root	Isotig22466	2	14	-2.936	0.000925454	TAIR|locus:2158621 - symbol:FRO1 "AT5G67590" species:3702 "Arabidopsis thaliana" [GO:0005739 "mitochondrion" evidence=IDA] [GO:0006970 "response to osmotic stress" evidence=IMP] [GO:0008137 "NADH dehydrogenase (ubiquinone) activity" evidence=ISS] [GO:0009631 "cold acclimation" evidence=IMP] [GO:0005747 "mitochondrial respiratory chain complex I" evidence=IDA] [GO:0050897 "cobalt ion binding" evidence=IDA] InterPro:IPR006885 Pfam:PF04800 EMBL:CP002688 GO:GO:0006810 GO:GO:0006970 GO:GO:0022900 TCDB:3.D.1.6.3 GO:GO:0050897 GO:GO:0005747 GO:GO:0016651 EMBL:AB013390 GO:GO:0009631 EMBL:AK118663 EMBL:BT003675 EMBL:AY086840 IPI:IPI00524802 RefSeq:NP_201560.1 UniGene:At.28805 ProteinModelPortal:Q9FJW4 SMR:Q9FJW4 IntAct:Q9FJW4 STRING:Q9FJW4 PRIDE:Q9FJW4 GeneID:836895 KEGG:ath:AT5G67590 GeneFarm:1830 TAIR:At5g67590 eggNOG:NOG79671 InParanoid:Q9FJW4 KO:K03937 OMA:VAYCERE PhylomeDB:Q9FJW4 ProtClustDB:CLSN2916625 BioCyc:ARA:AT5G67590-MONOMER BioCyc:MetaCyc:AT5G67590-MONOMER Genevestigator:Q9FJW4 PANTHER:PTHR12219 Uniprot:Q9FJW4
Root	Isotig22628	31	0	5.825	1.45E-08	No hit
Root	Isotig22676	1	15	-4.036	9.83E-05	No hit
Root	Isotig22690	5	22	-2.266	0.000318925	TAIR|locus:2052981 - symbol:HB1 "hemoglobin 1" species:3702 "Arabidopsis thaliana" [GO:0005618 "cell wall" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0001666 "response to hypoxia" evidence=TAS] [GO:0005344 "oxygen transporter activity" evidence=IDA] [GO:0019825 "oxygen binding" evidence=IDA] InterPro:IPR000971 InterPro:IPR001032 InterPro:IPR012292 InterPro:IPR019824 Pfam:PF00042 PRINTS:PR00188 PROSITE:PS00208 PROSITE:PS01033 GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 GO:GO:0005618 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0019825 GO:GO:0001666 GO:GO:0020037 GO:GO:0015671 Gene3D:G3DSA:1.10.490.10 InterPro:IPR009050 SUPFAM:SSF46458 EMBL:AC007134 EMBL:U94998 EMBL:BT006405 IPI:IPI00548638 PIR:C84536 RefSeq:NP_179204.1 UniGene:At.40321 ProteinModelPortal:O24520 SMR:O24520 STRING:O24520 PRIDE:O24520 EnsemblPlants:AT2G16060.1 GeneID:816103 KEGG:ath:AT2G16060 TAIR:At2g16060 eggNOG:NOG276286 HOGENOM:HBG317398 InParanoid:O24520 OMA:KEAVPEM PhylomeDB:O24520 ArrayExpress:O24520 Genevestigator:O24520 GermOnline:AT2G16060 Uniprot:O24520

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Root	Isotig22731	0	14	-4.936	8.24E-05	TAIR|locus:2185148 - symbol:AT5G02090 "AT5G02090" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002688 GenomeReviews:BA000015_GR EMBL:AL162508 EMBL:BT005481 EMBL:AK118214 IPI:IPI00548819 PIR:T48230 RefSeq:NP_195829.1 UniGene:At.33463 PRIDE:Q9LZM2 DNASU:831871 EnsemblPlants:AT5G02090.1 GeneID:831871 KEGG:ath:AT5G02090 TAIR:At5g02090 eggNOG:NOG315952 InParanoid:Q9LZM2 OMA:IVMYKRE PhylomeDB:Q9LZM2 ProtClustDB:CLSN2916750 Genevestigator:Q9LZM2 Uniprot:Q9LZM2
Root	Isotig22737	0	12	-4.714	0.000297064	TAIR|locus:2060529 - symbol:ERD15 "AT2G41430" species:3702 "Arabidopsis thaliana" [GO:0009617 "response to bacterium" evidence=IEP] [GO:0005737 "cytoplasm" evidence=ISS] [GO:0009644 "response to high light intensity" evidence=IEP] [GO:0005515 "protein binding" evidence=IPI] [GO:0009414 "response to water deprivation" evidence=NAS] EMBL:CP002685 GO:GO:0009617 GO:GO:0005515 GO:GO:0009414 GO:GO:0009644 EMBL:AC004625 EMBL:AC005662 UniGene:At.24137 EMBL:AF372909 EMBL:AY056399 EMBL:AY065120 EMBL:AY081636 EMBL:BT002663 EMBL:D30719 EMBL:AK317136 IPI:IPI00543434 PIR:T02438 RefSeq:NP_001189727.1 RefSeq:NP_181674.1 RefSeq:NP_850350.1 RefSeq:NP_973658.1 UniGene:At.23985 UniGene:At.24253 UniGene:At.69477 UniGene:At.73065 IntAct:Q39096 STRING:Q39096 PRIDE:Q39096 EnsemblPlants:AT2G41430.1 EnsemblPlants:AT2G41430.2 EnsemblPlants:AT2G41430.4 EnsemblPlants:AT2G41430.5 GeneID:818741 KEGG:ath:AT2G41430 TAIR:At2g41430 eggNOG:NOG300714 InParanoid:Q39096 OMA:ENENGGG PhylomeDB:Q39096 ProtClustDB:CLSN2683774 ArrayExpress:Q39096 Genevestigator:Q39096 Uniprot:Q39096
Root	Isotig22774	0	14	-4.936	8.24E-05	TAIR|locus:2089313 - symbol:AT3G16660 "AT3G16660" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:AB022217 InterPro:IPR006041 Pfam:PF01190 IPI:IPI00529614 TAIR:At3g16660 InParanoid:Q9LUR8 PhylomeDB:Q9LUR8 Genevestigator:Q9LUR8 Uniprot:Q9LUR8
Root	Isotig22780	0	11	-4.588	0.000569522	TAIR|locus:2143641 - symbol:AT5G27660 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004252 "serine-type endopeptidase activity" evidence=IEA] [GO:0006508 "proteolysis" evidence=IEA;ISS] [GO:0008236 "serine-type peptidase activity" evidence=ISS] InterPro:IPR001254 InterPro:IPR001478 InterPro:IPR001940 InterPro:IPR009003 PRINTS:PR00834 PROSITE:PS50106 SMART:SM00020 SMART:SM00228 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0006508 GO:GO:0004252 EMBL:AC007478 SUPFAM:SSF50494 SUPFAM:SSF50156 eggNOG:COG0265 HOGENOM:HBG585708 EMBL:AC069556 IPI:IPI00541824 IPI:IPI01020060 RefSeq:NP_198118.3 UniGene:At.48106 ProteinModelPortal:Q3E6S8 PRIDE:Q3E6S8 GeneID:832828 KEGG:ath:AT5G27660 GeneFarm:2266 TAIR:At5g27660 InParanoid:Q3E6S8 OMA:KSGRVIR PhylomeDB:Q3E6S8 Genevestigator:Q3E6S8 GermOnline:AT5G27660 Uniprot:Q3E6S8
Root	Isotig22781	12	0	4.456	0.000626491	No hit
Root	Isotig22823	13	1	3.571	0.000882483	No hit
Root	Isotig22882	31	0	5.825	1.45E-08	TAIR|locus:2206629 - symbol:AtLEA4-1 "AT1G32560" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0009793 "embryo development ending in seed dormancy" evidence=ISS] [GO:0006970 "response to osmotic stress" evidence=IMP] [GO:0009414 "response to water deprivation" evidence=IMP] [GO:0048316 "seed development" evidence=IMP] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR005513 Pfam:PF03760 ProDom:PD005538 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009506 GO:GO:0009790 GO:GO:0009414 GO:GO:0006970 GO:GO:0048316 EMBL:AC055769 EMBL:AY063826 EMBL:AY096424 EMBL:X89505 IPI:IPI00545826 PIR:S71249 RefSeq:NP_174534.1 UniGene:At.5386 STRING:Q39138 PRIDE:Q39138 EnsemblPlants:AT1G32560.1 GeneID:840150 KEGG:ath:AT1G32560 TAIR:At1g32560 eggNOG:NOG312967 InParanoid:Q39138 OMA:HAEDKLM PhylomeDB:Q39138 ProtClustDB:CLSN2720625 ArrayExpress:Q39138 Genevestigator:Q39138 Uniprot:Q39138
Root	Isotig22969	0	15	-5.036	4.38E-05	TAIR|locus:2134966 - symbol:AT4G24130 "AT4G24130" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0005634 "nucleus" evidence=IDA] EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005634 EMBL:AC002343 EMBL:AL161560 EMBL:AL109619 InterPro:IPR007493 Gene3D:G3DSA:2.30.240.10 Pfam:PF04398 SUPFAM:SSF141562 EMBL:BT008528 EMBL:AK118183 IPI:IPI00523393 PIR:T13461 RefSeq:NP_194144.1 UniGene:At.43869 PRIDE:O22978 EnsemblPlants:AT4G24130.1 GeneID:828513 KEGG:ath:AT4G24130 TAIR:At4g24130 eggNOG:NOG301239

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						HOGENOM:HBG749450 InParanoid:O22978 OMA:TNTRVSY PhylomeDB:O22978 ProtClustDB:CLSN2685388 Genevestigator:O22978 Uniprot:O22978
Root	Isotig23030	0	16	-5.129	2.34E-05	No hit
Root	Isotig23083	0	46	-6.653	9.06E-13	No hit
Root	Isotig23122	6	161	-4.875	1.60E-40	TAIR|locus:2153619 - symbol:AT5G05960 "AT5G05960" species:3702 "Arabidopsis thaliana" [GO:0006869 "lipid transport" evidence=ISS] [GO:0008289 "lipid binding" evidence=ISS] InterPro:IPR013770 EMBL:CP002688 InterPro:IPR016140 SMART:SM00499 SUPFAM:SSF47699 GO:GO:0006869 Gene3D:G3DSA:1.10.110.10 Pfam:PF14368 UniGene:At.43072 UniGene:At.66777 EMBL:AY086919 EMBL:BT024550 IPI:IPI00526394 RefSeq:NP_568160.1 ProteinModelPortal:Q8LBY9 SMR:Q8LBY9 STRING:Q8LBY9 EnsemblPlants:AT5G05960.1 GeneID:830481 KEGG:ath:AT5G05960 TAIR:At5g05960 eggNOG:NOG262474 InParanoid:Q8LBY9 OMA:KLAPCAM PhylomeDB:Q8LBY9 ProtClustDB:CLSN2917576 Genevestigator:Q8LBY9 Uniprot:Q8LBY9
Root	Isotig23146	15	1	3.778	0.000266457	TAIR|locus:2045482 - symbol:AT2G32090 "AT2G32090" species:3702 "Arabidopsis thaliana" [GO:0004462 "lactoylglutathione lyase activity" evidence=ISS] [GO:0005975 "carbohydrate metabolic process" evidence=ISS] EMBL:CP002685 GO:GO:0016829 EMBL:AC006223 EMBL:AY058893 EMBL:AY079042 IPI:IPI00533148 PIR:H84728 RefSeq:NP_565737.1 UniGene:At.20803 ProteinModelPortal:Q9SKZ0 SMR:Q9SKZ0 PRIDE:Q9SKZ0 EnsemblPlants:AT2G32090.1 GeneID:817769 KEGG:ath:AT2G32090 TAIR:At2g32090 InParanoid:Q9SKZ0 OMA:PDGRTRQ PhylomeDB:Q9SKZ0 ProtClustDB:CLSN2688622 ArrayExpress:Q9SKZ0 Genevestigator:Q9SKZ0 Uniprot:Q9SKZ0
Root	Isotig23163	13	1	3.571	0.000882483	No hit
Root	Isotig23270	0	25	-5.773	1.02E-07	TAIR|locus:2099044 - symbol:WRKY69 "AT3G58710" species:3702 "Arabidopsis thaliana" [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA;ISS] InterPro:IPR003657 Pfam:PF03106 PROSITE:PS50811 SMART:SM00774 GO:GO:0005634 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0043565 GO:GO:0003700 GO:GO:0006351 EMBL:AL353032 Gene3D:G3DSA:2.20.25.80 SUPFAM:SSF118290 HOGENOM:HBG749713 ProtClustDB:CLSN2690431 EMBL:AF421156 EMBL:BT029470 EMBL:AY084233 IPI:IPI00527147 IPI:IPI00530116 PIR:T49154 RefSeq:NP_567073.2 RefSeq:NP_851020.1 ProteinModelPortal:Q93WV5 SMR:Q93WV5 PRIDE:Q93WV5 EnsemblPlants:AT3G58710.2 GeneID:825040 KEGG:ath:AT3G58710 TAIR:At3g58710 eggNOG:NOG295795 OMA:CEDSKIS PhylomeDB:Q93WV5 ArrayExpress:Q93WV5 Genevestigator:Q93WV5 GermOnline:AT3G58710 Uniprot:Q93WV5
Root	Isotig23304	0	14	-4.936	8.24E-05	TAIR|locus:2084918 - symbol:PR4 "AT3G04720" species:3702 "Arabidopsis thaliana" [GO:0009627 "systemic acquired resistance" evidence=IEP] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0080027 "response to herbivore" evidence=IEP] [GO:0009817 "defense response to fungus, incompatible interaction" evidence=IDA] [GO:0008061 "chitin binding" evidence=ISS] [GO:0009615 "response to virus" evidence=IEP] [GO:0009723 "response to ethylene stimulus" evidence=IEP] InterPro:IPR001002 InterPro:IPR001153 InterPro:IPR018226 InterPro:IPR018371 Pfam:PF00187 Pfam:PF00967 PRINTS:PR00451 PRINTS:PR00602 ProDom:PD000609 ProDom:PD004535 PROSITE:PS00026 PROSITE:PS00771 PROSITE:PS00772 PROSITE:PS50941 PROSITE:PS51174 SMART:SM00270 GO:GO:0042742 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0009651 GO:GO:0009817 GO:GO:0009627 GO:GO:0009723 GO:GO:0009615 GO:GO:0080027 CAZy:CBM18 GO:GO:0008061 Gene3D:G3DSA:3.30.60.10 SUPFAM:SSF57016 EMBL:AC011437 InterPro:IPR014733 InterPro:IPR009009 Gene3D:G3DSA:2.40.40.10 SUPFAM:SSF50685 EMBL:U01880 EMBL:AF370536 EMBL:BT000046 EMBL:AY088644 IPI:IPI00529373 RefSeq:NP_187123.1 UniGene:At.252 ProteinModelPortal:P43082 SMR:P43082 IntAct:P43082 STRING:P43082 PRIDE:P43082 EnsemblPlants:AT3G04720.1 GeneID:819632 KEGG:ath:AT3G04720 TAIR:At3g04720 eggNOG:NOG306084 HOGENOM:HBG588395 InParanoid:P43082 OMA:QQGHLIV PhylomeDB:P43082 ProtClustDB:CLSN2914702 ArrayExpress:P43082 Genevestigator:P43082 GermOnline:AT3G04720 Uniprot:P43082
Root	Isotig23340	0	12	-4.714	0.000297064	No hit
Root	Isotig23426	38	0	6.119	3.74E-10	TAIR|locus:2084918 - symbol:PR4 "AT3G04720" species:3702 "Arabidopsis thaliana" [GO:0009627 "systemic acquired resistance" evidence=IEP] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0080027 "response to herbivore" evidence=IEP] [GO:0009817 "defense response to fungus, incompatible interaction" evidence=IDA] [GO:0008061 "chitin binding" evidence=ISS] [GO:0009615 "response to virus" evidence=IEP] [GO:0009723 "response to ethylene stimulus" evidence=IEP] InterPro:IPR001002 InterPro:IPR001153 InterPro:IPR018226 InterPro:IPR018371 Pfam:PF00187 Pfam:PF00967 PRINTS:PR00451 PRINTS:PR00602 ProDom:PD000609

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						ProDom:PD004535 PROSITE:PS00026 PROSITE:PS00771 PROSITE:PS00772 PROSITE:PS50941 PROSITE:PS51174 SMART:SM00270 GO:GO:0042742 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0009651 GO:GO:0009817 GO:GO:0009627 GO:GO:0009723 GO:GO:0009615 GO:GO:0080027 CAZy:CBM18 GO:GO:0008061 Gene3D:G3DSA:3.30.60.10 SUPFAM:SSF57016 EMBL:AC011437 InterPro:IPR014733 InterPro:IPR009009 Gene3D:G3DSA:2.40.40.10 SUPFAM:SSF50685 EMBL:U01880 EMBL:AF370536 EMBL:BT000046 EMBL:AY088644 IPI:IPI00529373 RefSeq:NP_187123.1 UniGene:At.252 ProteinModelPortal:P43082 SMR:P43082 IntAct:P43082 STRING:P43082 PRIDE:P43082 EnsemblPlants:AT3G04720.1 GeneID:819632 KEGG:ath:AT3G04720 TAIR:At3g04720 eggNOG:NOG306084 HOGENOM:HBG588395 InParanoid:P43082 OMA:QQGHLIV PhylomeDB:P43082 ProtClustDB:CLSN2914702 ArrayExpress:P43082 Genevestigator:P43082 GermOnline:AT3G04720 Uniprot:P43082
Root	Isotig23447	13	0	4.571	0.000344357	No hit
Root	Isotig23454	0	14	-4.936	8.24E-05	TAIR|locus:2167255 - symbol:AT5G17350 "AT5G17350" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] EMBL:CP002688 GenomeReviews:BA000015_GR EMBL:AL391142 HOGENOM:HBG594031 EMBL:AY084862 EMBL:AK228808 IPI:IPI00541082 PIR:T51572 RefSeq:NP_197237.1 UniGene:At.31563 STRING:Q9LF49 PRIDE:Q9LF49 EnsemblPlants:AT5G17350.1 GeneID:831601 KEGG:ath:AT5G17350 TAIR:At5g17350 eggNOG:NOG294516 InParanoid:Q9LF49 OMA:ELMMEIP PhylomeDB:Q9LF49 ProtClustDB:CLSN2684078 Genevestigator:Q9LF49 Uniprot:Q9LF49
Root	Isotig23765	57	16	1.704	4.39E-06	TAIR|locus:2153619 - symbol:AT5G05960 "AT5G05960" species:3702 "Arabidopsis thaliana" [GO:0006869 "lipid transport" evidence=ISS] [GO:0008289 "lipid binding" evidence=ISS] InterPro:IPR013770 EMBL:CP002688 InterPro:IPR016140 SMART:SM00499 SUPFAM:SSF47699 GO:GO:0006869 Gene3D:G3DSA:1.10.110.10 Pfam:PF14368 UniGene:At.43072 UniGene:At.66777 EMBL:AY086919 EMBL:BT024550 IPI:IPI00526394 RefSeq:NP_568160.1 ProteinModelPortal:Q8LBY9 SMR:Q8LBY9 STRING:Q8LBY9 EnsemblPlants:AT5G05960.1 GeneID:830481 KEGG:ath:AT5G05960 TAIR:At5g05960 eggNOG:NOG262474 InParanoid:Q8LBY9 OMA:KLAPCAM PhylomeDB:Q8LBY9 ProtClustDB:CLSN2917576 Genevestigator:Q8LBY9 Uniprot:Q8LBY9
Root	Isotig23769	0	16	-5.129	2.34E-05	TAIR|locus:2093247 - symbol:AT3G15630 "AT3G15630" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002686 GenomeReviews:BA000014_GR EMBL:AB017071 EMBL:AY052241 EMBL:AY060508 IPI:IPI00533188 RefSeq:NP_566521.1 UniGene:At.20536 STRING:Q9LW16 EnsemblPlants:AT3G15630.1 GeneID:820805 KEGG:ath:AT3G15630 TAIR:At3g15630 eggNOG:NOG293987 HOGENOM:HBG597979 InParanoid:Q9LW16 OMA:TIISCSA PhylomeDB:Q9LW16 ProtClustDB:CLSN2688413 Genevestigator:Q9LW16 Uniprot:Q9LW16
Root	Isotig23822	0	14	-4.936	8.24E-05	No hit
Root	Isotig23834	44	0	6.330	1.78E-11	TAIR|locus:2084918 - symbol:PR4 "AT3G04720" species:3702 "Arabidopsis thaliana" [GO:0009627 "systemic acquired resistance" evidence=IEP] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0080027 "response to herbivore" evidence=IEP] [GO:0009817 "defense response to fungus, incompatible interaction" evidence=IDA] [GO:0008061 "chitin binding" evidence=ISS] [GO:0009615 "response to virus" evidence=IEP] [GO:0009723 "response to ethylene stimulus" evidence=IEP] InterPro:IPR001002 InterPro:IPR001153 InterPro:IPR018226 InterPro:IPR018371 Pfam:PF00187 Pfam:PF00967 PRINTS:PR00451 PRINTS:PR00602 ProDom:PD000609 ProDom:PD004535 PROSITE:PS00026 PROSITE:PS00771 PROSITE:PS00772 PROSITE:PS50941 PROSITE:PS51174 SMART:SM00270 GO:GO:0042742 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0009651 GO:GO:0009817 GO:GO:0009627 GO:GO:0009723 GO:GO:0009615 GO:GO:0080027 CAZy:CBM18 GO:GO:0008061 Gene3D:G3DSA:3.30.60.10 SUPFAM:SSF57016 EMBL:AC011437 InterPro:IPR014733 InterPro:IPR009009 Gene3D:G3DSA:2.40.40.10 SUPFAM:SSF50685 EMBL:U01880 EMBL:AF370536 EMBL:BT000046 EMBL:AY088644 IPI:IPI00529373 RefSeq:NP_187123.1 UniGene:At.252 ProteinModelPortal:P43082 SMR:P43082 IntAct:P43082 STRING:P43082 PRIDE:P43082 EnsemblPlants:AT3G04720.1 GeneID:819632 KEGG:ath:AT3G04720 TAIR:At3g04720 eggNOG:NOG306084 HOGENOM:HBG588395 InParanoid:P43082 OMA:QQGHLIV PhylomeDB:P43082 ProtClustDB:CLSN2914702 ArrayExpress:P43082 Genevestigator:P43082 GermOnline:AT3G04720 Uniprot:P43082
Root	Isotig23872	14	1	3.678	0.000484579	No hit
Root	Isotig23922	15	0	4.778	0.000105609	TAIR|locus:2157587 - symbol:AT5G42290 "AT5G42290" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002688 GenomeReviews:BA000015_GR EMBL:AB023032

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EMBL:BT012116 EMBL:BT015703 IPI:IPI00530015 RefSeq:NP_199044.1 UniGene:At.30181 DNASU:834234 EnsemblPlants:AT5G42290.1 GeneID:834234 KEGG:ath:AT5G42290 TAIR:At5g42290 eggNOG:NOG255036 HOGENOM:HBG142075 InParanoid:Q9FH00 OMA:PPNISEM PhylomeDB:Q9FH00 ProtClustDB:CLSN2686582 Genevestigator:Q9FH00 Uniprot:Q9FH00
Root	Isotig23964	1	12	-3.714	0.000699736	No hit
Root	Isotig23986	36	0	6.041	1.05E-09	No hit
Root	Isotig24040	12	0	4.456	0.000626491	UNIPROTKB|F1PA85 - symbol:ESRP2 "Uncharacterized protein" species:9615 "Canis lupus familiaris" [GO:0000166 "nucleotide binding" evidence=IEA] [GO:0003676 "nucleic acid binding" evidence=IEA] InterPro:IPR000504 InterPro:IPR012337 InterPro:IPR012677 SMART:SM00360 GO:GO:0000166 Gene3D:G3DSA:3.30.70.330 GO:GO:0003676 SUPFAM:SSF53098 GeneTree:ENSGT00620000087828 OMA:SVFQAYQ Ensembl:ENSCAFT00000032365 Uniprot:F1PA85
Root	Isotig24050	0	14	-4.936	8.24E-05	SGD|S000028422 - symbol:TAR1 "Mitochondrial protein potentially involved in respiratory metabolism" species:4932 "Saccharomyces cerevisiae" [GO:0003674 "molecular_function" evidence=ND] [GO:0043457 "regulation of cellular respiration" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IEA;IMP] SGD:S000028422 GO:GO:0005739 EMBL:BK006945 EMBL:U53879 GO:GO:0043457 EMBL:Z73326 EMBL:AF479964 RefSeq:NP_690845.1 ProteinModelPortal:Q8TGM6 STRING:Q8TGM6 EnsemblFungi:YLR154W-C GeneID:1466405 KEGG:sce:YLR154W-C CYGD:YLR154w-c eggNOG:NOG79861 OMA:SCSKEHR OrthoDB:EOG466ZX8 NextBio:967146 Genevestigator:Q8TGM6 GermOnline:YLR154W-C Uniprot:Q8TGM6
Root	Isotig24056	0	12	-4.714	0.000297064	No hit
Root	Isotig24281	12	0	4.456	0.000626491	TAIR|locus:2133144 - symbol:AT4G21020 "AT4G21020" species:3702 "Arabidopsis thaliana" [GO:0009793 "embryo development ending in seed dormancy" evidence=ISS] EMBL:CP002687 GenomeReviews:CT486007_GR EMBL:AL080282 EMBL:AL161554 ProtClustDB:CLSN2687244 EMBL:AY072166 EMBL:AY117321 IPI:IPI00539152 PIR:T10644 RefSeq:NP_193834.1 UniGene:At.32674 PRIDE:Q9SUB2 EnsemblPlants:AT4G21020.1 GeneID:827849 KEGG:ath:AT4G21020 TAIR:At4g21020 eggNOG:NOG268376 HOGENOM:HBG744068 InParanoid:Q9SUB2 OMA:EDTKERA PhylomeDB:Q9SUB2 Genevestigator:Q9SUB2 Uniprot:Q9SUB2
Root	Isotig24412	33	161	-2.415	4.80E-24	No hit
Root	Isotig24447	0	15	-5.036	4.38E-05	No hit
Root	Isotig24547	16	0	4.871	5.89E-05	TAIR|locus:2089265 - symbol:AT3G12960 "AT3G12960" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002686 GenomeReviews:BA000014_GR EMBL:AB026645 EMBL:BT014911 EMBL:BT015752 IPI:IPI00534491 RefSeq:NP_187902.1 UniGene:At.39516 PRIDE:Q9LE44 ProMEX:Q9LE44 DNASU:820482 EnsemblPlants:AT3G12960.1 GeneID:820482 KEGG:ath:AT3G12960 TAIR:At3g12960 eggNOG:NOG319744 InParanoid:Q9LE44 OMA:KHGTPLE PhylomeDB:Q9LE44 Genevestigator:Q9LE44 Uniprot:Q9LE44
Root	Isotig24574	15	1	3.778	0.000266457	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig24594	18	0	5.041	1.86E-05	TAIR|locus:2062933 - symbol:AT2G46140 "AT2G46140" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0009269 "response to desiccation" evidence=IEA;ISS] [GO:0009793 "embryo development ending in seed dormancy" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR013990 SMART:SM00769 InterPro:IPR004864 GO:GO:0005829 GO:GO:0005886 EMBL:CP002685 GenomeReviews:CT485783_GR InterPro:IPR013783 Gene3D:G3DSA:2.60.40.10 EMBL:AC005397 GO:GO:0009269 HOGENOM:HBG320411 ProtClustDB:CLSN2682861 Pfam:PF03168 EMBL:BT005673 EMBL:BT004206 EMBL:AY086763 IPI:IPI00531665 PIR:B84899 RefSeq:NP_182137.1 UniGene:At.36550 PDB:1YYC PDBsum:1YYC ProteinModelPortal:O82355 SMR:O82355 PRIDE:O82355 DNASU:819221 EnsemblPlants:AT2G46140.1 GeneID:819221

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						KEGG:ath:AT2G46140 TAIR:At2g46140 eggNOG:NOG292167 InParanoid:O82355 OMA:DIDYQLD PhylomeDB:O82355 ArrayExpress:O82355 Genevestigator:O82355 GermOnline:AT2G46140 Uniprot:O82355
Root	Isotig24604	0	13	-4.829	0.000155955	TAIR|locus:2150640 - symbol:AT5G03870 species:3702 "Arabidopsis thaliana" [GO:0009055 "electron carrier activity" evidence=IEA] [GO:0015035 "protein disulfide oxidoreductase activity" evidence=IEA] [GO:0045454 "cell redox homeostasis" evidence=IEA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR002109 Pfam:PF00462 PROSITE:PS51354 GO:GO:0009506 EMBL:CP002688 GO:GO:0009055 EMBL:AL162873 EMBL:AB005235 InterPro:IPR012336 Gene3D:G3DSA:3.40.30.10 SUPFAM:SSF52833 GO:GO:0045454 GO:GO:0015035 IPI:IPI00516358 PIR:T48414 RefSeq:NP_196007.1 UniGene:At.33212 ProteinModelPortal:Q9LZC2 SMR:Q9LZC2 PRIDE:Q9LZC2 EnsemblPlants:AT5G03870.1 GeneID:831685 KEGG:ath:AT5G03870 TAIR:At5g03870 InParanoid:Q9LZC2 OMA:LEVINAW PhylomeDB:Q9LZC2 ProtClustDB:CLSN2686214 Genevestigator:Q9LZC2 Uniprot:Q9LZC2
Root	Isotig24886	0	17	-5.216	1.26E-05	No hit
Root	Isotig25062	0	12	-4.714	0.000297064	TAIR|locus:2082568 - symbol:BG1 ""beta-1,3-glucanase 1"" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=IEA;ISS] [GO:0005975 "carbohydrate metabolic process" evidence=IEA] [GO:0043169 "cation binding" evidence=IEA] InterPro:IPR000490 InterPro:IPR013781 Pfam:PF00332 PROSITE:PS00587 EMBL:CP002686 GO:GO:0043169 InterPro:IPR017853 Gene3D:G3DSA:3.20.20.80 SUPFAM:SSF51445 GO:GO:0005975 GO:GO:0004553 EMBL:AL137080 CAZy:GH17 HSSP:P12257 EMBL:DQ446773 IPI:IPI00535175 PIR:T45805 RefSeq:NP_191286.1 UniGene:At.34848 ProteinModelPortal:Q9M2M0 SMR:Q9M2M0 PRIDE:Q9M2M0 EnsemblPlants:AT3G57270.1 GeneID:824894 KEGG:ath:AT3G57270 TAIR:At3g57270 InParanoid:Q9M2M0 OMA:MEPIIRF ProtClustDB:CLSN2915358 Genevestigator:Q9M2M0 Uniprot:Q9M2M0
Root	Isotig25078	22	48	-1.255	0.000453212	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Root	Isotig25116	0	11	-4.588	0.000569522	TAIR|locus:2103085 - symbol:GAPC1 "AT3G04120" species:3702 "Arabidopsis thaliana" [GO:0006096 "glycolysis" evidence=ISS;IDA;TAS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0006979 "response to oxidative stress" evidence=IEP;IDA] [GO:0005740 "mitochondrial envelope" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA;TAS] [GO:0006094 "gluconeogenesis" evidence=TAS] [GO:0042542 "response to hydrogen peroxide" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0008886 "glyceraldehyde-3-phosphate dehydrogenase (NADP+) (non-phosphorylating) activity" evidence=IDA] [GO:0010154 "fruit development" evidence=IMP] [GO:0048316 "seed development" evidence=IMP] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] [GO:0004365 "glyceraldehyde-3-phosphate dehydrogenase (NAD+) (phosphorylating) activity" evidence=TAS] [GO:0006950 "response to stress" evidence=IEP] [GO:0009408 "response to heat" evidence=IEP] [GO:0009744 "response to sucrose stimulus" evidence=IEP] InterPro:IPR006424 InterPro:IPR016040 InterPro:IPR020828 InterPro:IPR020829 InterPro:IPR020830 InterPro:IPR020831 Pfam:PF00044 Pfam:PF02800 PIRSF:PIRSF000149 PRINTS:PR00078 PROSITE:PS00071 SMART:SM00846 GO:GO:0005829 GO:GO:0005886 GO:GO:0048046 GO:GO:0005634 GO:GO:0046686 GO:GO:0005774 GO:GO:0009507 EMBL:CP002686 GenomeReviews:BA000014_GR Gene3D:G3DSA:3.40.50.720 GO:GO:0051287 GO:GO:0050661 GO:GO:0005507 GO:GO:0006094 GO:GO:0009651 GO:GO:0009408 GO:GO:0005740 GO:GO:0009744 GO:GO:0048316 GO:GO:0042542 GO:GO:0006096 EMBL:AC016829 eggNOG:COG0057 HOGENOM:HBG571736 PANTHER:PTHR10836 GO:GO:0004365 KO:K00134 TIGRFAMs:TIGR01534 OMA:CESTGVF EMBL:M64116 EMBL:M64119 EMBL:AY052267 EMBL:AY060521 EMBL:AY140084 EMBL:F20074 IPI:IPI00527494 PIR:JQ1287 RefSeq:NP_187062.1 UniGene:At.22963 UniGene:At.24406 UniGene:At.71328 ProteinModelPortal:P25858 SMR:P25858 STRING:P25858 PRIDE:P25858 EnsemblPlants:AT3G04120.1

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GeneID:819567 KEGG:ath:AT3G04120 TAIR:At3g04120 InParanoid:P25858 PhylomeDB:P25858 ProtClustDB:PLN02358 ArrayExpress:P25858 Genevestigator:P25858 GermOnline:AT3G04120 GO:GO:0008886 Uniprot:P25858
Root	Isotig25165	14	97	-2.922	3.40E-18	TAIR|locus:2153619 - symbol:AT5G05960 "AT5G05960" species:3702 "Arabidopsis thaliana" [GO:0006869 "lipid transport" evidence=ISS] [GO:0008289 "lipid binding" evidence=ISS] InterPro:IPR013770 EMBL:CP002688 InterPro:IPR016140 SMART:SM00499 SUPFAM:SSF47699 GO:GO:0006869 Gene3D:G3DSA:1.10.110.10 Pfam:PF14368 UniGene:At.43072 UniGene:At.66777 EMBL:AY086919 EMBL:BT024550 IPI:IPI00526394 RefSeq:NP_568160.1 ProteinModelPortal:Q8LBY9 SMR:Q8LBY9 STRING:Q8LBY9 EnsemblPlants:AT5G05960.1 GeneID:830481 KEGG:ath:AT5G05960 TAIR:At5g05960 eggNOG:NOG262474 InParanoid:Q8LBY9 OMA:KLAPCAM PhylomeDB:Q8LBY9 ProtClustDB:CLSN2917576 Genevestigator:Q8LBY9 Uniprot:Q8LBY9
Root	Isotig25210	0	12	-4.714	0.000297064	ZFIN|ZDB-GENE-070410-9 - symbol:zgc:158463 "zgc:158463" species:7955 "Danio rerio" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] ZFIN:ZDB-GENE-070410-9 EMBL:BX296557 EMBL:BX537263 EMBL:BC129240 IPI:IPI00837201 RefSeq:NP_001091866.1 RefSeq:XP_003200836.1 UniGene:Dr.155369 Ensembl:ENSDART00000102863 Ensembl:ENSDART00000126982 GeneID:100037361 GeneID:100151188 KEGG:dre:100037361 KEGG:dre:100151188 eggNOG:NOG298153 GeneTree:ENSGT00390000016898 InParanoid:A2VD29 OMA:ACHQHAL OrthoDB:EOG4FJ8BF Bgee:A2VD29 Uniprot:A2VD29
Root	Isotig25284	53	2	4.599	4.61E-13	No hit
Root	Isotig25774	2	15	-3.036	0.000493759	No hit
Root	Isotig25782	0	14	-4.936	8.24E-05	TAIR|locus:2135625 - symbol:AT4G12490 "AT4G12490" species:3702 "Arabidopsis thaliana" [GO:0006869 "lipid transport" evidence=ISS] [GO:0008289 "lipid binding" evidence=ISS] [GO:0050832 "defense response to fungus" evidence=IMP] InterPro:IPR013770 Pfam:PF00234 EMBL:CP002687 GenomeReviews:CT486007_GR InterPro:IPR016140 SMART:SM00499 SUPFAM:SSF47699 GO:GO:0050832 GO:GO:0006869 Gene3D:G3DSA:1.10.110.10 EMBL:AL161534 EMBL:AL049730 HSSP:P24337 HOGENOM:HBG602760 ProtClustDB:CLSN2916012 UniGene:At.48850 EMBL:AY052336 EMBL:AY061906 IPI:IPI00524589 PIR:T07641 RefSeq:NP_192986.1 ProteinModelPortal:Q9SU34 SMR:Q9SU34 EnsemblPlants:AT4G12490.1 GeneID:826861 KEGG:ath:AT4G12490 TAIR:At4g12490 eggNOG:NOG328035 InParanoid:Q9SU34 OMA:RCNPSPK PhylomeDB:Q9SU34 ArrayExpress:Q9SU34 Genevestigator:Q9SU34 Uniprot:Q9SU34
Root	Isotig26339	0	11	-4.588	0.000569522	No hit
Root	Isotig26698	0	13	-4.829	0.000155955	No hit
Root	Isotig26702	0	12	-4.714	0.000297064	WB|WBGene00017233 - symbol:F07G11.9 species:6239 "Caenorhabditis elegans" [GO:0008061 "chitin binding" evidence=IEA] [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=IEA] [GO:0005975 "carbohydrate metabolic process" evidence=IEA] [GO:0016998 "cell wall macromolecule catabolic process" evidence=IEA] [GO:0004568 "chitinase activity" evidence=IEA] [GO:0006032 "chitin catabolic process" evidence=IEA] InterPro:IPR001002 InterPro:IPR001223 InterPro:IPR001579 InterPro:IPR002482 InterPro:IPR011583 InterPro:IPR013781 InterPro:IPR018392 Pfam:PF00704 Pfam:PF01476 PROSITE:PS01095 SMART:SM00257 SMART:SM00270 SMART:SM00636 GO:GO:0043169 InterPro:IPR017853 Gene3D:G3DSA:3.20.20.80 SUPFAM:SSF51445 GO:GO:0008061 GO:GO:0004568 GO:GO:0006032 GO:GO:0016998 eggNOG:COG3325 InterPro:IPR010264 Pfam:PF05938 EMBL:FO080517 RefSeq:NP_504862.1 PRIDE:O16237 GeneID:179121 KEGG:cel:F07G11.9 CTD:179121 WormBase:F07G11.9 HOGENOM:HBG386694 Uniprot:O16237
Root	Isotig27050	0	57	-6.962	3.07E-15	No hit
Root	Isotig27136	17	0	4.958	3.30E-05	No hit
Root	Isotig27909	18	0	5.041	1.86E-05	No hit
Root	Isotig28027	0	16	-5.129	2.34E-05	No hit
Root	Isotig28220	0	13	-4.829	0.000155955	No hit
Root	Isotig28490	13	1	3.571	0.000882483	TAIR|locus:2011251 - symbol:AT1G19130 "AT1G19130" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR011051 InterPro:IPR014710 Gene3D:G3DSA:2.60.120.10 SUPFAM:SSF51182 EMBL:CP002684 GO:GO:0005829 KO:K09705 InterPro:IPR009327 Pfam:PF06172 EMBL:AK117302 IPI:IPI00536403 RefSeq:NP_564073.4 UniGene:At.15081 UniGene:At.22114 ProteinModelPortal:Q8GYZ3 SMR:Q8GYZ3 STRING:Q8GYZ3 PRIDE:Q8GYZ3 DNASU:838496 EnsemblPlants:AT1G19130.1 GeneID:838496

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						KEGG:ath:AT1G19130 TAIR:At1g19130 PhylomeDB:Q8GYZ3 ProtClustDB:CLSN2696036 Genevestigator:Q8GYZ3 Uniprot:Q8GYZ3
Root	Isotig28925	0	14	-4.936	8.24E-05	No hit
Root	Isotig28939	20	0	5.193	5.94E-06	No hit
Root	Isotig29736	20	0	5.193	5.94E-06	TAIR|locus:2089860 - symbol:CERK1 "AT3G21630" species:3702 "Arabidopsis thaliana" [GO:0016301 "kinase activity" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0019199 "transmembrane receptor protein kinase activity" evidence=IMP;IDA] [GO:0032491 "detection of molecule of fungal origin" evidence=IEP;IMP] [GO:0035556 "intracellular signal transduction" evidence=IDA] [GO:0009817 "defense response to fungus, incompatible interaction" evidence=IMP] [GO:0010200 "response to chitin" evidence=IMP] [GO:0032499 "detection of peptidoglycan" evidence=IMP] InterPro:IPR000719 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 InterPro:IPR018392 Pfam:PF00069 Pfam:PF01476 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 GO:GO:0005886 GO:GO:0005524 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0035556 eggNOG:COG0515 SUPFAM:SSF56112 GO:GO:0004674 GO:GO:0009817 GO:GO:0010200 GO:GO:0005622 GO:GO:0016998 GO:GO:0019199 EMBL:AB367524 IPI:IPI00521578 RefSeq:NP_566689.2 UniGene:At.5663 ProteinModelPortal:A8R7E6 SMR:A8R7E6 STRING:A8R7E6 PRIDE:A8R7E6 EnsemblPlants:AT3G21630.1 GeneID:821717 KEGG:ath:AT3G21630 TAIR:At3g21630 HOGENOM:HBG317612 InParanoid:A8R7E6 KO:K13429 OMA:YPLRPED PhylomeDB:A8R7E6 ProtClustDB:CLSN2918177 Genevestigator:A8R7E6 GO:GO:0032491 Uniprot:A8R7E6
Root	Isotig30210	1	14	-3.936	0.000188601	No hit
Root	Isotig30221	0	14	-4.936	8.24E-05	UNIPROTKB|P04210 - symbol:P04210 "Ig lambda chain V-1 region" species:9031 "Gallus gallus" [GO:0003823 "antigen binding" evidence=IEA] InterPro:IPR007110 PROSITE:PS50835 InterPro:IPR013783 Gene3D:G3DSA:2.60.40.10 GO:GO:0003823 InterPro:IPR013106 Pfam:PF07686 InterPro:IPR003596 SMART:SM00406 HOVERGEN:HBG018013 GeneTree:ENSGT00530000063029 EMBL:M12317 IPI:IPI00582126 PIR:A01992 ProteinModelPortal:P04210 SMR:P04210 Ensembl:ENSGALT00000009518 Ensembl:ENSGALT00000009519 HOGENOM:HBG506495 InParanoid:P04210 Uniprot:P04210
Root	Isotig30992	567	860	-0.730	2.86E-21	UNIPROTKB|Q6NSD8 - symbol:FGA "FGA protein" species:9606 "Homo sapiens" [GO:0005102 "receptor binding" evidence=IEA] [GO:0005577 "fibrinogen complex" evidence=IEA] [GO:0007165 "signal transduction" evidence=IEA] [GO:0030168 "platelet activation" evidence=IEA] [GO:0030674 "protein binding, bridging" evidence=IEA] [GO:0051258 "protein polymerization" evidence=IEA] InterPro:IPR012290 Pfam:PF08702 GO:GO:0007165 GO:GO:0030168 GO:GO:0005102 GO:GO:0005577 GO:GO:0030674 GO:GO:0051258 GeneTree:ENSGT00650000092930 Gene3D:G3DSA:1.20.5.50 UniGene:Hs.351593 HGNC:HGNC:3661 EMBL:AC107385 IPI:IPI00871469 EMBL:BC070246 ProteinModelPortal:Q6NSD8 SMR:Q6NSD8 STRING:Q6NSD8 PRIDE:Q6NSD8 Ensembl:ENST00000457487 HOVERGEN:HBG062035 ArrayExpress:Q6NSD8 Bgee:Q6NSD8 Uniprot:Q6NSD8
Root	Isotig31334	26	1	4.571	4.15E-07	No hit
Leaf	Contig00003	991	688	1.055	6.34E-51	No hit
Leaf	Contig00004	31379	29705	0.608	0	No hit
Leaf	Contig00035	674	573	0.763	4.84E-21	No hit
Leaf	Contig00083	283	286	0.514	1.83E-05	SGD|S000028422 - symbol:TAR1 "Mitochondrial protein potentially involved in respiratory metabolism" species:4932 "Saccharomyces cerevisiae" [GO:0003674 "molecular_function" evidence=ND] [GO:0043457 "regulation of cellular respiration" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IEA;IMP] SGD:S000028422 GO:GO:0005739 EMBL:BK006945 EMBL:U53879 GO:GO:0043457 EMBL:Z73326 EMBL:AF479964 RefSeq:NP_690845.1 ProteinModelPortal:Q8TGM6 STRING:Q8TGM6 EnsemblFungi:YLR154W-C GeneID:1466405 KEGG:sce:YLR154W-C CYGD:YLR154w-c eggNOG:NOG79861 OMA:SCSKEHR OrthoDB:EOG466ZX8 NextBio:967146 Genevestigator:Q8TGM6 GermOnline:YLR154W-C Uniprot:Q8TGM6
Leaf	Contig00084	680	543	0.854	2.25E-25	No hit
Leaf	Contig00093	1231	1157	0.618	3.72E-26	No hit
Leaf	Contig00096	5520	6593	0.273	3.97E-26	SGD|S000028422 - symbol:TAR1 "Mitochondrial protein potentially involved in respiratory metabolism" species:4932 "Saccharomyces cerevisiae" [GO:0003674 "molecular_function" evidence=ND] [GO:0043457 "regulation of cellular respiration" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IEA;IMP] SGD:S000028422 GO:GO:0005739 EMBL:BK006945 EMBL:U53879 GO:GO:0043457 EMBL:Z73326 EMBL:AF479964 RefSeq:NP_690845.1 ProteinModelPortal:Q8TGM6 STRING:Q8TGM6 EnsemblFungi:YLR154W-

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						C GeneID:1466405 KEGG:sce:YLR154W-C CYGD:YLR154w-c eggNOG:NOG79861 OMA:SCSKEHR OrthoDB:EOG466ZX8 NextBio:967146 Genevestigator:Q8TGM6 GermOnline:YLR154W-C Uniprot:Q8TGM6
Leaf	Contig00107	453	345	0.922	1.25E-19	No hit
Leaf	Contig00145	24190	25784	0.437	8.78E-278	RGD|727924 - symbol:LOC257642 "rRNA promoter binding protein" species:10116 "Rattus norvegicus" [GO:0003690 "double-stranded DNA binding" evidence=IDA] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=IDA] [GO:0008134 "transcription factor binding" evidence=IDA] [GO:0008283 "cell proliferation" evidence=IDA] [GO:0009303 "rRNA transcription" evidence=IDA] RGD:727924 GO:GO:0008134 GO:GO:0008283 GO:GO:0003700 GO:GO:0003690 GO:GO:0009303 EMBL:U77931 IPI:IPI00195015 RefSeq:NP_671477.1 GeneID:257642 KEGG:rno:257642 NextBio:624170 Genevestigator:Q99JC0 Uniprot:Q99JC0
Leaf	Contig00179	3111	2754	0.705	5.61E-80	No hit
Leaf	Contig00182	1091	990	0.669	1.27E-26	CGD|CAL0002846 - symbol:CSA1 species:5476 "Candida albicans" [GO:0009277 "fungal-type cell wall" evidence=ISS;IDA] [GO:0009986 "cell surface" evidence=ISS;IDA] [GO:0020037 "heme binding" evidence=IGI] [GO:0006879 "cellular iron ion homeostasis" evidence=IMP] [GO:0005933 "cellular bud" evidence=IDA] [GO:0046658 "anchored to plasma membrane" evidence=ISS;IMP] [GO:0030446 "hyphal cell wall" evidence=IDA] [GO:0044011 "single-species biofilm formation on inanimate substrate" evidence=IMP] CGD:CAL0002846 EMBL:AACQ01000024 InterPro:IPR008427 Pfam:PF05730 RefSeq:XP_720404.1 RefSeq:XP_888643.1 GeneID:3638009 GeneID:3704110 KEGG:cal:CaO19.7114 KEGG:cal:CaO19_7114 InterPro:IPR014005 SMART:SM00747 Uniprot:G1UB63
Leaf	Contig00241	16514	18852	0.338	1.26E-115	SGD|S000028422 - symbol:TAR1 "Mitochondrial protein potentially involved in respiratory metabolism" species:4932 "Saccharomyces cerevisiae" [GO:0003674 "molecular_function" evidence=ND] [GO:0043457 "regulation of cellular respiration" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IEA;IMP] SGD:S000028422 GO:GO:0005739 EMBL:BK006945 EMBL:U53879 GO:GO:0043457 EMBL:Z73326 EMBL:AF479964 RefSeq:NP_690845.1 ProteinModelPortal:Q8TGM6 STRING:Q8TGM6 EnsemblFungi:YLR154W-C GeneID:1466405 KEGG:sce:YLR154W-C CYGD:YLR154w-c eggNOG:NOG79861 OMA:SCSKEHR OrthoDB:EOG466ZX8 NextBio:967146 Genevestigator:Q8TGM6 GermOnline:YLR154W-C Uniprot:Q8TGM6
Leaf	Contig00271	113	82	0.992	1.52E-06	No hit
Leaf	Contig00276	71	48	1.094	3.62E-05	TAIR|locus:2120993 - symbol:CGL1 "AT4G38240" species:3702 "Arabidopsis thaliana" [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS;IMP] [GO:0005794 "Golgi apparatus" evidence=IC;IDA;TAS] [GO:0003827 "alpha-1,3-mannosylglycoprotein 2-beta-N-acetylglucosaminyltransferase activity" evidence=IDA] [GO:0006972 "hyperosmotic response" evidence=IMP] [GO:0006491 "N-glycan processing" evidence=IMP] [GO:0006486 "protein glycosylation" evidence=IMP] [GO:0016262 "protein N-acetylglucosaminyltransferase activity" evidence=IMP] InterPro:IPR004139 Pfam:PF03071 GO:GO:0016021 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0000139 GO:GO:0046872 GO:GO:0006972 EMBL:AL035538 EMBL:AL161593 GO:GO:0016262 EMBL:AL035539 GO:GO:0006491 EMBL:AJ243198 EMBL:AJ249881 EMBL:AY099838 EMBL:BT000334 IPI:IPI00545584 PIR:JC7084 PIR:T05651 RefSeq:NP_195537.2 RefSeq:NP_849517.1 UniGene:At.22245 HSSP:P27115 ProteinModelPortal:Q9XGM8 SMR:Q9XGM8 STRING:Q9XGM8 CAZy:GT13 PRIDE:Q9XGM8 EnsemblPlants:AT4G38240.1 EnsemblPlants:AT4G38240.2 GeneID:829981 KEGG:ath:AT4G38240 TAIR:At4g38240 eggNOG:NOG148227 HOGENOM:HBG717617 InParanoid:Q9XGM8 KO:K00726 OMA:PPDHRKF PhylomeDB:Q9XGM8 ProtClustDB:CLSN2680320 Genevestigator:Q9XGM8 GO:GO:0003827 PANTHER:PTHR10468 Uniprot:Q9XGM8
Leaf	Isotig00001	67	41	1.237	9.50E-06	TAIR|locus:2036134 - symbol:AVP1 "AT1G15690" species:3702 "Arabidopsis thaliana" [GO:0009414 "response to water deprivation" evidence=IMP] [GO:0009651 "response to salt stress" evidence=IMP] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009678 "hydrogen-translocating pyrophosphatase activity" evidence=IDA] [GO:0009705 "plant-type vacuole membrane" evidence=IDA] [GO:0010248 "establishment or maintenance of transmembrane electrochemical gradient" evidence=TAS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009926 "auxin polar transport" evidence=IGI] [GO:0010008 "endosome membrane" evidence=IDA] [GO:0000325 "plant-type vacuole" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048366 "leaf development" evidence=IMP] [GO:0005829 "cytosol" evidence=RCA] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR004131 Pfam:PF03030 PIRSF:PIRSF001265 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005739 GO:GO:0005886 GO:GO:0009926 GO:GO:0009941 GO:GO:0009651 GO:GO:0009414

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0010008 GO:GO:0009705 GO:GO:0048366 GO:GO:0015992 EMBL:AC034256 UniGene:At.21942 UniGene:At.66944 EMBL:M81892 EMBL:AB015138 EMBL:AY065016 EMBL:AY078953 EMBL:BT002481 EMBL:Z17694 EMBL:Z17695 EMBL:AK221989 IPI:IPI00521876 PIR:A38230 RefSeq:NP_173021.1 UniGene:At.67102 UniGene:At.74973 STRING:P31414 TCDB:3.A.10.1.1 PRIDE:P31414 EnsemblPlants:AT1G15690.1 GeneID:838138 KEGG:ath:AT1G15690 GeneFarm:5159 TAIR:At1g15690 eggNOG:COG3808 InParanoid:P31414 KO:K01507 OMA:MAITSIV PhylomeDB:P31414 ProtClustDB:PLN02255 BRENDA:3.6.1.1 ArrayExpress:P31414 Genevestigator:P31414 GermOnline:AT1G15690 GO:GO:0009678 GO:GO:0004427 GO:GO:0010248 TIGRFAMs:TIGR01104 Uniprot:P31414
Leaf	Isotig00002	57	16	2.362	1.41E-10	TAIR|locus:2036134 - symbol:AVP1 "AT1G15690" species:3702 "Arabidopsis thaliana" [GO:0009414 "response to water deprivation" evidence=IMP] [GO:0009651 "response to salt stress" evidence=IMP] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009678 "hydrogen-translocating pyrophosphatase activity" evidence=IDA] [GO:0009705 "plant-type vacuole membrane" evidence=IDA] [GO:0010248 "establishment or maintenance of transmembrane electrochemical gradient" evidence=TAS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009926 "auxin polar transport" evidence=IGI] [GO:0010008 "endosome membrane" evidence=IDA] [GO:0000325 "plant-type vacuole" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048366 "leaf development" evidence=IMP] [GO:0005829 "cytosol" evidence=RCA] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR004131 Pfam:PF03030 PIRSF:PIRSF001265 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005739 GO:GO:0005886 GO:GO:0009926 GO:GO:0009941 GO:GO:0009651 GO:GO:0009414 GO:GO:0010008 GO:GO:0009705 GO:GO:0048366 GO:GO:0015992 EMBL:AC034256 UniGene:At.21942 UniGene:At.66944 EMBL:M81892 EMBL:AB015138 EMBL:AY065016 EMBL:AY078953 EMBL:BT002481 EMBL:Z17694 EMBL:Z17695 EMBL:AK221989 IPI:IPI00521876 PIR:A38230 RefSeq:NP_173021.1 UniGene:At.67102 UniGene:At.74973 STRING:P31414 TCDB:3.A.10.1.1 PRIDE:P31414 EnsemblPlants:AT1G15690.1 GeneID:838138 KEGG:ath:AT1G15690 GeneFarm:5159 TAIR:At1g15690 eggNOG:COG3808 InParanoid:P31414 KO:K01507 OMA:MAITSIV PhylomeDB:P31414 ProtClustDB:PLN02255 BRENDA:3.6.1.1 ArrayExpress:P31414 Genevestigator:P31414 GermOnline:AT1G15690 GO:GO:0009678 GO:GO:0004427 GO:GO:0010248 TIGRFAMs:TIGR01104 Uniprot:P31414
Leaf	Isotig00003	228	1624	-2.303	7.02E-174	TAIR|locus:2033686 - symbol:RBCS1A "AT1G67090" species:3702 "Arabidopsis thaliana" [GO:0009573 "chloroplast ribulose bisphosphate carboxylase complex" evidence=ISS] [GO:0015977 "carbon fixation" evidence=ISS] [GO:0016984 "ribulose-bisphosphate carboxylase activity" evidence=ISS] [GO:0031977 "thylakoid lumen" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009637 "response to blue light" evidence=IEP] [GO:0010114 "response to red light" evidence=IEP] [GO:0010218 "response to far red light" evidence=IEP] [GO:0015979 "photosynthesis" evidence=IMP] [GO:0080158 "chloroplast ribulose bisphosphate carboxylase complex biogenesis" evidence=IMP] InterPro:IPR000894 Pfam:PF00101 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0048046 GO:GO:0009570 GO:GO:0004497 GO:GO:0005507 GO:GO:0009409 GO:GO:0009637 GO:GO:0010218 GO:GO:0010114 GO:GO:0031969 EMBL:AC007152 GO:GO:0009853 GO:GO:0009535 GO:GO:0022626 GO:GO:0031977 EMBL:AC004146 GO:GO:0019253 UniGene:At.46639 GO:GO:0016984 UniGene:At.37531 Gene3D:G3DSA:3.30.190.10 EMBL:X13611 EMBL:AF325011 EMBL:AF325004 EMBL:AF372874 EMBL:AF410291 EMBL:AY054188 EMBL:AY054581 EMBL:AY058831 EMBL:AY059940 EMBL:AY062612 EMBL:AY062711 EMBL:AY065101 EMBL:AY093380 EMBL:AY093388 EMBL:AY097366 EMBL:BT000362 EMBL:BT002076 EMBL:X68342 IPI:IPI00539020 PIR:G96694 PIR:S03720 RefSeq:NP_176880.1 UniGene:At.12721 UniGene:At.30194 UniGene:At.49098 UniGene:At.67454 UniGene:At.68122 UniGene:At.70053 UniGene:At.75196 ProteinModelPortal:P10795 SMR:P10795 IntAct:P10795 MINT:MINT-2584041 STRING:P10795 World-2DPAGE:0003:P10795 PRIDE:P10795 ProMEX:P10795 EnsemblPlants:AT1G67090.1 GeneID:843029 KEGG:ath:AT1G67090 TAIR:At1g67090 eggNOG:COG4451 HOGENOM:HBG608223 InParanoid:P10795 KO:K01602 OMA:AFPATRK PhylomeDB:P10795 ProtClustDB:PLN02289 ArrayExpress:P10795 Genevestigator:P10795 InterPro:IPR024681 InterPro:IPR024680 Pfam:PF12338 PRINTS:PR00152 SMART:SM00961 SUPFAM:SSF55239 Uniprot:P10795

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig00004	237	1676	-2.293	1.97E-178	TAIR|locus:2033686 - symbol:RBCS1A "AT1G67090" species:3702 "Arabidopsis thaliana" [GO:0009573 "chloroplast ribulose bisphosphate carboxylase complex" evidence=ISS] [GO:0015977 "carbon fixation" evidence=ISS] [GO:0016984 "ribulose-bisphosphate carboxylase activity" evidence=ISS] [GO:0031977 "thylakoid lumen" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009637 "response to blue light" evidence=IEP] [GO:0010114 "response to red light" evidence=IEP] [GO:0010218 "response to far red light" evidence=IEP] [GO:0015979 "photosynthesis" evidence=IMP] [GO:0080158 "chloroplast ribulose bisphosphate carboxylase complex biogenesis" evidence=IMP] InterPro:IPR000894 Pfam:PF00101 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0048046 GO:GO:0009570 GO:GO:0004497 GO:GO:0005507 GO:GO:0009409 GO:GO:0009637 GO:GO:0010218 GO:GO:0010114 GO:GO:0031969 EMBL:AC007152 GO:GO:0009853 GO:GO:0009535 GO:GO:0022626 GO:GO:0031977 EMBL:AC004146 GO:GO:0019253 UniGene:At.46639 GO:GO:0016984 UniGene:At.37531 Gene3D:G3DSA:3.30.190.10 EMBL:X13611 EMBL:AF325011 EMBL:AF325004 EMBL:AF372874 EMBL:AF410291 EMBL:AY054188 EMBL:AY054581 EMBL:AY058831 EMBL:AY059940 EMBL:AY062612 EMBL:AY062711 EMBL:AY065101 EMBL:AY093380 EMBL:AY093388 EMBL:AY097366 EMBL:BT000362 EMBL:BT002076 EMBL:X68342 IPI:IPI00539020 PIR:G96694 PIR:S03720 RefSeq:NP_176880.1 UniGene:At.12721 UniGene:At.30194 UniGene:At.49098 UniGene:At.67454 UniGene:At.68122 UniGene:At.70053 UniGene:At.75196 ProteinModelPortal:P10795 SMR:P10795 IntAct:P10795 MINT:MINT-2584041 STRING:P10795 World-2DPAGE:0003:P10795 PRIDE:P10795 ProMEX:P10795 EnsemblPlants:AT1G67090.1 GeneID:843029 KEGG:ath:AT1G67090 TAIR:At1g67090 eggNOG:COG4451 HOGENOM:HBG608223 InParanoid:P10795 KO:K01602 OMA:AFPATRK PhylomeDB:P10795 ProtClustDB:PLN02289 ArrayExpress:P10795 Genevestigator:P10795 InterPro:IPR024681 InterPro:IPR024680 Pfam:PF12338 PRINTS:PR00152 SMART:SM00961 SUPFAM:SSF55239 Uniprot:P10795
Leaf	Isotig00005	228	1631	-2.310	3.52E-175	TAIR|locus:2033686 - symbol:RBCS1A "AT1G67090" species:3702 "Arabidopsis thaliana" [GO:0009573 "chloroplast ribulose bisphosphate carboxylase complex" evidence=ISS] [GO:0015977 "carbon fixation" evidence=ISS] [GO:0016984 "ribulose-bisphosphate carboxylase activity" evidence=ISS] [GO:0031977 "thylakoid lumen" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009637 "response to blue light" evidence=IEP] [GO:0010114 "response to red light" evidence=IEP] [GO:0010218 "response to far red light" evidence=IEP] [GO:0015979 "photosynthesis" evidence=IMP] [GO:0080158 "chloroplast ribulose bisphosphate carboxylase complex biogenesis" evidence=IMP] InterPro:IPR000894 Pfam:PF00101 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0048046 GO:GO:0009570 GO:GO:0004497 GO:GO:0005507 GO:GO:0009409 GO:GO:0009637 GO:GO:0010218 GO:GO:0010114 GO:GO:0031969 EMBL:AC007152 GO:GO:0009853 GO:GO:0009535 GO:GO:0022626 GO:GO:0031977 EMBL:AC004146 GO:GO:0019253 UniGene:At.46639 GO:GO:0016984 UniGene:At.37531 Gene3D:G3DSA:3.30.190.10 EMBL:X13611 EMBL:AF325011 EMBL:AF325004 EMBL:AF372874 EMBL:AF410291 EMBL:AY054188 EMBL:AY054581 EMBL:AY058831 EMBL:AY059940 EMBL:AY062612 EMBL:AY062711 EMBL:AY065101 EMBL:AY093380 EMBL:AY093388 EMBL:AY097366 EMBL:BT000362 EMBL:BT002076 EMBL:X68342 IPI:IPI00539020 PIR:G96694 PIR:S03720 RefSeq:NP_176880.1 UniGene:At.12721 UniGene:At.30194 UniGene:At.49098 UniGene:At.67454 UniGene:At.68122 UniGene:At.70053 UniGene:At.75196 ProteinModelPortal:P10795 SMR:P10795 IntAct:P10795 MINT:MINT-2584041 STRING:P10795 World-2DPAGE:0003:P10795 PRIDE:P10795 ProMEX:P10795 EnsemblPlants:AT1G67090.1 GeneID:843029 KEGG:ath:AT1G67090 TAIR:At1g67090 eggNOG:COG4451 HOGENOM:HBG608223 InParanoid:P10795 KO:K01602 OMA:AFPATRK PhylomeDB:P10795 ProtClustDB:PLN02289 ArrayExpress:P10795 Genevestigator:P10795 InterPro:IPR024681 InterPro:IPR024680 Pfam:PF12338 PRINTS:PR00152 SMART:SM00961 SUPFAM:SSF55239 Uniprot:P10795
Leaf	Isotig00006	237	1683	-2.299	9.93E-180	TAIR|locus:2033686 - symbol:RBCS1A "AT1G67090" species:3702 "Arabidopsis thaliana" [GO:0009573 "chloroplast ribulose bisphosphate carboxylase complex" evidence=ISS] [GO:0015977 "carbon fixation" evidence=ISS] [GO:0016984 "ribulose-bisphosphate carboxylase activity" evidence=ISS] [GO:0031977 "thylakoid

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						lumen" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009637 "response to blue light" evidence=IEP] [GO:0010114 "response to red light" evidence=IEP] [GO:0010218 "response to far red light" evidence=IEP] [GO:0015979 "photosynthesis" evidence=IMP] [GO:0080158 "chloroplast ribulose bisphosphate carboxylase complex biogenesis" evidence=IMP] InterPro:IPR000894 Pfam:PF00101 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0048046 GO:GO:0009570 GO:GO:0004497 GO:GO:0005507 GO:GO:0009409 GO:GO:0009637 GO:GO:0010218 GO:GO:0010114 GO:GO:0031969 EMBL:AC007152 GO:GO:0009853 GO:GO:0009535 GO:GO:0022626 GO:GO:0031977 EMBL:AC004146 GO:GO:0019253 UniGene:At.46639 GO:GO:0016984 UniGene:At.37531 Gene3D:G3DSA:3.30.190.10 EMBL:X13611 EMBL:AF325011 EMBL:AF325004 EMBL:AF372874 EMBL:AF410291 EMBL:AY054188 EMBL:AY054581 EMBL:AY058831 EMBL:AY059940 EMBL:AY062612 EMBL:AY062711 EMBL:AY065101 EMBL:AY093380 EMBL:AY093388 EMBL:AY097366 EMBL:BT000362 EMBL:BT002076 EMBL:X68342 IPI:IPI00539020 PIR:G96694 PIR:S03720 RefSeq:NP_176880.1 UniGene:At.12721 UniGene:At.30194 UniGene:At.49098 UniGene:At.67454 UniGene:At.68122 UniGene:At.70053 UniGene:At.75196 ProteinModelPortal:P10795 SMR:P10795 IntAct:P10795 MINT:MINT-2584041 STRING:P10795 World-2DPAGE:0003:P10795 PRIDE:P10795 ProMEX:P10795 EnsemblPlants:AT1G67090.1 GeneID:843029 KEGG:ath:AT1G67090 TAIR:At1g67090 eggNOG:COG4451 HOGENOM:HBG608223 InParanoid:P10795 KO:K01602 OMA:AFPATRK PhylomeDB:P10795 ProtClustDB:PLN02289 ArrayExpress:P10795 Genevestigator:P10795 InterPro:IPR024681 InterPro:IPR024680 Pfam:PF12338 PRINTS:PR00152 SMART:SM00961 SUPFAM:SSF55239 Uniprot:P10795
Leaf	Isotig00007	345	2349	-2.238	2.59E-242	TAIR|locus:2033686 - symbol:RBCS1A "AT1G67090" species:3702 "Arabidopsis thaliana" [GO:0009573 "chloroplast ribulose bisphosphate carboxylase complex" evidence=ISS] [GO:0015977 "carbon fixation" evidence=ISS] [GO:0016984 "ribulose-bisphosphate carboxylase activity" evidence=ISS] [GO:0031977 "thylakoid lumen" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009637 "response to blue light" evidence=IEP] [GO:0010114 "response to red light" evidence=IEP] [GO:0010218 "response to far red light" evidence=IEP] [GO:0015979 "photosynthesis" evidence=IMP] [GO:0080158 "chloroplast ribulose bisphosphate carboxylase complex biogenesis" evidence=IMP] InterPro:IPR000894 Pfam:PF00101 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0048046 GO:GO:0009570 GO:GO:0004497 GO:GO:0005507 GO:GO:0009409 GO:GO:0009637 GO:GO:0010218 GO:GO:0010114 GO:GO:0031969 EMBL:AC007152 GO:GO:0009853 GO:GO:0009535 GO:GO:0022626 GO:GO:0031977 EMBL:AC004146 GO:GO:0019253 UniGene:At.46639 GO:GO:0016984 UniGene:At.37531 Gene3D:G3DSA:3.30.190.10 EMBL:X13611 EMBL:AF325011 EMBL:AF325004 EMBL:AF372874 EMBL:AF410291 EMBL:AY054188 EMBL:AY054581 EMBL:AY058831 EMBL:AY059940 EMBL:AY062612 EMBL:AY062711 EMBL:AY065101 EMBL:AY093380 EMBL:AY093388 EMBL:AY097366 EMBL:BT000362 EMBL:BT002076 EMBL:X68342 IPI:IPI00539020 PIR:G96694 PIR:S03720 RefSeq:NP_176880.1 UniGene:At.12721 UniGene:At.30194 UniGene:At.49098 UniGene:At.67454 UniGene:At.68122 UniGene:At.70053 UniGene:At.75196 ProteinModelPortal:P10795 SMR:P10795 IntAct:P10795 MINT:MINT-2584041 STRING:P10795 World-2DPAGE:0003:P10795 PRIDE:P10795 ProMEX:P10795 EnsemblPlants:AT1G67090.1 GeneID:843029 KEGG:ath:AT1G67090 TAIR:At1g67090 eggNOG:COG4451 HOGENOM:HBG608223 InParanoid:P10795 KO:K01602 OMA:AFPATRK PhylomeDB:P10795 ProtClustDB:PLN02289 ArrayExpress:P10795 Genevestigator:P10795 InterPro:IPR024681 InterPro:IPR024680 Pfam:PF12338 PRINTS:PR00152 SMART:SM00961 SUPFAM:SSF55239 Uniprot:P10795
Leaf	Isotig00008	345	2356	-2.243	1.35E-243	TAIR|locus:2033686 - symbol:RBCS1A "AT1G67090" species:3702 "Arabidopsis thaliana" [GO:0009573 "chloroplast ribulose bisphosphate carboxylase complex" evidence=ISS] [GO:0015977 "carbon fixation" evidence=ISS] [GO:0016984 "ribulose-bisphosphate carboxylase activity" evidence=ISS] [GO:0031977 "thylakoid lumen" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0009570

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						"chloroplast stroma" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009637 "response to blue light" evidence=IEP] [GO:0010114 "response to red light" evidence=IEP] [GO:0010218 "response to far red light" evidence=IEP] [GO:0015979 "photosynthesis" evidence=IMP] [GO:0080158 "chloroplast ribulose bisphosphate carboxylase complex biogenesis" evidence=IMP] InterPro:IPR000894 Pfam:PF00101 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0048046 GO:GO:0009570 GO:GO:0004497 GO:GO:0005507 GO:GO:0009409 GO:GO:0009637 GO:GO:0010218 GO:GO:0010114 GO:GO:0031969 EMBL:AC007152 GO:GO:0009853 GO:GO:0009535 GO:GO:0022626 GO:GO:0031977 EMBL:AC004146 GO:GO:0019253 UniGene:At.46639 GO:GO:0016984 UniGene:At.37531 Gene3D:G3DSA:3.30.190.10 EMBL:X13611 EMBL:AF325011 EMBL:AF325004 EMBL:AF372874 EMBL:AF410291 EMBL:AY054188 EMBL:AY054581 EMBL:AY058831 EMBL:AY059940 EMBL:AY062612 EMBL:AY062711 EMBL:AY065101 EMBL:AY093380 EMBL:AY093388 EMBL:AY097366 EMBL:BT000362 EMBL:BT002076 EMBL:X68342 IPI:IPI00539020 PIR:G96694 PIR:S03720 RefSeq:NP_176880.1 UniGene:At.12721 UniGene:At.30194 UniGene:At.49098 UniGene:At.67454 UniGene:At.68122 UniGene:At.70053 UniGene:At.75196 ProteinModelPortal:P10795 SMR:P10795 IntAct:P10795 MINT:MINT-2584041 STRING:P10795 World-2DPAGE:0003:P10795 PRIDE:P10795 ProMEX:P10795 EnsemblPlants:AT1G67090.1 GeneID:843029 KEGG:ath:AT1G67090 TAIR:At1g67090 eggNOG:COG4451 HOGENOM:HBG608223 InParanoid:P10795 KO:K01602 OMA:AFPATRK PhylomeDB:P10795 ProtClustDB:PLN02289 ArrayExpress:P10795 Genevestigator:P10795 InterPro:IPR024681 InterPro:IPR024680 Pfam:PF12338 PRINTS:PR00152 SMART:SM00961 SUPFAM:SSF55239 Uniprot:P10795
Leaf	Isotig00009	228	1624	-2.303	7.02E-174	TAIR|locus:2033686 - symbol:RBCS1A "AT1G67090" species:3702 "Arabidopsis thaliana" [GO:0009573 "chloroplast ribulose bisphosphate carboxylase complex" evidence=ISS] [GO:0015977 "carbon fixation" evidence=ISS] [GO:0016984 "ribulose-bisphosphate carboxylase activity" evidence=ISS] [GO:0031977 "thylakoid lumen" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009637 "response to blue light" evidence=IEP] [GO:0010114 "response to red light" evidence=IEP] [GO:0010218 "response to far red light" evidence=IEP] [GO:0015979 "photosynthesis" evidence=IMP] [GO:0080158 "chloroplast ribulose bisphosphate carboxylase complex biogenesis" evidence=IMP] InterPro:IPR000894 Pfam:PF00101 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0048046 GO:GO:0009570 GO:GO:0004497 GO:GO:0005507 GO:GO:0009409 GO:GO:0009637 GO:GO:0010218 GO:GO:0010114 GO:GO:0031969 EMBL:AC007152 GO:GO:0009853 GO:GO:0009535 GO:GO:0022626 GO:GO:0031977 EMBL:AC004146 GO:GO:0019253 UniGene:At.46639 GO:GO:0016984 UniGene:At.37531 Gene3D:G3DSA:3.30.190.10 EMBL:X13611 EMBL:AF325011 EMBL:AF325004 EMBL:AF372874 EMBL:AF410291 EMBL:AY054188 EMBL:AY054581 EMBL:AY058831 EMBL:AY059940 EMBL:AY062612 EMBL:AY062711 EMBL:AY065101 EMBL:AY093380 EMBL:AY093388 EMBL:AY097366 EMBL:BT000362 EMBL:BT002076 EMBL:X68342 IPI:IPI00539020 PIR:G96694 PIR:S03720 RefSeq:NP_176880.1 UniGene:At.12721 UniGene:At.30194 UniGene:At.49098 UniGene:At.67454 UniGene:At.68122 UniGene:At.70053 UniGene:At.75196 ProteinModelPortal:P10795 SMR:P10795 IntAct:P10795 MINT:MINT-2584041 STRING:P10795 World-2DPAGE:0003:P10795 PRIDE:P10795 ProMEX:P10795 EnsemblPlants:AT1G67090.1 GeneID:843029 KEGG:ath:AT1G67090 TAIR:At1g67090 eggNOG:COG4451 HOGENOM:HBG608223 InParanoid:P10795 KO:K01602 OMA:AFPATRK PhylomeDB:P10795 ProtClustDB:PLN02289 ArrayExpress:P10795 Genevestigator:P10795 InterPro:IPR024681 InterPro:IPR024680 Pfam:PF12338 PRINTS:PR00152 SMART:SM00961 SUPFAM:SSF55239 Uniprot:P10795
Leaf	Isotig00010	237	1676	-2.293	1.97E-178	TAIR|locus:2033686 - symbol:RBCS1A "AT1G67090" species:3702 "Arabidopsis thaliana" [GO:0009573 "chloroplast ribulose bisphosphate carboxylase complex" evidence=ISS] [GO:0015977 "carbon fixation" evidence=ISS] [GO:0016984 "ribulose-bisphosphate carboxylase activity" evidence=ISS] [GO:0031977 "thylakoid lumen" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009637 "response to blue light" evidence=IEP] [GO:0010114 "response to red light" evidence=IEP] [GO:0010218 "response to far red light" evidence=IEP]

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						[GO:0015979 "photosynthesis" evidence=IMP] [GO:0080158 "chloroplast ribulose bisphosphate carboxylase complex biogenesis" evidence=IMP] InterPro:IPR000894 Pfam:PF00101 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0048046 GO:GO:0009570 GO:GO:0004497 GO:GO:0005507 GO:GO:0009409 GO:GO:0009637 GO:GO:0010218 GO:GO:0010114 GO:GO:0031969 EMBL:AC007152 GO:GO:0009853 GO:GO:0009535 GO:GO:0022626 GO:GO:0031977 EMBL:AC004146 GO:GO:0019253 UniGene:At.46639 GO:GO:0016984 UniGene:At.37531 Gene3D:G3DSA:3.30.190.10 EMBL:X13611 EMBL:AF325011 EMBL:AF325004 EMBL:AF372874 EMBL:AF410291 EMBL:AY054188 EMBL:AY054581 EMBL:AY058831 EMBL:AY059940 EMBL:AY062612 EMBL:AY062711 EMBL:AY065101 EMBL:AY093380 EMBL:AY093388 EMBL:AY097366 EMBL:BT000362 EMBL:BT002076 EMBL:X68342 IPI:IPI00539020 PIR:G96694 PIR:S03720 RefSeq:NP_176880.1 UniGene:At.12721 UniGene:At.30194 UniGene:At.49098 UniGene:At.67454 UniGene:At.68122 UniGene:At.70053 UniGene:At.75196 ProteinModelPortal:P10795 SMR:P10795 IntAct:P10795 MINT:MINT-2584041 STRING:P10795 World-2DPAGE:0003:P10795 PRIDE:P10795 ProMEX:P10795 EnsemblPlants:AT1G67090.1 GeneID:843029 KEGG:ath:AT1G67090 TAIR:At1g67090 eggNOG:COG4451 HOGENOM:HBG608223 InParanoid:P10795 KO:K01602 OMA:AFPATRK PhylomeDB:P10795 ProtClustDB:PLN02289 ArrayExpress:P10795 Genevestigator:P10795 InterPro:IPR024681 InterPro:IPR024680 Pfam:PF12338 PRINTS:PR00152 SMART:SM00961 SUPFAM:SSF55239 Uniprot:P10795
Leaf	Isotig00011	228	1631	-2.310	3.52E-175	TAIR|locus:2033686 - symbol:RBCS1A "AT1G67090" species:3702 "Arabidopsis thaliana" [GO:0009573 "chloroplast ribulose bisphosphate carboxylase complex" evidence=ISS] [GO:0015977 "carbon fixation" evidence=ISS] [GO:0016984 "ribulose-bisphosphate carboxylase activity" evidence=ISS] [GO:0031977 "thylakoid lumen" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009637 "response to blue light" evidence=IEP] [GO:0010114 "response to red light" evidence=IEP] [GO:0010218 "response to far red light" evidence=IEP] [GO:0015979 "photosynthesis" evidence=IMP] [GO:0080158 "chloroplast ribulose bisphosphate carboxylase complex biogenesis" evidence=IMP] InterPro:IPR000894 Pfam:PF00101 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0048046 GO:GO:0009570 GO:GO:0004497 GO:GO:0005507 GO:GO:0009409 GO:GO:0009637 GO:GO:0010218 GO:GO:0010114 GO:GO:0031969 EMBL:AC007152 GO:GO:0009853 GO:GO:0009535 GO:GO:0022626 GO:GO:0031977 EMBL:AC004146 GO:GO:0019253 UniGene:At.46639 GO:GO:0016984 UniGene:At.37531 Gene3D:G3DSA:3.30.190.10 EMBL:X13611 EMBL:AF325011 EMBL:AF325004 EMBL:AF372874 EMBL:AF410291 EMBL:AY054188 EMBL:AY054581 EMBL:AY058831 EMBL:AY059940 EMBL:AY062612 EMBL:AY062711 EMBL:AY065101 EMBL:AY093380 EMBL:AY093388 EMBL:AY097366 EMBL:BT000362 EMBL:BT002076 EMBL:X68342 IPI:IPI00539020 PIR:G96694 PIR:S03720 RefSeq:NP_176880.1 UniGene:At.12721 UniGene:At.30194 UniGene:At.49098 UniGene:At.67454 UniGene:At.68122 UniGene:At.70053 UniGene:At.75196 ProteinModelPortal:P10795 SMR:P10795 IntAct:P10795 MINT:MINT-2584041 STRING:P10795 World-2DPAGE:0003:P10795 PRIDE:P10795 ProMEX:P10795 EnsemblPlants:AT1G67090.1 GeneID:843029 KEGG:ath:AT1G67090 TAIR:At1g67090 eggNOG:COG4451 HOGENOM:HBG608223 InParanoid:P10795 KO:K01602 OMA:AFPATRK PhylomeDB:P10795 ProtClustDB:PLN02289 ArrayExpress:P10795 Genevestigator:P10795 InterPro:IPR024681 InterPro:IPR024680 Pfam:PF12338 PRINTS:PR00152 SMART:SM00961 SUPFAM:SSF55239 Uniprot:P10795
Leaf	Isotig00012	237	1683	-2.299	9.93E-180	TAIR|locus:2033686 - symbol:RBCS1A "AT1G67090" species:3702 "Arabidopsis thaliana" [GO:0009573 "chloroplast ribulose bisphosphate carboxylase complex" evidence=ISS] [GO:0015977 "carbon fixation" evidence=ISS] [GO:0016984 "ribulose-bisphosphate carboxylase activity" evidence=ISS] [GO:0031977 "thylakoid lumen" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009637 "response to blue light" evidence=IEP] [GO:0010114 "response to red light" evidence=IEP] [GO:0010218 "response to far red light" evidence=IEP] [GO:0015979 "photosynthesis" evidence=IMP] [GO:0080158 "chloroplast ribulose bisphosphate carboxylase complex biogenesis" evidence=IMP] InterPro:IPR000894 Pfam:PF00101 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0048046 GO:GO:0009570 GO:GO:0004497 GO:GO:0005507

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0009409 GO:GO:0009637 GO:GO:0010218 GO:GO:0010114 GO:GO:0031969 EMBL:AC007152 GO:GO:0009853 GO:GO:0009535 GO:GO:0022626 GO:GO:0031977 EMBL:AC004146 GO:GO:0019253 UniGene:At.46639 GO:GO:0016984 UniGene:At.37531 Gene3D:G3DSA:3.30.190.10 EMBL:X13611 EMBL:AF325011 EMBL:AF325004 EMBL:AF372874 EMBL:AF410291 EMBL:AY054188 EMBL:AY054581 EMBL:AY058831 EMBL:AY059940 EMBL:AY062612 EMBL:AY062711 EMBL:AY065101 EMBL:AY093380 EMBL:AY093388 EMBL:AY097366 EMBL:BT000362 EMBL:BT002076 EMBL:X68342 IPI:IPI00539020 PIR:G96694 PIR:S03720 RefSeq:NP_176880.1 UniGene:At.12721 UniGene:At.30194 UniGene:At.49098 UniGene:At.67454 UniGene:At.68122 UniGene:At.70053 UniGene:At.75196 ProteinModelPortal:P10795 SMR:P10795 IntAct:P10795 MINT:MINT-2584041 STRING:P10795 World-2DPAGE:0003:P10795 PRIDE:P10795 ProMEX:P10795 EnsemblPlants:AT1G67090.1 GeneID:843029 KEGG:ath:AT1G67090 TAIR:At1g67090 eggNOG:COG4451 HOGENOM:HBG608223 InParanoid:P10795 KO:K01602 OMA:AFPATRK PhylomeDB:P10795 ProtClustDB:PLN02289 ArrayExpress:P10795 Genevestigator:P10795 InterPro:IPR024681 InterPro:IPR024680 Pfam:PF12338 PRINTS:PR00152 SMART:SM00961 SUPFAM:SSF55239 Uniprot:P10795
Leaf	Isotig00013	345	2349	-2.238	2.59E-242	TAIR|locus:2033686 - symbol:RBCS1A "AT1G67090" species:3702 "Arabidopsis thaliana" [GO:0009573 "chloroplast ribulose bisphosphate carboxylase complex" evidence=ISS] [GO:0015977 "carbon fixation" evidence=ISS] [GO:0016984 "ribulose-bisphosphate carboxylase activity" evidence=ISS] [GO:0031977 "thylakoid lumen" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009637 "response to blue light" evidence=IEP] [GO:0010114 "response to red light" evidence=IEP] [GO:0010218 "response to far red light" evidence=IEP] [GO:0015979 "photosynthesis" evidence=IMP] [GO:0080158 "chloroplast ribulose bisphosphate carboxylase complex biogenesis" evidence=IMP] InterPro:IPR000894 Pfam:PF00101 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0048046 GO:GO:0009570 GO:GO:0004497 GO:GO:0005507 GO:GO:0009409 GO:GO:0009637 GO:GO:0010218 GO:GO:0010114 GO:GO:0031969 EMBL:AC007152 GO:GO:0009853 GO:GO:0009535 GO:GO:0022626 GO:GO:0031977 EMBL:AC004146 GO:GO:0019253 UniGene:At.46639 GO:GO:0016984 UniGene:At.37531 Gene3D:G3DSA:3.30.190.10 EMBL:X13611 EMBL:AF325011 EMBL:AF325004 EMBL:AF372874 EMBL:AF410291 EMBL:AY054188 EMBL:AY054581 EMBL:AY058831 EMBL:AY059940 EMBL:AY062612 EMBL:AY062711 EMBL:AY065101 EMBL:AY093380 EMBL:AY093388 EMBL:AY097366 EMBL:BT000362 EMBL:BT002076 EMBL:X68342 IPI:IPI00539020 PIR:G96694 PIR:S03720 RefSeq:NP_176880.1 UniGene:At.12721 UniGene:At.30194 UniGene:At.49098 UniGene:At.67454 UniGene:At.68122 UniGene:At.70053 UniGene:At.75196 ProteinModelPortal:P10795 SMR:P10795 IntAct:P10795 MINT:MINT-2584041 STRING:P10795 World-2DPAGE:0003:P10795 PRIDE:P10795 ProMEX:P10795 EnsemblPlants:AT1G67090.1 GeneID:843029 KEGG:ath:AT1G67090 TAIR:At1g67090 eggNOG:COG4451 HOGENOM:HBG608223 InParanoid:P10795 KO:K01602 OMA:AFPATRK PhylomeDB:P10795 ProtClustDB:PLN02289 ArrayExpress:P10795 Genevestigator:P10795 InterPro:IPR024681 InterPro:IPR024680 Pfam:PF12338 PRINTS:PR00152 SMART:SM00961 SUPFAM:SSF55239 Uniprot:P10795
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Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EMBL:AF325011 EMBL:AF325004 EMBL:AF372874 EMBL:AF410291 EMBL:AY054188 EMBL:AY054581 EMBL:AY058831 EMBL:AY059940 EMBL:AY062612 EMBL:AY062711 EMBL:AY065101 EMBL:AY093380 EMBL:AY093388 EMBL:AY097366 EMBL:BT000362 EMBL:BT002076 EMBL:X68342 IPI:IPI00539020 PIR:G96694 PIR:S03720 RefSeq:NP_176880.1 UniGene:At.12721 UniGene:At.30194 UniGene:At.49098 UniGene:At.67454 UniGene:At.68122 UniGene:At.70053 UniGene:At.75196 ProteinModelPortal:P10795 SMR:P10795 IntAct:P10795 MINT:MINT-2584041 STRING:P10795 World-2DPAGE:0003:P10795 PRIDE:P10795 ProMEX:P10795 EnsemblPlants:AT1G67090.1 GeneID:843029 KEGG:ath:AT1G67090 TAIR:At1g67090 eggNOG:COG4451 HOGENOM:HBG608223 InParanoid:P10795 KO:K01602 OMA:AFPATRK PhylomeDB:P10795 ProtClustDB:PLN02289 ArrayExpress:P10795 Genevestigator:P10795 InterPro:IPR024681 InterPro:IPR024680 Pfam:PF12338 PRINTS:PR00152 SMART:SM00961 SUPFAM:SSF55239 Uniprot:P10795
Leaf	Isotig00016	227	1612	-2.299	3.21E-172	UNIPROTKB|P69249 - symbol:RBCS "Ribulose bisphosphate carboxylase small chain, chloroplastic" species:4097 "Nicotiana tabacum" [GO:0005515 "protein binding" evidence=IPI] InterPro:IPR000894 Pfam:PF00101 GO:GO:0009507 GO:GO:0005515 GO:GO:0004497 GO:GO:0009853 GO:GO:0015979 GO:GO:0015977 GO:GO:0016984 Gene3D:G3DSA:3.30.190.10 InterPro:IPR024681 InterPro:IPR024680 Pfam:PF12338 PRINTS:PR00152 SUPFAM:SSF55239 EMBL:X02353 EMBL:M32419 PIR:A22934 PDB:1EJ7 PDB:1RLC PDB:1RLD PDB:3RUB PDB:4RUB PDBsum:1EJ7 PDBsum:1RLC PDBsum:1RLD PDBsum:3RUB PDBsum:4RUB ProteinModelPortal:P69249 SMR:P69249 DIP:DIP-40635N IntAct:P69249 MINT:MINT-1176585 Uniprot:P69249
Leaf	Isotig00017	227	1619	-2.305	1.61E-173	UNIPROTKB|P69249 - symbol:RBCS "Ribulose bisphosphate carboxylase small chain, chloroplastic" species:4097 "Nicotiana tabacum" [GO:0005515 "protein binding" evidence=IPI] InterPro:IPR000894 Pfam:PF00101 GO:GO:0009507 GO:GO:0005515 GO:GO:0004497 GO:GO:0009853 GO:GO:0015979 GO:GO:0015977 GO:GO:0016984 Gene3D:G3DSA:3.30.190.10 InterPro:IPR024681 InterPro:IPR024680 Pfam:PF12338 PRINTS:PR00152 SUPFAM:SSF55239 EMBL:X02353 EMBL:M32419 PIR:A22934 PDB:1EJ7 PDB:1RLC PDB:1RLD PDB:3RUB PDB:4RUB PDBsum:1EJ7 PDBsum:1RLC PDBsum:1RLD PDBsum:3RUB PDBsum:4RUB ProteinModelPortal:P69249 SMR:P69249 DIP:DIP-40635N IntAct:P69249 MINT:MINT-1176585 Uniprot:P69249
Leaf	Isotig00019	227	1612	-2.299	3.21E-172	UNIPROTKB|P69249 - symbol:RBCS "Ribulose bisphosphate carboxylase small chain, chloroplastic" species:4097 "Nicotiana tabacum" [GO:0005515 "protein binding" evidence=IPI] InterPro:IPR000894 Pfam:PF00101 GO:GO:0009507 GO:GO:0005515 GO:GO:0004497 GO:GO:0009853 GO:GO:0015979 GO:GO:0015977 GO:GO:0016984 Gene3D:G3DSA:3.30.190.10 InterPro:IPR024681 InterPro:IPR024680 Pfam:PF12338 PRINTS:PR00152 SUPFAM:SSF55239 EMBL:X02353 EMBL:M32419 PIR:A22934 PDB:1EJ7 PDB:1RLC PDB:1RLD PDB:3RUB PDB:4RUB PDBsum:1EJ7 PDBsum:1RLC PDBsum:1RLD PDBsum:3RUB PDBsum:4RUB ProteinModelPortal:P69249 SMR:P69249 DIP:DIP-40635N IntAct:P69249 MINT:MINT-1176585 Uniprot:P69249
Leaf	Isotig00020	227	1619	-2.305	1.61E-173	UNIPROTKB|P69249 - symbol:RBCS "Ribulose bisphosphate carboxylase small chain, chloroplastic" species:4097 "Nicotiana tabacum" [GO:0005515 "protein binding" evidence=IPI] InterPro:IPR000894 Pfam:PF00101 GO:GO:0009507 GO:GO:0005515 GO:GO:0004497 GO:GO:0009853 GO:GO:0015979 GO:GO:0015977 GO:GO:0016984 Gene3D:G3DSA:3.30.190.10 InterPro:IPR024681 InterPro:IPR024680 Pfam:PF12338 PRINTS:PR00152 SUPFAM:SSF55239 EMBL:X02353 EMBL:M32419 PIR:A22934 PDB:1EJ7 PDB:1RLC PDB:1RLD PDB:3RUB PDB:4RUB PDBsum:1EJ7 PDBsum:1RLC PDBsum:1RLD PDBsum:3RUB PDBsum:4RUB ProteinModelPortal:P69249 SMR:P69249 DIP:DIP-40635N IntAct:P69249 MINT:MINT-1176585 Uniprot:P69249
Leaf	Isotig00021	219	1611	-2.350	1.30E-176	TAIR|locus:2033686 - symbol:RBCS1A "AT1G67090" species:3702 "Arabidopsis thaliana" [GO:0009573 "chloroplast ribulose bisphosphate carboxylase complex" evidence=ISS] [GO:0015977 "carbon fixation" evidence=ISS] [GO:0016984 "ribulose-bisphosphate carboxylase activity" evidence=ISS] [GO:0031977 "thylakoid lumen" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009637 "response to blue light" evidence=IEP] [GO:0010114 "response to red light" evidence=IEP] [GO:0010218 "response to far red light" evidence=IEP] [GO:0015979 "photosynthesis" evidence=IMP] [GO:0080158 "chloroplast ribulose bisphosphate carboxylase complex biogenesis" evidence=IMP] InterPro:IPR000894 Pfam:PF00101 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0048046 GO:GO:0009570 GO:GO:0004497 GO:GO:0005507 GO:GO:0009409 GO:GO:0009637 GO:GO:0010218 GO:GO:0010114 GO:GO:0031969 EMBL:AC007152 GO:GO:0009853 GO:GO:0009535 GO:GO:0022626 GO:GO:0031977 EMBL:AC004146 GO:GO:0019253

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						UniGene:At.46639 GO:GO:0016984 UniGene:At.37531 Gene3D:G3DSA:3.30.190.10 EMBL:X13611 EMBL:AF325011 EMBL:AF325004 EMBL:AF372874 EMBL:AF410291 EMBL:AY054188 EMBL:AY054581 EMBL:AY058831 EMBL:AY059940 EMBL:AY062612 EMBL:AY062711 EMBL:AY065101 EMBL:AY093380 EMBL:AY093388 EMBL:AY097366 EMBL:BT000362 EMBL:BT002076 EMBL:X68342 IPI:IPI00539020 PIR:G96694 PIR:S03720 RefSeq:NP_176880.1 UniGene:At.12721 UniGene:At.30194 UniGene:At.49098 UniGene:At.67454 UniGene:At.68122 UniGene:At.70053 UniGene:At.75196 ProteinModelPortal:P10795 SMR:P10795 IntAct:P10795 MINT:MINT-2584041 STRING:P10795 World-2DPAGE:0003:P10795 PRIDE:P10795 ProMEX:P10795 EnsemblPlants:AT1G67090.1 GeneID:843029 KEGG:ath:AT1G67090 TAIR:At1g67090 eggNOG:COG4451 HOGENOM:HBG608223 InParanoid:P10795 KO:K01602 OMA:AFPATRK PhylomeDB:P10795 ProtClustDB:PLN02289 ArrayExpress:P10795 Genevestigator:P10795 InterPro:IPR024681 InterPro:IPR024680 Pfam:PF12338 PRINTS:PR00152 SMART:SM00961 SUPFAM:SSF55239 Uniprot:P10795
Leaf	Isotig00022	228	1663	-2.338	3.84E-181	TAIR|locus:2033686 - symbol:RBCS1A "AT1G67090" species:3702 "Arabidopsis thaliana" [GO:0009573 "chloroplast ribulose bisphosphate carboxylase complex" evidence=ISS] [GO:0015977 "carbon fixation" evidence=ISS] [GO:0016984 "ribulose-bisphosphate carboxylase activity" evidence=ISS] [GO:0031977 "thylakoid lumen" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009637 "response to blue light" evidence=IEP] [GO:0010114 "response to red light" evidence=IEP] [GO:0010218 "response to far red light" evidence=IEP] [GO:0015979 "photosynthesis" evidence=IMP] [GO:0080158 "chloroplast ribulose bisphosphate carboxylase complex biogenesis" evidence=IMP] InterPro:IPR000894 Pfam:PF00101 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0048046 GO:GO:0009570 GO:GO:0004497 GO:GO:0005507 GO:GO:0009409 GO:GO:0009637 GO:GO:0010218 GO:GO:0010114 GO:GO:0031969 EMBL:AC007152 GO:GO:0009853 GO:GO:0009535 GO:GO:0022626 GO:GO:0031977 EMBL:AC004146 GO:GO:0019253 UniGene:At.46639 GO:GO:0016984 UniGene:At.37531 Gene3D:G3DSA:3.30.190.10 EMBL:X13611 EMBL:AF325011 EMBL:AF325004 EMBL:AF372874 EMBL:AF410291 EMBL:AY054188 EMBL:AY054581 EMBL:AY058831 EMBL:AY059940 EMBL:AY062612 EMBL:AY062711 EMBL:AY065101 EMBL:AY093380 EMBL:AY093388 EMBL:AY097366 EMBL:BT000362 EMBL:BT002076 EMBL:X68342 IPI:IPI00539020 PIR:G96694 PIR:S03720 RefSeq:NP_176880.1 UniGene:At.12721 UniGene:At.30194 UniGene:At.49098 UniGene:At.67454 UniGene:At.68122 UniGene:At.70053 UniGene:At.75196 ProteinModelPortal:P10795 SMR:P10795 IntAct:P10795 MINT:MINT-2584041 STRING:P10795 World-2DPAGE:0003:P10795 PRIDE:P10795 ProMEX:P10795 EnsemblPlants:AT1G67090.1 GeneID:843029 KEGG:ath:AT1G67090 TAIR:At1g67090 eggNOG:COG4451 HOGENOM:HBG608223 InParanoid:P10795 KO:K01602 OMA:AFPATRK PhylomeDB:P10795 ProtClustDB:PLN02289 ArrayExpress:P10795 Genevestigator:P10795 InterPro:IPR024681 InterPro:IPR024680 Pfam:PF12338 PRINTS:PR00152 SMART:SM00961 SUPFAM:SSF55239 Uniprot:P10795
Leaf	Isotig00024	219	1618	-2.356	6.35E-178	TAIR|locus:2033686 - symbol:RBCS1A "AT1G67090" species:3702 "Arabidopsis thaliana" [GO:0009573 "chloroplast ribulose bisphosphate carboxylase complex" evidence=ISS] [GO:0015977 "carbon fixation" evidence=ISS] [GO:0016984 "ribulose-bisphosphate carboxylase activity" evidence=ISS] [GO:0031977 "thylakoid lumen" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009637 "response to blue light" evidence=IEP] [GO:0010114 "response to red light" evidence=IEP] [GO:0010218 "response to far red light" evidence=IEP] [GO:0015979 "photosynthesis" evidence=IMP] [GO:0080158 "chloroplast ribulose bisphosphate carboxylase complex biogenesis" evidence=IMP] InterPro:IPR000894 Pfam:PF00101 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0048046 GO:GO:0009570 GO:GO:0004497 GO:GO:0005507 GO:GO:0009409 GO:GO:0009637 GO:GO:0010218 GO:GO:0010114 GO:GO:0031969 EMBL:AC007152 GO:GO:0009853 GO:GO:0009535 GO:GO:0022626 GO:GO:0031977 EMBL:AC004146 GO:GO:0019253 UniGene:At.46639 GO:GO:0016984 UniGene:At.37531 Gene3D:G3DSA:3.30.190.10 EMBL:X13611 EMBL:AF325011 EMBL:AF325004 EMBL:AF372874 EMBL:AF410291 EMBL:AY054188 EMBL:AY054581 EMBL:AY058831 EMBL:AY059940 EMBL:AY062612 EMBL:AY062711 EMBL:AY065101 EMBL:AY093380

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EMBL:AY093388 EMBL:AY097366 EMBL:BT000362 EMBL:BT002076 EMBL:X68342 IPI:IPI00539020 PIR:G96694 PIR:S03720 RefSeq:NP_176880.1 UniGene:At.12721 UniGene:At.30194 UniGene:At.49098 UniGene:At.67454 UniGene:At.68122 UniGene:At.70053 UniGene:At.75196 ProteinModelPortal:P10795 SMR:P10795 IntAct:P10795 MINT:MINT-2584041 STRING:P10795 World-2DPAGE:0003:P10795 PRIDE:P10795 ProMEX:P10795 EnsemblPlants:AT1G67090.1 GeneID:843029 KEGG:ath:AT1G67090 TAIR:At1g67090 eggNOG:COG4451 HOGENOM:HBG608223 InParanoid:P10795 KO:K01602 OMA:AFPATRK PhylomeDB:P10795 ProtClustDB:PLN02289 ArrayExpress:P10795 Genevestigator:P10795 InterPro:IPR024681 InterPro:IPR024680 Pfam:PF12338 PRINTS:PR00152 SMART:SM00961 SUPFAM:SSF55239 Uniprot:P10795
Leaf	Isotig00025	228	1670	-2.344	1.89E-182	TAIR|locus:2033686 - symbol:RBCS1A "AT1G67090" species:3702 "Arabidopsis thaliana" [GO:0009573 "chloroplast ribulose bisphosphate carboxylase complex" evidence=ISS] [GO:0015977 "carbon fixation" evidence=ISS] [GO:0016984 "ribulose-bisphosphate carboxylase activity" evidence=ISS] [GO:0031977 "thylakoid lumen" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009637 "response to blue light" evidence=IEP] [GO:0010114 "response to red light" evidence=IEP] [GO:0010218 "response to far red light" evidence=IEP] [GO:0015979 "photosynthesis" evidence=IMP] [GO:0080158 "chloroplast ribulose bisphosphate carboxylase complex biogenesis" evidence=IMP] InterPro:IPR000894 Pfam:PF00101 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0048046 GO:GO:0009570 GO:GO:0004497 GO:GO:0005507 GO:GO:0009409 GO:GO:0009637 GO:GO:0010218 GO:GO:0010114 GO:GO:0031969 EMBL:AC007152 GO:GO:0009853 GO:GO:0009535 GO:GO:0022626 GO:GO:0031977 EMBL:AC004146 GO:GO:0019253 UniGene:At.46639 GO:GO:0016984 UniGene:At.37531 Gene3D:G3DSA:3.30.190.10 EMBL:X13611 EMBL:AF325011 EMBL:AF325004 EMBL:AF372874 EMBL:AF410291 EMBL:AY054188 EMBL:AY054581 EMBL:AY058831 EMBL:AY059940 EMBL:AY062612 EMBL:AY062711 EMBL:AY065101 EMBL:AY093380 EMBL:AY093388 EMBL:AY097366 EMBL:BT000362 EMBL:BT002076 EMBL:X68342 IPI:IPI00539020 PIR:G96694 PIR:S03720 RefSeq:NP_176880.1 UniGene:At.12721 UniGene:At.30194 UniGene:At.49098 UniGene:At.67454 UniGene:At.68122 UniGene:At.70053 UniGene:At.75196 ProteinModelPortal:P10795 SMR:P10795 IntAct:P10795 MINT:MINT-2584041 STRING:P10795 World-2DPAGE:0003:P10795 PRIDE:P10795 ProMEX:P10795 EnsemblPlants:AT1G67090.1 GeneID:843029 KEGG:ath:AT1G67090 TAIR:At1g67090 eggNOG:COG4451 HOGENOM:HBG608223 InParanoid:P10795 KO:K01602 OMA:AFPATRK PhylomeDB:P10795 ProtClustDB:PLN02289 ArrayExpress:P10795 Genevestigator:P10795 InterPro:IPR024681 InterPro:IPR024680 Pfam:PF12338 PRINTS:PR00152 SMART:SM00961 SUPFAM:SSF55239 Uniprot:P10795
Leaf	Isotig00027	130	855	-2.188	6.55E-87	TAIR|locus:2033686 - symbol:RBCS1A "AT1G67090" species:3702 "Arabidopsis thaliana" [GO:0009573 "chloroplast ribulose bisphosphate carboxylase complex" evidence=ISS] [GO:0015977 "carbon fixation" evidence=ISS] [GO:0016984 "ribulose-bisphosphate carboxylase activity" evidence=ISS] [GO:0031977 "thylakoid lumen" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009637 "response to blue light" evidence=IEP] [GO:0010114 "response to red light" evidence=IEP] [GO:0010218 "response to far red light" evidence=IEP] [GO:0015979 "photosynthesis" evidence=IMP] [GO:0080158 "chloroplast ribulose bisphosphate carboxylase complex biogenesis" evidence=IMP] InterPro:IPR000894 Pfam:PF00101 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0048046 GO:GO:0009570 GO:GO:0004497 GO:GO:0005507 GO:GO:0009409 GO:GO:0009637 GO:GO:0010218 GO:GO:0010114 GO:GO:0031969 EMBL:AC007152 GO:GO:0009853 GO:GO:0009535 GO:GO:0022626 GO:GO:0031977 EMBL:AC004146 GO:GO:0019253 UniGene:At.46639 GO:GO:0016984 UniGene:At.37531 Gene3D:G3DSA:3.30.190.10 EMBL:X13611 EMBL:AF325011 EMBL:AF325004 EMBL:AF372874 EMBL:AF410291 EMBL:AY054188 EMBL:AY054581 EMBL:AY058831 EMBL:AY059940 EMBL:AY062612 EMBL:AY062711 EMBL:AY065101 EMBL:AY093380 EMBL:AY093388 EMBL:AY097366 EMBL:BT000362 EMBL:BT002076 EMBL:X68342 IPI:IPI00539020 PIR:G96694 PIR:S03720 RefSeq:NP_176880.1 UniGene:At.12721 UniGene:At.30194 UniGene:At.49098 UniGene:At.67454 UniGene:At.68122 UniGene:At.70053 UniGene:At.75196 ProteinModelPortal:P10795 SMR:P10795 IntAct:P10795

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						MINT:MINT-2584041 STRING:P10795 World-2DPAGE:0003:P10795 PRIDE:P10795 ProMEX:P10795 EnsemblPlants:AT1G67090.1 GeneID:843029 KEGG:ath:AT1G67090 TAIR:At1g67090 eggNOG:COG4451 HOGENOM:HBG608223 InParanoid:P10795 KO:K01602 OMA:AFPATRK PhylomeDB:P10795 ProtClustDB:PLN02289 ArrayExpress:P10795 Genevestigator:P10795 InterPro:IPR024681 InterPro:IPR024680 Pfam:PF12338 PRINTS:PR00152 SMART:SM00961 SUPFAM:SSF55239 Uniprot:P10795
Leaf	Isotig00028	336	2336	-2.269	6.75E-245	TAIR|locus:2033686 - symbol:RBCS1A "AT1G67090" species:3702 "Arabidopsis thaliana" [GO:0009573 "chloroplast ribulose bisphosphate carboxylase complex" evidence=ISS] [GO:0015977 "carbon fixation" evidence=ISS] [GO:0016984 "ribulose-bisphosphate carboxylase activity" evidence=ISS] [GO:0031977 "thylakoid lumen" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009637 "response to blue light" evidence=IEP] [GO:0010114 "response to red light" evidence=IEP] [GO:0010218 "response to far red light" evidence=IEP] [GO:0015979 "photosynthesis" evidence=IMP] [GO:0080158 "chloroplast ribulose bisphosphate carboxylase complex biogenesis" evidence=IMP] InterPro:IPR000894 Pfam:PF00101 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0048046 GO:GO:0009570 GO:GO:0004497 GO:GO:0005507 GO:GO:0009409 GO:GO:0009637 GO:GO:0010218 GO:GO:0010114 GO:GO:0031969 EMBL:AC007152 GO:GO:0009853 GO:GO:0009535 GO:GO:0022626 GO:GO:0031977 EMBL:AC004146 GO:GO:0019253 UniGene:At.46639 GO:GO:0016984 UniGene:At.37531 Gene3D:G3DSA:3.30.190.10 EMBL:X13611 EMBL:AF325011 EMBL:AF325004 EMBL:AF372874 EMBL:AF410291 EMBL:AY054188 EMBL:AY054581 EMBL:AY058831 EMBL:AY059940 EMBL:AY062612 EMBL:AY062711 EMBL:AY065101 EMBL:AY093380 EMBL:AY093388 EMBL:AY097366 EMBL:BT000362 EMBL:BT002076 EMBL:X68342 IPI:IPI00539020 PIR:G96694 PIR:S03720 RefSeq:NP_176880.1 UniGene:At.12721 UniGene:At.30194 UniGene:At.49098 UniGene:At.67454 UniGene:At.68122 UniGene:At.70053 UniGene:At.75196 ProteinModelPortal:P10795 SMR:P10795 IntAct:P10795 MINT:MINT-2584041 STRING:P10795 World-2DPAGE:0003:P10795 PRIDE:P10795 ProMEX:P10795 EnsemblPlants:AT1G67090.1 GeneID:843029 KEGG:ath:AT1G67090 TAIR:At1g67090 eggNOG:COG4451 HOGENOM:HBG608223 InParanoid:P10795 KO:K01602 OMA:AFPATRK PhylomeDB:P10795 ProtClustDB:PLN02289 ArrayExpress:P10795 Genevestigator:P10795 InterPro:IPR024681 InterPro:IPR024680 Pfam:PF12338 PRINTS:PR00152 SMART:SM00961 SUPFAM:SSF55239 Uniprot:P10795
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Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						ProtClustDB:PLN02289 ArrayExpress:P10795 Genevestigator:P10795 InterPro:IPR024681 InterPro:IPR024680 Pfam:PF12338 PRINTS:PR00152 SMART:SM00961 SUPFAM:SSF55239 Uniprot:P10795
Leaf	Isotig00031	229	1623	-2.296	3.96E-173	TAIR|locus:2033686 - symbol:RBCS1A "AT1G67090" species:3702 "Arabidopsis thaliana" [GO:0009573 "chloroplast ribulose bisphosphate carboxylase complex" evidence=ISS] [GO:0015977 "carbon fixation" evidence=ISS] [GO:0016984 "ribulose-bisphosphate carboxylase activity" evidence=ISS] [GO:0031977 "thylakoid lumen" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009637 "response to blue light" evidence=IEP] [GO:0010114 "response to red light" evidence=IEP] [GO:0010218 "response to far red light" evidence=IEP] [GO:0015979 "photosynthesis" evidence=IMP] [GO:0080158 "chloroplast ribulose bisphosphate carboxylase complex biogenesis" evidence=IMP] InterPro:IPR000894 Pfam:PF00101 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0048046 GO:GO:0009570 GO:GO:0004497 GO:GO:0005507 GO:GO:0009409 GO:GO:0009637 GO:GO:0010218 GO:GO:0010114 GO:GO:0031969 EMBL:AC007152 GO:GO:0009853 GO:GO:0009535 GO:GO:0022626 GO:GO:0031977 EMBL:AC004146 GO:GO:0019253 UniGene:At.46639 GO:GO:0016984 UniGene:At.37531 Gene3D:G3DSA:3.30.190.10 EMBL:X13611 EMBL:AF325011 EMBL:AF325004 EMBL:AF372874 EMBL:AF410291 EMBL:AY054188 EMBL:AY054581 EMBL:AY058831 EMBL:AY059940 EMBL:AY062612 EMBL:AY062711 EMBL:AY065101 EMBL:AY093380 EMBL:AY093388 EMBL:AY097366 EMBL:BT000362 EMBL:BT002076 EMBL:X68342 IPI:IPI00539020 PIR:G96694 PIR:S03720 RefSeq:NP_176880.1 UniGene:At.12721 UniGene:At.30194 UniGene:At.49098 UniGene:At.67454 UniGene:At.68122 UniGene:At.70053 UniGene:At.75196 ProteinModelPortal:P10795 SMR:P10795 IntAct:P10795 MINT:MINT-2584041 STRING:P10795 World-2DPAGE:0003:P10795 PRIDE:P10795 ProMEX:P10795 EnsemblPlants:AT1G67090.1 GeneID:843029 KEGG:ath:AT1G67090 TAIR:At1g67090 eggNOG:COG4451 HOGENOM:HBG608223 InParanoid:P10795 KO:K01602 OMA:AFPATRK PhylomeDB:P10795 ProtClustDB:PLN02289 ArrayExpress:P10795 Genevestigator:P10795 InterPro:IPR024681 InterPro:IPR024680 Pfam:PF12338 PRINTS:PR00152 SMART:SM00961 SUPFAM:SSF55239 Uniprot:P10795
Leaf	Isotig00032	238	1675	-2.286	1.10E-177	TAIR|locus:2033686 - symbol:RBCS1A "AT1G67090" species:3702 "Arabidopsis thaliana" [GO:0009573 "chloroplast ribulose bisphosphate carboxylase complex" evidence=ISS] [GO:0015977 "carbon fixation" evidence=ISS] [GO:0016984 "ribulose-bisphosphate carboxylase activity" evidence=ISS] [GO:0031977 "thylakoid lumen" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009637 "response to blue light" evidence=IEP] [GO:0010114 "response to red light" evidence=IEP] [GO:0010218 "response to far red light" evidence=IEP] [GO:0015979 "photosynthesis" evidence=IMP] [GO:0080158 "chloroplast ribulose bisphosphate carboxylase complex biogenesis" evidence=IMP] InterPro:IPR000894 Pfam:PF00101 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0048046 GO:GO:0009570 GO:GO:0004497 GO:GO:0005507 GO:GO:0009409 GO:GO:0009637 GO:GO:0010218 GO:GO:0010114 GO:GO:0031969 EMBL:AC007152 GO:GO:0009853 GO:GO:0009535 GO:GO:0022626 GO:GO:0031977 EMBL:AC004146 GO:GO:0019253 UniGene:At.46639 GO:GO:0016984 UniGene:At.37531 Gene3D:G3DSA:3.30.190.10 EMBL:X13611 EMBL:AF325011 EMBL:AF325004 EMBL:AF372874 EMBL:AF410291 EMBL:AY054188 EMBL:AY054581 EMBL:AY058831 EMBL:AY059940 EMBL:AY062612 EMBL:AY062711 EMBL:AY065101 EMBL:AY093380 EMBL:AY093388 EMBL:AY097366 EMBL:BT000362 EMBL:BT002076 EMBL:X68342 IPI:IPI00539020 PIR:G96694 PIR:S03720 RefSeq:NP_176880.1 UniGene:At.12721 UniGene:At.30194 UniGene:At.49098 UniGene:At.67454 UniGene:At.68122 UniGene:At.70053 UniGene:At.75196 ProteinModelPortal:P10795 SMR:P10795 IntAct:P10795 MINT:MINT-2584041 STRING:P10795 World-2DPAGE:0003:P10795 PRIDE:P10795 ProMEX:P10795 EnsemblPlants:AT1G67090.1 GeneID:843029 KEGG:ath:AT1G67090 TAIR:At1g67090 eggNOG:COG4451 HOGENOM:HBG608223 InParanoid:P10795 KO:K01602 OMA:AFPATRK PhylomeDB:P10795 ProtClustDB:PLN02289 ArrayExpress:P10795 Genevestigator:P10795 InterPro:IPR024681 InterPro:IPR024680 Pfam:PF12338 PRINTS:PR00152 SMART:SM00961 SUPFAM:SSF55239 Uniprot:P10795

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig00033	222	1593	-2.314	1.57E-171	TAIR|locus:2033686 - symbol:RBCS1A "AT1G67090" species:3702 "Arabidopsis thaliana" [GO:0009573 "chloroplast ribulose bisphosphate carboxylase complex" evidence=ISS] [GO:0015977 "carbon fixation" evidence=ISS] [GO:0016984 "ribulose-bisphosphate carboxylase activity" evidence=ISS] [GO:0031977 "thylakoid lumen" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009637 "response to blue light" evidence=IEP] [GO:0010114 "response to red light" evidence=IEP] [GO:0010218 "response to far red light" evidence=IEP] [GO:0015979 "photosynthesis" evidence=IMP] [GO:0080158 "chloroplast ribulose bisphosphate carboxylase complex biogenesis" evidence=IMP] InterPro:IPR000894 Pfam:PF00101 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0048046 GO:GO:0009570 GO:GO:0004497 GO:GO:0005507 GO:GO:0009409 GO:GO:0009637 GO:GO:0010218 GO:GO:0010114 GO:GO:0031969 EMBL:AC007152 GO:GO:0009853 GO:GO:0009535 GO:GO:0022626 GO:GO:0031977 EMBL:AC004146 GO:GO:0019253 UniGene:At.46639 GO:GO:0016984 UniGene:At.37531 Gene3D:G3DSA:3.30.190.10 EMBL:X13611 EMBL:AF325011 EMBL:AF325004 EMBL:AF372874 EMBL:AF410291 EMBL:AY054188 EMBL:AY054581 EMBL:AY058831 EMBL:AY059940 EMBL:AY062612 EMBL:AY062711 EMBL:AY065101 EMBL:AY093380 EMBL:AY093388 EMBL:AY097366 EMBL:BT000362 EMBL:BT002076 EMBL:X68342 IPI:IPI00539020 PIR:G96694 PIR:S03720 RefSeq:NP_176880.1 UniGene:At.12721 UniGene:At.30194 UniGene:At.49098 UniGene:At.67454 UniGene:At.68122 UniGene:At.70053 UniGene:At.75196 ProteinModelPortal:P10795 SMR:P10795 IntAct:P10795 MINT:MINT-2584041 STRING:P10795 World-2DPAGE:0003:P10795 PRIDE:P10795 ProMEX:P10795 EnsemblPlants:AT1G67090.1 GeneID:843029 KEGG:ath:AT1G67090 TAIR:At1g67090 eggNOG:COG4451 HOGENOM:HBG608223 InParanoid:P10795 KO:K01602 OMA:AFPATRK PhylomeDB:P10795 ProtClustDB:PLN02289 ArrayExpress:P10795 Genevestigator:P10795 InterPro:IPR024681 InterPro:IPR024680 Pfam:PF12338 PRINTS:PR00152 SMART:SM00961 SUPFAM:SSF55239 Uniprot:P10795
Leaf	Isotig00034	231	1645	-2.303	4.46E-176	TAIR|locus:2033686 - symbol:RBCS1A "AT1G67090" species:3702 "Arabidopsis thaliana" [GO:0009573 "chloroplast ribulose bisphosphate carboxylase complex" evidence=ISS] [GO:0015977 "carbon fixation" evidence=ISS] [GO:0016984 "ribulose-bisphosphate carboxylase activity" evidence=ISS] [GO:0031977 "thylakoid lumen" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009637 "response to blue light" evidence=IEP] [GO:0010114 "response to red light" evidence=IEP] [GO:0010218 "response to far red light" evidence=IEP] [GO:0015979 "photosynthesis" evidence=IMP] [GO:0080158 "chloroplast ribulose bisphosphate carboxylase complex biogenesis" evidence=IMP] InterPro:IPR000894 Pfam:PF00101 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0048046 GO:GO:0009570 GO:GO:0004497 GO:GO:0005507 GO:GO:0009409 GO:GO:0009637 GO:GO:0010218 GO:GO:0010114 GO:GO:0031969 EMBL:AC007152 GO:GO:0009853 GO:GO:0009535 GO:GO:0022626 GO:GO:0031977 EMBL:AC004146 GO:GO:0019253 UniGene:At.46639 GO:GO:0016984 UniGene:At.37531 Gene3D:G3DSA:3.30.190.10 EMBL:X13611 EMBL:AF325011 EMBL:AF325004 EMBL:AF372874 EMBL:AF410291 EMBL:AY054188 EMBL:AY054581 EMBL:AY058831 EMBL:AY059940 EMBL:AY062612 EMBL:AY062711 EMBL:AY065101 EMBL:AY093380 EMBL:AY093388 EMBL:AY097366 EMBL:BT000362 EMBL:BT002076 EMBL:X68342 IPI:IPI00539020 PIR:G96694 PIR:S03720 RefSeq:NP_176880.1 UniGene:At.12721 UniGene:At.30194 UniGene:At.49098 UniGene:At.67454 UniGene:At.68122 UniGene:At.70053 UniGene:At.75196 ProteinModelPortal:P10795 SMR:P10795 IntAct:P10795 MINT:MINT-2584041 STRING:P10795 World-2DPAGE:0003:P10795 PRIDE:P10795 ProMEX:P10795 EnsemblPlants:AT1G67090.1 GeneID:843029 KEGG:ath:AT1G67090 TAIR:At1g67090 eggNOG:COG4451 HOGENOM:HBG608223 InParanoid:P10795 KO:K01602 OMA:AFPATRK PhylomeDB:P10795 ProtClustDB:PLN02289 ArrayExpress:P10795 Genevestigator:P10795 InterPro:IPR024681 InterPro:IPR024680 Pfam:PF12338 PRINTS:PR00152 SMART:SM00961 SUPFAM:SSF55239 Uniprot:P10795
Leaf	Isotig00035	346	2348	-2.234	1.39E-241	TAIR|locus:2033686 - symbol:RBCS1A "AT1G67090" species:3702 "Arabidopsis thaliana" [GO:0009573 "chloroplast ribulose bisphosphate carboxylase complex" evidence=ISS] [GO:0015977 "carbon fixation" evidence=ISS] [GO:0016984 "ribulose-bisphosphate carboxylase activity" evidence=ISS] [GO:0031977 "thylakoid

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						lumen" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009637 "response to blue light" evidence=IEP] [GO:0010114 "response to red light" evidence=IEP] [GO:0010218 "response to far red light" evidence=IEP] [GO:0015979 "photosynthesis" evidence=IMP] [GO:0080158 "chloroplast ribulose bisphosphate carboxylase complex biogenesis" evidence=IMP] InterPro:IPR000894 Pfam:PF00101 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0048046 GO:GO:0009570 GO:GO:0004497 GO:GO:0005507 GO:GO:0009409 GO:GO:0009637 GO:GO:0010218 GO:GO:0010114 GO:GO:0031969 EMBL:AC007152 GO:GO:0009853 GO:GO:0009535 GO:GO:0022626 GO:GO:0031977 EMBL:AC004146 GO:GO:0019253 UniGene:At.46639 GO:GO:0016984 UniGene:At.37531 Gene3D:G3DSA:3.30.190.10 EMBL:X13611 EMBL:AF325011 EMBL:AF325004 EMBL:AF372874 EMBL:AF410291 EMBL:AY054188 EMBL:AY054581 EMBL:AY058831 EMBL:AY059940 EMBL:AY062612 EMBL:AY062711 EMBL:AY065101 EMBL:AY093380 EMBL:AY093388 EMBL:AY097366 EMBL:BT000362 EMBL:BT002076 EMBL:X68342 IPI:IPI00539020 PIR:G96694 PIR:S03720 RefSeq:NP_176880.1 UniGene:At.12721 UniGene:At.30194 UniGene:At.49098 UniGene:At.67454 UniGene:At.68122 UniGene:At.70053 UniGene:At.75196 ProteinModelPortal:P10795 SMR:P10795 IntAct:P10795 MINT:MINT-2584041 STRING:P10795 World-2DPAGE:0003:P10795 PRIDE:P10795 ProMEX:P10795 EnsemblPlants:AT1G67090.1 GeneID:843029 KEGG:ath:AT1G67090 TAIR:At1g67090 eggNOG:COG4451 HOGENOM:HBG608223 InParanoid:P10795 KO:K01602 OMA:AFPATRK PhylomeDB:P10795 ProtClustDB:PLN02289 ArrayExpress:P10795 Genevestigator:P10795 InterPro:IPR024681 InterPro:IPR024680 Pfam:PF12338 PRINTS:PR00152 SMART:SM00961 SUPFAM:SSF55239 Uniprot:P10795
Leaf	Isotig00036	339	2318	-2.245	6.28E-240	TAIR|locus:2033686 - symbol:RBCS1A "AT1G67090" species:3702 "Arabidopsis thaliana" [GO:0009573 "chloroplast ribulose bisphosphate carboxylase complex" evidence=ISS] [GO:0015977 "carbon fixation" evidence=ISS] [GO:0016984 "ribulose-bisphosphate carboxylase activity" evidence=ISS] [GO:0031977 "thylakoid lumen" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009637 "response to blue light" evidence=IEP] [GO:0010114 "response to red light" evidence=IEP] [GO:0010218 "response to far red light" evidence=IEP] [GO:0015979 "photosynthesis" evidence=IMP] [GO:0080158 "chloroplast ribulose bisphosphate carboxylase complex biogenesis" evidence=IMP] InterPro:IPR000894 Pfam:PF00101 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0048046 GO:GO:0009570 GO:GO:0004497 GO:GO:0005507 GO:GO:0009409 GO:GO:0009637 GO:GO:0010218 GO:GO:0010114 GO:GO:0031969 EMBL:AC007152 GO:GO:0009853 GO:GO:0009535 GO:GO:0022626 GO:GO:0031977 EMBL:AC004146 GO:GO:0019253 UniGene:At.46639 GO:GO:0016984 UniGene:At.37531 Gene3D:G3DSA:3.30.190.10 EMBL:X13611 EMBL:AF325011 EMBL:AF325004 EMBL:AF372874 EMBL:AF410291 EMBL:AY054188 EMBL:AY054581 EMBL:AY058831 EMBL:AY059940 EMBL:AY062612 EMBL:AY062711 EMBL:AY065101 EMBL:AY093380 EMBL:AY093388 EMBL:AY097366 EMBL:BT000362 EMBL:BT002076 EMBL:X68342 IPI:IPI00539020 PIR:G96694 PIR:S03720 RefSeq:NP_176880.1 UniGene:At.12721 UniGene:At.30194 UniGene:At.49098 UniGene:At.67454 UniGene:At.68122 UniGene:At.70053 UniGene:At.75196 ProteinModelPortal:P10795 SMR:P10795 IntAct:P10795 MINT:MINT-2584041 STRING:P10795 World-2DPAGE:0003:P10795 PRIDE:P10795 ProMEX:P10795 EnsemblPlants:AT1G67090.1 GeneID:843029 KEGG:ath:AT1G67090 TAIR:At1g67090 eggNOG:COG4451 HOGENOM:HBG608223 InParanoid:P10795 KO:K01602 OMA:AFPATRK PhylomeDB:P10795 ProtClustDB:PLN02289 ArrayExpress:P10795 Genevestigator:P10795 InterPro:IPR024681 InterPro:IPR024680 Pfam:PF12338 PRINTS:PR00152 SMART:SM00961 SUPFAM:SSF55239 Uniprot:P10795
Leaf	Isotig00037	218	1615	-2.360	6.08E-178	TAIR|locus:2033686 - symbol:RBCS1A "AT1G67090" species:3702 "Arabidopsis thaliana" [GO:0009573 "chloroplast ribulose bisphosphate carboxylase complex" evidence=ISS] [GO:0015977 "carbon fixation" evidence=ISS] [GO:0016984 "ribulose-bisphosphate carboxylase activity" evidence=ISS] [GO:0031977 "thylakoid lumen" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0009570

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						"chloroplast stroma" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009637 "response to blue light" evidence=IEP] [GO:0010114 "response to red light" evidence=IEP] [GO:0010218 "response to far red light" evidence=IEP] [GO:0015979 "photosynthesis" evidence=IMP] [GO:0080158 "chloroplast ribulose bisphosphate carboxylase complex biogenesis" evidence=IMP] InterPro:IPR000894 Pfam:PF00101 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0048046 GO:GO:0009570 GO:GO:0004497 GO:GO:0005507 GO:GO:0009409 GO:GO:0009637 GO:GO:0010218 GO:GO:0010114 GO:GO:0031969 EMBL:AC007152 GO:GO:0009853 GO:GO:0009535 GO:GO:0022626 GO:GO:0031977 EMBL:AC004146 GO:GO:0019253 UniGene:At.46639 GO:GO:0016984 UniGene:At.37531 Gene3D:G3DSA:3.30.190.10 EMBL:X13611 EMBL:AF325011 EMBL:AF325004 EMBL:AF372874 EMBL:AF410291 EMBL:AY054188 EMBL:AY054581 EMBL:AY058831 EMBL:AY059940 EMBL:AY062612 EMBL:AY062711 EMBL:AY065101 EMBL:AY093380 EMBL:AY093388 EMBL:AY097366 EMBL:BT000362 EMBL:BT002076 EMBL:X68342 IPI:IPI00539020 PIR:G96694 PIR:S03720 RefSeq:NP_176880.1 UniGene:At.12721 UniGene:At.30194 UniGene:At.49098 UniGene:At.67454 UniGene:At.68122 UniGene:At.70053 UniGene:At.75196 ProteinModelPortal:P10795 SMR:P10795 IntAct:P10795 MINT:MINT-2584041 STRING:P10795 World-2DPAGE:0003:P10795 PRIDE:P10795 ProMEX:P10795 EnsemblPlants:AT1G67090.1 GeneID:843029 KEGG:ath:AT1G67090 TAIR:At1g67090 eggNOG:COG4451 HOGENOM:HBG608223 InParanoid:P10795 KO:K01602 OMA:AFPATRK PhylomeDB:P10795 ProtClustDB:PLN02289 ArrayExpress:P10795 Genevestigator:P10795 InterPro:IPR024681 InterPro:IPR024680 Pfam:PF12338 PRINTS:PR00152 SMART:SM00961 SUPFAM:SSF55239 Uniprot:P10795
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Leaf	Isotig00039	218	1622	-2.366	2.95E-179	TAIR|locus:2033686 - symbol:RBCS1A "AT1G67090" species:3702 "Arabidopsis thaliana" [GO:0009573 "chloroplast ribulose bisphosphate carboxylase complex" evidence=ISS] [GO:0015977 "carbon fixation" evidence=ISS] [GO:0016984 "ribulose-bisphosphate carboxylase activity" evidence=ISS] [GO:0031977 "thylakoid lumen" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009637 "response to blue light" evidence=IEP] [GO:0010114 "response to red light" evidence=IEP] [GO:0010218 "response to far red light" evidence=IEP]

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						[GO:0015979 "photosynthesis" evidence=IMP] [GO:0080158 "chloroplast ribulose bisphosphate carboxylase complex biogenesis" evidence=IMP] InterPro:IPR000894 Pfam:PF00101 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0048046 GO:GO:0009570 GO:GO:0004497 GO:GO:0005507 GO:GO:0009409 GO:GO:0009637 GO:GO:0010218 GO:GO:0010114 GO:GO:0031969 EMBL:AC007152 GO:GO:0009853 GO:GO:0009535 GO:GO:0022626 GO:GO:0031977 EMBL:AC004146 GO:GO:0019253 UniGene:At.46639 GO:GO:0016984 UniGene:At.37531 Gene3D:G3DSA:3.30.190.10 EMBL:X13611 EMBL:AF325011 EMBL:AF325004 EMBL:AF372874 EMBL:AF410291 EMBL:AY054188 EMBL:AY054581 EMBL:AY058831 EMBL:AY059940 EMBL:AY062612 EMBL:AY062711 EMBL:AY065101 EMBL:AY093380 EMBL:AY093388 EMBL:AY097366 EMBL:BT000362 EMBL:BT002076 EMBL:X68342 IPI:IPI00539020 PIR:G96694 PIR:S03720 RefSeq:NP_176880.1 UniGene:At.12721 UniGene:At.30194 UniGene:At.49098 UniGene:At.67454 UniGene:At.68122 UniGene:At.70053 UniGene:At.75196 ProteinModelPortal:P10795 SMR:P10795 IntAct:P10795 MINT:MINT-2584041 STRING:P10795 World-2DPAGE:0003:P10795 PRIDE:P10795 ProMEX:P10795 EnsemblPlants:AT1G67090.1 GeneID:843029 KEGG:ath:AT1G67090 TAIR:At1g67090 eggNOG:COG4451 HOGENOM:HBG608223 InParanoid:P10795 KO:K01602 OMA:AFPATRK PhylomeDB:P10795 ProtClustDB:PLN02289 ArrayExpress:P10795 Genevestigator:P10795 InterPro:IPR024681 InterPro:IPR024680 Pfam:PF12338 PRINTS:PR00152 SMART:SM00961 SUPFAM:SSF55239 Uniprot:P10795
Leaf	Isotig00040	227	1674	-2.354	8.87E-184	TAIR|locus:2033686 - symbol:RBCS1A "AT1G67090" species:3702 "Arabidopsis thaliana" [GO:0009573 "chloroplast ribulose bisphosphate carboxylase complex" evidence=ISS] [GO:0015977 "carbon fixation" evidence=ISS] [GO:0016984 "ribulose-bisphosphate carboxylase activity" evidence=ISS] [GO:0031977 "thylakoid lumen" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009637 "response to blue light" evidence=IEP] [GO:0010114 "response to red light" evidence=IEP] [GO:0010218 "response to far red light" evidence=IEP] [GO:0015979 "photosynthesis" evidence=IMP] [GO:0080158 "chloroplast ribulose bisphosphate carboxylase complex biogenesis" evidence=IMP] InterPro:IPR000894 Pfam:PF00101 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0048046 GO:GO:0009570 GO:GO:0004497 GO:GO:0005507 GO:GO:0009409 GO:GO:0009637 GO:GO:0010218 GO:GO:0010114 GO:GO:0031969 EMBL:AC007152 GO:GO:0009853 GO:GO:0009535 GO:GO:0022626 GO:GO:0031977 EMBL:AC004146 GO:GO:0019253 UniGene:At.46639 GO:GO:0016984 UniGene:At.37531 Gene3D:G3DSA:3.30.190.10 EMBL:X13611 EMBL:AF325011 EMBL:AF325004 EMBL:AF372874 EMBL:AF410291 EMBL:AY054188 EMBL:AY054581 EMBL:AY058831 EMBL:AY059940 EMBL:AY062612 EMBL:AY062711 EMBL:AY065101 EMBL:AY093380 EMBL:AY093388 EMBL:AY097366 EMBL:BT000362 EMBL:BT002076 EMBL:X68342 IPI:IPI00539020 PIR:G96694 PIR:S03720 RefSeq:NP_176880.1 UniGene:At.12721 UniGene:At.30194 UniGene:At.49098 UniGene:At.67454 UniGene:At.68122 UniGene:At.70053 UniGene:At.75196 ProteinModelPortal:P10795 SMR:P10795 IntAct:P10795 MINT:MINT-2584041 STRING:P10795 World-2DPAGE:0003:P10795 PRIDE:P10795 ProMEX:P10795 EnsemblPlants:AT1G67090.1 GeneID:843029 KEGG:ath:AT1G67090 TAIR:At1g67090 eggNOG:COG4451 HOGENOM:HBG608223 InParanoid:P10795 KO:K01602 OMA:AFPATRK PhylomeDB:P10795 ProtClustDB:PLN02289 ArrayExpress:P10795 Genevestigator:P10795 InterPro:IPR024681 InterPro:IPR024680 Pfam:PF12338 PRINTS:PR00152 SMART:SM00961 SUPFAM:SSF55239 Uniprot:P10795
Leaf	Isotig00042	129	855	-2.200	1.91E-87	TAIR|locus:2033686 - symbol:RBCS1A "AT1G67090" species:3702 "Arabidopsis thaliana" [GO:0009573 "chloroplast ribulose bisphosphate carboxylase complex" evidence=ISS] [GO:0015977 "carbon fixation" evidence=ISS] [GO:0016984 "ribulose-bisphosphate carboxylase activity" evidence=ISS] [GO:0031977 "thylakoid lumen" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009637 "response to blue light" evidence=IEP] [GO:0010114 "response to red light" evidence=IEP] [GO:0010218 "response to far red light" evidence=IEP] [GO:0015979 "photosynthesis" evidence=IMP] [GO:0080158 "chloroplast ribulose bisphosphate carboxylase complex biogenesis" evidence=IMP] InterPro:IPR000894 Pfam:PF00101 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0048046 GO:GO:0009570 GO:GO:0004497 GO:GO:0005507

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0009409 GO:GO:0009637 GO:GO:0010218 GO:GO:0010114 GO:GO:0031969 EMBL:AC007152 GO:GO:0009853 GO:GO:0009535 GO:GO:0022626 GO:GO:0031977 EMBL:AC004146 GO:GO:0019253 UniGene:At.46639 GO:GO:0016984 UniGene:At.37531 Gene3D:G3DSA:3.30.190.10 EMBL:X13611 EMBL:AF325011 EMBL:AF325004 EMBL:AF372874 EMBL:AF410291 EMBL:AY054188 EMBL:AY054581 EMBL:AY058831 EMBL:AY059940 EMBL:AY062612 EMBL:AY062711 EMBL:AY065101 EMBL:AY093380 EMBL:AY093388 EMBL:AY097366 EMBL:BT000362 EMBL:BT002076 EMBL:X68342 IPI:IPI00539020 PIR:G96694 PIR:S03720 RefSeq:NP_176880.1 UniGene:At.12721 UniGene:At.30194 UniGene:At.49098 UniGene:At.67454 UniGene:At.68122 UniGene:At.70053 UniGene:At.75196 ProteinModelPortal:P10795 SMR:P10795 IntAct:P10795 MINT:MINT-2584041 STRING:P10795 World-2DPAGE:0003:P10795 PRIDE:P10795 ProMEX:P10795 EnsemblPlants:AT1G67090.1 GeneID:843029 KEGG:ath:AT1G67090 TAIR:At1g67090 eggNOG:COG4451 HOGENOM:HBG608223 InParanoid:P10795 KO:K01602 OMA:AFPATRK PhylomeDB:P10795 ProtClustDB:PLN02289 ArrayExpress:P10795 Genevestigator:P10795 InterPro:IPR024681 InterPro:IPR024680 Pfam:PF12338 PRINTS:PR00152 SMART:SM00961 SUPFAM:SSF55239 Uniprot:P10795
Leaf	Isotig00043	335	2340	-2.275	3.42E-246	TAIR|locus:2033686 - symbol:RBCS1A "AT1G67090" species:3702 "Arabidopsis thaliana" [GO:0009573 "chloroplast ribulose bisphosphate carboxylase complex" evidence=ISS] [GO:0015977 "carbon fixation" evidence=ISS] [GO:0016984 "ribulose-bisphosphate carboxylase activity" evidence=ISS] [GO:0031977 "thylakoid lumen" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009637 "response to blue light" evidence=IEP] [GO:0010114 "response to red light" evidence=IEP] [GO:0010218 "response to far red light" evidence=IEP] [GO:0015979 "photosynthesis" evidence=IMP] [GO:0080158 "chloroplast ribulose bisphosphate carboxylase complex biogenesis" evidence=IMP] InterPro:IPR000894 Pfam:PF00101 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0048046 GO:GO:0009570 GO:GO:0004497 GO:GO:0005507 GO:GO:0009409 GO:GO:0009637 GO:GO:0010218 GO:GO:0010114 GO:GO:0031969 EMBL:AC007152 GO:GO:0009853 GO:GO:0009535 GO:GO:0022626 GO:GO:0031977 EMBL:AC004146 GO:GO:0019253 UniGene:At.46639 GO:GO:0016984 UniGene:At.37531 Gene3D:G3DSA:3.30.190.10 EMBL:X13611 EMBL:AF325011 EMBL:AF325004 EMBL:AF372874 EMBL:AF410291 EMBL:AY054188 EMBL:AY054581 EMBL:AY058831 EMBL:AY059940 EMBL:AY062612 EMBL:AY062711 EMBL:AY065101 EMBL:AY093380 EMBL:AY093388 EMBL:AY097366 EMBL:BT000362 EMBL:BT002076 EMBL:X68342 IPI:IPI00539020 PIR:G96694 PIR:S03720 RefSeq:NP_176880.1 UniGene:At.12721 UniGene:At.30194 UniGene:At.49098 UniGene:At.67454 UniGene:At.68122 UniGene:At.70053 UniGene:At.75196 ProteinModelPortal:P10795 SMR:P10795 IntAct:P10795 MINT:MINT-2584041 STRING:P10795 World-2DPAGE:0003:P10795 PRIDE:P10795 ProMEX:P10795 EnsemblPlants:AT1G67090.1 GeneID:843029 KEGG:ath:AT1G67090 TAIR:At1g67090 eggNOG:COG4451 HOGENOM:HBG608223 InParanoid:P10795 KO:K01602 OMA:AFPATRK PhylomeDB:P10795 ProtClustDB:PLN02289 ArrayExpress:P10795 Genevestigator:P10795 InterPro:IPR024681 InterPro:IPR024680 Pfam:PF12338 PRINTS:PR00152 SMART:SM00961 SUPFAM:SSF55239 Uniprot:P10795
Leaf	Isotig00044	335	2347	-2.280	1.74E-247	TAIR|locus:2033686 - symbol:RBCS1A "AT1G67090" species:3702 "Arabidopsis thaliana" [GO:0009573 "chloroplast ribulose bisphosphate carboxylase complex" evidence=ISS] [GO:0015977 "carbon fixation" evidence=ISS] [GO:0016984 "ribulose-bisphosphate carboxylase activity" evidence=ISS] [GO:0031977 "thylakoid lumen" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009637 "response to blue light" evidence=IEP] [GO:0010114 "response to red light" evidence=IEP] [GO:0010218 "response to far red light" evidence=IEP] [GO:0015979 "photosynthesis" evidence=IMP] [GO:0080158 "chloroplast ribulose bisphosphate carboxylase complex biogenesis" evidence=IMP] InterPro:IPR000894 Pfam:PF00101 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0048046 GO:GO:0009570 GO:GO:0004497 GO:GO:0005507 GO:GO:0009409 GO:GO:0009637 GO:GO:0010218 GO:GO:0010114 GO:GO:0031969 EMBL:AC007152 GO:GO:0009853 GO:GO:0009535 GO:GO:0022626 GO:GO:0031977 EMBL:AC004146 GO:GO:0019253 UniGene:At.46639 GO:GO:0016984 UniGene:At.37531 Gene3D:G3DSA:3.30.190.10 EMBL:X13611

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EMBL:AF325011 EMBL:AF325004 EMBL:AF372874 EMBL:AF410291 EMBL:AY054188 EMBL:AY054581 EMBL:AY058831 EMBL:AY059940 EMBL:AY062612 EMBL:AY062711 EMBL:AY065101 EMBL:AY093380 EMBL:AY093388 EMBL:AY097366 EMBL:BT000362 EMBL:BT002076 EMBL:X68342 IPI:IPI00539020 PIR:G96694 PIR:S03720 RefSeq:NP_176880.1 UniGene:At.12721 UniGene:At.30194 UniGene:At.49098 UniGene:At.67454 UniGene:At.68122 UniGene:At.70053 UniGene:At.75196 ProteinModelPortal:P10795 SMR:P10795 IntAct:P10795 MINT:MINT-2584041 STRING:P10795 World-2DPAGE:0003:P10795 PRIDE:P10795 ProMEX:P10795 EnsemblPlants:AT1G67090.1 GeneID:843029 KEGG:ath:AT1G67090 TAIR:At1g67090 eggNOG:COG4451 HOGENOM:HBG608223 InParanoid:P10795 KO:K01602 OMA:AFPATRK PhylomeDB:P10795 ProtClustDB:PLN02289 ArrayExpress:P10795 Genevestigator:P10795 InterPro:IPR024681 InterPro:IPR024680 Pfam:PF12338 PRINTS:PR00152 SMART:SM00961 SUPFAM:SSF55239 Uniprot:P10795
Leaf	Isotig00050	218	1599	-2.346	6.06E-175	UNIPROTKB|P69249 - symbol:RBCS "Ribulose bisphosphate carboxylase small chain, chloroplastic" species:4097 "Nicotiana tabacum" [GO:0005515 "protein binding" evidence=IPI] InterPro:IPR000894 Pfam:PF00101 GO:GO:0009507 GO:GO:0005515 GO:GO:0004497 GO:GO:0009853 GO:GO:0015979 GO:GO:0015977 GO:GO:0016984 Gene3D:G3DSA:3.30.190.10 InterPro:IPR024681 InterPro:IPR024680 Pfam:PF12338 PRINTS:PR00152 SUPFAM:SSF55239 EMBL:X02353 EMBL:M32419 PIR:A22934 PDB:1EJ7 PDB:1RLC PDB:1RLD PDB:3RUB PDB:4RUB PDBsum:1EJ7 PDBsum:1RLC PDBsum:1RLD PDBsum:3RUB PDBsum:4RUB ProteinModelPortal:P69249 SMR:P69249 DIP:DIP-40635N IntAct:P69249 MINT:MINT-1176585 Uniprot:P69249
Leaf	Isotig00051	218	1606	-2.352	2.96E-176	UNIPROTKB|P69249 - symbol:RBCS "Ribulose bisphosphate carboxylase small chain, chloroplastic" species:4097 "Nicotiana tabacum" [GO:0005515 "protein binding" evidence=IPI] InterPro:IPR000894 Pfam:PF00101 GO:GO:0009507 GO:GO:0005515 GO:GO:0004497 GO:GO:0009853 GO:GO:0015979 GO:GO:0015977 GO:GO:0016984 Gene3D:G3DSA:3.30.190.10 InterPro:IPR024681 InterPro:IPR024680 Pfam:PF12338 PRINTS:PR00152 SUPFAM:SSF55239 EMBL:X02353 EMBL:M32419 PIR:A22934 PDB:1EJ7 PDB:1RLC PDB:1RLD PDB:3RUB PDB:4RUB PDBsum:1EJ7 PDBsum:1RLC PDBsum:1RLD PDBsum:3RUB PDBsum:4RUB ProteinModelPortal:P69249 SMR:P69249 DIP:DIP-40635N IntAct:P69249 MINT:MINT-1176585 Uniprot:P69249
Leaf	Isotig00053	10	1	3.851	0.00071293	TAIR|locus:2018124 - symbol:RABG3d "RAB GTPase homolog G3D" species:3702 "Arabidopsis thaliana" [GO:0005525 "GTP binding" evidence=IEA;ISS] [GO:0007264 "small GTPase mediated signal transduction" evidence=IEA] [GO:0015031 "protein transport" evidence=IEA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR001806 InterPro:IPR003579 InterPro:IPR005225 Pfam:PF00071 PRINTS:PR00449 SMART:SM00175 GO:GO:0005525 TIGRFAMs:TIGR00231 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005886 GO:GO:0005774 GO:GO:0015031 GO:GO:0007264 EMBL:AC037424 PROSITE:PS51419 eggNOG:COG1100 HOGENOM:HBG745225 KO:K07976 HSSP:P32939 ProtClustDB:CLSN2679478 EMBL:AB071847 EMBL:AY074361 EMBL:AY096407 IPI:IPI00528726 PIR:H96562 RefSeq:NP_175638.1 UniGene:At.22905 ProteinModelPortal:Q9C820 SMR:Q9C820 IntAct:Q9C820 PRIDE:Q9C820 EnsemblPlants:AT1G52280.1 GeneID:841658 KEGG:ath:AT1G52280 TAIR:At1g52280 InParanoid:Q9C820 OMA:LVHANIS PhylomeDB:Q9C820 ArrayExpress:Q9C820 Genevestigator:Q9C820 Uniprot:Q9C820
Leaf	Isotig00054	228	1611	-2.292	1.80E-171	UNIPROTKB|P69249 - symbol:RBCS "Ribulose bisphosphate carboxylase small chain, chloroplastic" species:4097 "Nicotiana tabacum" [GO:0005515 "protein binding" evidence=IPI] InterPro:IPR000894 Pfam:PF00101 GO:GO:0009507 GO:GO:0005515 GO:GO:0004497 GO:GO:0009853 GO:GO:0015979 GO:GO:0015977 GO:GO:0016984 Gene3D:G3DSA:3.30.190.10 InterPro:IPR024681 InterPro:IPR024680 Pfam:PF12338 PRINTS:PR00152 SUPFAM:SSF55239 EMBL:X02353 EMBL:M32419 PIR:A22934 PDB:1EJ7 PDB:1RLC PDB:1RLD PDB:3RUB PDB:4RUB PDBsum:1EJ7 PDBsum:1RLC PDBsum:1RLD PDBsum:3RUB PDBsum:4RUB ProteinModelPortal:P69249 SMR:P69249 DIP:DIP-40635N IntAct:P69249 MINT:MINT-1176585 Uniprot:P69249
Leaf	Isotig00055	221	1581	-2.310	7.22E-170	UNIPROTKB|P69249 - symbol:RBCS "Ribulose bisphosphate carboxylase small chain, chloroplastic" species:4097 "Nicotiana tabacum" [GO:0005515 "protein binding" evidence=IPI] InterPro:IPR000894 Pfam:PF00101 GO:GO:0009507 GO:GO:0005515 GO:GO:0004497 GO:GO:0009853 GO:GO:0015979 GO:GO:0015977 GO:GO:0016984 Gene3D:G3DSA:3.30.190.10 InterPro:IPR024681 InterPro:IPR024680 Pfam:PF12338 PRINTS:PR00152 SUPFAM:SSF55239 EMBL:X02353 EMBL:M32419 PIR:A22934 PDB:1EJ7 PDB:1RLC PDB:1RLD PDB:3RUB PDB:4RUB PDBsum:1EJ7 PDBsum:1RLC PDBsum:1RLD PDBsum:3RUB PDBsum:4RUB ProteinModelPortal:P69249 SMR:P69249 DIP:DIP-40635N IntAct:P69249 MINT:MINT-1176585 Uniprot:P69249

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig00056	217	1603	-2.356	2.84E-176	UNIPROTKB|P69249 - symbol:RBCS "Ribulose bisphosphate carboxylase small chain, chloroplastic" species:4097 "Nicotiana tabacum" [GO:0005515 "protein binding" evidence=IPI] InterPro:IPR000894 Pfam:PF00101 GO:GO:0009507 GO:GO:0005515 GO:GO:0004497 GO:GO:0009853 GO:GO:0015979 GO:GO:0015977 GO:GO:0016984 Gene3D:G3DSA:3.30.190.10 InterPro:IPR024681 InterPro:IPR024680 Pfam:PF12338 PRINTS:PR00152 SUPFAM:SSF55239 EMBL:X02353 EMBL:M32419 PIR:A22934 PDB:1EJ7 PDB:1RLC PDB:1RLD PDB:3RUB PDB:4RUB PDBsum:1EJ7 PDBsum:1RLC PDBsum:1RLD PDBsum:3RUB PDBsum:4RUB ProteinModelPortal:P69249 SMR:P69249 DIP:DIP-40635N IntAct:P69249 MINT:MINT-1176585 Uniprot:P69249
Leaf	Isotig00057	217	1610	-2.362	1.38E-177	UNIPROTKB|P69249 - symbol:RBCS "Ribulose bisphosphate carboxylase small chain, chloroplastic" species:4097 "Nicotiana tabacum" [GO:0005515 "protein binding" evidence=IPI] InterPro:IPR000894 Pfam:PF00101 GO:GO:0009507 GO:GO:0005515 GO:GO:0004497 GO:GO:0009853 GO:GO:0015979 GO:GO:0015977 GO:GO:0016984 Gene3D:G3DSA:3.30.190.10 InterPro:IPR024681 InterPro:IPR024680 Pfam:PF12338 PRINTS:PR00152 SUPFAM:SSF55239 EMBL:X02353 EMBL:M32419 PIR:A22934 PDB:1EJ7 PDB:1RLC PDB:1RLD PDB:3RUB PDB:4RUB PDBsum:1EJ7 PDBsum:1RLC PDBsum:1RLD PDBsum:3RUB PDBsum:4RUB ProteinModelPortal:P69249 SMR:P69249 DIP:DIP-40635N IntAct:P69249 MINT:MINT-1176585 Uniprot:P69249
Leaf	Isotig00060	60	485	-2.486	5.52E-58	TAIR|locus:2009864 - symbol:GAPB "AT1G42970" species:3702 "Arabidopsis thaliana" [GO:0006096 "glycolysis" evidence=ISS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=ISS;IDA] [GO:0047100 "glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) activity" evidence=ISS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009416 "response to light stimulus" evidence=IEP] [GO:0009744 "response to sucrose stimulus" evidence=IEP] [GO:0019253 "reductive pentose-phosphate cycle" evidence=NAS] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0004365 "glyceraldehyde-3-phosphate dehydrogenase (NAD+) (phosphorylating) activity" evidence=NAS] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0009409 "response to cold" evidence=IEP] [GO:0010319 "stromule" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] InterPro:IPR006424 InterPro:IPR016040 InterPro:IPR020828 InterPro:IPR020829 InterPro:IPR020830 InterPro:IPR020831 Pfam:PF00044 Pfam:PF02800 PRINTS:PR00078 PROSITE:PS00071 SMART:SM00846 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0048046 GO:GO:0009570 GO:GO:0046686 Gene3D:G3DSA:3.40.50.720 GO:GO:0051287 GO:GO:0050661 GO:GO:0006006 GO:GO:0010319 GO:GO:0009409 GO:GO:0031969 GO:GO:0009744 GO:GO:0009416 GO:GO:0009535 EMBL:AC068324 GO:GO:0019253 InterPro:IPR003823 Pfam:PF02672 eggNOG:COG0057 HOGENOM:HBG571736 PANTHER:PTHR10836 GO:GO:0004365 TIGRFAMs:TIGR01534 KO:K05298 BRENDA:1.2.1.13 GO:GO:0047100 EMBL:M64115 EMBL:M64118 EMBL:AY039961 EMBL:AY039539 EMBL:AY079402 EMBL:AY095991 EMBL:AY140091 EMBL:BT002267 IPI:IPI00541680 PIR:C96497 PIR:JQ1286 RefSeq:NP_174996.1 UniGene:At.21749 UniGene:At.67261 ProteinModelPortal:P25857 SMR:P25857 IntAct:P25857 STRING:P25857 SWISS-2DPAGE:P25857 PRIDE:P25857 ProMEX:P25857 EnsemblPlants:AT1G42970.1 GeneID:840895 KEGG:ath:AT1G42970 TAIR:At1g42970 InParanoid:P25857 OMA:IGRNAFK PhylomeDB:P25857 ProtClustDB:PLN02237 ArrayExpress:P25857 Genevestigator:P25857 GermOnline:AT1G42970 Uniprot:P25857
Leaf	Isotig00061	40	371	-2.684	1.42E-48	TAIR|locus:2009864 - symbol:GAPB "AT1G42970" species:3702 "Arabidopsis thaliana" [GO:0006096 "glycolysis" evidence=ISS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=ISS;IDA] [GO:0047100 "glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) activity" evidence=ISS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009416 "response to light stimulus" evidence=IEP] [GO:0009744 "response to sucrose stimulus" evidence=IEP] [GO:0019253 "reductive pentose-phosphate cycle" evidence=NAS] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0004365 "glyceraldehyde-3-phosphate dehydrogenase (NAD+) (phosphorylating) activity" evidence=NAS] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0009409 "response to cold" evidence=IEP] [GO:0010319 "stromule" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] InterPro:IPR006424 InterPro:IPR016040 InterPro:IPR020828 InterPro:IPR020829 InterPro:IPR020830 InterPro:IPR020831 Pfam:PF00044 Pfam:PF02800 PRINTS:PR00078 PROSITE:PS00071 SMART:SM00846 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0048046 GO:GO:0009570 GO:GO:0046686 Gene3D:G3DSA:3.40.50.720 GO:GO:0051287 GO:GO:0050661 GO:GO:0006006 GO:GO:0010319 GO:GO:0009409 GO:GO:0031969 GO:GO:0009744 GO:GO:0009416 GO:GO:0009535 EMBL:AC068324 GO:GO:0019253 InterPro:IPR003823 Pfam:PF02672 eggNOG:COG0057

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						HOGENOM:HBG571736 PANTHER:PTHR10836 GO:GO:0004365 TIGRFAMs:TIGR01534 KO:K05298 BRENDA:1.2.1.13 GO:GO:0047100 EMBL:M64115 EMBL:M64118 EMBL:AY039961 EMBL:AY039539 EMBL:AY079402 EMBL:AY095991 EMBL:AY140091 EMBL:BT002267 IPI:IPI00541680 PIR:C96497 PIR:JQ1286 RefSeq:NP_174996.1 UniGene:At.21749 UniGene:At.67261 ProteinModelPortal:P25857 SMR:P25857 IntAct:P25857 STRING:P25857 SWISS-2DPAGE:P25857 PRIDE:P25857 ProMEX:P25857 EnsemblPlants:AT1G42970.1 GeneID:840895 KEGG:ath:AT1G42970 TAIR:At1g42970 InParanoid:P25857 OMA:IGRNAFK PhylomeDB:P25857 ProtClustDB:PLN02237 ArrayExpress:P25857 Genevestigator:P25857 GermOnline:AT1G42970 Uniprot:P25857
Leaf	Isotig00062	53	348	-2.186	2.28E-36	TAIR|locus:2009864 - symbol:GAPB "AT1G42970" species:3702 "Arabidopsis thaliana" [GO:0006096 "glycolysis" evidence=ISS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=ISS;IDA] [GO:0047100 "glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) activity" evidence=ISS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009416 "response to light stimulus" evidence=IEP] [GO:0009744 "response to sucrose stimulus" evidence=IEP] [GO:0019253 "reductive pentose-phosphate cycle" evidence=NAS] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0004365 "glyceraldehyde-3-phosphate dehydrogenase (NAD+) (phosphorylating) activity" evidence=NAS] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0009409 "response to cold" evidence=IEP] [GO:0010319 "stromule" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] InterPro:IPR006424 InterPro:IPR016040 InterPro:IPR020828 InterPro:IPR020829 InterPro:IPR020830 InterPro:IPR020831 Pfam:PF00044 Pfam:PF02800 PRINTS:PR00078 PROSITE:PS00071 SMART:SM00846 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0048046 GO:GO:0009570 GO:GO:0046686 Gene3D:G3DSA:3.40.50.720 GO:GO:0051287 GO:GO:0050661 GO:GO:0006006 GO:GO:0010319 GO:GO:0009409 GO:GO:0031969 GO:GO:0009744 GO:GO:0009416 GO:GO:0009535 EMBL:AC068324 GO:GO:0019253 InterPro:IPR003823 Pfam:PF02672 eggNOG:COG0057 HOGENOM:HBG571736 PANTHER:PTHR10836 GO:GO:0004365 TIGRFAMs:TIGR01534 KO:K05298 BRENDA:1.2.1.13 GO:GO:0047100 EMBL:M64115 EMBL:M64118 EMBL:AY039961 EMBL:AY039539 EMBL:AY079402 EMBL:AY095991 EMBL:AY140091 EMBL:BT002267 IPI:IPI00541680 PIR:C96497 PIR:JQ1286 RefSeq:NP_174996.1 UniGene:At.21749 UniGene:At.67261 ProteinModelPortal:P25857 SMR:P25857 IntAct:P25857 STRING:P25857 SWISS-2DPAGE:P25857 PRIDE:P25857 ProMEX:P25857 EnsemblPlants:AT1G42970.1 GeneID:840895 KEGG:ath:AT1G42970 TAIR:At1g42970 InParanoid:P25857 OMA:IGRNAFK PhylomeDB:P25857 ProtClustDB:PLN02237 ArrayExpress:P25857 Genevestigator:P25857 GermOnline:AT1G42970 Uniprot:P25857
Leaf	Isotig00064	33	180	-1.919	8.41E-17	TAIR|locus:2162540 - symbol:LHCB3 "AT5G54270" species:3702 "Arabidopsis thaliana" [GO:0015979 "photosynthesis" evidence=ISS;IMP] [GO:0030076 "light-harvesting complex" evidence=ISS] [GO:0005198 "structural molecule activity" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] InterPro:IPR001344 Pfam:PF00504 EMBL:CP002688 GO:GO:0005198 EMBL:AB010695 GO:GO:0009535 UniGene:At.49175 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 UniGene:At.10812 UniGene:At.32199 UniGene:At.66422 ProtClustDB:PLN00025 UniGene:At.21173 EMBL:AF134126 EMBL:AF143691 EMBL:AF361858 EMBL:AF372917 EMBL:AY057735 IPI:IPI00532626 PIR:T52318 RefSeq:NP_200238.1 UniGene:At.70236 ProteinModelPortal:Q9S7M0 SMR:Q9S7M0 STRING:Q9S7M0 PRIDE:Q9S7M0 EnsemblPlants:AT5G54270.1 GeneID:835515 KEGG:ath:AT5G54270 TAIR:At5g54270 InParanoid:Q9S7M0 KO:K08914 OMA:ADDPVTF PhylomeDB:Q9S7M0 Genevestigator:Q9S7M0 Uniprot:Q9S7M0
Leaf	Isotig00065	33	182	-1.934	3.84E-17	TAIR|locus:2162540 - symbol:LHCB3 "AT5G54270" species:3702 "Arabidopsis thaliana" [GO:0015979 "photosynthesis" evidence=ISS;IMP] [GO:0030076 "light-harvesting complex" evidence=ISS] [GO:0005198 "structural molecule activity" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] InterPro:IPR001344 Pfam:PF00504 EMBL:CP002688 GO:GO:0005198 EMBL:AB010695 GO:GO:0009535 UniGene:At.49175 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 UniGene:At.10812 UniGene:At.32199 UniGene:At.66422 ProtClustDB:PLN00025 UniGene:At.21173 EMBL:AF134126 EMBL:AF143691 EMBL:AF361858 EMBL:AF372917 EMBL:AY057735 IPI:IPI00532626 PIR:T52318 RefSeq:NP_200238.1 UniGene:At.70236

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						ProteinModelPortal:Q9S7M0 SMR:Q9S7M0 STRING:Q9S7M0 PRIDE:Q9S7M0 EnsemblPlants:AT5G54270.1 GeneID:835515 KEGG:ath:AT5G54270 TAIR:At5g54270 InParanoid:Q9S7M0 KO:K08914 OMA:ADDPVTF PhylomeDB:Q9S7M0 Genevestigator:Q9S7M0 Uniprot:Q9S7M0
Leaf	Isotig00066	23	180	-2.439	3.97E-22	TAIR|locus:2162540 - symbol:LHCB3 "AT5G54270" species:3702 "Arabidopsis thaliana" [GO:0015979 "photosynthesis" evidence=ISS;IMP] [GO:0030076 "light-harvesting complex" evidence=ISS] [GO:0005198 "structural molecule activity" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] InterPro:IPR001344 Pfam:PF00504 EMBL:CP002688 GO:GO:0005198 EMBL:AB010695 GO:GO:0009535 UniGene:At.49175 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 UniGene:At.10812 UniGene:At.32199 UniGene:At.66422 ProtClustDB:PLN00025 UniGene:At.21173 EMBL:AF134126 EMBL:AF143691 EMBL:AF361858 EMBL:AF372917 EMBL:AY057735 IPI:IPI00532626 PIR:T52318 RefSeq:NP_200238.1 UniGene:At.70236 ProteinModelPortal:Q9S7M0 SMR:Q9S7M0 STRING:Q9S7M0 PRIDE:Q9S7M0 EnsemblPlants:AT5G54270.1 GeneID:835515 KEGG:ath:AT5G54270 TAIR:At5g54270 InParanoid:Q9S7M0 KO:K08914 OMA:ADDPVTF PhylomeDB:Q9S7M0 Genevestigator:Q9S7M0 Uniprot:Q9S7M0
Leaf	Isotig00067	23	182	-2.455	1.64E-22	TAIR|locus:2162540 - symbol:LHCB3 "AT5G54270" species:3702 "Arabidopsis thaliana" [GO:0015979 "photosynthesis" evidence=ISS;IMP] [GO:0030076 "light-harvesting complex" evidence=ISS] [GO:0005198 "structural molecule activity" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] InterPro:IPR001344 Pfam:PF00504 EMBL:CP002688 GO:GO:0005198 EMBL:AB010695 GO:GO:0009535 UniGene:At.49175 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 UniGene:At.10812 UniGene:At.32199 UniGene:At.66422 ProtClustDB:PLN00025 UniGene:At.21173 EMBL:AF134126 EMBL:AF143691 EMBL:AF361858 EMBL:AF372917 EMBL:AY057735 IPI:IPI00532626 PIR:T52318 RefSeq:NP_200238.1 UniGene:At.70236 ProteinModelPortal:Q9S7M0 SMR:Q9S7M0 STRING:Q9S7M0 PRIDE:Q9S7M0 EnsemblPlants:AT5G54270.1 GeneID:835515 KEGG:ath:AT5G54270 TAIR:At5g54270 InParanoid:Q9S7M0 KO:K08914 OMA:ADDPVTF PhylomeDB:Q9S7M0 Genevestigator:Q9S7M0 Uniprot:Q9S7M0
Leaf	Isotig00068	36	21	1.307	0.000708525	TAIR|locus:505006307 - symbol:AT2G38905 "AT2G38905" species:3702 "Arabidopsis thaliana" [GO:0009409 "response to cold" evidence=ISS] [GO:0016021 "integral to membrane" evidence=IEA] [GO:0042538 "hyperosmotic salinity response" evidence=ISS] InterPro:IPR000612 Pfam:PF01679 PROSITE:PS01309 GO:GO:0016021 EMBL:CP002685 GenomeReviews:CT485783_GR EMBL:AC005770 HOGENOM:HBG741476 PANTHER:PTHR21659 ProtClustDB:CLSN2688798 EMBL:AY052231 EMBL:AY060504 IPI:IPI00533167 RefSeq:NP_565897.1 UniGene:At.26429 EnsemblPlants:AT2G38905.1 GeneID:818475 KEGG:ath:AT2G38905 TAIR:At2g38905 eggNOG:NOG331170 InParanoid:Q941D7 OMA:WINIILC PhylomeDB:Q941D7 ArrayExpress:Q941D7 Genevestigator:Q941D7 Uniprot:Q941D7
Leaf	Isotig00070	27	8	2.284	1.51E-05	TAIR|locus:505006307 - symbol:AT2G38905 "AT2G38905" species:3702 "Arabidopsis thaliana" [GO:0009409 "response to cold" evidence=ISS] [GO:0016021 "integral to membrane" evidence=IEA] [GO:0042538 "hyperosmotic salinity response" evidence=ISS] InterPro:IPR000612 Pfam:PF01679 PROSITE:PS01309 GO:GO:0016021 EMBL:CP002685 GenomeReviews:CT485783_GR EMBL:AC005770 HOGENOM:HBG741476 PANTHER:PTHR21659 ProtClustDB:CLSN2688798 EMBL:AY052231 EMBL:AY060504 IPI:IPI00533167 RefSeq:NP_565897.1 UniGene:At.26429 EnsemblPlants:AT2G38905.1 GeneID:818475 KEGG:ath:AT2G38905 TAIR:At2g38905 eggNOG:NOG331170 InParanoid:Q941D7 OMA:WINIILC PhylomeDB:Q941D7 ArrayExpress:Q941D7 Genevestigator:Q941D7 Uniprot:Q941D7
Leaf	Isotig00071	37	20	1.416	0.000260659	TAIR|locus:2205235 - symbol:LOS1 "AT1G56070" species:3702 "Arabidopsis thaliana" [GO:0003746 "translation elongation factor activity" evidence=ISS] [GO:0008135 "translation factor activity, nucleic acid binding" evidence=ISS] [GO:0009409 "response to cold" evidence=IMP] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR000640 InterPro:IPR000795 InterPro:IPR004161 InterPro:IPR005225 InterPro:IPR005517 Pfam:PF00009 Pfam:PF00679 Pfam:PF03144 Pfam:PF03764 PRINTS:PR00315 PROSITE:PS00301 SMART:SM00838 SMART:SM00889 GO:GO:0005525 TIGRFAMs:TIGR00231

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EMBL:CP002684 GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 GO:GO:0005774 GO:GO:0009507 GO:GO:0005730 GO:GO:0003924 GO:GO:0005507 GO:GO:0009409 GO:GO:0003746 InterPro:IPR020568 InterPro:IPR014721 Gene3D:G3DSA:3.30.230.10 SUPFAM:SSF54211 InterPro:IPR009000 SUPFAM:SSF50447 InterPro:IPR009022 Gene3D:G3DSA:3.30.70.240 SUPFAM:SSF54980 KO:K03234 OMA:GVMTQTE HSSP:P32324 EMBL:AF367331 EMBL:AY054461 EMBL:BT000661 EMBL:BT000722 EMBL:BT002714 IPI:IPI00517335 RefSeq:NP_849818.1 UniGene:At.47544 ProteinModelPortal:Q9ASR1 SMR:Q9ASR1 STRING:Q9ASR1 PRIDE:Q9ASR1 ProMEX:Q9ASR1 EnsemblPlants:AT1G56070.1 GeneID:842058 KEGG:ath:AT1G56070 TAIR:At1g56070 InParanoid:Q9ASR1 PhylomeDB:Q9ASR1 ProtClustDB:PLN00116 Genevestigator:Q9ASR1 Uniprot:Q9ASR1
Leaf	Isotig00072	37	20	1.416	0.000260659	TAIR|locus:2205235 - symbol:LOS1 "AT1G56070" species:3702 "Arabidopsis thaliana" [GO:0003746 "translation elongation factor activity" evidence=ISS] [GO:0008135 "translation factor activity, nucleic acid binding" evidence=ISS] [GO:0009409 "response to cold" evidence=IMP] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR000640 InterPro:IPR000795 InterPro:IPR004161 InterPro:IPR005225 InterPro:IPR005517 Pfam:PF00009 Pfam:PF00679 Pfam:PF03144 Pfam:PF03764 PRINTS:PR00315 PROSITE:PS00301 SMART:SM00838 SMART:SM00889 GO:GO:0005525 TIGRFAMs:TIGR00231 EMBL:CP002684 GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 GO:GO:0005774 GO:GO:0009507 GO:GO:0005730 GO:GO:0003924 GO:GO:0005507 GO:GO:0009409 GO:GO:0003746 InterPro:IPR020568 InterPro:IPR014721 Gene3D:G3DSA:3.30.230.10 SUPFAM:SSF54211 InterPro:IPR009000 SUPFAM:SSF50447 InterPro:IPR009022 Gene3D:G3DSA:3.30.70.240 SUPFAM:SSF54980 KO:K03234 OMA:GVMTQTE HSSP:P32324 EMBL:AF367331 EMBL:AY054461 EMBL:BT000661 EMBL:BT000722 EMBL:BT002714 IPI:IPI00517335 RefSeq:NP_849818.1 UniGene:At.47544 ProteinModelPortal:Q9ASR1 SMR:Q9ASR1 STRING:Q9ASR1 PRIDE:Q9ASR1 ProMEX:Q9ASR1 EnsemblPlants:AT1G56070.1 GeneID:842058 KEGG:ath:AT1G56070 TAIR:At1g56070 InParanoid:Q9ASR1 PhylomeDB:Q9ASR1 ProtClustDB:PLN00116 Genevestigator:Q9ASR1 Uniprot:Q9ASR1
Leaf	Isotig00073	38	20	1.455	0.000159477	TAIR|locus:2205235 - symbol:LOS1 "AT1G56070" species:3702 "Arabidopsis thaliana" [GO:0003746 "translation elongation factor activity" evidence=ISS] [GO:0008135 "translation factor activity, nucleic acid binding" evidence=ISS] [GO:0009409 "response to cold" evidence=IMP] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR000640 InterPro:IPR000795 InterPro:IPR004161 InterPro:IPR005225 InterPro:IPR005517 Pfam:PF00009 Pfam:PF00679 Pfam:PF03144 Pfam:PF03764 PRINTS:PR00315 PROSITE:PS00301 SMART:SM00838 SMART:SM00889 GO:GO:0005525 TIGRFAMs:TIGR00231 EMBL:CP002684 GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 GO:GO:0005774 GO:GO:0009507 GO:GO:0005730 GO:GO:0003924 GO:GO:0005507 GO:GO:0009409 GO:GO:0003746 InterPro:IPR020568 InterPro:IPR014721 Gene3D:G3DSA:3.30.230.10 SUPFAM:SSF54211 InterPro:IPR009000 SUPFAM:SSF50447 InterPro:IPR009022 Gene3D:G3DSA:3.30.70.240 SUPFAM:SSF54980 KO:K03234 OMA:GVMTQTE HSSP:P32324 EMBL:AF367331 EMBL:AY054461 EMBL:BT000661 EMBL:BT000722 EMBL:BT002714 IPI:IPI00517335 RefSeq:NP_849818.1 UniGene:At.47544 ProteinModelPortal:Q9ASR1 SMR:Q9ASR1 STRING:Q9ASR1 PRIDE:Q9ASR1 ProMEX:Q9ASR1 EnsemblPlants:AT1G56070.1 GeneID:842058 KEGG:ath:AT1G56070 TAIR:At1g56070 InParanoid:Q9ASR1 PhylomeDB:Q9ASR1 ProtClustDB:PLN00116 Genevestigator:Q9ASR1 Uniprot:Q9ASR1
Leaf	Isotig00074	38	20	1.455	0.000159477	TAIR|locus:2205235 - symbol:LOS1 "AT1G56070" species:3702 "Arabidopsis thaliana" [GO:0003746 "translation elongation factor activity" evidence=ISS] [GO:0008135 "translation factor activity, nucleic acid binding" evidence=ISS] [GO:0009409 "response to cold" evidence=IMP] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR000640 InterPro:IPR000795 InterPro:IPR004161 InterPro:IPR005225

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						InterPro:IPR005517 Pfam:PF00009 Pfam:PF00679 Pfam:PF03144 Pfam:PF03764 PRINTS:PR00315 PROSITE:PS00301 SMART:SM00838 SMART:SM00889 GO:GO:0005525 TIGRFAMs:TIGR00231 EMBL:CP002684 GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 GO:GO:0005774 GO:GO:0009507 GO:GO:0005730 GO:GO:0003924 GO:GO:0005507 GO:GO:0009409 GO:GO:0003746 InterPro:IPR020568 InterPro:IPR014721 Gene3D:G3DSA:3.30.230.10 SUPFAM:SSF54211 InterPro:IPR009000 SUPFAM:SSF50447 InterPro:IPR009022 Gene3D:G3DSA:3.30.70.240 SUPFAM:SSF54980 KO:K03234 OMA:GVMTQTE HSSP:P32324 EMBL:AF367331 EMBL:AY054461 EMBL:BT000661 EMBL:BT000722 EMBL:BT002714 IPI:IPI00517335 RefSeq:NP_849818.1 UniGene:At.47544 ProteinModelPortal:Q9ASR1 SMR:Q9ASR1 STRING:Q9ASR1 PRIDE:Q9ASR1 ProMEX:Q9ASR1 EnsemblPlants:AT1G56070.1 GeneID:842058 KEGG:ath:AT1G56070 TAIR:At1g56070 InParanoid:Q9ASR1 PhylomeDB:Q9ASR1 ProtClustDB:PLN00116 Genevestigator:Q9ASR1 Uniprot:Q9ASR1
Leaf	Isotig00075	36	19	1.451	0.000244889	TAIR|locus:2205235 - symbol:LOS1 "AT1G56070" species:3702 "Arabidopsis thaliana" [GO:0003746 "translation elongation factor activity" evidence=ISS] [GO:0008135 "translation factor activity, nucleic acid binding" evidence=ISS] [GO:0009409 "response to cold" evidence=IMP] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR000640 InterPro:IPR000795 InterPro:IPR004161 InterPro:IPR005225 InterPro:IPR005517 Pfam:PF00009 Pfam:PF00679 Pfam:PF03144 Pfam:PF03764 PRINTS:PR00315 PROSITE:PS00301 SMART:SM00838 SMART:SM00889 GO:GO:0005525 TIGRFAMs:TIGR00231 EMBL:CP002684 GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 GO:GO:0005774 GO:GO:0009507 GO:GO:0005730 GO:GO:0003924 GO:GO:0005507 GO:GO:0009409 GO:GO:0003746 InterPro:IPR020568 InterPro:IPR014721 Gene3D:G3DSA:3.30.230.10 SUPFAM:SSF54211 InterPro:IPR009000 SUPFAM:SSF50447 InterPro:IPR009022 Gene3D:G3DSA:3.30.70.240 SUPFAM:SSF54980 KO:K03234 OMA:GVMTQTE HSSP:P32324 EMBL:AF367331 EMBL:AY054461 EMBL:BT000661 EMBL:BT000722 EMBL:BT002714 IPI:IPI00517335 RefSeq:NP_849818.1 UniGene:At.47544 ProteinModelPortal:Q9ASR1 SMR:Q9ASR1 STRING:Q9ASR1 PRIDE:Q9ASR1 ProMEX:Q9ASR1 EnsemblPlants:AT1G56070.1 GeneID:842058 KEGG:ath:AT1G56070 TAIR:At1g56070 InParanoid:Q9ASR1 PhylomeDB:Q9ASR1 ProtClustDB:PLN00116 Genevestigator:Q9ASR1 Uniprot:Q9ASR1
Leaf	Isotig00076	37	19	1.490	0.000148623	TAIR|locus:2205235 - symbol:LOS1 "AT1G56070" species:3702 "Arabidopsis thaliana" [GO:0003746 "translation elongation factor activity" evidence=ISS] [GO:0008135 "translation factor activity, nucleic acid binding" evidence=ISS] [GO:0009409 "response to cold" evidence=IMP] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR000640 InterPro:IPR000795 InterPro:IPR004161 InterPro:IPR005225 InterPro:IPR005517 Pfam:PF00009 Pfam:PF00679 Pfam:PF03144 Pfam:PF03764 PRINTS:PR00315 PROSITE:PS00301 SMART:SM00838 SMART:SM00889 GO:GO:0005525 TIGRFAMs:TIGR00231 EMBL:CP002684 GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 GO:GO:0005774 GO:GO:0009507 GO:GO:0005730 GO:GO:0003924 GO:GO:0005507 GO:GO:0009409 GO:GO:0003746 InterPro:IPR020568 InterPro:IPR014721 Gene3D:G3DSA:3.30.230.10 SUPFAM:SSF54211 InterPro:IPR009000 SUPFAM:SSF50447 InterPro:IPR009022 Gene3D:G3DSA:3.30.70.240 SUPFAM:SSF54980 KO:K03234 OMA:GVMTQTE HSSP:P32324 EMBL:AF367331 EMBL:AY054461 EMBL:BT000661 EMBL:BT000722 EMBL:BT002714 IPI:IPI00517335 RefSeq:NP_849818.1 UniGene:At.47544 ProteinModelPortal:Q9ASR1 SMR:Q9ASR1 STRING:Q9ASR1 PRIDE:Q9ASR1 ProMEX:Q9ASR1 EnsemblPlants:AT1G56070.1 GeneID:842058 KEGG:ath:AT1G56070 TAIR:At1g56070 InParanoid:Q9ASR1 PhylomeDB:Q9ASR1 ProtClustDB:PLN00116 Genevestigator:Q9ASR1 Uniprot:Q9ASR1
Leaf	Isotig00077	37	20	1.416	0.000260659	TAIR|locus:2205235 - symbol:LOS1 "AT1G56070" species:3702 "Arabidopsis thaliana" [GO:0003746 "translation elongation factor activity" evidence=ISS] [GO:0008135 "translation factor activity, nucleic acid binding" evidence=ISS] [GO:0009409 "response to cold" evidence=IMP] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009507 "chloroplast"

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR000640 InterPro:IPR000795 InterPro:IPR004161 InterPro:IPR005225 InterPro:IPR005517 Pfam:PF00009 Pfam:PF00679 Pfam:PF03144 Pfam:PF03764 PRINTS:PR00315 PROSITE:PS00301 SMART:SM00838 SMART:SM00889 GO:GO:0005525 TIGRFAMs:TIGR00231 EMBL:CP002684 GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 GO:GO:0005774 GO:GO:0009507 GO:GO:0005730 GO:GO:0003924 GO:GO:0005507 GO:GO:0009409 GO:GO:0003746 InterPro:IPR020568 InterPro:IPR014721 Gene3D:G3DSA:3.30.230.10 SUPFAM:SSF54211 InterPro:IPR009000 SUPFAM:SSF50447 InterPro:IPR009022 Gene3D:G3DSA:3.30.70.240 SUPFAM:SSF54980 KO:K03234 OMA:GVMTQTE HSSP:P32324 EMBL:AF367331 EMBL:AY054461 EMBL:BT000661 EMBL:BT000722 EMBL:BT002714 IPI:IPI00517335 RefSeq:NP_849818.1 UniGene:At.47544 ProteinModelPortal:Q9ASR1 SMR:Q9ASR1 STRING:Q9ASR1 PRIDE:Q9ASR1 ProMEX:Q9ASR1 EnsemblPlants:AT1G56070.1 GeneID:842058 KEGG:ath:AT1G56070 TAIR:At1g56070 InParanoid:Q9ASR1 PhylomeDB:Q9ASR1 ProtClustDB:PLN00116 Genevestigator:Q9ASR1 Uniprot:Q9ASR1
Leaf	Isotig00078	37	20	1.416	0.000260659	TAIR|locus:2205235 - symbol:LOS1 "AT1G56070" species:3702 "Arabidopsis thaliana" [GO:0003746 "translation elongation factor activity" evidence=ISS] [GO:0008135 "translation factor activity, nucleic acid binding" evidence=ISS] [GO:0009409 "response to cold" evidence=IMP] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR000640 InterPro:IPR000795 InterPro:IPR004161 InterPro:IPR005225 InterPro:IPR005517 Pfam:PF00009 Pfam:PF00679 Pfam:PF03144 Pfam:PF03764 PRINTS:PR00315 PROSITE:PS00301 SMART:SM00838 SMART:SM00889 GO:GO:0005525 TIGRFAMs:TIGR00231 EMBL:CP002684 GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 GO:GO:0005774 GO:GO:0009507 GO:GO:0005730 GO:GO:0003924 GO:GO:0005507 GO:GO:0009409 GO:GO:0003746 InterPro:IPR020568 InterPro:IPR014721 Gene3D:G3DSA:3.30.230.10 SUPFAM:SSF54211 InterPro:IPR009000 SUPFAM:SSF50447 InterPro:IPR009022 Gene3D:G3DSA:3.30.70.240 SUPFAM:SSF54980 KO:K03234 OMA:GVMTQTE HSSP:P32324 EMBL:AF367331 EMBL:AY054461 EMBL:BT000661 EMBL:BT000722 EMBL:BT002714 IPI:IPI00517335 RefSeq:NP_849818.1 UniGene:At.47544 ProteinModelPortal:Q9ASR1 SMR:Q9ASR1 STRING:Q9ASR1 PRIDE:Q9ASR1 ProMEX:Q9ASR1 EnsemblPlants:AT1G56070.1 GeneID:842058 KEGG:ath:AT1G56070 TAIR:At1g56070 InParanoid:Q9ASR1 PhylomeDB:Q9ASR1 ProtClustDB:PLN00116 Genevestigator:Q9ASR1 Uniprot:Q9ASR1
Leaf	Isotig00079	36	19	1.451	0.000244889	TAIR|locus:2205235 - symbol:LOS1 "AT1G56070" species:3702 "Arabidopsis thaliana" [GO:0003746 "translation elongation factor activity" evidence=ISS] [GO:0008135 "translation factor activity, nucleic acid binding" evidence=ISS] [GO:0009409 "response to cold" evidence=IMP] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR000640 InterPro:IPR000795 InterPro:IPR004161 InterPro:IPR005225 InterPro:IPR005517 Pfam:PF00009 Pfam:PF00679 Pfam:PF03144 Pfam:PF03764 PRINTS:PR00315 PROSITE:PS00301 SMART:SM00838 SMART:SM00889 GO:GO:0005525 TIGRFAMs:TIGR00231 EMBL:CP002684 GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 GO:GO:0005774 GO:GO:0009507 GO:GO:0005730 GO:GO:0003924 GO:GO:0005507 GO:GO:0009409 GO:GO:0003746 InterPro:IPR020568 InterPro:IPR014721 Gene3D:G3DSA:3.30.230.10 SUPFAM:SSF54211 InterPro:IPR009000 SUPFAM:SSF50447 InterPro:IPR009022 Gene3D:G3DSA:3.30.70.240 SUPFAM:SSF54980 KO:K03234 OMA:GVMTQTE HSSP:P32324 EMBL:AF367331 EMBL:AY054461 EMBL:BT000661 EMBL:BT000722 EMBL:BT002714 IPI:IPI00517335 RefSeq:NP_849818.1 UniGene:At.47544 ProteinModelPortal:Q9ASR1 SMR:Q9ASR1 STRING:Q9ASR1 PRIDE:Q9ASR1 ProMEX:Q9ASR1 EnsemblPlants:AT1G56070.1 GeneID:842058 KEGG:ath:AT1G56070 TAIR:At1g56070 InParanoid:Q9ASR1 PhylomeDB:Q9ASR1 ProtClustDB:PLN00116 Genevestigator:Q9ASR1 Uniprot:Q9ASR1
Leaf	Isotig00080	36	19	1.451	0.000244889	TAIR|locus:2205235 - symbol:LOS1 "AT1G56070" species:3702 "Arabidopsis thaliana" [GO:0003746 "translation elongation factor activity" evidence=ISS] [GO:0008135 "translation factor activity, nucleic acid binding" evidence=ISS] [GO:0009409 "response to cold" evidence=IMP] [GO:0005730 "nucleolus" evidence=IDA]

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						[GO:0005507 "copper ion binding" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR000640 InterPro:IPR000795 InterPro:IPR004161 InterPro:IPR005225 InterPro:IPR005517 Pfam:PF00009 Pfam:PF00679 Pfam:PF03144 Pfam:PF03764 PRINTS:PR00315 PROSITE:PS00301 SMART:SM00838 SMART:SM00889 GO:GO:0005525 TIGRFAMs:TIGR00231 EMBL:CP002684 GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 GO:GO:0005774 GO:GO:0009507 GO:GO:0005730 GO:GO:0003924 GO:GO:0005507 GO:GO:0009409 GO:GO:0003746 InterPro:IPR020568 InterPro:IPR014721 Gene3D:G3DSA:3.30.230.10 SUPFAM:SSF54211 InterPro:IPR009000 SUPFAM:SSF50447 InterPro:IPR009022 Gene3D:G3DSA:3.30.70.240 SUPFAM:SSF54980 KO:K03234 OMA:GVMTQTE HSSP:P32324 EMBL:AF367331 EMBL:AY054461 EMBL:BT000661 EMBL:BT000722 EMBL:BT002714 IPI:IPI00517335 RefSeq:NP_849818.1 UniGene:At.47544 ProteinModelPortal:Q9ASR1 SMR:Q9ASR1 STRING:Q9ASR1 PRIDE:Q9ASR1 ProMEX:Q9ASR1 EnsemblPlants:AT1G56070.1 GeneID:842058 KEGG:ath:AT1G56070 TAIR:At1g56070 InParanoid:Q9ASR1 PhylomeDB:Q9ASR1 ProtClustDB:PLN00116 Genevestigator:Q9ASR1 Uniprot:Q9ASR1
Leaf	Isotig00081	37	19	1.490	0.000148623	TAIR|locus:2205235 - symbol:LOS1 "AT1G56070" species:3702 "Arabidopsis thaliana" [GO:0003746 "translation elongation factor activity" evidence=ISS] [GO:0008135 "translation factor activity, nucleic acid binding" evidence=ISS] [GO:0009409 "response to cold" evidence=IMP] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR000640 InterPro:IPR000795 InterPro:IPR004161 InterPro:IPR005225 InterPro:IPR005517 Pfam:PF00009 Pfam:PF00679 Pfam:PF03144 Pfam:PF03764 PRINTS:PR00315 PROSITE:PS00301 SMART:SM00838 SMART:SM00889 GO:GO:0005525 TIGRFAMs:TIGR00231 EMBL:CP002684 GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 GO:GO:0005774 GO:GO:0009507 GO:GO:0005730 GO:GO:0003924 GO:GO:0005507 GO:GO:0009409 GO:GO:0003746 InterPro:IPR020568 InterPro:IPR014721 Gene3D:G3DSA:3.30.230.10 SUPFAM:SSF54211 InterPro:IPR009000 SUPFAM:SSF50447 InterPro:IPR009022 Gene3D:G3DSA:3.30.70.240 SUPFAM:SSF54980 KO:K03234 OMA:GVMTQTE HSSP:P32324 EMBL:AF367331 EMBL:AY054461 EMBL:BT000661 EMBL:BT000722 EMBL:BT002714 IPI:IPI00517335 RefSeq:NP_849818.1 UniGene:At.47544 ProteinModelPortal:Q9ASR1 SMR:Q9ASR1 STRING:Q9ASR1 PRIDE:Q9ASR1 ProMEX:Q9ASR1 EnsemblPlants:AT1G56070.1 GeneID:842058 KEGG:ath:AT1G56070 TAIR:At1g56070 InParanoid:Q9ASR1 PhylomeDB:Q9ASR1 ProtClustDB:PLN00116 Genevestigator:Q9ASR1 Uniprot:Q9ASR1
Leaf	Isotig00082	36	19	1.451	0.000244889	TAIR|locus:2205235 - symbol:LOS1 "AT1G56070" species:3702 "Arabidopsis thaliana" [GO:0003746 "translation elongation factor activity" evidence=ISS] [GO:0008135 "translation factor activity, nucleic acid binding" evidence=ISS] [GO:0009409 "response to cold" evidence=IMP] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR000640 InterPro:IPR000795 InterPro:IPR004161 InterPro:IPR005225 InterPro:IPR005517 Pfam:PF00009 Pfam:PF00679 Pfam:PF03144 Pfam:PF03764 PRINTS:PR00315 PROSITE:PS00301 SMART:SM00838 SMART:SM00889 GO:GO:0005525 TIGRFAMs:TIGR00231 EMBL:CP002684 GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 GO:GO:0005774 GO:GO:0009507 GO:GO:0005730 GO:GO:0003924 GO:GO:0005507 GO:GO:0009409 GO:GO:0003746 InterPro:IPR020568 InterPro:IPR014721 Gene3D:G3DSA:3.30.230.10 SUPFAM:SSF54211 InterPro:IPR009000 SUPFAM:SSF50447 InterPro:IPR009022 Gene3D:G3DSA:3.30.70.240 SUPFAM:SSF54980 KO:K03234 OMA:GVMTQTE HSSP:P32324 EMBL:AF367331 EMBL:AY054461 EMBL:BT000661 EMBL:BT000722 EMBL:BT002714 IPI:IPI00517335 RefSeq:NP_849818.1 UniGene:At.47544 ProteinModelPortal:Q9ASR1 SMR:Q9ASR1 STRING:Q9ASR1 PRIDE:Q9ASR1 ProMEX:Q9ASR1 EnsemblPlants:AT1G56070.1 GeneID:842058 KEGG:ath:AT1G56070 TAIR:At1g56070 InParanoid:Q9ASR1 PhylomeDB:Q9ASR1 ProtClustDB:PLN00116 Genevestigator:Q9ASR1 Uniprot:Q9ASR1

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig00083	27	9	2.114	3.70E-05	TAIR|locus:2205235 - symbol:LOS1 "AT1G56070" species:3702 "Arabidopsis thaliana" [GO:0003746 "translation elongation factor activity" evidence=ISS] [GO:0008135 "translation factor activity, nucleic acid binding" evidence=ISS] [GO:0009409 "response to cold" evidence=IMP] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR000640 InterPro:IPR000795 InterPro:IPR004161 InterPro:IPR005225 InterPro:IPR005517 Pfam:PF00009 Pfam:PF00679 Pfam:PF03144 Pfam:PF03764 PRINTS:PR00315 PROSITE:PS00301 SMART:SM00838 SMART:SM00889 GO:GO:0005525 TIGRFAMs:TIGR00231 EMBL:CP002684 GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 GO:GO:0005774 GO:GO:0009507 GO:GO:0005730 GO:GO:0003924 GO:GO:0005507 GO:GO:0009409 GO:GO:0003746 InterPro:IPR020568 InterPro:IPR014721 Gene3D:G3DSA:3.30.230.10 SUPFAM:SSF54211 InterPro:IPR009000 SUPFAM:SSF50447 InterPro:IPR009022 Gene3D:G3DSA:3.30.70.240 SUPFAM:SSF54980 KO:K03234 OMA:GVMTQTE HSSP:P32324 EMBL:AF367331 EMBL:AY054461 EMBL:BT000661 EMBL:BT000722 EMBL:BT002714 IPI:IPI00517335 RefSeq:NP_849818.1 UniGene:At.47544 ProteinModelPortal:Q9ASR1 SMR:Q9ASR1 STRING:Q9ASR1 PRIDE:Q9ASR1 ProMEX:Q9ASR1 EnsemblPlants:AT1G56070.1 GeneID:842058 KEGG:ath:AT1G56070 TAIR:At1g56070 InParanoid:Q9ASR1 PhylomeDB:Q9ASR1 ProtClustDB:PLN00116 Genevestigator:Q9ASR1 Uniprot:Q9ASR1
Leaf	Isotig00084	27	9	2.114	3.70E-05	TAIR|locus:2205235 - symbol:LOS1 "AT1G56070" species:3702 "Arabidopsis thaliana" [GO:0003746 "translation elongation factor activity" evidence=ISS] [GO:0008135 "translation factor activity, nucleic acid binding" evidence=ISS] [GO:0009409 "response to cold" evidence=IMP] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR000640 InterPro:IPR000795 InterPro:IPR004161 InterPro:IPR005225 InterPro:IPR005517 Pfam:PF00009 Pfam:PF00679 Pfam:PF03144 Pfam:PF03764 PRINTS:PR00315 PROSITE:PS00301 SMART:SM00838 SMART:SM00889 GO:GO:0005525 TIGRFAMs:TIGR00231 EMBL:CP002684 GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 GO:GO:0005774 GO:GO:0009507 GO:GO:0005730 GO:GO:0003924 GO:GO:0005507 GO:GO:0009409 GO:GO:0003746 InterPro:IPR020568 InterPro:IPR014721 Gene3D:G3DSA:3.30.230.10 SUPFAM:SSF54211 InterPro:IPR009000 SUPFAM:SSF50447 InterPro:IPR009022 Gene3D:G3DSA:3.30.70.240 SUPFAM:SSF54980 KO:K03234 OMA:GVMTQTE HSSP:P32324 EMBL:AF367331 EMBL:AY054461 EMBL:BT000661 EMBL:BT000722 EMBL:BT002714 IPI:IPI00517335 RefSeq:NP_849818.1 UniGene:At.47544 ProteinModelPortal:Q9ASR1 SMR:Q9ASR1 STRING:Q9ASR1 PRIDE:Q9ASR1 ProMEX:Q9ASR1 EnsemblPlants:AT1G56070.1 GeneID:842058 KEGG:ath:AT1G56070 TAIR:At1g56070 InParanoid:Q9ASR1 PhylomeDB:Q9ASR1 ProtClustDB:PLN00116 Genevestigator:Q9ASR1 Uniprot:Q9ASR1
Leaf	Isotig00085	27	13	1.583	0.000705488	TAIR|locus:2205235 - symbol:LOS1 "AT1G56070" species:3702 "Arabidopsis thaliana" [GO:0003746 "translation elongation factor activity" evidence=ISS] [GO:0008135 "translation factor activity, nucleic acid binding" evidence=ISS] [GO:0009409 "response to cold" evidence=IMP] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR000640 InterPro:IPR000795 InterPro:IPR004161 InterPro:IPR005225 InterPro:IPR005517 Pfam:PF00009 Pfam:PF00679 Pfam:PF03144 Pfam:PF03764 PRINTS:PR00315 PROSITE:PS00301 SMART:SM00838 SMART:SM00889 GO:GO:0005525 TIGRFAMs:TIGR00231 EMBL:CP002684 GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 GO:GO:0005774 GO:GO:0009507 GO:GO:0005730 GO:GO:0003924 GO:GO:0005507 GO:GO:0009409 GO:GO:0003746 InterPro:IPR020568 InterPro:IPR014721 Gene3D:G3DSA:3.30.230.10 SUPFAM:SSF54211 InterPro:IPR009000 SUPFAM:SSF50447 InterPro:IPR009022 Gene3D:G3DSA:3.30.70.240 SUPFAM:SSF54980 KO:K03234 OMA:GVMTQTE HSSP:P32324 EMBL:AF367331 EMBL:AY054461 EMBL:BT000661 EMBL:BT000722 EMBL:BT002714 IPI:IPI00517335 RefSeq:NP_849818.1 UniGene:At.47544 ProteinModelPortal:Q9ASR1 SMR:Q9ASR1 STRING:Q9ASR1 PRIDE:Q9ASR1 ProMEX:Q9ASR1 EnsemblPlants:AT1G56070.1 GeneID:842058 KEGG:ath:AT1G56070

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						TAIR:At1g56070 InParanoid:Q9ASR1 PhylomeDB:Q9ASR1 ProtClustDB:PLN00116 Genevestigator:Q9ASR1 Uniprot:Q9ASR1
Leaf	Isotig00086	27	13	1.583	0.000705488	TAIR|locus:2205235 - symbol:LOS1 "AT1G56070" species:3702 "Arabidopsis thaliana" [GO:0003746 "translation elongation factor activity" evidence=ISS] [GO:0008135 "translation factor activity, nucleic acid binding" evidence=ISS] [GO:0009409 "response to cold" evidence=IMP] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR000640 InterPro:IPR000795 InterPro:IPR004161 InterPro:IPR005225 InterPro:IPR005517 Pfam:PF00009 Pfam:PF00679 Pfam:PF03144 Pfam:PF03764 PRINTS:PR00315 PROSITE:PS00301 SMART:SM00838 SMART:SM00889 GO:GO:0005525 TIGRFAMs:TIGR00231 EMBL:CP002684 GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 GO:GO:0005774 GO:GO:0009507 GO:GO:0005730 GO:GO:0003924 GO:GO:0005507 GO:GO:0009409 GO:GO:0003746 InterPro:IPR020568 InterPro:IPR014721 Gene3D:G3DSA:3.30.230.10 SUPFAM:SSF54211 InterPro:IPR009000 SUPFAM:SSF50447 InterPro:IPR009022 Gene3D:G3DSA:3.30.70.240 SUPFAM:SSF54980 KO:K03234 OMA:GVMTQTE HSSP:P32324 EMBL:AF367331 EMBL:AY054461 EMBL:BT000661 EMBL:BT000722 EMBL:BT002714 IPI:IPI00517335 RefSeq:NP_849818.1 UniGene:At.47544 ProteinModelPortal:Q9ASR1 SMR:Q9ASR1 STRING:Q9ASR1 PRIDE:Q9ASR1 ProMEX:Q9ASR1 EnsemblPlants:AT1G56070.1 GeneID:842058 KEGG:ath:AT1G56070 TAIR:At1g56070 InParanoid:Q9ASR1 PhylomeDB:Q9ASR1 ProtClustDB:PLN00116 Genevestigator:Q9ASR1 Uniprot:Q9ASR1
Leaf	Isotig00087	26	8	2.229	2.86E-05	TAIR|locus:2205235 - symbol:LOS1 "AT1G56070" species:3702 "Arabidopsis thaliana" [GO:0003746 "translation elongation factor activity" evidence=ISS] [GO:0008135 "translation factor activity, nucleic acid binding" evidence=ISS] [GO:0009409 "response to cold" evidence=IMP] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR000640 InterPro:IPR000795 InterPro:IPR004161 InterPro:IPR005225 InterPro:IPR005517 Pfam:PF00009 Pfam:PF00679 Pfam:PF03144 Pfam:PF03764 PRINTS:PR00315 PROSITE:PS00301 SMART:SM00838 SMART:SM00889 GO:GO:0005525 TIGRFAMs:TIGR00231 EMBL:CP002684 GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 GO:GO:0005774 GO:GO:0009507 GO:GO:0005730 GO:GO:0003924 GO:GO:0005507 GO:GO:0009409 GO:GO:0003746 InterPro:IPR020568 InterPro:IPR014721 Gene3D:G3DSA:3.30.230.10 SUPFAM:SSF54211 InterPro:IPR009000 SUPFAM:SSF50447 InterPro:IPR009022 Gene3D:G3DSA:3.30.70.240 SUPFAM:SSF54980 KO:K03234 OMA:GVMTQTE HSSP:P32324 EMBL:AF367331 EMBL:AY054461 EMBL:BT000661 EMBL:BT000722 EMBL:BT002714 IPI:IPI00517335 RefSeq:NP_849818.1 UniGene:At.47544 ProteinModelPortal:Q9ASR1 SMR:Q9ASR1 STRING:Q9ASR1 PRIDE:Q9ASR1 ProMEX:Q9ASR1 EnsemblPlants:AT1G56070.1 GeneID:842058 KEGG:ath:AT1G56070 TAIR:At1g56070 InParanoid:Q9ASR1 PhylomeDB:Q9ASR1 ProtClustDB:PLN00116 Genevestigator:Q9ASR1 Uniprot:Q9ASR1
Leaf	Isotig00088	26	12	1.644	0.000635683	TAIR|locus:2205235 - symbol:LOS1 "AT1G56070" species:3702 "Arabidopsis thaliana" [GO:0003746 "translation elongation factor activity" evidence=ISS] [GO:0008135 "translation factor activity, nucleic acid binding" evidence=ISS] [GO:0009409 "response to cold" evidence=IMP] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR000640 InterPro:IPR000795 InterPro:IPR004161 InterPro:IPR005225 InterPro:IPR005517 Pfam:PF00009 Pfam:PF00679 Pfam:PF03144 Pfam:PF03764 PRINTS:PR00315 PROSITE:PS00301 SMART:SM00838 SMART:SM00889 GO:GO:0005525 TIGRFAMs:TIGR00231 EMBL:CP002684 GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 GO:GO:0005774 GO:GO:0009507 GO:GO:0005730 GO:GO:0003924 GO:GO:0005507 GO:GO:0009409 GO:GO:0003746 InterPro:IPR020568 InterPro:IPR014721 Gene3D:G3DSA:3.30.230.10 SUPFAM:SSF54211 InterPro:IPR009000 SUPFAM:SSF50447 InterPro:IPR009022 Gene3D:G3DSA:3.30.70.240 SUPFAM:SSF54980 KO:K03234 OMA:GVMTQTE HSSP:P32324 EMBL:AF367331 EMBL:AY054461 EMBL:BT000661 EMBL:BT000722 EMBL:BT002714 IPI:IPI00517335

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						RefSeq:NP_849818.1 UniGene:At.47544 ProteinModelPortal:Q9ASR1 SMR:Q9ASR1 STRING:Q9ASR1 PRIDE:Q9ASR1 ProMEX:Q9ASR1 EnsemblPlants:AT1G56070.1 GeneID:842058 KEGG:ath:AT1G56070 TAIR:At1g56070 InParanoid:Q9ASR1 PhylomeDB:Q9ASR1 ProtClustDB:PLN00116 Genevestigator:Q9ASR1 Uniprot:Q9ASR1
Leaf	Isotig00089	26	8	2.229	2.86E-05	TAIR|locus:2205235 - symbol:LOS1 "AT1G56070" species:3702 "Arabidopsis thaliana" [GO:0003746 "translation elongation factor activity" evidence=ISS] [GO:0008135 "translation factor activity, nucleic acid binding" evidence=ISS] [GO:0009409 "response to cold" evidence=IMP] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR000640 InterPro:IPR000795 InterPro:IPR004161 InterPro:IPR005225 InterPro:IPR005517 Pfam:PF00009 Pfam:PF00679 Pfam:PF03144 Pfam:PF03764 PRINTS:PR00315 PROSITE:PS00301 SMART:SM00838 SMART:SM00889 GO:GO:0005525 TIGRFAMs:TIGR00231 EMBL:CP002684 GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 GO:GO:0005774 GO:GO:0009507 GO:GO:0005730 GO:GO:0003924 GO:GO:0005507 GO:GO:0009409 GO:GO:0003746 InterPro:IPR020568 InterPro:IPR014721 Gene3D:G3DSA:3.30.230.10 SUPFAM:SSF54211 InterPro:IPR009000 SUPFAM:SSF50447 InterPro:IPR009022 Gene3D:G3DSA:3.30.70.240 SUPFAM:SSF54980 KO:K03234 OMA:GVMTQTE HSSP:P32324 EMBL:AF367331 EMBL:AY054461 EMBL:BT000661 EMBL:BT000722 EMBL:BT002714 IPI:IPI00517335 RefSeq:NP_849818.1 UniGene:At.47544 ProteinModelPortal:Q9ASR1 SMR:Q9ASR1 STRING:Q9ASR1 PRIDE:Q9ASR1 ProMEX:Q9ASR1 EnsemblPlants:AT1G56070.1 GeneID:842058 KEGG:ath:AT1G56070 TAIR:At1g56070 InParanoid:Q9ASR1 PhylomeDB:Q9ASR1 ProtClustDB:PLN00116 Genevestigator:Q9ASR1 Uniprot:Q9ASR1
Leaf	Isotig00090	26	12	1.644	0.000635683	TAIR|locus:2205235 - symbol:LOS1 "AT1G56070" species:3702 "Arabidopsis thaliana" [GO:0003746 "translation elongation factor activity" evidence=ISS] [GO:0008135 "translation factor activity, nucleic acid binding" evidence=ISS] [GO:0009409 "response to cold" evidence=IMP] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR000640 InterPro:IPR000795 InterPro:IPR004161 InterPro:IPR005225 InterPro:IPR005517 Pfam:PF00009 Pfam:PF00679 Pfam:PF03144 Pfam:PF03764 PRINTS:PR00315 PROSITE:PS00301 SMART:SM00838 SMART:SM00889 GO:GO:0005525 TIGRFAMs:TIGR00231 EMBL:CP002684 GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 GO:GO:0005774 GO:GO:0009507 GO:GO:0005730 GO:GO:0003924 GO:GO:0005507 GO:GO:0009409 GO:GO:0003746 InterPro:IPR020568 InterPro:IPR014721 Gene3D:G3DSA:3.30.230.10 SUPFAM:SSF54211 InterPro:IPR009000 SUPFAM:SSF50447 InterPro:IPR009022 Gene3D:G3DSA:3.30.70.240 SUPFAM:SSF54980 KO:K03234 OMA:GVMTQTE HSSP:P32324 EMBL:AF367331 EMBL:AY054461 EMBL:BT000661 EMBL:BT000722 EMBL:BT002714 IPI:IPI00517335 RefSeq:NP_849818.1 UniGene:At.47544 ProteinModelPortal:Q9ASR1 SMR:Q9ASR1 STRING:Q9ASR1 PRIDE:Q9ASR1 ProMEX:Q9ASR1 EnsemblPlants:AT1G56070.1 GeneID:842058 KEGG:ath:AT1G56070 TAIR:At1g56070 InParanoid:Q9ASR1 PhylomeDB:Q9ASR1 ProtClustDB:PLN00116 Genevestigator:Q9ASR1 Uniprot:Q9ASR1
Leaf	Isotig00091	17	4	2.616	0.000204438	TAIR|locus:2205235 - symbol:LOS1 "AT1G56070" species:3702 "Arabidopsis thaliana" [GO:0003746 "translation elongation factor activity" evidence=ISS] [GO:0008135 "translation factor activity, nucleic acid binding" evidence=ISS] [GO:0009409 "response to cold" evidence=IMP] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR000640 InterPro:IPR000795 InterPro:IPR004161 InterPro:IPR005225 InterPro:IPR005517 Pfam:PF00009 Pfam:PF00679 Pfam:PF03144 Pfam:PF03764 PRINTS:PR00315 PROSITE:PS00301 SMART:SM00838 SMART:SM00889 GO:GO:0005525 TIGRFAMs:TIGR00231 EMBL:CP002684 GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 GO:GO:0005774 GO:GO:0009507 GO:GO:0005730 GO:GO:0003924 GO:GO:0005507 GO:GO:0009409 GO:GO:0003746 InterPro:IPR020568 InterPro:IPR014721 Gene3D:G3DSA:3.30.230.10 SUPFAM:SSF54211 InterPro:IPR009000 SUPFAM:SSF50447

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						InterPro:IPR009022 Gene3D:G3DSA:3.30.70.240 SUPFAM:SSF54980 KO:K03234 OMA:GVMTQTE HSSP:P32324 EMBL:AF367331 EMBL:AY054461 EMBL:BT000661 EMBL:BT000722 EMBL:BT002714 IPI:IPI00517335 RefSeq:NP_849818.1 UniGene:At.47544 ProteinModelPortal:Q9ASR1 SMR:Q9ASR1 STRING:Q9ASR1 PRIDE:Q9ASR1 ProMEX:Q9ASR1 EnsemblPlants:AT1G56070.1 GeneID:842058 KEGG:ath:AT1G56070 TAIR:At1g56070 InParanoid:Q9ASR1 PhylomeDB:Q9ASR1 ProtClustDB:PLN00116 Genevestigator:Q9ASR1 Uniprot:Q9ASR1
Leaf	Isotig00092	17	4	2.616	0.000204438	TAIR|locus:2205235 - symbol:LOS1 "AT1G56070" species:3702 "Arabidopsis thaliana" [GO:0003746 "translation elongation factor activity" evidence=ISS] [GO:0008135 "translation factor activity, nucleic acid binding" evidence=ISS] [GO:0009409 "response to cold" evidence=IMP] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR000640 InterPro:IPR000795 InterPro:IPR004161 InterPro:IPR005225 InterPro:IPR005517 Pfam:PF00009 Pfam:PF00679 Pfam:PF03144 Pfam:PF03764 PRINTS:PR00315 PROSITE:PS00301 SMART:SM00838 SMART:SM00889 GO:GO:0005525 TIGRFAMs:TIGR00231 EMBL:CP002684 GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 GO:GO:0005774 GO:GO:0009507 GO:GO:0005730 GO:GO:0003924 GO:GO:0005507 GO:GO:0009409 GO:GO:0003746 InterPro:IPR020568 InterPro:IPR014721 Gene3D:G3DSA:3.30.230.10 SUPFAM:SSF54211 InterPro:IPR009000 SUPFAM:SSF50447 InterPro:IPR009022 Gene3D:G3DSA:3.30.70.240 SUPFAM:SSF54980 KO:K03234 OMA:GVMTQTE HSSP:P32324 EMBL:AF367331 EMBL:AY054461 EMBL:BT000661 EMBL:BT000722 EMBL:BT002714 IPI:IPI00517335 RefSeq:NP_849818.1 UniGene:At.47544 ProteinModelPortal:Q9ASR1 SMR:Q9ASR1 STRING:Q9ASR1 PRIDE:Q9ASR1 ProMEX:Q9ASR1 EnsemblPlants:AT1G56070.1 GeneID:842058 KEGG:ath:AT1G56070 TAIR:At1g56070 InParanoid:Q9ASR1 PhylomeDB:Q9ASR1 ProtClustDB:PLN00116 Genevestigator:Q9ASR1 Uniprot:Q9ASR1
Leaf	Isotig00093	16	3	2.944	0.000128177	TAIR|locus:2205235 - symbol:LOS1 "AT1G56070" species:3702 "Arabidopsis thaliana" [GO:0003746 "translation elongation factor activity" evidence=ISS] [GO:0008135 "translation factor activity, nucleic acid binding" evidence=ISS] [GO:0009409 "response to cold" evidence=IMP] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR000640 InterPro:IPR000795 InterPro:IPR004161 InterPro:IPR005225 InterPro:IPR005517 Pfam:PF00009 Pfam:PF00679 Pfam:PF03144 Pfam:PF03764 PRINTS:PR00315 PROSITE:PS00301 SMART:SM00838 SMART:SM00889 GO:GO:0005525 TIGRFAMs:TIGR00231 EMBL:CP002684 GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 GO:GO:0005774 GO:GO:0009507 GO:GO:0005730 GO:GO:0003924 GO:GO:0005507 GO:GO:0009409 GO:GO:0003746 InterPro:IPR020568 InterPro:IPR014721 Gene3D:G3DSA:3.30.230.10 SUPFAM:SSF54211 InterPro:IPR009000 SUPFAM:SSF50447 InterPro:IPR009022 Gene3D:G3DSA:3.30.70.240 SUPFAM:SSF54980 KO:K03234 OMA:GVMTQTE HSSP:P32324 EMBL:AF367331 EMBL:AY054461 EMBL:BT000661 EMBL:BT000722 EMBL:BT002714 IPI:IPI00517335 RefSeq:NP_849818.1 UniGene:At.47544 ProteinModelPortal:Q9ASR1 SMR:Q9ASR1 STRING:Q9ASR1 PRIDE:Q9ASR1 ProMEX:Q9ASR1 EnsemblPlants:AT1G56070.1 GeneID:842058 KEGG:ath:AT1G56070 TAIR:At1g56070 InParanoid:Q9ASR1 PhylomeDB:Q9ASR1 ProtClustDB:PLN00116 Genevestigator:Q9ASR1 Uniprot:Q9ASR1
Leaf	Isotig00094	16	3	2.944	0.000128177	TAIR|locus:2205235 - symbol:LOS1 "AT1G56070" species:3702 "Arabidopsis thaliana" [GO:0003746 "translation elongation factor activity" evidence=ISS] [GO:0008135 "translation factor activity, nucleic acid binding" evidence=ISS] [GO:0009409 "response to cold" evidence=IMP] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR000640 InterPro:IPR000795 InterPro:IPR004161 InterPro:IPR005225 InterPro:IPR005517 Pfam:PF00009 Pfam:PF00679 Pfam:PF03144 Pfam:PF03764 PRINTS:PR00315 PROSITE:PS00301 SMART:SM00838 SMART:SM00889 GO:GO:0005525 TIGRFAMs:TIGR00231 EMBL:CP002684 GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 GO:GO:0005774 GO:GO:0009507

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0005730 GO:GO:0003924 GO:GO:0005507 GO:GO:0009409 GO:GO:0003746 InterPro:IPR020568 InterPro:IPR014721 Gene3D:G3DSA:3.30.230.10 SUPFAM:SSF54211 InterPro:IPR009000 SUPFAM:SSF50447 InterPro:IPR009022 Gene3D:G3DSA:3.30.70.240 SUPFAM:SSF54980 KO:K03234 OMA:GVMTQTE HSSP:P32324 EMBL:AF367331 EMBL:AY054461 EMBL:BT000661 EMBL:BT000722 EMBL:BT002714 IPI:IPI00517335 RefSeq:NP_849818.1 UniGene:At.47544 ProteinModelPortal:Q9ASR1 SMR:Q9ASR1 STRING:Q9ASR1 PRIDE:Q9ASR1 ProMEX:Q9ASR1 EnsemblPlants:AT1G56070.1 GeneID:842058 KEGG:ath:AT1G56070 TAIR:At1g56070 InParanoid:Q9ASR1 PhylomeDB:Q9ASR1 ProtClustDB:PLN00116 Genevestigator:Q9ASR1 Uniprot:Q9ASR1
Leaf	Isotig00095	215	555	-0.839	1.23E-14	TAIR|locus:2123777 - symbol:GLDP1 "AT4G33010" species:3702 "Arabidopsis thaliana" [GO:0004375 "glycine dehydrogenase (decarboxylating) activity" evidence=ISS] [GO:0005960 "glycine cleavage complex" evidence=ISS] [GO:0019464 "glycine decarboxylation via glycine cleavage system" evidence=ISS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0006546 "glycine catabolic process" evidence=IMP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] InterPro:IPR003437 InterPro:IPR015421 InterPro:IPR020580 InterPro:IPR020581 Pfam:PF02347 GO:GO:0005739 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0048046 GO:GO:0009570 GO:GO:0046686 GO:GO:0005515 GO:GO:0030170 InterPro:IPR015424 Gene3D:G3DSA:3.40.640.10 SUPFAM:SSF53383 GO:GO:0009941 GO:GO:0009534 EMBL:AL031804 EMBL:AL161582 GO:GO:0006546 GO:GO:0004375 UniGene:At.24550 HOGENOM:HBG286723 KO:K00281 ProtClustDB:PLN02414 PANTHER:PTHR11773 TIGRFAMs:TIGR00461 EMBL:AY063903 EMBL:AY091186 EMBL:AY042800 EMBL:AY128922 EMBL:AY065004 EMBL:BT001132 EMBL:BT000446 IPI:IPI00536025 PIR:T05309 RefSeq:NP_195027.1 UniGene:At.22214 ProteinModelPortal:Q94B78 SMR:Q94B78 IntAct:Q94B78 STRING:Q94B78 PRIDE:Q94B78 ProMEX:Q94B78 EnsemblPlants:AT4G33010.1 GeneID:829438 KEGG:ath:AT4G33010 GeneFarm:1737 TAIR:At4g33010 InParanoid:Q94B78 OMA:VPMSEYQ PhylomeDB:Q94B78 ArrayExpress:Q94B78 Genevestigator:Q94B78 GermOnline:AT4G33010 Uniprot:Q94B78
Leaf	Isotig00096	217	602	-0.943	7.52E-19	TAIR|locus:2123777 - symbol:GLDP1 "AT4G33010" species:3702 "Arabidopsis thaliana" [GO:0004375 "glycine dehydrogenase (decarboxylating) activity" evidence=ISS] [GO:0005960 "glycine cleavage complex" evidence=ISS] [GO:0019464 "glycine decarboxylation via glycine cleavage system" evidence=ISS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0006546 "glycine catabolic process" evidence=IMP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] InterPro:IPR003437 InterPro:IPR015421 InterPro:IPR020580 InterPro:IPR020581 Pfam:PF02347 GO:GO:0005739 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0048046 GO:GO:0009570 GO:GO:0046686 GO:GO:0005515 GO:GO:0030170 InterPro:IPR015424 Gene3D:G3DSA:3.40.640.10 SUPFAM:SSF53383 GO:GO:0009941 GO:GO:0009534 EMBL:AL031804 EMBL:AL161582 GO:GO:0006546 GO:GO:0004375 UniGene:At.24550 HOGENOM:HBG286723 KO:K00281 ProtClustDB:PLN02414 PANTHER:PTHR11773 TIGRFAMs:TIGR00461 EMBL:AY063903 EMBL:AY091186 EMBL:AY042800 EMBL:AY128922 EMBL:AY065004 EMBL:BT001132 EMBL:BT000446 IPI:IPI00536025 PIR:T05309 RefSeq:NP_195027.1 UniGene:At.22214 ProteinModelPortal:Q94B78 SMR:Q94B78 IntAct:Q94B78 STRING:Q94B78 PRIDE:Q94B78 ProMEX:Q94B78 EnsemblPlants:AT4G33010.1 GeneID:829438 KEGG:ath:AT4G33010 GeneFarm:1737 TAIR:At4g33010 InParanoid:Q94B78 OMA:VPMSEYQ PhylomeDB:Q94B78 ArrayExpress:Q94B78 Genevestigator:Q94B78 GermOnline:AT4G33010 Uniprot:Q94B78
Leaf	Isotig00097	194	490	-0.808	2.32E-12	TAIR|locus:2123777 - symbol:GLDP1 "AT4G33010" species:3702 "Arabidopsis thaliana" [GO:0004375 "glycine dehydrogenase (decarboxylating) activity" evidence=ISS] [GO:0005960 "glycine cleavage complex" evidence=ISS] [GO:0019464 "glycine decarboxylation via glycine cleavage system" evidence=ISS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0006546 "glycine catabolic process" evidence=IMP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] InterPro:IPR003437 InterPro:IPR015421 InterPro:IPR020580 InterPro:IPR020581 Pfam:PF02347 GO:GO:0005739 EMBL:CP002687

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GenomeReviews:CT486007_GR GO:GO:0048046 GO:GO:0009570 GO:GO:0046686 GO:GO:0005515 GO:GO:0030170 InterPro:IPR015424 Gene3D:G3DSA:3.40.640.10 SUPFAM:SSF53383 GO:GO:0009941 GO:GO:0009534 EMBL:AL031804 EMBL:AL161582 GO:GO:0006546 GO:GO:0004375 UniGene:At.24550 HOGENOM:HBG286723 KO:K00281 ProtClustDB:PLN02414 PANTHER:PTHR11773 TIGRFAMs:TIGR00461 EMBL:AY063903 EMBL:AY091186 EMBL:AY042800 EMBL:AY128922 EMBL:AY065004 EMBL:BT001132 EMBL:BT000446 IPI:IPI00536025 PIR:T05309 RefSeq:NP_195027.1 UniGene:At.22214 ProteinModelPortal:Q94B78 SMR:Q94B78 IntAct:Q94B78 STRING:Q94B78 PRIDE:Q94B78 ProMEX:Q94B78 EnsemblPlants:AT4G33010.1 GeneID:829438 KEGG:ath:AT4G33010 GeneFarm:1737 TAIR:At4g33010 InParanoid:Q94B78 OMA:VPMSEYQ PhylomeDB:Q94B78 ArrayExpress:Q94B78 Genevestigator:Q94B78 GermOnline:AT4G33010 Uniprot:Q94B78
Leaf	Isotig00098	196	537	-0.925	1.72E-16	TAIR|locus:2123777 - symbol:GLDP1 "AT4G33010" species:3702 "Arabidopsis thaliana" [GO:0004375 "glycine dehydrogenase (decarboxylating) activity" evidence=ISS] [GO:0005960 "glycine cleavage complex" evidence=ISS] [GO:0019464 "glycine decarboxylation via glycine cleavage system" evidence=ISS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0006546 "glycine catabolic process" evidence=IMP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] InterPro:IPR003437 InterPro:IPR015421 InterPro:IPR020580 InterPro:IPR020581 Pfam:PF02347 GO:GO:0005739 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0048046 GO:GO:0009570 GO:GO:0046686 GO:GO:0005515 GO:GO:0030170 InterPro:IPR015424 Gene3D:G3DSA:3.40.640.10 SUPFAM:SSF53383 GO:GO:0009941 GO:GO:0009534 EMBL:AL031804 EMBL:AL161582 GO:GO:0006546 GO:GO:0004375 UniGene:At.24550 HOGENOM:HBG286723 KO:K00281 ProtClustDB:PLN02414 PANTHER:PTHR11773 TIGRFAMs:TIGR00461 EMBL:AY063903 EMBL:AY091186 EMBL:AY042800 EMBL:AY128922 EMBL:AY065004 EMBL:BT001132 EMBL:BT000446 IPI:IPI00536025 PIR:T05309 RefSeq:NP_195027.1 UniGene:At.22214 ProteinModelPortal:Q94B78 SMR:Q94B78 IntAct:Q94B78 STRING:Q94B78 PRIDE:Q94B78 ProMEX:Q94B78 EnsemblPlants:AT4G33010.1 GeneID:829438 KEGG:ath:AT4G33010 GeneFarm:1737 TAIR:At4g33010 InParanoid:Q94B78 OMA:VPMSEYQ PhylomeDB:Q94B78 ArrayExpress:Q94B78 Genevestigator:Q94B78 GermOnline:AT4G33010 Uniprot:Q94B78
Leaf	Isotig00101	31	163	-1.866	7.56E-15	TAIR|locus:2200868 - symbol:LHCA3 "photosystem I light harvesting complex gene 3" species:3702 "Arabidopsis thaliana" [GO:0009765 "photosynthesis, light harvesting" evidence=IEA] [GO:0015979 "photosynthesis" evidence=ISS] [GO:0016168 "chlorophyll binding" evidence=ISS] [GO:0030076 "light-harvesting complex" evidence=ISS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] InterPro:IPR001344 Pfam:PF00504 EMBL:CP002684 GO:GO:0009535 GO:GO:0010287 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 UniGene:At.2877 EMBL:AC005850 UniGene:At.21403 EMBL:AY059879 EMBL:AY093370 IPI:IPI00532189 PIR:E96640 RefSeq:NP_001185280.1 RefSeq:NP_176347.1 UniGene:At.20472 UniGene:At.71924 UniGene:At.71944 ProteinModelPortal:Q9SY97 SMR:Q9SY97 STRING:Q9SY97 PRIDE:Q9SY97 ProMEX:Q9SY97 EnsemblPlants:AT1G61520.1 EnsemblPlants:AT1G61520.3 GeneID:842446 KEGG:ath:AT1G61520 TAIR:At1g61520 InParanoid:Q9SY97 KO:K08909 OMA:PGSMGKQ PhylomeDB:Q9SY97 ProtClustDB:PLN00048 ArrayExpress:Q9SY97 Genevestigator:Q9SY97 Uniprot:Q9SY97
Leaf	Isotig00102	61	272	-1.628	6.68E-20	TAIR|locus:2200868 - symbol:LHCA3 "photosystem I light harvesting complex gene 3" species:3702 "Arabidopsis thaliana" [GO:0009765 "photosynthesis, light harvesting" evidence=IEA] [GO:0015979 "photosynthesis" evidence=ISS] [GO:0016168 "chlorophyll binding" evidence=ISS] [GO:0030076 "light-harvesting complex" evidence=ISS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] InterPro:IPR001344 Pfam:PF00504 EMBL:CP002684 GO:GO:0009535 GO:GO:0010287 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 UniGene:At.2877 EMBL:AC005850 UniGene:At.21403 EMBL:AY059879 EMBL:AY093370 IPI:IPI00532189 PIR:E96640 RefSeq:NP_001185280.1 RefSeq:NP_176347.1 UniGene:At.20472 UniGene:At.71924 UniGene:At.71944

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						ProteinModelPortal:Q9SY97 SMR:Q9SY97 STRING:Q9SY97 PRIDE:Q9SY97 ProMEX:Q9SY97 EnsemblPlants:AT1G61520.1 EnsemblPlants:AT1G61520.3 GeneID:842446 KEGG:ath:AT1G61520 TAIR:At1g61520 InParanoid:Q9SY97 KO:K08909 OMA:PGSMGKQ PhylomeDB:Q9SY97 ProtClustDB:PLN00048 ArrayExpress:Q9SY97 Genevestigator:Q9SY97 Uniprot:Q9SY97
Leaf	Isotig00103	63	319	-1.811	1.56E-26	TAIR|locus:2200868 - symbol:LHCA3 "photosystem I light harvesting complex gene 3" species:3702 "Arabidopsis thaliana" [GO:0009765 "photosynthesis, light harvesting" evidence=IEA] [GO:0015979 "photosynthesis" evidence=ISS] [GO:0016168 "chlorophyll binding" evidence=ISS] [GO:0030076 "light-harvesting complex" evidence=ISS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] InterPro:IPR001344 Pfam:PF00504 EMBL:CP002684 GO:GO:0009535 GO:GO:0010287 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 UniGene:At.2877 EMBL:AC005850 UniGene:At.21403 EMBL:AY059879 EMBL:AY093370 IPI:IPI00532189 PIR:E96640 RefSeq:NP_001185280.1 RefSeq:NP_176347.1 UniGene:At.20472 UniGene:At.71924 UniGene:At.71944 ProteinModelPortal:Q9SY97 SMR:Q9SY97 STRING:Q9SY97 PRIDE:Q9SY97 ProMEX:Q9SY97 EnsemblPlants:AT1G61520.1 EnsemblPlants:AT1G61520.3 GeneID:842446 KEGG:ath:AT1G61520 TAIR:At1g61520 InParanoid:Q9SY97 KO:K08909 OMA:PGSMGKQ PhylomeDB:Q9SY97 ProtClustDB:PLN00048 ArrayExpress:Q9SY97 Genevestigator:Q9SY97 Uniprot:Q9SY97
Leaf	Isotig00124	31	16	1.483	0.000541208	TAIR|locus:2011415 - symbol:ICME-LIKE1 "AT1G26120" species:3702 "Arabidopsis thaliana" [GO:0004091 "carboxylesterase activity" evidence=IBA] [GO:0008152 "metabolic process" evidence=IBA] [GO:0016787 "hydrolase activity" evidence=IEA] [GO:0000139 "Golgi membrane" evidence=IDA] [GO:0005789 "endoplasmic reticulum membrane" evidence=IDA] InterPro:IPR013094 Pfam:PF07859 GO:GO:0016021 EMBL:CP002684 GO:GO:0000139 GO:GO:0005789 eggNOG:COG0657 EMBL:AC079829 EMBL:AC084221 EMBL:AY070374 EMBL:AY091332 EMBL:AK318861 IPI:IPI00522967 IPI:IPI01023330 PIR:C86387 RefSeq:NP_173937.2 UniGene:At.28380 ProteinModelPortal:Q8VYP9 MEROPS:S09.A21 PRIDE:C0Z2P7 GeneID:839153 KEGG:ath:AT1G26120 TAIR:At1g26120 HOGENOM:HBG316445 InParanoid:Q8VYP9 OMA:RLVPEFM PhylomeDB:Q8VYP9 ProtClustDB:CLSN2718708 Genevestigator:Q8VYP9 GO:GO:0052689 Uniprot:Q8VYP9
Leaf	Isotig00125	31	16	1.483	0.000541208	TAIR|locus:2011415 - symbol:ICME-LIKE1 "AT1G26120" species:3702 "Arabidopsis thaliana" [GO:0004091 "carboxylesterase activity" evidence=IBA] [GO:0008152 "metabolic process" evidence=IBA] [GO:0016787 "hydrolase activity" evidence=IEA] [GO:0000139 "Golgi membrane" evidence=IDA] [GO:0005789 "endoplasmic reticulum membrane" evidence=IDA] InterPro:IPR013094 Pfam:PF07859 GO:GO:0016021 EMBL:CP002684 GO:GO:0000139 GO:GO:0005789 eggNOG:COG0657 EMBL:AC079829 EMBL:AC084221 EMBL:AY070374 EMBL:AY091332 EMBL:AK318861 IPI:IPI00522967 IPI:IPI01023330 PIR:C86387 RefSeq:NP_173937.2 UniGene:At.28380 ProteinModelPortal:Q8VYP9 MEROPS:S09.A21 PRIDE:C0Z2P7 GeneID:839153 KEGG:ath:AT1G26120 TAIR:At1g26120 HOGENOM:HBG316445 InParanoid:Q8VYP9 OMA:RLVPEFM PhylomeDB:Q8VYP9 ProtClustDB:CLSN2718708 Genevestigator:Q8VYP9 GO:GO:0052689 Uniprot:Q8VYP9
Leaf	Isotig00126	31	16	1.483	0.000541208	TAIR|locus:2011415 - symbol:ICME-LIKE1 "AT1G26120" species:3702 "Arabidopsis thaliana" [GO:0004091 "carboxylesterase activity" evidence=IBA] [GO:0008152 "metabolic process" evidence=IBA] [GO:0016787 "hydrolase activity" evidence=IEA] [GO:0000139 "Golgi membrane" evidence=IDA] [GO:0005789 "endoplasmic reticulum membrane" evidence=IDA] InterPro:IPR013094 Pfam:PF07859 GO:GO:0016021 EMBL:CP002684 GO:GO:0000139 GO:GO:0005789 eggNOG:COG0657 EMBL:AC079829 EMBL:AC084221 EMBL:AY070374 EMBL:AY091332 EMBL:AK318861 IPI:IPI00522967 IPI:IPI01023330 PIR:C86387 RefSeq:NP_173937.2 UniGene:At.28380 ProteinModelPortal:Q8VYP9 MEROPS:S09.A21 PRIDE:C0Z2P7 GeneID:839153 KEGG:ath:AT1G26120 TAIR:At1g26120 HOGENOM:HBG316445 InParanoid:Q8VYP9 OMA:RLVPEFM PhylomeDB:Q8VYP9 ProtClustDB:CLSN2718708 Genevestigator:Q8VYP9 GO:GO:0052689 Uniprot:Q8VYP9
Leaf	Isotig00127	32	16	1.529	0.000324709	TAIR|locus:2011415 - symbol:ICME-LIKE1 "AT1G26120" species:3702 "Arabidopsis thaliana" [GO:0004091 "carboxylesterase activity" evidence=IBA] [GO:0008152 "metabolic process" evidence=IBA] [GO:0016787 "hydrolase activity" evidence=IEA] [GO:0000139 "Golgi membrane" evidence=IDA] [GO:0005789 "endoplasmic reticulum membrane" evidence=IDA] InterPro:IPR013094 Pfam:PF07859 GO:GO:0016021 EMBL:CP002684 GO:GO:0000139 GO:GO:0005789 eggNOG:COG0657 EMBL:AC079829 EMBL:AC084221 EMBL:AY070374 EMBL:AY091332 EMBL:AK318861 IPI:IPI00522967 IPI:IPI01023330 PIR:C86387 RefSeq:NP_173937.2 UniGene:At.28380 ProteinModelPortal:Q8VYP9 MEROPS:S09.A21 PRIDE:C0Z2P7 GeneID:839153

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						KEGG:ath:AT1G26120 TAIR:At1g26120 HOGENOM:HBG316445 InParanoid:Q8VYP9 OMA:RLVPEFM PhylomeDB:Q8VYP9 ProtClustDB:CLSN2718708 Genevestigator:Q8VYP9 GO:GO:0052689 Uniprot:Q8VYP9
Leaf	Isotig00128	32	16	1.529	0.000324709	TAIR|locus:2011415 - symbol:ICME-LIKE1 "AT1G26120" species:3702 "Arabidopsis thaliana" [GO:0004091 "carboxylesterase activity" evidence=IBA] [GO:0008152 "metabolic process" evidence=IBA] [GO:0016787 "hydrolase activity" evidence=IEA] [GO:0000139 "Golgi membrane" evidence=IDA] [GO:0005789 "endoplasmic reticulum membrane" evidence=IDA] InterPro:IPR013094 Pfam:PF07859 GO:GO:0016021 EMBL:CP002684 GO:GO:0000139 GO:GO:0005789 eggNOG:COG0657 EMBL:AC079829 EMBL:AC084221 EMBL:AY070374 EMBL:AY091332 EMBL:AK318861 IPI:IPI00522967 IPI:IPI01023330 PIR:C86387 RefSeq:NP_173937.2 UniGene:At.28380 ProteinModelPortal:Q8VYP9 MEROPS:S09.A21 PRIDE:C0Z2P7 GeneID:839153 KEGG:ath:AT1G26120 TAIR:At1g26120 HOGENOM:HBG316445 InParanoid:Q8VYP9 OMA:RLVPEFM PhylomeDB:Q8VYP9 ProtClustDB:CLSN2718708 Genevestigator:Q8VYP9 GO:GO:0052689 Uniprot:Q8VYP9
Leaf	Isotig00129	31	16	1.483	0.000541208	TAIR|locus:2011415 - symbol:ICME-LIKE1 "AT1G26120" species:3702 "Arabidopsis thaliana" [GO:0004091 "carboxylesterase activity" evidence=IBA] [GO:0008152 "metabolic process" evidence=IBA] [GO:0016787 "hydrolase activity" evidence=IEA] [GO:0000139 "Golgi membrane" evidence=IDA] [GO:0005789 "endoplasmic reticulum membrane" evidence=IDA] InterPro:IPR013094 Pfam:PF07859 GO:GO:0016021 EMBL:CP002684 GO:GO:0000139 GO:GO:0005789 eggNOG:COG0657 EMBL:AC079829 EMBL:AC084221 EMBL:AY070374 EMBL:AY091332 EMBL:AK318861 IPI:IPI00522967 IPI:IPI01023330 PIR:C86387 RefSeq:NP_173937.2 UniGene:At.28380 ProteinModelPortal:Q8VYP9 MEROPS:S09.A21 PRIDE:C0Z2P7 GeneID:839153 KEGG:ath:AT1G26120 TAIR:At1g26120 HOGENOM:HBG316445 InParanoid:Q8VYP9 OMA:RLVPEFM PhylomeDB:Q8VYP9 ProtClustDB:CLSN2718708 Genevestigator:Q8VYP9 GO:GO:0052689 Uniprot:Q8VYP9
Leaf	Isotig00130	32	16	1.529	0.000324709	TAIR|locus:2011415 - symbol:ICME-LIKE1 "AT1G26120" species:3702 "Arabidopsis thaliana" [GO:0004091 "carboxylesterase activity" evidence=IBA] [GO:0008152 "metabolic process" evidence=IBA] [GO:0016787 "hydrolase activity" evidence=IEA] [GO:0000139 "Golgi membrane" evidence=IDA] [GO:0005789 "endoplasmic reticulum membrane" evidence=IDA] InterPro:IPR013094 Pfam:PF07859 GO:GO:0016021 EMBL:CP002684 GO:GO:0000139 GO:GO:0005789 eggNOG:COG0657 EMBL:AC079829 EMBL:AC084221 EMBL:AY070374 EMBL:AY091332 EMBL:AK318861 IPI:IPI00522967 IPI:IPI01023330 PIR:C86387 RefSeq:NP_173937.2 UniGene:At.28380 ProteinModelPortal:Q8VYP9 MEROPS:S09.A21 PRIDE:C0Z2P7 GeneID:839153 KEGG:ath:AT1G26120 TAIR:At1g26120 HOGENOM:HBG316445 InParanoid:Q8VYP9 OMA:RLVPEFM PhylomeDB:Q8VYP9 ProtClustDB:CLSN2718708 Genevestigator:Q8VYP9 GO:GO:0052689 Uniprot:Q8VYP9
Leaf	Isotig00131	31	16	1.483	0.000541208	TAIR|locus:2011415 - symbol:ICME-LIKE1 "AT1G26120" species:3702 "Arabidopsis thaliana" [GO:0004091 "carboxylesterase activity" evidence=IBA] [GO:0008152 "metabolic process" evidence=IBA] [GO:0016787 "hydrolase activity" evidence=IEA] [GO:0000139 "Golgi membrane" evidence=IDA] [GO:0005789 "endoplasmic reticulum membrane" evidence=IDA] InterPro:IPR013094 Pfam:PF07859 GO:GO:0016021 EMBL:CP002684 GO:GO:0000139 GO:GO:0005789 eggNOG:COG0657 EMBL:AC079829 EMBL:AC084221 EMBL:AY070374 EMBL:AY091332 EMBL:AK318861 IPI:IPI00522967 IPI:IPI01023330 PIR:C86387 RefSeq:NP_173937.2 UniGene:At.28380 ProteinModelPortal:Q8VYP9 MEROPS:S09.A21 PRIDE:C0Z2P7 GeneID:839153 KEGG:ath:AT1G26120 TAIR:At1g26120 HOGENOM:HBG316445 InParanoid:Q8VYP9 OMA:RLVPEFM PhylomeDB:Q8VYP9 ProtClustDB:CLSN2718708 Genevestigator:Q8VYP9 GO:GO:0052689 Uniprot:Q8VYP9
Leaf	Isotig00132	32	16	1.529	0.000324709	TAIR|locus:2011415 - symbol:ICME-LIKE1 "AT1G26120" species:3702 "Arabidopsis thaliana" [GO:0004091 "carboxylesterase activity" evidence=IBA] [GO:0008152 "metabolic process" evidence=IBA] [GO:0016787 "hydrolase activity" evidence=IEA] [GO:0000139 "Golgi membrane" evidence=IDA] [GO:0005789 "endoplasmic reticulum membrane" evidence=IDA] InterPro:IPR013094 Pfam:PF07859 GO:GO:0016021 EMBL:CP002684 GO:GO:0000139 GO:GO:0005789 eggNOG:COG0657 EMBL:AC079829 EMBL:AC084221 EMBL:AY070374 EMBL:AY091332 EMBL:AK318861 IPI:IPI00522967 IPI:IPI01023330 PIR:C86387 RefSeq:NP_173937.2 UniGene:At.28380 ProteinModelPortal:Q8VYP9 MEROPS:S09.A21 PRIDE:C0Z2P7 GeneID:839153 KEGG:ath:AT1G26120 TAIR:At1g26120 HOGENOM:HBG316445 InParanoid:Q8VYP9 OMA:RLVPEFM PhylomeDB:Q8VYP9 ProtClustDB:CLSN2718708 Genevestigator:Q8VYP9 GO:GO:0052689 Uniprot:Q8VYP9
Leaf	Isotig00133	31	16	1.483	0.000541208	TAIR|locus:2011415 - symbol:ICME-LIKE1 "AT1G26120" species:3702 "Arabidopsis thaliana" [GO:0004091 "carboxylesterase activity" evidence=IBA] [GO:0008152 "metabolic process" evidence=IBA] [GO:0016787 "hydrolase activity" evidence=IEA] [GO:0000139 "Golgi membrane" evidence=IDA] [GO:0005789 "endoplasmic reticulum membrane" evidence=IDA] InterPro:IPR013094 Pfam:PF07859 GO:GO:0016021 EMBL:CP002684 GO:GO:0000139 GO:GO:0005789 eggNOG:COG0657 EMBL:AC079829 EMBL:AC084221 EMBL:AY070374

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EMBL:AY091332 EMBL:AK318861 IPI:IPI00522967 IPI:IPI01023330 PIR:C86387 RefSeq:NP_173937.2 UniGene:At.28380 ProteinModelPortal:Q8VYP9 MEROPS:S09.A21 PRIDE:C0Z2P7 GeneID:839153 KEGG:ath:AT1G26120 TAIR:At1g26120 HOGENOM:HBG316445 InParanoid:Q8VYP9 OMA:RLVPEFM PhylomeDB:Q8VYP9 ProtClustDB:CLSN2718708 Genevestigator:Q8VYP9 GO:GO:0052689 Uniprot:Q8VYP9
Leaf	Isotig00134	32	16	1.529	0.000324709	TAIR|locus:2011415 - symbol:ICME-LIKE1 "AT1G26120" species:3702 "Arabidopsis thaliana" [GO:0004091 "carboxylesterase activity" evidence=IBA] [GO:0008152 "metabolic process" evidence=IBA] [GO:0016787 "hydrolase activity" evidence=IEA] [GO:0000139 "Golgi membrane" evidence=IDA] [GO:0005789 "endoplasmic reticulum membrane" evidence=IDA] InterPro:IPR013094 Pfam:PF07859 GO:GO:0016021 EMBL:CP002684 GO:GO:0000139 GO:GO:0005789 eggNOG:COG0657 EMBL:AC079829 EMBL:AC084221 EMBL:AY070374 EMBL:AY091332 EMBL:AK318861 IPI:IPI00522967 IPI:IPI01023330 PIR:C86387 RefSeq:NP_173937.2 UniGene:At.28380 ProteinModelPortal:Q8VYP9 MEROPS:S09.A21 PRIDE:C0Z2P7 GeneID:839153 KEGG:ath:AT1G26120 TAIR:At1g26120 HOGENOM:HBG316445 InParanoid:Q8VYP9 OMA:RLVPEFM PhylomeDB:Q8VYP9 ProtClustDB:CLSN2718708 Genevestigator:Q8VYP9 GO:GO:0052689 Uniprot:Q8VYP9
Leaf	Isotig00135	32	16	1.529	0.000324709	TAIR|locus:2011415 - symbol:ICME-LIKE1 "AT1G26120" species:3702 "Arabidopsis thaliana" [GO:0004091 "carboxylesterase activity" evidence=IBA] [GO:0008152 "metabolic process" evidence=IBA] [GO:0016787 "hydrolase activity" evidence=IEA] [GO:0000139 "Golgi membrane" evidence=IDA] [GO:0005789 "endoplasmic reticulum membrane" evidence=IDA] InterPro:IPR013094 Pfam:PF07859 GO:GO:0016021 EMBL:CP002684 GO:GO:0000139 GO:GO:0005789 eggNOG:COG0657 EMBL:AC079829 EMBL:AC084221 EMBL:AY070374 EMBL:AY091332 EMBL:AK318861 IPI:IPI00522967 IPI:IPI01023330 PIR:C86387 RefSeq:NP_173937.2 UniGene:At.28380 ProteinModelPortal:Q8VYP9 MEROPS:S09.A21 PRIDE:C0Z2P7 GeneID:839153 KEGG:ath:AT1G26120 TAIR:At1g26120 HOGENOM:HBG316445 InParanoid:Q8VYP9 OMA:RLVPEFM PhylomeDB:Q8VYP9 ProtClustDB:CLSN2718708 Genevestigator:Q8VYP9 GO:GO:0052689 Uniprot:Q8VYP9
Leaf	Isotig00136	31	16	1.483	0.000541208	TAIR|locus:2011415 - symbol:ICME-LIKE1 "AT1G26120" species:3702 "Arabidopsis thaliana" [GO:0004091 "carboxylesterase activity" evidence=IBA] [GO:0008152 "metabolic process" evidence=IBA] [GO:0016787 "hydrolase activity" evidence=IEA] [GO:0000139 "Golgi membrane" evidence=IDA] [GO:0005789 "endoplasmic reticulum membrane" evidence=IDA] InterPro:IPR013094 Pfam:PF07859 GO:GO:0016021 EMBL:CP002684 GO:GO:0000139 GO:GO:0005789 eggNOG:COG0657 EMBL:AC079829 EMBL:AC084221 EMBL:AY070374 EMBL:AY091332 EMBL:AK318861 IPI:IPI00522967 IPI:IPI01023330 PIR:C86387 RefSeq:NP_173937.2 UniGene:At.28380 ProteinModelPortal:Q8VYP9 MEROPS:S09.A21 PRIDE:C0Z2P7 GeneID:839153 KEGG:ath:AT1G26120 TAIR:At1g26120 HOGENOM:HBG316445 InParanoid:Q8VYP9 OMA:RLVPEFM PhylomeDB:Q8VYP9 ProtClustDB:CLSN2718708 Genevestigator:Q8VYP9 GO:GO:0052689 Uniprot:Q8VYP9
Leaf	Isotig00137	32	16	1.529	0.000324709	TAIR|locus:2011415 - symbol:ICME-LIKE1 "AT1G26120" species:3702 "Arabidopsis thaliana" [GO:0004091 "carboxylesterase activity" evidence=IBA] [GO:0008152 "metabolic process" evidence=IBA] [GO:0016787 "hydrolase activity" evidence=IEA] [GO:0000139 "Golgi membrane" evidence=IDA] [GO:0005789 "endoplasmic reticulum membrane" evidence=IDA] InterPro:IPR013094 Pfam:PF07859 GO:GO:0016021 EMBL:CP002684 GO:GO:0000139 GO:GO:0005789 eggNOG:COG0657 EMBL:AC079829 EMBL:AC084221 EMBL:AY070374 EMBL:AY091332 EMBL:AK318861 IPI:IPI00522967 IPI:IPI01023330 PIR:C86387 RefSeq:NP_173937.2 UniGene:At.28380 ProteinModelPortal:Q8VYP9 MEROPS:S09.A21 PRIDE:C0Z2P7 GeneID:839153 KEGG:ath:AT1G26120 TAIR:At1g26120 HOGENOM:HBG316445 InParanoid:Q8VYP9 OMA:RLVPEFM PhylomeDB:Q8VYP9 ProtClustDB:CLSN2718708 Genevestigator:Q8VYP9 GO:GO:0052689 Uniprot:Q8VYP9
Leaf	Isotig00138	32	16	1.529	0.000324709	TAIR|locus:2011415 - symbol:ICME-LIKE1 "AT1G26120" species:3702 "Arabidopsis thaliana" [GO:0004091 "carboxylesterase activity" evidence=IBA] [GO:0008152 "metabolic process" evidence=IBA] [GO:0016787 "hydrolase activity" evidence=IEA] [GO:0000139 "Golgi membrane" evidence=IDA] [GO:0005789 "endoplasmic reticulum membrane" evidence=IDA] InterPro:IPR013094 Pfam:PF07859 GO:GO:0016021 EMBL:CP002684 GO:GO:0000139 GO:GO:0005789 eggNOG:COG0657 EMBL:AC079829 EMBL:AC084221 EMBL:AY070374 EMBL:AY091332 EMBL:AK318861 IPI:IPI00522967 IPI:IPI01023330 PIR:C86387 RefSeq:NP_173937.2 UniGene:At.28380 ProteinModelPortal:Q8VYP9 MEROPS:S09.A21 PRIDE:C0Z2P7 GeneID:839153 KEGG:ath:AT1G26120 TAIR:At1g26120 HOGENOM:HBG316445 InParanoid:Q8VYP9 OMA:RLVPEFM PhylomeDB:Q8VYP9 ProtClustDB:CLSN2718708 Genevestigator:Q8VYP9 GO:GO:0052689 Uniprot:Q8VYP9
Leaf	Isotig00139	31	16	1.483	0.000541208	TAIR|locus:2011415 - symbol:ICME-LIKE1 "AT1G26120" species:3702 "Arabidopsis thaliana" [GO:0004091 "carboxylesterase activity" evidence=IBA] [GO:0008152 "metabolic process" evidence=IBA] [GO:0016787 "hydrolase activity" evidence=IEA] [GO:0000139 "Golgi membrane" evidence=IDA] [GO:0005789 "endoplasmic

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						reticulum membrane" evidence=IDA] InterPro:IPR013094 Pfam:PF07859 GO:GO:0016021 EMBL:CP002684 GO:GO:0000139 GO:GO:0005789 eggNOG:COG0657 EMBL:AC079829 EMBL:AC084221 EMBL:AY070374 EMBL:AY091332 EMBL:AK318861 IPI:IPI00522967 IPI:IPI01023330 PIR:C86387 RefSeq:NP_173937.2 UniGene:At.28380 ProteinModelPortal:Q8VYP9 MEROPS:S09.A21 PRIDE:C0Z2P7 GeneID:839153 KEGG:ath:AT1G26120 TAIR:At1g26120 HOGENOM:HBG316445 InParanoid:Q8VYP9 OMA:RLVPEFM PhylomeDB:Q8VYP9 ProtClustDB:CLSN2718708 Genevestigator:Q8VYP9 GO:GO:0052689 Uniprot:Q8VYP9
Leaf	Isotig00140	26	6	2.644	3.85E-06	TAIR|locus:2011415 - symbol:ICME-LIKE1 "AT1G26120" species:3702 "Arabidopsis thaliana" [GO:0004091 "carboxylesterase activity" evidence=IBA] [GO:0008152 "metabolic process" evidence=IBA] [GO:0016787 "hydrolase activity" evidence=IEA] [GO:0000139 "Golgi membrane" evidence=IDA] [GO:0005789 "endoplasmic reticulum membrane" evidence=IDA] InterPro:IPR013094 Pfam:PF07859 GO:GO:0016021 EMBL:CP002684 GO:GO:0000139 GO:GO:0005789 eggNOG:COG0657 EMBL:AC079829 EMBL:AC084221 EMBL:AY070374 EMBL:AY091332 EMBL:AK318861 IPI:IPI00522967 IPI:IPI01023330 PIR:C86387 RefSeq:NP_173937.2 UniGene:At.28380 ProteinModelPortal:Q8VYP9 MEROPS:S09.A21 PRIDE:C0Z2P7 GeneID:839153 KEGG:ath:AT1G26120 TAIR:At1g26120 HOGENOM:HBG316445 InParanoid:Q8VYP9 OMA:RLVPEFM PhylomeDB:Q8VYP9 ProtClustDB:CLSN2718708 Genevestigator:Q8VYP9 GO:GO:0052689 Uniprot:Q8VYP9
Leaf	Isotig00141	26	6	2.644	3.85E-06	TAIR|locus:2011415 - symbol:ICME-LIKE1 "AT1G26120" species:3702 "Arabidopsis thaliana" [GO:0004091 "carboxylesterase activity" evidence=IBA] [GO:0008152 "metabolic process" evidence=IBA] [GO:0016787 "hydrolase activity" evidence=IEA] [GO:0000139 "Golgi membrane" evidence=IDA] [GO:0005789 "endoplasmic reticulum membrane" evidence=IDA] InterPro:IPR013094 Pfam:PF07859 GO:GO:0016021 EMBL:CP002684 GO:GO:0000139 GO:GO:0005789 eggNOG:COG0657 EMBL:AC079829 EMBL:AC084221 EMBL:AY070374 EMBL:AY091332 EMBL:AK318861 IPI:IPI00522967 IPI:IPI01023330 PIR:C86387 RefSeq:NP_173937.2 UniGene:At.28380 ProteinModelPortal:Q8VYP9 MEROPS:S09.A21 PRIDE:C0Z2P7 GeneID:839153 KEGG:ath:AT1G26120 TAIR:At1g26120 HOGENOM:HBG316445 InParanoid:Q8VYP9 OMA:RLVPEFM PhylomeDB:Q8VYP9 ProtClustDB:CLSN2718708 Genevestigator:Q8VYP9 GO:GO:0052689 Uniprot:Q8VYP9
Leaf	Isotig00142	26	6	2.644	3.85E-06	TAIR|locus:2011415 - symbol:ICME-LIKE1 "AT1G26120" species:3702 "Arabidopsis thaliana" [GO:0004091 "carboxylesterase activity" evidence=IBA] [GO:0008152 "metabolic process" evidence=IBA] [GO:0016787 "hydrolase activity" evidence=IEA] [GO:0000139 "Golgi membrane" evidence=IDA] [GO:0005789 "endoplasmic reticulum membrane" evidence=IDA] InterPro:IPR013094 Pfam:PF07859 GO:GO:0016021 EMBL:CP002684 GO:GO:0000139 GO:GO:0005789 eggNOG:COG0657 EMBL:AC079829 EMBL:AC084221 EMBL:AY070374 EMBL:AY091332 EMBL:AK318861 IPI:IPI00522967 IPI:IPI01023330 PIR:C86387 RefSeq:NP_173937.2 UniGene:At.28380 ProteinModelPortal:Q8VYP9 MEROPS:S09.A21 PRIDE:C0Z2P7 GeneID:839153 KEGG:ath:AT1G26120 TAIR:At1g26120 HOGENOM:HBG316445 InParanoid:Q8VYP9 OMA:RLVPEFM PhylomeDB:Q8VYP9 ProtClustDB:CLSN2718708 Genevestigator:Q8VYP9 GO:GO:0052689 Uniprot:Q8VYP9
Leaf	Isotig00143	26	6	2.644	3.85E-06	TAIR|locus:2011415 - symbol:ICME-LIKE1 "AT1G26120" species:3702 "Arabidopsis thaliana" [GO:0004091 "carboxylesterase activity" evidence=IBA] [GO:0008152 "metabolic process" evidence=IBA] [GO:0016787 "hydrolase activity" evidence=IEA] [GO:0000139 "Golgi membrane" evidence=IDA] [GO:0005789 "endoplasmic reticulum membrane" evidence=IDA] InterPro:IPR013094 Pfam:PF07859 GO:GO:0016021 EMBL:CP002684 GO:GO:0000139 GO:GO:0005789 eggNOG:COG0657 EMBL:AC079829 EMBL:AC084221 EMBL:AY070374 EMBL:AY091332 EMBL:AK318861 IPI:IPI00522967 IPI:IPI01023330 PIR:C86387 RefSeq:NP_173937.2 UniGene:At.28380 ProteinModelPortal:Q8VYP9 MEROPS:S09.A21 PRIDE:C0Z2P7 GeneID:839153 KEGG:ath:AT1G26120 TAIR:At1g26120 HOGENOM:HBG316445 InParanoid:Q8VYP9 OMA:RLVPEFM PhylomeDB:Q8VYP9 ProtClustDB:CLSN2718708 Genevestigator:Q8VYP9 GO:GO:0052689 Uniprot:Q8VYP9
Leaf	Isotig00144	67	306	-1.662	8.07E-23	TAIR|locus:2173234 - symbol:GUN5 "GENOMES UNCOUPLED 5" species:3702 "Arabidopsis thaliana" [GO:0009058 "biosynthetic process" evidence=IEA] [GO:0015995 "chlorophyll biosynthetic process" evidence=IEA] [GO:0009706 "chloroplast inner membrane" evidence=NAS] [GO:0016851 "magnesium chelatase activity" evidence=ISS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0010007 "magnesium chelatase complex" evidence=TAS] InterPro:IPR003672 InterPro:IPR011771 InterPro:IPR016040 InterPro:IPR022571 Pfam:PF02514 Pfam:PF11965 GO:GO:0005739 EMBL:CP002688 GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 EMBL:AB006704 GO:GO:0009706 GO:GO:0015995 GO:GO:0010007 GO:GO:0016851 EMBL:AY070133 EMBL:BT002311 IPI:IPI00548533 RefSeq:NP_196867.1 UniGene:At.23621 STRING:Q9FNB0 PRIDE:Q9FNB0 EnsemblPlants:AT5G13630.1 GeneID:831207

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						KEGG:ath:AT5G13630 TAIR:At5g13630 InParanoid:Q9FNB0 KO:K03403 OMA:VLWGSDN PhylomeDB:Q9FNB0 ProtClustDB:PLN03069 Genevestigator:Q9FNB0 TIGRFAMs:TIGR02025 Uniprot:Q9FNB0
Leaf	Isotig00145	69	316	-1.666	1.38E-23	TAIR|locus:2173234 - symbol:GUN5 "GENOMES UNCOUPLED 5" species:3702 "Arabidopsis thaliana" [GO:0009058 "biosynthetic process" evidence=IEA] [GO:0015995 "chlorophyll biosynthetic process" evidence=IEA] [GO:0009706 "chloroplast inner membrane" evidence=NAS] [GO:0016851 "magnesium chelatase activity" evidence=ISS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0010007 "magnesium chelatase complex" evidence=TAS] InterPro:IPR003672 InterPro:IPR011771 InterPro:IPR016040 InterPro:IPR022571 Pfam:PF02514 Pfam:PF11965 GO:GO:0005739 EMBL:CP002688 GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 EMBL:AB006704 GO:GO:0009706 GO:GO:0015995 GO:GO:0010007 GO:GO:0016851 EMBL:AY070133 EMBL:BT002311 IPI:IPI00548533 RefSeq:NP_196867.1 UniGene:At.23621 STRING:Q9FNB0 PRIDE:Q9FNB0 EnsemblPlants:AT5G13630.1 GeneID:831207 KEGG:ath:AT5G13630 TAIR:At5g13630 InParanoid:Q9FNB0 KO:K03403 OMA:VLWGSDN PhylomeDB:Q9FNB0 ProtClustDB:PLN03069 Genevestigator:Q9FNB0 TIGRFAMs:TIGR02025 Uniprot:Q9FNB0
Leaf	Isotig00146	70	307	-1.604	8.00E-22	TAIR|locus:2173234 - symbol:GUN5 "GENOMES UNCOUPLED 5" species:3702 "Arabidopsis thaliana" [GO:0009058 "biosynthetic process" evidence=IEA] [GO:0015995 "chlorophyll biosynthetic process" evidence=IEA] [GO:0009706 "chloroplast inner membrane" evidence=NAS] [GO:0016851 "magnesium chelatase activity" evidence=ISS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0010007 "magnesium chelatase complex" evidence=TAS] InterPro:IPR003672 InterPro:IPR011771 InterPro:IPR016040 InterPro:IPR022571 Pfam:PF02514 Pfam:PF11965 GO:GO:0005739 EMBL:CP002688 GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 EMBL:AB006704 GO:GO:0009706 GO:GO:0015995 GO:GO:0010007 GO:GO:0016851 EMBL:AY070133 EMBL:BT002311 IPI:IPI00548533 RefSeq:NP_196867.1 UniGene:At.23621 STRING:Q9FNB0 PRIDE:Q9FNB0 EnsemblPlants:AT5G13630.1 GeneID:831207 KEGG:ath:AT5G13630 TAIR:At5g13630 InParanoid:Q9FNB0 KO:K03403 OMA:VLWGSDN PhylomeDB:Q9FNB0 ProtClustDB:PLN03069 Genevestigator:Q9FNB0 TIGRFAMs:TIGR02025 Uniprot:Q9FNB0
Leaf	Isotig00147	67	305	-1.658	1.15E-22	TAIR|locus:2173234 - symbol:GUN5 "GENOMES UNCOUPLED 5" species:3702 "Arabidopsis thaliana" [GO:0009058 "biosynthetic process" evidence=IEA] [GO:0015995 "chlorophyll biosynthetic process" evidence=IEA] [GO:0009706 "chloroplast inner membrane" evidence=NAS] [GO:0016851 "magnesium chelatase activity" evidence=ISS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0010007 "magnesium chelatase complex" evidence=TAS] InterPro:IPR003672 InterPro:IPR011771 InterPro:IPR016040 InterPro:IPR022571 Pfam:PF02514 Pfam:PF11965 GO:GO:0005739 EMBL:CP002688 GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 EMBL:AB006704 GO:GO:0009706 GO:GO:0015995 GO:GO:0010007 GO:GO:0016851 EMBL:AY070133 EMBL:BT002311 IPI:IPI00548533 RefSeq:NP_196867.1 UniGene:At.23621 STRING:Q9FNB0 PRIDE:Q9FNB0 EnsemblPlants:AT5G13630.1 GeneID:831207 KEGG:ath:AT5G13630 TAIR:At5g13630 InParanoid:Q9FNB0 KO:K03403 OMA:VLWGSDN PhylomeDB:Q9FNB0 ProtClustDB:PLN03069 Genevestigator:Q9FNB0 TIGRFAMs:TIGR02025 Uniprot:Q9FNB0
Leaf	Isotig00148	72	317	-1.609	1.38E-22	TAIR|locus:2173234 - symbol:GUN5 "GENOMES UNCOUPLED 5" species:3702 "Arabidopsis thaliana" [GO:0009058 "biosynthetic process" evidence=IEA] [GO:0015995 "chlorophyll biosynthetic process" evidence=IEA] [GO:0009706 "chloroplast inner membrane" evidence=NAS] [GO:0016851 "magnesium chelatase activity" evidence=ISS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0010007 "magnesium chelatase complex" evidence=TAS] InterPro:IPR003672 InterPro:IPR011771 InterPro:IPR016040 InterPro:IPR022571 Pfam:PF02514 Pfam:PF11965 GO:GO:0005739 EMBL:CP002688 GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 EMBL:AB006704 GO:GO:0009706 GO:GO:0015995 GO:GO:0010007 GO:GO:0016851 EMBL:AY070133 EMBL:BT002311 IPI:IPI00548533 RefSeq:NP_196867.1 UniGene:At.23621 STRING:Q9FNB0 PRIDE:Q9FNB0 EnsemblPlants:AT5G13630.1 GeneID:831207 KEGG:ath:AT5G13630 TAIR:At5g13630 InParanoid:Q9FNB0 KO:K03403 OMA:VLWGSDN PhylomeDB:Q9FNB0 ProtClustDB:PLN03069 Genevestigator:Q9FNB0 TIGRFAMs:TIGR02025 Uniprot:Q9FNB0
Leaf	Isotig00149	69	315	-1.662	1.97E-23	TAIR|locus:2173234 - symbol:GUN5 "GENOMES UNCOUPLED 5" species:3702 "Arabidopsis thaliana" [GO:0009058 "biosynthetic process" evidence=IEA] [GO:0015995 "chlorophyll biosynthetic process" evidence=IEA] [GO:0009706 "chloroplast inner membrane" evidence=NAS] [GO:0016851 "magnesium chelatase activity" evidence=ISS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0010007 "magnesium chelatase complex" evidence=TAS] InterPro:IPR003672 InterPro:IPR011771 InterPro:IPR016040 InterPro:IPR022571 Pfam:PF02514 Pfam:PF11965 GO:GO:0005739 EMBL:CP002688

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 EMBL:AB006704 GO:GO:0009706 GO:GO:0015995 GO:GO:0010007 GO:GO:0016851 EMBL:AY070133 EMBL:BT002311 IPI:IPI00548533 RefSeq:NP_196867.1 UniGene:At.23621 STRING:Q9FNB0 PRIDE:Q9FNB0 EnsemblPlants:AT5G13630.1 GeneID:831207 KEGG:ath:AT5G13630 TAIR:At5g13630 InParanoid:Q9FNB0 KO:K03403 OMA:VLWGSDN PhylomeDB:Q9FNB0 ProtClustDB:PLN03069 Genevestigator:Q9FNB0 TIGRFAMs:TIGR02025 Uniprot:Q9FNB0
Leaf	Isotig00150	70	306	-1.599	1.13E-21	TAIR|locus:2173234 - symbol:GUN5 "GENOMES UNCOUPLED 5" species:3702 "Arabidopsis thaliana" [GO:0009058 "biosynthetic process" evidence=IEA] [GO:0015995 "chlorophyll biosynthetic process" evidence=IEA] [GO:0009706 "chloroplast inner membrane" evidence=NAS] [GO:0016851 "magnesium chelatase activity" evidence=ISS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0010007 "magnesium chelatase complex" evidence=TAS] InterPro:IPR003672 InterPro:IPR011771 InterPro:IPR016040 InterPro:IPR022571 Pfam:PF02514 Pfam:PF11965 GO:GO:0005739 EMBL:CP002688 GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 EMBL:AB006704 GO:GO:0009706 GO:GO:0015995 GO:GO:0010007 GO:GO:0016851 EMBL:AY070133 EMBL:BT002311 IPI:IPI00548533 RefSeq:NP_196867.1 UniGene:At.23621 STRING:Q9FNB0 PRIDE:Q9FNB0 EnsemblPlants:AT5G13630.1 GeneID:831207 KEGG:ath:AT5G13630 TAIR:At5g13630 InParanoid:Q9FNB0 KO:K03403 OMA:VLWGSDN PhylomeDB:Q9FNB0 ProtClustDB:PLN03069 Genevestigator:Q9FNB0 TIGRFAMs:TIGR02025 Uniprot:Q9FNB0
Leaf	Isotig00151	72	316	-1.605	1.95E-22	TAIR|locus:2173234 - symbol:GUN5 "GENOMES UNCOUPLED 5" species:3702 "Arabidopsis thaliana" [GO:0009058 "biosynthetic process" evidence=IEA] [GO:0015995 "chlorophyll biosynthetic process" evidence=IEA] [GO:0009706 "chloroplast inner membrane" evidence=NAS] [GO:0016851 "magnesium chelatase activity" evidence=ISS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0010007 "magnesium chelatase complex" evidence=TAS] InterPro:IPR003672 InterPro:IPR011771 InterPro:IPR016040 InterPro:IPR022571 Pfam:PF02514 Pfam:PF11965 GO:GO:0005739 EMBL:CP002688 GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 EMBL:AB006704 GO:GO:0009706 GO:GO:0015995 GO:GO:0010007 GO:GO:0016851 EMBL:AY070133 EMBL:BT002311 IPI:IPI00548533 RefSeq:NP_196867.1 UniGene:At.23621 STRING:Q9FNB0 PRIDE:Q9FNB0 EnsemblPlants:AT5G13630.1 GeneID:831207 KEGG:ath:AT5G13630 TAIR:At5g13630 InParanoid:Q9FNB0 KO:K03403 OMA:VLWGSDN PhylomeDB:Q9FNB0 ProtClustDB:PLN03069 Genevestigator:Q9FNB0 TIGRFAMs:TIGR02025 Uniprot:Q9FNB0
Leaf	Isotig00152	66	286	-1.587	3.82E-20	TAIR|locus:2173234 - symbol:GUN5 "GENOMES UNCOUPLED 5" species:3702 "Arabidopsis thaliana" [GO:0009058 "biosynthetic process" evidence=IEA] [GO:0015995 "chlorophyll biosynthetic process" evidence=IEA] [GO:0009706 "chloroplast inner membrane" evidence=NAS] [GO:0016851 "magnesium chelatase activity" evidence=ISS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0010007 "magnesium chelatase complex" evidence=TAS] InterPro:IPR003672 InterPro:IPR011771 InterPro:IPR016040 InterPro:IPR022571 Pfam:PF02514 Pfam:PF11965 GO:GO:0005739 EMBL:CP002688 GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 EMBL:AB006704 GO:GO:0009706 GO:GO:0015995 GO:GO:0010007 GO:GO:0016851 EMBL:AY070133 EMBL:BT002311 IPI:IPI00548533 RefSeq:NP_196867.1 UniGene:At.23621 STRING:Q9FNB0 PRIDE:Q9FNB0 EnsemblPlants:AT5G13630.1 GeneID:831207 KEGG:ath:AT5G13630 TAIR:At5g13630 InParanoid:Q9FNB0 KO:K03403 OMA:VLWGSDN PhylomeDB:Q9FNB0 ProtClustDB:PLN03069 Genevestigator:Q9FNB0 TIGRFAMs:TIGR02025 Uniprot:Q9FNB0
Leaf	Isotig00153	68	296	-1.593	6.58E-21	TAIR|locus:2173234 - symbol:GUN5 "GENOMES UNCOUPLED 5" species:3702 "Arabidopsis thaliana" [GO:0009058 "biosynthetic process" evidence=IEA] [GO:0015995 "chlorophyll biosynthetic process" evidence=IEA] [GO:0009706 "chloroplast inner membrane" evidence=NAS] [GO:0016851 "magnesium chelatase activity" evidence=ISS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0010007 "magnesium chelatase complex" evidence=TAS] InterPro:IPR003672 InterPro:IPR011771 InterPro:IPR016040 InterPro:IPR022571 Pfam:PF02514 Pfam:PF11965 GO:GO:0005739 EMBL:CP002688 GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 EMBL:AB006704 GO:GO:0009706 GO:GO:0015995 GO:GO:0010007 GO:GO:0016851 EMBL:AY070133 EMBL:BT002311 IPI:IPI00548533 RefSeq:NP_196867.1 UniGene:At.23621 STRING:Q9FNB0 PRIDE:Q9FNB0 EnsemblPlants:AT5G13630.1 GeneID:831207 KEGG:ath:AT5G13630 TAIR:At5g13630 InParanoid:Q9FNB0 KO:K03403 OMA:VLWGSDN PhylomeDB:Q9FNB0 ProtClustDB:PLN03069 Genevestigator:Q9FNB0 TIGRFAMs:TIGR02025 Uniprot:Q9FNB0
Leaf	Isotig00154	42	227	-1.905	1.32E-20	TAIR|locus:2173234 - symbol:GUN5 "GENOMES UNCOUPLED 5" species:3702 "Arabidopsis thaliana" [GO:0009058 "biosynthetic process" evidence=IEA] [GO:0015995 "chlorophyll biosynthetic process" evidence=IEA] [GO:0009706 "chloroplast inner membrane" evidence=NAS] [GO:0016851 "magnesium chelatase activity"

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						evidence=ISS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0010007 "magnesium chelatase complex" evidence=TAS] InterPro:IPR003672 InterPro:IPR011771 InterPro:IPR016040 InterPro:IPR022571 Pfam:PF02514 Pfam:PF11965 GO:GO:0005739 EMBL:CP002688 GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 EMBL:AB006704 GO:GO:0009706 GO:GO:0015995 GO:GO:0010007 GO:GO:0016851 EMBL:AY070133 EMBL:BT002311 IPI:IPI00548533 RefSeq:NP_196867.1 UniGene:At.23621 STRING:Q9FNB0 PRIDE:Q9FNB0 EnsemblPlants:AT5G13630.1 GeneID:831207 KEGG:ath:AT5G13630 TAIR:At5g13630 InParanoid:Q9FNB0 KO:K03403 OMA:VLWGSDN PhylomeDB:Q9FNB0 ProtClustDB:PLN03069 Genevestigator:Q9FNB0 TIGRFAMs:TIGR02025 Uniprot:Q9FNB0
Leaf	Isotig00155	66	285	-1.581	5.40E-20	TAIR|locus:2173234 - symbol:GUN5 "GENOMES UNCOUPLED 5" species:3702 "Arabidopsis thaliana" [GO:0009058 "biosynthetic process" evidence=IEA] [GO:0015995 "chlorophyll biosynthetic process" evidence=IEA] [GO:0009706 "chloroplast inner membrane" evidence=NAS] [GO:0016851 "magnesium chelatase activity" evidence=ISS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0010007 "magnesium chelatase complex" evidence=TAS] InterPro:IPR003672 InterPro:IPR011771 InterPro:IPR016040 InterPro:IPR022571 Pfam:PF02514 Pfam:PF11965 GO:GO:0005739 EMBL:CP002688 GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 EMBL:AB006704 GO:GO:0009706 GO:GO:0015995 GO:GO:0010007 GO:GO:0016851 EMBL:AY070133 EMBL:BT002311 IPI:IPI00548533 RefSeq:NP_196867.1 UniGene:At.23621 STRING:Q9FNB0 PRIDE:Q9FNB0 EnsemblPlants:AT5G13630.1 GeneID:831207 KEGG:ath:AT5G13630 TAIR:At5g13630 InParanoid:Q9FNB0 KO:K03403 OMA:VLWGSDN PhylomeDB:Q9FNB0 ProtClustDB:PLN03069 Genevestigator:Q9FNB0 TIGRFAMs:TIGR02025 Uniprot:Q9FNB0
Leaf	Isotig00156	45	228	-1.812	1.97E-19	TAIR|locus:2173234 - symbol:GUN5 "GENOMES UNCOUPLED 5" species:3702 "Arabidopsis thaliana" [GO:0009058 "biosynthetic process" evidence=IEA] [GO:0015995 "chlorophyll biosynthetic process" evidence=IEA] [GO:0009706 "chloroplast inner membrane" evidence=NAS] [GO:0016851 "magnesium chelatase activity" evidence=ISS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0010007 "magnesium chelatase complex" evidence=TAS] InterPro:IPR003672 InterPro:IPR011771 InterPro:IPR016040 InterPro:IPR022571 Pfam:PF02514 Pfam:PF11965 GO:GO:0005739 EMBL:CP002688 GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 EMBL:AB006704 GO:GO:0009706 GO:GO:0015995 GO:GO:0010007 GO:GO:0016851 EMBL:AY070133 EMBL:BT002311 IPI:IPI00548533 RefSeq:NP_196867.1 UniGene:At.23621 STRING:Q9FNB0 PRIDE:Q9FNB0 EnsemblPlants:AT5G13630.1 GeneID:831207 KEGG:ath:AT5G13630 TAIR:At5g13630 InParanoid:Q9FNB0 KO:K03403 OMA:VLWGSDN PhylomeDB:Q9FNB0 ProtClustDB:PLN03069 Genevestigator:Q9FNB0 TIGRFAMs:TIGR02025 Uniprot:Q9FNB0
Leaf	Isotig00157	68	295	-1.588	9.31E-21	TAIR|locus:2173234 - symbol:GUN5 "GENOMES UNCOUPLED 5" species:3702 "Arabidopsis thaliana" [GO:0009058 "biosynthetic process" evidence=IEA] [GO:0015995 "chlorophyll biosynthetic process" evidence=IEA] [GO:0009706 "chloroplast inner membrane" evidence=NAS] [GO:0016851 "magnesium chelatase activity" evidence=ISS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0010007 "magnesium chelatase complex" evidence=TAS] InterPro:IPR003672 InterPro:IPR011771 InterPro:IPR016040 InterPro:IPR022571 Pfam:PF02514 Pfam:PF11965 GO:GO:0005739 EMBL:CP002688 GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 EMBL:AB006704 GO:GO:0009706 GO:GO:0015995 GO:GO:0010007 GO:GO:0016851 EMBL:AY070133 EMBL:BT002311 IPI:IPI00548533 RefSeq:NP_196867.1 UniGene:At.23621 STRING:Q9FNB0 PRIDE:Q9FNB0 EnsemblPlants:AT5G13630.1 GeneID:831207 KEGG:ath:AT5G13630 TAIR:At5g13630 InParanoid:Q9FNB0 KO:K03403 OMA:VLWGSDN PhylomeDB:Q9FNB0 ProtClustDB:PLN03069 Genevestigator:Q9FNB0 TIGRFAMs:TIGR02025 Uniprot:Q9FNB0
Leaf	Isotig00158	42	226	-1.899	1.95E-20	TAIR|locus:2173234 - symbol:GUN5 "GENOMES UNCOUPLED 5" species:3702 "Arabidopsis thaliana" [GO:0009058 "biosynthetic process" evidence=IEA] [GO:0015995 "chlorophyll biosynthetic process" evidence=IEA] [GO:0009706 "chloroplast inner membrane" evidence=NAS] [GO:0016851 "magnesium chelatase activity" evidence=ISS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0010007 "magnesium chelatase complex" evidence=TAS] InterPro:IPR003672 InterPro:IPR011771 InterPro:IPR016040 InterPro:IPR022571 Pfam:PF02514 Pfam:PF11965 GO:GO:0005739 EMBL:CP002688 GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 EMBL:AB006704 GO:GO:0009706 GO:GO:0015995 GO:GO:0010007 GO:GO:0016851 EMBL:AY070133 EMBL:BT002311 IPI:IPI00548533 RefSeq:NP_196867.1 UniGene:At.23621 STRING:Q9FNB0 PRIDE:Q9FNB0 EnsemblPlants:AT5G13630.1 GeneID:831207 KEGG:ath:AT5G13630 TAIR:At5g13630 InParanoid:Q9FNB0 KO:K03403 OMA:VLWGSDN PhylomeDB:Q9FNB0 ProtClustDB:PLN03069 Genevestigator:Q9FNB0 TIGRFAMs:TIGR02025 Uniprot:Q9FNB0

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig00159	45	227	-1.806	2.87E-19	TAIR|locus:2173234 - symbol:GUN5 "GENOMES UNCOUPLED 5" species:3702 "Arabidopsis thaliana" [GO:0009058 "biosynthetic process" evidence=IEA] [GO:0015995 "chlorophyll biosynthetic process" evidence=IEA] [GO:0009706 "chloroplast inner membrane" evidence=NAS] [GO:0016851 "magnesium chelatase activity" evidence=ISS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0010007 "magnesium chelatase complex" evidence=TAS] InterPro:IPR003672 InterPro:IPR011771 InterPro:IPR016040 InterPro:IPR022571 Pfam:PF02514 Pfam:PF11965 GO:GO:0005739 EMBL:CP002688 GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 EMBL:AB006704 GO:GO:0009706 GO:GO:0015995 GO:GO:0010007 GO:GO:0016851 EMBL:AY070133 EMBL:BT002311 IPI:IPI00548533 RefSeq:NP_196867.1 UniGene:At.23621 STRING:Q9FNB0 PRIDE:Q9FNB0 EnsemblPlants:AT5G13630.1 GeneID:831207 KEGG:ath:AT5G13630 TAIR:At5g13630 InParanoid:Q9FNB0 KO:K03403 OMA:VLWGSDN PhylomeDB:Q9FNB0 ProtClustDB:PLN03069 Genevestigator:Q9FNB0 TIGRFAMs:TIGR02025 Uniprot:Q9FNB0
Leaf	Isotig00160	41	207	-1.807	1.01E-17	TAIR|locus:2173234 - symbol:GUN5 "GENOMES UNCOUPLED 5" species:3702 "Arabidopsis thaliana" [GO:0009058 "biosynthetic process" evidence=IEA] [GO:0015995 "chlorophyll biosynthetic process" evidence=IEA] [GO:0009706 "chloroplast inner membrane" evidence=NAS] [GO:0016851 "magnesium chelatase activity" evidence=ISS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0010007 "magnesium chelatase complex" evidence=TAS] InterPro:IPR003672 InterPro:IPR011771 InterPro:IPR016040 InterPro:IPR022571 Pfam:PF02514 Pfam:PF11965 GO:GO:0005739 EMBL:CP002688 GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 EMBL:AB006704 GO:GO:0009706 GO:GO:0015995 GO:GO:0010007 GO:GO:0016851 EMBL:AY070133 EMBL:BT002311 IPI:IPI00548533 RefSeq:NP_196867.1 UniGene:At.23621 STRING:Q9FNB0 PRIDE:Q9FNB0 EnsemblPlants:AT5G13630.1 GeneID:831207 KEGG:ath:AT5G13630 TAIR:At5g13630 InParanoid:Q9FNB0 KO:K03403 OMA:VLWGSDN PhylomeDB:Q9FNB0 ProtClustDB:PLN03069 Genevestigator:Q9FNB0 TIGRFAMs:TIGR02025 Uniprot:Q9FNB0
Leaf	Isotig00161	41	206	-1.800	1.47E-17	TAIR|locus:2173234 - symbol:GUN5 "GENOMES UNCOUPLED 5" species:3702 "Arabidopsis thaliana" [GO:0009058 "biosynthetic process" evidence=IEA] [GO:0015995 "chlorophyll biosynthetic process" evidence=IEA] [GO:0009706 "chloroplast inner membrane" evidence=NAS] [GO:0016851 "magnesium chelatase activity" evidence=ISS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0010007 "magnesium chelatase complex" evidence=TAS] InterPro:IPR003672 InterPro:IPR011771 InterPro:IPR016040 InterPro:IPR022571 Pfam:PF02514 Pfam:PF11965 GO:GO:0005739 EMBL:CP002688 GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 EMBL:AB006704 GO:GO:0009706 GO:GO:0015995 GO:GO:0010007 GO:GO:0016851 EMBL:AY070133 EMBL:BT002311 IPI:IPI00548533 RefSeq:NP_196867.1 UniGene:At.23621 STRING:Q9FNB0 PRIDE:Q9FNB0 EnsemblPlants:AT5G13630.1 GeneID:831207 KEGG:ath:AT5G13630 TAIR:At5g13630 InParanoid:Q9FNB0 KO:K03403 OMA:VLWGSDN PhylomeDB:Q9FNB0 ProtClustDB:PLN03069 Genevestigator:Q9FNB0 TIGRFAMs:TIGR02025 Uniprot:Q9FNB0
Leaf	Isotig00188	13	1	4.229	7.21E-05	No hit
Leaf	Isotig00189	14	0	5.336	1.79E-05	No hit
Leaf	Isotig00205	62	35	1.354	4.94E-06	TAIR|locus:2162550 - symbol:ATM2 "AT5G54280" species:3702 "Arabidopsis thaliana" [GO:0003774 "motor activity" evidence=ISS] [GO:0016459 "myosin complex" evidence=ISS] [GO:0030048 "actin filament-based movement" evidence=TAS] [GO:0005886 "plasma membrane" evidence=IDA] InterPro:IPR000048 InterPro:IPR001609 Pfam:PF00063 Pfam:PF00612 PRINTS:PR00193 PROSITE:PS50096 SMART:SM00015 SMART:SM00242 GO:GO:0005886 GO:GO:0005524 GenomeReviews:BA000015_GR GO:GO:0003774 GO:GO:0016459 GO:GO:0030048 eggNOG:COG5022 HOGENOM:HBG317080 EMBL:AK229471 IPI:IPI00516976 ProteinModelPortal:Q0WNH0 SMR:Q0WNH0 STRING:Q0WNH0 PRIDE:Q0WNH0 TAIR:At5g54280 PhylomeDB:Q0WNH0 Genevestigator:Q0WNH0 Uniprot:Q0WNH0
Leaf	Isotig00206	62	35	1.354	4.94E-06	TAIR|locus:2162550 - symbol:ATM2 "AT5G54280" species:3702 "Arabidopsis thaliana" [GO:0003774 "motor activity" evidence=ISS] [GO:0016459 "myosin complex" evidence=ISS] [GO:0030048 "actin filament-based movement" evidence=TAS] [GO:0005886 "plasma membrane" evidence=IDA] InterPro:IPR000048 InterPro:IPR001609 Pfam:PF00063 Pfam:PF00612 PRINTS:PR00193 PROSITE:PS50096 SMART:SM00015 SMART:SM00242 GO:GO:0005886 GO:GO:0005524 GenomeReviews:BA000015_GR GO:GO:0003774 GO:GO:0016459 GO:GO:0030048 eggNOG:COG5022 HOGENOM:HBG317080 EMBL:AK229471 IPI:IPI00516976 ProteinModelPortal:Q0WNH0 SMR:Q0WNH0 STRING:Q0WNH0 PRIDE:Q0WNH0 TAIR:At5g54280 PhylomeDB:Q0WNH0 Genevestigator:Q0WNH0 Uniprot:Q0WNH0

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig00207	55	28	1.503	3.26E-06	TAIR|locus:2162550 - symbol:ATM2 "AT5G54280" species:3702 "Arabidopsis thaliana" [GO:0003774 "motor activity" evidence=ISS] [GO:0016459 "myosin complex" evidence=ISS] [GO:0030048 "actin filament-based movement" evidence=TAS] [GO:0005886 "plasma membrane" evidence=IDA] InterPro:IPR000048 InterPro:IPR001609 Pfam:PF00063 Pfam:PF00612 PRINTS:PR00193 PROSITE:PS50096 SMART:SM00015 SMART:SM00242 GO:GO:0005886 GO:GO:0005524 GenomeReviews:BA000015_GR GO:GO:0003774 GO:GO:0016459 GO:GO:0030048 eggNOG:COG5022 HOGENOM:HBG317080 EMBL:AK229471 IPI:IPI00516976 ProteinModelPortal:Q0WNH0 SMR:Q0WNH0 STRING:Q0WNH0 PRIDE:Q0WNH0 TAIR:At5g54280 PhylomeDB:Q0WNH0 Genevestigator:Q0WNH0 Uniprot:Q0WNH0
Leaf	Isotig00208	55	28	1.503	3.26E-06	TAIR|locus:2162550 - symbol:ATM2 "AT5G54280" species:3702 "Arabidopsis thaliana" [GO:0003774 "motor activity" evidence=ISS] [GO:0016459 "myosin complex" evidence=ISS] [GO:0030048 "actin filament-based movement" evidence=TAS] [GO:0005886 "plasma membrane" evidence=IDA] InterPro:IPR000048 InterPro:IPR001609 Pfam:PF00063 Pfam:PF00612 PRINTS:PR00193 PROSITE:PS50096 SMART:SM00015 SMART:SM00242 GO:GO:0005886 GO:GO:0005524 GenomeReviews:BA000015_GR GO:GO:0003774 GO:GO:0016459 GO:GO:0030048 eggNOG:COG5022 HOGENOM:HBG317080 EMBL:AK229471 IPI:IPI00516976 ProteinModelPortal:Q0WNH0 SMR:Q0WNH0 STRING:Q0WNH0 PRIDE:Q0WNH0 TAIR:At5g54280 PhylomeDB:Q0WNH0 Genevestigator:Q0WNH0 Uniprot:Q0WNH0
Leaf	Isotig00209	48	24	1.529	1.07E-05	TAIR|locus:2162550 - symbol:ATM2 "AT5G54280" species:3702 "Arabidopsis thaliana" [GO:0003774 "motor activity" evidence=ISS] [GO:0016459 "myosin complex" evidence=ISS] [GO:0030048 "actin filament-based movement" evidence=TAS] [GO:0005886 "plasma membrane" evidence=IDA] InterPro:IPR000048 InterPro:IPR001609 Pfam:PF00063 Pfam:PF00612 PRINTS:PR00193 PROSITE:PS50096 SMART:SM00015 SMART:SM00242 GO:GO:0005886 GO:GO:0005524 GenomeReviews:BA000015_GR GO:GO:0003774 GO:GO:0016459 GO:GO:0030048 eggNOG:COG5022 HOGENOM:HBG317080 EMBL:AK229471 IPI:IPI00516976 ProteinModelPortal:Q0WNH0 SMR:Q0WNH0 STRING:Q0WNH0 PRIDE:Q0WNH0 TAIR:At5g54280 PhylomeDB:Q0WNH0 Genevestigator:Q0WNH0 Uniprot:Q0WNH0
Leaf	Isotig00210	48	24	1.529	1.07E-05	TAIR|locus:2162550 - symbol:ATM2 "AT5G54280" species:3702 "Arabidopsis thaliana" [GO:0003774 "motor activity" evidence=ISS] [GO:0016459 "myosin complex" evidence=ISS] [GO:0030048 "actin filament-based movement" evidence=TAS] [GO:0005886 "plasma membrane" evidence=IDA] InterPro:IPR000048 InterPro:IPR001609 Pfam:PF00063 Pfam:PF00612 PRINTS:PR00193 PROSITE:PS50096 SMART:SM00015 SMART:SM00242 GO:GO:0005886 GO:GO:0005524 GenomeReviews:BA000015_GR GO:GO:0003774 GO:GO:0016459 GO:GO:0030048 eggNOG:COG5022 HOGENOM:HBG317080 EMBL:AK229471 IPI:IPI00516976 ProteinModelPortal:Q0WNH0 SMR:Q0WNH0 STRING:Q0WNH0 PRIDE:Q0WNH0 TAIR:At5g54280 PhylomeDB:Q0WNH0 Genevestigator:Q0WNH0 Uniprot:Q0WNH0
Leaf	Isotig00215	62	269	-1.588	4.55E-19	TAIR|locus:2033087 - symbol:PSBP-1 "AT1G06680" species:3702 "Arabidopsis thaliana" [GO:0009543 "chloroplast thylakoid lumen" evidence=ISS;IDA] [GO:0009654 "oxygen evolving complex" evidence=ISS] [GO:0030095 "chloroplast photosystem II" evidence=ISS] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0019898 "extrinsic to membrane" evidence=TAS] [GO:0031977 "thylakoid lumen" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0042742 "defense response to bacterium" evidence=IEP] [GO:0008266 "poly(U) RNA binding" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0019684 "photosynthesis, light reaction" evidence=TAS] InterPro:IPR002683 Pfam:PF01789 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0048046 GO:GO:0009570 GO:GO:0042742 GO:GO:0005509 GO:GO:0008266 GO:GO:0019898 GO:GO:0009941 EMBL:AC007592 GO:GO:0009535 UniGene:At.23738 GO:GO:0009543 GO:GO:0019684 InterPro:IPR016124 InterPro:IPR016123 Gene3D:G3DSA:3.40.1000.10 SUPFAM:SSF55724 GO:GO:0009654 KO:K02717 UniGene:At.3352 EMBL:X98108 EMBL:AY056416 EMBL:AY070469 EMBL:AY074308 EMBL:AY096487 EMBL:AY087305 EMBL:Z25620 IPI:IPI00540742 IPI:IPI00891781 PIR:JC5271 RefSeq:NP_001117239.1 RefSeq:NP_172153.1 UniGene:At.42209 UniGene:At.47605 ProteinModelPortal:Q42029 SMR:Q42029 IntAct:Q42029 STRING:Q42029 SWISS-2DPAGE:Q42029 PRIDE:Q42029 ProMEX:Q42029 DNASU:837178 EnsemblPlants:AT1G06680.1 GeneID:837178 KEGG:ath:AT1G06680 TAIR:At1g06680 eggNOG:NOG318473 HOGENOM:HBG319237 InParanoid:Q42029 OMA:MASTSCF PhylomeDB:Q42029 ProtClustDB:PLN00042 ArrayExpress:Q42029 Genevestigator:Q42029 GermOnline:AT1G06680 Uniprot:Q42029

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig00216	62	268	-1.583	6.43E-19	TAIR|locus:2033087 - symbol:PSBP-1 "AT1G06680" species:3702 "Arabidopsis thaliana" [GO:0009543 "chloroplast thylakoid lumen" evidence=ISS;IDA] [GO:0009654 "oxygen evolving complex" evidence=ISS] [GO:0030095 "chloroplast photosystem II" evidence=ISS] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0019898 "extrinsic to membrane" evidence=TAS] [GO:0031977 "thylakoid lumen" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0042742 "defense response to bacterium" evidence=IEP] [GO:0008266 "poly(U) RNA binding" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0019684 "photosynthesis, light reaction" evidence=TAS] InterPro:IPR002683 Pfam:PF01789 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0048046 GO:GO:0009570 GO:GO:0042742 GO:GO:0005509 GO:GO:0008266 GO:GO:0019898 GO:GO:0009941 EMBL:AC007592 GO:GO:0009535 UniGene:At.23738 GO:GO:0009543 GO:GO:0019684 InterPro:IPR016124 InterPro:IPR016123 Gene3D:G3DSA:3.40.1000.10 SUPFAM:SSF55724 GO:GO:0009654 KO:K02717 UniGene:At.3352 EMBL:X98108 EMBL:AY056416 EMBL:AY070469 EMBL:AY074308 EMBL:AY096487 EMBL:AY087305 EMBL:Z25620 IPI:IPI00540742 IPI:IPI00891781 PIR:JC5271 RefSeq:NP_001117239.1 RefSeq:NP_172153.1 UniGene:At.42209 UniGene:At.47605 ProteinModelPortal:Q42029 SMR:Q42029 IntAct:Q42029 STRING:Q42029 SWISS-2DPAGE:Q42029 PRIDE:Q42029 ProMEX:Q42029 DNASU:837178 EnsemblPlants:AT1G06680.1 GeneID:837178 KEGG:ath:AT1G06680 TAIR:At1g06680 eggNOG:NOG318473 HOGENOM:HBG319237 InParanoid:Q42029 OMA:MASTSCF PhylomeDB:Q42029 ProtClustDB:PLN00042 ArrayExpress:Q42029 Genevestigator:Q42029 GermOnline:AT1G06680 Uniprot:Q42029
Leaf	Isotig00217	65	272	-1.536	2.01E-18	TAIR|locus:2033087 - symbol:PSBP-1 "AT1G06680" species:3702 "Arabidopsis thaliana" [GO:0009543 "chloroplast thylakoid lumen" evidence=ISS;IDA] [GO:0009654 "oxygen evolving complex" evidence=ISS] [GO:0030095 "chloroplast photosystem II" evidence=ISS] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0019898 "extrinsic to membrane" evidence=TAS] [GO:0031977 "thylakoid lumen" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0042742 "defense response to bacterium" evidence=IEP] [GO:0008266 "poly(U) RNA binding" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0019684 "photosynthesis, light reaction" evidence=TAS] InterPro:IPR002683 Pfam:PF01789 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0048046 GO:GO:0009570 GO:GO:0042742 GO:GO:0005509 GO:GO:0008266 GO:GO:0019898 GO:GO:0009941 EMBL:AC007592 GO:GO:0009535 UniGene:At.23738 GO:GO:0009543 GO:GO:0019684 InterPro:IPR016124 InterPro:IPR016123 Gene3D:G3DSA:3.40.1000.10 SUPFAM:SSF55724 GO:GO:0009654 KO:K02717 UniGene:At.3352 EMBL:X98108 EMBL:AY056416 EMBL:AY070469 EMBL:AY074308 EMBL:AY096487 EMBL:AY087305 EMBL:Z25620 IPI:IPI00540742 IPI:IPI00891781 PIR:JC5271 RefSeq:NP_001117239.1 RefSeq:NP_172153.1 UniGene:At.42209 UniGene:At.47605 ProteinModelPortal:Q42029 SMR:Q42029 IntAct:Q42029 STRING:Q42029 SWISS-2DPAGE:Q42029 PRIDE:Q42029 ProMEX:Q42029 DNASU:837178 EnsemblPlants:AT1G06680.1 GeneID:837178 KEGG:ath:AT1G06680 TAIR:At1g06680 eggNOG:NOG318473 HOGENOM:HBG319237 InParanoid:Q42029 OMA:MASTSCF PhylomeDB:Q42029 ProtClustDB:PLN00042 ArrayExpress:Q42029 Genevestigator:Q42029 GermOnline:AT1G06680 Uniprot:Q42029
Leaf	Isotig00218	58	273	-1.706	3.10E-21	TAIR|locus:2033087 - symbol:PSBP-1 "AT1G06680" species:3702 "Arabidopsis thaliana" [GO:0009543 "chloroplast thylakoid lumen" evidence=ISS;IDA] [GO:0009654 "oxygen evolving complex" evidence=ISS] [GO:0030095 "chloroplast photosystem II" evidence=ISS] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0019898 "extrinsic to membrane" evidence=TAS] [GO:0031977 "thylakoid lumen" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0042742 "defense response to bacterium" evidence=IEP] [GO:0008266 "poly(U) RNA binding" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0019684 "photosynthesis, light reaction" evidence=TAS] InterPro:IPR002683 Pfam:PF01789 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0048046 GO:GO:0009570 GO:GO:0042742 GO:GO:0005509 GO:GO:0008266 GO:GO:0019898 GO:GO:0009941 EMBL:AC007592 GO:GO:0009535 UniGene:At.23738 GO:GO:0009543 GO:GO:0019684 InterPro:IPR016124 InterPro:IPR016123 Gene3D:G3DSA:3.40.1000.10 SUPFAM:SSF55724 GO:GO:0009654 KO:K02717 UniGene:At.3352 EMBL:X98108 EMBL:AY056416 EMBL:AY070469 EMBL:AY074308 EMBL:AY096487 EMBL:AY087305 EMBL:Z25620 IPI:IPI00540742 IPI:IPI00891781 PIR:JC5271 RefSeq:NP_001117239.1 RefSeq:NP_172153.1 UniGene:At.42209 UniGene:At.47605 ProteinModelPortal:Q42029 SMR:Q42029

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						IntAct:Q42029 STRING:Q42029 SWISS-2DPAGE:Q42029 PRIDE:Q42029 ProMEX:Q42029 DNASU:837178 EnsemblPlants:AT1G06680.1 GeneID:837178 KEGG:ath:AT1G06680 TAIR:At1g06680 eggNOG:NOG318473 HOGENOM:HBG319237 InParanoid:Q42029 OMA:MASTSCF PhylomeDB:Q42029 ProtClustDB:PLN00042 ArrayExpress:Q42029 Genevestigator:Q42029 GermOnline:AT1G06680 Uniprot:Q42029
Leaf	Isotig00219	58	272	-1.701	4.46E-21	TAIR|locus:2033087 - symbol:PSBP-1 "AT1G06680" species:3702 "Arabidopsis thaliana" [GO:0009543 "chloroplast thylakoid lumen" evidence=ISS;IDA] [GO:0009654 "oxygen evolving complex" evidence=ISS] [GO:0030095 "chloroplast photosystem II" evidence=ISS] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0019898 "extrinsic to membrane" evidence=TAS] [GO:0031977 "thylakoid lumen" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0042742 "defense response to bacterium" evidence=IEP] [GO:0008266 "poly(U) RNA binding" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0019684 "photosynthesis, light reaction" evidence=TAS] InterPro:IPR002683 Pfam:PF01789 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0048046 GO:GO:0009570 GO:GO:0042742 GO:GO:0005509 GO:GO:0008266 GO:GO:0019898 GO:GO:0009941 EMBL:AC007592 GO:GO:0009535 UniGene:At.23738 GO:GO:0009543 GO:GO:0019684 InterPro:IPR016124 InterPro:IPR016123 Gene3D:G3DSA:3.40.1000.10 SUPFAM:SSF55724 GO:GO:0009654 KO:K02717 UniGene:At.3352 EMBL:X98108 EMBL:AY056416 EMBL:AY070469 EMBL:AY074308 EMBL:AY096487 EMBL:AY087305 EMBL:Z25620 IPI:IPI00540742 IPI:IPI00891781 PIR:JC5271 RefSeq:NP_001117239.1 RefSeq:NP_172153.1 UniGene:At.42209 UniGene:At.47605 ProteinModelPortal:Q42029 SMR:Q42029 IntAct:Q42029 STRING:Q42029 SWISS-2DPAGE:Q42029 PRIDE:Q42029 ProMEX:Q42029 DNASU:837178 EnsemblPlants:AT1G06680.1 GeneID:837178 KEGG:ath:AT1G06680 TAIR:At1g06680 eggNOG:NOG318473 HOGENOM:HBG319237 InParanoid:Q42029 OMA:MASTSCF PhylomeDB:Q42029 ProtClustDB:PLN00042 ArrayExpress:Q42029 Genevestigator:Q42029 GermOnline:AT1G06680 Uniprot:Q42029
Leaf	Isotig00220	61	276	-1.649	1.62E-20	TAIR|locus:2033087 - symbol:PSBP-1 "AT1G06680" species:3702 "Arabidopsis thaliana" [GO:0009543 "chloroplast thylakoid lumen" evidence=ISS;IDA] [GO:0009654 "oxygen evolving complex" evidence=ISS] [GO:0030095 "chloroplast photosystem II" evidence=ISS] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0019898 "extrinsic to membrane" evidence=TAS] [GO:0031977 "thylakoid lumen" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0042742 "defense response to bacterium" evidence=IEP] [GO:0008266 "poly(U) RNA binding" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0019684 "photosynthesis, light reaction" evidence=TAS] InterPro:IPR002683 Pfam:PF01789 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0048046 GO:GO:0009570 GO:GO:0042742 GO:GO:0005509 GO:GO:0008266 GO:GO:0019898 GO:GO:0009941 EMBL:AC007592 GO:GO:0009535 UniGene:At.23738 GO:GO:0009543 GO:GO:0019684 InterPro:IPR016124 InterPro:IPR016123 Gene3D:G3DSA:3.40.1000.10 SUPFAM:SSF55724 GO:GO:0009654 KO:K02717 UniGene:At.3352 EMBL:X98108 EMBL:AY056416 EMBL:AY070469 EMBL:AY074308 EMBL:AY096487 EMBL:AY087305 EMBL:Z25620 IPI:IPI00540742 IPI:IPI00891781 PIR:JC5271 RefSeq:NP_001117239.1 RefSeq:NP_172153.1 UniGene:At.42209 UniGene:At.47605 ProteinModelPortal:Q42029 SMR:Q42029 IntAct:Q42029 STRING:Q42029 SWISS-2DPAGE:Q42029 PRIDE:Q42029 ProMEX:Q42029 DNASU:837178 EnsemblPlants:AT1G06680.1 GeneID:837178 KEGG:ath:AT1G06680 TAIR:At1g06680 eggNOG:NOG318473 HOGENOM:HBG319237 InParanoid:Q42029 OMA:MASTSCF PhylomeDB:Q42029 ProtClustDB:PLN00042 ArrayExpress:Q42029 Genevestigator:Q42029 GermOnline:AT1G06680 Uniprot:Q42029
Leaf	Isotig00221	56	214	-1.405	3.66E-13	TAIR|locus:2161423 - symbol:APE2 "AT5G46110" species:3702 "Arabidopsis thaliana" [GO:0015297 "antiporter activity" evidence=ISS] [GO:0015120 "phosphoglycerate transmembrane transporter activity" evidence=IDA] [GO:0015713 "phosphoglycerate transport" evidence=IDA] [GO:0015717 "triose phosphate transport" evidence=IMP] [GO:0035436 "triose phosphate transmembrane transport" evidence=IDA] [GO:0071917 "triose-phosphate transmembrane transporter activity" evidence=IMP;IDA] [GO:0009643 "photosynthetic acclimation" evidence=IMP] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] InterPro:IPR004696 Pfam:PF03151 GO:GO:0016021 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0031969 EMBL:AB006698 InterPro:IPR004853 KO:K15283 GO:GO:0015120 GO:GO:0071917 TIGRFAMs:TIGR00817 GO:GO:0009643 UniGene:At.26418 EMBL:AF097648 EMBL:AY037211 EMBL:AY050811 EMBL:AY056790

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EMBL:AY091414 EMBL:BT002683 EMBL:AY087499 EMBL:AK222032 IPI:IPI00846992 PIR:T51692 RefSeq:NP_851138.1 UniGene:At.25255 IntAct:Q9ZSR7 STRING:Q9ZSR7 PRIDE:Q9ZSR7 EnsemblPlants:AT5G46110.1 GeneID:834652 KEGG:ath:AT5G46110 TAIR:At5g46110 eggNOG:NOG265656 InParanoid:Q9ZSR7 OMA:AASQFIM ProtClustDB:CLSN2680450 ArrayExpress:Q9ZSR7 Genevestigator:Q9ZSR7 Uniprot:Q9ZSR7
Leaf	Isotig00222	57	211	-1.359	1.97E-12	TAIR|locus:2161423 - symbol:APE2 "AT5G46110" species:3702 "Arabidopsis thaliana" [GO:0015297 "antiporter activity" evidence=ISS] [GO:0015120 "phosphoglycerate transmembrane transporter activity" evidence=IDA] [GO:0015713 "phosphoglycerate transport" evidence=IDA] [GO:0015717 "triose phosphate transport" evidence=IMP] [GO:0035436 "triose phosphate transmembrane transport" evidence=IDA] [GO:0071917 "triose-phosphate transmembrane transporter activity" evidence=IMP;IDA] [GO:0009643 "photosynthetic acclimation" evidence=IMP] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] InterPro:IPR004696 Pfam:PF03151 GO:GO:0016021 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0031969 EMBL:AB006698 InterPro:IPR004853 KO:K15283 GO:GO:0015120 GO:GO:0071917 TIGRFAMs:TIGR00817 GO:GO:0009643 UniGene:At.26418 EMBL:AF097648 EMBL:AY037211 EMBL:AY050811 EMBL:AY056790 EMBL:AY091414 EMBL:BT002683 EMBL:AY087499 EMBL:AK222032 IPI:IPI00846992 PIR:T51692 RefSeq:NP_851138.1 UniGene:At.25255 IntAct:Q9ZSR7 STRING:Q9ZSR7 PRIDE:Q9ZSR7 EnsemblPlants:AT5G46110.1 GeneID:834652 KEGG:ath:AT5G46110 TAIR:At5g46110 eggNOG:NOG265656 InParanoid:Q9ZSR7 OMA:AASQFIM ProtClustDB:CLSN2680450 ArrayExpress:Q9ZSR7 Genevestigator:Q9ZSR7 Uniprot:Q9ZSR7
Leaf	Isotig00227	52	223	-1.572	7.55E-16	TAIR|locus:2082767 - symbol:LHCA2 "AT3G61470" species:3702 "Arabidopsis thaliana" [GO:0009768 "photosynthesis, light harvesting in photosystem I" evidence=TAS] [GO:0009782 "photosystem I antenna complex" evidence=TAS] [GO:0015979 "photosynthesis" evidence=ISS] [GO:0016168 "chlorophyll binding" evidence=ISS] [GO:0030076 "light-harvesting complex" evidence=ISS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] InterPro:IPR001344 Pfam:PF00504 EMBL:CP002686 GO:GO:0009535 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 TCDB:5.B.4.1.1 KO:K08908 EMBL:AF134120 EMBL:AY054670 EMBL:AY065429 EMBL:AY072483 EMBL:BT002070 IPI:IPI00543126 PIR:T50550 RefSeq:NP_191706.2 UniGene:At.46743 UniGene:At.55066 ProteinModelPortal:Q9SYW8 SMR:Q9SYW8 STRING:Q9SYW8 PRIDE:Q9SYW8 EnsemblPlants:AT3G61470.1 GeneID:825320 KEGG:ath:AT3G61470 TAIR:At3g61470 InParanoid:Q9SYW8 PhylomeDB:Q9SYW8 ProtClustDB:CLSN2696878 ArrayExpress:Q9SYW8 Genevestigator:Q9SYW8 Uniprot:Q9SYW8
Leaf	Isotig00228	44	287	-2.177	3.92E-30	TAIR|locus:2079117 - symbol:LHCA4 "AT3G47470" species:3702 "Arabidopsis thaliana" [GO:0015979 "photosynthesis" evidence=ISS] [GO:0016168 "chlorophyll binding" evidence=ISS;NAS] [GO:0030076 "light-harvesting complex" evidence=ISS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0080167 "response to karrikin" evidence=IEP] InterPro:IPR001344 Pfam:PF00504 GO:GO:0016021 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0046872 GO:GO:0009941 GO:GO:0080167 GO:GO:0018298 GO:GO:0009535 GO:GO:0010287 EMBL:AL132955 EMBL:M63931 EMBL:AY093080 EMBL:BT000093 EMBL:AY086470 IPI:IPI00523187 PIR:T45707 RefSeq:NP_190331.3 UniGene:At.21346 UniGene:At.27524 UniGene:At.35504 UniGene:At.35803 UniGene:At.66361 UniGene:At.68076 UniGene:At.71101 ProteinModelPortal:P27521 SMR:P27521 STRING:P27521 PRIDE:P27521 EnsemblPlants:AT3G47470.1 GeneID:823901 KEGG:ath:AT3G47470 TAIR:At3g47470 eggNOG:NOG249845 HOGENOM:HBG618504 InParanoid:P27521 KO:K08910 OMA:WFVQAEL PhylomeDB:P27521 ProtClustDB:PLN00101 ArrayExpress:P27521 Genevestigator:P27521 GermOnline:AT3G47470 GO:GO:0009522 GO:GO:0009523 GO:GO:0016168 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 Uniprot:P27521
Leaf	Isotig00229	44	289	-2.187	1.70E-30	TAIR|locus:2079117 - symbol:LHCA4 "AT3G47470" species:3702 "Arabidopsis thaliana" [GO:0015979 "photosynthesis" evidence=ISS] [GO:0016168 "chlorophyll binding" evidence=ISS;NAS] [GO:0030076 "light-harvesting complex" evidence=ISS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009535 "chloroplast

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0080167 "response to karrikin" evidence=IEP] InterPro:IPR001344 Pfam:PF00504 GO:GO:0016021 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0046872 GO:GO:0009941 GO:GO:0080167 GO:GO:0018298 GO:GO:0009535 GO:GO:0010287 EMBL:AL132955 EMBL:M63931 EMBL:AY093080 EMBL:BT000093 EMBL:AY086470 IPI:IPI00523187 PIR:T45707 RefSeq:NP_190331.3 UniGene:At.21346 UniGene:At.27524 UniGene:At.35504 UniGene:At.35803 UniGene:At.66361 UniGene:At.68076 UniGene:At.71101 ProteinModelPortal:P27521 SMR:P27521 STRING:P27521 PRIDE:P27521 EnsemblPlants:AT3G47470.1 GeneID:823901 KEGG:ath:AT3G47470 TAIR:At3g47470 eggNOG:NOG249845 HOGENOM:HBG618504 InParanoid:P27521 KO:K08910 OMA:WFVQAEL PhylomeDB:P27521 ProtClustDB:PLN00101 ArrayExpress:P27521 Genevestigator:P27521 GermOnline:AT3G47470 GO:GO:0009522 GO:GO:0009523 GO:GO:0016168 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 Uniprot:P27521
Leaf	Isotig00230	41	226	-1.934	6.72E-21	TAIR|locus:2079117 - symbol:LHCA4 "AT3G47470" species:3702 "Arabidopsis thaliana" [GO:0015979 "photosynthesis" evidence=ISS] [GO:0016168 "chlorophyll binding" evidence=ISS;NAS] [GO:0030076 "light-harvesting complex" evidence=ISS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0080167 "response to karrikin" evidence=IEP] InterPro:IPR001344 Pfam:PF00504 GO:GO:0016021 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0046872 GO:GO:0009941 GO:GO:0080167 GO:GO:0018298 GO:GO:0009535 GO:GO:0010287 EMBL:AL132955 EMBL:M63931 EMBL:AY093080 EMBL:BT000093 EMBL:AY086470 IPI:IPI00523187 PIR:T45707 RefSeq:NP_190331.3 UniGene:At.21346 UniGene:At.27524 UniGene:At.35504 UniGene:At.35803 UniGene:At.66361 UniGene:At.68076 UniGene:At.71101 ProteinModelPortal:P27521 SMR:P27521 STRING:P27521 PRIDE:P27521 EnsemblPlants:AT3G47470.1 GeneID:823901 KEGG:ath:AT3G47470 TAIR:At3g47470 eggNOG:NOG249845 HOGENOM:HBG618504 InParanoid:P27521 KO:K08910 OMA:WFVQAEL PhylomeDB:P27521 ProtClustDB:PLN00101 ArrayExpress:P27521 Genevestigator:P27521 GermOnline:AT3G47470 GO:GO:0009522 GO:GO:0009523 GO:GO:0016168 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 Uniprot:P27521
Leaf	Isotig00231	52	223	-1.572	7.55E-16	TAIR|locus:2082767 - symbol:LHCA2 "AT3G61470" species:3702 "Arabidopsis thaliana" [GO:0009768 "photosynthesis, light harvesting in photosystem I" evidence=TAS] [GO:0009782 "photosystem I antenna complex" evidence=TAS] [GO:0015979 "photosynthesis" evidence=ISS] [GO:0016168 "chlorophyll binding" evidence=ISS] [GO:0030076 "light-harvesting complex" evidence=ISS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] InterPro:IPR001344 Pfam:PF00504 EMBL:CP002686 GO:GO:0009535 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 TCDB:5.B.4.1.1 KO:K08908 EMBL:AF134120 EMBL:AY054670 EMBL:AY065429 EMBL:AY072483 EMBL:BT002070 IPI:IPI00543126 PIR:T50550 RefSeq:NP_191706.2 UniGene:At.46743 UniGene:At.55066 ProteinModelPortal:Q9SYW8 SMR:Q9SYW8 STRING:Q9SYW8 PRIDE:Q9SYW8 EnsemblPlants:AT3G61470.1 GeneID:825320 KEGG:ath:AT3G61470 TAIR:At3g61470 InParanoid:Q9SYW8 PhylomeDB:Q9SYW8 ProtClustDB:CLSN2696878 ArrayExpress:Q9SYW8 Genevestigator:Q9SYW8 Uniprot:Q9SYW8
Leaf	Isotig00232	44	210	-1.726	6.05E-17	TAIR|locus:2082767 - symbol:LHCA2 "AT3G61470" species:3702 "Arabidopsis thaliana" [GO:0009768 "photosynthesis, light harvesting in photosystem I" evidence=TAS] [GO:0009782 "photosystem I antenna complex" evidence=TAS] [GO:0015979 "photosynthesis" evidence=ISS] [GO:0016168 "chlorophyll binding" evidence=ISS] [GO:0030076 "light-harvesting complex" evidence=ISS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] InterPro:IPR001344 Pfam:PF00504 EMBL:CP002686 GO:GO:0009535 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 TCDB:5.B.4.1.1 KO:K08908 EMBL:AF134120 EMBL:AY054670 EMBL:AY065429 EMBL:AY072483 EMBL:BT002070 IPI:IPI00543126 PIR:T50550 RefSeq:NP_191706.2 UniGene:At.46743 UniGene:At.55066 ProteinModelPortal:Q9SYW8

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						SMR:Q9SYW8 STRING:Q9SYW8 PRIDE:Q9SYW8 EnsemblPlants:AT3G61470.1 GeneID:825320 KEGG:ath:AT3G61470 TAIR:At3g61470 InParanoid:Q9SYW8 PhylomeDB:Q9SYW8 ProtClustDB:CLSN2696878 ArrayExpress:Q9SYW8 Genevestigator:Q9SYW8 Uniprot:Q9SYW8
Leaf	Isotig00233	44	210	-1.726	6.05E-17	TAIR|locus:2082767 - symbol:LHCA2 "AT3G61470" species:3702 "Arabidopsis thaliana" [GO:0009768 "photosynthesis, light harvesting in photosystem I" evidence=TAS] [GO:0009782 "photosystem I antenna complex" evidence=TAS] [GO:0015979 "photosynthesis" evidence=ISS] [GO:0016168 "chlorophyll binding" evidence=ISS] [GO:0030076 "light-harvesting complex" evidence=ISS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] InterPro:IPR001344 Pfam:PF00504 EMBL:CP002686 GO:GO:0009535 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 TCDB:5.B.4.1.1 KO:K08908 EMBL:AF134120 EMBL:AY054670 EMBL:AY065429 EMBL:AY072483 EMBL:BT002070 IPI:IPI00543126 PIR:T50550 RefSeq:NP_191706.2 UniGene:At.46743 UniGene:At.55066 ProteinModelPortal:Q9SYW8 SMR:Q9SYW8 STRING:Q9SYW8 PRIDE:Q9SYW8 EnsemblPlants:AT3G61470.1 GeneID:825320 KEGG:ath:AT3G61470 TAIR:At3g61470 InParanoid:Q9SYW8 PhylomeDB:Q9SYW8 ProtClustDB:CLSN2696878 ArrayExpress:Q9SYW8 Genevestigator:Q9SYW8 Uniprot:Q9SYW8
Leaf	Isotig00255	31	8	2.483	1.11E-06	TAIR|locus:2026177 - symbol:AT1G62660 species:3702 "Arabidopsis thaliana" [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=IEA;ISS] [GO:0071370 "cellular response to gibberellin stimulus" evidence=IEP] [GO:0000325 "plant-type vacuole" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0009617 "response to bacterium" evidence=IEP] InterPro:IPR001362 InterPro:IPR018053 InterPro:IPR021792 Pfam:PF11837 PROSITE:PS00609 SMART:SM00640 EMBL:CP002684 GO:GO:0005975 InterPro:IPR008985 SUPFAM:SSF49899 InterPro:IPR023296 SUPFAM:SSF75005 CAZy:GH32 KO:K01193 GO:GO:0004575 InterPro:IPR013189 InterPro:IPR013148 Pfam:PF08244 Pfam:PF00251 ProtClustDB:CLSN2687777 EMBL:AY048269 EMBL:AY062481 EMBL:AY063904 EMBL:AY114066 EMBL:X99111 IPI:IPI00517592 PIR:S71268 RefSeq:NP_564798.1 UniGene:At.24113 UniGene:At.67066 ProteinModelPortal:Q43348 SMR:Q43348 STRING:Q43348 PRIDE:Q43348 ProMEX:Q43348 EnsemblPlants:AT1G62660.1 GeneID:842563 KEGG:ath:AT1G62660 TAIR:At1g62660 InParanoid:Q43348 OMA:HSIVEGF PhylomeDB:Q43348 ArrayExpress:Q43348 Genevestigator:Q43348 Uniprot:Q43348
Leaf	Isotig00256	31	8	2.483	1.11E-06	TAIR|locus:2026177 - symbol:AT1G62660 species:3702 "Arabidopsis thaliana" [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=IEA;ISS] [GO:0071370 "cellular response to gibberellin stimulus" evidence=IEP] [GO:0000325 "plant-type vacuole" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0009617 "response to bacterium" evidence=IEP] InterPro:IPR001362 InterPro:IPR018053 InterPro:IPR021792 Pfam:PF11837 PROSITE:PS00609 SMART:SM00640 EMBL:CP002684 GO:GO:0005975 InterPro:IPR008985 SUPFAM:SSF49899 InterPro:IPR023296 SUPFAM:SSF75005 CAZy:GH32 KO:K01193 GO:GO:0004575 InterPro:IPR013189 InterPro:IPR013148 Pfam:PF08244 Pfam:PF00251 ProtClustDB:CLSN2687777 EMBL:AY048269 EMBL:AY062481 EMBL:AY063904 EMBL:AY114066 EMBL:X99111 IPI:IPI00517592 PIR:S71268 RefSeq:NP_564798.1 UniGene:At.24113 UniGene:At.67066 ProteinModelPortal:Q43348 SMR:Q43348 STRING:Q43348 PRIDE:Q43348 ProMEX:Q43348 EnsemblPlants:AT1G62660.1 GeneID:842563 KEGG:ath:AT1G62660 TAIR:At1g62660 InParanoid:Q43348 OMA:HSIVEGF PhylomeDB:Q43348 ArrayExpress:Q43348 Genevestigator:Q43348 Uniprot:Q43348
Leaf	Isotig00259	23	9	1.883	0.000416531	TAIR|locus:2026177 - symbol:AT1G62660 species:3702 "Arabidopsis thaliana" [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=IEA;ISS] [GO:0071370 "cellular response to gibberellin stimulus" evidence=IEP] [GO:0000325 "plant-type vacuole" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0009617 "response to bacterium" evidence=IEP] InterPro:IPR001362 InterPro:IPR018053 InterPro:IPR021792 Pfam:PF11837 PROSITE:PS00609 SMART:SM00640 EMBL:CP002684 GO:GO:0005975 InterPro:IPR008985 SUPFAM:SSF49899 InterPro:IPR023296 SUPFAM:SSF75005 CAZy:GH32 KO:K01193 GO:GO:0004575 InterPro:IPR013189 InterPro:IPR013148 Pfam:PF08244 Pfam:PF00251 ProtClustDB:CLSN2687777 EMBL:AY048269 EMBL:AY062481 EMBL:AY063904 EMBL:AY114066 EMBL:X99111 IPI:IPI00517592 PIR:S71268 RefSeq:NP_564798.1 UniGene:At.24113 UniGene:At.67066 ProteinModelPortal:Q43348 SMR:Q43348 STRING:Q43348 PRIDE:Q43348 ProMEX:Q43348 EnsemblPlants:AT1G62660.1 GeneID:842563 KEGG:ath:AT1G62660 TAIR:At1g62660 InParanoid:Q43348 OMA:HSIVEGF PhylomeDB:Q43348 ArrayExpress:Q43348 Genevestigator:Q43348 Uniprot:Q43348

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig00260	23	9	1.883	0.000416531	TAIR|locus:2026177 - symbol:AT1G62660 species:3702 "Arabidopsis thaliana" [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=IEA;ISS] [GO:0071370 "cellular response to gibberellin stimulus" evidence=IEP] [GO:0000325 "plant-type vacuole" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0009617 "response to bacterium" evidence=IEP] InterPro:IPR001362 InterPro:IPR018053 InterPro:IPR021792 Pfam:PF11837 PROSITE:PS00609 SMART:SM00640 EMBL:CP002684 GO:GO:0005975 InterPro:IPR008985 SUPFAM:SSF49899 InterPro:IPR023296 SUPFAM:SSF75005 CAZy:GH32 KO:K01193 GO:GO:0004575 InterPro:IPR013189 InterPro:IPR013148 Pfam:PF08244 Pfam:PF00251 ProtClustDB:CLSN2687777 EMBL:AY048269 EMBL:AY062481 EMBL:AY063904 EMBL:AY114066 EMBL:X99111 IPI:IPI00517592 PIR:S71268 RefSeq:NP_564798.1 UniGene:At.24113 UniGene:At.67066 ProteinModelPortal:Q43348 SMR:Q43348 STRING:Q43348 PRIDE:Q43348 ProMEX:Q43348 EnsemblPlants:AT1G62660.1 GeneID:842563 KEGG:ath:AT1G62660 TAIR:At1g62660 InParanoid:Q43348 OMA:HSIVEGF PhylomeDB:Q43348 ArrayExpress:Q43348 Genevestigator:Q43348 Uniprot:Q43348
Leaf	Isotig00261	25	9	2.003	0.000126076	TAIR|locus:2026177 - symbol:AT1G62660 species:3702 "Arabidopsis thaliana" [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=IEA;ISS] [GO:0071370 "cellular response to gibberellin stimulus" evidence=IEP] [GO:0000325 "plant-type vacuole" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0009617 "response to bacterium" evidence=IEP] InterPro:IPR001362 InterPro:IPR018053 InterPro:IPR021792 Pfam:PF11837 PROSITE:PS00609 SMART:SM00640 EMBL:CP002684 GO:GO:0005975 InterPro:IPR008985 SUPFAM:SSF49899 InterPro:IPR023296 SUPFAM:SSF75005 CAZy:GH32 KO:K01193 GO:GO:0004575 InterPro:IPR013189 InterPro:IPR013148 Pfam:PF08244 Pfam:PF00251 ProtClustDB:CLSN2687777 EMBL:AY048269 EMBL:AY062481 EMBL:AY063904 EMBL:AY114066 EMBL:X99111 IPI:IPI00517592 PIR:S71268 RefSeq:NP_564798.1 UniGene:At.24113 UniGene:At.67066 ProteinModelPortal:Q43348 SMR:Q43348 STRING:Q43348 PRIDE:Q43348 ProMEX:Q43348 EnsemblPlants:AT1G62660.1 GeneID:842563 KEGG:ath:AT1G62660 TAIR:At1g62660 InParanoid:Q43348 OMA:HSIVEGF PhylomeDB:Q43348 ArrayExpress:Q43348 Genevestigator:Q43348 Uniprot:Q43348
Leaf	Isotig00262	25	9	2.003	0.000126076	TAIR|locus:2026177 - symbol:AT1G62660 species:3702 "Arabidopsis thaliana" [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=IEA;ISS] [GO:0071370 "cellular response to gibberellin stimulus" evidence=IEP] [GO:0000325 "plant-type vacuole" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0009617 "response to bacterium" evidence=IEP] InterPro:IPR001362 InterPro:IPR018053 InterPro:IPR021792 Pfam:PF11837 PROSITE:PS00609 SMART:SM00640 EMBL:CP002684 GO:GO:0005975 InterPro:IPR008985 SUPFAM:SSF49899 InterPro:IPR023296 SUPFAM:SSF75005 CAZy:GH32 KO:K01193 GO:GO:0004575 InterPro:IPR013189 InterPro:IPR013148 Pfam:PF08244 Pfam:PF00251 ProtClustDB:CLSN2687777 EMBL:AY048269 EMBL:AY062481 EMBL:AY063904 EMBL:AY114066 EMBL:X99111 IPI:IPI00517592 PIR:S71268 RefSeq:NP_564798.1 UniGene:At.24113 UniGene:At.67066 ProteinModelPortal:Q43348 SMR:Q43348 STRING:Q43348 PRIDE:Q43348 ProMEX:Q43348 EnsemblPlants:AT1G62660.1 GeneID:842563 KEGG:ath:AT1G62660 TAIR:At1g62660 InParanoid:Q43348 OMA:HSIVEGF PhylomeDB:Q43348 ArrayExpress:Q43348 Genevestigator:Q43348 Uniprot:Q43348
Leaf	Isotig00263	11	0	4.988	0.000159591	TAIR|locus:2201966 - symbol:ATBETAFRUCT4 "AT1G12240" species:3702 "Arabidopsis thaliana" [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=ISS] [GO:0071370 "cellular response to gibberellin stimulus" evidence=IEP] [GO:0000325 "plant-type vacuole" evidence=IDA] [GO:0005773 "vacuole" evidence=ISS;IDA] [GO:0080022 "primary root development" evidence=IMP] [GO:0009617 "response to bacterium" evidence=IEP] [GO:0009505 "plant-type cell wall" evidence=IDA] [GO:0004564 "beta-fructofuranosidase activity" evidence=ISS] InterPro:IPR001362 InterPro:IPR018053 InterPro:IPR021792 Pfam:PF11837 PROSITE:PS00609 SMART:SM00640 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005975 InterPro:IPR008985 SUPFAM:SSF49899 InterPro:IPR023296 Gene3D:G3DSA:2.115.10.20 SUPFAM:SSF75005 GO:GO:0009505 EMBL:AC022522 CAZy:GH32 eggNOG:COG1621 HOGENOM:HBG317462 KO:K01193 GO:GO:0004575 InterPro:IPR013189 InterPro:IPR013148 Pfam:PF08244 Pfam:PF00251 EMBL:AY046009 EMBL:AY142666 EMBL:Y11559 IPI:IPI00545554 PIR:E86257 PIR:S71276 RefSeq:NP_563901.1 UniGene:At.24440 ProteinModelPortal:Q39041 SMR:Q39041 IntAct:Q39041 STRING:Q39041 PRIDE:Q39041 ProMEX:Q39041 EnsemblPlants:AT1G12240.1 GeneID:837777 KEGG:ath:AT1G12240 TAIR:At1g12240 InParanoid:Q39041 OMA:HQSISPR PhylomeDB:Q39041 ProtClustDB:CLSN2687777 ArrayExpress:Q39041 Genevestigator:Q39041 Uniprot:Q39041

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig00282	131	91	1.055	5.12E-08	TAIR|locus:2141385 - symbol:SAM-2 "AT4G01850" species:3702 "Arabidopsis thaliana" [GO:0004478 "methionine adenosyltransferase activity" evidence=ISS] [GO:0006556 "S-adenosylmethionine biosynthetic process" evidence=ISS] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0071281 "cellular response to iron ion" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA;RCA] [GO:0070062 "extracellular vesicular exosome" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR002133 InterPro:IPR022628 InterPro:IPR022629 InterPro:IPR022630 InterPro:IPR022631 InterPro:IPR022636 Pfam:PF00438 Pfam:PF02772 Pfam:PF02773 PIRSF:PIRSF000497 PROSITE:PS00376 PROSITE:PS00377 GO:GO:0005829 GO:GO:0009506 GO:GO:0005524 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005618 GO:GO:0071281 GO:GO:0005730 GO:GO:0005507 EMBL:AC007138 EMBL:AL161493 GO:GO:0070062 GO:GO:0006730 KO:K00789 GO:GO:0006556 UniGene:At.24731 eggNOG:COG0192 HOGENOM:HBG443662 ProtClustDB:PLN02243 GO:GO:0004478 PANTHER:PTHR11964 SUPFAM:SSF55973 TIGRFAMs:TIGR01034 EMBL:M33217 EMBL:AY072327 EMBL:AY094454 EMBL:BT000575 EMBL:Z33778 EMBL:Z29136 IPI:IPI00529348 PIR:JQ0410 RefSeq:NP_001078345.1 RefSeq:NP_192094.1 UniGene:At.24433 UniGene:At.71920 ProteinModelPortal:P17562 SMR:P17562 STRING:P17562 PRIDE:P17562 ProMEX:P17562 EnsemblPlants:AT4G01850.1 EnsemblPlants:AT4G01850.2 GeneID:826987 KEGG:ath:AT4G01850 TAIR:At4g01850 InParanoid:P17562 OMA:ATIDYEK PhylomeDB:P17562 ArrayExpress:P17562 Genevestigator:P17562 GermOnline:AT4G01850 Uniprot:P17562
Leaf	Isotig00284	115	80	1.053	3.48E-07	TAIR|locus:2141385 - symbol:SAM-2 "AT4G01850" species:3702 "Arabidopsis thaliana" [GO:0004478 "methionine adenosyltransferase activity" evidence=ISS] [GO:0006556 "S-adenosylmethionine biosynthetic process" evidence=ISS] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0071281 "cellular response to iron ion" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA;RCA] [GO:0070062 "extracellular vesicular exosome" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR002133 InterPro:IPR022628 InterPro:IPR022629 InterPro:IPR022630 InterPro:IPR022631 InterPro:IPR022636 Pfam:PF00438 Pfam:PF02772 Pfam:PF02773 PIRSF:PIRSF000497 PROSITE:PS00376 PROSITE:PS00377 GO:GO:0005829 GO:GO:0009506 GO:GO:0005524 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005618 GO:GO:0071281 GO:GO:0005730 GO:GO:0005507 EMBL:AC007138 EMBL:AL161493 GO:GO:0070062 GO:GO:0006730 KO:K00789 GO:GO:0006556 UniGene:At.24731 eggNOG:COG0192 HOGENOM:HBG443662 ProtClustDB:PLN02243 GO:GO:0004478 PANTHER:PTHR11964 SUPFAM:SSF55973 TIGRFAMs:TIGR01034 EMBL:M33217 EMBL:AY072327 EMBL:AY094454 EMBL:BT000575 EMBL:Z33778 EMBL:Z29136 IPI:IPI00529348 PIR:JQ0410 RefSeq:NP_001078345.1 RefSeq:NP_192094.1 UniGene:At.24433 UniGene:At.71920 ProteinModelPortal:P17562 SMR:P17562 STRING:P17562 PRIDE:P17562 ProMEX:P17562 EnsemblPlants:AT4G01850.1 EnsemblPlants:AT4G01850.2 GeneID:826987 KEGG:ath:AT4G01850 TAIR:At4g01850 InParanoid:P17562 OMA:ATIDYEK PhylomeDB:P17562 ArrayExpress:P17562 Genevestigator:P17562 GermOnline:AT4G01850 Uniprot:P17562
Leaf	Isotig00285	123	87	1.029	2.33E-07	TAIR|locus:2141385 - symbol:SAM-2 "AT4G01850" species:3702 "Arabidopsis thaliana" [GO:0004478 "methionine adenosyltransferase activity" evidence=ISS] [GO:0006556 "S-adenosylmethionine biosynthetic process" evidence=ISS] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0071281 "cellular response to iron ion" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA;RCA] [GO:0070062 "extracellular vesicular exosome" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR002133 InterPro:IPR022628 InterPro:IPR022629 InterPro:IPR022630 InterPro:IPR022631 InterPro:IPR022636 Pfam:PF00438 Pfam:PF02772 Pfam:PF02773 PIRSF:PIRSF000497 PROSITE:PS00376 PROSITE:PS00377 GO:GO:0005829 GO:GO:0009506 GO:GO:0005524 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005618 GO:GO:0071281 GO:GO:0005730 GO:GO:0005507 EMBL:AC007138 EMBL:AL161493 GO:GO:0070062 GO:GO:0006730 KO:K00789 GO:GO:0006556 UniGene:At.24731 eggNOG:COG0192 HOGENOM:HBG443662 ProtClustDB:PLN02243 GO:GO:0004478 PANTHER:PTHR11964 SUPFAM:SSF55973 TIGRFAMs:TIGR01034 EMBL:M33217 EMBL:AY072327 EMBL:AY094454 EMBL:BT000575 EMBL:Z33778 EMBL:Z29136 IPI:IPI00529348 PIR:JQ0410 RefSeq:NP_001078345.1 RefSeq:NP_192094.1 UniGene:At.24433 UniGene:At.71920 ProteinModelPortal:P17562 SMR:P17562 STRING:P17562 PRIDE:P17562 ProMEX:P17562 EnsemblPlants:AT4G01850.1 EnsemblPlants:AT4G01850.2 GeneID:826987 KEGG:ath:AT4G01850 TAIR:At4g01850 InParanoid:P17562

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						OMA:ATIDYEK PhylomeDB:P17562 ArrayExpress:P17562 Genevestigator:P17562 GermOnline:AT4G01850 Uniprot:P17562
Leaf	Isotig00286	153	94	1.232	2.59E-11	TAIR|locus:2058011 - symbol:MAT3 "AT2G36880" species:3702 "Arabidopsis thaliana" [GO:0004478 "methionine adenosyltransferase activity" evidence=ISS] [GO:0006556 "S-adenosylmethionine biosynthetic process" evidence=ISS] [GO:0006730 "one-carbon metabolic process" evidence=IEA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR002133 InterPro:IPR022628 InterPro:IPR022629 InterPro:IPR022630 InterPro:IPR022631 InterPro:IPR022636 Pfam:PF00438 Pfam:PF02772 Pfam:PF02773 PIRSF:PIRSF000497 PROSITE:PS00376 PROSITE:PS00377 GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 GO:GO:0005524 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0005507 EMBL:AC006922 GO:GO:0009809 GO:GO:0006730 KO:K00789 GO:GO:0006556 eggNOG:COG0192 HOGENOM:HBG443662 ProtClustDB:PLN02243 GO:GO:0004478 PANTHER:PTHR11964 SUPFAM:SSF55973 TIGRFAMs:TIGR01034 EMBL:AF367310 EMBL:AY133601 IPI:IPI00527972 PIR:G84785 RefSeq:NP_001118458.1 RefSeq:NP_181225.1 UniGene:At.23534 HSSP:P13444 ProteinModelPortal:Q9SJL8 SMR:Q9SJL8 STRING:Q9SJL8 PRIDE:Q9SJL8 EnsemblPlants:AT2G36880.1 EnsemblPlants:AT2G36880.2 GeneID:818260 KEGG:ath:AT2G36880 TAIR:At2g36880 InParanoid:Q9SJL8 OMA:RSTCREI PhylomeDB:Q9SJL8 ArrayExpress:Q9SJL8 Genevestigator:Q9SJL8 Uniprot:Q9SJL8
Leaf	Isotig00287	107	76	1.022	1.59E-06	TAIR|locus:2141385 - symbol:SAM-2 "AT4G01850" species:3702 "Arabidopsis thaliana" [GO:0004478 "methionine adenosyltransferase activity" evidence=ISS] [GO:0006556 "S-adenosylmethionine biosynthetic process" evidence=ISS] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0071281 "cellular response to iron ion" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA;RCA] [GO:0070062 "extracellular vesicular exosome" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR002133 InterPro:IPR022628 InterPro:IPR022629 InterPro:IPR022630 InterPro:IPR022631 InterPro:IPR022636 Pfam:PF00438 Pfam:PF02772 Pfam:PF02773 PIRSF:PIRSF000497 PROSITE:PS00376 PROSITE:PS00377 GO:GO:0005829 GO:GO:0009506 GO:GO:0005524 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005618 GO:GO:0071281 GO:GO:0005730 GO:GO:0005507 EMBL:AC007138 EMBL:AL161493 GO:GO:0070062 GO:GO:0006730 KO:K00789 GO:GO:0006556 UniGene:At.24731 eggNOG:COG0192 HOGENOM:HBG443662 ProtClustDB:PLN02243 GO:GO:0004478 PANTHER:PTHR11964 SUPFAM:SSF55973 TIGRFAMs:TIGR01034 EMBL:M33217 EMBL:AY072327 EMBL:AY094454 EMBL:BT000575 EMBL:Z33778 EMBL:Z29136 IPI:IPI00529348 PIR:JQ0410 RefSeq:NP_001078345.1 RefSeq:NP_192094.1 UniGene:At.24433 UniGene:At.71920 ProteinModelPortal:P17562 SMR:P17562 STRING:P17562 PRIDE:P17562 ProMEX:P17562 EnsemblPlants:AT4G01850.1 EnsemblPlants:AT4G01850.2 GeneID:826987 KEGG:ath:AT4G01850 TAIR:At4g01850 InParanoid:P17562 OMA:ATIDYEK PhylomeDB:P17562 ArrayExpress:P17562 Genevestigator:P17562 GermOnline:AT4G01850 Uniprot:P17562
Leaf	Isotig00288	137	83	1.252	1.65E-10	TAIR|locus:2058011 - symbol:MAT3 "AT2G36880" species:3702 "Arabidopsis thaliana" [GO:0004478 "methionine adenosyltransferase activity" evidence=ISS] [GO:0006556 "S-adenosylmethionine biosynthetic process" evidence=ISS] [GO:0006730 "one-carbon metabolic process" evidence=IEA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR002133 InterPro:IPR022628 InterPro:IPR022629 InterPro:IPR022630 InterPro:IPR022631 InterPro:IPR022636 Pfam:PF00438 Pfam:PF02772 Pfam:PF02773 PIRSF:PIRSF000497 PROSITE:PS00376 PROSITE:PS00377 GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 GO:GO:0005524 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0005507 EMBL:AC006922 GO:GO:0009809 GO:GO:0006730 KO:K00789 GO:GO:0006556 eggNOG:COG0192 HOGENOM:HBG443662 ProtClustDB:PLN02243 GO:GO:0004478 PANTHER:PTHR11964 SUPFAM:SSF55973 TIGRFAMs:TIGR01034 EMBL:AF367310 EMBL:AY133601 IPI:IPI00527972 PIR:G84785 RefSeq:NP_001118458.1 RefSeq:NP_181225.1 UniGene:At.23534 HSSP:P13444 ProteinModelPortal:Q9SJL8 SMR:Q9SJL8 STRING:Q9SJL8 PRIDE:Q9SJL8 EnsemblPlants:AT2G36880.1 EnsemblPlants:AT2G36880.2 GeneID:818260 KEGG:ath:AT2G36880 TAIR:At2g36880 InParanoid:Q9SJL8 OMA:RSTCREI PhylomeDB:Q9SJL8 ArrayExpress:Q9SJL8 Genevestigator:Q9SJL8 Uniprot:Q9SJL8
Leaf	Isotig00290	77	528	-2.249	3.85E-56	TAIR|locus:2010361 - symbol:GAPA-2 "glyceraldehyde 3-phosphate dehydrogenase A subunit 2" species:3702 "Arabidopsis thaliana" [GO:0006006 "glucose metabolic process" evidence=IEA] [GO:0006096 "glycolysis"

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						evidence=ISS] [GO:0051287 "NAD binding" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] InterPro:IPR006424 InterPro:IPR016040 InterPro:IPR020828 InterPro:IPR020829 InterPro:IPR020830 InterPro:IPR020831 Pfam:PF00044 Pfam:PF02800 PIRSF:PIRSF000149 PRINTS:PR00078 PROSITE:PS00071 SMART:SM00846 EMBL:CP002684 GO:GO:0048046 GO:GO:0009570 GO:GO:0016020 Gene3D:G3DSA:3.40.50.720 GO:GO:0051287 GO:GO:0050661 GO:GO:0016620 GO:GO:0009941 GO:GO:0006006 EMBL:AC012187 HOGENOM:HBG571736 PANTHER:PTHR10836 TIGRFAMs:TIGR01534 KO:K05298 ProtClustDB:PLN03096 EMBL:BT008637 EMBL:BT015867 IPI:IPI00544582 PIR:F86262 RefSeq:NP_172750.1 UniGene:At.28212 HSSP:P19866 ProteinModelPortal:Q9LPW0 SMR:Q9LPW0 STRING:Q9LPW0 PRIDE:Q9LPW0 ProMEX:Q9LPW0 EnsemblPlants:AT1G12900.1 GeneID:837848 KEGG:ath:AT1G12900 TAIR:At1g12900 InParanoid:Q9LPW0 OMA:INVTSDP PhylomeDB:Q9LPW0 ArrayExpress:Q9LPW0 Genevestigator:Q9LPW0 Uniprot:Q9LPW0
Leaf	Isotig00291	77	528	-2.249	3.85E-56	TAIR|locus:2010361 - symbol:GAPA-2 "glyceraldehyde 3-phosphate dehydrogenase A subunit 2" species:3702 "Arabidopsis thaliana" [GO:0006006 "glucose metabolic process" evidence=IEA] [GO:0006096 "glycolysis" evidence=ISS] [GO:0051287 "NAD binding" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] InterPro:IPR006424 InterPro:IPR016040 InterPro:IPR020828 InterPro:IPR020829 InterPro:IPR020830 InterPro:IPR020831 Pfam:PF00044 Pfam:PF02800 PIRSF:PIRSF000149 PRINTS:PR00078 PROSITE:PS00071 SMART:SM00846 EMBL:CP002684 GO:GO:0048046 GO:GO:0009570 GO:GO:0016020 Gene3D:G3DSA:3.40.50.720 GO:GO:0051287 GO:GO:0050661 GO:GO:0016620 GO:GO:0009941 GO:GO:0006006 EMBL:AC012187 HOGENOM:HBG571736 PANTHER:PTHR10836 TIGRFAMs:TIGR01534 KO:K05298 ProtClustDB:PLN03096 EMBL:BT008637 EMBL:BT015867 IPI:IPI00544582 PIR:F86262 RefSeq:NP_172750.1 UniGene:At.28212 HSSP:P19866 ProteinModelPortal:Q9LPW0 SMR:Q9LPW0 STRING:Q9LPW0 PRIDE:Q9LPW0 ProMEX:Q9LPW0 EnsemblPlants:AT1G12900.1 GeneID:837848 KEGG:ath:AT1G12900 TAIR:At1g12900 InParanoid:Q9LPW0 OMA:INVTSDP PhylomeDB:Q9LPW0 ArrayExpress:Q9LPW0 Genevestigator:Q9LPW0 Uniprot:Q9LPW0
Leaf	Isotig00292	100	643	-2.156	1.27E-64	TAIR|locus:2010361 - symbol:GAPA-2 "glyceraldehyde 3-phosphate dehydrogenase A subunit 2" species:3702 "Arabidopsis thaliana" [GO:0006006 "glucose metabolic process" evidence=IEA] [GO:0006096 "glycolysis" evidence=ISS] [GO:0051287 "NAD binding" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] InterPro:IPR006424 InterPro:IPR016040 InterPro:IPR020828 InterPro:IPR020829 InterPro:IPR020830 InterPro:IPR020831 Pfam:PF00044 Pfam:PF02800 PIRSF:PIRSF000149 PRINTS:PR00078 PROSITE:PS00071 SMART:SM00846 EMBL:CP002684 GO:GO:0048046 GO:GO:0009570 GO:GO:0016020 Gene3D:G3DSA:3.40.50.720 GO:GO:0051287 GO:GO:0050661 GO:GO:0016620 GO:GO:0009941 GO:GO:0006006 EMBL:AC012187 HOGENOM:HBG571736 PANTHER:PTHR10836 TIGRFAMs:TIGR01534 KO:K05298 ProtClustDB:PLN03096 EMBL:BT008637 EMBL:BT015867 IPI:IPI00544582 PIR:F86262 RefSeq:NP_172750.1 UniGene:At.28212 HSSP:P19866 ProteinModelPortal:Q9LPW0 SMR:Q9LPW0 STRING:Q9LPW0 PRIDE:Q9LPW0 ProMEX:Q9LPW0 EnsemblPlants:AT1G12900.1 GeneID:837848 KEGG:ath:AT1G12900 TAIR:At1g12900 InParanoid:Q9LPW0 OMA:INVTSDP PhylomeDB:Q9LPW0 ArrayExpress:Q9LPW0 Genevestigator:Q9LPW0 Uniprot:Q9LPW0
Leaf	Isotig00293	100	643	-2.156	1.27E-64	TAIR|locus:2010361 - symbol:GAPA-2 "glyceraldehyde 3-phosphate dehydrogenase A subunit 2" species:3702 "Arabidopsis thaliana" [GO:0006006 "glucose metabolic process" evidence=IEA] [GO:0006096 "glycolysis" evidence=ISS] [GO:0051287 "NAD binding" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] InterPro:IPR006424 InterPro:IPR016040 InterPro:IPR020828 InterPro:IPR020829 InterPro:IPR020830 InterPro:IPR020831 Pfam:PF00044 Pfam:PF02800 PIRSF:PIRSF000149 PRINTS:PR00078 PROSITE:PS00071 SMART:SM00846 EMBL:CP002684 GO:GO:0048046 GO:GO:0009570 GO:GO:0016020 Gene3D:G3DSA:3.40.50.720 GO:GO:0051287 GO:GO:0050661

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0016620 GO:GO:0009941 GO:GO:0006006 EMBL:AC012187 HOGENOM:HBG571736 PANTHER:PTHR10836 TIGRFAMs:TIGR01534 KO:K05298 ProtClustDB:PLN03096 EMBL:BT008637 EMBL:BT015867 IPI:IPI00544582 PIR:F86262 RefSeq:NP_172750.1 UniGene:At.28212 HSSP:P19866 ProteinModelPortal:Q9LPW0 SMR:Q9LPW0 STRING:Q9LPW0 PRIDE:Q9LPW0 ProMEX:Q9LPW0 EnsemblPlants:AT1G12900.1 GeneID:837848 KEGG:ath:AT1G12900 TAIR:At1g12900 InParanoid:Q9LPW0 OMA:INVTSDP PhylomeDB:Q9LPW0 ArrayExpress:Q9LPW0 Genevestigator:Q9LPW0 Uniprot:Q9LPW0
Leaf	Isotig00294	100	643	-2.156	1.27E-64	TAIR|locus:2010361 - symbol:GAPA-2 "glyceraldehyde 3-phosphate dehydrogenase A subunit 2" species:3702 "Arabidopsis thaliana" [GO:0006006 "glucose metabolic process" evidence=IEA] [GO:0006096 "glycolysis" evidence=ISS] [GO:0051287 "NAD binding" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] InterPro:IPR006424 InterPro:IPR016040 InterPro:IPR020828 InterPro:IPR020829 InterPro:IPR020830 InterPro:IPR020831 Pfam:PF00044 Pfam:PF02800 PIRSF:PIRSF000149 PRINTS:PR00078 PROSITE:PS00071 SMART:SM00846 EMBL:CP002684 GO:GO:0048046 GO:GO:0009570 GO:GO:0016020 Gene3D:G3DSA:3.40.50.720 GO:GO:0051287 GO:GO:0050661 GO:GO:0016620 GO:GO:0009941 GO:GO:0006006 EMBL:AC012187 HOGENOM:HBG571736 PANTHER:PTHR10836 TIGRFAMs:TIGR01534 KO:K05298 ProtClustDB:PLN03096 EMBL:BT008637 EMBL:BT015867 IPI:IPI00544582 PIR:F86262 RefSeq:NP_172750.1 UniGene:At.28212 HSSP:P19866 ProteinModelPortal:Q9LPW0 SMR:Q9LPW0 STRING:Q9LPW0 PRIDE:Q9LPW0 ProMEX:Q9LPW0 EnsemblPlants:AT1G12900.1 GeneID:837848 KEGG:ath:AT1G12900 TAIR:At1g12900 InParanoid:Q9LPW0 OMA:INVTSDP PhylomeDB:Q9LPW0 ArrayExpress:Q9LPW0 Genevestigator:Q9LPW0 Uniprot:Q9LPW0
Leaf	Isotig00295	100	643	-2.156	1.27E-64	TAIR|locus:2010361 - symbol:GAPA-2 "glyceraldehyde 3-phosphate dehydrogenase A subunit 2" species:3702 "Arabidopsis thaliana" [GO:0006006 "glucose metabolic process" evidence=IEA] [GO:0006096 "glycolysis" evidence=ISS] [GO:0051287 "NAD binding" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] InterPro:IPR006424 InterPro:IPR016040 InterPro:IPR020828 InterPro:IPR020829 InterPro:IPR020830 InterPro:IPR020831 Pfam:PF00044 Pfam:PF02800 PIRSF:PIRSF000149 PRINTS:PR00078 PROSITE:PS00071 SMART:SM00846 EMBL:CP002684 GO:GO:0048046 GO:GO:0009570 GO:GO:0016020 Gene3D:G3DSA:3.40.50.720 GO:GO:0051287 GO:GO:0050661 GO:GO:0016620 GO:GO:0009941 GO:GO:0006006 EMBL:AC012187 HOGENOM:HBG571736 PANTHER:PTHR10836 TIGRFAMs:TIGR01534 KO:K05298 ProtClustDB:PLN03096 EMBL:BT008637 EMBL:BT015867 IPI:IPI00544582 PIR:F86262 RefSeq:NP_172750.1 UniGene:At.28212 HSSP:P19866 ProteinModelPortal:Q9LPW0 SMR:Q9LPW0 STRING:Q9LPW0 PRIDE:Q9LPW0 ProMEX:Q9LPW0 EnsemblPlants:AT1G12900.1 GeneID:837848 KEGG:ath:AT1G12900 TAIR:At1g12900 InParanoid:Q9LPW0 OMA:INVTSDP PhylomeDB:Q9LPW0 ArrayExpress:Q9LPW0 Genevestigator:Q9LPW0 Uniprot:Q9LPW0
Leaf	Isotig00300	11	0	4.988	0.000159591	No hit
Leaf	Isotig00301	11	0	4.988	0.000159591	No hit
Leaf	Isotig00309	31	118	-1.399	7.46E-08	TAIR|locus:2007367 - symbol:F2KP "AT1G07110" species:3702 "Arabidopsis thaliana" [GO:0004331 "fructose-2,6-bisphosphate 2-phosphatase activity" evidence=IMP] [GO:0006000 "fructose metabolic process" evidence=IDA] [GO:0043609 "regulation of carbon utilization" evidence=IMP] [GO:0006002 "fructose 6-phosphate metabolic process" evidence=IDA] [GO:0006003 "fructose 2,6-bisphosphate metabolic process" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001345 InterPro:IPR002044 InterPro:IPR003094 InterPro:IPR013079 InterPro:IPR013784 InterPro:IPR016260 Pfam:PF00686 Pfam:PF01591 PIRSF:PIRSF000709 PRINTS:PR00991 PROSITE:PS00175 PROSITE:PS51166 SMART:SM01065 Pfam:PF00300 EMBL:CP002684 GO:GO:0005829 GO:GO:0005886 GO:GO:0005524 InterPro:IPR013783 Gene3D:G3DSA:2.60.40.10 eggNOG:COG0406 GO:GO:0003873 GO:GO:0004331 GO:GO:0006003 InterPro:IPR013078 PANTHER:PTHR10606 SMART:SM00855 SUPFAM:SSF49452 EMBL:AC067971 GO:GO:2001070 GO:GO:0006002 KO:K01103 BRENDA:3.1.3.46 HSSP:P07953 BRENDA:2.7.1.105 EMBL:AF190739 EMBL:AF242859 EMBL:AB035288 EMBL:AY128346 IPI:IPI00535340 PIR:H86205 RefSeq:NP_172191.1 UniGene:At.15685 ProteinModelPortal:Q9MB58 SMR:Q9MB58 STRING:Q9MB58 PRIDE:Q9SP17 ProMEX:Q9MB58 EnsemblPlants:AT1G07110.1 GeneID:837221 KEGG:ath:AT1G07110

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						TAIR:At1g07110 InParanoid:Q9MB58 OMA:EMPLHTI PhylomeDB:Q9MB58 ProtClustDB:CLSN2914245 ArrayExpress:Q8L7N6 Genevestigator:Q9MB58 GO:GO:0043609 Uniprot:Q9MB58
Leaf	Isotig00310	31	118	-1.399	7.46E-08	TAIR|locus:2007367 - symbol:F2KP "AT1G07110" species:3702 "Arabidopsis thaliana" [GO:0004331 "fructose-2,6-bisphosphate 2-phosphatase activity" evidence=IMP] [GO:0006000 "fructose metabolic process" evidence=IDA] [GO:0043609 "regulation of carbon utilization" evidence=IMP] [GO:0006002 "fructose 6-phosphate metabolic process" evidence=IDA] [GO:0006003 "fructose 2,6-bisphosphate metabolic process" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001345 InterPro:IPR002044 InterPro:IPR003094 InterPro:IPR013079 InterPro:IPR013784 InterPro:IPR016260 Pfam:PF00686 Pfam:PF01591 PIRSF:PIRSF000709 PRINTS:PR00991 PROSITE:PS00175 PROSITE:PS51166 SMART:SM01065 Pfam:PF00300 EMBL:CP002684 GO:GO:0005829 GO:GO:0005886 GO:GO:0005524 InterPro:IPR013783 Gene3D:G3DSA:2.60.40.10 eggNOG:COG0406 GO:GO:0003873 GO:GO:0004331 GO:GO:0006003 InterPro:IPR013078 PANTHER:PTHR10606 SMART:SM00855 SUPFAM:SSF49452 EMBL:AC067971 GO:GO:2001070 GO:GO:0006002 KO:K01103 BRENDA:3.1.3.46 HSSP:P07953 BRENDA:2.7.1.105 EMBL:AF190739 EMBL:AF242859 EMBL:AB035288 EMBL:AY128346 IPI:IPI00535340 PIR:H86205 RefSeq:NP_172191.1 UniGene:At.15685 ProteinModelPortal:Q9MB58 SMR:Q9MB58 STRING:Q9MB58 PRIDE:Q9SP17 ProMEX:Q9MB58 EnsemblPlants:AT1G07110.1 GeneID:837221 KEGG:ath:AT1G07110 TAIR:At1g07110 InParanoid:Q9MB58 OMA:EMPLHTI PhylomeDB:Q9MB58 ProtClustDB:CLSN2914245 ArrayExpress:Q8L7N6 Genevestigator:Q9MB58 GO:GO:0043609 Uniprot:Q9MB58
Leaf	Isotig00311	30	120	-1.471	1.78E-08	TAIR|locus:2007367 - symbol:F2KP "AT1G07110" species:3702 "Arabidopsis thaliana" [GO:0004331 "fructose-2,6-bisphosphate 2-phosphatase activity" evidence=IMP] [GO:0006000 "fructose metabolic process" evidence=IDA] [GO:0043609 "regulation of carbon utilization" evidence=IMP] [GO:0006002 "fructose 6-phosphate metabolic process" evidence=IDA] [GO:0006003 "fructose 2,6-bisphosphate metabolic process" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001345 InterPro:IPR002044 InterPro:IPR003094 InterPro:IPR013079 InterPro:IPR013784 InterPro:IPR016260 Pfam:PF00686 Pfam:PF01591 PIRSF:PIRSF000709 PRINTS:PR00991 PROSITE:PS00175 PROSITE:PS51166 SMART:SM01065 Pfam:PF00300 EMBL:CP002684 GO:GO:0005829 GO:GO:0005886 GO:GO:0005524 InterPro:IPR013783 Gene3D:G3DSA:2.60.40.10 eggNOG:COG0406 GO:GO:0003873 GO:GO:0004331 GO:GO:0006003 InterPro:IPR013078 PANTHER:PTHR10606 SMART:SM00855 SUPFAM:SSF49452 EMBL:AC067971 GO:GO:2001070 GO:GO:0006002 KO:K01103 BRENDA:3.1.3.46 HSSP:P07953 BRENDA:2.7.1.105 EMBL:AF190739 EMBL:AF242859 EMBL:AB035288 EMBL:AY128346 IPI:IPI00535340 PIR:H86205 RefSeq:NP_172191.1 UniGene:At.15685 ProteinModelPortal:Q9MB58 SMR:Q9MB58 STRING:Q9MB58 PRIDE:Q9SP17 ProMEX:Q9MB58 EnsemblPlants:AT1G07110.1 GeneID:837221 KEGG:ath:AT1G07110 TAIR:At1g07110 InParanoid:Q9MB58 OMA:EMPLHTI PhylomeDB:Q9MB58 ProtClustDB:CLSN2914245 ArrayExpress:Q8L7N6 Genevestigator:Q9MB58 GO:GO:0043609 Uniprot:Q9MB58
Leaf	Isotig00312	30	120	-1.471	1.78E-08	TAIR|locus:2007367 - symbol:F2KP "AT1G07110" species:3702 "Arabidopsis thaliana" [GO:0004331 "fructose-2,6-bisphosphate 2-phosphatase activity" evidence=IMP] [GO:0006000 "fructose metabolic process" evidence=IDA] [GO:0043609 "regulation of carbon utilization" evidence=IMP] [GO:0006002 "fructose 6-phosphate metabolic process" evidence=IDA] [GO:0006003 "fructose 2,6-bisphosphate metabolic process" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001345 InterPro:IPR002044 InterPro:IPR003094 InterPro:IPR013079 InterPro:IPR013784 InterPro:IPR016260 Pfam:PF00686 Pfam:PF01591 PIRSF:PIRSF000709 PRINTS:PR00991 PROSITE:PS00175 PROSITE:PS51166 SMART:SM01065 Pfam:PF00300 EMBL:CP002684 GO:GO:0005829 GO:GO:0005886 GO:GO:0005524 InterPro:IPR013783 Gene3D:G3DSA:2.60.40.10 eggNOG:COG0406 GO:GO:0003873 GO:GO:0004331 GO:GO:0006003 InterPro:IPR013078 PANTHER:PTHR10606 SMART:SM00855 SUPFAM:SSF49452 EMBL:AC067971 GO:GO:2001070 GO:GO:0006002 KO:K01103 BRENDA:3.1.3.46 HSSP:P07953 BRENDA:2.7.1.105 EMBL:AF190739 EMBL:AF242859 EMBL:AB035288 EMBL:AY128346 IPI:IPI00535340 PIR:H86205 RefSeq:NP_172191.1 UniGene:At.15685 ProteinModelPortal:Q9MB58 SMR:Q9MB58 STRING:Q9MB58 PRIDE:Q9SP17 ProMEX:Q9MB58 EnsemblPlants:AT1G07110.1 GeneID:837221 KEGG:ath:AT1G07110 TAIR:At1g07110 InParanoid:Q9MB58 OMA:EMPLHTI PhylomeDB:Q9MB58 ProtClustDB:CLSN2914245 ArrayExpress:Q8L7N6 Genevestigator:Q9MB58 GO:GO:0043609 Uniprot:Q9MB58
Leaf	Isotig00313	31	117	-1.387	1.03E-07	TAIR|locus:2007367 - symbol:F2KP "AT1G07110" species:3702 "Arabidopsis thaliana" [GO:0004331 "fructose-2,6-bisphosphate 2-phosphatase activity" evidence=IMP] [GO:0006000 "fructose metabolic process" evidence=IDA]

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						[GO:0043609 "regulation of carbon utilization" evidence=IMP] [GO:0006002 "fructose 6-phosphate metabolic process" evidence=IDA] [GO:0006003 "fructose 2,6-bisphosphate metabolic process" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001345 InterPro:IPR002044 InterPro:IPR003094 InterPro:IPR013079 InterPro:IPR013784 InterPro:IPR016260 Pfam:PF00686 Pfam:PF01591 PIRSF:PIRSF000709 PRINTS:PR00991 PROSITE:PS00175 PROSITE:PS51166 SMART:SM01065 Pfam:PF00300 EMBL:CP002684 GO:GO:0005829 GO:GO:0005886 GO:GO:0005524 InterPro:IPR013783 Gene3D:G3DSA:2.60.40.10 eggNOG:COG0406 GO:GO:0003873 GO:GO:0004331 GO:GO:0006003 InterPro:IPR013078 PANTHER:PTHR10606 SMART:SM00855 SUPFAM:SSF49452 EMBL:AC067971 GO:GO:2001070 GO:GO:0006002 KO:K01103 BRENDA:3.1.3.46 HSSP:P07953 BRENDA:2.7.1.105 EMBL:AF190739 EMBL:AF242859 EMBL:AB035288 EMBL:AY128346 IPI:IPI00535340 PIR:H86205 RefSeq:NP_172191.1 UniGene:At.15685 ProteinModelPortal:Q9MB58 SMR:Q9MB58 STRING:Q9MB58 PRIDE:Q9SP17 ProMEX:Q9MB58 EnsemblPlants:AT1G07110.1 GeneID:837221 KEGG:ath:AT1G07110 TAIR:At1g07110 InParanoid:Q9MB58 OMA:EMPLHTI PhylomeDB:Q9MB58 ProtClustDB:CLSN2914245 ArrayExpress:Q8L7N6 Genevestigator:Q9MB58 GO:GO:0043609 Uniprot:Q9MB58
Leaf	Isotig00314	30	119	-1.459	2.48E-08	TAIR|locus:2007367 - symbol:F2KP "AT1G07110" species:3702 "Arabidopsis thaliana" [GO:0004331 "fructose-2,6-bisphosphate 2-phosphatase activity" evidence=IMP] [GO:0006000 "fructose metabolic process" evidence=IDA] [GO:0043609 "regulation of carbon utilization" evidence=IMP] [GO:0006002 "fructose 6-phosphate metabolic process" evidence=IDA] [GO:0006003 "fructose 2,6-bisphosphate metabolic process" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001345 InterPro:IPR002044 InterPro:IPR003094 InterPro:IPR013079 InterPro:IPR013784 InterPro:IPR016260 Pfam:PF00686 Pfam:PF01591 PIRSF:PIRSF000709 PRINTS:PR00991 PROSITE:PS00175 PROSITE:PS51166 SMART:SM01065 Pfam:PF00300 EMBL:CP002684 GO:GO:0005829 GO:GO:0005886 GO:GO:0005524 InterPro:IPR013783 Gene3D:G3DSA:2.60.40.10 eggNOG:COG0406 GO:GO:0003873 GO:GO:0004331 GO:GO:0006003 InterPro:IPR013078 PANTHER:PTHR10606 SMART:SM00855 SUPFAM:SSF49452 EMBL:AC067971 GO:GO:2001070 GO:GO:0006002 KO:K01103 BRENDA:3.1.3.46 HSSP:P07953 BRENDA:2.7.1.105 EMBL:AF190739 EMBL:AF242859 EMBL:AB035288 EMBL:AY128346 IPI:IPI00535340 PIR:H86205 RefSeq:NP_172191.1 UniGene:At.15685 ProteinModelPortal:Q9MB58 SMR:Q9MB58 STRING:Q9MB58 PRIDE:Q9SP17 ProMEX:Q9MB58 EnsemblPlants:AT1G07110.1 GeneID:837221 KEGG:ath:AT1G07110 TAIR:At1g07110 InParanoid:Q9MB58 OMA:EMPLHTI PhylomeDB:Q9MB58 ProtClustDB:CLSN2914245 ArrayExpress:Q8L7N6 Genevestigator:Q9MB58 GO:GO:0043609 Uniprot:Q9MB58
Leaf	Isotig00315	30	118	-1.447	3.46E-08	TAIR|locus:2007367 - symbol:F2KP "AT1G07110" species:3702 "Arabidopsis thaliana" [GO:0004331 "fructose-2,6-bisphosphate 2-phosphatase activity" evidence=IMP] [GO:0006000 "fructose metabolic process" evidence=IDA] [GO:0043609 "regulation of carbon utilization" evidence=IMP] [GO:0006002 "fructose 6-phosphate metabolic process" evidence=IDA] [GO:0006003 "fructose 2,6-bisphosphate metabolic process" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001345 InterPro:IPR002044 InterPro:IPR003094 InterPro:IPR013079 InterPro:IPR013784 InterPro:IPR016260 Pfam:PF00686 Pfam:PF01591 PIRSF:PIRSF000709 PRINTS:PR00991 PROSITE:PS00175 PROSITE:PS51166 SMART:SM01065 Pfam:PF00300 EMBL:CP002684 GO:GO:0005829 GO:GO:0005886 GO:GO:0005524 InterPro:IPR013783 Gene3D:G3DSA:2.60.40.10 eggNOG:COG0406 GO:GO:0003873 GO:GO:0004331 GO:GO:0006003 InterPro:IPR013078 PANTHER:PTHR10606 SMART:SM00855 SUPFAM:SSF49452 EMBL:AC067971 GO:GO:2001070 GO:GO:0006002 KO:K01103 BRENDA:3.1.3.46 HSSP:P07953 BRENDA:2.7.1.105 EMBL:AF190739 EMBL:AF242859 EMBL:AB035288 EMBL:AY128346 IPI:IPI00535340 PIR:H86205 RefSeq:NP_172191.1 UniGene:At.15685 ProteinModelPortal:Q9MB58 SMR:Q9MB58 STRING:Q9MB58 PRIDE:Q9SP17 ProMEX:Q9MB58 EnsemblPlants:AT1G07110.1 GeneID:837221 KEGG:ath:AT1G07110 TAIR:At1g07110 InParanoid:Q9MB58 OMA:EMPLHTI PhylomeDB:Q9MB58 ProtClustDB:CLSN2914245 ArrayExpress:Q8L7N6 Genevestigator:Q9MB58 GO:GO:0043609 Uniprot:Q9MB58
Leaf	Isotig00316	30	118	-1.447	3.46E-08	TAIR|locus:2007367 - symbol:F2KP "AT1G07110" species:3702 "Arabidopsis thaliana" [GO:0004331 "fructose-2,6-bisphosphate 2-phosphatase activity" evidence=IMP] [GO:0006000 "fructose metabolic process" evidence=IDA] [GO:0043609 "regulation of carbon utilization" evidence=IMP] [GO:0006002 "fructose 6-phosphate metabolic process" evidence=IDA] [GO:0006003 "fructose 2,6-bisphosphate metabolic process" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001345 InterPro:IPR002044 InterPro:IPR003094 InterPro:IPR013079 InterPro:IPR013784 InterPro:IPR016260 Pfam:PF00686 Pfam:PF01591

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						PIRSF:PIRSF000709 PRINTS:PR00991 PROSITE:PS00175 PROSITE:PS51166 SMART:SM01065 Pfam:PF00300 EMBL:CP002684 GO:GO:0005829 GO:GO:0005886 GO:GO:0005524 InterPro:IPR013783 Gene3D:G3DSA:2.60.40.10 eggNOG:COG0406 GO:GO:0003873 GO:GO:0004331 GO:GO:0006003 InterPro:IPR013078 PANTHER:PTHR10606 SMART:SM00855 SUPFAM:SSF49452 EMBL:AC067971 GO:GO:2001070 GO:GO:0006002 KO:K01103 BRENDA:3.1.3.46 HSSP:P07953 BRENDA:2.7.1.105 EMBL:AF190739 EMBL:AF242859 EMBL:AB035288 EMBL:AY128346 IPI:IPI00535340 PIR:H86205 RefSeq:NP_172191.1 UniGene:At.15685 ProteinModelPortal:Q9MB58 SMR:Q9MB58 STRING:Q9MB58 PRIDE:Q9SP17 ProMEX:Q9MB58 EnsemblPlants:AT1G07110.1 GeneID:837221 KEGG:ath:AT1G07110 TAIR:At1g07110 InParanoid:Q9MB58 OMA:EMPLHTI PhylomeDB:Q9MB58 ProtClustDB:CLSN2914245 ArrayExpress:Q8L7N6 Genevestigator:Q9MB58 GO:GO:0043609 Uniprot:Q9MB58
Leaf	Isotig00317	29	120	-1.520	7.91E-09	TAIR|locus:2007367 - symbol:F2KP "AT1G07110" species:3702 "Arabidopsis thaliana" [GO:0004331 "fructose-2,6-bisphosphate 2-phosphatase activity" evidence=IMP] [GO:0006000 "fructose metabolic process" evidence=IDA] [GO:0043609 "regulation of carbon utilization" evidence=IMP] [GO:0006002 "fructose 6-phosphate metabolic process" evidence=IDA] [GO:0006003 "fructose 2,6-bisphosphate metabolic process" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001345 InterPro:IPR002044 InterPro:IPR003094 InterPro:IPR013079 InterPro:IPR013784 InterPro:IPR016260 Pfam:PF00686 Pfam:PF01591 PIRSF:PIRSF000709 PRINTS:PR00991 PROSITE:PS00175 PROSITE:PS51166 SMART:SM01065 Pfam:PF00300 EMBL:CP002684 GO:GO:0005829 GO:GO:0005886 GO:GO:0005524 InterPro:IPR013783 Gene3D:G3DSA:2.60.40.10 eggNOG:COG0406 GO:GO:0003873 GO:GO:0004331 GO:GO:0006003 InterPro:IPR013078 PANTHER:PTHR10606 SMART:SM00855 SUPFAM:SSF49452 EMBL:AC067971 GO:GO:2001070 GO:GO:0006002 KO:K01103 BRENDA:3.1.3.46 HSSP:P07953 BRENDA:2.7.1.105 EMBL:AF190739 EMBL:AF242859 EMBL:AB035288 EMBL:AY128346 IPI:IPI00535340 PIR:H86205 RefSeq:NP_172191.1 UniGene:At.15685 ProteinModelPortal:Q9MB58 SMR:Q9MB58 STRING:Q9MB58 PRIDE:Q9SP17 ProMEX:Q9MB58 EnsemblPlants:AT1G07110.1 GeneID:837221 KEGG:ath:AT1G07110 TAIR:At1g07110 InParanoid:Q9MB58 OMA:EMPLHTI PhylomeDB:Q9MB58 ProtClustDB:CLSN2914245 ArrayExpress:Q8L7N6 Genevestigator:Q9MB58 GO:GO:0043609 Uniprot:Q9MB58
Leaf	Isotig00318	29	120	-1.520	7.91E-09	TAIR|locus:2007367 - symbol:F2KP "AT1G07110" species:3702 "Arabidopsis thaliana" [GO:0004331 "fructose-2,6-bisphosphate 2-phosphatase activity" evidence=IMP] [GO:0006000 "fructose metabolic process" evidence=IDA] [GO:0043609 "regulation of carbon utilization" evidence=IMP] [GO:0006002 "fructose 6-phosphate metabolic process" evidence=IDA] [GO:0006003 "fructose 2,6-bisphosphate metabolic process" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001345 InterPro:IPR002044 InterPro:IPR003094 InterPro:IPR013079 InterPro:IPR013784 InterPro:IPR016260 Pfam:PF00686 Pfam:PF01591 PIRSF:PIRSF000709 PRINTS:PR00991 PROSITE:PS00175 PROSITE:PS51166 SMART:SM01065 Pfam:PF00300 EMBL:CP002684 GO:GO:0005829 GO:GO:0005886 GO:GO:0005524 InterPro:IPR013783 Gene3D:G3DSA:2.60.40.10 eggNOG:COG0406 GO:GO:0003873 GO:GO:0004331 GO:GO:0006003 InterPro:IPR013078 PANTHER:PTHR10606 SMART:SM00855 SUPFAM:SSF49452 EMBL:AC067971 GO:GO:2001070 GO:GO:0006002 KO:K01103 BRENDA:3.1.3.46 HSSP:P07953 BRENDA:2.7.1.105 EMBL:AF190739 EMBL:AF242859 EMBL:AB035288 EMBL:AY128346 IPI:IPI00535340 PIR:H86205 RefSeq:NP_172191.1 UniGene:At.15685 ProteinModelPortal:Q9MB58 SMR:Q9MB58 STRING:Q9MB58 PRIDE:Q9SP17 ProMEX:Q9MB58 EnsemblPlants:AT1G07110.1 GeneID:837221 KEGG:ath:AT1G07110 TAIR:At1g07110 InParanoid:Q9MB58 OMA:EMPLHTI PhylomeDB:Q9MB58 ProtClustDB:CLSN2914245 ArrayExpress:Q8L7N6 Genevestigator:Q9MB58 GO:GO:0043609 Uniprot:Q9MB58
Leaf	Isotig00319	30	117	-1.435	4.82E-08	TAIR|locus:2007367 - symbol:F2KP "AT1G07110" species:3702 "Arabidopsis thaliana" [GO:0004331 "fructose-2,6-bisphosphate 2-phosphatase activity" evidence=IMP] [GO:0006000 "fructose metabolic process" evidence=IDA] [GO:0043609 "regulation of carbon utilization" evidence=IMP] [GO:0006002 "fructose 6-phosphate metabolic process" evidence=IDA] [GO:0006003 "fructose 2,6-bisphosphate metabolic process" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001345 InterPro:IPR002044 InterPro:IPR003094 InterPro:IPR013079 InterPro:IPR013784 InterPro:IPR016260 Pfam:PF00686 Pfam:PF01591 PIRSF:PIRSF000709 PRINTS:PR00991 PROSITE:PS00175 PROSITE:PS51166 SMART:SM01065 Pfam:PF00300 EMBL:CP002684 GO:GO:0005829 GO:GO:0005886 GO:GO:0005524 InterPro:IPR013783 Gene3D:G3DSA:2.60.40.10 eggNOG:COG0406 GO:GO:0003873 GO:GO:0004331 GO:GO:0006003 InterPro:IPR013078 PANTHER:PTHR10606 SMART:SM00855 SUPFAM:SSF49452 EMBL:AC067971

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:2001070 GO:GO:0006002 KO:K01103 BRENDA:3.1.3.46 HSSP:P07953 BRENDA:2.7.1.105 EMBL:AF190739 EMBL:AF242859 EMBL:AB035288 EMBL:AY128346 IPI:IPI00535340 PIR:H86205 RefSeq:NP_172191.1 UniGene:At.15685 ProteinModelPortal:Q9MB58 SMR:Q9MB58 STRING:Q9MB58 PRIDE:Q9SP17 ProMEX:Q9MB58 EnsemblPlants:AT1G07110.1 GeneID:837221 KEGG:ath:AT1G07110 TAIR:At1g07110 InParanoid:Q9MB58 OMA:EMPLHTI PhylomeDB:Q9MB58 ProtClustDB:CLSN2914245 ArrayExpress:Q8L7N6 Genevestigator:Q9MB58 GO:GO:0043609 Uniprot:Q9MB58
Leaf	Isotig00320	29	119	-1.508	1.11E-08	TAIR|locus:2007367 - symbol:F2KP "AT1G07110" species:3702 "Arabidopsis thaliana" [GO:0004331 "fructose-2,6-bisphosphate 2-phosphatase activity" evidence=IMP] [GO:0006000 "fructose metabolic process" evidence=IDA] [GO:0043609 "regulation of carbon utilization" evidence=IMP] [GO:0006002 "fructose 6-phosphate metabolic process" evidence=IDA] [GO:0006003 "fructose 2,6-bisphosphate metabolic process" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001345 InterPro:IPR002044 InterPro:IPR003094 InterPro:IPR013079 InterPro:IPR013784 InterPro:IPR016260 Pfam:PF00686 Pfam:PF01591 PIRSF:PIRSF000709 PRINTS:PR00991 PROSITE:PS00175 PROSITE:PS51166 SMART:SM01065 Pfam:PF00300 EMBL:CP002684 GO:GO:0005829 GO:GO:0005886 GO:GO:0005524 InterPro:IPR013783 Gene3D:G3DSA:2.60.40.10 eggNOG:COG0406 GO:GO:0003873 GO:GO:0004331 GO:GO:0006003 InterPro:IPR013078 PANTHER:PTHR10606 SMART:SM00855 SUPFAM:SSF49452 EMBL:AC067971 GO:GO:2001070 GO:GO:0006002 KO:K01103 BRENDA:3.1.3.46 HSSP:P07953 BRENDA:2.7.1.105 EMBL:AF190739 EMBL:AF242859 EMBL:AB035288 EMBL:AY128346 IPI:IPI00535340 PIR:H86205 RefSeq:NP_172191.1 UniGene:At.15685 ProteinModelPortal:Q9MB58 SMR:Q9MB58 STRING:Q9MB58 PRIDE:Q9SP17 ProMEX:Q9MB58 EnsemblPlants:AT1G07110.1 GeneID:837221 KEGG:ath:AT1G07110 TAIR:At1g07110 InParanoid:Q9MB58 OMA:EMPLHTI PhylomeDB:Q9MB58 ProtClustDB:CLSN2914245 ArrayExpress:Q8L7N6 Genevestigator:Q9MB58 GO:GO:0043609 Uniprot:Q9MB58
Leaf	Isotig00346	19	7	1.970	0.000947153	SGD|S000007362 - symbol:YPR158C-D "Retrotransposon TYA Gag and TYB Pol genes" species:4932 "Saccharomyces cerevisiae" [GO:0000943 "retrotransposon nucleocapsid" evidence=ISS] [GO:0003887 "DNA-directed DNA polymerase activity" evidence=IEA;ISS] [GO:0008233 "peptidase activity" evidence=IEA;ISS] [GO:0004540 "ribonuclease activity" evidence=ISS] [GO:0032197 "transposition, RNA-mediated" evidence=ISS] [GO:0003964 "RNA-directed DNA polymerase activity" evidence=IEA;ISS] [GO:0003723 "RNA binding" evidence=IEA;ISS] [GO:0004523 "ribonuclease H activity" evidence=IEA] [GO:0003676 "nucleic acid binding" evidence=IEA] [GO:0004190 "aspartic-type endopeptidase activity" evidence=IEA] [GO:0005737 "cytoplasm" evidence=IEA] [GO:0006508 "proteolysis" evidence=IEA] [GO:0015074 "DNA integration" evidence=IEA] [GO:0000166 "nucleotide binding" evidence=IEA] [GO:0003677 "DNA binding" evidence=IEA] [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004518 "nuclease activity" evidence=IEA] [GO:0004519 "endonuclease activity" evidence=IEA] [GO:0005524 "ATP binding" evidence=IEA] [GO:0005634 "nucleus" evidence=IEA] [GO:0006310 "DNA recombination" evidence=IEA] [GO:0008152 "metabolic process" evidence=IEA] [GO:0016740 "transferase activity" evidence=IEA] [GO:0016779 "nucleotidyltransferase activity" evidence=IEA] [GO:0016787 "hydrolase activity" evidence=IEA] [GO:0032196 "transposition" evidence=IEA] [GO:0046797 "viral procapsid maturation" evidence=IEA] [GO:0046872 "metal ion binding" evidence=IEA] InterPro:IPR001584 InterPro:IPR001969 InterPro:IPR012337 InterPro:IPR015820 Pfam:PF00665 Pfam:PF01021 PROSITE:PS00141 PROSITE:PS50994 SGD:S000007362 GO:GO:0005524 GO:GO:0005634 GO:GO:0005737 GO:GO:0046872 GO:GO:0003677 GO:GO:0006508 GO:GO:0003723 EMBL:BK006949 GO:GO:0006310 SUPFAM:SSF53098 GO:GO:0003964 GO:GO:0004523 GO:GO:0004190 EMBL:U28371 GO:GO:0003887 GO:GO:0015074 GO:GO:0032196 GO:GO:0046797 InterPro:IPR013103 Pfam:PF07727 eggNOG:NOG283194 GeneTree:ENSGT00640000091659 HOGENOM:HBG204407 PIR:S69982 RefSeq:NP_058195.1 ProteinModelPortal:P0C2J1 IntAct:P0C2J1 STRING:P0C2J1 EnsemblFungi:YPR158C-D GeneID:856284 KEGG:sce:YPR158C-D NextBio:981613 Genevestigator:P0C2J1 Uniprot:P0C2J1
Leaf	Isotig00347	19	7	1.970	0.000947153	SGD|S000007362 - symbol:YPR158C-D "Retrotransposon TYA Gag and TYB Pol genes" species:4932 "Saccharomyces cerevisiae" [GO:0000943 "retrotransposon nucleocapsid" evidence=ISS] [GO:0003887 "DNA-directed DNA polymerase activity" evidence=IEA;ISS] [GO:0008233 "peptidase activity" evidence=IEA;ISS] [GO:0004540 "ribonuclease activity" evidence=ISS] [GO:0032197 "transposition, RNA-mediated" evidence=ISS] [GO:0003964 "RNA-directed DNA polymerase activity" evidence=IEA;ISS] [GO:0003723 "RNA binding" evidence=IEA;ISS] [GO:0004523 "ribonuclease H activity" evidence=IEA] [GO:0003676 "nucleic acid binding" evidence=IEA] [GO:0004190 "aspartic-type endopeptidase activity" evidence=IEA] [GO:0005737 "cytoplasm"

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						evidence=IEA] [GO:0006508 "proteolysis" evidence=IEA] [GO:0015074 "DNA integration" evidence=IEA] [GO:0000166 "nucleotide binding" evidence=IEA] [GO:0003677 "DNA binding" evidence=IEA] [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004518 "nuclease activity" evidence=IEA] [GO:0004519 "endonuclease activity" evidence=IEA] [GO:0005524 "ATP binding" evidence=IEA] [GO:0005634 "nucleus" evidence=IEA] [GO:0006310 "DNA recombination" evidence=IEA] [GO:0008152 "metabolic process" evidence=IEA] [GO:0016740 "transferase activity" evidence=IEA] [GO:0016779 "nucleotidyltransferase activity" evidence=IEA] [GO:0016787 "hydrolase activity" evidence=IEA] [GO:0032196 "transposition" evidence=IEA] [GO:0046797 "viral procapsid maturation" evidence=IEA] [GO:0046872 "metal ion binding" evidence=IEA] InterPro:IPR001584 InterPro:IPR001969 InterPro:IPR012337 InterPro:IPR015820 Pfam:PF00665 Pfam:PF01021 PROSITE:PS00141 PROSITE:PS50994 SGD:S000007362 GO:GO:0005524 GO:GO:0005634 GO:GO:0005737 GO:GO:0046872 GO:GO:0003677 GO:GO:0006508 GO:GO:0003723 EMBL:BK006949 GO:GO:0006310 SUPFAM:SSF53098 GO:GO:0003964 GO:GO:0004523 GO:GO:0004190 EMBL:U28371 GO:GO:0003887 GO:GO:0015074 GO:GO:0032196 GO:GO:0046797 InterPro:IPR013103 Pfam:PF07727 eggNOG:NOG283194 GeneTree:ENSGT00640000091659 HOGENOM:HBG204407 PIR:S69982 RefSeq:NP_058195.1 ProteinModelPortal:P0C2J1 IntAct:P0C2J1 STRING:P0C2J1 EnsemblFungi:YPR158C-D GeneID:856284 KEGG:sce:YPR158C-D NextBio:981613 Genevestigator:P0C2J1 Uniprot:P0C2J1
Leaf	Isotig00351	9	0	4.699	0.000718283	TAIR|locus:2155894 - symbol:SUS2 "AT5G49190" species:3702 "Arabidopsis thaliana" [GO:0005986 "sucrose biosynthetic process" evidence=ISS] [GO:0008194 "UDP-glycosyltransferase activity" evidence=ISS] [GO:0016157 "sucrose synthase activity" evidence=ISS;IMP] [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0001666 "response to hypoxia" evidence=IEP] [GO:0009505 "plant-type cell wall" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0005982 "starch metabolic process" evidence=IMP] [GO:0005985 "sucrose metabolic process" evidence=IMP] [GO:0010431 "seed maturation" evidence=IMP] InterPro:IPR000368 InterPro:IPR001296 InterPro:IPR012820 Pfam:PF00534 Pfam:PF00862 GO:GO:0005829 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0016020 GO:GO:0001666 GO:GO:0009058 GO:GO:0009505 eggNOG:COG0438 GO:GO:0010431 CAZy:GT4 EMBL:AB016872 GO:GO:0005985 GO:GO:0005982 HOGENOM:HBG286768 GO:GO:0016157 PANTHER:PTHR12526:SF27 TIGRFAMs:TIGR02470 EMBL:X60987 IPI:IPI00539012 PIR:S19125 RefSeq:NP_199730.1 UniGene:At.8597 ProteinModelPortal:Q00917 STRING:Q00917 PRIDE:Q00917 GeneID:834978 KEGG:ath:AT5G49190 TAIR:At5g49190 InParanoid:Q00917 PhylomeDB:Q00917 ArrayExpress:Q00917 Genevestigator:Q00917 GermOnline:AT5G49190 Uniprot:Q00917
Leaf	Isotig00352	9	0	4.699	0.000718283	TAIR|locus:2155894 - symbol:SUS2 "AT5G49190" species:3702 "Arabidopsis thaliana" [GO:0005986 "sucrose biosynthetic process" evidence=ISS] [GO:0008194 "UDP-glycosyltransferase activity" evidence=ISS] [GO:0016157 "sucrose synthase activity" evidence=ISS;IMP] [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0001666 "response to hypoxia" evidence=IEP] [GO:0009505 "plant-type cell wall" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0005982 "starch metabolic process" evidence=IMP] [GO:0005985 "sucrose metabolic process" evidence=IMP] [GO:0010431 "seed maturation" evidence=IMP] InterPro:IPR000368 InterPro:IPR001296 InterPro:IPR012820 Pfam:PF00534 Pfam:PF00862 GO:GO:0005829 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0016020 GO:GO:0001666 GO:GO:0009058 GO:GO:0009505 eggNOG:COG0438 GO:GO:0010431 CAZy:GT4 EMBL:AB016872 GO:GO:0005985 GO:GO:0005982 HOGENOM:HBG286768 GO:GO:0016157 PANTHER:PTHR12526:SF27 TIGRFAMs:TIGR02470 EMBL:X60987 IPI:IPI00539012 PIR:S19125 RefSeq:NP_199730.1 UniGene:At.8597 ProteinModelPortal:Q00917 STRING:Q00917 PRIDE:Q00917 GeneID:834978 KEGG:ath:AT5G49190 TAIR:At5g49190 InParanoid:Q00917 PhylomeDB:Q00917 ArrayExpress:Q00917 Genevestigator:Q00917 GermOnline:AT5G49190 Uniprot:Q00917
Leaf	Isotig00353	9	0	4.699	0.000718283	TAIR|locus:2155894 - symbol:SUS2 "AT5G49190" species:3702 "Arabidopsis thaliana" [GO:0005986 "sucrose biosynthetic process" evidence=ISS] [GO:0008194 "UDP-glycosyltransferase activity" evidence=ISS] [GO:0016157 "sucrose synthase activity" evidence=ISS;IMP] [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0001666 "response to hypoxia" evidence=IEP] [GO:0009505 "plant-type cell wall" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0005982 "starch metabolic process" evidence=IMP] [GO:0005985 "sucrose metabolic process" evidence=IMP] [GO:0010431 "seed maturation" evidence=IMP] InterPro:IPR000368 InterPro:IPR001296 InterPro:IPR012820 Pfam:PF00534 Pfam:PF00862 GO:GO:0005829 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0016020

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0001666 GO:GO:0009058 GO:GO:0009505 eggNOG:COG0438 GO:GO:0010431 CAZy:GT4 EMBL:AB016872 GO:GO:0005985 GO:GO:0005982 HOGENOM:HBG286768 GO:GO:0016157 PANTHER:PTHR12526:SF27 TIGRFAMs:TIGR02470 EMBL:X60987 IPI:IPI00539012 PIR:S19125 RefSeq:NP_199730.1 UniGene:At.8597 ProteinModelPortal:Q00917 STRING:Q00917 PRIDE:Q00917 GeneID:834978 KEGG:ath:AT5G49190 TAIR:At5g49190 InParanoid:Q00917 PhylomeDB:Q00917 ArrayExpress:Q00917 Genevestigator:Q00917 GermOnline:AT5G49190 Uniprot:Q00917
Leaf	Isotig00354	9	0	4.699	0.000718283	TAIR|locus:2137829 - symbol:SUS3 "AT4G02280" species:3702 "Arabidopsis thaliana" [GO:0005986 "sucrose biosynthetic process" evidence=ISS] [GO:0008194 "UDP-glycosyltransferase activity" evidence=ISS] [GO:0016157 "sucrose synthase activity" evidence=ISS;IDA] [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0005982 "starch metabolic process" evidence=IMP] [GO:0005985 "sucrose metabolic process" evidence=IMP] [GO:0010431 "seed maturation" evidence=IMP] InterPro:IPR000368 InterPro:IPR001296 InterPro:IPR012820 Pfam:PF00534 Pfam:PF00862 EMBL:CP002687 GO:GO:0009058 GO:GO:0010431 CAZy:GT4 EMBL:AL161494 GO:GO:0005985 GO:GO:0005982 KO:K00695 ProtClustDB:PLN00142 GO:GO:0016157 PANTHER:PTHR12526:SF27 TIGRFAMs:TIGR02470 EMBL:AY051001 EMBL:AY056784 EMBL:AY142511 IPI:IPI00528989 PIR:B85029 RefSeq:NP_192137.1 UniGene:At.3877 ProteinModelPortal:Q9M111 SMR:Q9M111 IntAct:Q9M111 STRING:Q9M111 PRIDE:Q9M111 EnsemblPlants:AT4G02280.1 GeneID:828081 KEGG:ath:AT4G02280 TAIR:At4g02280 InParanoid:Q9M111 OMA:WKYVSKL PhylomeDB:Q9M111 Genevestigator:Q9M111 Uniprot:Q9M111
Leaf	Isotig00355	9	0	4.699	0.000718283	TAIR|locus:2155894 - symbol:SUS2 "AT5G49190" species:3702 "Arabidopsis thaliana" [GO:0005986 "sucrose biosynthetic process" evidence=ISS] [GO:0008194 "UDP-glycosyltransferase activity" evidence=ISS] [GO:0016157 "sucrose synthase activity" evidence=ISS;IMP] [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0001666 "response to hypoxia" evidence=IEP] [GO:0009505 "plant-type cell wall" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0005982 "starch metabolic process" evidence=IMP] [GO:0005985 "sucrose metabolic process" evidence=IMP] [GO:0010431 "seed maturation" evidence=IMP] InterPro:IPR000368 InterPro:IPR001296 InterPro:IPR012820 Pfam:PF00534 Pfam:PF00862 GO:GO:0005829 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0016020 GO:GO:0001666 GO:GO:0009058 GO:GO:0009505 eggNOG:COG0438 GO:GO:0010431 CAZy:GT4 EMBL:AB016872 GO:GO:0005985 GO:GO:0005982 HOGENOM:HBG286768 GO:GO:0016157 PANTHER:PTHR12526:SF27 TIGRFAMs:TIGR02470 EMBL:X60987 IPI:IPI00539012 PIR:S19125 RefSeq:NP_199730.1 UniGene:At.8597 ProteinModelPortal:Q00917 STRING:Q00917 PRIDE:Q00917 GeneID:834978 KEGG:ath:AT5G49190 TAIR:At5g49190 InParanoid:Q00917 PhylomeDB:Q00917 ArrayExpress:Q00917 Genevestigator:Q00917 GermOnline:AT5G49190 Uniprot:Q00917
Leaf	Isotig00356	9	0	4.699	0.000718283	TAIR|locus:2137829 - symbol:SUS3 "AT4G02280" species:3702 "Arabidopsis thaliana" [GO:0005986 "sucrose biosynthetic process" evidence=ISS] [GO:0008194 "UDP-glycosyltransferase activity" evidence=ISS] [GO:0016157 "sucrose synthase activity" evidence=ISS;IDA] [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0005982 "starch metabolic process" evidence=IMP] [GO:0005985 "sucrose metabolic process" evidence=IMP] [GO:0010431 "seed maturation" evidence=IMP] InterPro:IPR000368 InterPro:IPR001296 InterPro:IPR012820 Pfam:PF00534 Pfam:PF00862 EMBL:CP002687 GO:GO:0009058 GO:GO:0010431 CAZy:GT4 EMBL:AL161494 GO:GO:0005985 GO:GO:0005982 KO:K00695 ProtClustDB:PLN00142 GO:GO:0016157 PANTHER:PTHR12526:SF27 TIGRFAMs:TIGR02470 EMBL:AY051001 EMBL:AY056784 EMBL:AY142511 IPI:IPI00528989 PIR:B85029 RefSeq:NP_192137.1 UniGene:At.3877 ProteinModelPortal:Q9M111 SMR:Q9M111 IntAct:Q9M111 STRING:Q9M111 PRIDE:Q9M111 EnsemblPlants:AT4G02280.1 GeneID:828081 KEGG:ath:AT4G02280 TAIR:At4g02280 InParanoid:Q9M111 OMA:WKYVSKL PhylomeDB:Q9M111 Genevestigator:Q9M111 Uniprot:Q9M111
Leaf	Isotig00357	9	0	4.699	0.000718283	TAIR|locus:2137829 - symbol:SUS3 "AT4G02280" species:3702 "Arabidopsis thaliana" [GO:0005986 "sucrose biosynthetic process" evidence=ISS] [GO:0008194 "UDP-glycosyltransferase activity" evidence=ISS] [GO:0016157 "sucrose synthase activity" evidence=ISS;IDA] [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0005982 "starch metabolic process" evidence=IMP] [GO:0005985 "sucrose metabolic process" evidence=IMP] [GO:0010431 "seed maturation" evidence=IMP] InterPro:IPR000368 InterPro:IPR001296 InterPro:IPR012820 Pfam:PF00534 Pfam:PF00862 EMBL:CP002687 GO:GO:0009058 GO:GO:0010431 CAZy:GT4 EMBL:AL161494 GO:GO:0005985 GO:GO:0005982 KO:K00695 ProtClustDB:PLN00142 GO:GO:0016157 PANTHER:PTHR12526:SF27 TIGRFAMs:TIGR02470 EMBL:AY051001 EMBL:AY056784 EMBL:AY142511

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						IPI:IPI00528989 PIR:B85029 RefSeq:NP_192137.1 UniGene:At.3877 ProteinModelPortal:Q9M111 SMR:Q9M111 IntAct:Q9M111 STRING:Q9M111 PRIDE:Q9M111 EnsemblPlants:AT4G02280.1 GeneID:828081 KEGG:ath:AT4G02280 TAIR:At4g02280 InParanoid:Q9M111 OMA:WKYVSKL PhylomeDB:Q9M111 Genevestigator:Q9M111 Uniprot:Q9M111
Leaf	Isotig00358	9	0	4.699	0.000718283	TAIR|locus:2137829 - symbol:SUS3 "AT4G02280" species:3702 "Arabidopsis thaliana" [GO:0005986 "sucrose biosynthetic process" evidence=ISS] [GO:0008194 "UDP-glycosyltransferase activity" evidence=ISS] [GO:0016157 "sucrose synthase activity" evidence=ISS;IDA] [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0005982 "starch metabolic process" evidence=IMP] [GO:0005985 "sucrose metabolic process" evidence=IMP] [GO:0010431 "seed maturation" evidence=IMP] InterPro:IPR000368 InterPro:IPR001296 InterPro:IPR012820 Pfam:PF00534 Pfam:PF00862 EMBL:CP002687 GO:GO:0009058 GO:GO:0010431 CAZy:GT4 EMBL:AL161494 GO:GO:0005985 GO:GO:0005982 KO:K00695 ProtClustDB:PLN00142 GO:GO:0016157 PANTHER:PTHR12526:SF27 TIGRFAMs:TIGR02470 EMBL:AY051001 EMBL:AY056784 EMBL:AY142511 IPI:IPI00528989 PIR:B85029 RefSeq:NP_192137.1 UniGene:At.3877 ProteinModelPortal:Q9M111 SMR:Q9M111 IntAct:Q9M111 STRING:Q9M111 PRIDE:Q9M111 EnsemblPlants:AT4G02280.1 GeneID:828081 KEGG:ath:AT4G02280 TAIR:At4g02280 InParanoid:Q9M111 OMA:WKYVSKL PhylomeDB:Q9M111 Genevestigator:Q9M111 Uniprot:Q9M111
Leaf	Isotig00367	18	84	-1.693	1.79E-07	TAIR|locus:2175851 - symbol:HDS "AT5G60600" species:3702 "Arabidopsis thaliana" [GO:0008299 "isoprenoid biosynthetic process" evidence=ISS] [GO:0046429 "4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase activity" evidence=IGI;ISS;IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0019288 "isopentenyl diphosphate biosynthetic process, mevalonate-independent pathway" evidence=TAS] [GO:0051539 "4 iron, 4 sulfur cluster binding" evidence=IDA] [GO:0009617 "response to bacterium" evidence=IMP] [GO:0009862 "systemic acquired resistance, salicylic acid mediated signaling pathway" evidence=IMP] [GO:0009570 "chloroplast stroma" evidence=IDA] InterPro:IPR004588 InterPro:IPR017178 Pfam:PF04551 PIRSF:PIRSF037336 GO:GO:0009570 GenomeReviews:BA000015_GR GO:GO:0009617 GO:GO:0005506 GO:GO:0009941 GO:GO:0051539 GO:GO:0009862 GO:GO:0019288 GO:GO:0016114 HOGENOM:HBG335271 GO:GO:0046429 HAMAP:MF_00159 TIGRFAMs:TIGR00612 EMBL:AY094472 IPI:IPI00530209 ProteinModelPortal:Q8LPQ4 STRING:Q8LPQ4 PRIDE:Q8LPQ4 TAIR:At5g60600 InParanoid:Q8LPQ4 PhylomeDB:Q8LPQ4 Genevestigator:Q8LPQ4 Uniprot:Q8LPQ4
Leaf	Isotig00368	18	82	-1.659	3.74E-07	TAIR|locus:2175851 - symbol:HDS "AT5G60600" species:3702 "Arabidopsis thaliana" [GO:0008299 "isoprenoid biosynthetic process" evidence=ISS] [GO:0046429 "4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase activity" evidence=IGI;ISS;IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0019288 "isopentenyl diphosphate biosynthetic process, mevalonate-independent pathway" evidence=TAS] [GO:0051539 "4 iron, 4 sulfur cluster binding" evidence=IDA] [GO:0009617 "response to bacterium" evidence=IMP] [GO:0009862 "systemic acquired resistance, salicylic acid mediated signaling pathway" evidence=IMP] [GO:0009570 "chloroplast stroma" evidence=IDA] InterPro:IPR004588 InterPro:IPR017178 Pfam:PF04551 PIRSF:PIRSF037336 GO:GO:0009570 GenomeReviews:BA000015_GR GO:GO:0009617 GO:GO:0005506 GO:GO:0009941 GO:GO:0051539 GO:GO:0009862 GO:GO:0019288 GO:GO:0016114 HOGENOM:HBG335271 GO:GO:0046429 HAMAP:MF_00159 TIGRFAMs:TIGR00612 EMBL:AY094472 IPI:IPI00530209 ProteinModelPortal:Q8LPQ4 STRING:Q8LPQ4 PRIDE:Q8LPQ4 TAIR:At5g60600 InParanoid:Q8LPQ4 PhylomeDB:Q8LPQ4 Genevestigator:Q8LPQ4 Uniprot:Q8LPQ4
Leaf	Isotig00369	18	84	-1.693	1.79E-07	TAIR|locus:2175851 - symbol:HDS "AT5G60600" species:3702 "Arabidopsis thaliana" [GO:0008299 "isoprenoid biosynthetic process" evidence=ISS] [GO:0046429 "4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase activity" evidence=IGI;ISS;IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0019288 "isopentenyl diphosphate biosynthetic process, mevalonate-independent pathway" evidence=TAS] [GO:0051539 "4 iron, 4 sulfur cluster binding" evidence=IDA] [GO:0009617 "response to bacterium" evidence=IMP] [GO:0009862 "systemic acquired resistance, salicylic acid mediated signaling pathway" evidence=IMP] [GO:0009570 "chloroplast stroma" evidence=IDA] InterPro:IPR004588 InterPro:IPR017178 Pfam:PF04551 PIRSF:PIRSF037336 GO:GO:0009570 GenomeReviews:BA000015_GR GO:GO:0009617 GO:GO:0005506 GO:GO:0009941 GO:GO:0051539 GO:GO:0009862 GO:GO:0019288 GO:GO:0016114 HOGENOM:HBG335271 GO:GO:0046429 HAMAP:MF_00159 TIGRFAMs:TIGR00612 EMBL:AY094472 IPI:IPI00530209 ProteinModelPortal:Q8LPQ4 STRING:Q8LPQ4 PRIDE:Q8LPQ4 TAIR:At5g60600 InParanoid:Q8LPQ4 PhylomeDB:Q8LPQ4 Genevestigator:Q8LPQ4 Uniprot:Q8LPQ4

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig00370	18	82	-1.659	3.74E-07	TAIR|locus:2175851 - symbol:HDS "AT5G60600" species:3702 "Arabidopsis thaliana" [GO:0008299 "isoprenoid biosynthetic process" evidence=ISS] [GO:0046429 "4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase activity" evidence=IGI;ISS;IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0019288 "isopentenyl diphosphate biosynthetic process, mevalonate-independent pathway" evidence=TAS] [GO:0051539 "4 iron, 4 sulfur cluster binding" evidence=IDA] [GO:0009617 "response to bacterium" evidence=IMP] [GO:0009862 "systemic acquired resistance, salicylic acid mediated signaling pathway" evidence=IMP] [GO:0009570 "chloroplast stroma" evidence=IDA] InterPro:IPR004588 InterPro:IPR017178 Pfam:PF04551 PIRSF:PIRSF037336 GO:GO:0009570 GenomeReviews:BA000015_GR GO:GO:0009617 GO:GO:0005506 GO:GO:0009941 GO:GO:0051539 GO:GO:0009862 GO:GO:0019288 GO:GO:0016114 HOGENOM:HBG335271 GO:GO:0046429 HAMAP:MF_00159 TIGRFAMs:TIGR00612 EMBL:AY094472 IPI:IPI00530209 ProteinModelPortal:Q8LPQ4 STRING:Q8LPQ4 PRIDE:Q8LPQ4 TAIR:At5g60600 InParanoid:Q8LPQ4 PhylomeDB:Q8LPQ4 Genevestigator:Q8LPQ4 Uniprot:Q8LPQ4
Leaf	Isotig00371	18	82	-1.659	3.74E-07	TAIR|locus:2175851 - symbol:HDS "AT5G60600" species:3702 "Arabidopsis thaliana" [GO:0008299 "isoprenoid biosynthetic process" evidence=ISS] [GO:0046429 "4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase activity" evidence=IGI;ISS;IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0019288 "isopentenyl diphosphate biosynthetic process, mevalonate-independent pathway" evidence=TAS] [GO:0051539 "4 iron, 4 sulfur cluster binding" evidence=IDA] [GO:0009617 "response to bacterium" evidence=IMP] [GO:0009862 "systemic acquired resistance, salicylic acid mediated signaling pathway" evidence=IMP] [GO:0009570 "chloroplast stroma" evidence=IDA] InterPro:IPR004588 InterPro:IPR017178 Pfam:PF04551 PIRSF:PIRSF037336 GO:GO:0009570 GenomeReviews:BA000015_GR GO:GO:0009617 GO:GO:0005506 GO:GO:0009941 GO:GO:0051539 GO:GO:0009862 GO:GO:0019288 GO:GO:0016114 HOGENOM:HBG335271 GO:GO:0046429 HAMAP:MF_00159 TIGRFAMs:TIGR00612 EMBL:AY094472 IPI:IPI00530209 ProteinModelPortal:Q8LPQ4 STRING:Q8LPQ4 PRIDE:Q8LPQ4 TAIR:At5g60600 InParanoid:Q8LPQ4 PhylomeDB:Q8LPQ4 Genevestigator:Q8LPQ4 Uniprot:Q8LPQ4
Leaf	Isotig00372	18	80	-1.623	7.74E-07	TAIR|locus:2175851 - symbol:HDS "AT5G60600" species:3702 "Arabidopsis thaliana" [GO:0008299 "isoprenoid biosynthetic process" evidence=ISS] [GO:0046429 "4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase activity" evidence=IGI;ISS;IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0019288 "isopentenyl diphosphate biosynthetic process, mevalonate-independent pathway" evidence=TAS] [GO:0051539 "4 iron, 4 sulfur cluster binding" evidence=IDA] [GO:0009617 "response to bacterium" evidence=IMP] [GO:0009862 "systemic acquired resistance, salicylic acid mediated signaling pathway" evidence=IMP] [GO:0009570 "chloroplast stroma" evidence=IDA] InterPro:IPR004588 InterPro:IPR017178 Pfam:PF04551 PIRSF:PIRSF037336 GO:GO:0009570 GenomeReviews:BA000015_GR GO:GO:0009617 GO:GO:0005506 GO:GO:0009941 GO:GO:0051539 GO:GO:0009862 GO:GO:0019288 GO:GO:0016114 HOGENOM:HBG335271 GO:GO:0046429 HAMAP:MF_00159 TIGRFAMs:TIGR00612 EMBL:AY094472 IPI:IPI00530209 ProteinModelPortal:Q8LPQ4 STRING:Q8LPQ4 PRIDE:Q8LPQ4 TAIR:At5g60600 InParanoid:Q8LPQ4 PhylomeDB:Q8LPQ4 Genevestigator:Q8LPQ4 Uniprot:Q8LPQ4
Leaf	Isotig00373	15	68	-1.652	3.96E-06	TAIR|locus:2175851 - symbol:HDS "AT5G60600" species:3702 "Arabidopsis thaliana" [GO:0008299 "isoprenoid biosynthetic process" evidence=ISS] [GO:0046429 "4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase activity" evidence=IGI;ISS;IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0019288 "isopentenyl diphosphate biosynthetic process, mevalonate-independent pathway" evidence=TAS] [GO:0051539 "4 iron, 4 sulfur cluster binding" evidence=IDA] [GO:0009617 "response to bacterium" evidence=IMP] [GO:0009862 "systemic acquired resistance, salicylic acid mediated signaling pathway" evidence=IMP] [GO:0009570 "chloroplast stroma" evidence=IDA] InterPro:IPR004588 InterPro:IPR017178 Pfam:PF04551 PIRSF:PIRSF037336 GO:GO:0009570 GenomeReviews:BA000015_GR GO:GO:0009617 GO:GO:0005506 GO:GO:0009941 GO:GO:0051539 GO:GO:0009862 GO:GO:0019288 GO:GO:0016114 HOGENOM:HBG335271 GO:GO:0046429 HAMAP:MF_00159 TIGRFAMs:TIGR00612 EMBL:AY094472 IPI:IPI00530209 ProteinModelPortal:Q8LPQ4 STRING:Q8LPQ4 PRIDE:Q8LPQ4 TAIR:At5g60600 InParanoid:Q8LPQ4 PhylomeDB:Q8LPQ4 Genevestigator:Q8LPQ4 Uniprot:Q8LPQ4
Leaf	Isotig00379	9	38	-1.549	0.000993089	TAIR|locus:2167225 - symbol:PSY "AT5G17230" species:3702 "Arabidopsis thaliana" [GO:0016117 "carotenoid biosynthetic process" evidence=IMP] [GO:0016767 "geranylgeranyl-diphosphate geranylgeranyltransferase activity" evidence=ISS;TAS] [GO:0046905 "phytoene synthase activity" evidence=TAS] [GO:0009507 "chloroplast" evidence=IDA] InterPro:IPR002060 InterPro:IPR019845 Pfam:PF00494 PROSITE:PS01044 PROSITE:PS01045

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009507 InterPro:IPR008949 Gene3D:G3DSA:1.10.600.10 SUPFAM:SSF48576 EMBL:AB005238 eggNOG:COG1562 GO:GO:0016767 GO:GO:0046905 EMBL:L25812 EMBL:AF009954 EMBL:BT000450 EMBL:BT002084 EMBL:AY085565 IPI:IPI00527204 RefSeq:NP_001031895.1 RefSeq:NP_197225.1 UniGene:At.23726 ProteinModelPortal:P37271 SMR:P37271 STRING:P37271 PRIDE:P37271 EnsemblPlants:AT5G17230.1 EnsemblPlants:AT5G17230.2 GeneID:831587 KEGG:ath:AT5G17230 TAIR:At5g17230 HOGENOM:HBG693191 InParanoid:P37271 KO:K02291 OMA:ELKLYCY PhylomeDB:P37271 ProtClustDB:PLN02632 BioCyc:ARA:AT5G17230-MONOMER BioCyc:MetaCyc:AT5G17230-MONOMER ArrayExpress:P37271 Genevestigator:P37271 GermOnline:AT5G17230 Uniprot:P37271
Leaf	Isotig00395	4	28	-2.278	0.00024892	TAIR|locus:2094869 - symbol:AT3G24460 species:3702 "Arabidopsis thaliana" [GO:0016020 "membrane" evidence=IEA;ISS] InterPro:IPR005016 Pfam:PF03348 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0016020 eggNOG:NOG308011 PANTHER:PTHR10383 EMBL:AY064147 EMBL:BT010591 IPI:IPI00536041 RefSeq:NP_189089.3 UniGene:At.45826 PRIDE:Q8VZI4 EnsemblPlants:AT3G24460.1 GeneID:822036 KEGG:ath:AT3G24460 TAIR:At3g24460 HOGENOM:HBG317661 InParanoid:Q8VZI4 OMA:LIGWNTH PhylomeDB:Q8VZI4 ProtClustDB:CLSN2689411 Genevestigator:Q8VZI4 Uniprot:Q8VZI4
Leaf	Isotig00396	3	26	-2.587	0.000145202	TAIR|locus:2094869 - symbol:AT3G24460 species:3702 "Arabidopsis thaliana" [GO:0016020 "membrane" evidence=IEA;ISS] InterPro:IPR005016 Pfam:PF03348 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0016020 eggNOG:NOG308011 PANTHER:PTHR10383 EMBL:AY064147 EMBL:BT010591 IPI:IPI00536041 RefSeq:NP_189089.3 UniGene:At.45826 PRIDE:Q8VZI4 EnsemblPlants:AT3G24460.1 GeneID:822036 KEGG:ath:AT3G24460 TAIR:At3g24460 HOGENOM:HBG317661 InParanoid:Q8VZI4 OMA:LIGWNTH PhylomeDB:Q8VZI4 ProtClustDB:CLSN2689411 Genevestigator:Q8VZI4 Uniprot:Q8VZI4
Leaf	Isotig00397	3	26	-2.587	0.000145202	TAIR|locus:2094869 - symbol:AT3G24460 species:3702 "Arabidopsis thaliana" [GO:0016020 "membrane" evidence=IEA;ISS] InterPro:IPR005016 Pfam:PF03348 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0016020 eggNOG:NOG308011 PANTHER:PTHR10383 EMBL:AY064147 EMBL:BT010591 IPI:IPI00536041 RefSeq:NP_189089.3 UniGene:At.45826 PRIDE:Q8VZI4 EnsemblPlants:AT3G24460.1 GeneID:822036 KEGG:ath:AT3G24460 TAIR:At3g24460 HOGENOM:HBG317661 InParanoid:Q8VZI4 OMA:LIGWNTH PhylomeDB:Q8VZI4 ProtClustDB:CLSN2689411 Genevestigator:Q8VZI4 Uniprot:Q8VZI4
Leaf	Isotig00404	87	487	-1.956	9.16E-44	TAIR|locus:2120192 - symbol:FBA2 "fructose-bisphosphate aldolase 2" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004332 "fructose-bisphosphate aldolase activity" evidence=IEA] [GO:0006098 "pentose-phosphate shunt" evidence=TAS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0009579 "thylakoid" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] InterPro:IPR000741 InterPro:IPR013785 Pfam:PF00274 PROSITE:PS00158 GO:GO:0009737 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0048046 GO:GO:0046686 GO:GO:0016020 Gene3D:G3DSA:3.20.20.70 GO:GO:0009941 GO:GO:0006096 GO:GO:0009579 HSSP:P05062 eggNOG:COG3588 HOGENOM:HBG559178 KO:K01623 GO:GO:0004332 PANTHER:PTHR11627 UniGene:At.21716 GO:GO:0010287 EMBL:AL035679 EMBL:AL161594 EMBL:AF428455 EMBL:BT015870 EMBL:AK226247 IPI:IPI00541448 PIR:T06057 RefSeq:NP_568049.1 UniGene:At.24925 UniGene:At.75329 ProteinModelPortal:Q944G9 SMR:Q944G9 STRING:Q944G9 PRIDE:Q944G9 ProMEX:Q944G9 GeneID:830052 KEGG:ath:AT4G38970 TAIR:At4g38970 InParanoid:Q944G9 PhylomeDB:Q944G9 ProtClustDB:CLSN2917687 ArrayExpress:Q9SVJ6 Genevestigator:Q944G9 Uniprot:Q944G9
Leaf	Isotig00405	86	488	-1.976	2.08E-44	TAIR|locus:2120192 - symbol:FBA2 "fructose-bisphosphate aldolase 2" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004332 "fructose-bisphosphate aldolase activity" evidence=IEA] [GO:0006098 "pentose-phosphate shunt" evidence=TAS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0009579 "thylakoid" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] InterPro:IPR000741 InterPro:IPR013785 Pfam:PF00274 PROSITE:PS00158 GO:GO:0009737 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0048046 GO:GO:0046686 GO:GO:0016020 Gene3D:G3DSA:3.20.20.70 GO:GO:0009941 GO:GO:0006096 GO:GO:0009579 HSSP:P05062 eggNOG:COG3588 HOGENOM:HBG559178 KO:K01623 GO:GO:0004332

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						PANTHER:PTHR11627 UniGene:At.21716 GO:GO:0010287 EMBL:AL035679 EMBL:AL161594 EMBL:AF428455 EMBL:BT015870 EMBL:AK226247 IPI:IPI00541448 PIR:T06057 RefSeq:NP_568049.1 UniGene:At.24925 UniGene:At.75329 ProteinModelPortal:Q944G9 SMR:Q944G9 STRING:Q944G9 PRIDE:Q944G9 ProMEX:Q944G9 GeneID:830052 KEGG:ath:AT4G38970 TAIR:At4g38970 InParanoid:Q944G9 PhylomeDB:Q944G9 ProtClustDB:CLSN2917687 ArrayExpress:Q9SVJ6 Genevestigator:Q944G9 Uniprot:Q944G9
Leaf	Isotig00406	95	523	-1.932	3.87E-46	TAIR|locus:2120192 - symbol:FBA2 "fructose-bisphosphate aldolase 2" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004332 "fructose-bisphosphate aldolase activity" evidence=IEA] [GO:0006098 "pentose-phosphate shunt" evidence=TAS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0009579 "thylakoid" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] InterPro:IPR000741 InterPro:IPR013785 Pfam:PF00274 PROSITE:PS00158 GO:GO:0009737 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0048046 GO:GO:0046686 GO:GO:0016020 Gene3D:G3DSA:3.20.20.70 GO:GO:0009941 GO:GO:0006096 GO:GO:0009579 HSSP:P05062 eggNOG:COG3588 HOGENOM:HBG559178 KO:K01623 GO:GO:0004332 PANTHER:PTHR11627 UniGene:At.21716 GO:GO:0010287 EMBL:AL035679 EMBL:AL161594 EMBL:AF428455 EMBL:BT015870 EMBL:AK226247 IPI:IPI00541448 PIR:T06057 RefSeq:NP_568049.1 UniGene:At.24925 UniGene:At.75329 ProteinModelPortal:Q944G9 SMR:Q944G9 STRING:Q944G9 PRIDE:Q944G9 ProMEX:Q944G9 GeneID:830052 KEGG:ath:AT4G38970 TAIR:At4g38970 InParanoid:Q944G9 PhylomeDB:Q944G9 ProtClustDB:CLSN2917687 ArrayExpress:Q9SVJ6 Genevestigator:Q944G9 Uniprot:Q944G9
Leaf	Isotig00407	78	457	-2.022	6.37E-43	TAIR|locus:2120192 - symbol:FBA2 "fructose-bisphosphate aldolase 2" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004332 "fructose-bisphosphate aldolase activity" evidence=IEA] [GO:0006098 "pentose-phosphate shunt" evidence=TAS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0009579 "thylakoid" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] InterPro:IPR000741 InterPro:IPR013785 Pfam:PF00274 PROSITE:PS00158 GO:GO:0009737 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0048046 GO:GO:0046686 GO:GO:0016020 Gene3D:G3DSA:3.20.20.70 GO:GO:0009941 GO:GO:0006096 GO:GO:0009579 HSSP:P05062 eggNOG:COG3588 HOGENOM:HBG559178 KO:K01623 GO:GO:0004332 PANTHER:PTHR11627 UniGene:At.21716 GO:GO:0010287 EMBL:AL035679 EMBL:AL161594 EMBL:AF428455 EMBL:BT015870 EMBL:AK226247 IPI:IPI00541448 PIR:T06057 RefSeq:NP_568049.1 UniGene:At.24925 UniGene:At.75329 ProteinModelPortal:Q944G9 SMR:Q944G9 STRING:Q944G9 PRIDE:Q944G9 ProMEX:Q944G9 GeneID:830052 KEGG:ath:AT4G38970 TAIR:At4g38970 InParanoid:Q944G9 PhylomeDB:Q944G9 ProtClustDB:CLSN2917687 ArrayExpress:Q9SVJ6 Genevestigator:Q944G9 Uniprot:Q944G9
Leaf	Isotig00409	3	81	-4.226	1.63E-16	TAIR|locus:2163031 - symbol:GDPD2 "glycerophosphodiester phosphodiesterase 2" species:3702 "Arabidopsis thaliana" [GO:0006071 "glycerol metabolic process" evidence=IEA;ISS] [GO:0006629 "lipid metabolic process" evidence=IEA] [GO:0008081 "phosphoric diester hydrolase activity" evidence=IEA] [GO:0008889 "glycerophosphodiester phosphodiesterase activity" evidence=IEA;ISS] InterPro:IPR004129 InterPro:IPR017946 Pfam:PF03009 EMBL:CP002688 Gene3D:G3DSA:3.20.20.190 SUPFAM:SSF51695 GO:GO:0006629 GO:GO:0006071 EMBL:AB010072 GO:GO:0008889 EMBL:BT030021 EMBL:AK117378 IPI:IPI00539025 RefSeq:NP_198924.1 UniGene:At.49114 ProteinModelPortal:Q9FLM1 SMR:Q9FLM1 STRING:Q9FLM1 PRIDE:Q9FLM1 DNASU:834110 EnsemblPlants:AT5G41080.1 GeneID:834110 KEGG:ath:AT5G41080 TAIR:At5g41080 InParanoid:Q9FLM1 OMA:LTYGKLN PhylomeDB:Q9FLM1 ProtClustDB:CLSN2914815 Genevestigator:Q9FLM1 Uniprot:Q9FLM1
Leaf	Isotig00410	6	106	-3.614	2.96E-19	TAIR|locus:2163031 - symbol:GDPD2 "glycerophosphodiester phosphodiesterase 2" species:3702 "Arabidopsis thaliana" [GO:0006071 "glycerol metabolic process" evidence=IEA;ISS] [GO:0006629 "lipid metabolic process" evidence=IEA] [GO:0008081 "phosphoric diester hydrolase activity" evidence=IEA] [GO:0008889 "glycerophosphodiester phosphodiesterase activity" evidence=IEA;ISS] InterPro:IPR004129 InterPro:IPR017946 Pfam:PF03009 EMBL:CP002688 Gene3D:G3DSA:3.20.20.190 SUPFAM:SSF51695 GO:GO:0006629 GO:GO:0006071 EMBL:AB010072 GO:GO:0008889 EMBL:BT030021 EMBL:AK117378 IPI:IPI00539025 RefSeq:NP_198924.1 UniGene:At.49114 ProteinModelPortal:Q9FLM1 SMR:Q9FLM1 STRING:Q9FLM1

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						PRIDE:Q9FLM1 DNASU:834110 EnsemblPlants:AT5G41080.1 GeneID:834110 KEGG:ath:AT5G41080 TAIR:At5g41080 InParanoid:Q9FLM1 OMA:LTYGKLN PhylomeDB:Q9FLM1 ProtClustDB:CLSN2914815 Genevestigator:Q9FLM1 Uniprot:Q9FLM1
Leaf	Isotig00411	3	81	-4.226	1.63E-16	TAIR|locus:2078603 - symbol:SRG3 "AT3G02040" species:3702 "Arabidopsis thaliana" [GO:0006071 "glycerol metabolic process" evidence=ISS] [GO:0008889 "glycerophosphodiester phosphodiesterase activity" evidence=ISS;IDA] [GO:0009536 "plastid" evidence=IDA] [GO:0030643 "cellular phosphate ion homeostasis" evidence=IMP] InterPro:IPR004129 InterPro:IPR017946 Pfam:PF03009 EMBL:CP002686 Gene3D:G3DSA:3.20.20.190 SUPFAM:SSF51695 GO:GO:0006629 EMBL:AC011664 GO:GO:0006071 GO:GO:0009536 GO:GO:0030643 GO:GO:0008889 EMBL:AY072127 EMBL:AY114073 IPI:IPI00531878 RefSeq:NP_566159.1 UniGene:At.20730 UniGene:At.75107 ProteinModelPortal:Q9SGA2 SMR:Q9SGA2 PRIDE:Q9SGA2 EnsemblPlants:AT3G02040.1 GeneID:821175 KEGG:ath:AT3G02040 TAIR:At3g02040 InParanoid:Q9SGA2 OMA:AVAFVEF PhylomeDB:Q9SGA2 Genevestigator:Q9SGA2 Uniprot:Q9SGA2
Leaf	Isotig00412	3	81	-4.226	1.63E-16	TAIR|locus:2163031 - symbol:GDPD2 "glycerophosphodiester phosphodiesterase 2" species:3702 "Arabidopsis thaliana" [GO:0006071 "glycerol metabolic process" evidence=IEA;ISS] [GO:0006629 "lipid metabolic process" evidence=IEA] [GO:0008081 "phosphoric diester hydrolase activity" evidence=IEA] [GO:0008889 "glycerophosphodiester phosphodiesterase activity" evidence=IEA;ISS] InterPro:IPR004129 InterPro:IPR017946 Pfam:PF03009 EMBL:CP002688 Gene3D:G3DSA:3.20.20.190 SUPFAM:SSF51695 GO:GO:0006629 GO:GO:0006071 EMBL:AB010072 GO:GO:0008889 EMBL:BT030021 EMBL:AK117378 IPI:IPI00539025 RefSeq:NP_198924.1 UniGene:At.49114 ProteinModelPortal:Q9FLM1 SMR:Q9FLM1 STRING:Q9FLM1 PRIDE:Q9FLM1 DNASU:834110 EnsemblPlants:AT5G41080.1 GeneID:834110 KEGG:ath:AT5G41080 TAIR:At5g41080 InParanoid:Q9FLM1 OMA:LTYGKLN PhylomeDB:Q9FLM1 ProtClustDB:CLSN2914815 Genevestigator:Q9FLM1 Uniprot:Q9FLM1
Leaf	Isotig00413	6	106	-3.614	2.96E-19	TAIR|locus:2078603 - symbol:SRG3 "AT3G02040" species:3702 "Arabidopsis thaliana" [GO:0006071 "glycerol metabolic process" evidence=ISS] [GO:0008889 "glycerophosphodiester phosphodiesterase activity" evidence=ISS;IDA] [GO:0009536 "plastid" evidence=IDA] [GO:0030643 "cellular phosphate ion homeostasis" evidence=IMP] InterPro:IPR004129 InterPro:IPR017946 Pfam:PF03009 EMBL:CP002686 Gene3D:G3DSA:3.20.20.190 SUPFAM:SSF51695 GO:GO:0006629 EMBL:AC011664 GO:GO:0006071 GO:GO:0009536 GO:GO:0030643 GO:GO:0008889 EMBL:AY072127 EMBL:AY114073 IPI:IPI00531878 RefSeq:NP_566159.1 UniGene:At.20730 UniGene:At.75107 ProteinModelPortal:Q9SGA2 SMR:Q9SGA2 PRIDE:Q9SGA2 EnsemblPlants:AT3G02040.1 GeneID:821175 KEGG:ath:AT3G02040 TAIR:At3g02040 InParanoid:Q9SGA2 OMA:AVAFVEF PhylomeDB:Q9SGA2 Genevestigator:Q9SGA2 Uniprot:Q9SGA2
Leaf	Isotig00414	5	94	-3.704	1.55E-17	TAIR|locus:2078603 - symbol:SRG3 "AT3G02040" species:3702 "Arabidopsis thaliana" [GO:0006071 "glycerol metabolic process" evidence=ISS] [GO:0008889 "glycerophosphodiester phosphodiesterase activity" evidence=ISS;IDA] [GO:0009536 "plastid" evidence=IDA] [GO:0030643 "cellular phosphate ion homeostasis" evidence=IMP] InterPro:IPR004129 InterPro:IPR017946 Pfam:PF03009 EMBL:CP002686 Gene3D:G3DSA:3.20.20.190 SUPFAM:SSF51695 GO:GO:0006629 EMBL:AC011664 GO:GO:0006071 GO:GO:0009536 GO:GO:0030643 GO:GO:0008889 EMBL:AY072127 EMBL:AY114073 IPI:IPI00531878 RefSeq:NP_566159.1 UniGene:At.20730 UniGene:At.75107 ProteinModelPortal:Q9SGA2 SMR:Q9SGA2 PRIDE:Q9SGA2 EnsemblPlants:AT3G02040.1 GeneID:821175 KEGG:ath:AT3G02040 TAIR:At3g02040 InParanoid:Q9SGA2 OMA:AVAFVEF PhylomeDB:Q9SGA2 Genevestigator:Q9SGA2 Uniprot:Q9SGA2
Leaf	Isotig00415	6	106	-3.614	2.96E-19	TAIR|locus:2163031 - symbol:GDPD2 "glycerophosphodiester phosphodiesterase 2" species:3702 "Arabidopsis thaliana" [GO:0006071 "glycerol metabolic process" evidence=IEA;ISS] [GO:0006629 "lipid metabolic process" evidence=IEA] [GO:0008081 "phosphoric diester hydrolase activity" evidence=IEA] [GO:0008889 "glycerophosphodiester phosphodiesterase activity" evidence=IEA;ISS] InterPro:IPR004129 InterPro:IPR017946 Pfam:PF03009 EMBL:CP002688 Gene3D:G3DSA:3.20.20.190 SUPFAM:SSF51695 GO:GO:0006629 GO:GO:0006071 EMBL:AB010072 GO:GO:0008889 EMBL:BT030021 EMBL:AK117378 IPI:IPI00539025 RefSeq:NP_198924.1 UniGene:At.49114 ProteinModelPortal:Q9FLM1 SMR:Q9FLM1 STRING:Q9FLM1 PRIDE:Q9FLM1 DNASU:834110 EnsemblPlants:AT5G41080.1 GeneID:834110 KEGG:ath:AT5G41080 TAIR:At5g41080 InParanoid:Q9FLM1 OMA:LTYGKLN PhylomeDB:Q9FLM1 ProtClustDB:CLSN2914815 Genevestigator:Q9FLM1 Uniprot:Q9FLM1
Leaf	Isotig00416	3	81	-4.226	1.63E-16	TAIR|locus:2078603 - symbol:SRG3 "AT3G02040" species:3702 "Arabidopsis thaliana" [GO:0006071 "glycerol metabolic process" evidence=ISS] [GO:0008889 "glycerophosphodiester phosphodiesterase activity"

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						evidence=ISS;IDA] [GO:0009536 "plastid" evidence=IDA] [GO:0030643 "cellular phosphate ion homeostasis" evidence=IMP] InterPro:IPR004129 InterPro:IPR017946 Pfam:PF03009 EMBL:CP002686 Gene3D:G3DSA:3.20.20.190 SUPFAM:SSF51695 GO:GO:0006629 EMBL:AC011664 GO:GO:0006071 GO:GO:0009536 GO:GO:0030643 GO:GO:0008889 EMBL:AY072127 EMBL:AY114073 IPI:IPI00531878 RefSeq:NP_566159.1 UniGene:At.20730 UniGene:At.75107 ProteinModelPortal:Q9SGA2 SMR:Q9SGA2 PRIDE:Q9SGA2 EnsemblPlants:AT3G02040.1 GeneID:821175 KEGG:ath:AT3G02040 TAIR:At3g02040 InParanoid:Q9SGA2 OMA:AVAFVEF PhylomeDB:Q9SGA2 Genevestigator:Q9SGA2 Uniprot:Q9SGA2
Leaf	Isotig00417	5	94	-3.704	1.55E-17	TAIR|locus:2078603 - symbol:SRG3 "AT3G02040" species:3702 "Arabidopsis thaliana" [GO:0006071 "glycerol metabolic process" evidence=ISS] [GO:0008889 "glycerophosphodiester phosphodiesterase activity" evidence=ISS;IDA] [GO:0009536 "plastid" evidence=IDA] [GO:0030643 "cellular phosphate ion homeostasis" evidence=IMP] InterPro:IPR004129 InterPro:IPR017946 Pfam:PF03009 EMBL:CP002686 Gene3D:G3DSA:3.20.20.190 SUPFAM:SSF51695 GO:GO:0006629 EMBL:AC011664 GO:GO:0006071 GO:GO:0009536 GO:GO:0030643 GO:GO:0008889 EMBL:AY072127 EMBL:AY114073 IPI:IPI00531878 RefSeq:NP_566159.1 UniGene:At.20730 UniGene:At.75107 ProteinModelPortal:Q9SGA2 SMR:Q9SGA2 PRIDE:Q9SGA2 EnsemblPlants:AT3G02040.1 GeneID:821175 KEGG:ath:AT3G02040 TAIR:At3g02040 InParanoid:Q9SGA2 OMA:AVAFVEF PhylomeDB:Q9SGA2 Genevestigator:Q9SGA2 Uniprot:Q9SGA2
Leaf	Isotig00418	6	106	-3.614	2.96E-19	TAIR|locus:2078603 - symbol:SRG3 "AT3G02040" species:3702 "Arabidopsis thaliana" [GO:0006071 "glycerol metabolic process" evidence=ISS] [GO:0008889 "glycerophosphodiester phosphodiesterase activity" evidence=ISS;IDA] [GO:0009536 "plastid" evidence=IDA] [GO:0030643 "cellular phosphate ion homeostasis" evidence=IMP] InterPro:IPR004129 InterPro:IPR017946 Pfam:PF03009 EMBL:CP002686 Gene3D:G3DSA:3.20.20.190 SUPFAM:SSF51695 GO:GO:0006629 EMBL:AC011664 GO:GO:0006071 GO:GO:0009536 GO:GO:0030643 GO:GO:0008889 EMBL:AY072127 EMBL:AY114073 IPI:IPI00531878 RefSeq:NP_566159.1 UniGene:At.20730 UniGene:At.75107 ProteinModelPortal:Q9SGA2 SMR:Q9SGA2 PRIDE:Q9SGA2 EnsemblPlants:AT3G02040.1 GeneID:821175 KEGG:ath:AT3G02040 TAIR:At3g02040 InParanoid:Q9SGA2 OMA:AVAFVEF PhylomeDB:Q9SGA2 Genevestigator:Q9SGA2 Uniprot:Q9SGA2
Leaf	Isotig00428	96	15	3.207	1.60E-22	TAIR|locus:2093227 - symbol:PLDALPHA1 "AT3G15730" species:3702 "Arabidopsis thaliana" [GO:0004630 "phospholipase D activity" evidence=ISS;IDA;IMP] [GO:0005634 "nucleus" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0030136 "clathrin-coated vesicle" evidence=IDA] [GO:0006631 "fatty acid metabolic process" evidence=IMP;TAS] [GO:0005515 "protein binding" evidence=IPI] [GO:0009507 "chloroplast" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0009789 "positive regulation of abscisic acid mediated signaling pathway" evidence=IMP] [GO:0010119 "regulation of stomatal movement" evidence=IMP] [GO:0009845 "seed germination" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005546 "phosphatidylinositol-4,5-bisphosphate binding" evidence=IDA] InterPro:IPR000008 InterPro:IPR001736 InterPro:IPR008973 InterPro:IPR011402 Pfam:PF00168 Pfam:PF00614 PIRSF:PIRSF036470 PROSITE:PS50035 SMART:SM00155 SMART:SM00239 GO:GO:0005829 GO:GO:0005739 GO:GO:0005886 GO:GO:0009506 GO:GO:0005634 GO:GO:0005773 GO:GO:0046686 GO:GO:0009507 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005509 GO:GO:0005515 GO:GO:0009738 GO:GO:0009873 GO:GO:0009789 GO:GO:0010119 GO:GO:0046470 GO:GO:0016042 GO:GO:0006631 GO:GO:0030136 GO:GO:0009845 SUPFAM:SSF49562 PROSITE:PS50004 GO:GO:0005546 EMBL:AB017071 eggNOG:COG1502 InterPro:IPR015679 PANTHER:PTHR18896 GO:GO:0070290 GO:GO:0004630 KO:K01115 EMBL:U36381 EMBL:AF428278 IPI:IPI00527854 RefSeq:NP_188194.1 UniGene:At.23882 ProteinModelPortal:Q38882 SMR:Q38882 IntAct:Q38882 STRING:Q38882 PRIDE:Q38882 DNASU:820816 EnsemblPlants:AT3G15730.1 GeneID:820816 KEGG:ath:AT3G15730 TAIR:At3g15730 HOGENOM:HBG748198 InParanoid:Q38882 OMA:KLQYFDV PhylomeDB:Q38882 ProtClustDB:PLN02270 ArrayExpress:Q38882 Genevestigator:Q38882 GermOnline:AT3G15730 InterPro:IPR024632 Pfam:PF12357 Uniprot:Q38882
Leaf	Isotig00429	96	15	3.207	1.60E-22	TAIR|locus:2093227 - symbol:PLDALPHA1 "AT3G15730" species:3702 "Arabidopsis thaliana" [GO:0004630 "phospholipase D activity" evidence=ISS;IDA;IMP] [GO:0005634 "nucleus" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0030136 "clathrin-coated vesicle" evidence=IDA] [GO:0006631 "fatty acid metabolic process" evidence=IMP;TAS] [GO:0005515 "protein binding" evidence=IPI] [GO:0009507 "chloroplast" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0009789 "positive regulation of abscisic acid mediated

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						signaling pathway" evidence=IMP] [GO:0010119 "regulation of stomatal movement" evidence=IMP] [GO:0009845 "seed germination" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005546 "phosphatidylinositol-4,5-bisphosphate binding" evidence=IDA] InterPro:IPR000008 InterPro:IPR001736 InterPro:IPR008973 InterPro:IPR011402 Pfam:PF00168 Pfam:PF00614 PIRSF:PIRSF036470 PROSITE:PS50035 SMART:SM00155 SMART:SM00239 GO:GO:0005829 GO:GO:0005739 GO:GO:0005886 GO:GO:0009506 GO:GO:0005634 GO:GO:0005773 GO:GO:0046686 GO:GO:0009507 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005509 GO:GO:0005515 GO:GO:0009738 GO:GO:0009873 GO:GO:0009789 GO:GO:0010119 GO:GO:0046470 GO:GO:0016042 GO:GO:0006631 GO:GO:0030136 GO:GO:0009845 SUPFAM:SSF49562 PROSITE:PS50004 GO:GO:0005546 EMBL:AB017071 eggNOG:COG1502 InterPro:IPR015679 PANTHER:PTHR18896 GO:GO:0070290 GO:GO:0004630 KO:K01115 EMBL:U36381 EMBL:AF428278 IPI:IPI00527854 RefSeq:NP_188194.1 UniGene:At.23882 ProteinModelPortal:Q38882 SMR:Q38882 IntAct:Q38882 STRING:Q38882 PRIDE:Q38882 DNASU:820816 EnsemblPlants:AT3G15730.1 GeneID:820816 KEGG:ath:AT3G15730 TAIR:At3g15730 HOGENOM:HBG748198 InParanoid:Q38882 OMA:KLQYFDV PhylomeDB:Q38882 ProtClustDB:PLN02270 ArrayExpress:Q38882 Genevestigator:Q38882 GermOnline:AT3G15730 InterPro:IPR024632 Pfam:PF12357 Uniprot:Q38882
Leaf	Isotig00430	95	15	3.192	3.22E-22	TAIR|locus:2093227 - symbol:PLDALPHA1 "AT3G15730" species:3702 "Arabidopsis thaliana" [GO:0004630 "phospholipase D activity" evidence=ISS;IDA;IMP] [GO:0005634 "nucleus" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0030136 "clathrin-coated vesicle" evidence=IDA] [GO:0006631 "fatty acid metabolic process" evidence=IMP;TAS] [GO:0005515 "protein binding" evidence=IPI] [GO:0009507 "chloroplast" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0009789 "positive regulation of abscisic acid mediated signaling pathway" evidence=IMP] [GO:0010119 "regulation of stomatal movement" evidence=IMP] [GO:0009845 "seed germination" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005546 "phosphatidylinositol-4,5-bisphosphate binding" evidence=IDA] InterPro:IPR000008 InterPro:IPR001736 InterPro:IPR008973 InterPro:IPR011402 Pfam:PF00168 Pfam:PF00614 PIRSF:PIRSF036470 PROSITE:PS50035 SMART:SM00155 SMART:SM00239 GO:GO:0005829 GO:GO:0005739 GO:GO:0005886 GO:GO:0009506 GO:GO:0005634 GO:GO:0005773 GO:GO:0046686 GO:GO:0009507 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005509 GO:GO:0005515 GO:GO:0009738 GO:GO:0009873 GO:GO:0009789 GO:GO:0010119 GO:GO:0046470 GO:GO:0016042 GO:GO:0006631 GO:GO:0030136 GO:GO:0009845 SUPFAM:SSF49562 PROSITE:PS50004 GO:GO:0005546 EMBL:AB017071 eggNOG:COG1502 InterPro:IPR015679 PANTHER:PTHR18896 GO:GO:0070290 GO:GO:0004630 KO:K01115 EMBL:U36381 EMBL:AF428278 IPI:IPI00527854 RefSeq:NP_188194.1 UniGene:At.23882 ProteinModelPortal:Q38882 SMR:Q38882 IntAct:Q38882 STRING:Q38882 PRIDE:Q38882 DNASU:820816 EnsemblPlants:AT3G15730.1 GeneID:820816 KEGG:ath:AT3G15730 TAIR:At3g15730 HOGENOM:HBG748198 InParanoid:Q38882 OMA:KLQYFDV PhylomeDB:Q38882 ProtClustDB:PLN02270 ArrayExpress:Q38882 Genevestigator:Q38882 GermOnline:AT3G15730 InterPro:IPR024632 Pfam:PF12357 Uniprot:Q38882
Leaf	Isotig00431	95	15	3.192	3.22E-22	TAIR|locus:2093227 - symbol:PLDALPHA1 "AT3G15730" species:3702 "Arabidopsis thaliana" [GO:0004630 "phospholipase D activity" evidence=ISS;IDA;IMP] [GO:0005634 "nucleus" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0030136 "clathrin-coated vesicle" evidence=IDA] [GO:0006631 "fatty acid metabolic process" evidence=IMP;TAS] [GO:0005515 "protein binding" evidence=IPI] [GO:0009507 "chloroplast" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0009789 "positive regulation of abscisic acid mediated signaling pathway" evidence=IMP] [GO:0010119 "regulation of stomatal movement" evidence=IMP] [GO:0009845 "seed germination" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005546 "phosphatidylinositol-4,5-bisphosphate binding" evidence=IDA] InterPro:IPR000008 InterPro:IPR001736 InterPro:IPR008973 InterPro:IPR011402 Pfam:PF00168 Pfam:PF00614 PIRSF:PIRSF036470 PROSITE:PS50035 SMART:SM00155 SMART:SM00239 GO:GO:0005829 GO:GO:0005739 GO:GO:0005886 GO:GO:0009506 GO:GO:0005634 GO:GO:0005773 GO:GO:0046686 GO:GO:0009507 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005509 GO:GO:0005515 GO:GO:0009738 GO:GO:0009873 GO:GO:0009789 GO:GO:0010119 GO:GO:0046470 GO:GO:0016042 GO:GO:0006631 GO:GO:0030136 GO:GO:0009845 SUPFAM:SSF49562 PROSITE:PS50004 GO:GO:0005546 EMBL:AB017071 eggNOG:COG1502 InterPro:IPR015679 PANTHER:PTHR18896 GO:GO:0070290 GO:GO:0004630 KO:K01115 EMBL:U36381 EMBL:AF428278 IPI:IPI00527854 RefSeq:NP_188194.1 UniGene:At.23882 ProteinModelPortal:Q38882

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						SMR:Q38882 IntAct:Q38882 STRING:Q38882 PRIDE:Q38882 DNASU:820816 EnsemblPlants:AT3G15730.1 GeneID:820816 KEGG:ath:AT3G15730 TAIR:At3g15730 HOGENOM:HBG748198 InParanoid:Q38882 OMA:KLQYFDV PhylomeDB:Q38882 ProtClustDB:PLN02270 ArrayExpress:Q38882 Genevestigator:Q38882 GermOnline:AT3G15730 InterPro:IPR024632 Pfam:PF12357 Uniprot:Q38882
Leaf	Isotig00432	92	15	3.146	2.63E-21	TAIR|locus:2093227 - symbol:PLDALPHA1 "AT3G15730" species:3702 "Arabidopsis thaliana" [GO:0004630 "phospholipase D activity" evidence=ISS;IDA;IMP] [GO:0005634 "nucleus" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0030136 "clathrin-coated vesicle" evidence=IDA] [GO:0006631 "fatty acid metabolic process" evidence=IMP;TAS] [GO:0005515 "protein binding" evidence=IPI] [GO:0009507 "chloroplast" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0009789 "positive regulation of abscisic acid mediated signaling pathway" evidence=IMP] [GO:0010119 "regulation of stomatal movement" evidence=IMP] [GO:0009845 "seed germination" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005546 "phosphatidylinositol-4,5-bisphosphate binding" evidence=IDA] InterPro:IPR000008 InterPro:IPR001736 InterPro:IPR008973 InterPro:IPR011402 Pfam:PF00168 Pfam:PF00614 PIRSF:PIRSF036470 PROSITE:PS50035 SMART:SM00155 SMART:SM00239 GO:GO:0005829 GO:GO:0005739 GO:GO:0005886 GO:GO:0009506 GO:GO:0005634 GO:GO:0005773 GO:GO:0046686 GO:GO:0009507 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005509 GO:GO:0005515 GO:GO:0009738 GO:GO:0009873 GO:GO:0009789 GO:GO:0010119 GO:GO:0046470 GO:GO:0016042 GO:GO:0006631 GO:GO:0030136 GO:GO:0009845 SUPFAM:SSF49562 PROSITE:PS50004 GO:GO:0005546 EMBL:AB017071 eggNOG:COG1502 InterPro:IPR015679 PANTHER:PTHR18896 GO:GO:0070290 GO:GO:0004630 KO:K01115 EMBL:U36381 EMBL:AF428278 IPI:IPI00527854 RefSeq:NP_188194.1 UniGene:At.23882 ProteinModelPortal:Q38882 SMR:Q38882 IntAct:Q38882 STRING:Q38882 PRIDE:Q38882 DNASU:820816 EnsemblPlants:AT3G15730.1 GeneID:820816 KEGG:ath:AT3G15730 TAIR:At3g15730 HOGENOM:HBG748198 InParanoid:Q38882 OMA:KLQYFDV PhylomeDB:Q38882 ProtClustDB:PLN02270 ArrayExpress:Q38882 Genevestigator:Q38882 GermOnline:AT3G15730 InterPro:IPR024632 Pfam:PF12357 Uniprot:Q38882
Leaf	Isotig00433	92	15	3.146	2.63E-21	TAIR|locus:2093227 - symbol:PLDALPHA1 "AT3G15730" species:3702 "Arabidopsis thaliana" [GO:0004630 "phospholipase D activity" evidence=ISS;IDA;IMP] [GO:0005634 "nucleus" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0030136 "clathrin-coated vesicle" evidence=IDA] [GO:0006631 "fatty acid metabolic process" evidence=IMP;TAS] [GO:0005515 "protein binding" evidence=IPI] [GO:0009507 "chloroplast" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0009789 "positive regulation of abscisic acid mediated signaling pathway" evidence=IMP] [GO:0010119 "regulation of stomatal movement" evidence=IMP] [GO:0009845 "seed germination" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005546 "phosphatidylinositol-4,5-bisphosphate binding" evidence=IDA] InterPro:IPR000008 InterPro:IPR001736 InterPro:IPR008973 InterPro:IPR011402 Pfam:PF00168 Pfam:PF00614 PIRSF:PIRSF036470 PROSITE:PS50035 SMART:SM00155 SMART:SM00239 GO:GO:0005829 GO:GO:0005739 GO:GO:0005886 GO:GO:0009506 GO:GO:0005634 GO:GO:0005773 GO:GO:0046686 GO:GO:0009507 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005509 GO:GO:0005515 GO:GO:0009738 GO:GO:0009873 GO:GO:0009789 GO:GO:0010119 GO:GO:0046470 GO:GO:0016042 GO:GO:0006631 GO:GO:0030136 GO:GO:0009845 SUPFAM:SSF49562 PROSITE:PS50004 GO:GO:0005546 EMBL:AB017071 eggNOG:COG1502 InterPro:IPR015679 PANTHER:PTHR18896 GO:GO:0070290 GO:GO:0004630 KO:K01115 EMBL:U36381 EMBL:AF428278 IPI:IPI00527854 RefSeq:NP_188194.1 UniGene:At.23882 ProteinModelPortal:Q38882 SMR:Q38882 IntAct:Q38882 STRING:Q38882 PRIDE:Q38882 DNASU:820816 EnsemblPlants:AT3G15730.1 GeneID:820816 KEGG:ath:AT3G15730 TAIR:At3g15730 HOGENOM:HBG748198 InParanoid:Q38882 OMA:KLQYFDV PhylomeDB:Q38882 ProtClustDB:PLN02270 ArrayExpress:Q38882 Genevestigator:Q38882 GermOnline:AT3G15730 InterPro:IPR024632 Pfam:PF12357 Uniprot:Q38882
Leaf	Isotig00434	91	15	3.130	5.30E-21	TAIR|locus:2093227 - symbol:PLDALPHA1 "AT3G15730" species:3702 "Arabidopsis thaliana" [GO:0004630 "phospholipase D activity" evidence=ISS;IDA;IMP] [GO:0005634 "nucleus" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0030136 "clathrin-coated vesicle" evidence=IDA] [GO:0006631 "fatty acid metabolic process" evidence=IMP;TAS] [GO:0005515 "protein binding" evidence=IPI] [GO:0009507 "chloroplast" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0009789 "positive regulation of abscisic acid mediated

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						signaling pathway" evidence=IMP] [GO:0010119 "regulation of stomatal movement" evidence=IMP] [GO:0009845 "seed germination" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005546 "phosphatidylinositol-4,5-bisphosphate binding" evidence=IDA] InterPro:IPR000008 InterPro:IPR001736 InterPro:IPR008973 InterPro:IPR011402 Pfam:PF00168 Pfam:PF00614 PIRSF:PIRSF036470 PROSITE:PS50035 SMART:SM00155 SMART:SM00239 GO:GO:0005829 GO:GO:0005739 GO:GO:0005886 GO:GO:0009506 GO:GO:0005634 GO:GO:0005773 GO:GO:0046686 GO:GO:0009507 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005509 GO:GO:0005515 GO:GO:0009738 GO:GO:0009873 GO:GO:0009789 GO:GO:0010119 GO:GO:0046470 GO:GO:0016042 GO:GO:0006631 GO:GO:0030136 GO:GO:0009845 SUPFAM:SSF49562 PROSITE:PS50004 GO:GO:0005546 EMBL:AB017071 eggNOG:COG1502 InterPro:IPR015679 PANTHER:PTHR18896 GO:GO:0070290 GO:GO:0004630 KO:K01115 EMBL:U36381 EMBL:AF428278 IPI:IPI00527854 RefSeq:NP_188194.1 UniGene:At.23882 ProteinModelPortal:Q38882 SMR:Q38882 IntAct:Q38882 STRING:Q38882 PRIDE:Q38882 DNASU:820816 EnsemblPlants:AT3G15730.1 GeneID:820816 KEGG:ath:AT3G15730 TAIR:At3g15730 HOGENOM:HBG748198 InParanoid:Q38882 OMA:KLQYFDV PhylomeDB:Q38882 ProtClustDB:PLN02270 ArrayExpress:Q38882 Genevestigator:Q38882 GermOnline:AT3G15730 InterPro:IPR024632 Pfam:PF12357 Uniprot:Q38882
Leaf	Isotig00435	91	15	3.130	5.30E-21	TAIR|locus:2093227 - symbol:PLDALPHA1 "AT3G15730" species:3702 "Arabidopsis thaliana" [GO:0004630 "phospholipase D activity" evidence=ISS;IDA;IMP] [GO:0005634 "nucleus" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0030136 "clathrin-coated vesicle" evidence=IDA] [GO:0006631 "fatty acid metabolic process" evidence=IMP;TAS] [GO:0005515 "protein binding" evidence=IPI] [GO:0009507 "chloroplast" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0009789 "positive regulation of abscisic acid mediated signaling pathway" evidence=IMP] [GO:0010119 "regulation of stomatal movement" evidence=IMP] [GO:0009845 "seed germination" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005546 "phosphatidylinositol-4,5-bisphosphate binding" evidence=IDA] InterPro:IPR000008 InterPro:IPR001736 InterPro:IPR008973 InterPro:IPR011402 Pfam:PF00168 Pfam:PF00614 PIRSF:PIRSF036470 PROSITE:PS50035 SMART:SM00155 SMART:SM00239 GO:GO:0005829 GO:GO:0005739 GO:GO:0005886 GO:GO:0009506 GO:GO:0005634 GO:GO:0005773 GO:GO:0046686 GO:GO:0009507 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005509 GO:GO:0005515 GO:GO:0009738 GO:GO:0009873 GO:GO:0009789 GO:GO:0010119 GO:GO:0046470 GO:GO:0016042 GO:GO:0006631 GO:GO:0030136 GO:GO:0009845 SUPFAM:SSF49562 PROSITE:PS50004 GO:GO:0005546 EMBL:AB017071 eggNOG:COG1502 InterPro:IPR015679 PANTHER:PTHR18896 GO:GO:0070290 GO:GO:0004630 KO:K01115 EMBL:U36381 EMBL:AF428278 IPI:IPI00527854 RefSeq:NP_188194.1 UniGene:At.23882 ProteinModelPortal:Q38882 SMR:Q38882 IntAct:Q38882 STRING:Q38882 PRIDE:Q38882 DNASU:820816 EnsemblPlants:AT3G15730.1 GeneID:820816 KEGG:ath:AT3G15730 TAIR:At3g15730 HOGENOM:HBG748198 InParanoid:Q38882 OMA:KLQYFDV PhylomeDB:Q38882 ProtClustDB:PLN02270 ArrayExpress:Q38882 Genevestigator:Q38882 GermOnline:AT3G15730 InterPro:IPR024632 Pfam:PF12357 Uniprot:Q38882
Leaf	Isotig00436	129	58	1.682	1.05E-14	TAIR|locus:2088535 - symbol:XPL1 "AT3G18000" species:3702 "Arabidopsis thaliana" [GO:0000234 "phosphoethanolamine N-methyltransferase activity" evidence=IGI;ISS] [GO:0005737 "cytoplasm" evidence=ISS] [GO:0006656 "phosphatidylcholine biosynthetic process" evidence=IGI] [GO:0008168 "methyltransferase activity" evidence=ISS] [GO:0009555 "pollen development" evidence=IMP] [GO:0009826 "unidimensional cell growth" evidence=IMP] [GO:0042425 "choline biosynthetic process" evidence=IMP] [GO:0048528 "post-embryonic root development" evidence=IMP] [GO:0009860 "pollen tube growth" evidence=IMP] [GO:0010183 "pollen tube guidance" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR013216 Pfam:PF08241 GO:GO:0005829 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0009555 GO:GO:0009860 eggNOG:COG0500 GO:GO:0006656 GO:GO:0010183 EMBL:AB019230 GO:GO:0048528 EMBL:AF197940 EMBL:AF367299 EMBL:AY058175 EMBL:AY091683 EMBL:AY093093 IPI:IPI00542357 RefSeq:NP_188427.2 UniGene:At.21159 ProteinModelPortal:Q9FR44 SMR:Q9FR44 STRING:Q9FR44 PRIDE:Q9FR44 EnsemblPlants:AT3G18000.1 GeneID:821324 KEGG:ath:AT3G18000 TAIR:At3g18000 HOGENOM:HBG320513 InParanoid:Q9FR44 KO:K05929 OMA:DQRWGLF PhylomeDB:Q9FR44 ProtClustDB:PLN02336 Genevestigator:Q9FR44 GermOnline:AT3G18000 GO:GO:0000234 GO:GO:0042425 Uniprot:Q9FR44
Leaf	Isotig00437	129	58	1.682	1.05E-14	TAIR|locus:2088535 - symbol:XPL1 "AT3G18000" species:3702 "Arabidopsis thaliana" [GO:0000234 "phosphoethanolamine N-methyltransferase activity" evidence=IGI;ISS] [GO:0005737 "cytoplasm" evidence=ISS]

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						[GO:0006656 "phosphatidylcholine biosynthetic process" evidence=IGI] [GO:0008168 "methyltransferase activity" evidence=ISS] [GO:0009555 "pollen development" evidence=IMP] [GO:0009826 "unidimensional cell growth" evidence=IMP] [GO:0042425 "choline biosynthetic process" evidence=IMP] [GO:0048528 "post-embryonic root development" evidence=IMP] [GO:0009860 "pollen tube growth" evidence=IMP] [GO:0010183 "pollen tube guidance" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR013216 Pfam:PF08241 GO:GO:0005829 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0009555 GO:GO:0009860 eggNOG:COG0500 GO:GO:0006656 GO:GO:0010183 EMBL:AB019230 GO:GO:0048528 EMBL:AF197940 EMBL:AF367299 EMBL:AY058175 EMBL:AY091683 EMBL:AY093093 IPI:IPI00542357 RefSeq:NP_188427.2 UniGene:At.21159 ProteinModelPortal:Q9FR44 SMR:Q9FR44 STRING:Q9FR44 PRIDE:Q9FR44 EnsemblPlants:AT3G18000.1 GeneID:821324 KEGG:ath:AT3G18000 TAIR:At3g18000 HOGENOM:HBG320513 InParanoid:Q9FR44 KO:K05929 OMA:DQRWGLF PhylomeDB:Q9FR44 ProtClustDB:PLN02336 Genevestigator:Q9FR44 GermOnline:AT3G18000 GO:GO:0000234 GO:GO:0042425 Uniprot:Q9FR44
Leaf	Isotig00438	122	65	1.437	2.02E-11	TAIR|locus:2088535 - symbol:XPL1 "AT3G18000" species:3702 "Arabidopsis thaliana" [GO:0000234 "phosphoethanolamine N-methyltransferase activity" evidence=IGI;ISS] [GO:0005737 "cytoplasm" evidence=ISS] [GO:0006656 "phosphatidylcholine biosynthetic process" evidence=IGI] [GO:0008168 "methyltransferase activity" evidence=ISS] [GO:0009555 "pollen development" evidence=IMP] [GO:0009826 "unidimensional cell growth" evidence=IMP] [GO:0042425 "choline biosynthetic process" evidence=IMP] [GO:0048528 "post-embryonic root development" evidence=IMP] [GO:0009860 "pollen tube growth" evidence=IMP] [GO:0010183 "pollen tube guidance" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR013216 Pfam:PF08241 GO:GO:0005829 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0009555 GO:GO:0009860 eggNOG:COG0500 GO:GO:0006656 GO:GO:0010183 EMBL:AB019230 GO:GO:0048528 EMBL:AF197940 EMBL:AF367299 EMBL:AY058175 EMBL:AY091683 EMBL:AY093093 IPI:IPI00542357 RefSeq:NP_188427.2 UniGene:At.21159 ProteinModelPortal:Q9FR44 SMR:Q9FR44 STRING:Q9FR44 PRIDE:Q9FR44 EnsemblPlants:AT3G18000.1 GeneID:821324 KEGG:ath:AT3G18000 TAIR:At3g18000 HOGENOM:HBG320513 InParanoid:Q9FR44 KO:K05929 OMA:DQRWGLF PhylomeDB:Q9FR44 ProtClustDB:PLN02336 Genevestigator:Q9FR44 GermOnline:AT3G18000 GO:GO:0000234 GO:GO:0042425 Uniprot:Q9FR44
Leaf	Isotig00439	125	55	1.713	1.24E-14	TAIR|locus:2088535 - symbol:XPL1 "AT3G18000" species:3702 "Arabidopsis thaliana" [GO:0000234 "phosphoethanolamine N-methyltransferase activity" evidence=IGI;ISS] [GO:0005737 "cytoplasm" evidence=ISS] [GO:0006656 "phosphatidylcholine biosynthetic process" evidence=IGI] [GO:0008168 "methyltransferase activity" evidence=ISS] [GO:0009555 "pollen development" evidence=IMP] [GO:0009826 "unidimensional cell growth" evidence=IMP] [GO:0042425 "choline biosynthetic process" evidence=IMP] [GO:0048528 "post-embryonic root development" evidence=IMP] [GO:0009860 "pollen tube growth" evidence=IMP] [GO:0010183 "pollen tube guidance" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR013216 Pfam:PF08241 GO:GO:0005829 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0009555 GO:GO:0009860 eggNOG:COG0500 GO:GO:0006656 GO:GO:0010183 EMBL:AB019230 GO:GO:0048528 EMBL:AF197940 EMBL:AF367299 EMBL:AY058175 EMBL:AY091683 EMBL:AY093093 IPI:IPI00542357 RefSeq:NP_188427.2 UniGene:At.21159 ProteinModelPortal:Q9FR44 SMR:Q9FR44 STRING:Q9FR44 PRIDE:Q9FR44 EnsemblPlants:AT3G18000.1 GeneID:821324 KEGG:ath:AT3G18000 TAIR:At3g18000 HOGENOM:HBG320513 InParanoid:Q9FR44 KO:K05929 OMA:DQRWGLF PhylomeDB:Q9FR44 ProtClustDB:PLN02336 Genevestigator:Q9FR44 GermOnline:AT3G18000 GO:GO:0000234 GO:GO:0042425 Uniprot:Q9FR44
Leaf	Isotig00440	125	55	1.713	1.24E-14	TAIR|locus:2088535 - symbol:XPL1 "AT3G18000" species:3702 "Arabidopsis thaliana" [GO:0000234 "phosphoethanolamine N-methyltransferase activity" evidence=IGI;ISS] [GO:0005737 "cytoplasm" evidence=ISS] [GO:0006656 "phosphatidylcholine biosynthetic process" evidence=IGI] [GO:0008168 "methyltransferase activity" evidence=ISS] [GO:0009555 "pollen development" evidence=IMP] [GO:0009826 "unidimensional cell growth" evidence=IMP] [GO:0042425 "choline biosynthetic process" evidence=IMP] [GO:0048528 "post-embryonic root development" evidence=IMP] [GO:0009860 "pollen tube growth" evidence=IMP] [GO:0010183 "pollen tube guidance" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR013216 Pfam:PF08241 GO:GO:0005829 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0009555 GO:GO:0009860 eggNOG:COG0500 GO:GO:0006656 GO:GO:0010183 EMBL:AB019230 GO:GO:0048528 EMBL:AF197940 EMBL:AF367299 EMBL:AY058175 EMBL:AY091683 EMBL:AY093093 IPI:IPI00542357 RefSeq:NP_188427.2 UniGene:At.21159 ProteinModelPortal:Q9FR44 SMR:Q9FR44 STRING:Q9FR44 PRIDE:Q9FR44 EnsemblPlants:AT3G18000.1 GeneID:821324 KEGG:ath:AT3G18000 TAIR:At3g18000 HOGENOM:HBG320513

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						InParanoid:Q9FR44 KO:K05929 OMA:DQRWGLF PhylomeDB:Q9FR44 ProtClustDB:PLN02336 Genevestigator:Q9FR44 GermOnline:AT3G18000 GO:GO:0000234 GO:GO:0042425 Uniprot:Q9FR44
Leaf	Isotig00441	118	62	1.457	2.69E-11	TAIR|locus:2088535 - symbol:XPL1 "AT3G18000" species:3702 "Arabidopsis thaliana" [GO:0000234 "phosphoethanolamine N-methyltransferase activity" evidence=IGI;ISS] [GO:0005737 "cytoplasm" evidence=ISS] [GO:0006656 "phosphatidylcholine biosynthetic process" evidence=IGI] [GO:0008168 "methyltransferase activity" evidence=ISS] [GO:0009555 "pollen development" evidence=IMP] [GO:0009826 "unidimensional cell growth" evidence=IMP] [GO:0042425 "choline biosynthetic process" evidence=IMP] [GO:0048528 "post-embryonic root development" evidence=IMP] [GO:0009860 "pollen tube growth" evidence=IMP] [GO:0010183 "pollen tube guidance" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR013216 Pfam:PF08241 GO:GO:0005829 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0009555 GO:GO:0009860 eggNOG:COG0500 GO:GO:0006656 GO:GO:0010183 EMBL:AB019230 GO:GO:0048528 EMBL:AF197940 EMBL:AF367299 EMBL:AY058175 EMBL:AY091683 EMBL:AY093093 IPI:IPI00542357 RefSeq:NP_188427.2 UniGene:At.21159 ProteinModelPortal:Q9FR44 SMR:Q9FR44 STRING:Q9FR44 PRIDE:Q9FR44 EnsemblPlants:AT3G18000.1 GeneID:821324 KEGG:ath:AT3G18000 TAIR:At3g18000 HOGENOM:HBG320513 InParanoid:Q9FR44 KO:K05929 OMA:DQRWGLF PhylomeDB:Q9FR44 ProtClustDB:PLN02336 Genevestigator:Q9FR44 GermOnline:AT3G18000 GO:GO:0000234 GO:GO:0042425 Uniprot:Q9FR44
Leaf	Isotig00442	160	49	2.236	2.45E-25	TAIR|locus:2088535 - symbol:XPL1 "AT3G18000" species:3702 "Arabidopsis thaliana" [GO:0000234 "phosphoethanolamine N-methyltransferase activity" evidence=IGI;ISS] [GO:0005737 "cytoplasm" evidence=ISS] [GO:0006656 "phosphatidylcholine biosynthetic process" evidence=IGI] [GO:0008168 "methyltransferase activity" evidence=ISS] [GO:0009555 "pollen development" evidence=IMP] [GO:0009826 "unidimensional cell growth" evidence=IMP] [GO:0042425 "choline biosynthetic process" evidence=IMP] [GO:0048528 "post-embryonic root development" evidence=IMP] [GO:0009860 "pollen tube growth" evidence=IMP] [GO:0010183 "pollen tube guidance" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR013216 Pfam:PF08241 GO:GO:0005829 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0009555 GO:GO:0009860 eggNOG:COG0500 GO:GO:0006656 GO:GO:0010183 EMBL:AB019230 GO:GO:0048528 EMBL:AF197940 EMBL:AF367299 EMBL:AY058175 EMBL:AY091683 EMBL:AY093093 IPI:IPI00542357 RefSeq:NP_188427.2 UniGene:At.21159 ProteinModelPortal:Q9FR44 SMR:Q9FR44 STRING:Q9FR44 PRIDE:Q9FR44 EnsemblPlants:AT3G18000.1 GeneID:821324 KEGG:ath:AT3G18000 TAIR:At3g18000 HOGENOM:HBG320513 InParanoid:Q9FR44 KO:K05929 OMA:DQRWGLF PhylomeDB:Q9FR44 ProtClustDB:PLN02336 Genevestigator:Q9FR44 GermOnline:AT3G18000 GO:GO:0000234 GO:GO:0042425 Uniprot:Q9FR44
Leaf	Isotig00443	160	49	2.236	2.45E-25	TAIR|locus:2088535 - symbol:XPL1 "AT3G18000" species:3702 "Arabidopsis thaliana" [GO:0000234 "phosphoethanolamine N-methyltransferase activity" evidence=IGI;ISS] [GO:0005737 "cytoplasm" evidence=ISS] [GO:0006656 "phosphatidylcholine biosynthetic process" evidence=IGI] [GO:0008168 "methyltransferase activity" evidence=ISS] [GO:0009555 "pollen development" evidence=IMP] [GO:0009826 "unidimensional cell growth" evidence=IMP] [GO:0042425 "choline biosynthetic process" evidence=IMP] [GO:0048528 "post-embryonic root development" evidence=IMP] [GO:0009860 "pollen tube growth" evidence=IMP] [GO:0010183 "pollen tube guidance" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR013216 Pfam:PF08241 GO:GO:0005829 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0009555 GO:GO:0009860 eggNOG:COG0500 GO:GO:0006656 GO:GO:0010183 EMBL:AB019230 GO:GO:0048528 EMBL:AF197940 EMBL:AF367299 EMBL:AY058175 EMBL:AY091683 EMBL:AY093093 IPI:IPI00542357 RefSeq:NP_188427.2 UniGene:At.21159 ProteinModelPortal:Q9FR44 SMR:Q9FR44 STRING:Q9FR44 PRIDE:Q9FR44 EnsemblPlants:AT3G18000.1 GeneID:821324 KEGG:ath:AT3G18000 TAIR:At3g18000 HOGENOM:HBG320513 InParanoid:Q9FR44 KO:K05929 OMA:DQRWGLF PhylomeDB:Q9FR44 ProtClustDB:PLN02336 Genevestigator:Q9FR44 GermOnline:AT3G18000 GO:GO:0000234 GO:GO:0042425 Uniprot:Q9FR44
Leaf	Isotig00468	32	11	2.070	9.40E-06	TAIR|locus:2089955 - symbol:AT3G21690 "AT3G21690" species:3702 "Arabidopsis thaliana" [GO:0005215 "transporter activity" evidence=ISS] [GO:0006855 "drug transmembrane transport" evidence=IEA] [GO:0015238 "drug transmembrane transporter activity" evidence=IEA] [GO:0015297 "antiporter activity" evidence=IEA;ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0055085 "transmembrane transport" evidence=IEA] [GO:0005774 "vacuolar membrane" evidence=IDA] InterPro:IPR002528 Pfam:PF01554 GO:GO:0005774 EMBL:CP002686 EMBL:AB019232 GO:GO:0015238 GO:GO:0015297 KO:K03327 PANTHER:PTHR11206 TIGRFAMs:TIGR00797 EMBL:BT015408 IPI:IPI00544369 RefSeq:NP_188806.1 UniGene:At.43957 UniGene:At.67726 ProteinModelPortal:Q9LVD9 IntAct:Q9LVD9 PRIDE:Q9LVD9 EnsemblPlants:AT3G21690.1 GeneID:821723

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						KEGG:ath:AT3G21690 TAIR:At3g21690 InParanoid:Q9LVD9 OMA:SICMTIS PhylomeDB:Q9LVD9 ProtClustDB:CLSN2682181 Genevestigator:Q9LVD9 Uniprot:Q9LVD9
Leaf	Isotig00469	31	11	2.024	1.72E-05	TAIR|locus:2089955 - symbol:AT3G21690 "AT3G21690" species:3702 "Arabidopsis thaliana" [GO:0005215 "transporter activity" evidence=ISS] [GO:0006855 "drug transmembrane transport" evidence=IEA] [GO:0015238 "drug transmembrane transporter activity" evidence=IEA] [GO:0015297 "antiporter activity" evidence=IEA;ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0055085 "transmembrane transport" evidence=IEA] [GO:0005774 "vacuolar membrane" evidence=IDA] InterPro:IPR002528 Pfam:PF01554 GO:GO:0005774 EMBL:CP002686 EMBL:AB019232 GO:GO:0015238 GO:GO:0015297 KO:K03327 PANTHER:PTHR11206 TIGRFAMs:TIGR00797 EMBL:BT015408 IPI:IPI00544369 RefSeq:NP_188806.1 UniGene:At.43957 UniGene:At.67726 ProteinModelPortal:Q9LVD9 IntAct:Q9LVD9 PRIDE:Q9LVD9 EnsemblPlants:AT3G21690.1 GeneID:821723 KEGG:ath:AT3G21690 TAIR:At3g21690 InParanoid:Q9LVD9 OMA:SICMTIS PhylomeDB:Q9LVD9 ProtClustDB:CLSN2682181 Genevestigator:Q9LVD9 Uniprot:Q9LVD9
Leaf	Isotig00470	32	11	2.070	9.40E-06	TAIR|locus:2089955 - symbol:AT3G21690 "AT3G21690" species:3702 "Arabidopsis thaliana" [GO:0005215 "transporter activity" evidence=ISS] [GO:0006855 "drug transmembrane transport" evidence=IEA] [GO:0015238 "drug transmembrane transporter activity" evidence=IEA] [GO:0015297 "antiporter activity" evidence=IEA;ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0055085 "transmembrane transport" evidence=IEA] [GO:0005774 "vacuolar membrane" evidence=IDA] InterPro:IPR002528 Pfam:PF01554 GO:GO:0005774 EMBL:CP002686 EMBL:AB019232 GO:GO:0015238 GO:GO:0015297 KO:K03327 PANTHER:PTHR11206 TIGRFAMs:TIGR00797 EMBL:BT015408 IPI:IPI00544369 RefSeq:NP_188806.1 UniGene:At.43957 UniGene:At.67726 ProteinModelPortal:Q9LVD9 IntAct:Q9LVD9 PRIDE:Q9LVD9 EnsemblPlants:AT3G21690.1 GeneID:821723 KEGG:ath:AT3G21690 TAIR:At3g21690 InParanoid:Q9LVD9 OMA:SICMTIS PhylomeDB:Q9LVD9 ProtClustDB:CLSN2682181 Genevestigator:Q9LVD9 Uniprot:Q9LVD9
Leaf	Isotig00471	31	11	2.024	1.72E-05	TAIR|locus:2089955 - symbol:AT3G21690 "AT3G21690" species:3702 "Arabidopsis thaliana" [GO:0005215 "transporter activity" evidence=ISS] [GO:0006855 "drug transmembrane transport" evidence=IEA] [GO:0015238 "drug transmembrane transporter activity" evidence=IEA] [GO:0015297 "antiporter activity" evidence=IEA;ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0055085 "transmembrane transport" evidence=IEA] [GO:0005774 "vacuolar membrane" evidence=IDA] InterPro:IPR002528 Pfam:PF01554 GO:GO:0005774 EMBL:CP002686 EMBL:AB019232 GO:GO:0015238 GO:GO:0015297 KO:K03327 PANTHER:PTHR11206 TIGRFAMs:TIGR00797 EMBL:BT015408 IPI:IPI00544369 RefSeq:NP_188806.1 UniGene:At.43957 UniGene:At.67726 ProteinModelPortal:Q9LVD9 IntAct:Q9LVD9 PRIDE:Q9LVD9 EnsemblPlants:AT3G21690.1 GeneID:821723 KEGG:ath:AT3G21690 TAIR:At3g21690 InParanoid:Q9LVD9 OMA:SICMTIS PhylomeDB:Q9LVD9 ProtClustDB:CLSN2682181 Genevestigator:Q9LVD9 Uniprot:Q9LVD9
Leaf	Isotig00489	810	684	0.773	1.73E-25	UNIPROTKB|P09193 - symbol:psbC "Photosystem II 44 kDa reaction center protein" species:1111708 "Synechocystis sp. PCC 6803 substr. Kazusa" [GO:0030096 "plasma membrane-derived thylakoid photosystem II" evidence=IDA] InterPro:IPR000932 InterPro:IPR005869 Pfam:PF00421 GO:GO:0016021 GO:GO:0018298 EMBL:BA000022 GenomeReviews:BA000022_GR GO:GO:0042651 GO:GO:0009772 GO:GO:0016168 GO:GO:0030096 TCDB:3.E.2.2.2 GO:GO:0045156 HOGENOM:HBG284351 GO:GO:0030076 EMBL:M21538 EMBL:X07018 PIR:S06469 ProteinModelPortal:P09193 SMR:P09193 IntAct:P09193 STRING:P09193 KEGG:syn:sll0851 eggNOG:NOG05025 OMA:AWWSGNA PhylomeDB:P09193 ProtClustDB:CLSK892993 BioCyc:MetaCyc:PSBC-MONOMER BioCyc:SSP1148:SLL0851-MONOMER TIGRFAMs:TIGR01153 Uniprot:P09193
Leaf	Isotig00490	816	687	0.777	6.70E-26	UNIPROTKB|P09193 - symbol:psbC "Photosystem II 44 kDa reaction center protein" species:1111708 "Synechocystis sp. PCC 6803 substr. Kazusa" [GO:0030096 "plasma membrane-derived thylakoid photosystem II" evidence=IDA] InterPro:IPR000932 InterPro:IPR005869 Pfam:PF00421 GO:GO:0016021 GO:GO:0018298 EMBL:BA000022 GenomeReviews:BA000022_GR GO:GO:0042651 GO:GO:0009772 GO:GO:0016168 GO:GO:0030096 TCDB:3.E.2.2.2 GO:GO:0045156 HOGENOM:HBG284351 GO:GO:0030076 EMBL:M21538 EMBL:X07018 PIR:S06469 ProteinModelPortal:P09193 SMR:P09193 IntAct:P09193 STRING:P09193 KEGG:syn:sll0851 eggNOG:NOG05025 OMA:AWWSGNA PhylomeDB:P09193 ProtClustDB:CLSK892993 BioCyc:MetaCyc:PSBC-MONOMER BioCyc:SSP1148:SLL0851-MONOMER TIGRFAMs:TIGR01153 Uniprot:P09193
Leaf	Isotig00491	787	661	0.781	3.24E-25	UNIPROTKB|P09193 - symbol:psbC "Photosystem II 44 kDa reaction center protein" species:1111708 "Synechocystis sp. PCC 6803 substr. Kazusa" [GO:0030096 "plasma membrane-derived thylakoid photosystem II"

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						evidence=IDA] InterPro:IPR000932 InterPro:IPR005869 Pfam:PF00421 GO:GO:0016021 GO:GO:0018298 EMBL:BA000022 GenomeReviews:BA000022_GR GO:GO:0042651 GO:GO:0009772 GO:GO:0016168 GO:GO:0030096 TCDB:3.E.2.2.2 GO:GO:0045156 HOGENOM:HBG284351 GO:GO:0030076 EMBL:M21538 EMBL:X07018 PIR:S06469 ProteinModelPortal:P09193 SMR:P09193 IntAct:P09193 STRING:P09193 KEGG:syn:sll0851 eggNOG:NOG05025 OMA:AWWSGNA PhylomeDB:P09193 ProtClustDB:CLSK892993 BioCyc:MetaCyc:PSBC-MONOMER BioCyc:SSP1148:SLL0851-MONOMER TIGRFAMs:TIGR01153 Uniprot:P09193
Leaf	Isotig00492	793	664	0.785	1.25E-25	UNIPROTKB|P09193 - symbol:psbC "Photosystem II 44 kDa reaction center protein" species:1111708 "Synechocystis sp. PCC 6803 substr. Kazusa" [GO:0030096 "plasma membrane-derived thylakoid photosystem II" evidence=IDA] InterPro:IPR000932 InterPro:IPR005869 Pfam:PF00421 GO:GO:0016021 GO:GO:0018298 EMBL:BA000022 GenomeReviews:BA000022_GR GO:GO:0042651 GO:GO:0009772 GO:GO:0016168 GO:GO:0030096 TCDB:3.E.2.2.2 GO:GO:0045156 HOGENOM:HBG284351 GO:GO:0030076 EMBL:M21538 EMBL:X07018 PIR:S06469 ProteinModelPortal:P09193 SMR:P09193 IntAct:P09193 STRING:P09193 KEGG:syn:sll0851 eggNOG:NOG05025 OMA:AWWSGNA PhylomeDB:P09193 ProtClustDB:CLSK892993 BioCyc:MetaCyc:PSBC-MONOMER BioCyc:SSP1148:SLL0851-MONOMER TIGRFAMs:TIGR01153 Uniprot:P09193
Leaf	Isotig00493	281	217	0.902	2.43E-12	UNIPROTKB|P09193 - symbol:psbC "Photosystem II 44 kDa reaction center protein" species:1111708 "Synechocystis sp. PCC 6803 substr. Kazusa" [GO:0030096 "plasma membrane-derived thylakoid photosystem II" evidence=IDA] InterPro:IPR000932 InterPro:IPR005869 Pfam:PF00421 GO:GO:0016021 GO:GO:0018298 EMBL:BA000022 GenomeReviews:BA000022_GR GO:GO:0042651 GO:GO:0009772 GO:GO:0016168 GO:GO:0030096 TCDB:3.E.2.2.2 GO:GO:0045156 HOGENOM:HBG284351 GO:GO:0030076 EMBL:M21538 EMBL:X07018 PIR:S06469 ProteinModelPortal:P09193 SMR:P09193 IntAct:P09193 STRING:P09193 KEGG:syn:sll0851 eggNOG:NOG05025 OMA:AWWSGNA PhylomeDB:P09193 ProtClustDB:CLSK892993 BioCyc:MetaCyc:PSBC-MONOMER BioCyc:SSP1148:SLL0851-MONOMER TIGRFAMs:TIGR01153 Uniprot:P09193
Leaf	Isotig00495	49	13	2.443	1.31E-09	TAIR|locus:2094721 - symbol:ABCC8 "AT3G21250" species:3702 "Arabidopsis thaliana" [GO:0042626 "ATPase activity, coupled to transmembrane movement of substances" evidence=ISS] [GO:0000325 "plant-type vacuole" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] InterPro:IPR001140 InterPro:IPR003439 InterPro:IPR003593 InterPro:IPR011527 InterPro:IPR017871 Pfam:PF00005 Pfam:PF00664 PROSITE:PS00211 PROSITE:PS50893 SMART:SM00382 GO:GO:0016021 GO:GO:0005524 GO:GO:0005774 EMBL:CP002686 GenomeReviews:BA000014_GR EMBL:AB023045 eggNOG:COG1132 HOGENOM:HBG758042 InterPro:IPR017940 SUPFAM:SSF90123 PROSITE:PS50929 GO:GO:0008559 GO:GO:0000325 EMBL:AJ507057 IPI:IPI00540913 IPI:IPI00991516 RefSeq:NP_001189944.1 RefSeq:NP_188762.3 UniGene:At.38092 ProteinModelPortal:Q8LGU1 SMR:Q8LGU1 PRIDE:Q8LGU1 EnsemblPlants:AT3G21250.2 GeneID:821679 KEGG:ath:AT3G21250 TAIR:At3g21250 InParanoid:Q8LGU1 Genevestigator:Q8LGU1 GermOnline:AT3G21250 Uniprot:Q8LGU1
Leaf	Isotig00496	48	12	2.529	9.15E-10	TAIR|locus:2094721 - symbol:ABCC8 "AT3G21250" species:3702 "Arabidopsis thaliana" [GO:0042626 "ATPase activity, coupled to transmembrane movement of substances" evidence=ISS] [GO:0000325 "plant-type vacuole" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] InterPro:IPR001140 InterPro:IPR003439 InterPro:IPR003593 InterPro:IPR011527 InterPro:IPR017871 Pfam:PF00005 Pfam:PF00664 PROSITE:PS00211 PROSITE:PS50893 SMART:SM00382 GO:GO:0016021 GO:GO:0005524 GO:GO:0005774 EMBL:CP002686 GenomeReviews:BA000014_GR EMBL:AB023045 eggNOG:COG1132 HOGENOM:HBG758042 InterPro:IPR017940 SUPFAM:SSF90123 PROSITE:PS50929 GO:GO:0008559 GO:GO:0000325 EMBL:AJ507057 IPI:IPI00540913 IPI:IPI00991516 RefSeq:NP_001189944.1 RefSeq:NP_188762.3 UniGene:At.38092 ProteinModelPortal:Q8LGU1 SMR:Q8LGU1 PRIDE:Q8LGU1 EnsemblPlants:AT3G21250.2 GeneID:821679 KEGG:ath:AT3G21250 TAIR:At3g21250 InParanoid:Q8LGU1 Genevestigator:Q8LGU1 GermOnline:AT3G21250 Uniprot:Q8LGU1
Leaf	Isotig00497	37	13	2.038	2.39E-06	TAIR|locus:2094721 - symbol:ABCC8 "AT3G21250" species:3702 "Arabidopsis thaliana" [GO:0042626 "ATPase activity, coupled to transmembrane movement of substances" evidence=ISS] [GO:0000325 "plant-type vacuole" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] InterPro:IPR001140 InterPro:IPR003439 InterPro:IPR003593 InterPro:IPR011527 InterPro:IPR017871 Pfam:PF00005 Pfam:PF00664 PROSITE:PS00211 PROSITE:PS50893 SMART:SM00382 GO:GO:0016021 GO:GO:0005524 GO:GO:0005774 EMBL:CP002686

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GenomeReviews:BA000014_GR EMBL:AB023045 eggNOG:COG1132 HOGENOM:HBG758042 InterPro:IPR017940 SUPFAM:SSF90123 PROSITE:PS50929 GO:GO:0008559 GO:GO:0000325 EMBL:AJ507057 IPI:IPI00540913 IPI:IPI00991516 RefSeq:NP_001189944.1 RefSeq:NP_188762.3 UniGene:At.38092 ProteinModelPortal:Q8LGU1 SMR:Q8LGU1 PRIDE:Q8LGU1 EnsemblPlants:AT3G21250.2 GeneID:821679 KEGG:ath:AT3G21250 TAIR:At3g21250 InParanoid:Q8LGU1 Genevestigator:Q8LGU1 GermOnline:AT3G21250 Uniprot:Q8LGU1
Leaf	Isotig00498	36	12	2.114	1.90E-06	TAIR|locus:2094721 - symbol:ABCC8 "AT3G21250" species:3702 "Arabidopsis thaliana" [GO:0042626 "ATPase activity, coupled to transmembrane movement of substances" evidence=ISS] [GO:0000325 "plant-type vacuole" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] InterPro:IPR001140 InterPro:IPR003439 InterPro:IPR003593 InterPro:IPR011527 InterPro:IPR017871 Pfam:PF00005 Pfam:PF00664 PROSITE:PS00211 PROSITE:PS50893 SMART:SM00382 GO:GO:0016021 GO:GO:0005524 GO:GO:0005774 EMBL:CP002686 GenomeReviews:BA000014_GR EMBL:AB023045 eggNOG:COG1132 HOGENOM:HBG758042 InterPro:IPR017940 SUPFAM:SSF90123 PROSITE:PS50929 GO:GO:0008559 GO:GO:0000325 EMBL:AJ507057 IPI:IPI00540913 IPI:IPI00991516 RefSeq:NP_001189944.1 RefSeq:NP_188762.3 UniGene:At.38092 ProteinModelPortal:Q8LGU1 SMR:Q8LGU1 PRIDE:Q8LGU1 EnsemblPlants:AT3G21250.2 GeneID:821679 KEGG:ath:AT3G21250 TAIR:At3g21250 InParanoid:Q8LGU1 Genevestigator:Q8LGU1 GermOnline:AT3G21250 Uniprot:Q8LGU1
Leaf	Isotig00500	13	0	5.229	3.68E-05	TAIR|locus:2077750 - symbol:ABCC10 "ATP-binding cassette C10" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=IEA] [GO:0055085 "transmembrane transport" evidence=IEA] [GO:0042626 "ATPase activity, coupled to transmembrane movement of substances" evidence=ISS] [GO:0005774 "vacuolar membrane" evidence=IDA] InterPro:IPR001140 InterPro:IPR003439 InterPro:IPR003593 InterPro:IPR011527 InterPro:IPR017871 Pfam:PF00005 Pfam:PF00664 PROSITE:PS00211 PROSITE:PS50893 SMART:SM00382 GO:GO:0016021 GO:GO:0005524 GO:GO:0005774 EMBL:CP002686 GenomeReviews:BA000014_GR eggNOG:COG1132 HOGENOM:HBG758042 InterPro:IPR017940 SUPFAM:SSF90123 PROSITE:PS50929 EMBL:AL163527 IPI:IPI00539087 PIR:T47796 RefSeq:NP_191473.2 UniGene:At.34659 ProteinModelPortal:Q9LYS2 PRIDE:Q9LYS2 GeneID:825083 KEGG:ath:AT3G59140 TAIR:At3g59140 InParanoid:Q9LYS2 PhylomeDB:Q9LYS2 Genevestigator:Q9LYS2 GermOnline:AT3G59140 GO:GO:0008559 Uniprot:Q9LYS2
Leaf	Isotig00501	96	41	1.756	6.14E-12	TAIR|locus:2094138 - symbol:PREP1 "AT3G19170" species:3702 "Arabidopsis thaliana" [GO:0004222 "metalloendopeptidase activity" evidence=ISS;IDA] [GO:0006508 "proteolysis" evidence=ISS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0016485 "protein processing" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0048046 "apoplast" evidence=IDA] InterPro:IPR007863 InterPro:IPR011237 InterPro:IPR011249 InterPro:IPR011765 InterPro:IPR013578 Pfam:PF00675 Pfam:PF05193 Pfam:PF08367 PROSITE:PS00143 GO:GO:0048046 GO:GO:0009570 GO:GO:0046686 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005759 GO:GO:0008270 GO:GO:0006508 GO:GO:0009941 EMBL:AP000419 GO:GO:0004222 GO:GO:0016485 Gene3D:G3DSA:3.30.830.10 SUPFAM:SSF63411 eggNOG:COG1026 KO:K06972 HOGENOM:HBG413876 EMBL:AY090240 EMBL:AY091051 EMBL:BT006362 EMBL:BT002372 IPI:IPI00547030 RefSeq:NP_188548.2 UniGene:At.27915 PDB:2FGE PDBsum:2FGE ProteinModelPortal:Q9LJL3 SMR:Q9LJL3 MINT:MINT-7231907 STRING:Q9LJL3 MEROPS:M16.012 PRIDE:Q9LJL3 ProMEX:Q9LJL3 EnsemblPlants:AT3G19170.1 GeneID:821451 KEGG:ath:AT3G19170 GeneFarm:2137 TAIR:At3g19170 InParanoid:Q9LJL3 OMA:IAFKTIP PhylomeDB:Q9LJL3 ProtClustDB:CLSN2690450 ArrayExpress:Q8RUN6 Genevestigator:Q9LJL3 GermOnline:AT3G19170 Uniprot:Q9LJL3
Leaf	Isotig00502	97	41	1.771	3.58E-12	TAIR|locus:2094138 - symbol:PREP1 "AT3G19170" species:3702 "Arabidopsis thaliana" [GO:0004222 "metalloendopeptidase activity" evidence=ISS;IDA] [GO:0006508 "proteolysis" evidence=ISS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0016485 "protein processing" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0048046 "apoplast" evidence=IDA] InterPro:IPR007863 InterPro:IPR011237 InterPro:IPR011249 InterPro:IPR011765 InterPro:IPR013578 Pfam:PF00675 Pfam:PF05193 Pfam:PF08367 PROSITE:PS00143 GO:GO:0048046 GO:GO:0009570 GO:GO:0046686 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005759 GO:GO:0008270

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0006508 GO:GO:0009941 EMBL:AP000419 GO:GO:0004222 GO:GO:0016485 Gene3D:G3DSA:3.30.830.10 SUPFAM:SSF63411 eggNOG:COG1026 KO:K06972 HOGENOM:HBG413876 EMBL:AY090240 EMBL:AY091051 EMBL:BT006362 EMBL:BT002372 IPI:IPI00547030 RefSeq:NP_188548.2 UniGene:At.27915 PDB:2FGE PDBsum:2FGE ProteinModelPortal:Q9LJL3 SMR:Q9LJL3 MINT:MINT-7231907 STRING:Q9LJL3 MEROPS:M16.012 PRIDE:Q9LJL3 ProMEX:Q9LJL3 EnsemblPlants:AT3G19170.1 GeneID:821451 KEGG:ath:AT3G19170 GeneFarm:2137 TAIR:At3g19170 InParanoid:Q9LJL3 OMA:IAFKTIP PhylomeDB:Q9LJL3 ProtClustDB:CLSN2690450 ArrayExpress:Q8RUN6 Genevestigator:Q9LJL3 GermOnline:AT3G19170 Uniprot:Q9LJL3
Leaf	Isotig00503	70	37	1.449	3.24E-07	TAIR|locus:2094138 - symbol:PREP1 "AT3G19170" species:3702 "Arabidopsis thaliana" [GO:0004222 "metalloendopeptidase activity" evidence=ISS;IDA] [GO:0006508 "proteolysis" evidence=ISS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0016485 "protein processing" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0048046 "apoplast" evidence=IDA] InterPro:IPR007863 InterPro:IPR011237 InterPro:IPR011249 InterPro:IPR011765 InterPro:IPR013578 Pfam:PF00675 Pfam:PF05193 Pfam:PF08367 PROSITE:PS00143 GO:GO:0048046 GO:GO:0009570 GO:GO:0046686 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005759 GO:GO:0008270 GO:GO:0006508 GO:GO:0009941 EMBL:AP000419 GO:GO:0004222 GO:GO:0016485 Gene3D:G3DSA:3.30.830.10 SUPFAM:SSF63411 eggNOG:COG1026 KO:K06972 HOGENOM:HBG413876 EMBL:AY090240 EMBL:AY091051 EMBL:BT006362 EMBL:BT002372 IPI:IPI00547030 RefSeq:NP_188548.2 UniGene:At.27915 PDB:2FGE PDBsum:2FGE ProteinModelPortal:Q9LJL3 SMR:Q9LJL3 MINT:MINT-7231907 STRING:Q9LJL3 MEROPS:M16.012 PRIDE:Q9LJL3 ProMEX:Q9LJL3 EnsemblPlants:AT3G19170.1 GeneID:821451 KEGG:ath:AT3G19170 GeneFarm:2137 TAIR:At3g19170 InParanoid:Q9LJL3 OMA:IAFKTIP PhylomeDB:Q9LJL3 ProtClustDB:CLSN2690450 ArrayExpress:Q8RUN6 Genevestigator:Q9LJL3 GermOnline:AT3G19170 Uniprot:Q9LJL3
Leaf	Isotig00504	96	41	1.756	6.14E-12	TAIR|locus:2094138 - symbol:PREP1 "AT3G19170" species:3702 "Arabidopsis thaliana" [GO:0004222 "metalloendopeptidase activity" evidence=ISS;IDA] [GO:0006508 "proteolysis" evidence=ISS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0016485 "protein processing" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0048046 "apoplast" evidence=IDA] InterPro:IPR007863 InterPro:IPR011237 InterPro:IPR011249 InterPro:IPR011765 InterPro:IPR013578 Pfam:PF00675 Pfam:PF05193 Pfam:PF08367 PROSITE:PS00143 GO:GO:0048046 GO:GO:0009570 GO:GO:0046686 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005759 GO:GO:0008270 GO:GO:0006508 GO:GO:0009941 EMBL:AP000419 GO:GO:0004222 GO:GO:0016485 Gene3D:G3DSA:3.30.830.10 SUPFAM:SSF63411 eggNOG:COG1026 KO:K06972 HOGENOM:HBG413876 EMBL:AY090240 EMBL:AY091051 EMBL:BT006362 EMBL:BT002372 IPI:IPI00547030 RefSeq:NP_188548.2 UniGene:At.27915 PDB:2FGE PDBsum:2FGE ProteinModelPortal:Q9LJL3 SMR:Q9LJL3 MINT:MINT-7231907 STRING:Q9LJL3 MEROPS:M16.012 PRIDE:Q9LJL3 ProMEX:Q9LJL3 EnsemblPlants:AT3G19170.1 GeneID:821451 KEGG:ath:AT3G19170 GeneFarm:2137 TAIR:At3g19170 InParanoid:Q9LJL3 OMA:IAFKTIP PhylomeDB:Q9LJL3 ProtClustDB:CLSN2690450 ArrayExpress:Q8RUN6 Genevestigator:Q9LJL3 GermOnline:AT3G19170 Uniprot:Q9LJL3
Leaf	Isotig00505	97	41	1.771	3.58E-12	TAIR|locus:2094138 - symbol:PREP1 "AT3G19170" species:3702 "Arabidopsis thaliana" [GO:0004222 "metalloendopeptidase activity" evidence=ISS;IDA] [GO:0006508 "proteolysis" evidence=ISS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0016485 "protein processing" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0048046 "apoplast" evidence=IDA] InterPro:IPR007863 InterPro:IPR011237 InterPro:IPR011249 InterPro:IPR011765 InterPro:IPR013578 Pfam:PF00675 Pfam:PF05193 Pfam:PF08367 PROSITE:PS00143 GO:GO:0048046 GO:GO:0009570 GO:GO:0046686 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005759 GO:GO:0008270 GO:GO:0006508 GO:GO:0009941 EMBL:AP000419 GO:GO:0004222 GO:GO:0016485 Gene3D:G3DSA:3.30.830.10 SUPFAM:SSF63411 eggNOG:COG1026 KO:K06972 HOGENOM:HBG413876 EMBL:AY090240 EMBL:AY091051 EMBL:BT006362 EMBL:BT002372 IPI:IPI00547030 RefSeq:NP_188548.2 UniGene:At.27915 PDB:2FGE PDBsum:2FGE ProteinModelPortal:Q9LJL3 SMR:Q9LJL3 MINT:MINT-7231907

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						STRING:Q9LJL3 MEROPS:M16.012 PRIDE:Q9LJL3 ProMEX:Q9LJL3 EnsemblPlants:AT3G19170.1 GeneID:821451 KEGG:ath:AT3G19170 GeneFarm:2137 TAIR:At3g19170 InParanoid:Q9LJL3 OMA:IAFKTIP PhylomeDB:Q9LJL3 ProtClustDB:CLSN2690450 ArrayExpress:Q8RUN6 Genevestigator:Q9LJL3 GermOnline:AT3G19170 Uniprot:Q9LJL3
Leaf	Isotig00506	70	37	1.449	3.24E-07	TAIR|locus:2094138 - symbol:PREP1 "AT3G19170" species:3702 "Arabidopsis thaliana" [GO:0004222 "metalloendopeptidase activity" evidence=ISS;IDA] [GO:0006508 "proteolysis" evidence=ISS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0016485 "protein processing" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0048046 "apoplast" evidence=IDA] InterPro:IPR007863 InterPro:IPR011237 InterPro:IPR011249 InterPro:IPR011765 InterPro:IPR013578 Pfam:PF00675 Pfam:PF05193 Pfam:PF08367 PROSITE:PS00143 GO:GO:0048046 GO:GO:0009570 GO:GO:0046686 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005759 GO:GO:0008270 GO:GO:0006508 GO:GO:0009941 EMBL:AP000419 GO:GO:0004222 GO:GO:0016485 Gene3D:G3DSA:3.30.830.10 SUPFAM:SSF63411 eggNOG:COG1026 KO:K06972 HOGENOM:HBG413876 EMBL:AY090240 EMBL:AY091051 EMBL:BT006362 EMBL:BT002372 IPI:IPI00547030 RefSeq:NP_188548.2 UniGene:At.27915 PDB:2FGE PDBsum:2FGE ProteinModelPortal:Q9LJL3 SMR:Q9LJL3 MINT:MINT-7231907 STRING:Q9LJL3 MEROPS:M16.012 PRIDE:Q9LJL3 ProMEX:Q9LJL3 EnsemblPlants:AT3G19170.1 GeneID:821451 KEGG:ath:AT3G19170 GeneFarm:2137 TAIR:At3g19170 InParanoid:Q9LJL3 OMA:IAFKTIP PhylomeDB:Q9LJL3 ProtClustDB:CLSN2690450 ArrayExpress:Q8RUN6 Genevestigator:Q9LJL3 GermOnline:AT3G19170 Uniprot:Q9LJL3
Leaf	Isotig00507	27	8	2.284	1.51E-05	TAIR|locus:2149604 - symbol:AT5G52580 species:3702 "Arabidopsis thaliana" [GO:0005097 "Rab GTPase activator activity" evidence=IEA] [GO:0032313 "regulation of Rab GTPase activity" evidence=IEA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR000195 Pfam:PF00566 PROSITE:PS50086 SMART:SM00164 GO:GO:0005829 GenomeReviews:BA000015_GR eggNOG:COG5210 EMBL:AB025606 GO:GO:0005097 SUPFAM:SSF47923 HOGENOM:HBG715338 EMBL:DQ778955 EMBL:AK117830 IPI:IPI00526888 ProteinModelPortal:Q9LTF8 SMR:Q9LTF8 PRIDE:Q9LTF8 TAIR:At5g52580 InParanoid:Q9LTF8 OMA:CIEAGEN PhylomeDB:Q9LTF8 Genevestigator:Q9LTF8 Uniprot:Q9LTF8
Leaf	Isotig00508	27	8	2.284	1.51E-05	TAIR|locus:2149604 - symbol:AT5G52580 species:3702 "Arabidopsis thaliana" [GO:0005097 "Rab GTPase activator activity" evidence=IEA] [GO:0032313 "regulation of Rab GTPase activity" evidence=IEA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR000195 Pfam:PF00566 PROSITE:PS50086 SMART:SM00164 GO:GO:0005829 GenomeReviews:BA000015_GR eggNOG:COG5210 EMBL:AB025606 GO:GO:0005097 SUPFAM:SSF47923 HOGENOM:HBG715338 EMBL:DQ778955 EMBL:AK117830 IPI:IPI00526888 ProteinModelPortal:Q9LTF8 SMR:Q9LTF8 PRIDE:Q9LTF8 TAIR:At5g52580 InParanoid:Q9LTF8 OMA:CIEAGEN PhylomeDB:Q9LTF8 Genevestigator:Q9LTF8 Uniprot:Q9LTF8
Leaf	Isotig00509	26	8	2.229	2.86E-05	TAIR|locus:2149604 - symbol:AT5G52580 species:3702 "Arabidopsis thaliana" [GO:0005097 "Rab GTPase activator activity" evidence=IEA] [GO:0032313 "regulation of Rab GTPase activity" evidence=IEA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR000195 Pfam:PF00566 PROSITE:PS50086 SMART:SM00164 GO:GO:0005829 GenomeReviews:BA000015_GR eggNOG:COG5210 EMBL:AB025606 GO:GO:0005097 SUPFAM:SSF47923 HOGENOM:HBG715338 EMBL:DQ778955 EMBL:AK117830 IPI:IPI00526888 ProteinModelPortal:Q9LTF8 SMR:Q9LTF8 PRIDE:Q9LTF8 TAIR:At5g52580 InParanoid:Q9LTF8 OMA:CIEAGEN PhylomeDB:Q9LTF8 Genevestigator:Q9LTF8 Uniprot:Q9LTF8
Leaf	Isotig00510	27	9	2.114	3.70E-05	TAIR|locus:2149604 - symbol:AT5G52580 species:3702 "Arabidopsis thaliana" [GO:0005097 "Rab GTPase activator activity" evidence=IEA] [GO:0032313 "regulation of Rab GTPase activity" evidence=IEA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR000195 Pfam:PF00566 PROSITE:PS50086 SMART:SM00164 GO:GO:0005829 GenomeReviews:BA000015_GR eggNOG:COG5210 EMBL:AB025606 GO:GO:0005097 SUPFAM:SSF47923 HOGENOM:HBG715338 EMBL:DQ778955 EMBL:AK117830 IPI:IPI00526888 ProteinModelPortal:Q9LTF8 SMR:Q9LTF8 PRIDE:Q9LTF8 TAIR:At5g52580 InParanoid:Q9LTF8 OMA:CIEAGEN PhylomeDB:Q9LTF8 Genevestigator:Q9LTF8 Uniprot:Q9LTF8
Leaf	Isotig00511	27	9	2.114	3.70E-05	TAIR|locus:2149604 - symbol:AT5G52580 species:3702 "Arabidopsis thaliana" [GO:0005097 "Rab GTPase activator activity" evidence=IEA] [GO:0032313 "regulation of Rab GTPase activity" evidence=IEA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR000195 Pfam:PF00566 PROSITE:PS50086 SMART:SM00164 GO:GO:0005829 GenomeReviews:BA000015_GR eggNOG:COG5210 EMBL:AB025606 GO:GO:0005097

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						SUPFAM:SSF47923 HOGENOM:HBG715338 EMBL:DQ778955 EMBL:AK117830 IPI:IPI00526888 ProteinModelPortal:Q9LTF8 SMR:Q9LTF8 PRIDE:Q9LTF8 TAIR:At5g52580 InParanoid:Q9LTF8 OMA:CIEAGEN PhylomeDB:Q9LTF8 Genevestigator:Q9LTF8 Uniprot:Q9LTF8
Leaf	Isotig00512	26	9	2.059	6.86E-05	TAIR|locus:2149604 - symbol:AT5G52580 species:3702 "Arabidopsis thaliana" [GO:0005097 "Rab GTPase activator activity" evidence=IEA] [GO:0032313 "regulation of Rab GTPase activity" evidence=IEA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR000195 Pfam:PF00566 PROSITE:PS50086 SMART:SM00164 GO:GO:0005829 GenomeReviews:BA000015_GR eggNOG:COG5210 EMBL:AB025606 GO:GO:0005097 SUPFAM:SSF47923 HOGENOM:HBG715338 EMBL:DQ778955 EMBL:AK117830 IPI:IPI00526888 ProteinModelPortal:Q9LTF8 SMR:Q9LTF8 PRIDE:Q9LTF8 TAIR:At5g52580 InParanoid:Q9LTF8 OMA:CIEAGEN PhylomeDB:Q9LTF8 Genevestigator:Q9LTF8 Uniprot:Q9LTF8
Leaf	Isotig00517	32	99	-1.100	4.49E-05	TAIR|locus:2053654 - symbol:NIR1 "AT2G15620" species:3702 "Arabidopsis thaliana" [GO:0047889 "ferredoxin-nitrate reductase activity" evidence=ISS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0010167 "response to nitrate" evidence=IEP] [GO:0005829 "cytosol" evidence=RCA] [GO:0050421 "nitrite reductase (NO-forming) activity" evidence=ISS] InterPro:IPR005117 InterPro:IPR006066 InterPro:IPR006067 Pfam:PF01077 Pfam:PF03460 PRINTS:PR00397 PROSITE:PS00365 GO:GO:0005739 GO:GO:0048046 GO:GO:0009570 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0016020 GO:GO:0006810 GO:GO:0051539 GO:GO:0020037 GO:GO:0022900 GO:GO:0042128 GO:GO:0010167 EMBL:AC006248 eggNOG:COG0155 Gene3D:G3DSA:3.90.480.10 SUPFAM:SSF55124 EMBL:D14824 EMBL:AB006032 EMBL:AF360320 EMBL:AY045608 EMBL:AY093995 EMBL:AY142685 EMBL:BT000685 EMBL:BT000686 IPI:IPI00533476 PIR:C84531 RefSeq:NP_179164.1 UniGene:At.21870 ProteinModelPortal:Q39161 SMR:Q39161 IntAct:Q39161 STRING:Q39161 PRIDE:Q39161 EnsemblPlants:AT2G15620.1 GeneID:816055 KEGG:ath:AT2G15620 GeneFarm:4362 TAIR:At2g15620 HOGENOM:HBG578916 InParanoid:Q39161 KO:K00366 OMA:DKYFMLR PhylomeDB:Q39161 ProtClustDB:PLN02431 ArrayExpress:Q39161 Genevestigator:Q39161 GermOnline:AT2G15620 GO:GO:0048307 Uniprot:Q39161
Leaf	Isotig00518	32	99	-1.100	4.49E-05	TAIR|locus:2053654 - symbol:NIR1 "AT2G15620" species:3702 "Arabidopsis thaliana" [GO:0047889 "ferredoxin-nitrate reductase activity" evidence=ISS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0010167 "response to nitrate" evidence=IEP] [GO:0005829 "cytosol" evidence=RCA] [GO:0050421 "nitrite reductase (NO-forming) activity" evidence=ISS] InterPro:IPR005117 InterPro:IPR006066 InterPro:IPR006067 Pfam:PF01077 Pfam:PF03460 PRINTS:PR00397 PROSITE:PS00365 GO:GO:0005739 GO:GO:0048046 GO:GO:0009570 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0016020 GO:GO:0006810 GO:GO:0051539 GO:GO:0020037 GO:GO:0022900 GO:GO:0042128 GO:GO:0010167 EMBL:AC006248 eggNOG:COG0155 Gene3D:G3DSA:3.90.480.10 SUPFAM:SSF55124 EMBL:D14824 EMBL:AB006032 EMBL:AF360320 EMBL:AY045608 EMBL:AY093995 EMBL:AY142685 EMBL:BT000685 EMBL:BT000686 IPI:IPI00533476 PIR:C84531 RefSeq:NP_179164.1 UniGene:At.21870 ProteinModelPortal:Q39161 SMR:Q39161 IntAct:Q39161 STRING:Q39161 PRIDE:Q39161 EnsemblPlants:AT2G15620.1 GeneID:816055 KEGG:ath:AT2G15620 GeneFarm:4362 TAIR:At2g15620 HOGENOM:HBG578916 InParanoid:Q39161 KO:K00366 OMA:DKYFMLR PhylomeDB:Q39161 ProtClustDB:PLN02431 ArrayExpress:Q39161 Genevestigator:Q39161 GermOnline:AT2G15620 GO:GO:0048307 Uniprot:Q39161
Leaf	Isotig00546	36	95	-0.871	0.000993915	TAIR|locus:2102926 - symbol:AT3G30390 "AT3G30390" species:3702 "Arabidopsis thaliana" [GO:0006865 "amino acid transport" evidence=ISS] [GO:0015171 "amino acid transmembrane transporter activity" evidence=ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0005773 "vacuole" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] GO:GO:0016021 GO:GO:0005774 EMBL:CP002686 InterPro:IPR013057 Pfam:PF01490 HOGENOM:HBG601878 EMBL:AY052201 EMBL:AF428287 EMBL:AP001314 IPI:IPI00520585 RefSeq:NP_001030795.1 RefSeq:NP_566854.1 UniGene:At.21575 ProteinModelPortal:Q9LI61 STRING:Q9LI61 PRIDE:Q9LI61 EnsemblPlants:AT3G30390.1 EnsemblPlants:AT3G30390.2 GeneID:822740 KEGG:ath:AT3G30390 TAIR:At3g30390 InParanoid:Q9LI61 OMA:AFICHYN PhylomeDB:Q9LI61 ProtClustDB:CLSN2687270 Genevestigator:Q9LI61 Uniprot:Q9LI61
Leaf	Isotig00549	31	91	-1.025	0.000223335	No hit

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig00569	15	56	-1.372	0.000262802	TAIR|locus:2124044 - symbol:PORB "AT4G27440" species:3702 "Arabidopsis thaliana" [GO:0016491 "oxidoreductase activity" evidence=ISS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=NAS;IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0016630 "protochlorophyllide reductase activity" evidence=TAS] [GO:0016020 "membrane" evidence=IDA] [GO:0009723 "response to ethylene stimulus" evidence=IEP] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0015995 "chlorophyll biosynthetic process" evidence=TAS] InterPro:IPR002198 InterPro:IPR005979 InterPro:IPR016040 Pfam:PF00106 InterPro:IPR002347 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 GO:GO:0009723 EMBL:AL078467 EMBL:AL161571 eggNOG:COG1028 HOGENOM:HBG750976 PRINTS:PR00081 GO:GO:0015995 GO:GO:0009535 GO:GO:0015979 GO:GO:0009707 UniGene:At.23416 KO:K00218 ProtClustDB:PLN00015 BRENDA:1.3.1.33 GO:GO:0016630 PANTHER:PTHR24316:SF100 TIGRFAMs:TIGR01289 EMBL:U29785 EMBL:AY042883 EMBL:AY054206 EMBL:AY081465 IPI:IPI00549013 PIR:T08936 RefSeq:NP_001031731.1 RefSeq:NP_194474.1 UniGene:At.75221 ProteinModelPortal:P21218 SMR:P21218 IntAct:P21218 STRING:P21218 PRIDE:P21218 EnsemblPlants:AT4G27440.1 EnsemblPlants:AT4G27440.2 GeneID:828853 KEGG:ath:AT4G27440 TAIR:At4g27440 InParanoid:P21218 OMA:SETESGK PhylomeDB:P21218 ArrayExpress:P21218 Genevestigator:P21218 GermOnline:AT4G27440 Uniprot:P21218
Leaf	Isotig00570	14	54	-1.419	0.000236402	TAIR|locus:2124044 - symbol:PORB "AT4G27440" species:3702 "Arabidopsis thaliana" [GO:0016491 "oxidoreductase activity" evidence=ISS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=NAS;IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0016630 "protochlorophyllide reductase activity" evidence=TAS] [GO:0016020 "membrane" evidence=IDA] [GO:0009723 "response to ethylene stimulus" evidence=IEP] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0015995 "chlorophyll biosynthetic process" evidence=TAS] InterPro:IPR002198 InterPro:IPR005979 InterPro:IPR016040 Pfam:PF00106 InterPro:IPR002347 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 GO:GO:0009723 EMBL:AL078467 EMBL:AL161571 eggNOG:COG1028 HOGENOM:HBG750976 PRINTS:PR00081 GO:GO:0015995 GO:GO:0009535 GO:GO:0015979 GO:GO:0009707 UniGene:At.23416 KO:K00218 ProtClustDB:PLN00015 BRENDA:1.3.1.33 GO:GO:0016630 PANTHER:PTHR24316:SF100 TIGRFAMs:TIGR01289 EMBL:U29785 EMBL:AY042883 EMBL:AY054206 EMBL:AY081465 IPI:IPI00549013 PIR:T08936 RefSeq:NP_001031731.1 RefSeq:NP_194474.1 UniGene:At.75221 ProteinModelPortal:P21218 SMR:P21218 IntAct:P21218 STRING:P21218 PRIDE:P21218 EnsemblPlants:AT4G27440.1 EnsemblPlants:AT4G27440.2 GeneID:828853 KEGG:ath:AT4G27440 TAIR:At4g27440 InParanoid:P21218 OMA:SETESGK PhylomeDB:P21218 ArrayExpress:P21218 Genevestigator:P21218 GermOnline:AT4G27440 Uniprot:P21218
Leaf	Isotig00571	14	54	-1.419	0.000236402	TAIR|locus:2124044 - symbol:PORB "AT4G27440" species:3702 "Arabidopsis thaliana" [GO:0016491 "oxidoreductase activity" evidence=ISS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=NAS;IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0016630 "protochlorophyllide reductase activity" evidence=TAS] [GO:0016020 "membrane" evidence=IDA] [GO:0009723 "response to ethylene stimulus" evidence=IEP] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0015995 "chlorophyll biosynthetic process" evidence=TAS] InterPro:IPR002198 InterPro:IPR005979 InterPro:IPR016040 Pfam:PF00106 InterPro:IPR002347 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 GO:GO:0009723 EMBL:AL078467 EMBL:AL161571 eggNOG:COG1028 HOGENOM:HBG750976 PRINTS:PR00081 GO:GO:0015995 GO:GO:0009535 GO:GO:0015979 GO:GO:0009707 UniGene:At.23416 KO:K00218 ProtClustDB:PLN00015 BRENDA:1.3.1.33 GO:GO:0016630 PANTHER:PTHR24316:SF100 TIGRFAMs:TIGR01289 EMBL:U29785 EMBL:AY042883 EMBL:AY054206 EMBL:AY081465 IPI:IPI00549013 PIR:T08936 RefSeq:NP_001031731.1 RefSeq:NP_194474.1 UniGene:At.75221 ProteinModelPortal:P21218 SMR:P21218 IntAct:P21218 STRING:P21218 PRIDE:P21218 EnsemblPlants:AT4G27440.1 EnsemblPlants:AT4G27440.2 GeneID:828853 KEGG:ath:AT4G27440 TAIR:At4g27440 InParanoid:P21218 OMA:SETESGK PhylomeDB:P21218 ArrayExpress:P21218 Genevestigator:P21218 GermOnline:AT4G27440 Uniprot:P21218
Leaf	Isotig00572	15	56	-1.372	0.000262802	TAIR|locus:2153438 - symbol:PORA "AT5G54190" species:3702 "Arabidopsis thaliana" [GO:0016491 "oxidoreductase activity" evidence=ISS] [GO:0016630 "protochlorophyllide reductase activity" evidence=NAS;TAS] [GO:0009723 "response to ethylene stimulus" evidence=IEP] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0015995 "chlorophyll biosynthetic process" evidence=TAS]

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						[GO:0009507 "chloroplast" evidence=NAS] InterPro:IPR002198 InterPro:IPR005979 InterPro:IPR016040 Pfam:PF00106 InterPro:IPR002347 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 GO:GO:0009941 GO:GO:0009723 eggNOG:COG1028 HOGENOM:HBG750976 PRINTS:PR00081 GO:GO:0015995 GO:GO:0009534 GO:GO:0015979 EMBL:AB013387 EMBL:U29699 EMBL:BT003853 EMBL:BT005080 IPI:IPI00545356 RefSeq:NP_200230.1 UniGene:At.23877 ProteinModelPortal:Q42536 SMR:Q42536 IntAct:Q42536 STRING:Q42536 PRIDE:Q42536 EnsemblPlants:AT5G54190.1 GeneID:835507 KEGG:ath:AT5G54190 TAIR:At5g54190 InParanoid:Q42536 KO:K00218 OMA:SWGNRQK PhylomeDB:Q42536 ProtClustDB:PLN00015 BRENDA:1.3.1.33 ArrayExpress:Q42536 Genevestigator:Q42536 GO:GO:0016630 PANTHER:PTHR24316:SF100 TIGRFAMs:TIGR01289 Uniprot:Q42536
Leaf	Isotig00573	14	54	-1.419	0.000236402	TAIR|locus:2153438 - symbol:PORA "AT5G54190" species:3702 "Arabidopsis thaliana" [GO:0016491 "oxidoreductase activity" evidence=ISS] [GO:0016630 "protochlorophyllide reductase activity" evidence=NAS;TAS] [GO:0009723 "response to ethylene stimulus" evidence=IEP] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0015995 "chlorophyll biosynthetic process" evidence=TAS] [GO:0009507 "chloroplast" evidence=NAS] InterPro:IPR002198 InterPro:IPR005979 InterPro:IPR016040 Pfam:PF00106 InterPro:IPR002347 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 GO:GO:0009941 GO:GO:0009723 eggNOG:COG1028 HOGENOM:HBG750976 PRINTS:PR00081 GO:GO:0015995 GO:GO:0009534 GO:GO:0015979 EMBL:AB013387 EMBL:U29699 EMBL:BT003853 EMBL:BT005080 IPI:IPI00545356 RefSeq:NP_200230.1 UniGene:At.23877 ProteinModelPortal:Q42536 SMR:Q42536 IntAct:Q42536 STRING:Q42536 PRIDE:Q42536 EnsemblPlants:AT5G54190.1 GeneID:835507 KEGG:ath:AT5G54190 TAIR:At5g54190 InParanoid:Q42536 KO:K00218 OMA:SWGNRQK PhylomeDB:Q42536 ProtClustDB:PLN00015 BRENDA:1.3.1.33 ArrayExpress:Q42536 Genevestigator:Q42536 GO:GO:0016630 PANTHER:PTHR24316:SF100 TIGRFAMs:TIGR01289 Uniprot:Q42536
Leaf	Isotig00574	14	54	-1.419	0.000236402	TAIR|locus:2153438 - symbol:PORA "AT5G54190" species:3702 "Arabidopsis thaliana" [GO:0016491 "oxidoreductase activity" evidence=ISS] [GO:0016630 "protochlorophyllide reductase activity" evidence=NAS;TAS] [GO:0009723 "response to ethylene stimulus" evidence=IEP] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0015995 "chlorophyll biosynthetic process" evidence=TAS] [GO:0009507 "chloroplast" evidence=NAS] InterPro:IPR002198 InterPro:IPR005979 InterPro:IPR016040 Pfam:PF00106 InterPro:IPR002347 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 GO:GO:0009941 GO:GO:0009723 eggNOG:COG1028 HOGENOM:HBG750976 PRINTS:PR00081 GO:GO:0015995 GO:GO:0009534 GO:GO:0015979 EMBL:AB013387 EMBL:U29699 EMBL:BT003853 EMBL:BT005080 IPI:IPI00545356 RefSeq:NP_200230.1 UniGene:At.23877 ProteinModelPortal:Q42536 SMR:Q42536 IntAct:Q42536 STRING:Q42536 PRIDE:Q42536 EnsemblPlants:AT5G54190.1 GeneID:835507 KEGG:ath:AT5G54190 TAIR:At5g54190 InParanoid:Q42536 KO:K00218 OMA:SWGNRQK PhylomeDB:Q42536 ProtClustDB:PLN00015 BRENDA:1.3.1.33 ArrayExpress:Q42536 Genevestigator:Q42536 GO:GO:0016630 PANTHER:PTHR24316:SF100 TIGRFAMs:TIGR01289 Uniprot:Q42536
Leaf	Isotig00575	14	57	-1.497	8.44E-05	TAIR|locus:2153438 - symbol:PORA "AT5G54190" species:3702 "Arabidopsis thaliana" [GO:0016491 "oxidoreductase activity" evidence=ISS] [GO:0016630 "protochlorophyllide reductase activity" evidence=NAS;TAS] [GO:0009723 "response to ethylene stimulus" evidence=IEP] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0015995 "chlorophyll biosynthetic process" evidence=TAS] [GO:0009507 "chloroplast" evidence=NAS] InterPro:IPR002198 InterPro:IPR005979 InterPro:IPR016040 Pfam:PF00106 InterPro:IPR002347 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 GO:GO:0009941 GO:GO:0009723 eggNOG:COG1028 HOGENOM:HBG750976 PRINTS:PR00081 GO:GO:0015995 GO:GO:0009534 GO:GO:0015979 EMBL:AB013387 EMBL:U29699 EMBL:BT003853 EMBL:BT005080 IPI:IPI00545356 RefSeq:NP_200230.1 UniGene:At.23877 ProteinModelPortal:Q42536 SMR:Q42536 IntAct:Q42536 STRING:Q42536 PRIDE:Q42536 EnsemblPlants:AT5G54190.1 GeneID:835507 KEGG:ath:AT5G54190 TAIR:At5g54190 InParanoid:Q42536 KO:K00218 OMA:SWGNRQK PhylomeDB:Q42536 ProtClustDB:PLN00015 BRENDA:1.3.1.33 ArrayExpress:Q42536 Genevestigator:Q42536 GO:GO:0016630 PANTHER:PTHR24316:SF100 TIGRFAMs:TIGR01289 Uniprot:Q42536

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig00576	13	55	-1.552	7.29E-05	TAIR|locus:2153438 - symbol:PORA "AT5G54190" species:3702 "Arabidopsis thaliana" [GO:0016491 "oxidoreductase activity" evidence=ISS] [GO:0016630 "protochlorophyllide reductase activity" evidence=NAS;TAS] [GO:0009723 "response to ethylene stimulus" evidence=IEP] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0015995 "chlorophyll biosynthetic process" evidence=TAS] [GO:0009507 "chloroplast" evidence=NAS] InterPro:IPR002198 InterPro:IPR005979 InterPro:IPR016040 Pfam:PF00106 InterPro:IPR002347 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 GO:GO:0009941 GO:GO:0009723 eggNOG:COG1028 HOGENOM:HBG750976 PRINTS:PR00081 GO:GO:0015995 GO:GO:0009534 GO:GO:0015979 EMBL:AB013387 EMBL:U29699 EMBL:BT003853 EMBL:BT005080 IPI:IPI00545356 RefSeq:NP_200230.1 UniGene:At.23877 ProteinModelPortal:Q42536 SMR:Q42536 IntAct:Q42536 STRING:Q42536 PRIDE:Q42536 EnsemblPlants:AT5G54190.1 GeneID:835507 KEGG:ath:AT5G54190 TAIR:At5g54190 InParanoid:Q42536 KO:K00218 OMA:SWGNRQK PhylomeDB:Q42536 ProtClustDB:PLN00015 BRENDA:1.3.1.33 ArrayExpress:Q42536 Genevestigator:Q42536 GO:GO:0016630 PANTHER:PTHR24316:SF100 TIGRFAMs:TIGR01289 Uniprot:Q42536
Leaf	Isotig00577	13	55	-1.552	7.29E-05	TAIR|locus:2153438 - symbol:PORA "AT5G54190" species:3702 "Arabidopsis thaliana" [GO:0016491 "oxidoreductase activity" evidence=ISS] [GO:0016630 "protochlorophyllide reductase activity" evidence=NAS;TAS] [GO:0009723 "response to ethylene stimulus" evidence=IEP] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0015995 "chlorophyll biosynthetic process" evidence=TAS] [GO:0009507 "chloroplast" evidence=NAS] InterPro:IPR002198 InterPro:IPR005979 InterPro:IPR016040 Pfam:PF00106 InterPro:IPR002347 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 GO:GO:0009941 GO:GO:0009723 eggNOG:COG1028 HOGENOM:HBG750976 PRINTS:PR00081 GO:GO:0015995 GO:GO:0009534 GO:GO:0015979 EMBL:AB013387 EMBL:U29699 EMBL:BT003853 EMBL:BT005080 IPI:IPI00545356 RefSeq:NP_200230.1 UniGene:At.23877 ProteinModelPortal:Q42536 SMR:Q42536 IntAct:Q42536 STRING:Q42536 PRIDE:Q42536 EnsemblPlants:AT5G54190.1 GeneID:835507 KEGG:ath:AT5G54190 TAIR:At5g54190 InParanoid:Q42536 KO:K00218 OMA:SWGNRQK PhylomeDB:Q42536 ProtClustDB:PLN00015 BRENDA:1.3.1.33 ArrayExpress:Q42536 Genevestigator:Q42536 GO:GO:0016630 PANTHER:PTHR24316:SF100 TIGRFAMs:TIGR01289 Uniprot:Q42536
Leaf	Isotig00588	28	80	-0.986	0.00080368	TAIR|locus:2060364 - symbol:MIPS2 "AT2G22240" species:3702 "Arabidopsis thaliana" [GO:0004512 "inositol-3-phosphate synthase activity" evidence=IGI;ISS] [GO:0006021 "inositol biosynthetic process" evidence=ISS] [GO:0008654 "phospholipid biosynthetic process" evidence=ISS] [GO:0009733 "response to auxin stimulus" evidence=TAS] [GO:0016036 "cellular response to phosphate starvation" evidence=TAS] [GO:0009408 "response to heat" evidence=IEP] [GO:0009644 "response to high light intensity" evidence=IEP] [GO:0042542 "response to hydrogen peroxide" evidence=IEP] [GO:0010264 "myo-inositol hexakisphosphate biosynthetic process" evidence=IMP] [GO:0042742 "defense response to bacterium" evidence=IMP] [GO:0050832 "defense response to fungus" evidence=IMP] [GO:0051607 "defense response to virus" evidence=IMP] [GO:0005515 "protein binding" evidence=IPI] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0009793 "embryo development ending in seed dormancy" evidence=IGI] InterPro:IPR002587 InterPro:IPR016040 Pfam:PF07994 PIRSF:PIRSF015578 Pfam:PF01658 GO:GO:0005737 GO:GO:0042742 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0005515 GO:GO:0009733 GO:GO:0050832 GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 GO:GO:0008654 GO:GO:0009408 GO:GO:0051607 GO:GO:0009644 GO:GO:0042542 GO:GO:0016036 EMBL:AC007168 GO:GO:0006021 eggNOG:COG1260 HOGENOM:HBG316335 KO:K01858 ProtClustDB:PLN02438 GO:GO:0004512 GO:GO:0010264 InterPro:IPR013021 PANTHER:PTHR11510 OMA:TEVVHEN EMBL:U30250 EMBL:AY053415 EMBL:AY054202 EMBL:AY143904 IPI:IPI00536408 PIR:D84610 RefSeq:NP_179812.1 UniGene:At.14447 UniGene:At.48504 ProteinModelPortal:Q38862 SMR:Q38862 IntAct:Q38862 STRING:Q38862 PRIDE:Q38862 EnsemblPlants:AT2G22240.1 GeneID:816757 KEGG:ath:AT2G22240 TAIR:At2g22240 InParanoid:Q38862 PhylomeDB:Q38862 ArrayExpress:Q38862 Genevestigator:Q38862 GermOnline:AT2G22240 Uniprot:Q38862
Leaf	Isotig00592	28	80	-0.986	0.00080368	TAIR|locus:2060364 - symbol:MIPS2 "AT2G22240" species:3702 "Arabidopsis thaliana" [GO:0004512 "inositol-3-phosphate synthase activity" evidence=IGI;ISS] [GO:0006021 "inositol biosynthetic process" evidence=ISS] [GO:0008654 "phospholipid biosynthetic process" evidence=ISS] [GO:0009733 "response to auxin stimulus" evidence=TAS] [GO:0016036 "cellular response to phosphate starvation" evidence=TAS] [GO:0009408 "response to

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						heat" evidence=IEP] [GO:0009644 "response to high light intensity" evidence=IEP] [GO:0042542 "response to hydrogen peroxide" evidence=IEP] [GO:0010264 "myo-inositol hexakisphosphate biosynthetic process" evidence=IMP] [GO:0042742 "defense response to bacterium" evidence=IMP] [GO:0050832 "defense response to fungus" evidence=IMP] [GO:0051607 "defense response to virus" evidence=IMP] [GO:0005515 "protein binding" evidence=IPI] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0009793 "embryo development ending in seed dormancy" evidence=IGI] InterPro:IPR002587 InterPro:IPR016040 Pfam:PF07994 PIRSF:PIRSF015578 Pfam:PF01658 GO:GO:0005737 GO:GO:0042742 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0005515 GO:GO:0009733 GO:GO:0050832 GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 GO:GO:0008654 GO:GO:0009408 GO:GO:0051607 GO:GO:0009644 GO:GO:0042542 GO:GO:0016036 EMBL:AC007168 GO:GO:0006021 eggNOG:COG1260 HOGENOM:HBG316335 KO:K01858 ProtClustDB:PLN02438 GO:GO:0004512 GO:GO:0010264 InterPro:IPR013021 PANTHER:PTHR11510 OMA:TEVVHEN EMBL:U30250 EMBL:AY053415 EMBL:AY054202 EMBL:AY143904 IPI:IPI00536408 PIR:D84610 RefSeq:NP_179812.1 UniGene:At.14447 UniGene:At.48504 ProteinModelPortal:Q38862 SMR:Q38862 IntAct:Q38862 STRING:Q38862 PRIDE:Q38862 EnsemblPlants:AT2G22240.1 GeneID:816757 KEGG:ath:AT2G22240 TAIR:At2g22240 InParanoid:Q38862 PhylomeDB:Q38862 ArrayExpress:Q38862 Genevestigator:Q38862 GermOnline:AT2G22240 Uniprot:Q38862
Leaf	Isotig00610	27	11	1.824	0.000181563	TAIR|locus:2093691 - symbol:GR1 "glutathione-disulfide reductase" species:3702 "Arabidopsis thaliana" [GO:0004362 "glutathione-disulfide reductase activity" evidence=IEA;ISS] [GO:0006749 "glutathione metabolic process" evidence=IEA] [GO:0016491 "oxidoreductase activity" evidence=IEA] [GO:0045454 "cell redox homeostasis" evidence=IEA] [GO:0050660 "flavin adenine dinucleotide binding" evidence=IEA] [GO:0050661 "NADP binding" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0005777 "peroxisome" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] InterPro:IPR001327 InterPro:IPR004099 InterPro:IPR006324 InterPro:IPR012999 InterPro:IPR013027 InterPro:IPR016156 InterPro:IPR023753 Pfam:PF00070 Pfam:PF02852 Pfam:PF07992 PRINTS:PR00368 PROSITE:PS00076 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005777 GO:GO:0050660 GO:GO:0050661 GO:GO:0045454 Gene3D:G3DSA:3.30.390.30 SUPFAM:SSF55424 GO:GO:0006749 EMBL:AB028621 eggNOG:COG1249 HOGENOM:HBG515043 GO:GO:0004362 EMBL:U37697 EMBL:AF360228 EMBL:AY040029 EMBL:AY140042 EMBL:AY142628 EMBL:BT008870 IPI:IPI00526326 RefSeq:NP_001030756.2 RefSeq:NP_001118688.1 RefSeq:NP_189059.1 UniGene:At.24980 ProteinModelPortal:P48641 SMR:P48641 PRIDE:P48641 EnsemblPlants:AT3G24170.1 EnsemblPlants:AT3G24170.2 EnsemblPlants:AT3G24170.3 GeneID:822003 KEGG:ath:AT3G24170 TAIR:At3g24170 InParanoid:P48641 KO:K00383 OMA:RLTGANE PhylomeDB:P48641 ProtClustDB:PLN02507 ArrayExpress:P48641 Genevestigator:P48641 TIGRFAMs:TIGR01424 Uniprot:P48641
Leaf	Isotig00611	27	11	1.824	0.000181563	TAIR|locus:2093691 - symbol:GR1 "glutathione-disulfide reductase" species:3702 "Arabidopsis thaliana" [GO:0004362 "glutathione-disulfide reductase activity" evidence=IEA;ISS] [GO:0006749 "glutathione metabolic process" evidence=IEA] [GO:0016491 "oxidoreductase activity" evidence=IEA] [GO:0045454 "cell redox homeostasis" evidence=IEA] [GO:0050660 "flavin adenine dinucleotide binding" evidence=IEA] [GO:0050661 "NADP binding" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0005777 "peroxisome" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] InterPro:IPR001327 InterPro:IPR004099 InterPro:IPR006324 InterPro:IPR012999 InterPro:IPR013027 InterPro:IPR016156 InterPro:IPR023753 Pfam:PF00070 Pfam:PF02852 Pfam:PF07992 PRINTS:PR00368 PROSITE:PS00076 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005777 GO:GO:0050660 GO:GO:0050661 GO:GO:0045454 Gene3D:G3DSA:3.30.390.30 SUPFAM:SSF55424 GO:GO:0006749 EMBL:AB028621 eggNOG:COG1249 HOGENOM:HBG515043 GO:GO:0004362 EMBL:U37697 EMBL:AF360228 EMBL:AY040029 EMBL:AY140042 EMBL:AY142628 EMBL:BT008870 IPI:IPI00526326 RefSeq:NP_001030756.2 RefSeq:NP_001118688.1 RefSeq:NP_189059.1 UniGene:At.24980 ProteinModelPortal:P48641 SMR:P48641 PRIDE:P48641 EnsemblPlants:AT3G24170.1 EnsemblPlants:AT3G24170.2 EnsemblPlants:AT3G24170.3 GeneID:822003 KEGG:ath:AT3G24170 TAIR:At3g24170 InParanoid:P48641 KO:K00383 OMA:RLTGANE PhylomeDB:P48641 ProtClustDB:PLN02507 ArrayExpress:P48641 Genevestigator:P48641 TIGRFAMs:TIGR01424 Uniprot:P48641
Leaf	Isotig00612	29	14	1.580	0.000457445	TAIR|locus:2093691 - symbol:GR1 "glutathione-disulfide reductase" species:3702 "Arabidopsis thaliana" [GO:0004362 "glutathione-disulfide reductase activity" evidence=IEA;ISS] [GO:0006749 "glutathione metabolic process" evidence=IEA] [GO:0016491 "oxidoreductase activity" evidence=IEA] [GO:0045454 "cell redox homeostasis" evidence=IEA] [GO:0050660 "flavin adenine dinucleotide binding" evidence=IEA] [GO:0050661

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						"NADP binding" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0005777 "peroxisome" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] InterPro:IPR001327 InterPro:IPR004099 InterPro:IPR006324 InterPro:IPR012999 InterPro:IPR013027 InterPro:IPR016156 InterPro:IPR023753 Pfam:PF00070 Pfam:PF02852 Pfam:PF07992 PRINTS:PR00368 PROSITE:PS00076 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005777 GO:GO:0050660 GO:GO:0050661 GO:GO:0045454 Gene3D:G3DSA:3.30.390.30 SUPFAM:SSF55424 GO:GO:0006749 EMBL:AB028621 eggNOG:COG1249 HOGENOM:HBG515043 GO:GO:0004362 EMBL:U37697 EMBL:AF360228 EMBL:AY040029 EMBL:AY140042 EMBL:AY142628 EMBL:BT008870 IPI:IPI00526326 RefSeq:NP_001030756.2 RefSeq:NP_001118688.1 RefSeq:NP_189059.1 UniGene:At.24980 ProteinModelPortal:P48641 SMR:P48641 PRIDE:P48641 EnsemblPlants:AT3G24170.1 EnsemblPlants:AT3G24170.2 EnsemblPlants:AT3G24170.3 GeneID:822003 KEGG:ath:AT3G24170 TAIR:At3g24170 InParanoid:P48641 KO:K00383 OMA:RLTGANE PhylomeDB:P48641 ProtClustDB:PLN02507 ArrayExpress:P48641 Genevestigator:P48641 TIGRFAMs:TIGR01424 Uniprot:P48641
Leaf	Isotig00613	29	14	1.580	0.000457445	TAIR|locus:2093691 - symbol:GR1 "glutathione-disulfide reductase" species:3702 "Arabidopsis thaliana" [GO:0004362 "glutathione-disulfide reductase activity" evidence=IEA;ISS] [GO:0006749 "glutathione metabolic process" evidence=IEA] [GO:0016491 "oxidoreductase activity" evidence=IEA] [GO:0045454 "cell redox homeostasis" evidence=IEA] [GO:0050660 "flavin adenine dinucleotide binding" evidence=IEA] [GO:0050661 "NADP binding" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0005777 "peroxisome" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] InterPro:IPR001327 InterPro:IPR004099 InterPro:IPR006324 InterPro:IPR012999 InterPro:IPR013027 InterPro:IPR016156 InterPro:IPR023753 Pfam:PF00070 Pfam:PF02852 Pfam:PF07992 PRINTS:PR00368 PROSITE:PS00076 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005777 GO:GO:0050660 GO:GO:0050661 GO:GO:0045454 Gene3D:G3DSA:3.30.390.30 SUPFAM:SSF55424 GO:GO:0006749 EMBL:AB028621 eggNOG:COG1249 HOGENOM:HBG515043 GO:GO:0004362 EMBL:U37697 EMBL:AF360228 EMBL:AY040029 EMBL:AY140042 EMBL:AY142628 EMBL:BT008870 IPI:IPI00526326 RefSeq:NP_001030756.2 RefSeq:NP_001118688.1 RefSeq:NP_189059.1 UniGene:At.24980 ProteinModelPortal:P48641 SMR:P48641 PRIDE:P48641 EnsemblPlants:AT3G24170.1 EnsemblPlants:AT3G24170.2 EnsemblPlants:AT3G24170.3 GeneID:822003 KEGG:ath:AT3G24170 TAIR:At3g24170 InParanoid:P48641 KO:K00383 OMA:RLTGANE PhylomeDB:P48641 ProtClustDB:PLN02507 ArrayExpress:P48641 Genevestigator:P48641 TIGRFAMs:TIGR01424 Uniprot:P48641
Leaf	Isotig00614	29	13	1.686	0.000239693	TAIR|locus:2093691 - symbol:GR1 "glutathione-disulfide reductase" species:3702 "Arabidopsis thaliana" [GO:0004362 "glutathione-disulfide reductase activity" evidence=IEA;ISS] [GO:0006749 "glutathione metabolic process" evidence=IEA] [GO:0016491 "oxidoreductase activity" evidence=IEA] [GO:0045454 "cell redox homeostasis" evidence=IEA] [GO:0050660 "flavin adenine dinucleotide binding" evidence=IEA] [GO:0050661 "NADP binding" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0005777 "peroxisome" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] InterPro:IPR001327 InterPro:IPR004099 InterPro:IPR006324 InterPro:IPR012999 InterPro:IPR013027 InterPro:IPR016156 InterPro:IPR023753 Pfam:PF00070 Pfam:PF02852 Pfam:PF07992 PRINTS:PR00368 PROSITE:PS00076 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005777 GO:GO:0050660 GO:GO:0050661 GO:GO:0045454 Gene3D:G3DSA:3.30.390.30 SUPFAM:SSF55424 GO:GO:0006749 EMBL:AB028621 eggNOG:COG1249 HOGENOM:HBG515043 GO:GO:0004362 EMBL:U37697 EMBL:AF360228 EMBL:AY040029 EMBL:AY140042 EMBL:AY142628 EMBL:BT008870 IPI:IPI00526326 RefSeq:NP_001030756.2 RefSeq:NP_001118688.1 RefSeq:NP_189059.1 UniGene:At.24980 ProteinModelPortal:P48641 SMR:P48641 PRIDE:P48641 EnsemblPlants:AT3G24170.1 EnsemblPlants:AT3G24170.2 EnsemblPlants:AT3G24170.3 GeneID:822003 KEGG:ath:AT3G24170 TAIR:At3g24170 InParanoid:P48641 KO:K00383 OMA:RLTGANE PhylomeDB:P48641 ProtClustDB:PLN02507 ArrayExpress:P48641 Genevestigator:P48641 TIGRFAMs:TIGR01424 Uniprot:P48641
Leaf	Isotig00615	29	13	1.686	0.000239693	TAIR|locus:2093691 - symbol:GR1 "glutathione-disulfide reductase" species:3702 "Arabidopsis thaliana" [GO:0004362 "glutathione-disulfide reductase activity" evidence=IEA;ISS] [GO:0006749 "glutathione metabolic process" evidence=IEA] [GO:0016491 "oxidoreductase activity" evidence=IEA] [GO:0045454 "cell redox homeostasis" evidence=IEA] [GO:0050660 "flavin adenine dinucleotide binding" evidence=IEA] [GO:0050661 "NADP binding" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0005777 "peroxisome" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] InterPro:IPR001327 InterPro:IPR004099 InterPro:IPR006324 InterPro:IPR012999 InterPro:IPR013027 InterPro:IPR016156 InterPro:IPR023753 Pfam:PF00070 Pfam:PF02852 Pfam:PF07992 PRINTS:PR00368 PROSITE:PS00076 EMBL:CP002686

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GenomeReviews:BA000014_GR GO:GO:0005777 GO:GO:0050660 GO:GO:0050661 GO:GO:0045454 Gene3D:G3DSA:3.30.390.30 SUPFAM:SSF55424 GO:GO:0006749 EMBL:AB028621 eggNOG:COG1249 HOGENOM:HBG515043 GO:GO:0004362 EMBL:U37697 EMBL:AF360228 EMBL:AY040029 EMBL:AY140042 EMBL:AY142628 EMBL:BT008870 IPI:IPI00526326 RefSeq:NP_001030756.2 RefSeq:NP_001118688.1 RefSeq:NP_189059.1 UniGene:At.24980 ProteinModelPortal:P48641 SMR:P48641 PRIDE:P48641 EnsemblPlants:AT3G24170.1 EnsemblPlants:AT3G24170.2 EnsemblPlants:AT3G24170.3 GeneID:822003 KEGG:ath:AT3G24170 TAIR:At3g24170 InParanoid:P48641 KO:K00383 OMA:RLTGANE PhylomeDB:P48641 ProtClustDB:PLN02507 ArrayExpress:P48641 Genevestigator:P48641 TIGRFAMs:TIGR01424 Uniprot:P48641
Leaf	Isotig00626	103	92	0.692	0.000739581	TAIR|locus:2018848 - symbol:LOX3 "lipoxygenase 3" species:3702 "Arabidopsis thaliana" [GO:0005506 "iron ion binding" evidence=IEA] [GO:0016165 "lipoxygenase activity" evidence=IEA;IDA] [GO:0016702 "oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen" evidence=IEA] [GO:0046872 "metal ion binding" evidence=IEA] [GO:0009611 "response to wounding" evidence=IEP;TAS] [GO:0009644 "response to high light intensity" evidence=IEP] [GO:0009753 "response to jasmonic acid stimulus" evidence=IEP] [GO:0009620 "response to fungus" evidence=IEP] [GO:0009555 "pollen development" evidence=IGI] [GO:0009901 "anther dehiscence" evidence=IGI] [GO:0048653 "anther development" evidence=IGI] [GO:0080086 "stamen filament development" evidence=IGI] [GO:0009695 "jasmonic acid biosynthetic process" evidence=TAS] [GO:0006952 "defense response" evidence=TAS] [GO:0040007 "growth" evidence=TAS] InterPro:IPR000907 InterPro:IPR001024 InterPro:IPR001246 InterPro:IPR013819 InterPro:IPR020833 InterPro:IPR020834 Pfam:PF00305 Pfam:PF01477 PRINTS:PR00087 PRINTS:PR00468 PROSITE:PS00081 PROSITE:PS00711 PROSITE:PS50095 PROSITE:PS51393 SMART:SM00308 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009507 GO:GO:0009753 GO:GO:0009611 GO:GO:0005506 GO:GO:0009555 GO:GO:0009620 GO:GO:0009644 GO:GO:0009901 GO:GO:0031408 EMBL:AC022492 InterPro:IPR008976 Gene3D:G3DSA:2.60.60.20 SUPFAM:SSF49723 EMBL:AC007843 GO:GO:0080086 GO:GO:0016165 PANTHER:PTHR11771 SUPFAM:SSF48484 eggNOG:NOG69653 HOGENOM:HBG749429 KO:K00454 EMBL:AJ249794 EMBL:AY075625 EMBL:BT006348 IPI:IPI00544066 RefSeq:NP_564021.1 UniGene:At.20467 UniGene:At.64244 UniGene:At.67022 HSSP:P08170 ProteinModelPortal:Q9LNR3 SMR:Q9LNR3 IntAct:Q9LNR3 STRING:Q9LNR3 PRIDE:Q9LNR3 EnsemblPlants:AT1G17420.1 GeneID:838314 KEGG:ath:AT1G17420 TAIR:At1g17420 InParanoid:Q9LNR3 OMA:HVSSNDA PhylomeDB:Q9LNR3 ProtClustDB:PLN02264 Genevestigator:Q9LNR3 Uniprot:Q9LNR3
Leaf	Isotig00627	105	82	0.886	2.47E-05	TAIR|locus:2018848 - symbol:LOX3 "lipoxygenase 3" species:3702 "Arabidopsis thaliana" [GO:0005506 "iron ion binding" evidence=IEA] [GO:0016165 "lipoxygenase activity" evidence=IEA;IDA] [GO:0016702 "oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen" evidence=IEA] [GO:0046872 "metal ion binding" evidence=IEA] [GO:0009611 "response to wounding" evidence=IEP;TAS] [GO:0009644 "response to high light intensity" evidence=IEP] [GO:0009753 "response to jasmonic acid stimulus" evidence=IEP] [GO:0009620 "response to fungus" evidence=IEP] [GO:0009555 "pollen development" evidence=IGI] [GO:0009901 "anther dehiscence" evidence=IGI] [GO:0048653 "anther development" evidence=IGI] [GO:0080086 "stamen filament development" evidence=IGI] [GO:0009695 "jasmonic acid biosynthetic process" evidence=TAS] [GO:0006952 "defense response" evidence=TAS] [GO:0040007 "growth" evidence=TAS] InterPro:IPR000907 InterPro:IPR001024 InterPro:IPR001246 InterPro:IPR013819 InterPro:IPR020833 InterPro:IPR020834 Pfam:PF00305 Pfam:PF01477 PRINTS:PR00087 PRINTS:PR00468 PROSITE:PS00081 PROSITE:PS00711 PROSITE:PS50095 PROSITE:PS51393 SMART:SM00308 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009507 GO:GO:0009753 GO:GO:0009611 GO:GO:0005506 GO:GO:0009555 GO:GO:0009620 GO:GO:0009644 GO:GO:0009901 GO:GO:0031408 EMBL:AC022492 InterPro:IPR008976 Gene3D:G3DSA:2.60.60.20 SUPFAM:SSF49723 EMBL:AC007843 GO:GO:0080086 GO:GO:0016165 PANTHER:PTHR11771 SUPFAM:SSF48484 eggNOG:NOG69653 HOGENOM:HBG749429 KO:K00454 EMBL:AJ249794 EMBL:AY075625 EMBL:BT006348 IPI:IPI00544066 RefSeq:NP_564021.1 UniGene:At.20467 UniGene:At.64244 UniGene:At.67022 HSSP:P08170 ProteinModelPortal:Q9LNR3 SMR:Q9LNR3 IntAct:Q9LNR3 STRING:Q9LNR3 PRIDE:Q9LNR3 EnsemblPlants:AT1G17420.1 GeneID:838314 KEGG:ath:AT1G17420 TAIR:At1g17420 InParanoid:Q9LNR3 OMA:HVSSNDA PhylomeDB:Q9LNR3 ProtClustDB:PLN02264 Genevestigator:Q9LNR3 Uniprot:Q9LNR3
Leaf	Isotig00628	106	77	0.990	3.29E-06	TAIR|locus:2018848 - symbol:LOX3 "lipoxygenase 3" species:3702 "Arabidopsis thaliana" [GO:0005506 "iron ion binding" evidence=IEA] [GO:0016165 "lipoxygenase activity" evidence=IEA;IDA] [GO:0016702 "oxidoreductase

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen" evidence=IEA] [GO:0046872 "metal ion binding" evidence=IEA] [GO:0009611 "response to wounding" evidence=IEP;TAS] [GO:0009644 "response to high light intensity" evidence=IEP] [GO:0009753 "response to jasmonic acid stimulus" evidence=IEP] [GO:0009620 "response to fungus" evidence=IEP] [GO:0009555 "pollen development" evidence=IGI] [GO:0009901 "anther dehiscence" evidence=IGI] [GO:0048653 "anther development" evidence=IGI] [GO:0080086 "stamen filament development" evidence=IGI] [GO:0009695 "jasmonic acid biosynthetic process" evidence=TAS] [GO:0006952 "defense response" evidence=TAS] [GO:0040007 "growth" evidence=TAS] InterPro:IPR000907 InterPro:IPR001024 InterPro:IPR001246 InterPro:IPR013819 InterPro:IPR020833 InterPro:IPR020834 Pfam:PF00305 Pfam:PF01477 PRINTS:PR00087 PRINTS:PR00468 PROSITE:PS00081 PROSITE:PS00711 PROSITE:PS50095 PROSITE:PS51393 SMART:SM00308 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009507 GO:GO:0009753 GO:GO:0009611 GO:GO:0005506 GO:GO:0009555 GO:GO:0009620 GO:GO:0009644 GO:GO:0009901 GO:GO:0031408 EMBL:AC022492 InterPro:IPR008976 Gene3D:G3DSA:2.60.60.20 SUPFAM:SSF49723 EMBL:AC007843 GO:GO:0080086 GO:GO:0016165 PANTHER:PTHR11771 SUPFAM:SSF48484 eggNOG:NOG69653 HOGENOM:HBG749429 KO:K00454 EMBL:AJ249794 EMBL:AY075625 EMBL:BT006348 IPI:IPI00544066 RefSeq:NP_564021.1 UniGene:At.20467 UniGene:At.64244 UniGene:At.67022 HSSP:P08170 ProteinModelPortal:Q9LNR3 SMR:Q9LNR3 IntAct:Q9LNR3 STRING:Q9LNR3 PRIDE:Q9LNR3 EnsemblPlants:AT1G17420.1 GeneID:838314 KEGG:ath:AT1G17420 TAIR:At1g17420 InParanoid:Q9LNR3 OMA:HVSSNDA PhylomeDB:Q9LNR3 ProtClustDB:PLN02264 Genevestigator:Q9LNR3 Uniprot:Q9LNR3
Leaf	Isotig00631	86	74	0.746	0.000992824	TAIR|locus:2087837 - symbol:LOX5 species:3702 "Arabidopsis thaliana" [GO:0005506 "iron ion binding" evidence=IEA] [GO:0016165 "lipoxygenase activity" evidence=IEA;ISS;IDA] [GO:0016702 "oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen" evidence=IEA] [GO:0046872 "metal ion binding" evidence=IEA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0010386 "lateral root primordium development" evidence=IMP] [GO:0048364 "root development" evidence=IMP] InterPro:IPR000907 InterPro:IPR001024 InterPro:IPR001246 InterPro:IPR013819 InterPro:IPR020833 InterPro:IPR020834 Pfam:PF00305 Pfam:PF01477 PRINTS:PR00087 PRINTS:PR00468 PROSITE:PS00081 PROSITE:PS00711 PROSITE:PS50095 PROSITE:PS51393 SMART:SM00308 GO:GO:0009507 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005506 GO:GO:0031408 EMBL:AB022215 GO:GO:0010386 InterPro:IPR008976 Gene3D:G3DSA:2.60.60.20 SUPFAM:SSF49723 GO:GO:0016165 PANTHER:PTHR11771 SUPFAM:SSF48484 eggNOG:NOG69653 KO:K15718 ProtClustDB:PLN02337 HSSP:P08170 EMBL:AJ302043 IPI:IPI00543707 RefSeq:NP_188879.2 UniGene:At.37889 ProteinModelPortal:Q9LUW0 SMR:Q9LUW0 STRING:Q9LUW0 PRIDE:Q9LUW0 EnsemblPlants:AT3G22400.1 GeneID:821808 KEGG:ath:AT3G22400 TAIR:At3g22400 InParanoid:Q9LUW0 OMA:FDWDESM PhylomeDB:Q9LUW0 Genevestigator:Q9LUW0 Uniprot:Q9LUW0
Leaf	Isotig00633	44	22	1.529	2.49E-05	TAIR|locus:2089850 - symbol:AT3G21620 "AT3G21620" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0005886 "plasma membrane" evidence=IDA] InterPro:IPR003864 Pfam:PF02714 GO:GO:0005886 EMBL:CP002686 EMBL:AB019232 ProtClustDB:CLSN2682090 IPI:IPI00525780 RefSeq:NP_188799.1 UniGene:At.53420 PRIDE:Q9LVE4 EnsemblPlants:AT3G21620.1 GeneID:821716 KEGG:ath:AT3G21620 TAIR:At3g21620 InParanoid:Q9LVE4 OMA:MAYVITF PhylomeDB:Q9LVE4 Genevestigator:Q9LVE4 Uniprot:Q9LVE4
Leaf	Isotig00634	44	23	1.465	4.43E-05	TAIR|locus:2089850 - symbol:AT3G21620 "AT3G21620" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0005886 "plasma membrane" evidence=IDA] InterPro:IPR003864 Pfam:PF02714 GO:GO:0005886 EMBL:CP002686 EMBL:AB019232 ProtClustDB:CLSN2682090 IPI:IPI00525780 RefSeq:NP_188799.1 UniGene:At.53420 PRIDE:Q9LVE4 EnsemblPlants:AT3G21620.1 GeneID:821716 KEGG:ath:AT3G21620 TAIR:At3g21620 InParanoid:Q9LVE4 OMA:MAYVITF PhylomeDB:Q9LVE4 Genevestigator:Q9LVE4 Uniprot:Q9LVE4
Leaf	Isotig00635	43	18	1.785	3.25E-06	TAIR|locus:2089850 - symbol:AT3G21620 "AT3G21620" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0005886 "plasma membrane" evidence=IDA] InterPro:IPR003864 Pfam:PF02714 GO:GO:0005886 EMBL:CP002686 EMBL:AB019232 ProtClustDB:CLSN2682090 IPI:IPI00525780 RefSeq:NP_188799.1 UniGene:At.53420 PRIDE:Q9LVE4 EnsemblPlants:AT3G21620.1 GeneID:821716 KEGG:ath:AT3G21620 TAIR:At3g21620 InParanoid:Q9LVE4 OMA:MAYVITF PhylomeDB:Q9LVE4 Genevestigator:Q9LVE4 Uniprot:Q9LVE4

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig00636	43	19	1.707	6.44E-06	TAIR|locus:2089850 - symbol:AT3G21620 "AT3G21620" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0005886 "plasma membrane" evidence=IDA] InterPro:IPR003864 Pfam:PF02714 GO:GO:0005886 EMBL:CP002686 EMBL:AB019232 ProtClustDB:CLSN2682090 IPI:IPI00525780 RefSeq:NP_188799.1 UniGene:At.53420 PRIDE:Q9LVE4 EnsemblPlants:AT3G21620.1 GeneID:821716 KEGG:ath:AT3G21620 TAIR:At3g21620 InParanoid:Q9LVE4 OMA:MAYVITF PhylomeDB:Q9LVE4 Genevestigator:Q9LVE4 Uniprot:Q9LVE4
Leaf	Isotig00637	36	18	1.529	0.00013739	TAIR|locus:2089850 - symbol:AT3G21620 "AT3G21620" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0005886 "plasma membrane" evidence=IDA] InterPro:IPR003864 Pfam:PF02714 GO:GO:0005886 EMBL:CP002686 EMBL:AB019232 ProtClustDB:CLSN2682090 IPI:IPI00525780 RefSeq:NP_188799.1 UniGene:At.53420 PRIDE:Q9LVE4 EnsemblPlants:AT3G21620.1 GeneID:821716 KEGG:ath:AT3G21620 TAIR:At3g21620 InParanoid:Q9LVE4 OMA:MAYVITF PhylomeDB:Q9LVE4 Genevestigator:Q9LVE4 Uniprot:Q9LVE4
Leaf	Isotig00638	35	14	1.851	1.68E-05	TAIR|locus:2089850 - symbol:AT3G21620 "AT3G21620" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0005886 "plasma membrane" evidence=IDA] InterPro:IPR003864 Pfam:PF02714 GO:GO:0005886 EMBL:CP002686 EMBL:AB019232 ProtClustDB:CLSN2682090 IPI:IPI00525780 RefSeq:NP_188799.1 UniGene:At.53420 PRIDE:Q9LVE4 EnsemblPlants:AT3G21620.1 GeneID:821716 KEGG:ath:AT3G21620 TAIR:At3g21620 InParanoid:Q9LVE4 OMA:MAYVITF PhylomeDB:Q9LVE4 Genevestigator:Q9LVE4 Uniprot:Q9LVE4
Leaf	Isotig00645	55	0	7.310	1.30E-16	TAIR|locus:2007943 - symbol:HAB2 "homology to ABI2" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004722 "protein serine/threonine phosphatase activity" evidence=IEA;ISS] [GO:0006470 "protein dephosphorylation" evidence=IEA] InterPro:IPR000222 InterPro:IPR001932 Pfam:PF00481 PROSITE:PS01032 SMART:SM00331 SMART:SM00332 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0006470 GO:GO:0009738 GO:GO:0004722 GO:GO:0046872 EMBL:AC022492 eggNOG:COG0631 Gene3D:G3DSA:3.60.40.10 SUPFAM:SSF81606 GO:GO:0008287 InterPro:IPR015655 PANTHER:PTHR13832 HSSP:P35813 HOGENOM:HBG747569 KO:K14497 EMBL:AK118656 IPI:IPI00532752 RefSeq:NP_173199.2 UniGene:At.41827 ProteinModelPortal:Q9LNP9 SMR:Q9LNP9 DIP:DIP-48989N PRIDE:Q9LNP9 EnsemblPlants:AT1G17550.1 GeneID:838330 KEGG:ath:AT1G17550 TAIR:At1g17550 InParanoid:Q8GWS8 OMA:RRILAWH PhylomeDB:Q9LNP9 ProtClustDB:CLSN2679602 Genevestigator:Q9LNP9 Uniprot:Q9LNP9
Leaf	Isotig00646	54	0	7.284	2.28E-16	TAIR|locus:2007943 - symbol:HAB2 "homology to ABI2" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004722 "protein serine/threonine phosphatase activity" evidence=IEA;ISS] [GO:0006470 "protein dephosphorylation" evidence=IEA] InterPro:IPR000222 InterPro:IPR001932 Pfam:PF00481 PROSITE:PS01032 SMART:SM00331 SMART:SM00332 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0006470 GO:GO:0009738 GO:GO:0004722 GO:GO:0046872 EMBL:AC022492 eggNOG:COG0631 Gene3D:G3DSA:3.60.40.10 SUPFAM:SSF81606 GO:GO:0008287 InterPro:IPR015655 PANTHER:PTHR13832 HSSP:P35813 HOGENOM:HBG747569 KO:K14497 EMBL:AK118656 IPI:IPI00532752 RefSeq:NP_173199.2 UniGene:At.41827 ProteinModelPortal:Q9LNP9 SMR:Q9LNP9 DIP:DIP-48989N PRIDE:Q9LNP9 EnsemblPlants:AT1G17550.1 GeneID:838330 KEGG:ath:AT1G17550 TAIR:At1g17550 InParanoid:Q8GWS8 OMA:RRILAWH PhylomeDB:Q9LNP9 ProtClustDB:CLSN2679602 Genevestigator:Q9LNP9 Uniprot:Q9LNP9
Leaf	Isotig00647	48	0	7.114	7.13E-15	TAIR|locus:2030230 - symbol:HAB1 "AT1G72770" species:3702 "Arabidopsis thaliana" [GO:0004722 "protein serine/threonine phosphatase activity" evidence=ISS;IDA] [GO:0006470 "protein dephosphorylation" evidence=IEA] [GO:0008287 "protein serine/threonine phosphatase complex" evidence=IEA] [GO:0005515 "protein binding" evidence=IPI] InterPro:IPR000222 InterPro:IPR001932 Pfam:PF00481 PROSITE:PS01032 SMART:SM00331 SMART:SM00332 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005634 GO:GO:0005737 GO:GO:0005515 GO:GO:0006470 GO:GO:0009738 GO:GO:0004722 GO:GO:0046872 EMBL:AC010926 eggNOG:COG0631 Gene3D:G3DSA:3.60.40.10 SUPFAM:SSF81606 GO:GO:0008287 InterPro:IPR015655 PANTHER:PTHR13832 HOGENOM:HBG747569 ProtClustDB:CLSN2679602 EMBL:AJ003119 EMBL:BT015409 EMBL:AK230171 EMBL:AK318665 IPI:IPI00538917 IPI:IPI00846864 PIR:F96752 RefSeq:NP_001077815.1 RefSeq:NP_001185385.1 RefSeq:NP_177421.1 UniGene:At.46635 UniGene:At.67356 PDB:3KB3 PDB:3NMT PDB:3QN1 PDB:3RT0 PDBsum:3KB3 PDBsum:3NMT PDBsum:3QN1 PDBsum:3RT0 ProteinModelPortal:Q9CAJ0 SMR:Q9CAJ0 DIP:DIP-48988N IntAct:Q9CAJ0 STRING:Q9CAJ0 PRIDE:Q9CAJ0 EnsemblPlants:AT1G72770.1 EnsemblPlants:AT1G72770.3 GeneID:843609 KEGG:ath:AT1G72770 TAIR:At1g72770 InParanoid:Q9CAJ0 OMA:YARIENA PhylomeDB:Q9CAJ0 Genevestigator:Q9CAJ0 Uniprot:Q9CAJ0

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig00648	47	0	7.084	1.27E-14	TAIR|locus:2030230 - symbol:HAB1 "AT1G72770" species:3702 "Arabidopsis thaliana" [GO:0004722 "protein serine/threonine phosphatase activity" evidence=ISS;IDA] [GO:0006470 "protein dephosphorylation" evidence=IEA] [GO:0008287 "protein serine/threonine phosphatase complex" evidence=IEA] [GO:0005515 "protein binding" evidence=IPI] InterPro:IPR000222 InterPro:IPR001932 Pfam:PF00481 PROSITE:PS01032 SMART:SM00331 SMART:SM00332 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005634 GO:GO:0005737 GO:GO:0005515 GO:GO:0006470 GO:GO:0009738 GO:GO:0004722 GO:GO:0046872 EMBL:AC010926 eggNOG:COG0631 Gene3D:G3DSA:3.60.40.10 SUPFAM:SSF81606 GO:GO:0008287 InterPro:IPR015655 PANTHER:PTHR13832 HOGENOM:HBG747569 ProtClustDB:CLSN2679602 EMBL:AJ003119 EMBL:BT015409 EMBL:AK230171 EMBL:AK318665 IPI:IPI00538917 IPI:IPI00846864 PIR:F96752 RefSeq:NP_001077815.1 RefSeq:NP_001185385.1 RefSeq:NP_177421.1 UniGene:At.46635 UniGene:At.67356 PDB:3KB3 PDB:3NMT PDB:3QN1 PDB:3RT0 PDBsum:3KB3 PDBsum:3NMT PDBsum:3QN1 PDBsum:3RT0 ProteinModelPortal:Q9CAJ0 SMR:Q9CAJ0 DIP:DIP-48988N IntAct:Q9CAJ0 STRING:Q9CAJ0 PRIDE:Q9CAJ0 EnsemblPlants:AT1G72770.1 EnsemblPlants:AT1G72770.3 GeneID:843609 KEGG:ath:AT1G72770 TAIR:At1g72770 InParanoid:Q9CAJ0 OMA:YARIENA PhylomeDB:Q9CAJ0 Genevestigator:Q9CAJ0 Uniprot:Q9CAJ0
Leaf	Isotig00649	36	0	6.699	9.13E-12	TAIR|locus:2007943 - symbol:HAB2 "homology to ABI2" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004722 "protein serine/threonine phosphatase activity" evidence=IEA;ISS] [GO:0006470 "protein dephosphorylation" evidence=IEA] InterPro:IPR000222 InterPro:IPR001932 Pfam:PF00481 PROSITE:PS01032 SMART:SM00331 SMART:SM00332 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0006470 GO:GO:0009738 GO:GO:0004722 GO:GO:0046872 EMBL:AC022492 eggNOG:COG0631 Gene3D:G3DSA:3.60.40.10 SUPFAM:SSF81606 GO:GO:0008287 InterPro:IPR015655 PANTHER:PTHR13832 HSSP:P35813 HOGENOM:HBG747569 KO:K14497 EMBL:AK118656 IPI:IPI00532752 RefSeq:NP_173199.2 UniGene:At.41827 ProteinModelPortal:Q9LNP9 SMR:Q9LNP9 DIP:DIP-48989N PRIDE:Q9LNP9 EnsemblPlants:AT1G17550.1 GeneID:838330 KEGG:ath:AT1G17550 TAIR:At1g17550 InParanoid:Q8GWS8 OMA:RRILAWH PhylomeDB:Q9LNP9 ProtClustDB:CLSN2679602 Genevestigator:Q9LNP9 Uniprot:Q9LNP9
Leaf	Isotig00650	35	0	6.658	1.69E-11	TAIR|locus:2007943 - symbol:HAB2 "homology to ABI2" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004722 "protein serine/threonine phosphatase activity" evidence=IEA;ISS] [GO:0006470 "protein dephosphorylation" evidence=IEA] InterPro:IPR000222 InterPro:IPR001932 Pfam:PF00481 PROSITE:PS01032 SMART:SM00331 SMART:SM00332 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0006470 GO:GO:0009738 GO:GO:0004722 GO:GO:0046872 EMBL:AC022492 eggNOG:COG0631 Gene3D:G3DSA:3.60.40.10 SUPFAM:SSF81606 GO:GO:0008287 InterPro:IPR015655 PANTHER:PTHR13832 HSSP:P35813 HOGENOM:HBG747569 KO:K14497 EMBL:AK118656 IPI:IPI00532752 RefSeq:NP_173199.2 UniGene:At.41827 ProteinModelPortal:Q9LNP9 SMR:Q9LNP9 DIP:DIP-48989N PRIDE:Q9LNP9 EnsemblPlants:AT1G17550.1 GeneID:838330 KEGG:ath:AT1G17550 TAIR:At1g17550 InParanoid:Q8GWS8 OMA:RRILAWH PhylomeDB:Q9LNP9 ProtClustDB:CLSN2679602 Genevestigator:Q9LNP9 Uniprot:Q9LNP9
Leaf	Isotig00657	13	50	-1.414	0.000415544	TAIR|locus:2132313 - symbol:MLO1 "AT4G02600" species:3702 "Arabidopsis thaliana" [GO:0005516 "calmodulin binding" evidence=ISS] [GO:0005886 "plasma membrane" evidence=ISS;IDA] [GO:0006952 "defense response" evidence=ISS] [GO:0008219 "cell death" evidence=IEA;ISS] InterPro:IPR004326 Pfam:PF03094 GO:GO:0016021 GO:GO:0005886 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0006952 GO:GO:0008219 GO:GO:0005516 GO:GO:0009607 EMBL:AC002330 EMBL:AL161494 HOGENOM:HBG319688 KO:K08472 EMBL:Z95352 EMBL:AY072135 EMBL:AY113992 IPI:IPI00519393 PIR:T01089 RefSeq:NP_001031578.1 RefSeq:NP_192169.1 UniGene:At.20439 PRIDE:O49621 EnsemblPlants:AT4G02600.1 EnsemblPlants:AT4G02600.2 GeneID:828229 KEGG:ath:AT4G02600 TAIR:At4g02600 eggNOG:NOG266513 InParanoid:O49621 OMA:GWAQKVK PhylomeDB:O49621 ProtClustDB:CLSN2685759 ArrayExpress:O49621 Genevestigator:O49621 GermOnline:AT4G02600 Uniprot:O49621
Leaf	Isotig00658	11	50	-1.655	7.42E-05	TAIR|locus:2132313 - symbol:MLO1 "AT4G02600" species:3702 "Arabidopsis thaliana" [GO:0005516 "calmodulin binding" evidence=ISS] [GO:0005886 "plasma membrane" evidence=ISS;IDA] [GO:0006952 "defense response" evidence=ISS] [GO:0008219 "cell death" evidence=IEA;ISS] InterPro:IPR004326 Pfam:PF03094 GO:GO:0016021 GO:GO:0005886 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0006952 GO:GO:0008219 GO:GO:0005516 GO:GO:0009607 EMBL:AC002330 EMBL:AL161494 HOGENOM:HBG319688 KO:K08472 EMBL:Z95352 EMBL:AY072135 EMBL:AY113992 IPI:IPI00519393 PIR:T01089 RefSeq:NP_001031578.1 RefSeq:NP_192169.1 UniGene:At.20439 PRIDE:O49621 EnsemblPlants:AT4G02600.1 EnsemblPlants:AT4G02600.2 GeneID:828229 KEGG:ath:AT4G02600 TAIR:At4g02600 eggNOG:NOG266513

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						InParanoid:O49621 OMA:GWAQKVK PhylomeDB:O49621 ProtClustDB:CLSN2685759 ArrayExpress:O49621 Genevestigator:O49621 GermOnline:AT4G02600 Uniprot:O49621
Leaf	Isotig00659	13	50	-1.414	0.000415544	TAIR|locus:2132313 - symbol:MLO1 "AT4G02600" species:3702 "Arabidopsis thaliana" [GO:0005516 "calmodulin binding" evidence=ISS] [GO:0005886 "plasma membrane" evidence=ISS;IDA] [GO:0006952 "defense response" evidence=ISS] [GO:0008219 "cell death" evidence=IEA;ISS] InterPro:IPR004326 Pfam:PF03094 GO:GO:0016021 GO:GO:0005886 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0006952 GO:GO:0008219 GO:GO:0005516 GO:GO:0009607 EMBL:AC002330 EMBL:AL161494 HOGENOM:HBG319688 KO:K08472 EMBL:Z95352 EMBL:AY072135 EMBL:AY113992 IPI:IPI00519393 PIR:T01089 RefSeq:NP_001031578.1 RefSeq:NP_192169.1 UniGene:At.20439 PRIDE:O49621 EnsemblPlants:AT4G02600.1 EnsemblPlants:AT4G02600.2 GeneID:828229 KEGG:ath:AT4G02600 TAIR:At4g02600 eggNOG:NOG266513 InParanoid:O49621 OMA:GWAQKVK PhylomeDB:O49621 ProtClustDB:CLSN2685759 ArrayExpress:O49621 Genevestigator:O49621 GermOnline:AT4G02600 Uniprot:O49621
Leaf	Isotig00660	11	50	-1.655	7.42E-05	TAIR|locus:2132313 - symbol:MLO1 "AT4G02600" species:3702 "Arabidopsis thaliana" [GO:0005516 "calmodulin binding" evidence=ISS] [GO:0005886 "plasma membrane" evidence=ISS;IDA] [GO:0006952 "defense response" evidence=ISS] [GO:0008219 "cell death" evidence=IEA;ISS] InterPro:IPR004326 Pfam:PF03094 GO:GO:0016021 GO:GO:0005886 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0006952 GO:GO:0008219 GO:GO:0005516 GO:GO:0009607 EMBL:AC002330 EMBL:AL161494 HOGENOM:HBG319688 KO:K08472 EMBL:Z95352 EMBL:AY072135 EMBL:AY113992 IPI:IPI00519393 PIR:T01089 RefSeq:NP_001031578.1 RefSeq:NP_192169.1 UniGene:At.20439 PRIDE:O49621 EnsemblPlants:AT4G02600.1 EnsemblPlants:AT4G02600.2 GeneID:828229 KEGG:ath:AT4G02600 TAIR:At4g02600 eggNOG:NOG266513 InParanoid:O49621 OMA:GWAQKVK PhylomeDB:O49621 ProtClustDB:CLSN2685759 ArrayExpress:O49621 Genevestigator:O49621 GermOnline:AT4G02600 Uniprot:O49621
Leaf	Isotig00661	12	47	-1.441	0.000520297	TAIR|locus:2132313 - symbol:MLO1 "AT4G02600" species:3702 "Arabidopsis thaliana" [GO:0005516 "calmodulin binding" evidence=ISS] [GO:0005886 "plasma membrane" evidence=ISS;IDA] [GO:0006952 "defense response" evidence=ISS] [GO:0008219 "cell death" evidence=IEA;ISS] InterPro:IPR004326 Pfam:PF03094 GO:GO:0016021 GO:GO:0005886 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0006952 GO:GO:0008219 GO:GO:0005516 GO:GO:0009607 EMBL:AC002330 EMBL:AL161494 HOGENOM:HBG319688 KO:K08472 EMBL:Z95352 EMBL:AY072135 EMBL:AY113992 IPI:IPI00519393 PIR:T01089 RefSeq:NP_001031578.1 RefSeq:NP_192169.1 UniGene:At.20439 PRIDE:O49621 EnsemblPlants:AT4G02600.1 EnsemblPlants:AT4G02600.2 GeneID:828229 KEGG:ath:AT4G02600 TAIR:At4g02600 eggNOG:NOG266513 InParanoid:O49621 OMA:GWAQKVK PhylomeDB:O49621 ProtClustDB:CLSN2685759 ArrayExpress:O49621 Genevestigator:O49621 GermOnline:AT4G02600 Uniprot:O49621
Leaf	Isotig00662	10	47	-1.704	8.83E-05	TAIR|locus:2132313 - symbol:MLO1 "AT4G02600" species:3702 "Arabidopsis thaliana" [GO:0005516 "calmodulin binding" evidence=ISS] [GO:0005886 "plasma membrane" evidence=ISS;IDA] [GO:0006952 "defense response" evidence=ISS] [GO:0008219 "cell death" evidence=IEA;ISS] InterPro:IPR004326 Pfam:PF03094 GO:GO:0016021 GO:GO:0005886 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0006952 GO:GO:0008219 GO:GO:0005516 GO:GO:0009607 EMBL:AC002330 EMBL:AL161494 HOGENOM:HBG319688 KO:K08472 EMBL:Z95352 EMBL:AY072135 EMBL:AY113992 IPI:IPI00519393 PIR:T01089 RefSeq:NP_001031578.1 RefSeq:NP_192169.1 UniGene:At.20439 PRIDE:O49621 EnsemblPlants:AT4G02600.1 EnsemblPlants:AT4G02600.2 GeneID:828229 KEGG:ath:AT4G02600 TAIR:At4g02600 eggNOG:NOG266513 InParanoid:O49621 OMA:GWAQKVK PhylomeDB:O49621 ProtClustDB:CLSN2685759 ArrayExpress:O49621 Genevestigator:O49621 GermOnline:AT4G02600 Uniprot:O49621
Leaf	Isotig00687	23	109	-1.716	1.97E-09	TAIR|locus:2033583 - symbol:PGM2 "AT1G70730" species:3702 "Arabidopsis thaliana" [GO:0004614 "phosphoglucomutase activity" evidence=ISS;IDA] [GO:0005975 "carbohydrate metabolic process" evidence=ISS;IDA] [GO:0005992 "trehalose biosynthetic process" evidence=IBA] [GO:0006874 "cellular calcium ion homeostasis" evidence=IBA] [GO:0009570 "chloroplast stroma" evidence=IBA] [GO:0009590 "detection of gravity" evidence=IBA] [GO:0010319 "stromule" evidence=IBA] [GO:0019252 "starch biosynthetic process" evidence=IBA] [GO:0019255 "glucose 1-phosphate metabolic process" evidence=IBA] [GO:0019388 "galactose catabolic process" evidence=IBA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0044445 "cytosolic part" evidence=IDA] [GO:0048229 "gametophyte development" evidence=IGI] InterPro:IPR005841 InterPro:IPR005843 InterPro:IPR005844 InterPro:IPR005845 InterPro:IPR005846 InterPro:IPR016055

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						InterPro:IPR016066 Pfam:PF00408 Pfam:PF02878 Pfam:PF02879 Pfam:PF02880 PRINTS:PR00509 PROSITE:PS00710 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005886 GO:GO:0005634 GO:GO:0046686 GO:GO:0000287 GO:GO:0006006 EMBL:AC011663 Gene3D:G3DSA:3.40.120.10 SUPFAM:SSF53738 GO:GO:0004614 GO:GO:0044445 KO:K01835 eggNOG:COG0033 OMA:SIFFSID HOGENOM:HBG286308 ProtClustDB:PLN02307 GO:GO:0048229 EMBL:AY090231 EMBL:BT002627 IPI:IPI00533044 PIR:G96731 RefSeq:NP_177230.1 UniGene:At.35274 ProteinModelPortal:Q9SGC1 SMR:Q9SGC1 STRING:Q9SGC1 PRIDE:Q9SGC1 ProMEX:Q9SGC1 EnsemblPlants:AT1G70730.1 GeneID:843410 KEGG:ath:AT1G70730 TAIR:At1g70730 InParanoid:Q9SGC1 PhylomeDB:Q9SGC1 ArrayExpress:Q9SGC1 Genevestigator:Q9SGC1 GermOnline:AT1G70730 Uniprot:Q9SGC1
Leaf	Isotig00688	23	99	-1.577	7.29E-08	TAIR|locus:2033583 - symbol:PGM2 "AT1G70730" species:3702 "Arabidopsis thaliana" [GO:0004614 "phosphoglucomutase activity" evidence=ISS;IDA] [GO:0005975 "carbohydrate metabolic process" evidence=ISS;IDA] [GO:0005992 "trehalose biosynthetic process" evidence=IBA] [GO:0006874 "cellular calcium ion homeostasis" evidence=IBA] [GO:0009570 "chloroplast stroma" evidence=IBA] [GO:0009590 "detection of gravity" evidence=IBA] [GO:0010319 "stromule" evidence=IBA] [GO:0019252 "starch biosynthetic process" evidence=IBA] [GO:0019255 "glucose 1-phosphate metabolic process" evidence=IBA] [GO:0019388 "galactose catabolic process" evidence=IBA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0044445 "cytosolic part" evidence=IDA] [GO:0048229 "gametophyte development" evidence=IGI] InterPro:IPR005841 InterPro:IPR005843 InterPro:IPR005844 InterPro:IPR005845 InterPro:IPR005846 InterPro:IPR016055 InterPro:IPR016066 Pfam:PF00408 Pfam:PF02878 Pfam:PF02879 Pfam:PF02880 PRINTS:PR00509 PROSITE:PS00710 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005886 GO:GO:0005634 GO:GO:0046686 GO:GO:0000287 GO:GO:0006006 EMBL:AC011663 Gene3D:G3DSA:3.40.120.10 SUPFAM:SSF53738 GO:GO:0004614 GO:GO:0044445 KO:K01835 eggNOG:COG0033 OMA:SIFFSID HOGENOM:HBG286308 ProtClustDB:PLN02307 GO:GO:0048229 EMBL:AY090231 EMBL:BT002627 IPI:IPI00533044 PIR:G96731 RefSeq:NP_177230.1 UniGene:At.35274 ProteinModelPortal:Q9SGC1 SMR:Q9SGC1 STRING:Q9SGC1 PRIDE:Q9SGC1 ProMEX:Q9SGC1 EnsemblPlants:AT1G70730.1 GeneID:843410 KEGG:ath:AT1G70730 TAIR:At1g70730 InParanoid:Q9SGC1 PhylomeDB:Q9SGC1 ArrayExpress:Q9SGC1 Genevestigator:Q9SGC1 GermOnline:AT1G70730 Uniprot:Q9SGC1
Leaf	Isotig00689	23	112	-1.755	6.43E-10	TAIR|locus:2033583 - symbol:PGM2 "AT1G70730" species:3702 "Arabidopsis thaliana" [GO:0004614 "phosphoglucomutase activity" evidence=ISS;IDA] [GO:0005975 "carbohydrate metabolic process" evidence=ISS;IDA] [GO:0005992 "trehalose biosynthetic process" evidence=IBA] [GO:0006874 "cellular calcium ion homeostasis" evidence=IBA] [GO:0009570 "chloroplast stroma" evidence=IBA] [GO:0009590 "detection of gravity" evidence=IBA] [GO:0010319 "stromule" evidence=IBA] [GO:0019252 "starch biosynthetic process" evidence=IBA] [GO:0019255 "glucose 1-phosphate metabolic process" evidence=IBA] [GO:0019388 "galactose catabolic process" evidence=IBA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0044445 "cytosolic part" evidence=IDA] [GO:0048229 "gametophyte development" evidence=IGI] InterPro:IPR005841 InterPro:IPR005843 InterPro:IPR005844 InterPro:IPR005845 InterPro:IPR005846 InterPro:IPR016055 InterPro:IPR016066 Pfam:PF00408 Pfam:PF02878 Pfam:PF02879 Pfam:PF02880 PRINTS:PR00509 PROSITE:PS00710 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005886 GO:GO:0005634 GO:GO:0046686 GO:GO:0000287 GO:GO:0006006 EMBL:AC011663 Gene3D:G3DSA:3.40.120.10 SUPFAM:SSF53738 GO:GO:0004614 GO:GO:0044445 KO:K01835 eggNOG:COG0033 OMA:SIFFSID HOGENOM:HBG286308 ProtClustDB:PLN02307 GO:GO:0048229 EMBL:AY090231 EMBL:BT002627 IPI:IPI00533044 PIR:G96731 RefSeq:NP_177230.1 UniGene:At.35274 ProteinModelPortal:Q9SGC1 SMR:Q9SGC1 STRING:Q9SGC1 PRIDE:Q9SGC1 ProMEX:Q9SGC1 EnsemblPlants:AT1G70730.1 GeneID:843410 KEGG:ath:AT1G70730 TAIR:At1g70730 InParanoid:Q9SGC1 PhylomeDB:Q9SGC1 ArrayExpress:Q9SGC1 Genevestigator:Q9SGC1 GermOnline:AT1G70730 Uniprot:Q9SGC1
Leaf	Isotig00690	23	102	-1.620	2.51E-08	TAIR|locus:2033583 - symbol:PGM2 "AT1G70730" species:3702 "Arabidopsis thaliana" [GO:0004614 "phosphoglucomutase activity" evidence=ISS;IDA] [GO:0005975 "carbohydrate metabolic process" evidence=ISS;IDA] [GO:0005992 "trehalose biosynthetic process" evidence=IBA] [GO:0006874 "cellular calcium ion homeostasis" evidence=IBA] [GO:0009570 "chloroplast stroma" evidence=IBA] [GO:0009590 "detection of gravity" evidence=IBA] [GO:0010319 "stromule" evidence=IBA] [GO:0019252 "starch biosynthetic process" evidence=IBA]

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						[GO:0019255 "glucose 1-phosphate metabolic process" evidence=IBA] [GO:0019388 "galactose catabolic process" evidence=IBA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0044445 "cytosolic part" evidence=IDA] [GO:0048229 "gametophyte development" evidence=IGI] InterPro:IPR005841 InterPro:IPR005843 InterPro:IPR005844 InterPro:IPR005845 InterPro:IPR005846 InterPro:IPR016055 InterPro:IPR016066 Pfam:PF00408 Pfam:PF02878 Pfam:PF02879 Pfam:PF02880 PRINTS:PR00509 PROSITE:PS00710 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005886 GO:GO:0005634 GO:GO:0046686 GO:GO:0000287 GO:GO:0006006 EMBL:AC011663 Gene3D:G3DSA:3.40.120.10 SUPFAM:SSF53738 GO:GO:0004614 GO:GO:0044445 KO:K01835 eggNOG:COG0033 OMA:SIFFSID HOGENOM:HBG286308 ProtClustDB:PLN02307 GO:GO:0048229 EMBL:AY090231 EMBL:BT002627 IPI:IPI00533044 PIR:G96731 RefSeq:NP_177230.1 UniGene:At.35274 ProteinModelPortal:Q9SGC1 SMR:Q9SGC1 STRING:Q9SGC1 PRIDE:Q9SGC1 ProMEX:Q9SGC1 EnsemblPlants:AT1G70730.1 GeneID:843410 KEGG:ath:AT1G70730 TAIR:At1g70730 InParanoid:Q9SGC1 PhylomeDB:Q9SGC1 ArrayExpress:Q9SGC1 Genevestigator:Q9SGC1 GermOnline:AT1G70730 Uniprot:Q9SGC1
Leaf	Isotig00691	16	94	-2.026	4.52E-10	TAIR|locus:2033583 - symbol:PGM2 "AT1G70730" species:3702 "Arabidopsis thaliana" [GO:0004614 "phosphoglucomutase activity" evidence=ISS;IDA] [GO:0005975 "carbohydrate metabolic process" evidence=ISS;IDA] [GO:0005992 "trehalose biosynthetic process" evidence=IBA] [GO:0006874 "cellular calcium ion homeostasis" evidence=IBA] [GO:0009570 "chloroplast stroma" evidence=IBA] [GO:0009590 "detection of gravity" evidence=IBA] [GO:0010319 "stromule" evidence=IBA] [GO:0019252 "starch biosynthetic process" evidence=IBA] [GO:0019255 "glucose 1-phosphate metabolic process" evidence=IBA] [GO:0019388 "galactose catabolic process" evidence=IBA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0044445 "cytosolic part" evidence=IDA] [GO:0048229 "gametophyte development" evidence=IGI] InterPro:IPR005841 InterPro:IPR005843 InterPro:IPR005844 InterPro:IPR005845 InterPro:IPR005846 InterPro:IPR016055 InterPro:IPR016066 Pfam:PF00408 Pfam:PF02878 Pfam:PF02879 Pfam:PF02880 PRINTS:PR00509 PROSITE:PS00710 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005886 GO:GO:0005634 GO:GO:0046686 GO:GO:0000287 GO:GO:0006006 EMBL:AC011663 Gene3D:G3DSA:3.40.120.10 SUPFAM:SSF53738 GO:GO:0004614 GO:GO:0044445 KO:K01835 eggNOG:COG0033 OMA:SIFFSID HOGENOM:HBG286308 ProtClustDB:PLN02307 GO:GO:0048229 EMBL:AY090231 EMBL:BT002627 IPI:IPI00533044 PIR:G96731 RefSeq:NP_177230.1 UniGene:At.35274 ProteinModelPortal:Q9SGC1 SMR:Q9SGC1 STRING:Q9SGC1 PRIDE:Q9SGC1 ProMEX:Q9SGC1 EnsemblPlants:AT1G70730.1 GeneID:843410 KEGG:ath:AT1G70730 TAIR:At1g70730 InParanoid:Q9SGC1 PhylomeDB:Q9SGC1 ArrayExpress:Q9SGC1 Genevestigator:Q9SGC1 GermOnline:AT1G70730 Uniprot:Q9SGC1
Leaf	Isotig00702	10	98	-2.764	2.12E-14	TAIR|locus:2150059 - symbol:SQD2 "AT5G01220" species:3702 "Arabidopsis thaliana" [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0008194 "UDP-glycosyltransferase activity" evidence=IDA] [GO:0009247 "glycolipid biosynthetic process" evidence=IDA] [GO:0016036 "cellular response to phosphate starvation" evidence=IMP] [GO:0046506 "sulfolipid biosynthetic process" evidence=TAS] [GO:0046510 "UDP-sulfoquinovose:DAG sulfoquinovosyltransferase activity" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] InterPro:IPR001296 Pfam:PF00534 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009247 GO:GO:0009941 eggNOG:COG0438 CAZy:GT4 HOGENOM:HBG726846 GO:GO:0008194 EMBL:AF454354 EMBL:BT005796 IPI:IPI00548055 RefSeq:NP_568085.2 UniGene:At.47995 ProteinModelPortal:Q8S4F6 STRING:Q8S4F6 PRIDE:Q8S4F6 EnsemblPlants:AT5G01220.1 GeneID:831888 KEGG:ath:AT5G01220 TAIR:At5g01220 InParanoid:Q8S4F6 KO:K06119 OMA:LCTSTAM PhylomeDB:Q8S4F6 ProtClustDB:PLN02871 Genevestigator:Q8S4F6 Uniprot:Q8S4F6
Leaf	Isotig00703	5	66	-3.194	1.73E-11	TAIR|locus:2150059 - symbol:SQD2 "AT5G01220" species:3702 "Arabidopsis thaliana" [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0008194 "UDP-glycosyltransferase activity" evidence=IDA] [GO:0009247 "glycolipid biosynthetic process" evidence=IDA] [GO:0016036 "cellular response to phosphate starvation" evidence=IMP] [GO:0046506 "sulfolipid biosynthetic process" evidence=TAS] [GO:0046510 "UDP-sulfoquinovose:DAG sulfoquinovosyltransferase activity" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] InterPro:IPR001296 Pfam:PF00534 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009247 GO:GO:0009941 eggNOG:COG0438 CAZy:GT4 HOGENOM:HBG726846 GO:GO:0008194 EMBL:AF454354 EMBL:BT005796 IPI:IPI00548055

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						RefSeq:NP_568085.2 UniGene:At.47995 ProteinModelPortal:Q8S4F6 STRING:Q8S4F6 PRIDE:Q8S4F6 EnsemblPlants:AT5G01220.1 GeneID:831888 KEGG:ath:AT5G01220 TAIR:At5g01220 InParanoid:Q8S4F6 KO:K06119 OMA:LCTSTAM PhylomeDB:Q8S4F6 ProtClustDB:PLN02871 Genevestigator:Q8S4F6 Uniprot:Q8S4F6
Leaf	Isotig00704	7	79	-2.967	1.14E-12	TAIR|locus:2150059 - symbol:SQD2 "AT5G01220" species:3702 "Arabidopsis thaliana" [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0008194 "UDP-glycosyltransferase activity" evidence=IDA] [GO:0009247 "glycolipid biosynthetic process" evidence=IDA] [GO:0016036 "cellular response to phosphate starvation" evidence=IMP] [GO:0046506 "sulfolipid biosynthetic process" evidence=TAS] [GO:0046510 "UDP-sulfoquinovose:DAG sulfoquinovosyltransferase activity" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] InterPro:IPR001296 Pfam:PF00534 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009247 GO:GO:0009941 eggNOG:COG0438 CAZy:GT4 HOGENOM:HBG726846 GO:GO:0008194 EMBL:AF454354 EMBL:BT005796 IPI:IPI00548055 RefSeq:NP_568085.2 UniGene:At.47995 ProteinModelPortal:Q8S4F6 STRING:Q8S4F6 PRIDE:Q8S4F6 EnsemblPlants:AT5G01220.1 GeneID:831888 KEGG:ath:AT5G01220 TAIR:At5g01220 InParanoid:Q8S4F6 KO:K06119 OMA:LCTSTAM PhylomeDB:Q8S4F6 ProtClustDB:PLN02871 Genevestigator:Q8S4F6 Uniprot:Q8S4F6
Leaf	Isotig00705	10	97	-2.749	3.38E-14	TAIR|locus:2150059 - symbol:SQD2 "AT5G01220" species:3702 "Arabidopsis thaliana" [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0008194 "UDP-glycosyltransferase activity" evidence=IDA] [GO:0009247 "glycolipid biosynthetic process" evidence=IDA] [GO:0016036 "cellular response to phosphate starvation" evidence=IMP] [GO:0046506 "sulfolipid biosynthetic process" evidence=TAS] [GO:0046510 "UDP-sulfoquinovose:DAG sulfoquinovosyltransferase activity" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] InterPro:IPR001296 Pfam:PF00534 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009247 GO:GO:0009941 eggNOG:COG0438 CAZy:GT4 HOGENOM:HBG726846 GO:GO:0008194 EMBL:AF454354 EMBL:BT005796 IPI:IPI00548055 RefSeq:NP_568085.2 UniGene:At.47995 ProteinModelPortal:Q8S4F6 STRING:Q8S4F6 PRIDE:Q8S4F6 EnsemblPlants:AT5G01220.1 GeneID:831888 KEGG:ath:AT5G01220 TAIR:At5g01220 InParanoid:Q8S4F6 KO:K06119 OMA:LCTSTAM PhylomeDB:Q8S4F6 ProtClustDB:PLN02871 Genevestigator:Q8S4F6 Uniprot:Q8S4F6
Leaf	Isotig00706	7	78	-2.949	1.84E-12	TAIR|locus:2150059 - symbol:SQD2 "AT5G01220" species:3702 "Arabidopsis thaliana" [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0008194 "UDP-glycosyltransferase activity" evidence=IDA] [GO:0009247 "glycolipid biosynthetic process" evidence=IDA] [GO:0016036 "cellular response to phosphate starvation" evidence=IMP] [GO:0046506 "sulfolipid biosynthetic process" evidence=TAS] [GO:0046510 "UDP-sulfoquinovose:DAG sulfoquinovosyltransferase activity" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] InterPro:IPR001296 Pfam:PF00534 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009247 GO:GO:0009941 eggNOG:COG0438 CAZy:GT4 HOGENOM:HBG726846 GO:GO:0008194 EMBL:AF454354 EMBL:BT005796 IPI:IPI00548055 RefSeq:NP_568085.2 UniGene:At.47995 ProteinModelPortal:Q8S4F6 STRING:Q8S4F6 PRIDE:Q8S4F6 EnsemblPlants:AT5G01220.1 GeneID:831888 KEGG:ath:AT5G01220 TAIR:At5g01220 InParanoid:Q8S4F6 KO:K06119 OMA:LCTSTAM PhylomeDB:Q8S4F6 ProtClustDB:PLN02871 Genevestigator:Q8S4F6 Uniprot:Q8S4F6
Leaf	Isotig00707	55	167	-1.073	2.05E-07	UNIPROTKB|Q43848 - symbol:Q43848 "Transketolase, chloroplastic" species:4113 "Solanum tuberosum" [GO:0004802 "transketolase activity" evidence=ISS] [GO:0009535 "chloroplast thylakoid membrane" evidence=ISS] InterPro:IPR005476 InterPro:IPR005478 InterPro:IPR009014 InterPro:IPR015941 Pfam:PF02780 InterPro:IPR005475 Pfam:PF00456 Pfam:PF02779 InterPro:IPR005474 GO:GO:0046872 GO:GO:0009535 SMART:SM00861 InterPro:IPR020826 Gene3D:G3DSA:3.40.50.920 SUPFAM:SSF52922 PROSITE:PS00801 PROSITE:PS00802 GO:GO:0004802 TIGRFAMs:TIGR00232 EMBL:Z50099 PIR:S58083 ProteinModelPortal:Q43848 SMR:Q43848 PRIDE:Q43848 Uniprot:Q43848
Leaf	Isotig00722	142	639	-1.641	4.82E-45	TAIR|locus:2077972 - symbol:PSBO2 "AT3G50820" species:3702 "Arabidopsis thaliana" [GO:0009654 "oxygen evolving complex" evidence=ISS] [GO:0030095 "chloroplast photosystem II" evidence=ISS] [GO:0009543 "chloroplast thylakoid lumen" evidence=IDA] [GO:0031977 "thylakoid lumen" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0010242 "oxygen evolving activity" evidence=ISS] [GO:0019684 "photosynthesis, light reaction" evidence=ISS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0010207 "photosystem II assembly" evidence=IMP] [GO:0042549 "photosystem II stabilization" evidence=IMP] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0010205 "photoinhibition" evidence=IMP] [GO:0035304 "regulation of protein dephosphorylation" evidence=IMP] [GO:0008266 "poly(U) RNA binding" evidence=IDA] [GO:0005515 "protein

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						binding" evidence=IPI] [GO:0009534 "chloroplast thylakoid" evidence=IDA] InterPro:IPR002628 Pfam:PF01716 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005509 GO:GO:0005515 GO:GO:0008266 GO:GO:0019898 GO:GO:0010205 GO:GO:0009535 GO:GO:0010287 GO:GO:0031977 EMBL:AL049862 GO:GO:0035304 GO:GO:0010207 GO:GO:0009654 eggNOG:NOG05777 KO:K02716 ProtClustDB:PLN00037 GO:GO:0042549 EMBL:AJ145957 EMBL:AY050362 EMBL:AY116934 EMBL:AY088799 IPI:IPI00519769 PIR:T08403 RefSeq:NP_190651.1 UniGene:At.21117 ProteinModelPortal:Q9S841 SMR:Q9S841 IntAct:Q9S841 STRING:Q9S841 SWISS-2DPAGE:Q9S841 PRIDE:Q9S841 ProMEX:Q9S841 DNASU:824246 EnsemblPlants:AT3G50820.1 GeneID:824246 KEGG:ath:AT3G50820 TAIR:At3g50820 HOGENOM:HBG317982 InParanoid:Q9S841 OMA:KIAASPS PhylomeDB:Q9S841 ArrayExpress:Q9S841 Genevestigator:Q9S841 GermOnline:AT3G50820 Uniprot:Q9S841
Leaf	Isotig00723	142	634	-1.630	2.79E-44	TAIR|locus:2077972 - symbol:PSBO2 "AT3G50820" species:3702 "Arabidopsis thaliana" [GO:0009654 "oxygen evolving complex" evidence=ISS] [GO:0030095 "chloroplast photosystem II" evidence=ISS] [GO:0009543 "chloroplast thylakoid lumen" evidence=IDA] [GO:0031977 "thylakoid lumen" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0010242 "oxygen evolving activity" evidence=ISS] [GO:0019684 "photosynthesis, light reaction" evidence=ISS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0010207 "photosystem II assembly" evidence=IMP] [GO:0042549 "photosystem II stabilization" evidence=IMP] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0010205 "photoinhibition" evidence=IMP] [GO:0035304 "regulation of protein dephosphorylation" evidence=IMP] [GO:0008266 "poly(U) RNA binding" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0009534 "chloroplast thylakoid" evidence=IDA] InterPro:IPR002628 Pfam:PF01716 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005509 GO:GO:0005515 GO:GO:0008266 GO:GO:0019898 GO:GO:0010205 GO:GO:0009535 GO:GO:0010287 GO:GO:0031977 EMBL:AL049862 GO:GO:0035304 GO:GO:0010207 GO:GO:0009654 eggNOG:NOG05777 KO:K02716 ProtClustDB:PLN00037 GO:GO:0042549 EMBL:AJ145957 EMBL:AY050362 EMBL:AY116934 EMBL:AY088799 IPI:IPI00519769 PIR:T08403 RefSeq:NP_190651.1 UniGene:At.21117 ProteinModelPortal:Q9S841 SMR:Q9S841 IntAct:Q9S841 STRING:Q9S841 SWISS-2DPAGE:Q9S841 PRIDE:Q9S841 ProMEX:Q9S841 DNASU:824246 EnsemblPlants:AT3G50820.1 GeneID:824246 KEGG:ath:AT3G50820 TAIR:At3g50820 HOGENOM:HBG317982 InParanoid:Q9S841 OMA:KIAASPS PhylomeDB:Q9S841 ArrayExpress:Q9S841 Genevestigator:Q9S841 GermOnline:AT3G50820 Uniprot:Q9S841
Leaf	Isotig00724	141	639	-1.651	1.99E-45	TAIR|locus:2077972 - symbol:PSBO2 "AT3G50820" species:3702 "Arabidopsis thaliana" [GO:0009654 "oxygen evolving complex" evidence=ISS] [GO:0030095 "chloroplast photosystem II" evidence=ISS] [GO:0009543 "chloroplast thylakoid lumen" evidence=IDA] [GO:0031977 "thylakoid lumen" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0010242 "oxygen evolving activity" evidence=ISS] [GO:0019684 "photosynthesis, light reaction" evidence=ISS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0010207 "photosystem II assembly" evidence=IMP] [GO:0042549 "photosystem II stabilization" evidence=IMP] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0010205 "photoinhibition" evidence=IMP] [GO:0035304 "regulation of protein dephosphorylation" evidence=IMP] [GO:0008266 "poly(U) RNA binding" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0009534 "chloroplast thylakoid" evidence=IDA] InterPro:IPR002628 Pfam:PF01716 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005509 GO:GO:0005515 GO:GO:0008266 GO:GO:0019898 GO:GO:0010205 GO:GO:0009535 GO:GO:0010287 GO:GO:0031977 EMBL:AL049862 GO:GO:0035304 GO:GO:0010207 GO:GO:0009654 eggNOG:NOG05777 KO:K02716 ProtClustDB:PLN00037 GO:GO:0042549 EMBL:AJ145957 EMBL:AY050362 EMBL:AY116934 EMBL:AY088799 IPI:IPI00519769 PIR:T08403 RefSeq:NP_190651.1 UniGene:At.21117 ProteinModelPortal:Q9S841 SMR:Q9S841 IntAct:Q9S841 STRING:Q9S841 SWISS-2DPAGE:Q9S841 PRIDE:Q9S841 ProMEX:Q9S841 DNASU:824246 EnsemblPlants:AT3G50820.1 GeneID:824246 KEGG:ath:AT3G50820 TAIR:At3g50820 HOGENOM:HBG317982 InParanoid:Q9S841 OMA:KIAASPS PhylomeDB:Q9S841 ArrayExpress:Q9S841 Genevestigator:Q9S841 GermOnline:AT3G50820 Uniprot:Q9S841
Leaf	Isotig00725	141	634	-1.640	1.16E-44	TAIR|locus:2077972 - symbol:PSBO2 "AT3G50820" species:3702 "Arabidopsis thaliana" [GO:0009654 "oxygen evolving complex" evidence=ISS] [GO:0030095 "chloroplast photosystem II" evidence=ISS] [GO:0009543 "chloroplast thylakoid lumen" evidence=IDA] [GO:0031977 "thylakoid lumen" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0010242 "oxygen evolving activity" evidence=ISS] [GO:0019684 "photosynthesis,

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						light reaction" evidence=ISS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0010207 "photosystem II assembly" evidence=IMP] [GO:0042549 "photosystem II stabilization" evidence=IMP] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0010205 "photoinhibition" evidence=IMP] [GO:0035304 "regulation of protein dephosphorylation" evidence=IMP] [GO:0008266 "poly(U) RNA binding" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0009534 "chloroplast thylakoid" evidence=IDA] InterPro:IPR002628 Pfam:PF01716 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005509 GO:GO:0005515 GO:GO:0008266 GO:GO:0019898 GO:GO:0010205 GO:GO:0009535 GO:GO:0010287 GO:GO:0031977 EMBL:AL049862 GO:GO:0035304 GO:GO:0010207 GO:GO:0009654 eggNOG:NOG05777 KO:K02716 ProtClustDB:PLN00037 GO:GO:0042549 EMBL:AJ145957 EMBL:AY050362 EMBL:AY116934 EMBL:AY088799 IPI:IPI00519769 PIR:T08403 RefSeq:NP_190651.1 UniGene:At.21117 ProteinModelPortal:Q9S841 SMR:Q9S841 IntAct:Q9S841 STRING:Q9S841 SWISS-2DPAGE:Q9S841 PRIDE:Q9S841 ProMEX:Q9S841 DNASU:824246 EnsemblPlants:AT3G50820.1 GeneID:824246 KEGG:ath:AT3G50820 TAIR:At3g50820 HOGENOM:HBG317982 InParanoid:Q9S841 OMA:KIAASPS PhylomeDB:Q9S841 ArrayExpress:Q9S841 Genevestigator:Q9S841 GermOnline:AT3G50820 Uniprot:Q9S841
Leaf	Isotig00727	22	85	-1.421	3.86E-06	TAIR|locus:2026212 - symbol:SCO1 "AT1G62750" species:3702 "Arabidopsis thaliana" [GO:0003746 "translation elongation factor activity" evidence=ISS] [GO:0008135 "translation factor activity, nucleic acid binding" evidence=ISS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005525 "GTP binding" evidence=ISS] [GO:0009658 "chloroplast organization" evidence=IMP] [GO:0009791 "post-embryonic development" evidence=IMP] [GO:0009845 "seed germination" evidence=IMP] [GO:0005524 "ATP binding" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] InterPro:IPR000640 InterPro:IPR000795 InterPro:IPR004161 InterPro:IPR004540 InterPro:IPR005225 InterPro:IPR005517 Pfam:PF00009 Pfam:PF00679 Pfam:PF03144 Pfam:PF03764 PRINTS:PR00315 PROSITE:PS00301 SMART:SM00838 SMART:SM00889 GO:GO:0005525 TIGRFAMs:TIGR00231 EMBL:CP002684 GO:GO:0005739 GO:GO:0005524 GO:GO:0048046 GO:GO:0009570 GO:GO:0003924 GO:GO:0009941 EMBL:AC007190 GO:GO:0009658 GO:GO:0009845 GO:GO:0003746 InterPro:IPR020568 InterPro:IPR014721 Gene3D:G3DSA:3.30.230.10 SUPFAM:SSF54211 InterPro:IPR009000 SUPFAM:SSF50447 InterPro:IPR009022 Gene3D:G3DSA:3.30.70.240 SUPFAM:SSF54980 KO:K02355 HAMAP:MF_00054_B TIGRFAMs:TIGR00484 OMA:QGRAVYS HSSP:P13551 ProtClustDB:CLSN2681893 UniGene:At.21185 UniGene:At.48334 EMBL:AY142646 EMBL:BK005771 IPI:IPI00533633 PIR:E96652 RefSeq:NP_564801.1 ProteinModelPortal:Q9SI75 SMR:Q9SI75 STRING:Q9SI75 PRIDE:Q9SI75 ProMEX:Q9SI75 EnsemblPlants:AT1G62750.1 GeneID:842573 KEGG:ath:AT1G62750 TAIR:At1g62750 InParanoid:Q9SI75 PhylomeDB:Q9SI75 Genevestigator:Q9SI75 Uniprot:Q9SI75
Leaf	Isotig00728	25	78	-1.113	0.000257804	TAIR|locus:2026212 - symbol:SCO1 "AT1G62750" species:3702 "Arabidopsis thaliana" [GO:0003746 "translation elongation factor activity" evidence=ISS] [GO:0008135 "translation factor activity, nucleic acid binding" evidence=ISS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005525 "GTP binding" evidence=ISS] [GO:0009658 "chloroplast organization" evidence=IMP] [GO:0009791 "post-embryonic development" evidence=IMP] [GO:0009845 "seed germination" evidence=IMP] [GO:0005524 "ATP binding" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] InterPro:IPR000640 InterPro:IPR000795 InterPro:IPR004161 InterPro:IPR004540 InterPro:IPR005225 InterPro:IPR005517 Pfam:PF00009 Pfam:PF00679 Pfam:PF03144 Pfam:PF03764 PRINTS:PR00315 PROSITE:PS00301 SMART:SM00838 SMART:SM00889 GO:GO:0005525 TIGRFAMs:TIGR00231 EMBL:CP002684 GO:GO:0005739 GO:GO:0005524 GO:GO:0048046 GO:GO:0009570 GO:GO:0003924 GO:GO:0009941 EMBL:AC007190 GO:GO:0009658 GO:GO:0009845 GO:GO:0003746 InterPro:IPR020568 InterPro:IPR014721 Gene3D:G3DSA:3.30.230.10 SUPFAM:SSF54211 InterPro:IPR009000 SUPFAM:SSF50447 InterPro:IPR009022 Gene3D:G3DSA:3.30.70.240 SUPFAM:SSF54980 KO:K02355 HAMAP:MF_00054_B TIGRFAMs:TIGR00484 OMA:QGRAVYS HSSP:P13551 ProtClustDB:CLSN2681893 UniGene:At.21185 UniGene:At.48334 EMBL:AY142646 EMBL:BK005771 IPI:IPI00533633 PIR:E96652 RefSeq:NP_564801.1 ProteinModelPortal:Q9SI75 SMR:Q9SI75 STRING:Q9SI75 PRIDE:Q9SI75 ProMEX:Q9SI75 EnsemblPlants:AT1G62750.1 GeneID:842573 KEGG:ath:AT1G62750 TAIR:At1g62750 InParanoid:Q9SI75 PhylomeDB:Q9SI75 Genevestigator:Q9SI75 Uniprot:Q9SI75

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig00735	3	27	-2.641	9.01E-05	UNIPROTKB|Q86YZ3 - symbol:HRNR "Hornerin" species:9606 "Homo sapiens" [GO:0001533 "cornified envelope" evidence=IEA] [GO:0004640 "phosphoribosylanthranilate isomerase activity" evidence=IEA] [GO:0005509 "calcium ion binding" evidence=IEA] [GO:0006568 "tryptophan metabolic process" evidence=IEA] [GO:0017111 "nucleoside-triphosphatase activity" evidence=IEA] [GO:0031424 "keratinization" evidence=IEA] InterPro:IPR001240 InterPro:IPR001751 InterPro:IPR011992 InterPro:IPR020922 PROSITE:PS00303 Prosite:PS00018 GO:GO:0005509 InterPro:IPR018247 InterPro:IPR018249 Gene3D:G3DSA:1.10.238.10 PROSITE:PS50222 GO:GO:0006568 GO:GO:0017111 eggNOG:NOG12793 GO:GO:0031424 GeneTree:ENSGT00530000063634 InterPro:IPR013787 Pfam:PF01023 OrthoDB:EOG4RJG10 GO:GO:0004640 EMBL:AB104446 EMBL:BR000036 EMBL:AL589986 IPI:IPI00398625 RefSeq:NP_001009931.1 UniGene:Hs.490162 ProteinModelPortal:Q86YZ3 SMR:Q86YZ3 IntAct:Q86YZ3 MINT:MINT-2809380 STRING:Q86YZ3 PhosphoSite:Q86YZ3 DMDM:45476906 UCD-2DPAGE:Q86YZ3 PRIDE:Q86YZ3 Ensembl:ENST00000368801 GeneID:388697 KEGG:hsa:388697 UCSC:uc001ezt.1 CTD:388697 GeneCards:GC01M152184 H-InvDB:HIX0200013 HGNC:HGNC:20846 HPA:HPA031469 neXtProt:NX_Q86YZ3 PharmGKB:PA134936141 InParanoid:Q86YZ3 OMA:GHHESSS PhylomeDB:Q86YZ3 NextBio:102292 ArrayExpress:Q5U1F4 Bgee:Q86YZ3 CleanEx:HS_HRNR Genevestigator:Q86YZ3 GermOnline:ENSG00000197915 InterPro:IPR019822 Uniprot:Q86YZ3
Leaf	Isotig00752	29	8	2.387	4.14E-06	UNIPROTKB|F1PQT7 - symbol:F1PQT7 "Uncharacterized protein" species:9615 "Canis lupus familiaris" [GO:0045095 "keratin filament" evidence=IEA] InterPro:IPR002494 GO:GO:0045095 GeneTree:ENSGT00650000092979 PANTHER:PTHR23262 OMA:CCTEDSP Ensembl:ENSCAFT00000024050 Uniprot:F1PQT7
Leaf	Isotig00753	57	0	7.362	4.21E-17	TAIR|locus:2179117 - symbol:AT5G01300 "AT5G01300" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0008429 "phosphatidylethanolamine binding" evidence=ISS] Pfam:PF01161 EMBL:CP002688 GenomeReviews:BA000015_GR InterPro:IPR008914 Gene3D:G3DSA:3.90.280.10 SUPFAM:SSF49777 EMBL:AL161746 KO:K06910 HOGENOM:HBG649023 InterPro:IPR005247 TIGRFAMs:TIGR00481 UniGene:At.33912 UniGene:At.48967 EMBL:AY065369 EMBL:AY096477 IPI:IPI00535873 PIR:T48152 RefSeq:NP_195750.1 HSSP:P77368 ProteinModelPortal:Q9M042 SMR:Q9M042 PRIDE:Q9M042 ProMEX:Q9M042 EnsemblPlants:AT5G01300.1 GeneID:830983 KEGG:ath:AT5G01300 TAIR:At5g01300 InParanoid:Q9M042 OMA:LEWYNVP PhylomeDB:Q9M042 ProtClustDB:CLSN2687113 ArrayExpress:Q9M042 Genevestigator:Q9M042 Uniprot:Q9M042
Leaf	Isotig00754	57	0	7.362	4.21E-17	TAIR|locus:2179117 - symbol:AT5G01300 "AT5G01300" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0008429 "phosphatidylethanolamine binding" evidence=ISS] Pfam:PF01161 EMBL:CP002688 GenomeReviews:BA000015_GR InterPro:IPR008914 Gene3D:G3DSA:3.90.280.10 SUPFAM:SSF49777 EMBL:AL161746 KO:K06910 HOGENOM:HBG649023 InterPro:IPR005247 TIGRFAMs:TIGR00481 UniGene:At.33912 UniGene:At.48967 EMBL:AY065369 EMBL:AY096477 IPI:IPI00535873 PIR:T48152 RefSeq:NP_195750.1 HSSP:P77368 ProteinModelPortal:Q9M042 SMR:Q9M042 PRIDE:Q9M042 ProMEX:Q9M042 EnsemblPlants:AT5G01300.1 GeneID:830983 KEGG:ath:AT5G01300 TAIR:At5g01300 InParanoid:Q9M042 OMA:LEWYNVP PhylomeDB:Q9M042 ProtClustDB:CLSN2687113 ArrayExpress:Q9M042 Genevestigator:Q9M042 Uniprot:Q9M042
Leaf	Isotig00755	57	0	7.362	4.21E-17	TAIR|locus:2179117 - symbol:AT5G01300 "AT5G01300" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0008429 "phosphatidylethanolamine binding" evidence=ISS] Pfam:PF01161 EMBL:CP002688 GenomeReviews:BA000015_GR InterPro:IPR008914 Gene3D:G3DSA:3.90.280.10 SUPFAM:SSF49777 EMBL:AL161746 KO:K06910 HOGENOM:HBG649023 InterPro:IPR005247 TIGRFAMs:TIGR00481 UniGene:At.33912 UniGene:At.48967 EMBL:AY065369 EMBL:AY096477 IPI:IPI00535873 PIR:T48152 RefSeq:NP_195750.1 HSSP:P77368 ProteinModelPortal:Q9M042 SMR:Q9M042 PRIDE:Q9M042 ProMEX:Q9M042 EnsemblPlants:AT5G01300.1 GeneID:830983 KEGG:ath:AT5G01300 TAIR:At5g01300 InParanoid:Q9M042 OMA:LEWYNVP PhylomeDB:Q9M042 ProtClustDB:CLSN2687113 ArrayExpress:Q9M042 Genevestigator:Q9M042 Uniprot:Q9M042
Leaf	Isotig00756	57	0	7.362	4.21E-17	TAIR|locus:2179117 - symbol:AT5G01300 "AT5G01300" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0008429 "phosphatidylethanolamine binding" evidence=ISS] Pfam:PF01161 EMBL:CP002688

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GenomeReviews:BA000015_GR InterPro:IPR008914 Gene3D:G3DSA:3.90.280.10 SUPFAM:SSF49777 EMBL:AL161746 KO:K06910 HOGENOM:HBG649023 InterPro:IPR005247 TIGRFAMs:TIGR00481 UniGene:At.33912 UniGene:At.48967 EMBL:AY065369 EMBL:AY096477 IPI:IPI00535873 PIR:T48152 RefSeq:NP_195750.1 HSSP:P77368 ProteinModelPortal:Q9M042 SMR:Q9M042 PRIDE:Q9M042 ProMEX:Q9M042 EnsemblPlants:AT5G01300.1 GeneID:830983 KEGG:ath:AT5G01300 TAIR:At5g01300 InParanoid:Q9M042 OMA:LEWYNVP PhylomeDB:Q9M042 ProtClustDB:CLSN2687113 ArrayExpress:Q9M042 Genevestigator:Q9M042 Uniprot:Q9M042
Leaf	Isotig00757	57	0	7.362	4.21E-17	TAIR|locus:2179117 - symbol:AT5G01300 "AT5G01300" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0008429 "phosphatidylethanolamine binding" evidence=ISS] Pfam:PF01161 EMBL:CP002688 GenomeReviews:BA000015_GR InterPro:IPR008914 Gene3D:G3DSA:3.90.280.10 SUPFAM:SSF49777 EMBL:AL161746 KO:K06910 HOGENOM:HBG649023 InterPro:IPR005247 TIGRFAMs:TIGR00481 UniGene:At.33912 UniGene:At.48967 EMBL:AY065369 EMBL:AY096477 IPI:IPI00535873 PIR:T48152 RefSeq:NP_195750.1 HSSP:P77368 ProteinModelPortal:Q9M042 SMR:Q9M042 PRIDE:Q9M042 ProMEX:Q9M042 EnsemblPlants:AT5G01300.1 GeneID:830983 KEGG:ath:AT5G01300 TAIR:At5g01300 InParanoid:Q9M042 OMA:LEWYNVP PhylomeDB:Q9M042 ProtClustDB:CLSN2687113 ArrayExpress:Q9M042 Genevestigator:Q9M042 Uniprot:Q9M042
Leaf	Isotig00758	57	0	7.362	4.21E-17	TAIR|locus:2179117 - symbol:AT5G01300 "AT5G01300" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0008429 "phosphatidylethanolamine binding" evidence=ISS] Pfam:PF01161 EMBL:CP002688 GenomeReviews:BA000015_GR InterPro:IPR008914 Gene3D:G3DSA:3.90.280.10 SUPFAM:SSF49777 EMBL:AL161746 KO:K06910 HOGENOM:HBG649023 InterPro:IPR005247 TIGRFAMs:TIGR00481 UniGene:At.33912 UniGene:At.48967 EMBL:AY065369 EMBL:AY096477 IPI:IPI00535873 PIR:T48152 RefSeq:NP_195750.1 HSSP:P77368 ProteinModelPortal:Q9M042 SMR:Q9M042 PRIDE:Q9M042 ProMEX:Q9M042 EnsemblPlants:AT5G01300.1 GeneID:830983 KEGG:ath:AT5G01300 TAIR:At5g01300 InParanoid:Q9M042 OMA:LEWYNVP PhylomeDB:Q9M042 ProtClustDB:CLSN2687113 ArrayExpress:Q9M042 Genevestigator:Q9M042 Uniprot:Q9M042
Leaf	Isotig00759	57	0	7.362	4.21E-17	TAIR|locus:2179117 - symbol:AT5G01300 "AT5G01300" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0008429 "phosphatidylethanolamine binding" evidence=ISS] Pfam:PF01161 EMBL:CP002688 GenomeReviews:BA000015_GR InterPro:IPR008914 Gene3D:G3DSA:3.90.280.10 SUPFAM:SSF49777 EMBL:AL161746 KO:K06910 HOGENOM:HBG649023 InterPro:IPR005247 TIGRFAMs:TIGR00481 UniGene:At.33912 UniGene:At.48967 EMBL:AY065369 EMBL:AY096477 IPI:IPI00535873 PIR:T48152 RefSeq:NP_195750.1 HSSP:P77368 ProteinModelPortal:Q9M042 SMR:Q9M042 PRIDE:Q9M042 ProMEX:Q9M042 EnsemblPlants:AT5G01300.1 GeneID:830983 KEGG:ath:AT5G01300 TAIR:At5g01300 InParanoid:Q9M042 OMA:LEWYNVP PhylomeDB:Q9M042 ProtClustDB:CLSN2687113 ArrayExpress:Q9M042 Genevestigator:Q9M042 Uniprot:Q9M042
Leaf	Isotig00760	57	0	7.362	4.21E-17	TAIR|locus:2179117 - symbol:AT5G01300 "AT5G01300" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0008429 "phosphatidylethanolamine binding" evidence=ISS] Pfam:PF01161 EMBL:CP002688 GenomeReviews:BA000015_GR InterPro:IPR008914 Gene3D:G3DSA:3.90.280.10 SUPFAM:SSF49777 EMBL:AL161746 KO:K06910 HOGENOM:HBG649023 InterPro:IPR005247 TIGRFAMs:TIGR00481 UniGene:At.33912 UniGene:At.48967 EMBL:AY065369 EMBL:AY096477 IPI:IPI00535873 PIR:T48152 RefSeq:NP_195750.1 HSSP:P77368 ProteinModelPortal:Q9M042 SMR:Q9M042 PRIDE:Q9M042 ProMEX:Q9M042 EnsemblPlants:AT5G01300.1 GeneID:830983 KEGG:ath:AT5G01300 TAIR:At5g01300 InParanoid:Q9M042 OMA:LEWYNVP PhylomeDB:Q9M042 ProtClustDB:CLSN2687113 ArrayExpress:Q9M042 Genevestigator:Q9M042 Uniprot:Q9M042
Leaf	Isotig00761	41	15	1.980	1.10E-06	No hit
Leaf	Isotig00762	38	14	1.970	2.94E-06	No hit
Leaf	Isotig00763	42	15	2.014	6.10E-07	No hit
Leaf	Isotig00764	39	14	2.007	1.63E-06	No hit
Leaf	Isotig00765	34	14	1.809	2.96E-05	No hit

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig00766	31	13	1.783	7.89E-05	No hit
Leaf	Isotig00779	56	39	1.051	0.000383765	TAIR|locus:1005716172 - symbol:AT5G21326 species:3702 "Arabidopsis thaliana" [GO:0004672 "protein kinase activity" evidence=IEA;ISS] [GO:0004674 "protein serine/threonine kinase activity" evidence=IEA] [GO:0005524 "ATP binding" evidence=IEA;ISS] [GO:0006468 "protein phosphorylation" evidence=IEA;ISS] [GO:0007165 "signal transduction" evidence=IEA;ISS] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR000719 InterPro:IPR002290 InterPro:IPR004041 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 InterPro:IPR018451 Pfam:PF00069 Pfam:PF03822 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 PROSITE:PS50816 SMART:SM00220 GO:GO:0005829 GO:GO:0005524 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0007165 eggNOG:COG0515 SUPFAM:SSF56112 GO:GO:0004674 HOGENOM:HBG755340 EMBL:AC140977 HSSP:P49137 EMBL:BT014878 IPI:IPI00544603 RefSeq:NP_850861.2 UniGene:At.20987 UniGene:At.49214 ProteinModelPortal:Q84VQ3 SMR:Q84VQ3 PRIDE:Q84VQ3 EnsemblPlants:AT5G21326.1 GeneID:832246 KEGG:ath:AT5G21326 TAIR:At5g21326 InParanoid:Q84VQ3 OMA:HHISGAE PhylomeDB:Q84VQ3 ProtClustDB:CLSN2915155 Genevestigator:Q84VQ3 Uniprot:Q84VQ3
Leaf	Isotig00782	55	39	1.025	0.000565593	TAIR|locus:1005716172 - symbol:AT5G21326 species:3702 "Arabidopsis thaliana" [GO:0004672 "protein kinase activity" evidence=IEA;ISS] [GO:0004674 "protein serine/threonine kinase activity" evidence=IEA] [GO:0005524 "ATP binding" evidence=IEA;ISS] [GO:0006468 "protein phosphorylation" evidence=IEA;ISS] [GO:0007165 "signal transduction" evidence=IEA;ISS] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR000719 InterPro:IPR002290 InterPro:IPR004041 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 InterPro:IPR018451 Pfam:PF00069 Pfam:PF03822 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 PROSITE:PS50816 SMART:SM00220 GO:GO:0005829 GO:GO:0005524 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0007165 eggNOG:COG0515 SUPFAM:SSF56112 GO:GO:0004674 HOGENOM:HBG755340 EMBL:AC140977 HSSP:P49137 EMBL:BT014878 IPI:IPI00544603 RefSeq:NP_850861.2 UniGene:At.20987 UniGene:At.49214 ProteinModelPortal:Q84VQ3 SMR:Q84VQ3 PRIDE:Q84VQ3 EnsemblPlants:AT5G21326.1 GeneID:832246 KEGG:ath:AT5G21326 TAIR:At5g21326 InParanoid:Q84VQ3 OMA:HHISGAE PhylomeDB:Q84VQ3 ProtClustDB:CLSN2915155 Genevestigator:Q84VQ3 Uniprot:Q84VQ3
Leaf	Isotig00785	42	27	1.166	0.000821387	TAIR|locus:2008940 - symbol:APA1 "AT1G11910" species:3702 "Arabidopsis thaliana" [GO:0006508 "proteolysis" evidence=ISS;IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0004175 "endopeptidase activity" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR001461 InterPro:IPR001969 InterPro:IPR007856 InterPro:IPR009007 Pfam:PF00026 Pfam:PF05184 PRINTS:PR00792 PROSITE:PS00141 EMBL:CP002684 GO:GO:0005829 GO:GO:0009506 GO:GO:0005773 GO:GO:0006508 GO:GO:0006629 GO:GO:0009651 EMBL:AC002131 InterPro:IPR008138 InterPro:IPR011001 InterPro:IPR008139 Gene3D:G3DSA:1.10.225.10 Pfam:PF03489 SMART:SM00741 SUPFAM:SSF47862 PROSITE:PS50015 GO:GO:0004190 InterPro:IPR021109 SUPFAM:SSF50630 HOGENOM:HBG590923 Gene3D:G3DSA:2.40.70.10 PANTHER:PTHR13683 OMA:SGFMGID HSSP:P00797 KO:K08245 EMBL:AY056387 EMBL:AY056403 EMBL:AY063974 EMBL:AY088657 EMBL:BT001980 IPI:IPI00518049 PIR:F86253 RefSeq:NP_172655.1 UniGene:At.24544 UniGene:At.67307 ProteinModelPortal:O65390 SMR:O65390 IntAct:O65390 STRING:O65390 MEROPS:A01.020 PRIDE:O65390 ProMEX:O65390 EnsemblPlants:AT1G11910.1 GeneID:837740 KEGG:ath:AT1G11910 TAIR:At1g11910 InParanoid:O65390 PhylomeDB:O65390 ProtClustDB:CLSN2682210 ArrayExpress:O65390 Genevestigator:O65390 Uniprot:O65390
Leaf	Isotig00786	42	27	1.166	0.000821387	TAIR|locus:2008940 - symbol:APA1 "AT1G11910" species:3702 "Arabidopsis thaliana" [GO:0006508 "proteolysis" evidence=ISS;IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0004175 "endopeptidase activity" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR001461 InterPro:IPR001969 InterPro:IPR007856 InterPro:IPR009007 Pfam:PF00026 Pfam:PF05184 PRINTS:PR00792 PROSITE:PS00141 EMBL:CP002684 GO:GO:0005829 GO:GO:0009506 GO:GO:0005773 GO:GO:0006508 GO:GO:0006629 GO:GO:0009651 EMBL:AC002131 InterPro:IPR008138 InterPro:IPR011001 InterPro:IPR008139 Gene3D:G3DSA:1.10.225.10 Pfam:PF03489 SMART:SM00741 SUPFAM:SSF47862 PROSITE:PS50015 GO:GO:0004190 InterPro:IPR021109 SUPFAM:SSF50630 HOGENOM:HBG590923 Gene3D:G3DSA:2.40.70.10 PANTHER:PTHR13683 OMA:SGFMGID HSSP:P00797 KO:K08245 EMBL:AY056387 EMBL:AY056403 EMBL:AY063974 EMBL:AY088657 EMBL:BT001980 IPI:IPI00518049 PIR:F86253 RefSeq:NP_172655.1 UniGene:At.24544 UniGene:At.67307 ProteinModelPortal:O65390 SMR:O65390 IntAct:O65390 STRING:O65390 MEROPS:A01.020 PRIDE:O65390

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						ProMEX:O65390 EnsemblPlants:AT1G11910.1 GeneID:837740 KEGG:ath:AT1G11910 TAIR:At1g11910 InParanoid:O65390 PhylomeDB:O65390 ProtClustDB:CLSN2682210 ArrayExpress:O65390 Genevestigator:O65390 Uniprot:O65390
Leaf	Isotig00787	42	27	1.166	0.000821387	TAIR|locus:2008940 - symbol:APA1 "AT1G11910" species:3702 "Arabidopsis thaliana" [GO:0006508 "proteolysis" evidence=ISS;IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0004175 "endopeptidase activity" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR001461 InterPro:IPR001969 InterPro:IPR007856 InterPro:IPR009007 Pfam:PF00026 Pfam:PF05184 PRINTS:PR00792 PROSITE:PS00141 EMBL:CP002684 GO:GO:0005829 GO:GO:0009506 GO:GO:0005773 GO:GO:0006508 GO:GO:0006629 GO:GO:0009651 EMBL:AC002131 InterPro:IPR008138 InterPro:IPR011001 InterPro:IPR008139 Gene3D:G3DSA:1.10.225.10 Pfam:PF03489 SMART:SM00741 SUPFAM:SSF47862 PROSITE:PS50015 GO:GO:0004190 InterPro:IPR021109 SUPFAM:SSF50630 HOGENOM:HBG590923 Gene3D:G3DSA:2.40.70.10 PANTHER:PTHR13683 OMA:SGFMGID HSSP:P00797 KO:K08245 EMBL:AY056387 EMBL:AY056403 EMBL:AY063974 EMBL:AY088657 EMBL:BT001980 IPI:IPI00518049 PIR:F86253 RefSeq:NP_172655.1 UniGene:At.24544 UniGene:At.67307 ProteinModelPortal:O65390 SMR:O65390 IntAct:O65390 STRING:O65390 MEROPS:A01.020 PRIDE:O65390 ProMEX:O65390 EnsemblPlants:AT1G11910.1 GeneID:837740 KEGG:ath:AT1G11910 TAIR:At1g11910 InParanoid:O65390 PhylomeDB:O65390 ProtClustDB:CLSN2682210 ArrayExpress:O65390 Genevestigator:O65390 Uniprot:O65390
Leaf	Isotig00788	42	27	1.166	0.000821387	TAIR|locus:2008940 - symbol:APA1 "AT1G11910" species:3702 "Arabidopsis thaliana" [GO:0006508 "proteolysis" evidence=ISS;IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0004175 "endopeptidase activity" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR001461 InterPro:IPR001969 InterPro:IPR007856 InterPro:IPR009007 Pfam:PF00026 Pfam:PF05184 PRINTS:PR00792 PROSITE:PS00141 EMBL:CP002684 GO:GO:0005829 GO:GO:0009506 GO:GO:0005773 GO:GO:0006508 GO:GO:0006629 GO:GO:0009651 EMBL:AC002131 InterPro:IPR008138 InterPro:IPR011001 InterPro:IPR008139 Gene3D:G3DSA:1.10.225.10 Pfam:PF03489 SMART:SM00741 SUPFAM:SSF47862 PROSITE:PS50015 GO:GO:0004190 InterPro:IPR021109 SUPFAM:SSF50630 HOGENOM:HBG590923 Gene3D:G3DSA:2.40.70.10 PANTHER:PTHR13683 OMA:SGFMGID HSSP:P00797 KO:K08245 EMBL:AY056387 EMBL:AY056403 EMBL:AY063974 EMBL:AY088657 EMBL:BT001980 IPI:IPI00518049 PIR:F86253 RefSeq:NP_172655.1 UniGene:At.24544 UniGene:At.67307 ProteinModelPortal:O65390 SMR:O65390 IntAct:O65390 STRING:O65390 MEROPS:A01.020 PRIDE:O65390 ProMEX:O65390 EnsemblPlants:AT1G11910.1 GeneID:837740 KEGG:ath:AT1G11910 TAIR:At1g11910 InParanoid:O65390 PhylomeDB:O65390 ProtClustDB:CLSN2682210 ArrayExpress:O65390 Genevestigator:O65390 Uniprot:O65390
Leaf	Isotig00797	57	266	-1.693	1.55E-20	TAIR|locus:2160130 - symbol:THI1 "AT5G54770" species:3702 "Arabidopsis thaliana" [GO:0018131 "oxazole or thiazole biosynthetic process" evidence=IGI;IMP] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0042803 "protein homodimerization activity" evidence=IPI] [GO:0009409 "response to cold" evidence=IEP] [GO:0010319 "stromule" evidence=IDA] [GO:0008270 "zinc ion binding" evidence=IDA] [GO:0009228 "thiamine biosynthetic process" evidence=IGI;TAS] [GO:0006974 "response to DNA damage stimulus" evidence=IMP] InterPro:IPR002922 GO:GO:0005739 GO:GO:0009570 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0042803 GO:GO:0008270 GO:GO:0010319 GO:GO:0009409 GO:GO:0006974 GO:GO:0031969 GO:GO:0009579 GO:GO:0009228 EMBL:AB005232 GO:GO:0018131 EMBL:U17589 EMBL:AF419604 EMBL:AF428355 EMBL:AF428385 EMBL:AY054216 EMBL:AY058094 EMBL:AY143082 IPI:IPI00541324 PIR:S71191 RefSeq:NP_200288.1 UniGene:At.24888 PDB:1RP0 PDBsum:1RP0 ProteinModelPortal:Q38814 SMR:Q38814 IntAct:Q38814 STRING:Q38814 PRIDE:Q38814 EnsemblPlants:AT5G54770.1 GeneID:835567 KEGG:ath:AT5G54770 TAIR:At5g54770 eggNOG:COG1635 HOGENOM:HBG325902 InParanoid:Q38814 KO:K03146 OMA:GLHVDPL PhylomeDB:Q38814 ProtClustDB:PLN02661 ArrayExpress:Q38814 Genevestigator:Q38814 GermOnline:AT5G54770 PANTHER:PTHR10617:SF54 TIGRFAMs:TIGR00292 Uniprot:Q38814
Leaf	Isotig00798	57	266	-1.693	1.55E-20	TAIR|locus:2160130 - symbol:THI1 "AT5G54770" species:3702 "Arabidopsis thaliana" [GO:0018131 "oxazole or thiazole biosynthetic process" evidence=IGI;IMP] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009570 "chloroplast stroma"

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0042803 "protein homodimerization activity" evidence=IPI] [GO:0009409 "response to cold" evidence=IEP] [GO:0010319 "stromule" evidence=IDA] [GO:0008270 "zinc ion binding" evidence=IDA] [GO:0009228 "thiamine biosynthetic process" evidence=IGI;TAS] [GO:0006974 "response to DNA damage stimulus" evidence=IMP] InterPro:IPR002922 GO:GO:0005739 GO:GO:0009570 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0042803 GO:GO:0008270 GO:GO:0010319 GO:GO:0009409 GO:GO:0006974 GO:GO:0031969 GO:GO:0009579 GO:GO:0009228 EMBL:AB005232 GO:GO:0018131 EMBL:U17589 EMBL:AF419604 EMBL:AF428355 EMBL:AF428385 EMBL:AY054216 EMBL:AY058094 EMBL:AY143082 IPI:IPI00541324 PIR:S71191 RefSeq:NP_200288.1 UniGene:At.24888 PDB:1RP0 PDBsum:1RP0 ProteinModelPortal:Q38814 SMR:Q38814 IntAct:Q38814 STRING:Q38814 PRIDE:Q38814 EnsemblPlants:AT5G54770.1 GeneID:835567 KEGG:ath:AT5G54770 TAIR:At5g54770 eggNOG:COG1635 HOGENOM:HBG325902 InParanoid:Q38814 KO:K03146 OMA:GLHVDPL PhylomeDB:Q38814 ProtClustDB:PLN02661 ArrayExpress:Q38814 Genevestigator:Q38814 GermOnline:AT5G54770 PANTHER:PTHR10617:SF54 TIGRFAMs:TIGR00292 Uniprot:Q38814
Leaf	Isotig00799	64	266	-1.526	6.77E-18	TAIR|locus:2160130 - symbol:THI1 "AT5G54770" species:3702 "Arabidopsis thaliana" [GO:0018131 "oxazole or thiazole biosynthetic process" evidence=IGI;IMP] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0042803 "protein homodimerization activity" evidence=IPI] [GO:0009409 "response to cold" evidence=IEP] [GO:0010319 "stromule" evidence=IDA] [GO:0008270 "zinc ion binding" evidence=IDA] [GO:0009228 "thiamine biosynthetic process" evidence=IGI;TAS] [GO:0006974 "response to DNA damage stimulus" evidence=IMP] InterPro:IPR002922 GO:GO:0005739 GO:GO:0009570 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0042803 GO:GO:0008270 GO:GO:0010319 GO:GO:0009409 GO:GO:0006974 GO:GO:0031969 GO:GO:0009579 GO:GO:0009228 EMBL:AB005232 GO:GO:0018131 EMBL:U17589 EMBL:AF419604 EMBL:AF428355 EMBL:AF428385 EMBL:AY054216 EMBL:AY058094 EMBL:AY143082 IPI:IPI00541324 PIR:S71191 RefSeq:NP_200288.1 UniGene:At.24888 PDB:1RP0 PDBsum:1RP0 ProteinModelPortal:Q38814 SMR:Q38814 IntAct:Q38814 STRING:Q38814 PRIDE:Q38814 EnsemblPlants:AT5G54770.1 GeneID:835567 KEGG:ath:AT5G54770 TAIR:At5g54770 eggNOG:COG1635 HOGENOM:HBG325902 InParanoid:Q38814 KO:K03146 OMA:GLHVDPL PhylomeDB:Q38814 ProtClustDB:PLN02661 ArrayExpress:Q38814 Genevestigator:Q38814 GermOnline:AT5G54770 PANTHER:PTHR10617:SF54 TIGRFAMs:TIGR00292 Uniprot:Q38814
Leaf	Isotig00800	55	256	-1.690	9.14E-20	TAIR|locus:2160130 - symbol:THI1 "AT5G54770" species:3702 "Arabidopsis thaliana" [GO:0018131 "oxazole or thiazole biosynthetic process" evidence=IGI;IMP] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0042803 "protein homodimerization activity" evidence=IPI] [GO:0009409 "response to cold" evidence=IEP] [GO:0010319 "stromule" evidence=IDA] [GO:0008270 "zinc ion binding" evidence=IDA] [GO:0009228 "thiamine biosynthetic process" evidence=IGI;TAS] [GO:0006974 "response to DNA damage stimulus" evidence=IMP] InterPro:IPR002922 GO:GO:0005739 GO:GO:0009570 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0042803 GO:GO:0008270 GO:GO:0010319 GO:GO:0009409 GO:GO:0006974 GO:GO:0031969 GO:GO:0009579 GO:GO:0009228 EMBL:AB005232 GO:GO:0018131 EMBL:U17589 EMBL:AF419604 EMBL:AF428355 EMBL:AF428385 EMBL:AY054216 EMBL:AY058094 EMBL:AY143082 IPI:IPI00541324 PIR:S71191 RefSeq:NP_200288.1 UniGene:At.24888 PDB:1RP0 PDBsum:1RP0 ProteinModelPortal:Q38814 SMR:Q38814 IntAct:Q38814 STRING:Q38814 PRIDE:Q38814 EnsemblPlants:AT5G54770.1 GeneID:835567 KEGG:ath:AT5G54770 TAIR:At5g54770 eggNOG:COG1635 HOGENOM:HBG325902 InParanoid:Q38814 KO:K03146 OMA:GLHVDPL PhylomeDB:Q38814 ProtClustDB:PLN02661 ArrayExpress:Q38814 Genevestigator:Q38814 GermOnline:AT5G54770 PANTHER:PTHR10617:SF54 TIGRFAMs:TIGR00292 Uniprot:Q38814
Leaf	Isotig00801	64	266	-1.526	6.77E-18	TAIR|locus:2160130 - symbol:THI1 "AT5G54770" species:3702 "Arabidopsis thaliana" [GO:0018131 "oxazole or thiazole biosynthetic process" evidence=IGI;IMP] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0042803 "protein homodimerization activity" evidence=IPI] [GO:0009409 "response to cold" evidence=IEP] [GO:0010319 "stromule" evidence=IDA] [GO:0008270 "zinc ion binding" evidence=IDA] [GO:0009228 "thiamine biosynthetic process" evidence=IGI;TAS] [GO:0006974 "response to DNA damage stimulus" evidence=IMP] InterPro:IPR002922 GO:GO:0005739

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0009570 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0042803 GO:GO:0008270 GO:GO:0010319 GO:GO:0009409 GO:GO:0006974 GO:GO:0031969 GO:GO:0009579 GO:GO:0009228 EMBL:AB005232 GO:GO:0018131 EMBL:U17589 EMBL:AF419604 EMBL:AF428355 EMBL:AF428385 EMBL:AY054216 EMBL:AY058094 EMBL:AY143082 IPI:IPI00541324 PIR:S71191 RefSeq:NP_200288.1 UniGene:At.24888 PDB:1RP0 PDBsum:1RP0 ProteinModelPortal:Q38814 SMR:Q38814 IntAct:Q38814 STRING:Q38814 PRIDE:Q38814 EnsemblPlants:AT5G54770.1 GeneID:835567 KEGG:ath:AT5G54770 TAIR:At5g54770 eggNOG:COG1635 HOGENOM:HBG325902 InParanoid:Q38814 KO:K03146 OMA:GLHVDPL PhylomeDB:Q38814 ProtClustDB:PLN02661 ArrayExpress:Q38814 Genevestigator:Q38814 GermOnline:AT5G54770 PANTHER:PTHR10617:SF54 TIGRFAMs:TIGR00292 Uniprot:Q38814
Leaf	Isotig00802	55	256	-1.690	9.14E-20	TAIR|locus:2160130 - symbol:THI1 "AT5G54770" species:3702 "Arabidopsis thaliana" [GO:0018131 "oxazole or thiazole biosynthetic process" evidence=IGI;IMP] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0042803 "protein homodimerization activity" evidence=IPI] [GO:0009409 "response to cold" evidence=IEP] [GO:0010319 "stromule" evidence=IDA] [GO:0008270 "zinc ion binding" evidence=IDA] [GO:0009228 "thiamine biosynthetic process" evidence=IGI;TAS] [GO:0006974 "response to DNA damage stimulus" evidence=IMP] InterPro:IPR002922 GO:GO:0005739 GO:GO:0009570 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0042803 GO:GO:0008270 GO:GO:0010319 GO:GO:0009409 GO:GO:0006974 GO:GO:0031969 GO:GO:0009579 GO:GO:0009228 EMBL:AB005232 GO:GO:0018131 EMBL:U17589 EMBL:AF419604 EMBL:AF428355 EMBL:AF428385 EMBL:AY054216 EMBL:AY058094 EMBL:AY143082 IPI:IPI00541324 PIR:S71191 RefSeq:NP_200288.1 UniGene:At.24888 PDB:1RP0 PDBsum:1RP0 ProteinModelPortal:Q38814 SMR:Q38814 IntAct:Q38814 STRING:Q38814 PRIDE:Q38814 EnsemblPlants:AT5G54770.1 GeneID:835567 KEGG:ath:AT5G54770 TAIR:At5g54770 eggNOG:COG1635 HOGENOM:HBG325902 InParanoid:Q38814 KO:K03146 OMA:GLHVDPL PhylomeDB:Q38814 ProtClustDB:PLN02661 ArrayExpress:Q38814 Genevestigator:Q38814 GermOnline:AT5G54770 PANTHER:PTHR10617:SF54 TIGRFAMs:TIGR00292 Uniprot:Q38814
Leaf	Isotig00823	11	1	3.988	0.000330755	TAIR|locus:2025092 - symbol:SR45a "serine/arginine rich-like protein 45a" species:3702 "Arabidopsis thaliana" [GO:0000166 "nucleotide binding" evidence=IEA] [GO:0003676 "nucleic acid binding" evidence=IEA] [GO:0003723 "RNA binding" evidence=ISS] [GO:0008380 "RNA splicing" evidence=NAS] [GO:0009644 "response to high light intensity" evidence=IMP] [GO:0043484 "regulation of RNA splicing" evidence=IMP] InterPro:IPR000504 InterPro:IPR012677 Pfam:PF00076 PROSITE:PS50102 SMART:SM00360 EMBL:CP002684 GO:GO:0008380 GO:GO:0000166 Gene3D:G3DSA:3.30.70.330 GO:GO:0003676 GO:GO:0009644 GO:GO:0030529 GO:GO:0043484 eggNOG:COG0724 HSSP:Q14103 EMBL:BT005797 IPI:IPI00529615 RefSeq:NP_563787.2 UniGene:At.24511 ProteinModelPortal:Q84TH4 SMR:Q84TH4 STRING:Q84TH4 PRIDE:Q84TH4 EnsemblPlants:AT1G07350.1 GeneID:837246 KEGG:ath:AT1G07350 TAIR:At1g07350 InParanoid:Q84TH4 OMA:DPWTRES PhylomeDB:Q84TH4 ProtClustDB:CLSN2918464 Genevestigator:Q84TH4 Uniprot:Q84TH4
Leaf	Isotig00824	11	1	3.988	0.000330755	TAIR|locus:2025092 - symbol:SR45a "serine/arginine rich-like protein 45a" species:3702 "Arabidopsis thaliana" [GO:0000166 "nucleotide binding" evidence=IEA] [GO:0003676 "nucleic acid binding" evidence=IEA] [GO:0003723 "RNA binding" evidence=ISS] [GO:0008380 "RNA splicing" evidence=NAS] [GO:0009644 "response to high light intensity" evidence=IMP] [GO:0043484 "regulation of RNA splicing" evidence=IMP] InterPro:IPR000504 InterPro:IPR012677 Pfam:PF00076 PROSITE:PS50102 SMART:SM00360 EMBL:CP002684 GO:GO:0008380 GO:GO:0000166 Gene3D:G3DSA:3.30.70.330 GO:GO:0003676 GO:GO:0009644 GO:GO:0030529 GO:GO:0043484 eggNOG:COG0724 HSSP:Q14103 EMBL:BT005797 IPI:IPI00529615 RefSeq:NP_563787.2 UniGene:At.24511 ProteinModelPortal:Q84TH4 SMR:Q84TH4 STRING:Q84TH4 PRIDE:Q84TH4 EnsemblPlants:AT1G07350.1 GeneID:837246 KEGG:ath:AT1G07350 TAIR:At1g07350 InParanoid:Q84TH4 OMA:DPWTRES PhylomeDB:Q84TH4 ProtClustDB:CLSN2918464 Genevestigator:Q84TH4 Uniprot:Q84TH4
Leaf	Isotig00825	10	1	3.851	0.00071293	TAIR|locus:2025092 - symbol:SR45a "serine/arginine rich-like protein 45a" species:3702 "Arabidopsis thaliana" [GO:0000166 "nucleotide binding" evidence=IEA] [GO:0003676 "nucleic acid binding" evidence=IEA] [GO:0003723 "RNA binding" evidence=ISS] [GO:0008380 "RNA splicing" evidence=NAS] [GO:0009644 "response to high light intensity" evidence=IMP] [GO:0043484 "regulation of RNA splicing" evidence=IMP] InterPro:IPR000504 InterPro:IPR012677 Pfam:PF00076 PROSITE:PS50102 SMART:SM00360 EMBL:CP002684 GO:GO:0008380 GO:GO:0000166 Gene3D:G3DSA:3.30.70.330 GO:GO:0003676 GO:GO:0009644 GO:GO:0030529 GO:GO:0043484 eggNOG:COG0724 HSSP:Q14103 EMBL:BT005797 IPI:IPI00529615 RefSeq:NP_563787.2

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						UniGene:At.24511 ProteinModelPortal:Q84TH4 SMR:Q84TH4 STRING:Q84TH4 PRIDE:Q84TH4 EnsemblPlants:AT1G07350.1 GeneID:837246 KEGG:ath:AT1G07350 TAIR:At1g07350 InParanoid:Q84TH4 OMA:DPWTRES PhylomeDB:Q84TH4 ProtClustDB:CLSN2918464 Genevestigator:Q84TH4 Uniprot:Q84TH4
Leaf	Isotig00826	10	1	3.851	0.00071293	TAIR|locus:2025092 - symbol:SR45a "serine/arginine rich-like protein 45a" species:3702 "Arabidopsis thaliana" [GO:0000166 "nucleotide binding" evidence=IEA] [GO:0003676 "nucleic acid binding" evidence=IEA] [GO:0003723 "RNA binding" evidence=ISS] [GO:0008380 "RNA splicing" evidence=NAS] [GO:0009644 "response to high light intensity" evidence=IMP] [GO:0043484 "regulation of RNA splicing" evidence=IMP] InterPro:IPR000504 InterPro:IPR012677 Pfam:PF00076 PROSITE:PS50102 SMART:SM00360 EMBL:CP002684 GO:GO:0008380 GO:GO:0000166 Gene3D:G3DSA:3.30.70.330 GO:GO:0003676 GO:GO:0009644 GO:GO:0030529 GO:GO:0043484 eggNOG:COG0724 HSSP:Q14103 EMBL:BT005797 IPI:IPI00529615 RefSeq:NP_563787.2 UniGene:At.24511 ProteinModelPortal:Q84TH4 SMR:Q84TH4 STRING:Q84TH4 PRIDE:Q84TH4 EnsemblPlants:AT1G07350.1 GeneID:837246 KEGG:ath:AT1G07350 TAIR:At1g07350 InParanoid:Q84TH4 OMA:DPWTRES PhylomeDB:Q84TH4 ProtClustDB:CLSN2918464 Genevestigator:Q84TH4 Uniprot:Q84TH4
Leaf	Isotig00886	40	107	-0.891	0.000370043	TAIR|locus:2102385 - symbol:CHUP1 "CHLOROPLAST UNUSUAL POSITIONING 1" species:3702 "Arabidopsis thaliana" [GO:0009507 "chloroplast" evidence=IDA] [GO:0009707 "chloroplast outer membrane" evidence=IDA] [GO:0009902 "chloroplast relocation" evidence=IMP] EMBL:CP002686 GenomeReviews:BA000014_GR EMBL:AP001313 GO:GO:0009707 EMBL:AB087408 IPI:IPI00541711 RefSeq:NP_001189974.1 RefSeq:NP_189197.2 UniGene:At.27741 ProteinModelPortal:Q9LI74 STRING:Q9LI74 PRIDE:Q9LI74 EnsemblPlants:AT3G25690.1 EnsemblPlants:AT3G25690.2 GeneID:822157 KEGG:ath:AT3G25690 TAIR:At3g25690 eggNOG:NOG310144 HOGENOM:HBG589659 InParanoid:Q9LI74 OMA:GIPVDWL PhylomeDB:Q9LI74 ProtClustDB:CLSN2680868 Genevestigator:Q9LI74 GO:GO:0009902 Uniprot:Q9LI74
Leaf	Isotig00887	40	107	-0.891	0.000370043	TAIR|locus:2102385 - symbol:CHUP1 "CHLOROPLAST UNUSUAL POSITIONING 1" species:3702 "Arabidopsis thaliana" [GO:0009507 "chloroplast" evidence=IDA] [GO:0009707 "chloroplast outer membrane" evidence=IDA] [GO:0009902 "chloroplast relocation" evidence=IMP] EMBL:CP002686 GenomeReviews:BA000014_GR EMBL:AP001313 GO:GO:0009707 EMBL:AB087408 IPI:IPI00541711 RefSeq:NP_001189974.1 RefSeq:NP_189197.2 UniGene:At.27741 ProteinModelPortal:Q9LI74 STRING:Q9LI74 PRIDE:Q9LI74 EnsemblPlants:AT3G25690.1 EnsemblPlants:AT3G25690.2 GeneID:822157 KEGG:ath:AT3G25690 TAIR:At3g25690 eggNOG:NOG310144 HOGENOM:HBG589659 InParanoid:Q9LI74 OMA:GIPVDWL PhylomeDB:Q9LI74 ProtClustDB:CLSN2680868 Genevestigator:Q9LI74 GO:GO:0009902 Uniprot:Q9LI74
Leaf	Isotig00888	33	97	-1.027	0.00013526	TAIR|locus:2102385 - symbol:CHUP1 "CHLOROPLAST UNUSUAL POSITIONING 1" species:3702 "Arabidopsis thaliana" [GO:0009507 "chloroplast" evidence=IDA] [GO:0009707 "chloroplast outer membrane" evidence=IDA] [GO:0009902 "chloroplast relocation" evidence=IMP] EMBL:CP002686 GenomeReviews:BA000014_GR EMBL:AP001313 GO:GO:0009707 EMBL:AB087408 IPI:IPI00541711 RefSeq:NP_001189974.1 RefSeq:NP_189197.2 UniGene:At.27741 ProteinModelPortal:Q9LI74 STRING:Q9LI74 PRIDE:Q9LI74 EnsemblPlants:AT3G25690.1 EnsemblPlants:AT3G25690.2 GeneID:822157 KEGG:ath:AT3G25690 TAIR:At3g25690 eggNOG:NOG310144 HOGENOM:HBG589659 InParanoid:Q9LI74 OMA:GIPVDWL PhylomeDB:Q9LI74 ProtClustDB:CLSN2680868 Genevestigator:Q9LI74 GO:GO:0009902 Uniprot:Q9LI74
Leaf	Isotig00889	33	97	-1.027	0.00013526	TAIR|locus:2102385 - symbol:CHUP1 "CHLOROPLAST UNUSUAL POSITIONING 1" species:3702 "Arabidopsis thaliana" [GO:0009507 "chloroplast" evidence=IDA] [GO:0009707 "chloroplast outer membrane" evidence=IDA] [GO:0009902 "chloroplast relocation" evidence=IMP] EMBL:CP002686 GenomeReviews:BA000014_GR EMBL:AP001313 GO:GO:0009707 EMBL:AB087408 IPI:IPI00541711 RefSeq:NP_001189974.1 RefSeq:NP_189197.2 UniGene:At.27741 ProteinModelPortal:Q9LI74 STRING:Q9LI74 PRIDE:Q9LI74 EnsemblPlants:AT3G25690.1 EnsemblPlants:AT3G25690.2 GeneID:822157 KEGG:ath:AT3G25690 TAIR:At3g25690 eggNOG:NOG310144 HOGENOM:HBG589659 InParanoid:Q9LI74 OMA:GIPVDWL PhylomeDB:Q9LI74 ProtClustDB:CLSN2680868 Genevestigator:Q9LI74 GO:GO:0009902 Uniprot:Q9LI74
Leaf	Isotig00898	78	44	1.355	2.96E-07	TAIR|locus:2135897 - symbol:cpHsc70-1 "AT4G24280" species:3702 "Arabidopsis thaliana" [GO:0006457 "protein folding" evidence=TAS] [GO:0009408 "response to heat" evidence=IEP] [GO:0009532 "plastid stroma" evidence=TAS] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005524 "ATP binding" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0045036 "protein targeting to chloroplast" evidence=IMP]

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						InterPro:IPR001023 InterPro:IPR012725 PRINTS:PR00301 Pfam:PF00012 Prosite:PS00297 Prosite:PS00329 Prosite:PS01036 GO:GO:0005739 GO:GO:0005524 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0009570 GO:GO:0005634 GO:GO:0046686 GO:GO:0006457 GO:GO:0051082 GO:GO:0009941 GO:GO:0009409 EMBL:AL078637 EMBL:AL161561 GO:GO:0009579 GO:GO:0045036 eggNOG:COG0443 HOGENOM:HBG334976 InterPro:IPR018181 InterPro:IPR013126 PANTHER:PTHR19375 TIGRFAMs:TIGR02350 KO:K03283 EMBL:AY072138 EMBL:BT001950 IPI:IPI00531287 PIR:T09891 RefSeq:NP_194159.1 UniGene:At.25311 UniGene:At.67055 HSSP:P04475 ProteinModelPortal:Q9STW6 SMR:Q9STW6 STRING:Q9STW6 PRIDE:Q9STW6 ProMEX:Q9STW6 EnsemblPlants:AT4G24280.1 GeneID:828531 KEGG:ath:AT4G24280 TAIR:At4g24280 InParanoid:Q9STW6 OMA:TQSEINL PhylomeDB:Q9STW6 ProtClustDB:PLN03184 Genevestigator:Q9STW6 Uniprot:Q9STW6
Leaf	Isotig00899	78	43	1.388	1.78E-07	TAIR|locus:2135897 - symbol:cpHsc70-1 "AT4G24280" species:3702 "Arabidopsis thaliana" [GO:0006457 "protein folding" evidence=TAS] [GO:0009408 "response to heat" evidence=IEP] [GO:0009532 "plastid stroma" evidence=TAS] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005524 "ATP binding" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0045036 "protein targeting to chloroplast" evidence=IMP] InterPro:IPR001023 InterPro:IPR012725 PRINTS:PR00301 Pfam:PF00012 Prosite:PS00297 Prosite:PS00329 Prosite:PS01036 GO:GO:0005739 GO:GO:0005524 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0009570 GO:GO:0005634 GO:GO:0046686 GO:GO:0006457 GO:GO:0051082 GO:GO:0009941 GO:GO:0009409 EMBL:AL078637 EMBL:AL161561 GO:GO:0009579 GO:GO:0045036 eggNOG:COG0443 HOGENOM:HBG334976 InterPro:IPR018181 InterPro:IPR013126 PANTHER:PTHR19375 TIGRFAMs:TIGR02350 KO:K03283 EMBL:AY072138 EMBL:BT001950 IPI:IPI00531287 PIR:T09891 RefSeq:NP_194159.1 UniGene:At.25311 UniGene:At.67055 HSSP:P04475 ProteinModelPortal:Q9STW6 SMR:Q9STW6 STRING:Q9STW6 PRIDE:Q9STW6 ProMEX:Q9STW6 EnsemblPlants:AT4G24280.1 GeneID:828531 KEGG:ath:AT4G24280 TAIR:At4g24280 InParanoid:Q9STW6 OMA:TQSEINL PhylomeDB:Q9STW6 ProtClustDB:PLN03184 Genevestigator:Q9STW6 Uniprot:Q9STW6
Leaf	Isotig00900	78	44	1.355	2.96E-07	TAIR|locus:2135897 - symbol:cpHsc70-1 "AT4G24280" species:3702 "Arabidopsis thaliana" [GO:0006457 "protein folding" evidence=TAS] [GO:0009408 "response to heat" evidence=IEP] [GO:0009532 "plastid stroma" evidence=TAS] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005524 "ATP binding" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0045036 "protein targeting to chloroplast" evidence=IMP] InterPro:IPR001023 InterPro:IPR012725 PRINTS:PR00301 Pfam:PF00012 Prosite:PS00297 Prosite:PS00329 Prosite:PS01036 GO:GO:0005739 GO:GO:0005524 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0009570 GO:GO:0005634 GO:GO:0046686 GO:GO:0006457 GO:GO:0051082 GO:GO:0009941 GO:GO:0009409 EMBL:AL078637 EMBL:AL161561 GO:GO:0009579 GO:GO:0045036 eggNOG:COG0443 HOGENOM:HBG334976 InterPro:IPR018181 InterPro:IPR013126 PANTHER:PTHR19375 TIGRFAMs:TIGR02350 KO:K03283 EMBL:AY072138 EMBL:BT001950 IPI:IPI00531287 PIR:T09891 RefSeq:NP_194159.1 UniGene:At.25311 UniGene:At.67055 HSSP:P04475 ProteinModelPortal:Q9STW6 SMR:Q9STW6 STRING:Q9STW6 PRIDE:Q9STW6 ProMEX:Q9STW6 EnsemblPlants:AT4G24280.1 GeneID:828531 KEGG:ath:AT4G24280 TAIR:At4g24280 InParanoid:Q9STW6 OMA:TQSEINL PhylomeDB:Q9STW6 ProtClustDB:PLN03184 Genevestigator:Q9STW6 Uniprot:Q9STW6
Leaf	Isotig00901	78	43	1.388	1.78E-07	TAIR|locus:2135897 - symbol:cpHsc70-1 "AT4G24280" species:3702 "Arabidopsis thaliana" [GO:0006457 "protein folding" evidence=TAS] [GO:0009408 "response to heat" evidence=IEP] [GO:0009532 "plastid stroma" evidence=TAS] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005524 "ATP binding" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0045036 "protein targeting to chloroplast" evidence=IMP] InterPro:IPR001023 InterPro:IPR012725 PRINTS:PR00301 Pfam:PF00012 Prosite:PS00297 Prosite:PS00329

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						Prosite:PS01036 GO:GO:0005739 GO:GO:0005524 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0009570 GO:GO:0005634 GO:GO:0046686 GO:GO:0006457 GO:GO:0051082 GO:GO:0009941 GO:GO:0009409 EMBL:AL078637 EMBL:AL161561 GO:GO:0009579 GO:GO:0045036 eggNOG:COG0443 HOGENOM:HBG334976 InterPro:IPR018181 InterPro:IPR013126 PANTHER:PTHR19375 TIGRFAMs:TIGR02350 KO:K03283 EMBL:AY072138 EMBL:BT001950 IPI:IPI00531287 PIR:T09891 RefSeq:NP_194159.1 UniGene:At.25311 UniGene:At.67055 HSSP:P04475 ProteinModelPortal:Q9STW6 SMR:Q9STW6 STRING:Q9STW6 PRIDE:Q9STW6 ProMEX:Q9STW6 EnsemblPlants:AT4G24280.1 GeneID:828531 KEGG:ath:AT4G24280 TAIR:At4g24280 InParanoid:Q9STW6 OMA:TQSEINL PhylomeDB:Q9STW6 ProtClustDB:PLN03184 Genevestigator:Q9STW6 Uniprot:Q9STW6
Leaf	Isotig00902	13	49	-1.385	0.000582034	TAIR|locus:2029677 - symbol:NIA2 "AT1G37130" species:3702 "Arabidopsis thaliana" [GO:0006809 "nitric oxide biosynthetic process" evidence=IMP] [GO:0005773 "vacuole" evidence=IDA] [GO:0009416 "response to light stimulus" evidence=IMP] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009610 "response to symbiotic fungus" evidence=IEP] [GO:0008940 "nitrate reductase activity" evidence=ISS;IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009703 "nitrate reductase (NADH) activity" evidence=IDA] [GO:0042128 "nitrate assimilation" evidence=IMP] InterPro:IPR000572 InterPro:IPR001199 InterPro:IPR001433 InterPro:IPR001709 InterPro:IPR001834 InterPro:IPR005066 InterPro:IPR008335 InterPro:IPR012137 InterPro:IPR017927 InterPro:IPR017938 InterPro:IPR018506 InterPro:IPR022407 Pfam:PF00173 Pfam:PF00174 Pfam:PF00175 Pfam:PF03404 PIRSF:PIRSF000233 PRINTS:PR00363 PRINTS:PR00371 PRINTS:PR00406 PRINTS:PR00407 PROSITE:PS00191 PROSITE:PS00559 PROSITE:PS50255 PROSITE:PS51384 InterPro:IPR008333 Pfam:PF00970 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0005886 GO:GO:0005773 GO:GO:0009635 GO:GO:0009055 GO:GO:0050660 GO:GO:0020037 GO:GO:0009416 Gene3D:G3DSA:3.10.120.10 SUPFAM:SSF55856 InterPro:IPR014756 SUPFAM:SSF81296 GO:GO:0043546 eggNOG:COG0543 SUPFAM:SSF63380 GO:GO:0006809 GO:GO:0042128 GO:GO:0009610 GO:GO:0030151 KO:K00360 HOGENOM:HBG326850 ProtClustDB:PLN02252 GO:GO:0009703 Gene3D:G3DSA:2.60.40.650 Gene3D:G3DSA:3.90.420.10 SUPFAM:SSF56524 EMBL:J03240 EMBL:AC007505 EMBL:AF367272 EMBL:AF436835 EMBL:AY037183 EMBL:AY039914 EMBL:AY133530 EMBL:AY142568 EMBL:S45385 EMBL:X13435 IPI:IPI00544857 PIR:A31821 RefSeq:NP_174901.1 UniGene:At.23731 UniGene:At.72953 UniGene:At.74746 UniGene:At.74925 ProteinModelPortal:P11035 SMR:P11035 IntAct:P11035 STRING:P11035 PRIDE:P11035 ProMEX:P11035 EnsemblPlants:AT1G37130.1 GeneID:840630 KEGG:ath:AT1G37130 TAIR:At1g37130 InParanoid:P11035 OMA:RFEHPTQ PhylomeDB:P11035 BRENDA:1.7.1.1 Genevestigator:P11035 GermOnline:AT1G37130 Uniprot:P11035
Leaf	Isotig00903	13	49	-1.385	0.000582034	TAIR|locus:2029677 - symbol:NIA2 "AT1G37130" species:3702 "Arabidopsis thaliana" [GO:0006809 "nitric oxide biosynthetic process" evidence=IMP] [GO:0005773 "vacuole" evidence=IDA] [GO:0009416 "response to light stimulus" evidence=IMP] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009610 "response to symbiotic fungus" evidence=IEP] [GO:0008940 "nitrate reductase activity" evidence=ISS;IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009703 "nitrate reductase (NADH) activity" evidence=IDA] [GO:0042128 "nitrate assimilation" evidence=IMP] InterPro:IPR000572 InterPro:IPR001199 InterPro:IPR001433 InterPro:IPR001709 InterPro:IPR001834 InterPro:IPR005066 InterPro:IPR008335 InterPro:IPR012137 InterPro:IPR017927 InterPro:IPR017938 InterPro:IPR018506 InterPro:IPR022407 Pfam:PF00173 Pfam:PF00174 Pfam:PF00175 Pfam:PF03404 PIRSF:PIRSF000233 PRINTS:PR00363 PRINTS:PR00371 PRINTS:PR00406 PRINTS:PR00407 PROSITE:PS00191 PROSITE:PS00559 PROSITE:PS50255 PROSITE:PS51384 InterPro:IPR008333 Pfam:PF00970 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0005886 GO:GO:0005773 GO:GO:0009635 GO:GO:0009055 GO:GO:0050660 GO:GO:0020037 GO:GO:0009416 Gene3D:G3DSA:3.10.120.10 SUPFAM:SSF55856 InterPro:IPR014756 SUPFAM:SSF81296 GO:GO:0043546 eggNOG:COG0543 SUPFAM:SSF63380 GO:GO:0006809 GO:GO:0042128 GO:GO:0009610 GO:GO:0030151 KO:K00360 HOGENOM:HBG326850 ProtClustDB:PLN02252 GO:GO:0009703 Gene3D:G3DSA:2.60.40.650 Gene3D:G3DSA:3.90.420.10 SUPFAM:SSF56524 EMBL:J03240 EMBL:AC007505 EMBL:AF367272 EMBL:AF436835 EMBL:AY037183 EMBL:AY039914 EMBL:AY133530 EMBL:AY142568 EMBL:S45385 EMBL:X13435 IPI:IPI00544857 PIR:A31821 RefSeq:NP_174901.1 UniGene:At.23731 UniGene:At.72953 UniGene:At.74746 UniGene:At.74925 ProteinModelPortal:P11035 SMR:P11035 IntAct:P11035 STRING:P11035 PRIDE:P11035 ProMEX:P11035 EnsemblPlants:AT1G37130.1 GeneID:840630 KEGG:ath:AT1G37130 TAIR:At1g37130 InParanoid:P11035 OMA:RFEHPTQ PhylomeDB:P11035 BRENDA:1.7.1.1 Genevestigator:P11035 GermOnline:AT1G37130 Uniprot:P11035

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig00906	64	184	-0.995	3.03E-07	TAIR|locus:2075825 - symbol:SPD1 "SEEDLING PLASTID DEVELOPMENT 1" species:3702 "Arabidopsis thaliana" [GO:0000166 "nucleotide binding" evidence=IEA] [GO:0017111 "nucleoside-triphosphatase activity" evidence=IEA] [GO:0009507 "chloroplast" evidence=IDA] InterPro:IPR003593 SMART:SM00382 GO:GO:0005524 GO:GO:0009507 GO:GO:0017111 EMBL:AY056103 EMBL:BT004529 IPI:IPI00535779 ProteinModelPortal:Q940C8 SMR:Q940C8 STRING:Q940C8 PRIDE:Q940C8 TAIR:At3g10420 InParanoid:Q940C8 PhylomeDB:Q940C8 Genevestigator:Q940C8 Uniprot:Q940C8
Leaf	Isotig00907	64	183	-0.987	3.89E-07	TAIR|locus:2075825 - symbol:SPD1 "SEEDLING PLASTID DEVELOPMENT 1" species:3702 "Arabidopsis thaliana" [GO:0000166 "nucleotide binding" evidence=IEA] [GO:0017111 "nucleoside-triphosphatase activity" evidence=IEA] [GO:0009507 "chloroplast" evidence=IDA] InterPro:IPR003593 SMART:SM00382 GO:GO:0005524 GO:GO:0009507 GO:GO:0017111 EMBL:AY056103 EMBL:BT004529 IPI:IPI00535779 ProteinModelPortal:Q940C8 SMR:Q940C8 STRING:Q940C8 PRIDE:Q940C8 TAIR:At3g10420 InParanoid:Q940C8 PhylomeDB:Q940C8 Genevestigator:Q940C8 Uniprot:Q940C8
Leaf	Isotig00908	61	184	-1.064	6.20E-08	TAIR|locus:2075825 - symbol:SPD1 "SEEDLING PLASTID DEVELOPMENT 1" species:3702 "Arabidopsis thaliana" [GO:0000166 "nucleotide binding" evidence=IEA] [GO:0017111 "nucleoside-triphosphatase activity" evidence=IEA] [GO:0009507 "chloroplast" evidence=IDA] InterPro:IPR003593 SMART:SM00382 GO:GO:0005524 GO:GO:0009507 GO:GO:0017111 EMBL:AY056103 EMBL:BT004529 IPI:IPI00535779 ProteinModelPortal:Q940C8 SMR:Q940C8 STRING:Q940C8 PRIDE:Q940C8 TAIR:At3g10420 InParanoid:Q940C8 PhylomeDB:Q940C8 Genevestigator:Q940C8 Uniprot:Q940C8
Leaf	Isotig00909	61	183	-1.056	8.06E-08	TAIR|locus:2075825 - symbol:SPD1 "SEEDLING PLASTID DEVELOPMENT 1" species:3702 "Arabidopsis thaliana" [GO:0000166 "nucleotide binding" evidence=IEA] [GO:0017111 "nucleoside-triphosphatase activity" evidence=IEA] [GO:0009507 "chloroplast" evidence=IDA] InterPro:IPR003593 SMART:SM00382 GO:GO:0005524 GO:GO:0009507 GO:GO:0017111 EMBL:AY056103 EMBL:BT004529 IPI:IPI00535779 ProteinModelPortal:Q940C8 SMR:Q940C8 STRING:Q940C8 PRIDE:Q940C8 TAIR:At3g10420 InParanoid:Q940C8 PhylomeDB:Q940C8 Genevestigator:Q940C8 Uniprot:Q940C8
Leaf	Isotig00910	76	56	0.970	0.000108493	TAIR|locus:2077778 - symbol:AAC1 "AT3G08580" species:3702 "Arabidopsis thaliana" [GO:0005471 "ATP:ADP antiporter activity" evidence=ISS;IDA] [GO:0005743 "mitochondrial inner membrane" evidence=ISS] [GO:0006810 "transport" evidence=ISS] [GO:0005740 "mitochondrial envelope" evidence=TAS] [GO:0015865 "purine nucleotide transport" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR002067 InterPro:IPR002113 PRINTS:PR00926 PRINTS:PR00927 Pfam:PF00153 GO:GO:0016021 GO:GO:0005886 GO:GO:0005774 GO:GO:0005618 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005730 GO:GO:0005743 GO:GO:0009941 GO:GO:0005507 EMBL:AC012562 EMBL:AY034933 EMBL:AY042814 EMBL:AY054248 EMBL:AY074529 EMBL:BT000381 EMBL:BT002387 EMBL:X65549 EMBL:Z26399 IPI:IPI00546691 PIR:S21313 RefSeq:NP_187470.1 RefSeq:NP_850541.1 UniGene:At.15439 UniGene:At.23909 UniGene:At.67047 ProteinModelPortal:P31167 SMR:P31167 STRING:P31167 TCDB:2.A.29.1.5 PRIDE:P31167 EnsemblPlants:AT3G08580.1 EnsemblPlants:AT3G08580.2 GeneID:820005 KEGG:ath:AT3G08580 GeneFarm:3730 TAIR:At3g08580 eggNOG:NOG238123 HOGENOM:HBG610399 InParanoid:P31167 KO:K05863 OMA:GQAVKYD PhylomeDB:P31167 ProtClustDB:CLSN2684949 ArrayExpress:P31167 Genevestigator:P31167 GermOnline:AT3G08580 GO:GO:0005471 GO:GO:0015865 InterPro:IPR018108 InterPro:IPR023395 Gene3D:G3DSA:1.50.40.10 SUPFAM:SSF103506 PROSITE:PS50920 Uniprot:P31167
Leaf	Isotig00912	75	56	0.950	0.000155616	TAIR|locus:2077778 - symbol:AAC1 "AT3G08580" species:3702 "Arabidopsis thaliana" [GO:0005471 "ATP:ADP antiporter activity" evidence=ISS;IDA] [GO:0005743 "mitochondrial inner membrane" evidence=ISS] [GO:0006810 "transport" evidence=ISS] [GO:0005740 "mitochondrial envelope" evidence=TAS] [GO:0015865 "purine nucleotide transport" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR002067 InterPro:IPR002113 PRINTS:PR00926 PRINTS:PR00927 Pfam:PF00153 GO:GO:0016021

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0005886 GO:GO:0005774 GO:GO:0005618 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005730 GO:GO:0005743 GO:GO:0009941 GO:GO:0005507 EMBL:AC012562 EMBL:AY034933 EMBL:AY042814 EMBL:AY054248 EMBL:AY074529 EMBL:BT000381 EMBL:BT002387 EMBL:X65549 EMBL:Z26399 IPI:IPI00546691 PIR:S21313 RefSeq:NP_187470.1 RefSeq:NP_850541.1 UniGene:At.15439 UniGene:At.23909 UniGene:At.67047 ProteinModelPortal:P31167 SMR:P31167 STRING:P31167 TCDB:2.A.29.1.5 PRIDE:P31167 EnsemblPlants:AT3G08580.1 EnsemblPlants:AT3G08580.2 GeneID:820005 KEGG:ath:AT3G08580 GeneFarm:3730 TAIR:At3g08580 eggNOG:NOG238123 HOGENOM:HBG610399 InParanoid:P31167 KO:K05863 OMA:GQAVKYD PhylomeDB:P31167 ProtClustDB:CLSN2684949 ArrayExpress:P31167 Genevestigator:P31167 GermOnline:AT3G08580 GO:GO:0005471 GO:GO:0015865 InterPro:IPR018108 InterPro:IPR023395 Gene3D:G3DSA:1.50.40.10 SUPFAM:SSF103506 PROSITE:PS50920 Uniprot:P31167
Leaf	Isotig00918	30	97	-1.164	2.38E-05	TAIR|locus:2131591 - symbol:CAT2 "AT4G35090" species:3702 "Arabidopsis thaliana" [GO:0004096 "catalase activity" evidence=ISS;IMP] [GO:0005777 "peroxisome" evidence=IDA;NAS] [GO:0042744 "hydrogen peroxide catabolic process" evidence=NAS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0006995 "cellular response to nitrogen starvation" evidence=IEP] [GO:0009970 "cellular response to sulfate starvation" evidence=IEP] [GO:0016036 "cellular response to phosphate starvation" evidence=IEP] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0010319 "stromule" evidence=IDA] [GO:0006979 "response to oxidative stress" evidence=IMP] [GO:0008219 "cell death" evidence=IMP] [GO:0009648 "photoperiodism" evidence=IMP] [GO:0045454 "cell redox homeostasis" evidence=IMP] [GO:0009416 "response to light stimulus" evidence=IEP] [GO:0005515 "protein binding" evidence=IPI] [GO:0050897 "cobalt ion binding" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] InterPro:IPR002226 InterPro:IPR011614 InterPro:IPR018028 InterPro:IPR020835 InterPro:IPR024708 InterPro:IPR024711 Pfam:PF00199 PIRSF:PIRSF038928 PRINTS:PR00067 PROSITE:PS00437 PROSITE:PS00438 PROSITE:PS51402 SMART:SM01060 InterPro:IPR010582 GO:GO:0005739 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0009507 GO:GO:0005515 GO:GO:0008219 GO:GO:0010319 GO:GO:0009409 GO:GO:0009514 GO:GO:0020037 GO:GO:0050897 EMBL:AL022023 EMBL:AL161586 GO:GO:0016036 GO:GO:0045454 GO:GO:0022626 GO:GO:0006995 GO:GO:0042744 GO:GO:0009970 GO:GO:0004096 eggNOG:COG0753 KO:K03781 Gene3D:G3DSA:2.40.180.10 PANTHER:PTHR11465 Pfam:PF06628 SUPFAM:SSF56634 HOGENOM:HBG339355 ProtClustDB:PLN02609 OMA:DWVYNNT EMBL:X64271 EMBL:X94447 EMBL:AY074301 EMBL:AY113854 IPI:IPI00520641 PIR:T05779 RefSeq:NP_195235.1 UniGene:At.24350 UniGene:At.64718 ProteinModelPortal:P25819 SMR:P25819 IntAct:P25819 STRING:P25819 PeroxiBase:5141 PRIDE:P25819 ProMEX:P25819 EnsemblPlants:AT4G35090.1 GeneID:829661 KEGG:ath:AT4G35090 TAIR:At4g35090 InParanoid:P25819 PhylomeDB:P25819 BioCyc:MetaCyc:AT4G35090-MONOMER ArrayExpress:P25819 Genevestigator:P25819 GO:GO:0009648 Uniprot:P25819
Leaf	Isotig00921	7	37	-1.873	0.000203981	TAIR|locus:2035109 - symbol:LEA7 "AT1G52690" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0009793 "embryo development ending in seed dormancy" evidence=ISS] EMBL:CP002684 EMBL:AC008016 EMBL:AF385732 EMBL:AY093968 EMBL:AY087466 EMBL:BT000737 EMBL:BT000739 EMBL:X91919 IPI:IPI00526817 PIR:H96567 RefSeq:NP_175678.1 RefSeq:NP_974009.1 UniGene:At.21275 STRING:Q96270 PRIDE:Q96270 ProMEX:Q96270 DNASU:841701 EnsemblPlants:AT1G52690.1 EnsemblPlants:AT1G52690.2 GeneID:841701 KEGG:ath:AT1G52690 TAIR:At1g52690 InParanoid:Q96270 OMA:MASHQEQ PhylomeDB:Q96270 ProtClustDB:CLSN2679745 ArrayExpress:Q96270 Genevestigator:Q96270 Uniprot:Q96270
Leaf	Isotig00922	236	1261	-1.889	1.41E-105	TAIR|locus:2063922 - symbol:RCA "AT2G39730" species:3702 "Arabidopsis thaliana" [GO:0009507 "chloroplast" evidence=IDA;NAS] [GO:0030234 "enzyme regulator activity" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0005524 "ATP binding" evidence=IDA] [GO:0043531 "ADP binding" evidence=IDA] [GO:0046863 "ribulose-1,5-bisphosphate carboxylase/oxygenase activator activity" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0010319 "stromule" evidence=IDA] [GO:0042742 "defense response to bacterium" evidence=IEP] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009753 "response to jasmonic acid stimulus" evidence=IEP] [GO:0010150 "leaf senescence" evidence=IMP] [GO:0009416 "response to

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						light stimulus" evidence=IEP] InterPro:IPR003959 Pfam:PF00004 GO:GO:0005524 GO:GO:0048046 GO:GO:0005634 GO:GO:0005618 GO:GO:0042742 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009753 GO:GO:0009941 GO:GO:0043531 GO:GO:0010150 GO:GO:0010319 GO:GO:0009409 GO:GO:0009416 GO:GO:0009535 GO:GO:0010287 EMBL:AC003000 UniGene:At.25263 EMBL:X14212 EMBL:M86720 EMBL:AY052703 EMBL:AF325049 EMBL:AY056108 EMBL:BT000710 EMBL:AY088487 IPI:IPI00518163 IPI:IPI00526733 PIR:S04048 PIR:T01002 PIR:T01003 RefSeq:NP_565913.1 RefSeq:NP_850320.1 UniGene:At.25299 UniGene:At.25319 UniGene:At.47493 ProteinModelPortal:P10896 SMR:P10896 IntAct:P10896 STRING:P10896 SWISS-2DPAGE:P10896 World-2DPAGE:0003:P10896 PRIDE:P10896 ProMEX:P10896 EnsemblPlants:AT2G39730.1 GeneID:818558 KEGG:ath:AT2G39730 TAIR:At2g39730 eggNOG:NOG316327 HOGENOM:HBG320501 InParanoid:P10896 OMA:WAPTRDD PhylomeDB:P10896 ProtClustDB:PLN00020 ArrayExpress:P10896 Genevestigator:P10896 GO:GO:0046863 Uniprot:P10896
Leaf	Isotig00923	230	1254	-1.918	3.91E-107	TAIR|locus:2063922 - symbol:RCA "AT2G39730" species:3702 "Arabidopsis thaliana" [GO:0009507 "chloroplast" evidence=IDA;NAS] [GO:0030234 "enzyme regulator activity" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0005524 "ATP binding" evidence=IDA] [GO:0043531 "ADP binding" evidence=IDA] [GO:0046863 "ribulose-1,5-bisphosphate carboxylase/oxygenase activator activity" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0010319 "stromule" evidence=IDA] [GO:0042742 "defense response to bacterium" evidence=IEP] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009753 "response to jasmonic acid stimulus" evidence=IEP] [GO:0010150 "leaf senescence" evidence=IMP] [GO:0009416 "response to light stimulus" evidence=IEP] InterPro:IPR003959 Pfam:PF00004 GO:GO:0005524 GO:GO:0048046 GO:GO:0005634 GO:GO:0005618 GO:GO:0042742 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009753 GO:GO:0009941 GO:GO:0043531 GO:GO:0010150 GO:GO:0010319 GO:GO:0009409 GO:GO:0009416 GO:GO:0009535 GO:GO:0010287 EMBL:AC003000 UniGene:At.25263 EMBL:X14212 EMBL:M86720 EMBL:AY052703 EMBL:AF325049 EMBL:AY056108 EMBL:BT000710 EMBL:AY088487 IPI:IPI00518163 IPI:IPI00526733 PIR:S04048 PIR:T01002 PIR:T01003 RefSeq:NP_565913.1 RefSeq:NP_850320.1 UniGene:At.25299 UniGene:At.25319 UniGene:At.47493 ProteinModelPortal:P10896 SMR:P10896 IntAct:P10896 STRING:P10896 SWISS-2DPAGE:P10896 World-2DPAGE:0003:P10896 PRIDE:P10896 ProMEX:P10896 EnsemblPlants:AT2G39730.1 GeneID:818558 KEGG:ath:AT2G39730 TAIR:At2g39730 eggNOG:NOG316327 HOGENOM:HBG320501 InParanoid:P10896 OMA:WAPTRDD PhylomeDB:P10896 ProtClustDB:PLN00020 ArrayExpress:P10896 Genevestigator:P10896 GO:GO:0046863 Uniprot:P10896
Leaf	Isotig00924	229	1244	-1.913	6.53E-106	TAIR|locus:2063922 - symbol:RCA "AT2G39730" species:3702 "Arabidopsis thaliana" [GO:0009507 "chloroplast" evidence=IDA;NAS] [GO:0030234 "enzyme regulator activity" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0005524 "ATP binding" evidence=IDA] [GO:0043531 "ADP binding" evidence=IDA] [GO:0046863 "ribulose-1,5-bisphosphate carboxylase/oxygenase activator activity" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0010319 "stromule" evidence=IDA] [GO:0042742 "defense response to bacterium" evidence=IEP] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009753 "response to jasmonic acid stimulus" evidence=IEP] [GO:0010150 "leaf senescence" evidence=IMP] [GO:0009416 "response to light stimulus" evidence=IEP] InterPro:IPR003959 Pfam:PF00004 GO:GO:0005524 GO:GO:0048046 GO:GO:0005634 GO:GO:0005618 GO:GO:0042742 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009753 GO:GO:0009941 GO:GO:0043531 GO:GO:0010150 GO:GO:0010319 GO:GO:0009409 GO:GO:0009416 GO:GO:0009535 GO:GO:0010287 EMBL:AC003000 UniGene:At.25263 EMBL:X14212 EMBL:M86720 EMBL:AY052703 EMBL:AF325049 EMBL:AY056108 EMBL:BT000710 EMBL:AY088487 IPI:IPI00518163 IPI:IPI00526733 PIR:S04048 PIR:T01002 PIR:T01003 RefSeq:NP_565913.1 RefSeq:NP_850320.1 UniGene:At.25299 UniGene:At.25319 UniGene:At.47493 ProteinModelPortal:P10896 SMR:P10896 IntAct:P10896 STRING:P10896 SWISS-2DPAGE:P10896 World-2DPAGE:0003:P10896 PRIDE:P10896 ProMEX:P10896 EnsemblPlants:AT2G39730.1 GeneID:818558 KEGG:ath:AT2G39730 TAIR:At2g39730 eggNOG:NOG316327 HOGENOM:HBG320501 InParanoid:P10896 OMA:WAPTRDD PhylomeDB:P10896 ProtClustDB:PLN00020 ArrayExpress:P10896 Genevestigator:P10896 GO:GO:0046863 Uniprot:P10896

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig00925	235	1251	-1.883	2.32E-104	TAIR|locus:2063922 - symbol:RCA "AT2G39730" species:3702 "Arabidopsis thaliana" [GO:0009507 "chloroplast" evidence=IDA;NAS] [GO:0030234 "enzyme regulator activity" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0005524 "ATP binding" evidence=IDA] [GO:0043531 "ADP binding" evidence=IDA] [GO:0046863 "ribulose-1,5-bisphosphate carboxylase/oxygenase activator activity" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0010319 "stromule" evidence=IDA] [GO:0042742 "defense response to bacterium" evidence=IEP] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009753 "response to jasmonic acid stimulus" evidence=IEP] [GO:0010150 "leaf senescence" evidence=IMP] [GO:0009416 "response to light stimulus" evidence=IEP] InterPro:IPR003959 Pfam:PF00004 GO:GO:0005524 GO:GO:0048046 GO:GO:0005634 GO:GO:0005618 GO:GO:0042742 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009753 GO:GO:0009941 GO:GO:0043531 GO:GO:0010150 GO:GO:0010319 GO:GO:0009409 GO:GO:0009416 GO:GO:0009535 GO:GO:0010287 EMBL:AC003000 UniGene:At.25263 EMBL:X14212 EMBL:M86720 EMBL:AY052703 EMBL:AF325049 EMBL:AY056108 EMBL:BT000710 EMBL:AY088487 IPI:IPI00518163 IPI:IPI00526733 PIR:S04048 PIR:T01002 PIR:T01003 RefSeq:NP_565913.1 RefSeq:NP_850320.1 UniGene:At.25299 UniGene:At.25319 UniGene:At.47493 ProteinModelPortal:P10896 SMR:P10896 IntAct:P10896 STRING:P10896 SWISS-2DPAGE:P10896 World-2DPAGE:0003:P10896 PRIDE:P10896 ProMEX:P10896 EnsemblPlants:AT2G39730.1 GeneID:818558 KEGG:ath:AT2G39730 TAIR:At2g39730 eggNOG:NOG316327 HOGENOM:HBG320501 InParanoid:P10896 OMA:WAPTRDD PhylomeDB:P10896 ProtClustDB:PLN00020 ArrayExpress:P10896 Genevestigator:P10896 GO:GO:0046863 Uniprot:P10896
Leaf	Isotig00954	13	62	-1.725	5.56E-06	UNIPROTKB|Q9ZS34 - symbol:CHLP "Geranylgeranyl diphosphate reductase, chloroplastic" species:4097 "Nicotiana tabacum" [GO:0010189 "vitamin E biosynthetic process" evidence=IMP] [GO:0015995 "chlorophyll biosynthetic process" evidence=IMP] [GO:0033385 "geranylgeranyl diphosphate metabolic process" evidence=IMP] [GO:0033521 "phytyl diphosphate biosynthetic process" evidence=IMP] [GO:0045550 "geranylgeranyl reductase activity" evidence=NAS] InterPro:IPR003042 InterPro:IPR010253 InterPro:IPR011774 InterPro:IPR011777 InterPro:IPR016040 InterPro:IPR023753 Pfam:PF07992 PRINTS:PR00420 GO:GO:0009507 GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 GO:GO:0015995 GO:GO:0045550 GO:GO:0015979 GO:GO:0016628 TIGRFAMs:TIGR02023 TIGRFAMs:TIGR02028 TIGRFAMs:TIGR02032 EMBL:AJ007789 ProteinModelPortal:Q9ZS34 BioCyc:MetaCyc:MONOMER-14870 GO:GO:0033385 GO:GO:0033521 GO:GO:0010189 Uniprot:Q9ZS34
Leaf	Isotig00955	14	72	-1.834	3.28E-07	UNIPROTKB|Q9ZS34 - symbol:CHLP "Geranylgeranyl diphosphate reductase, chloroplastic" species:4097 "Nicotiana tabacum" [GO:0010189 "vitamin E biosynthetic process" evidence=IMP] [GO:0015995 "chlorophyll biosynthetic process" evidence=IMP] [GO:0033385 "geranylgeranyl diphosphate metabolic process" evidence=IMP] [GO:0033521 "phytyl diphosphate biosynthetic process" evidence=IMP] [GO:0045550 "geranylgeranyl reductase activity" evidence=NAS] InterPro:IPR003042 InterPro:IPR010253 InterPro:IPR011774 InterPro:IPR011777 InterPro:IPR016040 InterPro:IPR023753 Pfam:PF07992 PRINTS:PR00420 GO:GO:0009507 GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 GO:GO:0015995 GO:GO:0045550 GO:GO:0015979 GO:GO:0016628 TIGRFAMs:TIGR02023 TIGRFAMs:TIGR02028 TIGRFAMs:TIGR02032 EMBL:AJ007789 ProteinModelPortal:Q9ZS34 BioCyc:MetaCyc:MONOMER-14870 GO:GO:0033385 GO:GO:0033521 GO:GO:0010189 Uniprot:Q9ZS34
Leaf	Isotig00977	28	14	1.529	0.000772232	TAIR|locus:2092502 - symbol:HCHIB "AT3G12500" species:3702 "Arabidopsis thaliana" [GO:0004568 "chitinase activity" evidence=ISS;IDA] [GO:0050832 "defense response to fungus" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009871 "jasmonic acid and ethylene-dependent systemic resistance, ethylene mediated signaling pathway" evidence=IGI] InterPro:IPR000726 InterPro:IPR001002 InterPro:IPR016283 InterPro:IPR018371 Pfam:PF00182 Pfam:PF00187 PIRSF:PIRSF001060 PRINTS:PR00451 ProDom:PD000609 PROSITE:PS00026 PROSITE:PS00773 PROSITE:PS00774 PROSITE:PS50941 SMART:SM00270 GO:GO:0005829 GO:GO:0046686 GO:GO:0005774 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0050832 GO:GO:0031640 GO:GO:0009626 CAZy:CBM18 GO:GO:0008061 Gene3D:G3DSA:3.30.60.10 SUPFAM:SSF57016 EMBL:AP002047 EMBL:AC069474 GO:GO:0006032 GO:GO:0016998 KO:K01183 CAZy:GH19 InterPro:IPR023346 SUPFAM:SSF53955

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EMBL:M38240 EMBL:AB023448 EMBL:AB023449 EMBL:AB023450 EMBL:AB023451 EMBL:AB023452 EMBL:AB023453 EMBL:AB023454 EMBL:AB023455 EMBL:AB023456 EMBL:AB023457 EMBL:AB023458 EMBL:AB023459 EMBL:AB023460 EMBL:AB023461 EMBL:AB023462 EMBL:AB023463 EMBL:AY054628 EMBL:AY081519 IPI:IPI00537422 PIR:B45511 RefSeq:NP_566426.2 UniGene:At.296 UniGene:At.75237 ProteinModelPortal:P19171 SMR:P19171 STRING:P19171 PRIDE:P19171 EnsemblPlants:AT3G12500.1 GeneID:820429 KEGG:ath:AT3G12500 TAIR:At3g12500 eggNOG:COG3979 HOGENOM:HBG748705 InParanoid:P19171 PhylomeDB:P19171 ProtClustDB:CLSN2914971 ArrayExpress:P19171 Genevestigator:P19171 GermOnline:AT3G12500 GO:GO:0009871 Uniprot:P19171
Leaf	Isotig01014	106	227	-0.570	0.000452222	TAIR|locus:2146718 - symbol:GLU1 "glutamate synthase 1" species:3702 "Arabidopsis thaliana" [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009416 "response to light stimulus" evidence=IEP] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009853 "photorespiration" evidence=IMP;TAS] [GO:0016041 "glutamate synthase (ferredoxin) activity" evidence=ISS;IDA] [GO:0080114 "positive regulation of glycine hydroxymethyltransferase activity" evidence=IDA] InterPro:IPR000583 InterPro:IPR002489 InterPro:IPR002932 InterPro:IPR006982 InterPro:IPR013785 Pfam:PF00310 Pfam:PF01493 Pfam:PF01645 Pfam:PF04898 GO:GO:0005739 GO:GO:0048046 GO:GO:0009570 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005515 GO:GO:0016020 Gene3D:G3DSA:3.20.20.70 GO:GO:0046872 GO:GO:0009941 GO:GO:0009416 GO:GO:0051538 GO:GO:0006537 GO:GO:0009853 GO:GO:0006541 InterPro:IPR017932 PROSITE:PS51278 EMBL:AL391716 HOGENOM:HBG313993 Gene3D:G3DSA:2.160.20.60 SUPFAM:SSF69336 EMBL:Y09667 EMBL:U39287 IPI:IPI00539225 IPI:IPI00540577 RefSeq:NP_568134.1 RefSeq:NP_850763.1 UniGene:At.21961 UniGene:At.67926 ProteinModelPortal:Q9ZNZ7 IntAct:Q9ZNZ7 STRING:Q9ZNZ7 PRIDE:Q9ZNZ7 ProMEX:Q9ZNZ7 EnsemblPlants:AT5G04140.2 GeneID:830292 KEGG:ath:AT5G04140 TAIR:At5g04140 eggNOG:COG0069 InParanoid:Q9ZNZ7 KO:K00284 OMA:RTGGEYH PhylomeDB:Q9ZNZ7 ProtClustDB:CLSN2913236 ArrayExpress:Q9ZNZ7 Genevestigator:Q9ZNZ7 GermOnline:AT5G04140 GO:GO:0016041 GO:GO:0080114 Uniprot:Q9ZNZ7
Leaf	Isotig01015	92	221	-0.735	1.42E-05	TAIR|locus:2146718 - symbol:GLU1 "glutamate synthase 1" species:3702 "Arabidopsis thaliana" [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009416 "response to light stimulus" evidence=IEP] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009853 "photorespiration" evidence=IMP;TAS] [GO:0016041 "glutamate synthase (ferredoxin) activity" evidence=ISS;IDA] [GO:0080114 "positive regulation of glycine hydroxymethyltransferase activity" evidence=IDA] InterPro:IPR000583 InterPro:IPR002489 InterPro:IPR002932 InterPro:IPR006982 InterPro:IPR013785 Pfam:PF00310 Pfam:PF01493 Pfam:PF01645 Pfam:PF04898 GO:GO:0005739 GO:GO:0048046 GO:GO:0009570 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005515 GO:GO:0016020 Gene3D:G3DSA:3.20.20.70 GO:GO:0046872 GO:GO:0009941 GO:GO:0009416 GO:GO:0051538 GO:GO:0006537 GO:GO:0009853 GO:GO:0006541 InterPro:IPR017932 PROSITE:PS51278 EMBL:AL391716 HOGENOM:HBG313993 Gene3D:G3DSA:2.160.20.60 SUPFAM:SSF69336 EMBL:Y09667 EMBL:U39287 IPI:IPI00539225 IPI:IPI00540577 RefSeq:NP_568134.1 RefSeq:NP_850763.1 UniGene:At.21961 UniGene:At.67926 ProteinModelPortal:Q9ZNZ7 IntAct:Q9ZNZ7 STRING:Q9ZNZ7 PRIDE:Q9ZNZ7 ProMEX:Q9ZNZ7 EnsemblPlants:AT5G04140.2 GeneID:830292 KEGG:ath:AT5G04140 TAIR:At5g04140 eggNOG:COG0069 InParanoid:Q9ZNZ7 KO:K00284 OMA:RTGGEYH PhylomeDB:Q9ZNZ7 ProtClustDB:CLSN2913236 ArrayExpress:Q9ZNZ7 Genevestigator:Q9ZNZ7 GermOnline:AT5G04140 GO:GO:0016041 GO:GO:0080114 Uniprot:Q9ZNZ7
Leaf	Isotig01016	90	224	-0.787	3.60E-06	TAIR|locus:2146718 - symbol:GLU1 "glutamate synthase 1" species:3702 "Arabidopsis thaliana" [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009416 "response to light stimulus" evidence=IEP] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009853 "photorespiration" evidence=IMP;TAS] [GO:0016041 "glutamate synthase (ferredoxin) activity" evidence=ISS;IDA] [GO:0080114 "positive regulation of glycine hydroxymethyltransferase activity" evidence=IDA] InterPro:IPR000583 InterPro:IPR002489 InterPro:IPR002932 InterPro:IPR006982 InterPro:IPR013785 Pfam:PF00310 Pfam:PF01493 Pfam:PF01645 Pfam:PF04898

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0005739 GO:GO:0048046 GO:GO:0009570 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005515 GO:GO:0016020 Gene3D:G3DSA:3.20.20.70 GO:GO:0046872 GO:GO:0009941 GO:GO:0009416 GO:GO:0051538 GO:GO:0006537 GO:GO:0009853 GO:GO:0006541 InterPro:IPR017932 PROSITE:PS51278 EMBL:AL391716 HOGENOM:HBG313993 Gene3D:G3DSA:2.160.20.60 SUPFAM:SSF69336 EMBL:Y09667 EMBL:U39287 IPI:IPI00539225 IPI:IPI00540577 RefSeq:NP_568134.1 RefSeq:NP_850763.1 UniGene:At.21961 UniGene:At.67926 ProteinModelPortal:Q9ZNZ7 IntAct:Q9ZNZ7 STRING:Q9ZNZ7 PRIDE:Q9ZNZ7 ProMEX:Q9ZNZ7 EnsemblPlants:AT5G04140.2 GeneID:830292 KEGG:ath:AT5G04140 TAIR:At5g04140 eggNOG:COG0069 InParanoid:Q9ZNZ7 KO:K00284 OMA:RTGGEYH PhylomeDB:Q9ZNZ7 ProtClustDB:CLSN2913236 ArrayExpress:Q9ZNZ7 Genevestigator:Q9ZNZ7 GermOnline:AT5G04140 GO:GO:0016041 GO:GO:0080114 Uniprot:Q9ZNZ7
Leaf	Isotig01020	28	3	3.751	1.99E-08	TAIR|locus:2052005 - symbol:OZF1 "AT2G19810" species:3702 "Arabidopsis thaliana" [GO:0003676 "nucleic acid binding" evidence=ISS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=TAS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0006979 "response to oxidative stress" evidence=IMP] InterPro:IPR000571 PROSITE:PS50103 SMART:SM00356 GO:GO:0005886 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0006979 GO:GO:0006355 GO:GO:0003677 GO:GO:0008270 EMBL:AC005169 EMBL:AY136395 EMBL:BT002114 EMBL:AY084253 IPI:IPI00535519 PIR:D84581 RefSeq:NP_179571.1 UniGene:At.12895 ProteinModelPortal:O82199 SMR:O82199 PRIDE:O82199 EnsemblPlants:AT2G19810.1 GeneID:816500 KEGG:ath:AT2G19810 TAIR:At2g19810 eggNOG:NOG288631 HOGENOM:HBG744620 InParanoid:O82199 OMA:WENGLEE PhylomeDB:O82199 ProtClustDB:CLSN2691160 ArrayExpress:O82199 Genevestigator:O82199 Uniprot:O82199
Leaf	Isotig01021	28	3	3.751	1.99E-08	TAIR|locus:2052005 - symbol:OZF1 "AT2G19810" species:3702 "Arabidopsis thaliana" [GO:0003676 "nucleic acid binding" evidence=ISS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=TAS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0006979 "response to oxidative stress" evidence=IMP] InterPro:IPR000571 PROSITE:PS50103 SMART:SM00356 GO:GO:0005886 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0006979 GO:GO:0006355 GO:GO:0003677 GO:GO:0008270 EMBL:AC005169 EMBL:AY136395 EMBL:BT002114 EMBL:AY084253 IPI:IPI00535519 PIR:D84581 RefSeq:NP_179571.1 UniGene:At.12895 ProteinModelPortal:O82199 SMR:O82199 PRIDE:O82199 EnsemblPlants:AT2G19810.1 GeneID:816500 KEGG:ath:AT2G19810 TAIR:At2g19810 eggNOG:NOG288631 HOGENOM:HBG744620 InParanoid:O82199 OMA:WENGLEE PhylomeDB:O82199 ProtClustDB:CLSN2691160 ArrayExpress:O82199 Genevestigator:O82199 Uniprot:O82199
Leaf	Isotig01030	37	15	1.832	1.11E-05	TAIR|locus:2198225 - symbol:ATAF1 "AT1G01720" species:3702 "Arabidopsis thaliana" [GO:0007275 "multicellular organismal development" evidence=ISS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0009611 "response to wounding" evidence=IEP] [GO:0009788 "negative regulation of abscisic acid mediated signaling pathway" evidence=IMP] InterPro:IPR003441 Pfam:PF02365 PROSITE:PS51005 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005634 GO:GO:0009611 GO:GO:0006355 GO:GO:0003677 GO:GO:0006351 GO:GO:0009788 EMBL:AC009273 HOGENOM:HBG750044 SUPFAM:SSF101941 EMBL:X74755 EMBL:AF370617 IPI:IPI00547269 PIR:E86148 PIR:S37101 RefSeq:NP_171677.1 UniGene:At.134 UniGene:At.57938 ProteinModelPortal:Q39013 SMR:Q39013 STRING:Q39013 PRIDE:Q39013 EnsemblPlants:AT1G01720.1 GeneID:839265 KEGG:ath:AT1G01720 GeneFarm:4060 TAIR:At1g01720 eggNOG:NOG265262 InParanoid:Q39013 OMA:EIMEEKP PhylomeDB:Q39013 ProtClustDB:CLSN2714451 ArrayExpress:Q39013 Genevestigator:Q39013 GermOnline:AT1G01720 Uniprot:Q39013
Leaf	Isotig01031	34	13	1.916	1.41E-05	TAIR|locus:2198225 - symbol:ATAF1 "AT1G01720" species:3702 "Arabidopsis thaliana" [GO:0007275 "multicellular organismal development" evidence=ISS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0009611 "response to wounding" evidence=IEP] [GO:0009788 "negative regulation of abscisic acid mediated signaling pathway" evidence=IMP] InterPro:IPR003441 Pfam:PF02365 PROSITE:PS51005 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005634 GO:GO:0009611 GO:GO:0006355 GO:GO:0003677 GO:GO:0006351 GO:GO:0009788 EMBL:AC009273 HOGENOM:HBG750044 SUPFAM:SSF101941 EMBL:X74755 EMBL:AF370617 IPI:IPI00547269 PIR:E86148 PIR:S37101 RefSeq:NP_171677.1 UniGene:At.134 UniGene:At.57938 ProteinModelPortal:Q39013 SMR:Q39013

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						STRING:Q39013 PRIDE:Q39013 EnsemblPlants:AT1G01720.1 GeneID:839265 KEGG:ath:AT1G01720 GeneFarm:4060 TAIR:At1g01720 eggNOG:NOG265262 InParanoid:Q39013 OMA:EIMEEKP PhylomeDB:Q39013 ProtClustDB:CLSN2714451 ArrayExpress:Q39013 Genevestigator:Q39013 GermOnline:AT1G01720 Uniprot:Q39013
Leaf	Isotig01032	37	15	1.832	1.11E-05	TAIR|locus:2198225 - symbol:ATAF1 "AT1G01720" species:3702 "Arabidopsis thaliana" [GO:0007275 "multicellular organismal development" evidence=ISS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0009611 "response to wounding" evidence=IEP] [GO:0009788 "negative regulation of abscisic acid mediated signaling pathway" evidence=IMP] InterPro:IPR003441 Pfam:PF02365 PROSITE:PS51005 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005634 GO:GO:0009611 GO:GO:0006355 GO:GO:0003677 GO:GO:0006351 GO:GO:0009788 EMBL:AC009273 HOGENOM:HBG750044 SUPFAM:SSF101941 EMBL:X74755 EMBL:AF370617 IPI:IPI00547269 PIR:E86148 PIR:S37101 RefSeq:NP_171677.1 UniGene:At.134 UniGene:At.57938 ProteinModelPortal:Q39013 SMR:Q39013 STRING:Q39013 PRIDE:Q39013 EnsemblPlants:AT1G01720.1 GeneID:839265 KEGG:ath:AT1G01720 GeneFarm:4060 TAIR:At1g01720 eggNOG:NOG265262 InParanoid:Q39013 OMA:EIMEEKP PhylomeDB:Q39013 ProtClustDB:CLSN2714451 ArrayExpress:Q39013 Genevestigator:Q39013 GermOnline:AT1G01720 Uniprot:Q39013
Leaf	Isotig01033	36	15	1.792	1.96E-05	TAIR|locus:2198225 - symbol:ATAF1 "AT1G01720" species:3702 "Arabidopsis thaliana" [GO:0007275 "multicellular organismal development" evidence=ISS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0009611 "response to wounding" evidence=IEP] [GO:0009788 "negative regulation of abscisic acid mediated signaling pathway" evidence=IMP] InterPro:IPR003441 Pfam:PF02365 PROSITE:PS51005 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005634 GO:GO:0009611 GO:GO:0006355 GO:GO:0003677 GO:GO:0006351 GO:GO:0009788 EMBL:AC009273 HOGENOM:HBG750044 SUPFAM:SSF101941 EMBL:X74755 EMBL:AF370617 IPI:IPI00547269 PIR:E86148 PIR:S37101 RefSeq:NP_171677.1 UniGene:At.134 UniGene:At.57938 ProteinModelPortal:Q39013 SMR:Q39013 STRING:Q39013 PRIDE:Q39013 EnsemblPlants:AT1G01720.1 GeneID:839265 KEGG:ath:AT1G01720 GeneFarm:4060 TAIR:At1g01720 eggNOG:NOG265262 InParanoid:Q39013 OMA:EIMEEKP PhylomeDB:Q39013 ProtClustDB:CLSN2714451 ArrayExpress:Q39013 Genevestigator:Q39013 GermOnline:AT1G01720 Uniprot:Q39013
Leaf	Isotig01034	34	13	1.916	1.41E-05	TAIR|locus:2198225 - symbol:ATAF1 "AT1G01720" species:3702 "Arabidopsis thaliana" [GO:0007275 "multicellular organismal development" evidence=ISS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0009611 "response to wounding" evidence=IEP] [GO:0009788 "negative regulation of abscisic acid mediated signaling pathway" evidence=IMP] InterPro:IPR003441 Pfam:PF02365 PROSITE:PS51005 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005634 GO:GO:0009611 GO:GO:0006355 GO:GO:0003677 GO:GO:0006351 GO:GO:0009788 EMBL:AC009273 HOGENOM:HBG750044 SUPFAM:SSF101941 EMBL:X74755 EMBL:AF370617 IPI:IPI00547269 PIR:E86148 PIR:S37101 RefSeq:NP_171677.1 UniGene:At.134 UniGene:At.57938 ProteinModelPortal:Q39013 SMR:Q39013 STRING:Q39013 PRIDE:Q39013 EnsemblPlants:AT1G01720.1 GeneID:839265 KEGG:ath:AT1G01720 GeneFarm:4060 TAIR:At1g01720 eggNOG:NOG265262 InParanoid:Q39013 OMA:EIMEEKP PhylomeDB:Q39013 ProtClustDB:CLSN2714451 ArrayExpress:Q39013 Genevestigator:Q39013 GermOnline:AT1G01720 Uniprot:Q39013
Leaf	Isotig01035	33	13	1.873	2.52E-05	TAIR|locus:2198225 - symbol:ATAF1 "AT1G01720" species:3702 "Arabidopsis thaliana" [GO:0007275 "multicellular organismal development" evidence=ISS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0009611 "response to wounding" evidence=IEP] [GO:0009788 "negative regulation of abscisic acid mediated signaling pathway" evidence=IMP] InterPro:IPR003441 Pfam:PF02365 PROSITE:PS51005 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005634 GO:GO:0009611 GO:GO:0006355 GO:GO:0003677 GO:GO:0006351 GO:GO:0009788 EMBL:AC009273 HOGENOM:HBG750044 SUPFAM:SSF101941 EMBL:X74755 EMBL:AF370617 IPI:IPI00547269 PIR:E86148 PIR:S37101 RefSeq:NP_171677.1 UniGene:At.134 UniGene:At.57938 ProteinModelPortal:Q39013 SMR:Q39013 STRING:Q39013 PRIDE:Q39013 EnsemblPlants:AT1G01720.1 GeneID:839265 KEGG:ath:AT1G01720 GeneFarm:4060 TAIR:At1g01720 eggNOG:NOG265262 InParanoid:Q39013 OMA:EIMEEKP PhylomeDB:Q39013 ProtClustDB:CLSN2714451 ArrayExpress:Q39013 Genevestigator:Q39013 GermOnline:AT1G01720 Uniprot:Q39013

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig01048	79	213	-0.902	3.81E-07	TAIR|locus:2005518 - symbol:SHM1 "AT4G37930" species:3702 "Arabidopsis thaliana" [GO:0004372 "glycine hydroxymethyltransferase activity" evidence=ISS;TAS] [GO:0006544 "glycine metabolic process" evidence=ISS] [GO:0006563 "L-serine metabolic process" evidence=ISS] [GO:0019464 "glycine decarboxylation via glycine cleavage system" evidence=IMP] [GO:0005759 "mitochondrial matrix" evidence=ISS] [GO:0005634 "nucleus" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009626 "plant-type hypersensitive response" evidence=TAS] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0009409 "response to cold" evidence=IEP] [GO:0010319 "stromule" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009853 "photorespiration" evidence=IMP] [GO:0016020 "membrane" evidence=IDA] [GO:0008266 "poly(U) RNA binding" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] InterPro:IPR001085 InterPro:IPR015421 InterPro:IPR015422 InterPro:IPR019798 Pfam:PF00464 PIRSF:PIRSF000412 PROSITE:PS00096 GO:GO:0005739 GO:GO:0005886 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0048046 GO:GO:0009570 GO:GO:0005634 GO:GO:0046686 GO:GO:0005515 GO:GO:0030170 InterPro:IPR015424 Gene3D:G3DSA:3.40.640.10 Gene3D:G3DSA:3.90.1150.10 SUPFAM:SSF53383 EMBL:AL161592 GO:GO:0008266 GO:GO:0010319 GO:GO:0009409 GO:GO:0009626 EMBL:AL035538 GO:GO:0009853 GO:GO:0009534 GO:GO:0022626 GO:GO:0006544 GO:GO:0006730 eggNOG:COG0112 HOGENOM:HBG301263 KO:K00600 GO:GO:0004372 GO:GO:0006563 PANTHER:PTHR11680 OMA:DYARIKK EMBL:AJ271726 EMBL:AY054254 EMBL:AY057645 EMBL:AY070726 EMBL:AF428388 EMBL:BT006353 IPI:IPI00525727 PIR:T05620 RefSeq:NP_195506.1 UniGene:At.21766 ProteinModelPortal:Q9SZJ5 SMR:Q9SZJ5 IntAct:Q9SZJ5 STRING:Q9SZJ5 PRIDE:Q9SZJ5 ProMEX:Q9SZJ5 EnsemblPlants:AT4G37930.1 GeneID:829949 KEGG:ath:AT4G37930 TAIR:At4g37930 InParanoid:Q9SZJ5 PhylomeDB:Q9SZJ5 ProtClustDB:PLN03226 ArrayExpress:Q9SZJ5 Genevestigator:Q9SZJ5 GermOnline:AT4G37930 Uniprot:Q9SZJ5
Leaf	Isotig01049	90	250	-0.945	1.06E-08	TAIR|locus:2005518 - symbol:SHM1 "AT4G37930" species:3702 "Arabidopsis thaliana" [GO:0004372 "glycine hydroxymethyltransferase activity" evidence=ISS;TAS] [GO:0006544 "glycine metabolic process" evidence=ISS] [GO:0006563 "L-serine metabolic process" evidence=ISS] [GO:0019464 "glycine decarboxylation via glycine cleavage system" evidence=IMP] [GO:0005759 "mitochondrial matrix" evidence=ISS] [GO:0005634 "nucleus" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009626 "plant-type hypersensitive response" evidence=TAS] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0009409 "response to cold" evidence=IEP] [GO:0010319 "stromule" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009853 "photorespiration" evidence=IMP] [GO:0016020 "membrane" evidence=IDA] [GO:0008266 "poly(U) RNA binding" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] InterPro:IPR001085 InterPro:IPR015421 InterPro:IPR015422 InterPro:IPR019798 Pfam:PF00464 PIRSF:PIRSF000412 PROSITE:PS00096 GO:GO:0005739 GO:GO:0005886 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0048046 GO:GO:0009570 GO:GO:0005634 GO:GO:0046686 GO:GO:0005515 GO:GO:0030170 InterPro:IPR015424 Gene3D:G3DSA:3.40.640.10 Gene3D:G3DSA:3.90.1150.10 SUPFAM:SSF53383 EMBL:AL161592 GO:GO:0008266 GO:GO:0010319 GO:GO:0009409 GO:GO:0009626 EMBL:AL035538 GO:GO:0009853 GO:GO:0009534 GO:GO:0022626 GO:GO:0006544 GO:GO:0006730 eggNOG:COG0112 HOGENOM:HBG301263 KO:K00600 GO:GO:0004372 GO:GO:0006563 PANTHER:PTHR11680 OMA:DYARIKK EMBL:AJ271726 EMBL:AY054254 EMBL:AY057645 EMBL:AY070726 EMBL:AF428388 EMBL:BT006353 IPI:IPI00525727 PIR:T05620 RefSeq:NP_195506.1 UniGene:At.21766 ProteinModelPortal:Q9SZJ5 SMR:Q9SZJ5 IntAct:Q9SZJ5 STRING:Q9SZJ5 PRIDE:Q9SZJ5 ProMEX:Q9SZJ5 EnsemblPlants:AT4G37930.1 GeneID:829949 KEGG:ath:AT4G37930 TAIR:At4g37930 InParanoid:Q9SZJ5 PhylomeDB:Q9SZJ5 ProtClustDB:PLN03226 ArrayExpress:Q9SZJ5 Genevestigator:Q9SZJ5 GermOnline:AT4G37930 Uniprot:Q9SZJ5
Leaf	Isotig01050	31	112	-1.324	5.05E-07	TAIR|locus:2005518 - symbol:SHM1 "AT4G37930" species:3702 "Arabidopsis thaliana" [GO:0004372 "glycine hydroxymethyltransferase activity" evidence=ISS;TAS] [GO:0006544 "glycine metabolic process" evidence=ISS] [GO:0006563 "L-serine metabolic process" evidence=ISS] [GO:0019464 "glycine decarboxylation via glycine cleavage system" evidence=IMP] [GO:0005759 "mitochondrial matrix" evidence=ISS] [GO:0005634 "nucleus" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA]

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						[GO:0009626 "plant-type hypersensitive response" evidence=TAS] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0009409 "response to cold" evidence=IEP] [GO:0010319 "stromule" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009853 "photorespiration" evidence=IMP] [GO:0016020 "membrane" evidence=IDA] [GO:0008266 "poly(U) RNA binding" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] InterPro:IPR001085 InterPro:IPR015421 InterPro:IPR015422 InterPro:IPR019798 Pfam:PF00464 PIRSF:PIRSF000412 PROSITE:PS00096 GO:GO:0005739 GO:GO:0005886 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0048046 GO:GO:0009570 GO:GO:0005634 GO:GO:0046686 GO:GO:0005515 GO:GO:0030170 InterPro:IPR015424 Gene3D:G3DSA:3.40.640.10 Gene3D:G3DSA:3.90.1150.10 SUPFAM:SSF53383 EMBL:AL161592 GO:GO:0008266 GO:GO:0010319 GO:GO:0009409 GO:GO:0009626 EMBL:AL035538 GO:GO:0009853 GO:GO:0009534 GO:GO:0022626 GO:GO:0006544 GO:GO:0006730 eggNOG:COG0112 HOGENOM:HBG301263 KO:K00600 GO:GO:0004372 GO:GO:0006563 PANTHER:PTHR11680 OMA:DYARIKK EMBL:AJ271726 EMBL:AY054254 EMBL:AY057645 EMBL:AY070726 EMBL:AF428388 EMBL:BT006353 IPI:IPI00525727 PIR:T05620 RefSeq:NP_195506.1 UniGene:At.21766 ProteinModelPortal:Q9SZJ5 SMR:Q9SZJ5 IntAct:Q9SZJ5 STRING:Q9SZJ5 PRIDE:Q9SZJ5 ProMEX:Q9SZJ5 EnsemblPlants:AT4G37930.1 GeneID:829949 KEGG:ath:AT4G37930 TAIR:At4g37930 InParanoid:Q9SZJ5 PhylomeDB:Q9SZJ5 ProtClustDB:PLN03226 ArrayExpress:Q9SZJ5 Genevestigator:Q9SZJ5 GermOnline:AT4G37930 Uniprot:Q9SZJ5
Leaf	Isotig01051	69	218	-1.131	6.01E-10	TAIR|locus:2005518 - symbol:SHM1 "AT4G37930" species:3702 "Arabidopsis thaliana" [GO:0004372 "glycine hydroxymethyltransferase activity" evidence=ISS;TAS] [GO:0006544 "glycine metabolic process" evidence=ISS] [GO:0006563 "L-serine metabolic process" evidence=ISS] [GO:0019464 "glycine decarboxylation via glycine cleavage system" evidence=IMP] [GO:0005759 "mitochondrial matrix" evidence=ISS] [GO:0005634 "nucleus" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009626 "plant-type hypersensitive response" evidence=TAS] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0009409 "response to cold" evidence=IEP] [GO:0010319 "stromule" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009853 "photorespiration" evidence=IMP] [GO:0016020 "membrane" evidence=IDA] [GO:0008266 "poly(U) RNA binding" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] InterPro:IPR001085 InterPro:IPR015421 InterPro:IPR015422 InterPro:IPR019798 Pfam:PF00464 PIRSF:PIRSF000412 PROSITE:PS00096 GO:GO:0005739 GO:GO:0005886 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0048046 GO:GO:0009570 GO:GO:0005634 GO:GO:0046686 GO:GO:0005515 GO:GO:0030170 InterPro:IPR015424 Gene3D:G3DSA:3.40.640.10 Gene3D:G3DSA:3.90.1150.10 SUPFAM:SSF53383 EMBL:AL161592 GO:GO:0008266 GO:GO:0010319 GO:GO:0009409 GO:GO:0009626 EMBL:AL035538 GO:GO:0009853 GO:GO:0009534 GO:GO:0022626 GO:GO:0006544 GO:GO:0006730 eggNOG:COG0112 HOGENOM:HBG301263 KO:K00600 GO:GO:0004372 GO:GO:0006563 PANTHER:PTHR11680 OMA:DYARIKK EMBL:AJ271726 EMBL:AY054254 EMBL:AY057645 EMBL:AY070726 EMBL:AF428388 EMBL:BT006353 IPI:IPI00525727 PIR:T05620 RefSeq:NP_195506.1 UniGene:At.21766 ProteinModelPortal:Q9SZJ5 SMR:Q9SZJ5 IntAct:Q9SZJ5 STRING:Q9SZJ5 PRIDE:Q9SZJ5 ProMEX:Q9SZJ5 EnsemblPlants:AT4G37930.1 GeneID:829949 KEGG:ath:AT4G37930 TAIR:At4g37930 InParanoid:Q9SZJ5 PhylomeDB:Q9SZJ5 ProtClustDB:PLN03226 ArrayExpress:Q9SZJ5 Genevestigator:Q9SZJ5 GermOnline:AT4G37930 Uniprot:Q9SZJ5
Leaf	Isotig01052	80	255	-1.143	1.42E-11	TAIR|locus:2005518 - symbol:SHM1 "AT4G37930" species:3702 "Arabidopsis thaliana" [GO:0004372 "glycine hydroxymethyltransferase activity" evidence=ISS;TAS] [GO:0006544 "glycine metabolic process" evidence=ISS] [GO:0006563 "L-serine metabolic process" evidence=ISS] [GO:0019464 "glycine decarboxylation via glycine cleavage system" evidence=IMP] [GO:0005759 "mitochondrial matrix" evidence=ISS] [GO:0005634 "nucleus" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009626 "plant-type hypersensitive response" evidence=TAS] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0009409 "response to cold" evidence=IEP] [GO:0010319 "stromule" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009853 "photorespiration" evidence=IMP] [GO:0016020 "membrane" evidence=IDA] [GO:0008266 "poly(U) RNA binding" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI]

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						[GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] InterPro:IPR001085 InterPro:IPR015421 InterPro:IPR015422 InterPro:IPR019798 Pfam:PF00464 PIRSF:PIRSF000412 PROSITE:PS00096 GO:GO:0005739 GO:GO:0005886 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0048046 GO:GO:0009570 GO:GO:0005634 GO:GO:0046686 GO:GO:0005515 GO:GO:0030170 InterPro:IPR015424 Gene3D:G3DSA:3.40.640.10 Gene3D:G3DSA:3.90.1150.10 SUPFAM:SSF53383 EMBL:AL161592 GO:GO:0008266 GO:GO:0010319 GO:GO:0009409 GO:GO:0009626 EMBL:AL035538 GO:GO:0009853 GO:GO:0009534 GO:GO:0022626 GO:GO:0006544 GO:GO:0006730 eggNOG:COG0112 HOGENOM:HBG301263 KO:K00600 GO:GO:0004372 GO:GO:0006563 PANTHER:PTHR11680 OMA:DYARIKK EMBL:AJ271726 EMBL:AY054254 EMBL:AY057645 EMBL:AY070726 EMBL:AF428388 EMBL:BT006353 IPI:IPI00525727 PIR:T05620 RefSeq:NP_195506.1 UniGene:At.21766 ProteinModelPortal:Q9SZJ5 SMR:Q9SZJ5 IntAct:Q9SZJ5 STRING:Q9SZJ5 PRIDE:Q9SZJ5 ProMEX:Q9SZJ5 EnsemblPlants:AT4G37930.1 GeneID:829949 KEGG:ath:AT4G37930 TAIR:At4g37930 InParanoid:Q9SZJ5 PhylomeDB:Q9SZJ5 ProtClustDB:PLN03226 ArrayExpress:Q9SZJ5 Genevestigator:Q9SZJ5 GermOnline:AT4G37930 Uniprot:Q9SZJ5
Leaf	Isotig01053	24	0	6.114	1.86E-08	TAIR|locus:2077081 - symbol:AT3G22490 "AT3G22490" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0009793 "embryo development ending in seed dormancy" evidence=ISS] Pfam:PF04927 EMBL:CP002686 EMBL:AP000731 UniGene:At.64534 InterPro:IPR007011 ProtClustDB:CLSN2684142 EMBL:BT002907 EMBL:BT004425 IPI:IPI00543172 RefSeq:NP_188888.1 PRIDE:Q9LJ97 EnsemblPlants:AT3G22490.1 GeneID:821820 KEGG:ath:AT3G22490 TAIR:At3g22490 InParanoid:Q9LJ97 OMA:QTAGNKP PhylomeDB:Q9LJ97 ArrayExpress:Q9LJ97 Genevestigator:Q9LJ97 Uniprot:Q9LJ97
Leaf	Isotig01054	24	0	6.114	1.86E-08	TAIR|locus:2077081 - symbol:AT3G22490 "AT3G22490" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0009793 "embryo development ending in seed dormancy" evidence=ISS] Pfam:PF04927 EMBL:CP002686 EMBL:AP000731 UniGene:At.64534 InterPro:IPR007011 ProtClustDB:CLSN2684142 EMBL:BT002907 EMBL:BT004425 IPI:IPI00543172 RefSeq:NP_188888.1 PRIDE:Q9LJ97 EnsemblPlants:AT3G22490.1 GeneID:821820 KEGG:ath:AT3G22490 TAIR:At3g22490 InParanoid:Q9LJ97 OMA:QTAGNKP PhylomeDB:Q9LJ97 ArrayExpress:Q9LJ97 Genevestigator:Q9LJ97 Uniprot:Q9LJ97
Leaf	Isotig01055	24	2	4.114	8.70E-08	TAIR|locus:2077081 - symbol:AT3G22490 "AT3G22490" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0009793 "embryo development ending in seed dormancy" evidence=ISS] Pfam:PF04927 EMBL:CP002686 EMBL:AP000731 UniGene:At.64534 InterPro:IPR007011 ProtClustDB:CLSN2684142 EMBL:BT002907 EMBL:BT004425 IPI:IPI00543172 RefSeq:NP_188888.1 PRIDE:Q9LJ97 EnsemblPlants:AT3G22490.1 GeneID:821820 KEGG:ath:AT3G22490 TAIR:At3g22490 InParanoid:Q9LJ97 OMA:QTAGNKP PhylomeDB:Q9LJ97 ArrayExpress:Q9LJ97 Genevestigator:Q9LJ97 Uniprot:Q9LJ97
Leaf	Isotig01057	24	2	4.114	8.70E-08	TAIR|locus:2077081 - symbol:AT3G22490 "AT3G22490" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0009793 "embryo development ending in seed dormancy" evidence=ISS] Pfam:PF04927 EMBL:CP002686 EMBL:AP000731 UniGene:At.64534 InterPro:IPR007011 ProtClustDB:CLSN2684142 EMBL:BT002907 EMBL:BT004425 IPI:IPI00543172 RefSeq:NP_188888.1 PRIDE:Q9LJ97 EnsemblPlants:AT3G22490.1 GeneID:821820 KEGG:ath:AT3G22490 TAIR:At3g22490 InParanoid:Q9LJ97 OMA:QTAGNKP PhylomeDB:Q9LJ97 ArrayExpress:Q9LJ97 Genevestigator:Q9LJ97 Uniprot:Q9LJ97
Leaf	Isotig01063	20	6	2.266	0.000209978	TAIR|locus:2094508 - symbol:ATL5 "AT3G25520" species:3702 "Arabidopsis thaliana" [GO:0003735 "structural constituent of ribosome" evidence=ISS] [GO:0005840 "ribosome" evidence=ISS] [GO:0006412 "translation" evidence=ISS] [GO:0042254 "ribosome biogenesis" evidence=ISS] [GO:0005634 "nucleus" evidence=IDA] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0006913 "nucleocytoplasmic transport" evidence=TAS] [GO:0008097 "5S rRNA binding" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0022625 "cytosolic large ribosomal subunit" evidence=IDA] [GO:0009955 "adaxial/abaxial pattern specification" evidence=IGI] [GO:0008283 "cell proliferation" evidence=IMP] [GO:0009965 "leaf morphogenesis" evidence=IMP] [GO:0010015 "root morphogenesis" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] [GO:0005794 "Golgi

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						apparatus" evidence=RCA] InterPro:IPR005484 InterPro:IPR005485 Pfam:PF00861 PRINTS:PR00058 GO:GO:0005886 GO:GO:0005773 GO:GO:0009507 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005730 GO:GO:0006412 GO:GO:0008283 GO:GO:0006913 UniGene:At.23809 GO:GO:0003735 GO:GO:0009965 GO:GO:0008097 EMBL:AB025639 GO:GO:0022625 GO:GO:0010015 GO:GO:0009955 eggNOG:COG0256 EMBL:AY186611 EMBL:AY054161 EMBL:AY065103 EMBL:AY081701 EMBL:AY136319 EMBL:BT000411 EMBL:BT002427 EMBL:BT008705 EMBL:AY087197 IPI:IPI00548063 RefSeq:NP_566767.1 UniGene:At.25396 ProteinModelPortal:Q8LBI1 SMR:Q8LBI1 STRING:Q8LBI1 PRIDE:Q8LBI1 EnsemblPlants:AT3G25520.1 GeneID:822138 KEGG:ath:AT3G25520 GeneFarm:390 TAIR:At3g25520 HOGENOM:HBG391676 InParanoid:Q8LBI1 KO:K02932 OMA:YNAEAHR PhylomeDB:Q8LBI1 ProtClustDB:CLSN2687505 ArrayExpress:Q940R7 Genevestigator:Q8LBI1 GermOnline:AT3G25520 InterPro:IPR025607 PANTHER:PTHR23410 Pfam:PF14204 Uniprot:Q8LBI1
Leaf	Isotig01064	20	6	2.266	0.000209978	TAIR|locus:2094508 - symbol:ATL5 "AT3G25520" species:3702 "Arabidopsis thaliana" [GO:0003735 "structural constituent of ribosome" evidence=ISS] [GO:0005840 "ribosome" evidence=ISS] [GO:0006412 "translation" evidence=ISS] [GO:0042254 "ribosome biogenesis" evidence=ISS] [GO:0005634 "nucleus" evidence=IDA] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0006913 "nucleocytoplasmic transport" evidence=TAS] [GO:0008097 "5S rRNA binding" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0022625 "cytosolic large ribosomal subunit" evidence=IDA] [GO:0009955 "adaxial/abaxial pattern specification" evidence=IGI] [GO:0008283 "cell proliferation" evidence=IMP] [GO:0009965 "leaf morphogenesis" evidence=IMP] [GO:0010015 "root morphogenesis" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR005484 InterPro:IPR005485 Pfam:PF00861 PRINTS:PR00058 GO:GO:0005886 GO:GO:0005773 GO:GO:0009507 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005730 GO:GO:0006412 GO:GO:0008283 GO:GO:0006913 UniGene:At.23809 GO:GO:0003735 GO:GO:0009965 GO:GO:0008097 EMBL:AB025639 GO:GO:0022625 GO:GO:0010015 GO:GO:0009955 eggNOG:COG0256 EMBL:AY186611 EMBL:AY054161 EMBL:AY065103 EMBL:AY081701 EMBL:AY136319 EMBL:BT000411 EMBL:BT002427 EMBL:BT008705 EMBL:AY087197 IPI:IPI00548063 RefSeq:NP_566767.1 UniGene:At.25396 ProteinModelPortal:Q8LBI1 SMR:Q8LBI1 STRING:Q8LBI1 PRIDE:Q8LBI1 EnsemblPlants:AT3G25520.1 GeneID:822138 KEGG:ath:AT3G25520 GeneFarm:390 TAIR:At3g25520 HOGENOM:HBG391676 InParanoid:Q8LBI1 KO:K02932 OMA:YNAEAHR PhylomeDB:Q8LBI1 ProtClustDB:CLSN2687505 ArrayExpress:Q940R7 Genevestigator:Q8LBI1 GermOnline:AT3G25520 InterPro:IPR025607 PANTHER:PTHR23410 Pfam:PF14204 Uniprot:Q8LBI1
Leaf	Isotig01065	13	2	3.229	0.00031313	TAIR|locus:2094508 - symbol:ATL5 "AT3G25520" species:3702 "Arabidopsis thaliana" [GO:0003735 "structural constituent of ribosome" evidence=ISS] [GO:0005840 "ribosome" evidence=ISS] [GO:0006412 "translation" evidence=ISS] [GO:0042254 "ribosome biogenesis" evidence=ISS] [GO:0005634 "nucleus" evidence=IDA] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0006913 "nucleocytoplasmic transport" evidence=TAS] [GO:0008097 "5S rRNA binding" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0022625 "cytosolic large ribosomal subunit" evidence=IDA] [GO:0009955 "adaxial/abaxial pattern specification" evidence=IGI] [GO:0008283 "cell proliferation" evidence=IMP] [GO:0009965 "leaf morphogenesis" evidence=IMP] [GO:0010015 "root morphogenesis" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR005484 InterPro:IPR005485 Pfam:PF00861 PRINTS:PR00058 GO:GO:0005886 GO:GO:0005773 GO:GO:0009507 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005730 GO:GO:0006412 GO:GO:0008283 GO:GO:0006913 UniGene:At.23809 GO:GO:0003735 GO:GO:0009965 GO:GO:0008097 EMBL:AB025639 GO:GO:0022625 GO:GO:0010015 GO:GO:0009955 eggNOG:COG0256 EMBL:AY186611 EMBL:AY054161 EMBL:AY065103 EMBL:AY081701 EMBL:AY136319 EMBL:BT000411 EMBL:BT002427 EMBL:BT008705 EMBL:AY087197 IPI:IPI00548063 RefSeq:NP_566767.1 UniGene:At.25396 ProteinModelPortal:Q8LBI1 SMR:Q8LBI1 STRING:Q8LBI1 PRIDE:Q8LBI1 EnsemblPlants:AT3G25520.1 GeneID:822138 KEGG:ath:AT3G25520 GeneFarm:390 TAIR:At3g25520 HOGENOM:HBG391676 InParanoid:Q8LBI1 KO:K02932 OMA:YNAEAHR PhylomeDB:Q8LBI1 ProtClustDB:CLSN2687505 ArrayExpress:Q940R7 Genevestigator:Q8LBI1 GermOnline:AT3G25520 InterPro:IPR025607 PANTHER:PTHR23410 Pfam:PF14204 Uniprot:Q8LBI1

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig01066	13	2	3.229	0.00031313	TAIR|locus:2094508 - symbol:ATL5 "AT3G25520" species:3702 "Arabidopsis thaliana" [GO:0003735 "structural constituent of ribosome" evidence=ISS] [GO:0005840 "ribosome" evidence=ISS] [GO:0006412 "translation" evidence=ISS] [GO:0042254 "ribosome biogenesis" evidence=ISS] [GO:0005634 "nucleus" evidence=IDA] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0006913 "nucleocytoplasmic transport" evidence=TAS] [GO:0008097 "5S rRNA binding" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0022625 "cytosolic large ribosomal subunit" evidence=IDA] [GO:0009955 "adaxial/abaxial pattern specification" evidence=IGI] [GO:0008283 "cell proliferation" evidence=IMP] [GO:0009965 "leaf morphogenesis" evidence=IMP] [GO:0010015 "root morphogenesis" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR005484 InterPro:IPR005485 Pfam:PF00861 PRINTS:PR00058 GO:GO:0005886 GO:GO:0005773 GO:GO:0009507 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005730 GO:GO:0006412 GO:GO:0008283 GO:GO:0006913 UniGene:At.23809 GO:GO:0003735 GO:GO:0009965 GO:GO:0008097 EMBL:AB025639 GO:GO:0022625 GO:GO:0010015 GO:GO:0009955 eggNOG:COG0256 EMBL:AY186611 EMBL:AY054161 EMBL:AY065103 EMBL:AY081701 EMBL:AY136319 EMBL:BT000411 EMBL:BT002427 EMBL:BT008705 EMBL:AY087197 IPI:IPI00548063 RefSeq:NP_566767.1 UniGene:At.25396 ProteinModelPortal:Q8LBI1 SMR:Q8LBI1 STRING:Q8LBI1 PRIDE:Q8LBI1 EnsemblPlants:AT3G25520.1 GeneID:822138 KEGG:ath:AT3G25520 GeneFarm:390 TAIR:At3g25520 HOGENOM:HBG391676 InParanoid:Q8LBI1 KO:K02932 OMA:YNAEAHR PhylomeDB:Q8LBI1 ProtClustDB:CLSN2687505 ArrayExpress:Q940R7 Genevestigator:Q8LBI1 GermOnline:AT3G25520 InterPro:IPR025607 PANTHER:PTHR23410 Pfam:PF14204 Uniprot:Q8LBI1
Leaf	Isotig01068	11	1	3.988	0.000330755	TAIR|locus:2040711 - symbol:AT2G37730 "AT2G37730" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] EMBL:AC004684 EMBL:CP002685 GenomeReviews:CT485783_GR CAZy:GT31 InterPro:IPR006740 Pfam:PF04646 HOGENOM:HBG593120 IPI:IPI00523560 PIR:T02539 RefSeq:NP_565869.1 UniGene:At.53059 ProteinModelPortal:O80941 PRIDE:O80941 EnsemblPlants:AT2G37730.1 GeneID:818350 KEGG:ath:AT2G37730 TAIR:At2g37730 eggNOG:NOG298366 InParanoid:O80941 OMA:DIRGNPY PhylomeDB:O80941 ProtClustDB:CLSN2688758 ArrayExpress:O80941 Genevestigator:O80941 Uniprot:O80941
Leaf	Isotig01077	62	41	1.126	7.80E-05	TAIR|locus:2155821 - symbol:PHOT2 "AT5G58140" species:3702 "Arabidopsis thaliana" [GO:0016301 "kinase activity" evidence=ISS] [GO:0004674 "protein serine/threonine kinase activity" evidence=IMP;IDA] [GO:0009638 "phototropism" evidence=IGI;IMP] [GO:0010118 "stomatal movement" evidence=IGI;IMP] [GO:0009902 "chloroplast relocation" evidence=TAS] [GO:0016020 "membrane" evidence=ISS] [GO:0009637 "response to blue light" evidence=IGI] [GO:0010181 "FMN binding" evidence=IDA;TAS] [GO:0046777 "protein autophosphorylation" evidence=TAS] [GO:0005794 "Golgi apparatus" evidence=IDA] [GO:0009882 "blue light photoreceptor activity" evidence=IMP] [GO:0010362 "negative regulation of anion channel activity by blue light" evidence=IMP] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0042802 "identical protein binding" evidence=IPI] InterPro:IPR000014 InterPro:IPR000700 InterPro:IPR000719 InterPro:IPR001610 InterPro:IPR002290 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 Pfam:PF00069 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 PROSITE:PS50112 PROSITE:PS50113 SMART:SM00086 SMART:SM00091 SMART:SM00220 GO:GO:0005886 GO:GO:0005524 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0042802 GO:GO:0006355 GO:GO:0005794 SUPFAM:SSF56112 GO:GO:0004674 GO:GO:0046777 EMBL:AB019228 GO:GO:0010118 eggNOG:COG2202 GO:GO:0009882 GO:GO:0018298 TIGRFAMs:TIGR00229 GO:GO:0000155 GO:GO:0009638 GO:GO:0010181 EMBL:AB024029 GO:GO:0009902 HOGENOM:HBG407503 GO:GO:0010362 EMBL:AF053941 EMBL:AY093141 EMBL:BT008901 EMBL:U79744 IPI:IPI00528569 IPI:IPI00540112 PIR:T51600 RefSeq:NP_851210.1 RefSeq:NP_851211.1 UniGene:At.22044 PDB:2Z6D PDBsum:2Z6D ProteinModelPortal:P93025 SMR:P93025 DIP:DIP-53468N IntAct:P93025 MINT:MINT-6823418 STRING:P93025 PRIDE:P93025 EnsemblPlants:AT5G58140.1 EnsemblPlants:AT5G58140.2 GeneID:835926 KEGG:ath:AT5G58140 TAIR:At5g58140 InParanoid:P93025 OMA:CLITDFC PhylomeDB:P93025 ProtClustDB:CLSN2680555 ArrayExpress:Q8RWE6 Genevestigator:P93025 GermOnline:AT5G58140 Uniprot:P93025

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig01078	63	40	1.184	3.36E-05	TAIR|locus:2155821 - symbol:PHOT2 "AT5G58140" species:3702 "Arabidopsis thaliana" [GO:0016301 "kinase activity" evidence=ISS] [GO:0004674 "protein serine/threonine kinase activity" evidence=IMP;IDA] [GO:0009638 "phototropism" evidence=IGI;IMP] [GO:0010118 "stomatal movement" evidence=IGI;IMP] [GO:0009902 "chloroplast relocation" evidence=TAS] [GO:0016020 "membrane" evidence=ISS] [GO:0009637 "response to blue light" evidence=IGI] [GO:0010181 "FMN binding" evidence=IDA;TAS] [GO:0046777 "protein autophosphorylation" evidence=TAS] [GO:0005794 "Golgi apparatus" evidence=IDA] [GO:0009882 "blue light photoreceptor activity" evidence=IMP] [GO:0010362 "negative regulation of anion channel activity by blue light" evidence=IMP] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0042802 "identical protein binding" evidence=IPI] InterPro:IPR000014 InterPro:IPR000700 InterPro:IPR000719 InterPro:IPR001610 InterPro:IPR002290 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 Pfam:PF00069 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 PROSITE:PS50112 PROSITE:PS50113 SMART:SM00086 SMART:SM00091 SMART:SM00220 GO:GO:0005886 GO:GO:0005524 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0042802 GO:GO:0006355 GO:GO:0005794 SUPFAM:SSF56112 GO:GO:0004674 GO:GO:0046777 EMBL:AB019228 GO:GO:0010118 eggNOG:COG2202 GO:GO:0009882 GO:GO:0018298 TIGRFAMs:TIGR00229 GO:GO:0000155 GO:GO:0009638 GO:GO:0010181 EMBL:AB024029 GO:GO:0009902 HOGENOM:HBG407503 GO:GO:0010362 EMBL:AF053941 EMBL:AY093141 EMBL:BT008901 EMBL:U79744 IPI:IPI00528569 IPI:IPI00540112 PIR:T51600 RefSeq:NP_851210.1 RefSeq:NP_851211.1 UniGene:At.22044 PDB:2Z6D PDBsum:2Z6D ProteinModelPortal:P93025 SMR:P93025 DIP:DIP-53468N IntAct:P93025 MINT:MINT-6823418 STRING:P93025 PRIDE:P93025 EnsemblPlants:AT5G58140.1 EnsemblPlants:AT5G58140.2 GeneID:835926 KEGG:ath:AT5G58140 TAIR:At5g58140 InParanoid:P93025 OMA:CLITDFC PhylomeDB:P93025 ProtClustDB:CLSN2680555 ArrayExpress:Q8RWE6 Genevestigator:P93025 GermOnline:AT5G58140 Uniprot:P93025
Leaf	Isotig01079	63	40	1.184	3.36E-05	TAIR|locus:2155821 - symbol:PHOT2 "AT5G58140" species:3702 "Arabidopsis thaliana" [GO:0016301 "kinase activity" evidence=ISS] [GO:0004674 "protein serine/threonine kinase activity" evidence=IMP;IDA] [GO:0009638 "phototropism" evidence=IGI;IMP] [GO:0010118 "stomatal movement" evidence=IGI;IMP] [GO:0009902 "chloroplast relocation" evidence=TAS] [GO:0016020 "membrane" evidence=ISS] [GO:0009637 "response to blue light" evidence=IGI] [GO:0010181 "FMN binding" evidence=IDA;TAS] [GO:0046777 "protein autophosphorylation" evidence=TAS] [GO:0005794 "Golgi apparatus" evidence=IDA] [GO:0009882 "blue light photoreceptor activity" evidence=IMP] [GO:0010362 "negative regulation of anion channel activity by blue light" evidence=IMP] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0042802 "identical protein binding" evidence=IPI] InterPro:IPR000014 InterPro:IPR000700 InterPro:IPR000719 InterPro:IPR001610 InterPro:IPR002290 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 Pfam:PF00069 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 PROSITE:PS50112 PROSITE:PS50113 SMART:SM00086 SMART:SM00091 SMART:SM00220 GO:GO:0005886 GO:GO:0005524 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0042802 GO:GO:0006355 GO:GO:0005794 SUPFAM:SSF56112 GO:GO:0004674 GO:GO:0046777 EMBL:AB019228 GO:GO:0010118 eggNOG:COG2202 GO:GO:0009882 GO:GO:0018298 TIGRFAMs:TIGR00229 GO:GO:0000155 GO:GO:0009638 GO:GO:0010181 EMBL:AB024029 GO:GO:0009902 HOGENOM:HBG407503 GO:GO:0010362 EMBL:AF053941 EMBL:AY093141 EMBL:BT008901 EMBL:U79744 IPI:IPI00528569 IPI:IPI00540112 PIR:T51600 RefSeq:NP_851210.1 RefSeq:NP_851211.1 UniGene:At.22044 PDB:2Z6D PDBsum:2Z6D ProteinModelPortal:P93025 SMR:P93025 DIP:DIP-53468N IntAct:P93025 MINT:MINT-6823418 STRING:P93025 PRIDE:P93025 EnsemblPlants:AT5G58140.1 EnsemblPlants:AT5G58140.2 GeneID:835926 KEGG:ath:AT5G58140 TAIR:At5g58140 InParanoid:P93025 OMA:CLITDFC PhylomeDB:P93025 ProtClustDB:CLSN2680555 ArrayExpress:Q8RWE6 Genevestigator:P93025 GermOnline:AT5G58140 Uniprot:P93025
Leaf	Isotig01080	64	39	1.244	1.40E-05	TAIR|locus:2155821 - symbol:PHOT2 "AT5G58140" species:3702 "Arabidopsis thaliana" [GO:0016301 "kinase activity" evidence=ISS] [GO:0004674 "protein serine/threonine kinase activity" evidence=IMP;IDA] [GO:0009638 "phototropism" evidence=IGI;IMP] [GO:0010118 "stomatal movement" evidence=IGI;IMP] [GO:0009902 "chloroplast relocation" evidence=TAS] [GO:0016020 "membrane" evidence=ISS] [GO:0009637 "response to blue light" evidence=IGI] [GO:0010181 "FMN binding" evidence=IDA;TAS] [GO:0046777 "protein autophosphorylation" evidence=TAS] [GO:0005794 "Golgi apparatus" evidence=IDA] [GO:0009882 "blue light photoreceptor activity" evidence=IMP] [GO:0010362 "negative regulation of anion channel activity by blue light" evidence=IMP] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0042802 "identical protein binding" evidence=IPI] InterPro:IPR000014 InterPro:IPR000700 InterPro:IPR000719 InterPro:IPR001610 InterPro:IPR002290

<table>
<tr><th>Tissue</th><th>Identification</th><th># of reads (stress)</th><th># of reads (control)</th><th>Fold Change</th><th>p-value</th><th>Description</th></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td></td><td>InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 Pfam:PF00069 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 PROSITE:PS50112 PROSITE:PS50113 SMART:SM00086 SMART:SM00091 SMART:SM00220 GO:GO:0005886 GO:GO:0005524 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0042802 GO:GO:0006355 GO:GO:0005794 SUPFAM:SSF56112 GO:GO:0004674 GO:GO:0046777 EMBL:AB019228 GO:GO:0010118 eggNOG:COG2202 GO:GO:0009882 GO:GO:0018298 TIGRFAMs:TIGR00229 GO:GO:0000155 GO:GO:0009638 GO:GO:0010181 EMBL:AB024029 GO:GO:0009902 HOGENOM:HBG407503 GO:GO:0010362 EMBL:AF053941 EMBL:AY093141 EMBL:BT008901 EMBL:U79744 IPI:IPI00528569 IPI:IPI00540112 PIR:T51600 RefSeq:NP_851210.1 RefSeq:NP_851211.1 UniGene:At.22044 PDB:2Z6D PDBsum:2Z6D ProteinModelPortal:P93025 SMR:P93025 DIP:DIP-53468N IntAct:P93025 MINT:MINT-6823418 STRING:P93025 PRIDE:P93025 EnsemblPlants:AT5G58140.1 EnsemblPlants:AT5G58140.2 GeneID:835926 KEGG:ath:AT5G58140 TAIR:At5g58140 InParanoid:P93025 OMA:CLITDFC PhylomeDB:P93025 ProtClustDB:CLSN2680555 ArrayExpress:Q8RWE6 Genevestigator:P93025 GermOnline:AT5G58140 Uniprot:P93025</td></tr>
<tr><td>Leaf</td><td>Isotig01081</td><td>59</td><td>12</td><td>2.827</td><td>5.73E-13</td><td>TAIR|locus:2121899 - symbol:NBR1 "AT4G24690" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0008270 "zinc ion binding" evidence=IEA] [GO:0005737 "cytoplasm" evidence=IDA] InterPro:IPR000270 InterPro:IPR000433 InterPro:IPR000449 InterPro:IPR009060 Pfam:PF00564 Pfam:PF00569 Pfam:PF00627 PROSITE:PS50135 SMART:SM00291 SMART:SM00666 EMBL:CP002687 GO:GO:0005737 GO:GO:0008270 EMBL:AL035356 EMBL:AL161562 SUPFAM:SSF46934 EMBL:AY062827 EMBL:AY128759 EMBL:AY140081 EMBL:BT008425 IPI:IPI00543691 PIR:T05565 RefSeq:NP_194200.1 UniGene:At.24692 UniGene:At.71380 ProteinModelPortal:Q9SB64 SMR:Q9SB64 IntAct:Q9SB64 PRIDE:Q9SB64 EnsemblPlants:AT4G24690.1 GeneID:828571 KEGG:ath:AT4G24690 TAIR:At4g24690 InParanoid:Q9SB64 OMA:CGVSEWD PhylomeDB:Q9SB64 ProtClustDB:CLSN2685439 Genevestigator:Q9SB64 Uniprot:Q9SB64</td></tr>
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<tr><td>Leaf</td><td>Isotig01084</td><td>59</td><td>12</td><td>2.827</td><td>5.73E-13</td><td>TAIR|locus:2121899 - symbol:NBR1 "AT4G24690" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0008270 "zinc ion binding" evidence=IEA] [GO:0005737 "cytoplasm" evidence=IDA] InterPro:IPR000270 InterPro:IPR000433 InterPro:IPR000449 InterPro:IPR009060 Pfam:PF00564 Pfam:PF00569 Pfam:PF00627 PROSITE:PS50135 SMART:SM00291 SMART:SM00666 EMBL:CP002687 GO:GO:0005737 GO:GO:0008270 EMBL:AL035356 EMBL:AL161562 SUPFAM:SSF46934 EMBL:AY062827 EMBL:AY128759 EMBL:AY140081 EMBL:BT008425 IPI:IPI00543691 PIR:T05565 RefSeq:NP_194200.1 UniGene:At.24692 UniGene:At.71380 ProteinModelPortal:Q9SB64 SMR:Q9SB64 IntAct:Q9SB64 PRIDE:Q9SB64 EnsemblPlants:AT4G24690.1 GeneID:828571 KEGG:ath:AT4G24690 TAIR:At4g24690 InParanoid:Q9SB64 OMA:CGVSEWD PhylomeDB:Q9SB64 ProtClustDB:CLSN2685439 Genevestigator:Q9SB64 Uniprot:Q9SB64</td></tr>
<tr><td>Leaf</td><td>Isotig01085</td><td>32</td><td>2</td><td>4.529</td><td>2.43E-10</td><td>TAIR|locus:2172656 - symbol:AT5G22920 species:3702 "Arabidopsis thaliana" [GO:0008270 "zinc ion binding" evidence=IEA;ISS] InterPro:IPR001841 InterPro:IPR008913 Pfam:PF05495 PROSITE:PS50089 PROSITE:PS51266 SMART:SM00184 InterPro:IPR004039 EMBL:CP002688 GO:GO:0008270 InterPro:IPR013083</td></tr>
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Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						Gene3D:G3DSA:3.30.40.10 HSSP:Q9LRB7 EMBL:AB005243 Gene3D:G3DSA:2.20.28.10 InterPro:IPR017921 PROSITE:PS51270 KO:K10144 EMBL:AY052362 EMBL:BT002635 EMBL:DQ059131 IPI:IPI00531172 RefSeq:NP_197683.1 UniGene:At.19948 ProteinModelPortal:Q9FFB6 SMR:Q9FFB6 STRING:Q9FFB6 EnsemblPlants:AT5G22920.1 GeneID:832356 KEGG:ath:AT5G22920 TAIR:At5g22920 InParanoid:Q9FFB6 OMA:KVICSLC PhylomeDB:Q9FFB6 ProtClustDB:CLSN2686096 Genevestigator:Q9FFB6 Uniprot:Q9FFB6
Leaf	Isotig01086	32	2	4.529	2.43E-10	TAIR|locus:2172656 - symbol:AT5G22920 species:3702 "Arabidopsis thaliana" [GO:0008270 "zinc ion binding" evidence=IEA;ISS] InterPro:IPR001841 InterPro:IPR008913 Pfam:PF05495 PROSITE:PS50089 PROSITE:PS51266 SMART:SM00184 InterPro:IPR004039 EMBL:CP002688 GO:GO:0008270 InterPro:IPR013083 Gene3D:G3DSA:3.30.40.10 HSSP:Q9LRB7 EMBL:AB005243 Gene3D:G3DSA:2.20.28.10 InterPro:IPR017921 PROSITE:PS51270 KO:K10144 EMBL:AY052362 EMBL:BT002635 EMBL:DQ059131 IPI:IPI00531172 RefSeq:NP_197683.1 UniGene:At.19948 ProteinModelPortal:Q9FFB6 SMR:Q9FFB6 STRING:Q9FFB6 EnsemblPlants:AT5G22920.1 GeneID:832356 KEGG:ath:AT5G22920 TAIR:At5g22920 InParanoid:Q9FFB6 OMA:KVICSLC PhylomeDB:Q9FFB6 ProtClustDB:CLSN2686096 Genevestigator:Q9FFB6 Uniprot:Q9FFB6
Leaf	Isotig01087	32	2	4.529	2.43E-10	TAIR|locus:2172656 - symbol:AT5G22920 species:3702 "Arabidopsis thaliana" [GO:0008270 "zinc ion binding" evidence=IEA;ISS] InterPro:IPR001841 InterPro:IPR008913 Pfam:PF05495 PROSITE:PS50089 PROSITE:PS51266 SMART:SM00184 InterPro:IPR004039 EMBL:CP002688 GO:GO:0008270 InterPro:IPR013083 Gene3D:G3DSA:3.30.40.10 HSSP:Q9LRB7 EMBL:AB005243 Gene3D:G3DSA:2.20.28.10 InterPro:IPR017921 PROSITE:PS51270 KO:K10144 EMBL:AY052362 EMBL:BT002635 EMBL:DQ059131 IPI:IPI00531172 RefSeq:NP_197683.1 UniGene:At.19948 ProteinModelPortal:Q9FFB6 SMR:Q9FFB6 STRING:Q9FFB6 EnsemblPlants:AT5G22920.1 GeneID:832356 KEGG:ath:AT5G22920 TAIR:At5g22920 InParanoid:Q9FFB6 OMA:KVICSLC PhylomeDB:Q9FFB6 ProtClustDB:CLSN2686096 Genevestigator:Q9FFB6 Uniprot:Q9FFB6
Leaf	Isotig01088	32	2	4.529	2.43E-10	TAIR|locus:2172656 - symbol:AT5G22920 species:3702 "Arabidopsis thaliana" [GO:0008270 "zinc ion binding" evidence=IEA;ISS] InterPro:IPR001841 InterPro:IPR008913 Pfam:PF05495 PROSITE:PS50089 PROSITE:PS51266 SMART:SM00184 InterPro:IPR004039 EMBL:CP002688 GO:GO:0008270 InterPro:IPR013083 Gene3D:G3DSA:3.30.40.10 HSSP:Q9LRB7 EMBL:AB005243 Gene3D:G3DSA:2.20.28.10 InterPro:IPR017921 PROSITE:PS51270 KO:K10144 EMBL:AY052362 EMBL:BT002635 EMBL:DQ059131 IPI:IPI00531172 RefSeq:NP_197683.1 UniGene:At.19948 ProteinModelPortal:Q9FFB6 SMR:Q9FFB6 STRING:Q9FFB6 EnsemblPlants:AT5G22920.1 GeneID:832356 KEGG:ath:AT5G22920 TAIR:At5g22920 InParanoid:Q9FFB6 OMA:KVICSLC PhylomeDB:Q9FFB6 ProtClustDB:CLSN2686096 Genevestigator:Q9FFB6 Uniprot:Q9FFB6
Leaf	Isotig01093	8	39	-1.756	0.000263686	TAIR|locus:2058475 - symbol:DPE2 "AT2G40840" species:3702 "Arabidopsis thaliana" [GO:0004134 "4-alpha-glucanotransferase activity" evidence=IGI;ISS;IDA] [GO:0000023 "maltose metabolic process" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] [GO:0005983 "starch catabolic process" evidence=TAS] [GO:0005976 "polysaccharide metabolic process" evidence=TAS] [GO:0010297 "heteropolysaccharide binding" evidence=IDA] [GO:0000025 "maltose catabolic process" evidence=IDA] InterPro:IPR002044 InterPro:IPR003385 InterPro:IPR013781 InterPro:IPR013784 Pfam:PF00686 Pfam:PF02446 PROSITE:PS51166 SMART:SM01065 GO:GO:0005829 EMBL:CP002685 GenomeReviews:CT485783_GR InterPro:IPR013783 Gene3D:G3DSA:2.60.40.10 GO:GO:0043169 InterPro:IPR017853 Gene3D:G3DSA:3.20.20.80 SUPFAM:SSF51445 GO:GO:0005983 EMBL:AC002409 SUPFAM:SSF49452 CAZy:GH77 eggNOG:COG1640 KO:K00705 GO:GO:0004134 GO:GO:0000025 EMBL:AY081315 EMBL:BT010364 IPI:IPI00538294 PIR:T00748 RefSeq:NP_181616.3 UniGene:At.44028 ProteinModelPortal:Q8RXD9 SMR:Q8RXD9 STRING:Q8RXD9 CAZy:CBM20 PRIDE:Q8RXD9 ProMEX:Q8RXD9 EnsemblPlants:AT2G40840.1 GeneID:818682 KEGG:ath:AT2G40840 TAIR:At2g40840 HOGENOM:HBG557805 InParanoid:Q8RXD9 OMA:HYWRYRM PhylomeDB:Q8RXD9 ProtClustDB:PLN02950 Genevestigator:Q8RXD9 GO:GO:0010297 GO:GO:2001070 Uniprot:Q8RXD9
Leaf	Isotig01094	8	39	-1.756	0.000263686	TAIR|locus:2058475 - symbol:DPE2 "AT2G40840" species:3702 "Arabidopsis thaliana" [GO:0004134 "4-alpha-glucanotransferase activity" evidence=IGI;ISS;IDA] [GO:0000023 "maltose metabolic process" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] [GO:0005983 "starch catabolic process" evidence=TAS] [GO:0005976 "polysaccharide metabolic process" evidence=TAS] [GO:0010297 "heteropolysaccharide binding" evidence=IDA] [GO:0000025 "maltose catabolic process" evidence=IDA] InterPro:IPR002044 InterPro:IPR003385 InterPro:IPR013781 InterPro:IPR013784 Pfam:PF00686 Pfam:PF02446 PROSITE:PS51166 SMART:SM01065 GO:GO:0005829 EMBL:CP002685 GenomeReviews:CT485783_GR InterPro:IPR013783 Gene3D:G3DSA:2.60.40.10 GO:GO:0043169 InterPro:IPR017853 Gene3D:G3DSA:3.20.20.80 SUPFAM:SSF51445

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						GO:GO:0005983 EMBL:AC002409 SUPFAM:SSF49452 CAZy:GH77 eggNOG:COG1640 KO:K00705 GO:GO:0004134 GO:GO:0000025 EMBL:AY081315 EMBL:BT010364 IPI:IPI00538294 PIR:T00748 RefSeq:NP_181616.3 UniGene:At.44028 ProteinModelPortal:Q8RXD9 SMR:Q8RXD9 STRING:Q8RXD9 CAZy:CBM20 PRIDE:Q8RXD9 ProMEX:Q8RXD9 EnsemblPlants:AT2G40840.1 GeneID:818682 KEGG:ath:AT2G40840 TAIR:At2g40840 HOGENOM:HBG557805 InParanoid:Q8RXD9 OMA:HYWRYRM PhylomeDB:Q8RXD9 ProtClustDB:PLN02950 Genevestigator:Q8RXD9 GO:GO:0010297 GO:GO:2001070 Uniprot:Q8RXD9
Leaf	Isotig01095	8	37	-1.680	0.000570683	TAIR|locus:2058475 - symbol:DPE2 "AT2G40840" species:3702 "Arabidopsis thaliana" [GO:0004134 "4-alpha-glucanotransferase activity" evidence=IGI;ISS;IDA] [GO:0000023 "maltose metabolic process" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] [GO:0005983 "starch catabolic process" evidence=TAS] [GO:0005976 "polysaccharide metabolic process" evidence=TAS] [GO:0010297 "heteropolysaccharide binding" evidence=IDA] [GO:0000025 "maltose catabolic process" evidence=IDA] InterPro:IPR002044 InterPro:IPR003385 InterPro:IPR013781 InterPro:IPR013784 Pfam:PF00686 Pfam:PF02446 PROSITE:PS51166 SMART:SM01065 GO:GO:0005829 EMBL:CP002685 GenomeReviews:CT485783_GR InterPro:IPR013783 Gene3D:G3DSA:2.60.40.10 GO:GO:0043169 InterPro:IPR017853 Gene3D:G3DSA:3.20.20.80 SUPFAM:SSF51445 GO:GO:0005983 EMBL:AC002409 SUPFAM:SSF49452 CAZy:GH77 eggNOG:COG1640 KO:K00705 GO:GO:0004134 GO:GO:0000025 EMBL:AY081315 EMBL:BT010364 IPI:IPI00538294 PIR:T00748 RefSeq:NP_181616.3 UniGene:At.44028 ProteinModelPortal:Q8RXD9 SMR:Q8RXD9 STRING:Q8RXD9 CAZy:CBM20 PRIDE:Q8RXD9 ProMEX:Q8RXD9 EnsemblPlants:AT2G40840.1 GeneID:818682 KEGG:ath:AT2G40840 TAIR:At2g40840 HOGENOM:HBG557805 InParanoid:Q8RXD9 OMA:HYWRYRM PhylomeDB:Q8RXD9 ProtClustDB:PLN02950 Genevestigator:Q8RXD9 GO:GO:0010297 GO:GO:2001070 Uniprot:Q8RXD9
Leaf	Isotig01096	8	37	-1.680	0.000570683	TAIR|locus:2058475 - symbol:DPE2 "AT2G40840" species:3702 "Arabidopsis thaliana" [GO:0004134 "4-alpha-glucanotransferase activity" evidence=IGI;ISS;IDA] [GO:0000023 "maltose metabolic process" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] [GO:0005983 "starch catabolic process" evidence=TAS] [GO:0005976 "polysaccharide metabolic process" evidence=TAS] [GO:0010297 "heteropolysaccharide binding" evidence=IDA] [GO:0000025 "maltose catabolic process" evidence=IDA] InterPro:IPR002044 InterPro:IPR003385 InterPro:IPR013781 InterPro:IPR013784 Pfam:PF00686 Pfam:PF02446 PROSITE:PS51166 SMART:SM01065 GO:GO:0005829 EMBL:CP002685 GenomeReviews:CT485783_GR InterPro:IPR013783 Gene3D:G3DSA:2.60.40.10 GO:GO:0043169 InterPro:IPR017853 Gene3D:G3DSA:3.20.20.80 SUPFAM:SSF51445 GO:GO:0005983 EMBL:AC002409 SUPFAM:SSF49452 CAZy:GH77 eggNOG:COG1640 KO:K00705 GO:GO:0004134 GO:GO:0000025 EMBL:AY081315 EMBL:BT010364 IPI:IPI00538294 PIR:T00748 RefSeq:NP_181616.3 UniGene:At.44028 ProteinModelPortal:Q8RXD9 SMR:Q8RXD9 STRING:Q8RXD9 CAZy:CBM20 PRIDE:Q8RXD9 ProMEX:Q8RXD9 EnsemblPlants:AT2G40840.1 GeneID:818682 KEGG:ath:AT2G40840 TAIR:At2g40840 HOGENOM:HBG557805 InParanoid:Q8RXD9 OMA:HYWRYRM PhylomeDB:Q8RXD9 ProtClustDB:PLN02950 Genevestigator:Q8RXD9 GO:GO:0010297 GO:GO:2001070 Uniprot:Q8RXD9
Leaf	Isotig01105	21	2	3.921	8.06E-07	TAIR|locus:2128716 - symbol:TPC1 "AT4G03560" species:3702 "Arabidopsis thaliana" [GO:0005262 "calcium channel activity" evidence=IGI;ISS;IMP] [GO:0005245 "voltage-gated calcium channel activity" evidence=IGI;ISS] [GO:0005886 "plasma membrane" evidence=TAS] [GO:0006816 "calcium ion transport" evidence=IC;IMP] [GO:0005773 "vacuole" evidence=IDA] [GO:0000325 "plant-type vacuole" evidence=IDA] [GO:0009845 "seed germination" evidence=IMP] [GO:0010119 "regulation of stomatal movement" evidence=IMP] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0080141 "regulation of jasmonic acid biosynthetic process" evidence=IMP] [GO:0019722 "calcium-mediated signaling" evidence=IMP] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR002048 InterPro:IPR005821 InterPro:IPR011992 Pfam:PF00520 SMART:SM00054 GO:GO:0016021 GO:GO:0005886 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005774 GO:GO:0005509 GO:GO:0010119 GO:GO:0019722 InterPro:IPR018249 Gene3D:G3DSA:1.10.238.10 PROSITE:PS50222 GO:GO:0000325 GO:GO:0009845 GO:GO:0005245 EMBL:AC005142 EMBL:AF071527 EMBL:AL161497 GO:GO:0080141 EMBL:AB053952 EMBL:AF360372 IPI:IPI00542997 PIR:B85045 RefSeq:NP_567258.1 UniGene:At.3957 ProteinModelPortal:Q94KI8 IntAct:Q94KI8 STRING:Q94KI8 PRIDE:Q94KI8 EnsemblPlants:AT4G03560.1 GeneID:825655 KEGG:ath:AT4G03560 TAIR:At4g03560 eggNOG:NOG280094

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						HOGENOM:HBG591069 InParanoid:Q94KI8 OMA:LVMGNWQ PhylomeDB:Q94KI8 ProtClustDB:CLSN2689320 ArrayExpress:Q9ZT83 Genevestigator:Q94KI8 Uniprot:Q94KI8
Leaf	Isotig01106	21	2	3.921	8.06E-07	TAIR|locus:2128716 - symbol:TPC1 "AT4G03560" species:3702 "Arabidopsis thaliana" [GO:0005262 "calcium channel activity" evidence=IGI;ISS;IMP] [GO:0005245 "voltage-gated calcium channel activity" evidence=IGI;ISS] [GO:0005886 "plasma membrane" evidence=TAS] [GO:0006816 "calcium ion transport" evidence=IC;IMP] [GO:0005773 "vacuole" evidence=IDA] [GO:0000325 "plant-type vacuole" evidence=IDA] [GO:0009845 "seed germination" evidence=IMP] [GO:0010119 "regulation of stomatal movement" evidence=IMP] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0080141 "regulation of jasmonic acid biosynthetic process" evidence=IMP] [GO:0019722 "calcium-mediated signaling" evidence=IMP] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR002048 InterPro:IPR005821 InterPro:IPR011992 Pfam:PF00520 SMART:SM00054 GO:GO:0016021 GO:GO:0005886 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005774 GO:GO:0005509 GO:GO:0010119 GO:GO:0019722 InterPro:IPR018249 Gene3D:G3DSA:1.10.238.10 PROSITE:PS50222 GO:GO:0000325 GO:GO:0009845 GO:GO:0005245 EMBL:AC005142 EMBL:AF071527 EMBL:AL161497 GO:GO:0080141 EMBL:AB053952 EMBL:AF360372 IPI:IPI00542997 PIR:B85045 RefSeq:NP_567258.1 UniGene:At.3957 ProteinModelPortal:Q94KI8 IntAct:Q94KI8 STRING:Q94KI8 PRIDE:Q94KI8 EnsemblPlants:AT4G03560.1 GeneID:825655 KEGG:ath:AT4G03560 TAIR:At4g03560 eggNOG:NOG280094 HOGENOM:HBG591069 InParanoid:Q94KI8 OMA:LVMGNWQ PhylomeDB:Q94KI8 ProtClustDB:CLSN2689320 ArrayExpress:Q9ZT83 Genevestigator:Q94KI8 Uniprot:Q94KI8
Leaf	Isotig01107	19	2	3.777	3.57E-06	TAIR|locus:2128716 - symbol:TPC1 "AT4G03560" species:3702 "Arabidopsis thaliana" [GO:0005262 "calcium channel activity" evidence=IGI;ISS;IMP] [GO:0005245 "voltage-gated calcium channel activity" evidence=IGI;ISS] [GO:0005886 "plasma membrane" evidence=TAS] [GO:0006816 "calcium ion transport" evidence=IC;IMP] [GO:0005773 "vacuole" evidence=IDA] [GO:0000325 "plant-type vacuole" evidence=IDA] [GO:0009845 "seed germination" evidence=IMP] [GO:0010119 "regulation of stomatal movement" evidence=IMP] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0080141 "regulation of jasmonic acid biosynthetic process" evidence=IMP] [GO:0019722 "calcium-mediated signaling" evidence=IMP] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR002048 InterPro:IPR005821 InterPro:IPR011992 Pfam:PF00520 SMART:SM00054 GO:GO:0016021 GO:GO:0005886 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005774 GO:GO:0005509 GO:GO:0010119 GO:GO:0019722 InterPro:IPR018249 Gene3D:G3DSA:1.10.238.10 PROSITE:PS50222 GO:GO:0000325 GO:GO:0009845 GO:GO:0005245 EMBL:AC005142 EMBL:AF071527 EMBL:AL161497 GO:GO:0080141 EMBL:AB053952 EMBL:AF360372 IPI:IPI00542997 PIR:B85045 RefSeq:NP_567258.1 UniGene:At.3957 ProteinModelPortal:Q94KI8 IntAct:Q94KI8 STRING:Q94KI8 PRIDE:Q94KI8 EnsemblPlants:AT4G03560.1 GeneID:825655 KEGG:ath:AT4G03560 TAIR:At4g03560 eggNOG:NOG280094 HOGENOM:HBG591069 InParanoid:Q94KI8 OMA:LVMGNWQ PhylomeDB:Q94KI8 ProtClustDB:CLSN2689320 ArrayExpress:Q9ZT83 Genevestigator:Q94KI8 Uniprot:Q94KI8
Leaf	Isotig01108	19	2	3.777	3.57E-06	TAIR|locus:2128716 - symbol:TPC1 "AT4G03560" species:3702 "Arabidopsis thaliana" [GO:0005262 "calcium channel activity" evidence=IGI;ISS;IMP] [GO:0005245 "voltage-gated calcium channel activity" evidence=IGI;ISS] [GO:0005886 "plasma membrane" evidence=TAS] [GO:0006816 "calcium ion transport" evidence=IC;IMP] [GO:0005773 "vacuole" evidence=IDA] [GO:0000325 "plant-type vacuole" evidence=IDA] [GO:0009845 "seed germination" evidence=IMP] [GO:0010119 "regulation of stomatal movement" evidence=IMP] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0080141 "regulation of jasmonic acid biosynthetic process" evidence=IMP] [GO:0019722 "calcium-mediated signaling" evidence=IMP] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR002048 InterPro:IPR005821 InterPro:IPR011992 Pfam:PF00520 SMART:SM00054 GO:GO:0016021 GO:GO:0005886 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005774 GO:GO:0005509 GO:GO:0010119 GO:GO:0019722 InterPro:IPR018249 Gene3D:G3DSA:1.10.238.10 PROSITE:PS50222 GO:GO:0000325 GO:GO:0009845 GO:GO:0005245 EMBL:AC005142 EMBL:AF071527 EMBL:AL161497 GO:GO:0080141 EMBL:AB053952 EMBL:AF360372 IPI:IPI00542997 PIR:B85045 RefSeq:NP_567258.1 UniGene:At.3957 ProteinModelPortal:Q94KI8 IntAct:Q94KI8 STRING:Q94KI8 PRIDE:Q94KI8 EnsemblPlants:AT4G03560.1 GeneID:825655 KEGG:ath:AT4G03560 TAIR:At4g03560 eggNOG:NOG280094 HOGENOM:HBG591069 InParanoid:Q94KI8 OMA:LVMGNWQ PhylomeDB:Q94KI8 ProtClustDB:CLSN2689320 ArrayExpress:Q9ZT83 Genevestigator:Q94KI8 Uniprot:Q94KI8
Leaf	Isotig01113	70	20	2.336	1.62E-12	TAIR|locus:2089270 - symbol:NiaP "AT3G13050" species:3702 "Arabidopsis thaliana" [GO:0005351 "sugar:hydrogen symporter activity" evidence=ISS] [GO:0015144 "carbohydrate transmembrane transporter activity"

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						evidence=ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:2001142 "nicotinate transport" evidence=IDA] [GO:2001143 "N-methylnicotinate transport" evidence=IDA] InterPro:IPR005828 InterPro:IPR005829 Pfam:PF00083 PROSITE:PS00216 PROSITE:PS00217 GO:GO:0016021 GO:GO:0005886 GO:GO:0005524 EMBL:CP002686 GenomeReviews:BA000014_GR eggNOG:COG0477 InterPro:IPR016196 SUPFAM:SSF103473 InterPro:IPR020846 PROSITE:PS50850 GO:GO:0022857 EMBL:AB026645 HOGENOM:HBG715489 EMBL:AY054262 EMBL:BT004522 IPI:IPI00523791 IPI:IPI00546036 RefSeq:NP_187911.1 UniGene:At.26387 ProteinModelPortal:Q940M4 STRING:Q940M4 PRIDE:Q940M4 EnsemblPlants:AT3G13050.1 GeneID:820491 KEGG:ath:AT3G13050 TAIR:At3g13050 InParanoid:Q940M4 OMA:GRICISA PhylomeDB:Q940M4 ProtClustDB:CLSN2684648 Genevestigator:Q940M4 GO:GO:2001143 GO:GO:2001142 Uniprot:Q940M4
Leaf	Isotig01114	69	20	2.316	3.04E-12	TAIR|locus:2089270 - symbol:NiaP "AT3G13050" species:3702 "Arabidopsis thaliana" [GO:0005351 "sugar:hydrogen symporter activity" evidence=ISS] [GO:0015144 "carbohydrate transmembrane transporter activity" evidence=ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:2001142 "nicotinate transport" evidence=IDA] [GO:2001143 "N-methylnicotinate transport" evidence=IDA] InterPro:IPR005828 InterPro:IPR005829 Pfam:PF00083 PROSITE:PS00216 PROSITE:PS00217 GO:GO:0016021 GO:GO:0005886 GO:GO:0005524 EMBL:CP002686 GenomeReviews:BA000014_GR eggNOG:COG0477 InterPro:IPR016196 SUPFAM:SSF103473 InterPro:IPR020846 PROSITE:PS50850 GO:GO:0022857 EMBL:AB026645 HOGENOM:HBG715489 EMBL:AY054262 EMBL:BT004522 IPI:IPI00523791 IPI:IPI00546036 RefSeq:NP_187911.1 UniGene:At.26387 ProteinModelPortal:Q940M4 STRING:Q940M4 PRIDE:Q940M4 EnsemblPlants:AT3G13050.1 GeneID:820491 KEGG:ath:AT3G13050 TAIR:At3g13050 InParanoid:Q940M4 OMA:GRICISA PhylomeDB:Q940M4 ProtClustDB:CLSN2684648 Genevestigator:Q940M4 GO:GO:2001143 GO:GO:2001142 Uniprot:Q940M4
Leaf	Isotig01115	67	18	2.425	1.62E-12	TAIR|locus:2089270 - symbol:NiaP "AT3G13050" species:3702 "Arabidopsis thaliana" [GO:0005351 "sugar:hydrogen symporter activity" evidence=ISS] [GO:0015144 "carbohydrate transmembrane transporter activity" evidence=ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:2001142 "nicotinate transport" evidence=IDA] [GO:2001143 "N-methylnicotinate transport" evidence=IDA] InterPro:IPR005828 InterPro:IPR005829 Pfam:PF00083 PROSITE:PS00216 PROSITE:PS00217 GO:GO:0016021 GO:GO:0005886 GO:GO:0005524 EMBL:CP002686 GenomeReviews:BA000014_GR eggNOG:COG0477 InterPro:IPR016196 SUPFAM:SSF103473 InterPro:IPR020846 PROSITE:PS50850 GO:GO:0022857 EMBL:AB026645 HOGENOM:HBG715489 EMBL:AY054262 EMBL:BT004522 IPI:IPI00523791 IPI:IPI00546036 RefSeq:NP_187911.1 UniGene:At.26387 ProteinModelPortal:Q940M4 STRING:Q940M4 PRIDE:Q940M4 EnsemblPlants:AT3G13050.1 GeneID:820491 KEGG:ath:AT3G13050 TAIR:At3g13050 InParanoid:Q940M4 OMA:GRICISA PhylomeDB:Q940M4 ProtClustDB:CLSN2684648 Genevestigator:Q940M4 GO:GO:2001143 GO:GO:2001142 Uniprot:Q940M4
Leaf	Isotig01116	66	18	2.403	3.07E-12	TAIR|locus:2089270 - symbol:NiaP "AT3G13050" species:3702 "Arabidopsis thaliana" [GO:0005351 "sugar:hydrogen symporter activity" evidence=ISS] [GO:0015144 "carbohydrate transmembrane transporter activity" evidence=ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:2001142 "nicotinate transport" evidence=IDA] [GO:2001143 "N-methylnicotinate transport" evidence=IDA] InterPro:IPR005828 InterPro:IPR005829 Pfam:PF00083 PROSITE:PS00216 PROSITE:PS00217 GO:GO:0016021 GO:GO:0005886 GO:GO:0005524 EMBL:CP002686 GenomeReviews:BA000014_GR eggNOG:COG0477 InterPro:IPR016196 SUPFAM:SSF103473 InterPro:IPR020846 PROSITE:PS50850 GO:GO:0022857 EMBL:AB026645 HOGENOM:HBG715489 EMBL:AY054262 EMBL:BT004522 IPI:IPI00523791 IPI:IPI00546036 RefSeq:NP_187911.1 UniGene:At.26387 ProteinModelPortal:Q940M4 STRING:Q940M4 PRIDE:Q940M4 EnsemblPlants:AT3G13050.1 GeneID:820491 KEGG:ath:AT3G13050 TAIR:At3g13050 InParanoid:Q940M4 OMA:GRICISA PhylomeDB:Q940M4 ProtClustDB:CLSN2684648 Genevestigator:Q940M4 GO:GO:2001143 GO:GO:2001142 Uniprot:Q940M4
Leaf	Isotig01117	85	45	1.446	1.88E-08	TAIR|locus:2037493 - symbol:VHA-A "vacuolar ATP synthase subunit A" species:3702 "Arabidopsis thaliana" [GO:0005524 "ATP binding" evidence=IEA;ISS] [GO:0015992 "proton transport" evidence=ISS] [GO:0016820 "hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances" evidence=IEA] [GO:0046933 "hydrogen ion transporting ATP synthase activity, rotational mechanism" evidence=IEA;ISS] [GO:0046961 "proton-transporting ATPase activity, rotational mechanism" evidence=IEA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA]

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						[GO:0007030 "Golgi organization" evidence=IMP] [GO:0009555 "pollen development" evidence=IMP] [GO:0005618 "cell wall" evidence=IDA] [GO:0000325 "plant-type vacuole" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0002020 "protease binding" evidence=IPI] [GO:0005829 "cytosol" evidence=RCA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR000194 InterPro:IPR000793 InterPro:IPR004100 InterPro:IPR005725 InterPro:IPR018118 InterPro:IPR020003 InterPro:IPR022878 Pfam:PF00006 Pfam:PF00306 Pfam:PF02874 PROSITE:PS00152 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005886 GO:GO:0009506 GO:GO:0005524 GO:GO:0005774 GO:GO:0005618 GO:GO:0002020 GO:GO:0009941 GO:GO:0009651 GO:GO:0000325 GO:GO:0009555 GO:GO:0007030 GO:GO:0015991 GO:GO:0046933 GO:GO:0046961 SUPFAM:SSF50615 SUPFAM:SSF47917 InterPro:IPR024034 Gene3D:G3DSA:1.10.1140.10 EMBL:AC005679 TCDB:3.A.2.2.5 GO:GO:0033180 eggNOG:COG1155 KO:K02145 TIGRFAMs:TIGR01042 OMA:SENKITW EMBL:U65638 EMBL:AY059909 EMBL:AY081296 EMBL:BT002589 EMBL:BT008383 EMBL:AY085759 IPI:IPI00525922 PIR:E96818 RefSeq:NP_001031299.1 RefSeq:NP_178011.1 UniGene:At.24629 UniGene:At.67925 ProteinModelPortal:O23654 SMR:O23654 IntAct:O23654 STRING:O23654 PRIDE:O23654 EnsemblPlants:AT1G78900.1 EnsemblPlants:AT1G78900.2 GeneID:844228 KEGG:ath:AT1G78900 TAIR:At1g78900 HOGENOM:HBG288114 InParanoid:O23654 PhylomeDB:O23654 ProtClustDB:CLSN2679797 ArrayExpress:O23654 Genevestigator:O23654 GermOnline:AT1G78900 Uniprot:O23654
Leaf	Isotig01118	85	45	1.446	1.88E-08	TAIR|locus:2037493 - symbol:VHA-A "vacuolar ATP synthase subunit A" species:3702 "Arabidopsis thaliana" [GO:0005524 "ATP binding" evidence=IEA;ISS] [GO:0015992 "proton transport" evidence=ISS] [GO:0016820 "hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances" evidence=IEA] [GO:0046933 "hydrogen ion transporting ATP synthase activity, rotational mechanism" evidence=IEA;ISS] [GO:0046961 "proton-transporting ATPase activity, rotational mechanism" evidence=IEA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0007030 "Golgi organization" evidence=IMP] [GO:0009555 "pollen development" evidence=IMP] [GO:0005618 "cell wall" evidence=IDA] [GO:0000325 "plant-type vacuole" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0002020 "protease binding" evidence=IPI] [GO:0005829 "cytosol" evidence=RCA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR000194 InterPro:IPR000793 InterPro:IPR004100 InterPro:IPR005725 InterPro:IPR018118 InterPro:IPR020003 InterPro:IPR022878 Pfam:PF00006 Pfam:PF00306 Pfam:PF02874 PROSITE:PS00152 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005886 GO:GO:0009506 GO:GO:0005524 GO:GO:0005774 GO:GO:0005618 GO:GO:0002020 GO:GO:0009941 GO:GO:0009651 GO:GO:0000325 GO:GO:0009555 GO:GO:0007030 GO:GO:0015991 GO:GO:0046933 GO:GO:0046961 SUPFAM:SSF50615 SUPFAM:SSF47917 InterPro:IPR024034 Gene3D:G3DSA:1.10.1140.10 EMBL:AC005679 TCDB:3.A.2.2.5 GO:GO:0033180 eggNOG:COG1155 KO:K02145 TIGRFAMs:TIGR01042 OMA:SENKITW EMBL:U65638 EMBL:AY059909 EMBL:AY081296 EMBL:BT002589 EMBL:BT008383 EMBL:AY085759 IPI:IPI00525922 PIR:E96818 RefSeq:NP_001031299.1 RefSeq:NP_178011.1 UniGene:At.24629 UniGene:At.67925 ProteinModelPortal:O23654 SMR:O23654 IntAct:O23654 STRING:O23654 PRIDE:O23654 EnsemblPlants:AT1G78900.1 EnsemblPlants:AT1G78900.2 GeneID:844228 KEGG:ath:AT1G78900 TAIR:At1g78900 HOGENOM:HBG288114 InParanoid:O23654 PhylomeDB:O23654 ProtClustDB:CLSN2679797 ArrayExpress:O23654 Genevestigator:O23654 GermOnline:AT1G78900 Uniprot:O23654
Leaf	Isotig01119	88	46	1.465	7.68E-09	TAIR|locus:2037493 - symbol:VHA-A "vacuolar ATP synthase subunit A" species:3702 "Arabidopsis thaliana" [GO:0005524 "ATP binding" evidence=IEA;ISS] [GO:0015992 "proton transport" evidence=ISS] [GO:0016820 "hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances" evidence=IEA] [GO:0046933 "hydrogen ion transporting ATP synthase activity, rotational mechanism" evidence=IEA;ISS] [GO:0046961 "proton-transporting ATPase activity, rotational mechanism" evidence=IEA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0007030 "Golgi organization" evidence=IMP] [GO:0009555 "pollen development" evidence=IMP] [GO:0005618 "cell wall" evidence=IDA] [GO:0000325 "plant-type vacuole" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0002020 "protease binding" evidence=IPI] [GO:0005829 "cytosol" evidence=RCA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus"

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						evidence=IDA] InterPro:IPR000194 InterPro:IPR000793 InterPro:IPR004100 InterPro:IPR005725 InterPro:IPR018118 InterPro:IPR020003 InterPro:IPR022878 Pfam:PF00006 Pfam:PF00306 Pfam:PF02874 PROSITE:PS00152 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005886 GO:GO:0009506 GO:GO:0005524 GO:GO:0005774 GO:GO:0005618 GO:GO:0002020 GO:GO:0009941 GO:GO:0009651 GO:GO:0000325 GO:GO:0009555 GO:GO:0007030 GO:GO:0015991 GO:GO:0046933 GO:GO:0046961 SUPFAM:SSF50615 SUPFAM:SSF47917 InterPro:IPR024034 Gene3D:G3DSA:1.10.1140.10 EMBL:AC005679 TCDB:3.A.2.2.5 GO:GO:0033180 eggNOG:COG1155 KO:K02145 TIGRFAMs:TIGR01042 OMA:SENKITW EMBL:U65638 EMBL:AY059909 EMBL:AY081296 EMBL:BT002589 EMBL:BT008383 EMBL:AY085759 IPI:IPI00525922 PIR:E96818 RefSeq:NP_001031299.1 RefSeq:NP_178011.1 UniGene:At.24629 UniGene:At.67925 ProteinModelPortal:O23654 SMR:O23654 IntAct:O23654 STRING:O23654 PRIDE:O23654 EnsemblPlants:AT1G78900.1 EnsemblPlants:AT1G78900.2 GeneID:844228 KEGG:ath:AT1G78900 TAIR:At1g78900 HOGENOM:HBG288114 InParanoid:O23654 PhylomeDB:O23654 ProtClustDB:CLSN2679797 ArrayExpress:O23654 Genevestigator:O23654 GermOnline:AT1G78900 Uniprot:O23654
Leaf	Isotig01120	88	46	1.465	7.68E-09	TAIR|locus:2037493 - symbol:VHA-A "vacuolar ATP synthase subunit A" species:3702 "Arabidopsis thaliana" [GO:0005524 "ATP binding" evidence=IEA;ISS] [GO:0015992 "proton transport" evidence=ISS] [GO:0016820 "hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances" evidence=IEA] [GO:0046933 "hydrogen ion transporting ATP synthase activity, rotational mechanism" evidence=IEA;ISS] [GO:0046961 "proton-transporting ATPase activity, rotational mechanism" evidence=IEA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0007030 "Golgi organization" evidence=IMP] [GO:0009555 "pollen development" evidence=IMP] [GO:0005618 "cell wall" evidence=IDA] [GO:0000325 "plant-type vacuole" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0002020 "protease binding" evidence=IPI] [GO:0005829 "cytosol" evidence=RCA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR000194 InterPro:IPR000793 InterPro:IPR004100 InterPro:IPR005725 InterPro:IPR018118 InterPro:IPR020003 InterPro:IPR022878 Pfam:PF00006 Pfam:PF00306 Pfam:PF02874 PROSITE:PS00152 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005886 GO:GO:0009506 GO:GO:0005524 GO:GO:0005774 GO:GO:0005618 GO:GO:0002020 GO:GO:0009941 GO:GO:0009651 GO:GO:0000325 GO:GO:0009555 GO:GO:0007030 GO:GO:0015991 GO:GO:0046933 GO:GO:0046961 SUPFAM:SSF50615 SUPFAM:SSF47917 InterPro:IPR024034 Gene3D:G3DSA:1.10.1140.10 EMBL:AC005679 TCDB:3.A.2.2.5 GO:GO:0033180 eggNOG:COG1155 KO:K02145 TIGRFAMs:TIGR01042 OMA:SENKITW EMBL:U65638 EMBL:AY059909 EMBL:AY081296 EMBL:BT002589 EMBL:BT008383 EMBL:AY085759 IPI:IPI00525922 PIR:E96818 RefSeq:NP_001031299.1 RefSeq:NP_178011.1 UniGene:At.24629 UniGene:At.67925 ProteinModelPortal:O23654 SMR:O23654 IntAct:O23654 STRING:O23654 PRIDE:O23654 EnsemblPlants:AT1G78900.1 EnsemblPlants:AT1G78900.2 GeneID:844228 KEGG:ath:AT1G78900 TAIR:At1g78900 HOGENOM:HBG288114 InParanoid:O23654 PhylomeDB:O23654 ProtClustDB:CLSN2679797 ArrayExpress:O23654 Genevestigator:O23654 GermOnline:AT1G78900 Uniprot:O23654
Leaf	Isotig01133	19	7	1.970	0.000947153	TAIR|locus:2014540 - symbol:AT1G03290 "AT1G03290" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002684 GenomeReviews:CT485782_GR EMBL:AC005278 eggNOG:NOG316219 HOGENOM:HBG027356 ProtClustDB:CLSN2679654 IPI:IPI00532020 PIR:D86164 RefSeq:NP_001184898.1 RefSeq:NP_171828.1 UniGene:At.43158 ProteinModelPortal:Q9ZVT0 STRING:Q9ZVT0 PRIDE:Q9ZVT0 EnsemblPlants:AT1G03290.1 EnsemblPlants:AT1G03290.2 GeneID:838603 KEGG:ath:AT1G03290 TAIR:At1g03290 InParanoid:Q9ZVT0 OMA:TEMETVT PhylomeDB:Q9ZVT0 Genevestigator:Q9ZVT0 Uniprot:Q9ZVT0
Leaf	Isotig01134	19	7	1.970	0.000947153	TAIR|locus:2014540 - symbol:AT1G03290 "AT1G03290" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002684 GenomeReviews:CT485782_GR EMBL:AC005278 eggNOG:NOG316219 HOGENOM:HBG027356 ProtClustDB:CLSN2679654 IPI:IPI00532020 PIR:D86164 RefSeq:NP_001184898.1 RefSeq:NP_171828.1 UniGene:At.43158 ProteinModelPortal:Q9ZVT0 STRING:Q9ZVT0 PRIDE:Q9ZVT0 EnsemblPlants:AT1G03290.1 EnsemblPlants:AT1G03290.2 GeneID:838603

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						KEGG:ath:AT1G03290 TAIR:At1g03290 InParanoid:Q9ZVT0 OMA:TEMETVT PhylomeDB:Q9ZVT0 Genevestigator:Q9ZVT0 Uniprot:Q9ZVT0
Leaf	Isotig01135	19	7	1.970	0.000947153	TAIR|locus:2014540 - symbol:AT1G03290 "AT1G03290" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002684 GenomeReviews:CT485782_GR EMBL:AC005278 eggNOG:NOG316219 HOGENOM:HBG027356 ProtClustDB:CLSN2679654 IPI:IPI00532020 PIR:D86164 RefSeq:NP_001184898.1 RefSeq:NP_171828.1 UniGene:At.43158 ProteinModelPortal:Q9ZVT0 STRING:Q9ZVT0 PRIDE:Q9ZVT0 EnsemblPlants:AT1G03290.1 EnsemblPlants:AT1G03290.2 GeneID:838603 KEGG:ath:AT1G03290 TAIR:At1g03290 InParanoid:Q9ZVT0 OMA:TEMETVT PhylomeDB:Q9ZVT0 Genevestigator:Q9ZVT0 Uniprot:Q9ZVT0
Leaf	Isotig01136	19	7	1.970	0.000947153	TAIR|locus:2014540 - symbol:AT1G03290 "AT1G03290" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002684 GenomeReviews:CT485782_GR EMBL:AC005278 eggNOG:NOG316219 HOGENOM:HBG027356 ProtClustDB:CLSN2679654 IPI:IPI00532020 PIR:D86164 RefSeq:NP_001184898.1 RefSeq:NP_171828.1 UniGene:At.43158 ProteinModelPortal:Q9ZVT0 STRING:Q9ZVT0 PRIDE:Q9ZVT0 EnsemblPlants:AT1G03290.1 EnsemblPlants:AT1G03290.2 GeneID:838603 KEGG:ath:AT1G03290 TAIR:At1g03290 InParanoid:Q9ZVT0 OMA:TEMETVT PhylomeDB:Q9ZVT0 Genevestigator:Q9ZVT0 Uniprot:Q9ZVT0
Leaf	Isotig01141	70	14	2.851	3.17E-15	TAIR|locus:2087765 - symbol:emb2742 "embryo defective 2742" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0003883 "CTP synthase activity" evidence=IEA;ISS] [GO:0009793 "embryo development ending in seed dormancy" evidence=NAS] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA] HAMAP:MF_01227 InterPro:IPR004468 InterPro:IPR017456 Pfam:PF06418 Pfam:PF00117 GO:GO:0005829 GO:GO:0046686 EMBL:CP002686 GenomeReviews:BA000014_GR EMBL:AB024033 EMBL:AC069474 GO:GO:0006221 InterPro:IPR017926 PROSITE:PS51273 eggNOG:COG0504 HOGENOM:HBG597806 KO:K01937 GO:GO:0003883 PANTHER:PTHR11550 TIGRFAMs:TIGR00337 OMA:EQCSIAL ProtClustDB:PLN02327 EMBL:AY093110 EMBL:BT008360 IPI:IPI00542960 RefSeq:NP_187873.1 UniGene:At.5669 ProteinModelPortal:Q9LTW8 SMR:Q9LTW8 STRING:Q9LTW8 PRIDE:Q9LTW8 EnsemblPlants:AT3G12670.1 GeneID:820447 KEGG:ath:AT3G12670 TAIR:At3g12670 InParanoid:Q9LTW8 PhylomeDB:Q9LTW8 ArrayExpress:Q9LTW8 Genevestigator:Q9LTW8 Uniprot:Q9LTW8
Leaf	Isotig01142	65	14	2.744	9.40E-14	TAIR|locus:2087765 - symbol:emb2742 "embryo defective 2742" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0003883 "CTP synthase activity" evidence=IEA;ISS] [GO:0009793 "embryo development ending in seed dormancy" evidence=NAS] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA] HAMAP:MF_01227 InterPro:IPR004468 InterPro:IPR017456 Pfam:PF06418 Pfam:PF00117 GO:GO:0005829 GO:GO:0046686 EMBL:CP002686 GenomeReviews:BA000014_GR EMBL:AB024033 EMBL:AC069474 GO:GO:0006221 InterPro:IPR017926 PROSITE:PS51273 eggNOG:COG0504 HOGENOM:HBG597806 KO:K01937 GO:GO:0003883 PANTHER:PTHR11550 TIGRFAMs:TIGR00337 OMA:EQCSIAL ProtClustDB:PLN02327 EMBL:AY093110 EMBL:BT008360 IPI:IPI00542960 RefSeq:NP_187873.1 UniGene:At.5669 ProteinModelPortal:Q9LTW8 SMR:Q9LTW8 STRING:Q9LTW8 PRIDE:Q9LTW8 EnsemblPlants:AT3G12670.1 GeneID:820447 KEGG:ath:AT3G12670 TAIR:At3g12670 InParanoid:Q9LTW8 PhylomeDB:Q9LTW8 ArrayExpress:Q9LTW8 Genevestigator:Q9LTW8 Uniprot:Q9LTW8
Leaf	Isotig01143	67	11	3.136	6.74E-16	TAIR|locus:2087765 - symbol:emb2742 "embryo defective 2742" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0003883 "CTP synthase activity" evidence=IEA;ISS] [GO:0009793 "embryo development ending in seed dormancy" evidence=NAS] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA] HAMAP:MF_01227 InterPro:IPR004468 InterPro:IPR017456 Pfam:PF06418 Pfam:PF00117 GO:GO:0005829 GO:GO:0046686 EMBL:CP002686 GenomeReviews:BA000014_GR EMBL:AB024033 EMBL:AC069474 GO:GO:0006221 InterPro:IPR017926 PROSITE:PS51273 eggNOG:COG0504 HOGENOM:HBG597806 KO:K01937 GO:GO:0003883 PANTHER:PTHR11550 TIGRFAMs:TIGR00337 OMA:EQCSIAL ProtClustDB:PLN02327 EMBL:AY093110 EMBL:BT008360 IPI:IPI00542960 RefSeq:NP_187873.1 UniGene:At.5669 ProteinModelPortal:Q9LTW8 SMR:Q9LTW8 STRING:Q9LTW8 PRIDE:Q9LTW8 EnsemblPlants:AT3G12670.1 GeneID:820447 KEGG:ath:AT3G12670 TAIR:At3g12670 InParanoid:Q9LTW8 PhylomeDB:Q9LTW8 ArrayExpress:Q9LTW8 Genevestigator:Q9LTW8 Uniprot:Q9LTW8

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig01144	62	11	3.024	2.22E-14	TAIR|locus:2087765 - symbol:emb2742 "embryo defective 2742" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0003883 "CTP synthase activity" evidence=IEA;ISS] [GO:0009793 "embryo development ending in seed dormancy" evidence=NAS] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA] HAMAP:MF_01227 InterPro:IPR004468 InterPro:IPR017456 Pfam:PF06418 Pfam:PF00117 GO:GO:0005829 GO:GO:0046686 EMBL:CP002686 GenomeReviews:BA000014_GR EMBL:AB024033 EMBL:AC069474 GO:GO:0006221 InterPro:IPR017926 PROSITE:PS51273 eggNOG:COG0504 HOGENOM:HBG597806 KO:K01937 GO:GO:0003883 PANTHER:PTHR11550 TIGRFAMs:TIGR00337 OMA:EQCSIAL ProtClustDB:PLN02327 EMBL:AY093110 EMBL:BT008360 IPI:IPI00542960 RefSeq:NP_187873.1 UniGene:At.5669 ProteinModelPortal:Q9LTW8 SMR:Q9LTW8 STRING:Q9LTW8 PRIDE:Q9LTW8 EnsemblPlants:AT3G12670.1 GeneID:820447 KEGG:ath:AT3G12670 TAIR:At3g12670 InParanoid:Q9LTW8 PhylomeDB:Q9LTW8 ArrayExpress:Q9LTW8 Genevestigator:Q9LTW8 Uniprot:Q9LTW8
Leaf	Isotig01161	20	89	-1.625	1.82E-07	TAIR|locus:2125786 - symbol:APR1 "AT4G04610" species:3702 "Arabidopsis thaliana" [GO:0009973 "adenylyl-sulfate reductase activity" evidence=IDA] [GO:0009536 "plastid" evidence=TAS] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0000103 "sulfate assimilation" evidence=IGI;IDA] [GO:0009507 "chloroplast" evidence=ISS] [GO:0019419 "sulfate reduction" evidence=IDA] InterPro:IPR002500 InterPro:IPR004508 InterPro:IPR013766 Pfam:PF00085 Pfam:PF01507 PROSITE:PS00194 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0009570 GO:GO:0006950 GO:GO:0046872 GO:GO:0051539 EMBL:AL161501 InterPro:IPR012336 Gene3D:G3DSA:3.40.30.10 SUPFAM:SSF52833 GO:GO:0045454 PROSITE:PS51352 EMBL:U53864 EMBL:U43412 EMBL:AF016282 EMBL:AF074021 EMBL:AF424582 EMBL:BT002612 EMBL:AY088011 EMBL:AK220828 IPI:IPI00538168 PIR:B85058 RefSeq:NP_192370.1 UniGene:At.47507 UniGene:At.59149 ProteinModelPortal:P92979 SMR:P92979 STRING:P92979 PRIDE:P92979 EnsemblPlants:AT4G04610.1 GeneID:825793 KEGG:ath:AT4G04610 TAIR:At4g04610 eggNOG:COG0175 HOGENOM:HBG758022 InParanoid:P92979 KO:K05907 OMA:EASYDEL PhylomeDB:P92979 ProtClustDB:PLN02309 BRENDA:1.8.4.9 ArrayExpress:P92979 Genevestigator:P92979 GermOnline:AT4G04610 GO:GO:0033741 GO:GO:0009973 GO:GO:0019344 GO:GO:0000103 GO:GO:0019419 InterPro:IPR014729 Gene3D:G3DSA:3.40.50.620 TIGRFAMs:TIGR00424 Uniprot:P92979
Leaf	Isotig01162	20	88	-1.609	2.61E-07	TAIR|locus:2125786 - symbol:APR1 "AT4G04610" species:3702 "Arabidopsis thaliana" [GO:0009973 "adenylyl-sulfate reductase activity" evidence=IDA] [GO:0009536 "plastid" evidence=TAS] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0000103 "sulfate assimilation" evidence=IGI;IDA] [GO:0009507 "chloroplast" evidence=ISS] [GO:0019419 "sulfate reduction" evidence=IDA] InterPro:IPR002500 InterPro:IPR004508 InterPro:IPR013766 Pfam:PF00085 Pfam:PF01507 PROSITE:PS00194 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0009570 GO:GO:0006950 GO:GO:0046872 GO:GO:0051539 EMBL:AL161501 InterPro:IPR012336 Gene3D:G3DSA:3.40.30.10 SUPFAM:SSF52833 GO:GO:0045454 PROSITE:PS51352 EMBL:U53864 EMBL:U43412 EMBL:AF016282 EMBL:AF074021 EMBL:AF424582 EMBL:BT002612 EMBL:AY088011 EMBL:AK220828 IPI:IPI00538168 PIR:B85058 RefSeq:NP_192370.1 UniGene:At.47507 UniGene:At.59149 ProteinModelPortal:P92979 SMR:P92979 STRING:P92979 PRIDE:P92979 EnsemblPlants:AT4G04610.1 GeneID:825793 KEGG:ath:AT4G04610 TAIR:At4g04610 eggNOG:COG0175 HOGENOM:HBG758022 InParanoid:P92979 KO:K05907 OMA:EASYDEL PhylomeDB:P92979 ProtClustDB:PLN02309 BRENDA:1.8.4.9 ArrayExpress:P92979 Genevestigator:P92979 GermOnline:AT4G04610 GO:GO:0033741 GO:GO:0009973 GO:GO:0019344 GO:GO:0000103 GO:GO:0019419 InterPro:IPR014729 Gene3D:G3DSA:3.40.50.620 TIGRFAMs:TIGR00424 Uniprot:P92979
Leaf	Isotig01163	21	88	-1.538	6.20E-07	TAIR|locus:2125786 - symbol:APR1 "AT4G04610" species:3702 "Arabidopsis thaliana" [GO:0009973 "adenylyl-sulfate reductase activity" evidence=IDA] [GO:0009536 "plastid" evidence=TAS] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0000103 "sulfate assimilation" evidence=IGI;IDA] [GO:0009507 "chloroplast" evidence=ISS] [GO:0019419 "sulfate reduction" evidence=IDA] InterPro:IPR002500 InterPro:IPR004508 InterPro:IPR013766 Pfam:PF00085 Pfam:PF01507 PROSITE:PS00194 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0009570 GO:GO:0006950 GO:GO:0046872 GO:GO:0051539 EMBL:AL161501 InterPro:IPR012336 Gene3D:G3DSA:3.40.30.10 SUPFAM:SSF52833 GO:GO:0045454 PROSITE:PS51352 EMBL:U53864 EMBL:U43412 EMBL:AF016282 EMBL:AF074021 EMBL:AF424582 EMBL:BT002612 EMBL:AY088011 EMBL:AK220828 IPI:IPI00538168 PIR:B85058 RefSeq:NP_192370.1 UniGene:At.47507 UniGene:At.59149 ProteinModelPortal:P92979 SMR:P92979 STRING:P92979 PRIDE:P92979 EnsemblPlants:AT4G04610.1 GeneID:825793 KEGG:ath:AT4G04610

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						TAIR:At4g04610 eggNOG:COG0175 HOGENOM:HBG758022 InParanoid:P92979 KO:K05907 OMA:EASYDEL PhylomeDB:P92979 ProtClustDB:PLN02309 BRENDA:1.8.4.9 ArrayExpress:P92979 Genevestigator:P92979 GermOnline:AT4G04610 GO:GO:0033741 GO:GO:0009973 GO:GO:0019344 GO:GO:0000103 GO:GO:0019419 InterPro:IPR014729 Gene3D:G3DSA:3.40.50.620 TIGRFAMs:TIGR00424 Uniprot:P92979
Leaf	Isotig01164	21	87	-1.522	8.78E-07	TAIR|locus:2125786 - symbol:APR1 "AT4G04610" species:3702 "Arabidopsis thaliana" [GO:0009973 "adenylyl-sulfate reductase activity" evidence=IDA] [GO:0009536 "plastid" evidence=TAS] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0000103 "sulfate assimilation" evidence=IGI;IDA] [GO:0009507 "chloroplast" evidence=ISS] [GO:0019419 "sulfate reduction" evidence=IDA] InterPro:IPR002500 InterPro:IPR004508 InterPro:IPR013766 Pfam:PF00085 Pfam:PF01507 PROSITE:PS00194 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0009570 GO:GO:0006950 GO:GO:0046872 GO:GO:0051539 EMBL:AL161501 InterPro:IPR012336 Gene3D:G3DSA:3.40.30.10 SUPFAM:SSF52833 GO:GO:0045454 PROSITE:PS51352 EMBL:U53864 EMBL:U43412 EMBL:AF016282 EMBL:AF074021 EMBL:AF424582 EMBL:BT002612 EMBL:AY088011 EMBL:AK220828 IPI:IPI00538168 PIR:B85058 RefSeq:NP_192370.1 UniGene:At.47507 UniGene:At.59149 ProteinModelPortal:P92979 SMR:P92979 STRING:P92979 PRIDE:P92979 EnsemblPlants:AT4G04610.1 GeneID:825793 KEGG:ath:AT4G04610 TAIR:At4g04610 eggNOG:COG0175 HOGENOM:HBG758022 InParanoid:P92979 KO:K05907 OMA:EASYDEL PhylomeDB:P92979 ProtClustDB:PLN02309 BRENDA:1.8.4.9 ArrayExpress:P92979 Genevestigator:P92979 GermOnline:AT4G04610 GO:GO:0033741 GO:GO:0009973 GO:GO:0019344 GO:GO:0000103 GO:GO:0019419 InterPro:IPR014729 Gene3D:G3DSA:3.40.50.620 TIGRFAMs:TIGR00424 Uniprot:P92979
Leaf	Isotig01165	7	39	-1.949	9.01E-05	TAIR|locus:2169434 - symbol:CYP93D1 ""cytochrome P450, family 93, subfamily D, polypeptide 1"" species:3702 "Arabidopsis thaliana" [GO:0004497 "monooxygenase activity" evidence=IEA] [GO:0005506 "iron ion binding" evidence=IEA] [GO:0009055 "electron carrier activity" evidence=IEA] [GO:0019825 "oxygen binding" evidence=ISS] [GO:0020037 "heme binding" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] InterPro:IPR001128 InterPro:IPR002401 InterPro:IPR017972 Pfam:PF00067 PRINTS:PR00385 PRINTS:PR00463 PROSITE:PS00086 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009055 GO:GO:0004497 eggNOG:COG2124 GO:GO:0020037 Gene3D:G3DSA:1.10.630.10 SUPFAM:SSF48264 EMBL:AB010697 GO:GO:0016705 HOGENOM:HBG749920 IPI:IPI00540736 RefSeq:NP_196307.1 UniGene:At.54754 ProteinModelPortal:Q9FL56 SMR:Q9FL56 PRIDE:Q9FL56 EnsemblPlants:AT5G06900.1 GeneID:830580 KEGG:ath:AT5G06900 TAIR:At5g06900 InParanoid:Q9FL56 OMA:DEECAVA PhylomeDB:Q9FL56 ProtClustDB:CLSN2916540 Genevestigator:Q9FL56 Uniprot:Q9FL56
Leaf	Isotig01166	7	39	-1.949	9.01E-05	TAIR|locus:2169434 - symbol:CYP93D1 ""cytochrome P450, family 93, subfamily D, polypeptide 1"" species:3702 "Arabidopsis thaliana" [GO:0004497 "monooxygenase activity" evidence=IEA] [GO:0005506 "iron ion binding" evidence=IEA] [GO:0009055 "electron carrier activity" evidence=IEA] [GO:0019825 "oxygen binding" evidence=ISS] [GO:0020037 "heme binding" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] InterPro:IPR001128 InterPro:IPR002401 InterPro:IPR017972 Pfam:PF00067 PRINTS:PR00385 PRINTS:PR00463 PROSITE:PS00086 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009055 GO:GO:0004497 eggNOG:COG2124 GO:GO:0020037 Gene3D:G3DSA:1.10.630.10 SUPFAM:SSF48264 EMBL:AB010697 GO:GO:0016705 HOGENOM:HBG749920 IPI:IPI00540736 RefSeq:NP_196307.1 UniGene:At.54754 ProteinModelPortal:Q9FL56 SMR:Q9FL56 PRIDE:Q9FL56 EnsemblPlants:AT5G06900.1 GeneID:830580 KEGG:ath:AT5G06900 TAIR:At5g06900 InParanoid:Q9FL56 OMA:DEECAVA PhylomeDB:Q9FL56 ProtClustDB:CLSN2916540 Genevestigator:Q9FL56 Uniprot:Q9FL56
Leaf	Isotig01167	7	40	-1.986	5.96E-05	TAIR|locus:2169434 - symbol:CYP93D1 ""cytochrome P450, family 93, subfamily D, polypeptide 1"" species:3702 "Arabidopsis thaliana" [GO:0004497 "monooxygenase activity" evidence=IEA] [GO:0005506 "iron ion binding" evidence=IEA] [GO:0009055 "electron carrier activity" evidence=IEA] [GO:0019825 "oxygen binding" evidence=ISS] [GO:0020037 "heme binding" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] InterPro:IPR001128 InterPro:IPR002401 InterPro:IPR017972 Pfam:PF00067 PRINTS:PR00385 PRINTS:PR00463 PROSITE:PS00086 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009055 GO:GO:0004497 eggNOG:COG2124 GO:GO:0020037 Gene3D:G3DSA:1.10.630.10 SUPFAM:SSF48264 EMBL:AB010697 GO:GO:0016705 HOGENOM:HBG749920 IPI:IPI00540736 RefSeq:NP_196307.1 UniGene:At.54754 ProteinModelPortal:Q9FL56 SMR:Q9FL56 PRIDE:Q9FL56 EnsemblPlants:AT5G06900.1 GeneID:830580 KEGG:ath:AT5G06900 TAIR:At5g06900 InParanoid:Q9FL56 OMA:DEECAVA PhylomeDB:Q9FL56 ProtClustDB:CLSN2916540 Genevestigator:Q9FL56 Uniprot:Q9FL56

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig01168	7	40	-1.986	5.96E-05	TAIR|locus:2169434 - symbol:CYP93D1 ""cytochrome P450, family 93, subfamily D, polypeptide 1"" species:3702 "Arabidopsis thaliana" [GO:0004497 "monooxygenase activity" evidence=IEA] [GO:0005506 "iron ion binding" evidence=IEA] [GO:0009055 "electron carrier activity" evidence=IEA] [GO:0019825 "oxygen binding" evidence=ISS] [GO:0020037 "heme binding" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] InterPro:IPR001128 InterPro:IPR002401 InterPro:IPR017972 Pfam:PF00067 PRINTS:PR00385 PRINTS:PR00463 PROSITE:PS00086 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009055 GO:GO:0004497 eggNOG:COG2124 GO:GO:0020037 Gene3D:G3DSA:1.10.630.10 SUPFAM:SSF48264 EMBL:AB010697 GO:GO:0016705 HOGENOM:HBG749920 IPI:IPI00540736 RefSeq:NP_196307.1 UniGene:At.54754 ProteinModelPortal:Q9FL56 SMR:Q9FL56 PRIDE:Q9FL56 EnsemblPlants:AT5G06900.1 GeneID:830580 KEGG:ath:AT5G06900 TAIR:At5g06900 InParanoid:Q9FL56 OMA:DEECAVA PhylomeDB:Q9FL56 ProtClustDB:CLSN2916540 Genevestigator:Q9FL56 Uniprot:Q9FL56
Leaf	Isotig01169	23	7	2.245	7.72E-05	TAIR|locus:2093827 - symbol:UGD2 "AT3G29360" species:3702 "Arabidopsis thaliana" [GO:0003979 "UDP-glucose 6-dehydrogenase activity" evidence=IGI;ISS] [GO:0005634 "nucleus" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0005975 "carbohydrate metabolic process" evidence=IGI] [GO:0052546 "cell wall pectin metabolic process" evidence=IGI] InterPro:IPR001732 InterPro:IPR008927 InterPro:IPR014026 InterPro:IPR014027 InterPro:IPR016040 InterPro:IPR017476 Pfam:PF00984 Pfam:PF03720 Pfam:PF03721 PIRSF:PIRSF000124 SMART:SM00984 GO:GO:0005829 GO:GO:0005634 EMBL:CP002686 GenomeReviews:BA000014_GR Gene3D:G3DSA:3.40.50.720 GO:GO:0051287 SUPFAM:SSF48179 EMBL:AP001309 InterPro:IPR021157 Gene3D:G3DSA:1.20.5.100 GO:GO:0003979 eggNOG:COG1004 HOGENOM:HBG400967 KO:K00012 SUPFAM:SSF52413 TIGRFAMs:TIGR03026 EMBL:AF424576 EMBL:AY088902 EMBL:BT021126 EMBL:AK226539 EMBL:BT029164 IPI:IPI00545262 RefSeq:NP_001030792.1 RefSeq:NP_189582.1 UniGene:At.22975 ProteinModelPortal:Q9LIA8 SMR:Q9LIA8 IntAct:Q9LIA8 STRING:Q9LIA8 PRIDE:Q9LIA8 EnsemblPlants:AT3G29360.1 EnsemblPlants:AT3G29360.2 GeneID:822594 KEGG:ath:AT3G29360 TAIR:At3g29360 InParanoid:Q9LIA8 OMA:QMCPEIR PhylomeDB:Q9LIA8 ProtClustDB:PLN02353 Genevestigator:Q9LIA8 Uniprot:Q9LIA8
Leaf	Isotig01170	23	7	2.245	7.72E-05	TAIR|locus:2093827 - symbol:UGD2 "AT3G29360" species:3702 "Arabidopsis thaliana" [GO:0003979 "UDP-glucose 6-dehydrogenase activity" evidence=IGI;ISS] [GO:0005634 "nucleus" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0005975 "carbohydrate metabolic process" evidence=IGI] [GO:0052546 "cell wall pectin metabolic process" evidence=IGI] InterPro:IPR001732 InterPro:IPR008927 InterPro:IPR014026 InterPro:IPR014027 InterPro:IPR016040 InterPro:IPR017476 Pfam:PF00984 Pfam:PF03720 Pfam:PF03721 PIRSF:PIRSF000124 SMART:SM00984 GO:GO:0005829 GO:GO:0005634 EMBL:CP002686 GenomeReviews:BA000014_GR Gene3D:G3DSA:3.40.50.720 GO:GO:0051287 SUPFAM:SSF48179 EMBL:AP001309 InterPro:IPR021157 Gene3D:G3DSA:1.20.5.100 GO:GO:0003979 eggNOG:COG1004 HOGENOM:HBG400967 KO:K00012 SUPFAM:SSF52413 TIGRFAMs:TIGR03026 EMBL:AF424576 EMBL:AY088902 EMBL:BT021126 EMBL:AK226539 EMBL:BT029164 IPI:IPI00545262 RefSeq:NP_001030792.1 RefSeq:NP_189582.1 UniGene:At.22975 ProteinModelPortal:Q9LIA8 SMR:Q9LIA8 IntAct:Q9LIA8 STRING:Q9LIA8 PRIDE:Q9LIA8 EnsemblPlants:AT3G29360.1 EnsemblPlants:AT3G29360.2 GeneID:822594 KEGG:ath:AT3G29360 TAIR:At3g29360 InParanoid:Q9LIA8 OMA:QMCPEIR PhylomeDB:Q9LIA8 ProtClustDB:PLN02353 Genevestigator:Q9LIA8 Uniprot:Q9LIA8
Leaf	Isotig01171	22	6	2.403	5.66E-05	TAIR|locus:2093827 - symbol:UGD2 "AT3G29360" species:3702 "Arabidopsis thaliana" [GO:0003979 "UDP-glucose 6-dehydrogenase activity" evidence=IGI;ISS] [GO:0005634 "nucleus" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0005975 "carbohydrate metabolic process" evidence=IGI] [GO:0052546 "cell wall pectin metabolic process" evidence=IGI] InterPro:IPR001732 InterPro:IPR008927 InterPro:IPR014026 InterPro:IPR014027 InterPro:IPR016040 InterPro:IPR017476 Pfam:PF00984 Pfam:PF03720 Pfam:PF03721 PIRSF:PIRSF000124 SMART:SM00984 GO:GO:0005829 GO:GO:0005634 EMBL:CP002686 GenomeReviews:BA000014_GR Gene3D:G3DSA:3.40.50.720 GO:GO:0051287 SUPFAM:SSF48179 EMBL:AP001309 InterPro:IPR021157 Gene3D:G3DSA:1.20.5.100 GO:GO:0003979 eggNOG:COG1004 HOGENOM:HBG400967 KO:K00012 SUPFAM:SSF52413 TIGRFAMs:TIGR03026 EMBL:AF424576 EMBL:AY088902 EMBL:BT021126 EMBL:AK226539 EMBL:BT029164 IPI:IPI00545262 RefSeq:NP_001030792.1 RefSeq:NP_189582.1 UniGene:At.22975 ProteinModelPortal:Q9LIA8 SMR:Q9LIA8 IntAct:Q9LIA8 STRING:Q9LIA8 PRIDE:Q9LIA8 EnsemblPlants:AT3G29360.1 EnsemblPlants:AT3G29360.2 GeneID:822594 KEGG:ath:AT3G29360

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
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Leaf	Isotig01172	22	6	2.403	5.66E-05	TAIR|locus:2093827 - symbol:UGD2 "AT3G29360" species:3702 "Arabidopsis thaliana" [GO:0003979 "UDP-glucose 6-dehydrogenase activity" evidence=IGI;ISS] [GO:0005634 "nucleus" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0005975 "carbohydrate metabolic process" evidence=IGI] [GO:0052546 "cell wall pectin metabolic process" evidence=IGI] InterPro:IPR001732 InterPro:IPR008927 InterPro:IPR014026 InterPro:IPR014027 InterPro:IPR016040 InterPro:IPR017476 Pfam:PF00984 Pfam:PF03720 Pfam:PF03721 PIRSF:PIRSF000124 SMART:SM00984 GO:GO:0005829 GO:GO:0005634 EMBL:CP002686 GenomeReviews:BA000014_GR Gene3D:G3DSA:3.40.50.720 GO:GO:0051287 SUPFAM:SSF48179 EMBL:AP001309 InterPro:IPR021157 Gene3D:G3DSA:1.20.5.100 GO:GO:0003979 eggNOG:COG1004 HOGENOM:HBG400967 KO:K00012 SUPFAM:SSF52413 TIGRFAMs:TIGR03026 EMBL:AF424576 EMBL:AY088902 EMBL:BT021126 EMBL:AK226539 EMBL:BT029164 IPI:IPI00545262 RefSeq:NP_001030792.1 RefSeq:NP_189582.1 UniGene:At.22975 ProteinModelPortal:Q9LIA8 SMR:Q9LIA8 IntAct:Q9LIA8 STRING:Q9LIA8 PRIDE:Q9LIA8 EnsemblPlants:AT3G29360.1 EnsemblPlants:AT3G29360.2 GeneID:822594 KEGG:ath:AT3G29360 TAIR:At3g29360 InParanoid:Q9LIA8 OMA:QMCPEIR PhylomeDB:Q9LIA8 ProtClustDB:PLN02353 Genevestigator:Q9LIA8 Uniprot:Q9LIA8
Leaf	Isotig01185	9	0	4.699	0.000718283	TAIR|locus:2126634 - symbol:AT4G31080 "AT4G31080" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] GenomeReviews:CT486007_GR InterPro:IPR019273 Pfam:PF10058 EMBL:AK176449 IPI:IPI00525084 STRING:Q67YL9 PRIDE:Q67YL9 TAIR:At4g31080 PhylomeDB:Q67YL9 Genevestigator:Q67YL9 Uniprot:Q67YL9
Leaf	Isotig01187	9	0	4.699	0.000718283	TAIR|locus:2126634 - symbol:AT4G31080 "AT4G31080" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] GenomeReviews:CT486007_GR InterPro:IPR019273 Pfam:PF10058 EMBL:AK176449 IPI:IPI00525084 STRING:Q67YL9 PRIDE:Q67YL9 TAIR:At4g31080 PhylomeDB:Q67YL9 Genevestigator:Q67YL9 Uniprot:Q67YL9
Leaf	Isotig01209	44	10	2.666	1.58E-09	TAIR|locus:2142609 - symbol:ADK2 "AT5G03300" species:3702 "Arabidopsis thaliana" [GO:0016301 "kinase activity" evidence=ISS] [GO:0004001 "adenosine kinase activity" evidence=ISS;IDA] [GO:0006169 "adenosine salvage" evidence=TAS] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001805 InterPro:IPR002173 PRINTS:PR00989 PROSITE:PS00583 PROSITE:PS00584 Pfam:PF00294 GO:GO:0005829 GO:GO:0005886 GO:GO:0005524 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0044419 EMBL:AL162751 GO:GO:0005507 UniGene:At.16947 eggNOG:COG0524 HOGENOM:HBG314716 KO:K00856 ProtClustDB:PLN02548 BRENDA:2.7.1.20 GO:GO:0004001 GO:GO:0016773 GO:GO:0006169 InterPro:IPR011611 PANTHER:PTHR10584:SF24 EMBL:AF180895 EMBL:AF180897 EMBL:AB005240 EMBL:AY042855 EMBL:AY072485 IPI:IPI00523164 PIR:T48351 RefSeq:NP_195950.1 UniGene:At.1599 ProteinModelPortal:Q9LZG0 SMR:Q9LZG0 IntAct:Q9LZG0 STRING:Q9LZG0 PRIDE:Q9LZG0 EnsemblPlants:AT5G03300.1 GeneID:831882 KEGG:ath:AT5G03300 TAIR:At5g03300 InParanoid:Q9LZG0 OMA:AQWMIQQ PhylomeDB:Q9LZG0 ArrayExpress:Q9LZG0 Genevestigator:Q9LZG0 GermOnline:AT5G03300 Uniprot:Q9LZG0
Leaf	Isotig01210	44	10	2.666	1.58E-09	TAIR|locus:2142609 - symbol:ADK2 "AT5G03300" species:3702 "Arabidopsis thaliana" [GO:0016301 "kinase activity" evidence=ISS] [GO:0004001 "adenosine kinase activity" evidence=ISS;IDA] [GO:0006169 "adenosine salvage" evidence=TAS] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001805 InterPro:IPR002173 PRINTS:PR00989 PROSITE:PS00583 PROSITE:PS00584 Pfam:PF00294 GO:GO:0005829 GO:GO:0005886 GO:GO:0005524 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0044419 EMBL:AL162751 GO:GO:0005507 UniGene:At.16947 eggNOG:COG0524 HOGENOM:HBG314716 KO:K00856 ProtClustDB:PLN02548 BRENDA:2.7.1.20 GO:GO:0004001 GO:GO:0016773 GO:GO:0006169 InterPro:IPR011611 PANTHER:PTHR10584:SF24 EMBL:AF180895 EMBL:AF180897 EMBL:AB005240 EMBL:AY042855 EMBL:AY072485 IPI:IPI00523164 PIR:T48351 RefSeq:NP_195950.1 UniGene:At.1599 ProteinModelPortal:Q9LZG0 SMR:Q9LZG0 IntAct:Q9LZG0 STRING:Q9LZG0 PRIDE:Q9LZG0 EnsemblPlants:AT5G03300.1 GeneID:831882 KEGG:ath:AT5G03300 TAIR:At5g03300 InParanoid:Q9LZG0 OMA:AQWMIQQ PhylomeDB:Q9LZG0 ArrayExpress:Q9LZG0 Genevestigator:Q9LZG0 GermOnline:AT5G03300 Uniprot:Q9LZG0
Leaf	Isotig01211	44	10	2.666	1.58E-09	TAIR|locus:2142609 - symbol:ADK2 "AT5G03300" species:3702 "Arabidopsis thaliana" [GO:0016301 "kinase activity" evidence=ISS] [GO:0004001 "adenosine kinase activity" evidence=ISS;IDA] [GO:0006169 "adenosine

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						salvage" evidence=TAS] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001805 InterPro:IPR002173 PRINTS:PR00989 PROSITE:PS00583 PROSITE:PS00584 Pfam:PF00294 GO:GO:0005829 GO:GO:0005886 GO:GO:0005524 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0044419 EMBL:AL162751 GO:GO:0005507 UniGene:At.16947 eggNOG:COG0524 HOGENOM:HBG314716 KO:K00856 ProtClustDB:PLN02548 BRENDA:2.7.1.20 GO:GO:0004001 GO:GO:0016773 GO:GO:0006169 InterPro:IPR011611 PANTHER:PTHR10584:SF24 EMBL:AF180895 EMBL:AF180897 EMBL:AB005240 EMBL:AY042855 EMBL:AY072485 IPI:IPI00523164 PIR:T48351 RefSeq:NP_195950.1 UniGene:At.1599 ProteinModelPortal:Q9LZG0 SMR:Q9LZG0 IntAct:Q9LZG0 STRING:Q9LZG0 PRIDE:Q9LZG0 EnsemblPlants:AT5G03300.1 GeneID:831882 KEGG:ath:AT5G03300 TAIR:At5g03300 InParanoid:Q9LZG0 OMA:AQWMIQQ PhylomeDB:Q9LZG0 ArrayExpress:Q9LZG0 Genevestigator:Q9LZG0 GermOnline:AT5G03300 Uniprot:Q9LZG0
Leaf	Isotig01212	44	10	2.666	1.58E-09	TAIR|locus:2142609 - symbol:ADK2 "AT5G03300" species:3702 "Arabidopsis thaliana" [GO:0016301 "kinase activity" evidence=ISS] [GO:0004001 "adenosine kinase activity" evidence=ISS;IDA] [GO:0006169 "adenosine salvage" evidence=TAS] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001805 InterPro:IPR002173 PRINTS:PR00989 PROSITE:PS00583 PROSITE:PS00584 Pfam:PF00294 GO:GO:0005829 GO:GO:0005886 GO:GO:0005524 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0044419 EMBL:AL162751 GO:GO:0005507 UniGene:At.16947 eggNOG:COG0524 HOGENOM:HBG314716 KO:K00856 ProtClustDB:PLN02548 BRENDA:2.7.1.20 GO:GO:0004001 GO:GO:0016773 GO:GO:0006169 InterPro:IPR011611 PANTHER:PTHR10584:SF24 EMBL:AF180895 EMBL:AF180897 EMBL:AB005240 EMBL:AY042855 EMBL:AY072485 IPI:IPI00523164 PIR:T48351 RefSeq:NP_195950.1 UniGene:At.1599 ProteinModelPortal:Q9LZG0 SMR:Q9LZG0 IntAct:Q9LZG0 STRING:Q9LZG0 PRIDE:Q9LZG0 EnsemblPlants:AT5G03300.1 GeneID:831882 KEGG:ath:AT5G03300 TAIR:At5g03300 InParanoid:Q9LZG0 OMA:AQWMIQQ PhylomeDB:Q9LZG0 ArrayExpress:Q9LZG0 Genevestigator:Q9LZG0 GermOnline:AT5G03300 Uniprot:Q9LZG0
Leaf	Isotig01220	3	29	-2.744	3.44E-05	TAIR|locus:2011496 - symbol:AT1G52870 "AT1G52870" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0016021 "integral to membrane" evidence=IEA] InterPro:IPR007248 Pfam:PF04117 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR EMBL:AC019018 PANTHER:PTHR11266 EMBL:AF385726 EMBL:BT002228 IPI:IPI00519623 PIR:H96569 RefSeq:NP_564615.3 UniGene:At.23745 IntAct:Q9C933 STRING:Q9C933 EnsemblPlants:AT1G52870.2 GeneID:841720 KEGG:ath:AT1G52870 TAIR:At1g52870 HOGENOM:HBG746907 InParanoid:Q9C933 OMA:GFLRFES PhylomeDB:Q9C933 ProtClustDB:CLSN2688734 Genevestigator:Q9C933 Uniprot:Q9C933
Leaf	Isotig01249	3	52	-3.587	3.73E-10	TAIR|locus:2040934 - symbol:LHB1B2 "AT2G34420" species:3702 "Arabidopsis thaliana" [GO:0009769 "photosynthesis, light harvesting in photosystem II" evidence=TAS] [GO:0016168 "chlorophyll binding" evidence=ISS;TAS] [GO:0030076 "light-harvesting complex" evidence=ISS] [GO:0042651 "thylakoid membrane" evidence=TAS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0015979 "photosynthesis" evidence=ISS] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR001344 Pfam:PF00504 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009535 GO:GO:0010287 EMBL:AC004077 EMBL:AC004481 HOGENOM:HBG618504 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 UniGene:At.10812 UniGene:At.24351 UniGene:At.32199 UniGene:At.66422 UniGene:At.71449 UniGene:At.71528 KO:K08912 ProtClustDB:PLN00025 UniGene:At.23647 UniGene:At.27457 UniGene:At.24888 EMBL:AF372886 EMBL:AY039561 EMBL:AY045806 EMBL:AF428397 EMBL:AF419548 EMBL:AF419587 EMBL:AY065125 EMBL:AY079101 EMBL:AY079110 EMBL:AY081587 EMBL:AY142513 EMBL:AK229627 EMBL:X64460 IPI:IPI00530785 PIR:S23546 RefSeq:NP_565786.1 UniGene:At.24064 UniGene:At.71003 UniGene:At.71384 ProteinModelPortal:Q39141 SMR:Q39141 IntAct:Q39141 STRING:Q39141 PRIDE:Q39141 EnsemblPlants:AT2G34420.1 GeneID:818005 KEGG:ath:AT2G34420 TAIR:At2g34420 InParanoid:Q39141 OMA:SILAIWG PhylomeDB:Q39141 ArrayExpress:Q39141 Genevestigator:Q39141 Uniprot:Q39141
Leaf	Isotig01250	9	77	-2.568	7.41E-11	TAIR|locus:2040934 - symbol:LHB1B2 "AT2G34420" species:3702 "Arabidopsis thaliana" [GO:0009769 "photosynthesis, light harvesting in photosystem II" evidence=TAS] [GO:0016168 "chlorophyll binding"

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						evidence=ISS;TAS] [GO:0030076 "light-harvesting complex" evidence=ISS] [GO:0042651 "thylakoid membrane" evidence=TAS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0015979 "photosynthesis" evidence=ISS] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR001344 Pfam:PF00504 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009535 GO:GO:0010287 EMBL:AC004077 EMBL:AC004481 HOGENOM:HBG618504 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 UniGene:At.10812 UniGene:At.24351 UniGene:At.32199 UniGene:At.66422 UniGene:At.71449 UniGene:At.71528 KO:K08912 ProtClustDB:PLN00025 UniGene:At.23647 UniGene:At.27457 UniGene:At.24888 EMBL:AF372886 EMBL:AY039561 EMBL:AY045806 EMBL:AF428397 EMBL:AF419548 EMBL:AF419587 EMBL:AY065125 EMBL:AY079101 EMBL:AY079110 EMBL:AY081587 EMBL:AY142513 EMBL:AK229627 EMBL:X64460 IPI:IPI00530785 PIR:S23546 RefSeq:NP_565786.1 UniGene:At.24064 UniGene:At.71003 UniGene:At.71384 ProteinModelPortal:Q39141 SMR:Q39141 IntAct:Q39141 STRING:Q39141 PRIDE:Q39141 EnsemblPlants:AT2G34420.1 GeneID:818005 KEGG:ath:AT2G34420 TAIR:At2g34420 InParanoid:Q39141 OMA:SILAIWG PhylomeDB:Q39141 ArrayExpress:Q39141 Genevestigator:Q39141 Uniprot:Q39141
Leaf	Isotig01251	11	57	-1.845	5.07E-06	TAIR|locus:2040934 - symbol:LHB1B2 "AT2G34420" species:3702 "Arabidopsis thaliana" [GO:0009769 "photosynthesis, light harvesting in photosystem II" evidence=TAS] [GO:0016168 "chlorophyll binding" evidence=ISS;TAS] [GO:0030076 "light-harvesting complex" evidence=ISS] [GO:0042651 "thylakoid membrane" evidence=TAS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0015979 "photosynthesis" evidence=ISS] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR001344 Pfam:PF00504 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009535 GO:GO:0010287 EMBL:AC004077 EMBL:AC004481 HOGENOM:HBG618504 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 UniGene:At.10812 UniGene:At.24351 UniGene:At.32199 UniGene:At.66422 UniGene:At.71449 UniGene:At.71528 KO:K08912 ProtClustDB:PLN00025 UniGene:At.23647 UniGene:At.27457 UniGene:At.24888 EMBL:AF372886 EMBL:AY039561 EMBL:AY045806 EMBL:AF428397 EMBL:AF419548 EMBL:AF419587 EMBL:AY065125 EMBL:AY079101 EMBL:AY079110 EMBL:AY081587 EMBL:AY142513 EMBL:AK229627 EMBL:X64460 IPI:IPI00530785 PIR:S23546 RefSeq:NP_565786.1 UniGene:At.24064 UniGene:At.71003 UniGene:At.71384 ProteinModelPortal:Q39141 SMR:Q39141 IntAct:Q39141 STRING:Q39141 PRIDE:Q39141 EnsemblPlants:AT2G34420.1 GeneID:818005 KEGG:ath:AT2G34420 TAIR:At2g34420 InParanoid:Q39141 OMA:SILAIWG PhylomeDB:Q39141 ArrayExpress:Q39141 Genevestigator:Q39141 Uniprot:Q39141
Leaf	Isotig01253	6	86	-3.312	6.05E-15	TAIR|locus:2040934 - symbol:LHB1B2 "AT2G34420" species:3702 "Arabidopsis thaliana" [GO:0009769 "photosynthesis, light harvesting in photosystem II" evidence=TAS] [GO:0016168 "chlorophyll binding" evidence=ISS;TAS] [GO:0030076 "light-harvesting complex" evidence=ISS] [GO:0042651 "thylakoid membrane" evidence=TAS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0015979 "photosynthesis" evidence=ISS] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR001344 Pfam:PF00504 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009535 GO:GO:0010287 EMBL:AC004077 EMBL:AC004481 HOGENOM:HBG618504 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 UniGene:At.10812 UniGene:At.24351 UniGene:At.32199 UniGene:At.66422 UniGene:At.71449 UniGene:At.71528 KO:K08912 ProtClustDB:PLN00025 UniGene:At.23647 UniGene:At.27457 UniGene:At.24888 EMBL:AF372886 EMBL:AY039561 EMBL:AY045806 EMBL:AF428397 EMBL:AF419548 EMBL:AF419587 EMBL:AY065125 EMBL:AY079101 EMBL:AY079110 EMBL:AY081587 EMBL:AY142513 EMBL:AK229627 EMBL:X64460 IPI:IPI00530785 PIR:S23546 RefSeq:NP_565786.1 UniGene:At.24064 UniGene:At.71003 UniGene:At.71384 ProteinModelPortal:Q39141 SMR:Q39141 IntAct:Q39141 STRING:Q39141 PRIDE:Q39141 EnsemblPlants:AT2G34420.1 GeneID:818005 KEGG:ath:AT2G34420 TAIR:At2g34420 InParanoid:Q39141 OMA:SILAIWG PhylomeDB:Q39141 ArrayExpress:Q39141 Genevestigator:Q39141 Uniprot:Q39141

<table>
<tr><th>Tissue</th><th>Identification</th><th># of reads (stress)</th><th># of reads (control)</th><th>Fold Change</th><th>p-value</th><th>Description</th></tr>
<tr><td>Leaf</td><td>Isotig01254</td><td>10</td><td>73</td><td>-2.339</td><td>1.87E-09</td><td>TAIR|locus:2040934 - symbol:LHB1B2 "AT2G34420" species:3702 "Arabidopsis thaliana" [GO:0009769 "photosynthesis, light harvesting in photosystem II" evidence=TAS] [GO:0016168 "chlorophyll binding" evidence=ISS;TAS] [GO:0030076 "light-harvesting complex" evidence=ISS] [GO:0042651 "thylakoid membrane" evidence=TAS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0015979 "photosynthesis" evidence=ISS] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR001344 Pfam:PF00504 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009535 GO:GO:0010287 EMBL:AC004077 EMBL:AC004481 HOGENOM:HBG618504 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 UniGene:At.10812 UniGene:At.24351 UniGene:At.32199 UniGene:At.66422 UniGene:At.71449 UniGene:At.71528 KO:K08912 ProtClustDB:PLN00025 UniGene:At.23647 UniGene:At.27457 UniGene:At.24888 EMBL:AF372886 EMBL:AY039561 EMBL:AY045806 EMBL:AF428397 EMBL:AF419548 EMBL:AF419587 EMBL:AY065125 EMBL:AY079101 EMBL:AY079110 EMBL:AY081587 EMBL:AY142513 EMBL:AK229627 EMBL:X64460 IPI:IPI00530785 PIR:S23546 RefSeq:NP_565786.1 UniGene:At.24064 UniGene:At.71003 UniGene:At.71384 ProteinModelPortal:Q39141 SMR:Q39141 IntAct:Q39141 STRING:Q39141 PRIDE:Q39141 EnsemblPlants:AT2G34420.1 GeneID:818005 KEGG:ath:AT2G34420 TAIR:At2g34420 InParanoid:Q39141 OMA:SILAIWG PhylomeDB:Q39141 ArrayExpress:Q39141 Genevestigator:Q39141 Uniprot:Q39141</td></tr>
<tr><td>Leaf</td><td>Isotig01255</td><td>5</td><td>49</td><td>-2.764</td><td>6.50E-08</td><td>TAIR|locus:2040934 - symbol:LHB1B2 "AT2G34420" species:3702 "Arabidopsis thaliana" [GO:0009769 "photosynthesis, light harvesting in photosystem II" evidence=TAS] [GO:0016168 "chlorophyll binding" evidence=ISS;TAS] [GO:0030076 "light-harvesting complex" evidence=ISS] [GO:0042651 "thylakoid membrane" evidence=TAS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0015979 "photosynthesis" evidence=ISS] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR001344 Pfam:PF00504 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009535 GO:GO:0010287 EMBL:AC004077 EMBL:AC004481 HOGENOM:HBG618504 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 UniGene:At.10812 UniGene:At.24351 UniGene:At.32199 UniGene:At.66422 UniGene:At.71449 UniGene:At.71528 KO:K08912 ProtClustDB:PLN00025 UniGene:At.23647 UniGene:At.27457 UniGene:At.24888 EMBL:AF372886 EMBL:AY039561 EMBL:AY045806 EMBL:AF428397 EMBL:AF419548 EMBL:AF419587 EMBL:AY065125 EMBL:AY079101 EMBL:AY079110 EMBL:AY081587 EMBL:AY142513 EMBL:AK229627 EMBL:X64460 IPI:IPI00530785 PIR:S23546 RefSeq:NP_565786.1 UniGene:At.24064 UniGene:At.71003 UniGene:At.71384 ProteinModelPortal:Q39141 SMR:Q39141 IntAct:Q39141 STRING:Q39141 PRIDE:Q39141 EnsemblPlants:AT2G34420.1 GeneID:818005 KEGG:ath:AT2G34420 TAIR:At2g34420 InParanoid:Q39141 OMA:SILAIWG PhylomeDB:Q39141 ArrayExpress:Q39141 Genevestigator:Q39141 Uniprot:Q39141</td></tr>
<tr><td>Leaf</td><td>Isotig01256</td><td>0</td><td>40</td><td>-5.793</td><td>1.41E-09</td><td>TAIR|locus:2040934 - symbol:LHB1B2 "AT2G34420" species:3702 "Arabidopsis thaliana" [GO:0009769 "photosynthesis, light harvesting in photosystem II" evidence=TAS] [GO:0016168 "chlorophyll binding" evidence=ISS;TAS] [GO:0030076 "light-harvesting complex" evidence=ISS] [GO:0042651 "thylakoid membrane" evidence=TAS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0015979 "photosynthesis" evidence=ISS] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR001344 Pfam:PF00504 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009535 GO:GO:0010287 EMBL:AC004077 EMBL:AC004481 HOGENOM:HBG618504 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 UniGene:At.10812 UniGene:At.24351 UniGene:At.32199 UniGene:At.66422 UniGene:At.71449 UniGene:At.71528 KO:K08912 ProtClustDB:PLN00025 UniGene:At.23647 UniGene:At.27457 UniGene:At.24888 EMBL:AF372886 EMBL:AY039561 EMBL:AY045806 EMBL:AF428397 EMBL:AF419548 EMBL:AF419587 EMBL:AY065125 EMBL:AY079101 EMBL:AY079110 EMBL:AY081587 EMBL:AY142513 EMBL:AK229627 EMBL:X64460 IPI:IPI00530785 PIR:S23546 RefSeq:NP_565786.1 UniGene:At.24064 UniGene:At.71003 UniGene:At.71384 ProteinModelPortal:Q39141 SMR:Q39141 IntAct:Q39141 STRING:Q39141 PRIDE:Q39141 EnsemblPlants:AT2G34420.1 GeneID:818005</td></tr>
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Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						KEGG:ath:AT2G34420 TAIR:At2g34420 InParanoid:Q39141 OMA:SILAIWG PhylomeDB:Q39141 ArrayExpress:Q39141 Genevestigator:Q39141 Uniprot:Q39141
Leaf	Isotig01269	63	32	1.506	6.08E-07	TAIR|locus:2089378 - symbol:TCTP "AT3G16640" species:3702 "Arabidopsis thaliana" [GO:0005737 "cytoplasm" evidence=ISS] [GO:0009579 "thylakoid" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0042742 "defense response to bacterium" evidence=IEP] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0001558 "regulation of cell growth" evidence=IMP] [GO:0009860 "pollen tube growth" evidence=IMP] [GO:0010252 "auxin homeostasis" evidence=IMP] [GO:0048364 "root development" evidence=IMP] [GO:0048527 "lateral root development" evidence=IMP] [GO:0048768 "root hair cell tip growth" evidence=IMP] [GO:0090406 "pollen tube" evidence=IDA] [GO:0007346 "regulation of mitotic cell cycle" evidence=IMP] [GO:0008283 "cell proliferation" evidence=IMP] [GO:0009790 "embryo development" evidence=IMP] [GO:0009791 "post-embryonic development" evidence=IMP] [GO:0040014 "regulation of multicellular organism growth" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 GO:GO:0048046 GO:GO:0005634 GO:GO:0046686 GO:GO:0007346 GO:GO:0005774 GO:GO:0009507 GO:GO:0042742 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0001558 GO:GO:0009790 GO:GO:0008283 GO:GO:0040014 GO:GO:0048527 GO:GO:0009860 GO:GO:0048768 GO:GO:0009579 EMBL:AB022217 InterPro:IPR011057 SUPFAM:SSF51316 UniGene:At.34389 InterPro:IPR011323 Gene3D:G3DSA:2.170.150.10 GO:GO:0090406 GO:GO:0010252 eggNOG:NOG280126 InterPro:IPR018103 InterPro:IPR018105 PANTHER:PTHR11991 Pfam:PF00838 PRINTS:PR01653 PROSITE:PS01002 PROSITE:PS01003 EMBL:AF215897 EMBL:AF361815 EMBL:AY045802 EMBL:AY056065 EMBL:AY072337 EMBL:AY079333 EMBL:AY114601 EMBL:AY088605 EMBL:Z18387 IPI:IPI00531702 RefSeq:NP_188286.1 UniGene:At.47256 UniGene:At.74193 ProteinModelPortal:P31265 SMR:P31265 IntAct:P31265 STRING:P31265 PRIDE:P31265 ProMEX:P31265 EnsemblPlants:AT3G16640.1 GeneID:820916 KEGG:ath:AT3G16640 TAIR:At3g16640 HOGENOM:HBG507116 InParanoid:P31265 OMA:ASYMAHI PhylomeDB:P31265 ProtClustDB:CLSN2684008 ArrayExpress:P31265 Genevestigator:P31265 GermOnline:AT3G16640 Uniprot:P31265
Leaf	Isotig01270	63	32	1.506	6.08E-07	TAIR|locus:2089378 - symbol:TCTP "AT3G16640" species:3702 "Arabidopsis thaliana" [GO:0005737 "cytoplasm" evidence=ISS] [GO:0009579 "thylakoid" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0042742 "defense response to bacterium" evidence=IEP] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0001558 "regulation of cell growth" evidence=IMP] [GO:0009860 "pollen tube growth" evidence=IMP] [GO:0010252 "auxin homeostasis" evidence=IMP] [GO:0048364 "root development" evidence=IMP] [GO:0048527 "lateral root development" evidence=IMP] [GO:0048768 "root hair cell tip growth" evidence=IMP] [GO:0090406 "pollen tube" evidence=IDA] [GO:0007346 "regulation of mitotic cell cycle" evidence=IMP] [GO:0008283 "cell proliferation" evidence=IMP] [GO:0009790 "embryo development" evidence=IMP] [GO:0009791 "post-embryonic development" evidence=IMP] [GO:0040014 "regulation of multicellular organism growth" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 GO:GO:0048046 GO:GO:0005634 GO:GO:0046686 GO:GO:0007346 GO:GO:0005774 GO:GO:0009507 GO:GO:0042742 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0001558 GO:GO:0009790 GO:GO:0008283 GO:GO:0040014 GO:GO:0048527 GO:GO:0009860 GO:GO:0048768 GO:GO:0009579 EMBL:AB022217 InterPro:IPR011057 SUPFAM:SSF51316 UniGene:At.34389 InterPro:IPR011323 Gene3D:G3DSA:2.170.150.10 GO:GO:0090406 GO:GO:0010252 eggNOG:NOG280126 InterPro:IPR018103 InterPro:IPR018105 PANTHER:PTHR11991 Pfam:PF00838 PRINTS:PR01653 PROSITE:PS01002 PROSITE:PS01003 EMBL:AF215897 EMBL:AF361815 EMBL:AY045802 EMBL:AY056065 EMBL:AY072337 EMBL:AY079333 EMBL:AY114601 EMBL:AY088605 EMBL:Z18387 IPI:IPI00531702 RefSeq:NP_188286.1 UniGene:At.47256 UniGene:At.74193 ProteinModelPortal:P31265 SMR:P31265 IntAct:P31265 STRING:P31265 PRIDE:P31265 ProMEX:P31265 EnsemblPlants:AT3G16640.1 GeneID:820916 KEGG:ath:AT3G16640 TAIR:At3g16640 HOGENOM:HBG507116 InParanoid:P31265 OMA:ASYMAHI PhylomeDB:P31265 ProtClustDB:CLSN2684008 ArrayExpress:P31265 Genevestigator:P31265 GermOnline:AT3G16640 Uniprot:P31265

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig01271	63	32	1.506	6.08E-07	TAIR|locus:2089378 - symbol:TCTP "AT3G16640" species:3702 "Arabidopsis thaliana" [GO:0005737 "cytoplasm" evidence=ISS] [GO:0009579 "thylakoid" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0042742 "defense response to bacterium" evidence=IEP] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0001558 "regulation of cell growth" evidence=IMP] [GO:0009860 "pollen tube growth" evidence=IMP] [GO:0010252 "auxin homeostasis" evidence=IMP] [GO:0048364 "root development" evidence=IMP] [GO:0048527 "lateral root development" evidence=IMP] [GO:0048768 "root hair cell tip growth" evidence=IMP] [GO:0090406 "pollen tube" evidence=IDA] [GO:0007346 "regulation of mitotic cell cycle" evidence=IMP] [GO:0008283 "cell proliferation" evidence=IMP] [GO:0009790 "embryo development" evidence=IMP] [GO:0009791 "post-embryonic development" evidence=IMP] [GO:0040014 "regulation of multicellular organism growth" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 GO:GO:0048046 GO:GO:0005634 GO:GO:0046686 GO:GO:0007346 GO:GO:0005774 GO:GO:0009507 GO:GO:0042742 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0001558 GO:GO:0009790 GO:GO:0008283 GO:GO:0040014 GO:GO:0048527 GO:GO:0009860 GO:GO:0048768 GO:GO:0009579 EMBL:AB022217 InterPro:IPR011057 SUPFAM:SSF51316 UniGene:At.34389 InterPro:IPR011323 Gene3D:G3DSA:2.170.150.10 GO:GO:0090406 GO:GO:0010252 eggNOG:NOG280126 InterPro:IPR018103 InterPro:IPR018105 PANTHER:PTHR11991 Pfam:PF00838 PRINTS:PR01653 PROSITE:PS01002 PROSITE:PS01003 EMBL:AF215897 EMBL:AF361815 EMBL:AY045802 EMBL:AY056065 EMBL:AY072337 EMBL:AY079333 EMBL:AY114601 EMBL:AY088605 EMBL:Z18387 IPI:IPI00531702 RefSeq:NP_188286.1 UniGene:At.47256 UniGene:At.74193 ProteinModelPortal:P31265 SMR:P31265 IntAct:P31265 STRING:P31265 PRIDE:P31265 ProMEX:P31265 EnsemblPlants:AT3G16640.1 GeneID:820916 KEGG:ath:AT3G16640 TAIR:At3g16640 HOGENOM:HBG507116 InParanoid:P31265 OMA:ASYMAHI PhylomeDB:P31265 ProtClustDB:CLSN2684008 ArrayExpress:P31265 Genevestigator:P31265 GermOnline:AT3G16640 Uniprot:P31265
Leaf	Isotig01272	63	32	1.506	6.08E-07	TAIR|locus:2089378 - symbol:TCTP "AT3G16640" species:3702 "Arabidopsis thaliana" [GO:0005737 "cytoplasm" evidence=ISS] [GO:0009579 "thylakoid" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0042742 "defense response to bacterium" evidence=IEP] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0001558 "regulation of cell growth" evidence=IMP] [GO:0009860 "pollen tube growth" evidence=IMP] [GO:0010252 "auxin homeostasis" evidence=IMP] [GO:0048364 "root development" evidence=IMP] [GO:0048527 "lateral root development" evidence=IMP] [GO:0048768 "root hair cell tip growth" evidence=IMP] [GO:0090406 "pollen tube" evidence=IDA] [GO:0007346 "regulation of mitotic cell cycle" evidence=IMP] [GO:0008283 "cell proliferation" evidence=IMP] [GO:0009790 "embryo development" evidence=IMP] [GO:0009791 "post-embryonic development" evidence=IMP] [GO:0040014 "regulation of multicellular organism growth" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 GO:GO:0048046 GO:GO:0005634 GO:GO:0046686 GO:GO:0007346 GO:GO:0005774 GO:GO:0009507 GO:GO:0042742 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0001558 GO:GO:0009790 GO:GO:0008283 GO:GO:0040014 GO:GO:0048527 GO:GO:0009860 GO:GO:0048768 GO:GO:0009579 EMBL:AB022217 InterPro:IPR011057 SUPFAM:SSF51316 UniGene:At.34389 InterPro:IPR011323 Gene3D:G3DSA:2.170.150.10 GO:GO:0090406 GO:GO:0010252 eggNOG:NOG280126 InterPro:IPR018103 InterPro:IPR018105 PANTHER:PTHR11991 Pfam:PF00838 PRINTS:PR01653 PROSITE:PS01002 PROSITE:PS01003 EMBL:AF215897 EMBL:AF361815 EMBL:AY045802 EMBL:AY056065 EMBL:AY072337 EMBL:AY079333 EMBL:AY114601 EMBL:AY088605 EMBL:Z18387 IPI:IPI00531702 RefSeq:NP_188286.1 UniGene:At.47256 UniGene:At.74193 ProteinModelPortal:P31265 SMR:P31265 IntAct:P31265 STRING:P31265 PRIDE:P31265 ProMEX:P31265 EnsemblPlants:AT3G16640.1 GeneID:820916 KEGG:ath:AT3G16640 TAIR:At3g16640 HOGENOM:HBG507116 InParanoid:P31265 OMA:ASYMAHI PhylomeDB:P31265 ProtClustDB:CLSN2684008 ArrayExpress:P31265 Genevestigator:P31265 GermOnline:AT3G16640 Uniprot:P31265
Leaf	Isotig01277	559	489	0.722	3.19E-16	UNIPROTKB|P05429 - symbol:psbB "Photosystem II CP47 chlorophyll apoprotein" species:1111708 "Synechocystis sp. PCC 6803 substr. Kazusa" [GO:0030096 "plasma membrane-derived thylakoid photosystem II" evidence=IDA] InterPro:IPR000932 InterPro:IPR017486 Pfam:PF00421 GO:GO:0016021 GO:GO:0018298

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0009767 EMBL:BA000022 GenomeReviews:BA000022_GR GO:GO:0042651 GO:GO:0016168 GO:GO:0030096 EMBL:M17109 PIR:S06272 RefSeq:NP_442388.1 ProteinModelPortal:P05429 SMR:P05429 IntAct:P05429 STRING:P05429 GeneID:954481 KEGG:syn:slr0906 PATRIC:23842466 eggNOG:NOG05024 HOGENOM:HBG606154 KO:K02704 OMA:GPGMWVS PhylomeDB:P05429 ProtClustDB:CLSK893546 BioCyc:MetaCyc:PSBB-MONOMER BioCyc:SSP1148:SLR0906-MONOMER TIGRFAMs:TIGR03039 Uniprot:P05429
Leaf	Isotig01278	556	476	0.753	2.93E-17	UNIPROTKB|P05429 - symbol:psbB "Photosystem II CP47 chlorophyll apoprotein" species:1111708 "Synechocystis sp. PCC 6803 substr. Kazusa" [GO:0030096 "plasma membrane-derived thylakoid photosystem II" evidence=IDA] InterPro:IPR000932 InterPro:IPR017486 Pfam:PF00421 GO:GO:0016021 GO:GO:0018298 GO:GO:0009767 EMBL:BA000022 GenomeReviews:BA000022_GR GO:GO:0042651 GO:GO:0016168 GO:GO:0030096 EMBL:M17109 PIR:S06272 RefSeq:NP_442388.1 ProteinModelPortal:P05429 SMR:P05429 IntAct:P05429 STRING:P05429 GeneID:954481 KEGG:syn:slr0906 PATRIC:23842466 eggNOG:NOG05024 HOGENOM:HBG606154 KO:K02704 OMA:GPGMWVS PhylomeDB:P05429 ProtClustDB:CLSK893546 BioCyc:MetaCyc:PSBB-MONOMER BioCyc:SSP1148:SLR0906-MONOMER TIGRFAMs:TIGR03039 Uniprot:P05429
Leaf	Isotig01279	336	371	0.386	0.000334776	UNIPROTKB|P27179 - symbol:atpA "ATP synthase subunit alpha" species:1111708 "Synechocystis sp. PCC 6803 substr. Kazusa" [GO:0045260 "plasma membrane proton-transporting ATP synthase complex" evidence=IDA] HAMAP:MF_01346 InterPro:IPR000194 InterPro:IPR000793 InterPro:IPR004100 InterPro:IPR005294 InterPro:IPR018118 InterPro:IPR020003 Pfam:PF00006 Pfam:PF00306 Pfam:PF02874 PROSITE:PS00152 GO:GO:0005524 EMBL:BA000022 GenomeReviews:BA000022_GR GO:GO:0015991 GO:GO:0046933 GO:GO:0046961 GO:GO:0015986 GO:GO:0045261 InterPro:IPR023366 Gene3D:G3DSA:2.40.30.20 eggNOG:COG0056 SUPFAM:SSF50615 SUPFAM:SSF47917 TIGRFAMs:TIGR00962 HOGENOM:HBG565875 KO:K02111 ProtClustDB:PRK09281 OMA:GSDRDIK EMBL:X58128 PIR:S17751 RefSeq:NP_440055.1 ProteinModelPortal:P27179 SMR:P27179 IntAct:P27179 STRING:P27179 GeneID:953354 KEGG:syn:sll1326 PATRIC:23837190 PhylomeDB:P27179 BioCyc:SSP1148:SLL1326-MONOMER GO:GO:0045260 GO:GO:0042651 Uniprot:P27179
Leaf	Isotig01280	332	365	0.392	0.000295621	UNIPROTKB|P27179 - symbol:atpA "ATP synthase subunit alpha" species:1111708 "Synechocystis sp. PCC 6803 substr. Kazusa" [GO:0045260 "plasma membrane proton-transporting ATP synthase complex" evidence=IDA] HAMAP:MF_01346 InterPro:IPR000194 InterPro:IPR000793 InterPro:IPR004100 InterPro:IPR005294 InterPro:IPR018118 InterPro:IPR020003 Pfam:PF00006 Pfam:PF00306 Pfam:PF02874 PROSITE:PS00152 GO:GO:0005524 EMBL:BA000022 GenomeReviews:BA000022_GR GO:GO:0015991 GO:GO:0046933 GO:GO:0046961 GO:GO:0015986 GO:GO:0045261 InterPro:IPR023366 Gene3D:G3DSA:2.40.30.20 eggNOG:COG0056 SUPFAM:SSF50615 SUPFAM:SSF47917 TIGRFAMs:TIGR00962 HOGENOM:HBG565875 KO:K02111 ProtClustDB:PRK09281 OMA:GSDRDIK EMBL:X58128 PIR:S17751 RefSeq:NP_440055.1 ProteinModelPortal:P27179 SMR:P27179 IntAct:P27179 STRING:P27179 GeneID:953354 KEGG:syn:sll1326 PATRIC:23837190 PhylomeDB:P27179 BioCyc:SSP1148:SLL1326-MONOMER GO:GO:0045260 GO:GO:0042651 Uniprot:P27179
Leaf	Isotig01282	18	67	-1.367	6.82E-05	TAIR|locus:2198215 - symbol:KEA1 "K+ efflux antiporter 1" species:3702 "Arabidopsis thaliana" [GO:0006812 "cation transport" evidence=IEA] [GO:0006813 "potassium ion transport" evidence=IEA] [GO:0008152 "metabolic process" evidence=IEA] [GO:0015079 "potassium ion transmembrane transporter activity" evidence=ISS] [GO:0015386 "potassium:hydrogen antiporter activity" evidence=ISS] [GO:0055085 "transmembrane transport" evidence=IEA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] InterPro:IPR003148 InterPro:IPR004771 InterPro:IPR006153 InterPro:IPR016040 Pfam:PF00999 Pfam:PF02254 PROSITE:PS51201 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 GO:GO:0031969 GO:GO:0006813 EMBL:AC009273 eggNOG:COG1226 GO:GO:0015299 EMBL:AF003382 IPI:IPI00520129 PIR:E86149 PIR:F86149 RefSeq:NP_171684.2 UniGene:At.24894 ProteinModelPortal:Q9ZTZ7 SMR:Q9ZTZ7 STRING:Q9ZTZ7 PRIDE:Q9ZTZ7 EnsemblPlants:AT1G01790.1 GeneID:837332 KEGG:ath:AT1G01790 TAIR:At1g01790 HOGENOM:HBG319654 InParanoid:Q9LQ76 PhylomeDB:Q9ZTZ7 ProtClustDB:CLSN2695256 Genevestigator:Q9LQ76 TIGRFAMs:TIGR00932 Uniprot:Q9ZTZ7
Leaf	Isotig01283	18	67	-1.367	6.82E-05	TAIR|locus:2198215 - symbol:KEA1 "K+ efflux antiporter 1" species:3702 "Arabidopsis thaliana" [GO:0006812 "cation transport" evidence=IEA] [GO:0006813 "potassium ion transport" evidence=IEA] [GO:0008152 "metabolic

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						process" evidence=IEA] [GO:0015079 "potassium ion transmembrane transporter activity" evidence=ISS] [GO:0015386 "potassium:hydrogen antiporter activity" evidence=ISS] [GO:0055085 "transmembrane transport" evidence=IEA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] InterPro:IPR003148 InterPro:IPR004771 InterPro:IPR006153 InterPro:IPR016040 Pfam:PF00999 Pfam:PF02254 PROSITE:PS51201 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 GO:GO:0031969 GO:GO:0006813 EMBL:AC009273 eggNOG:COG1226 GO:GO:0015299 EMBL:AF003382 IPI:IPI00520129 PIR:E86149 PIR:F86149 RefSeq:NP_171684.2 UniGene:At.24894 ProteinModelPortal:Q9ZTZ7 SMR:Q9ZTZ7 STRING:Q9ZTZ7 PRIDE:Q9ZTZ7 EnsemblPlants:AT1G01790.1 GeneID:837332 KEGG:ath:AT1G01790 TAIR:At1g01790 HOGENOM:HBG319654 InParanoid:Q9LQ76 PhylomeDB:Q9ZTZ7 ProtClustDB:CLSN2695256 Genevestigator:Q9LQ76 TIGRFAMs:TIGR00932 Uniprot:Q9ZTZ7
Leaf	Isotig01285	18	6	2.114	0.000756754	TAIR|locus:2144118 - symbol:UBP12 "ubiquitin-specific protease 12" species:3702 "Arabidopsis thaliana" [GO:0004221 "ubiquitin thiolesterase activity" evidence=IEA] [GO:0004843 "ubiquitin-specific protease activity" evidence=ISS] [GO:0006511 "ubiquitin-dependent protein catabolic process" evidence=IEA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001394 InterPro:IPR002083 InterPro:IPR008974 InterPro:IPR018200 Pfam:PF00443 Pfam:PF00917 PROSITE:PS00972 PROSITE:PS00973 PROSITE:PS50144 PROSITE:PS50235 SMART:SM00061 GO:GO:0005829 EMBL:CP002688 GenomeReviews:BA000015_GR EMBL:AP002543 GO:GO:0006511 GO:GO:0008234 GO:GO:0004221 SUPFAM:SSF49599 InterPro:IPR013322 Gene3D:G3DSA:2.60.210.10 HSSP:Q93009 eggNOG:COG5077 EMBL:AF302663 EMBL:AF360198 EMBL:AY142616 IPI:IPI00540940 IPI:IPI00547717 RefSeq:NP_568171.1 RefSeq:NP_850783.1 UniGene:At.22362 UniGene:At.67352 ProteinModelPortal:Q9FPT1 SMR:Q9FPT1 STRING:Q9FPT1 PRIDE:Q9FPT1 EnsemblPlants:AT5G06600.1 GeneID:830548 KEGG:ath:AT5G06600 TAIR:At5g06600 HOGENOM:HBG385658 InParanoid:Q9FPT1 KO:K11838 OMA:GLEHADT PhylomeDB:Q9FPT1 ProtClustDB:CLSN2689510 ArrayExpress:Q9C5K1 Genevestigator:Q9FPT1 InterPro:IPR024729 Pfam:PF12436 Uniprot:Q9FPT1
Leaf	Isotig01286	18	4	2.699	0.000102062	TAIR|locus:2144118 - symbol:UBP12 "ubiquitin-specific protease 12" species:3702 "Arabidopsis thaliana" [GO:0004221 "ubiquitin thiolesterase activity" evidence=IEA] [GO:0004843 "ubiquitin-specific protease activity" evidence=ISS] [GO:0006511 "ubiquitin-dependent protein catabolic process" evidence=IEA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001394 InterPro:IPR002083 InterPro:IPR008974 InterPro:IPR018200 Pfam:PF00443 Pfam:PF00917 PROSITE:PS00972 PROSITE:PS00973 PROSITE:PS50144 PROSITE:PS50235 SMART:SM00061 GO:GO:0005829 EMBL:CP002688 GenomeReviews:BA000015_GR EMBL:AP002543 GO:GO:0006511 GO:GO:0008234 GO:GO:0004221 SUPFAM:SSF49599 InterPro:IPR013322 Gene3D:G3DSA:2.60.210.10 HSSP:Q93009 eggNOG:COG5077 EMBL:AF302663 EMBL:AF360198 EMBL:AY142616 IPI:IPI00540940 IPI:IPI00547717 RefSeq:NP_568171.1 RefSeq:NP_850783.1 UniGene:At.22362 UniGene:At.67352 ProteinModelPortal:Q9FPT1 SMR:Q9FPT1 STRING:Q9FPT1 PRIDE:Q9FPT1 EnsemblPlants:AT5G06600.1 GeneID:830548 KEGG:ath:AT5G06600 TAIR:At5g06600 HOGENOM:HBG385658 InParanoid:Q9FPT1 KO:K11838 OMA:GLEHADT PhylomeDB:Q9FPT1 ProtClustDB:CLSN2689510 ArrayExpress:Q9C5K1 Genevestigator:Q9FPT1 InterPro:IPR024729 Pfam:PF12436 Uniprot:Q9FPT1
Leaf	Isotig01287	18	4	2.699	0.000102062	TAIR|locus:2144118 - symbol:UBP12 "ubiquitin-specific protease 12" species:3702 "Arabidopsis thaliana" [GO:0004221 "ubiquitin thiolesterase activity" evidence=IEA] [GO:0004843 "ubiquitin-specific protease activity" evidence=ISS] [GO:0006511 "ubiquitin-dependent protein catabolic process" evidence=IEA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001394 InterPro:IPR002083 InterPro:IPR008974 InterPro:IPR018200 Pfam:PF00443 Pfam:PF00917 PROSITE:PS00972 PROSITE:PS00973 PROSITE:PS50144 PROSITE:PS50235 SMART:SM00061 GO:GO:0005829 EMBL:CP002688 GenomeReviews:BA000015_GR EMBL:AP002543 GO:GO:0006511 GO:GO:0008234 GO:GO:0004221 SUPFAM:SSF49599 InterPro:IPR013322 Gene3D:G3DSA:2.60.210.10 HSSP:Q93009 eggNOG:COG5077 EMBL:AF302663 EMBL:AF360198 EMBL:AY142616 IPI:IPI00540940 IPI:IPI00547717 RefSeq:NP_568171.1 RefSeq:NP_850783.1 UniGene:At.22362 UniGene:At.67352 ProteinModelPortal:Q9FPT1 SMR:Q9FPT1 STRING:Q9FPT1 PRIDE:Q9FPT1 EnsemblPlants:AT5G06600.1 GeneID:830548 KEGG:ath:AT5G06600 TAIR:At5g06600 HOGENOM:HBG385658 InParanoid:Q9FPT1 KO:K11838 OMA:GLEHADT PhylomeDB:Q9FPT1 ProtClustDB:CLSN2689510 ArrayExpress:Q9C5K1 Genevestigator:Q9FPT1 InterPro:IPR024729 Pfam:PF12436 Uniprot:Q9FPT1
Leaf	Isotig01294	3	42	-3.278	5.67E-08	TAIR|locus:2157032 - symbol:FRO7 "AT5G49740" species:3702 "Arabidopsis thaliana" [GO:0016020 "membrane" evidence=ISS] [GO:0016491 "oxidoreductase activity" evidence=ISS] [GO:0000293 "ferric-chelate reductase

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						activity" evidence=IMP;IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009767 "photosynthetic electron transport chain" evidence=IMP] InterPro:IPR000778 InterPro:IPR013112 InterPro:IPR013121 InterPro:IPR013130 InterPro:IPR017927 InterPro:IPR017938 Pfam:PF01794 Pfam:PF08022 Pfam:PF08030 PRINTS:PR00466 PROSITE:PS51384 GO:GO:0016021 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005506 GO:GO:0009055 GO:GO:0050660 GO:GO:0006811 GO:GO:0031969 GO:GO:0009767 SUPFAM:SSF63380 GO:GO:0000293 EMBL:AB025613 UniGene:At.29770 eggNOG:NOG264754 ProtClustDB:CLSN2690231 EMBL:AY912280 EMBL:AK227087 IPI:IPI00547178 RefSeq:NP_199785.2 UniGene:At.7122 ProteinModelPortal:Q3KTM0 STRING:Q3KTM0 PRIDE:Q3KTM0 EnsemblPlants:AT5G49740.1 GeneID:835037 KEGG:ath:AT5G49740 TAIR:At5g49740 HOGENOM:HBG316989 InParanoid:Q3KTM0 PhylomeDB:Q3KTM0 BioCyc:ARA:AT5G49740-MONOMER BioCyc:MetaCyc:AT5G49740-MONOMER BRENDA:1.16.1.7 Genevestigator:Q3KTM0 Uniprot:Q3KTM0
Leaf	Isotig01295	6	42	-2.278	7.23E-06	TAIR|locus:2157032 - symbol:FRO7 "AT5G49740" species:3702 "Arabidopsis thaliana" [GO:0016020 "membrane" evidence=ISS] [GO:0016491 "oxidoreductase activity" evidence=ISS] [GO:0000293 "ferric-chelate reductase activity" evidence=IMP;IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009767 "photosynthetic electron transport chain" evidence=IMP] InterPro:IPR000778 InterPro:IPR013112 InterPro:IPR013121 InterPro:IPR013130 InterPro:IPR017927 InterPro:IPR017938 Pfam:PF01794 Pfam:PF08022 Pfam:PF08030 PRINTS:PR00466 PROSITE:PS51384 GO:GO:0016021 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005506 GO:GO:0009055 GO:GO:0050660 GO:GO:0006811 GO:GO:0031969 GO:GO:0009767 SUPFAM:SSF63380 GO:GO:0000293 EMBL:AB025613 UniGene:At.29770 eggNOG:NOG264754 ProtClustDB:CLSN2690231 EMBL:AY912280 EMBL:AK227087 IPI:IPI00547178 RefSeq:NP_199785.2 UniGene:At.7122 ProteinModelPortal:Q3KTM0 STRING:Q3KTM0 PRIDE:Q3KTM0 EnsemblPlants:AT5G49740.1 GeneID:835037 KEGG:ath:AT5G49740 TAIR:At5g49740 HOGENOM:HBG316989 InParanoid:Q3KTM0 PhylomeDB:Q3KTM0 BioCyc:ARA:AT5G49740-MONOMER BioCyc:MetaCyc:AT5G49740-MONOMER BRENDA:1.16.1.7 Genevestigator:Q3KTM0 Uniprot:Q3KTM0
Leaf	Isotig01296	6	42	-2.278	7.23E-06	TAIR|locus:2157032 - symbol:FRO7 "AT5G49740" species:3702 "Arabidopsis thaliana" [GO:0016020 "membrane" evidence=ISS] [GO:0016491 "oxidoreductase activity" evidence=ISS] [GO:0000293 "ferric-chelate reductase activity" evidence=IMP;IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009767 "photosynthetic electron transport chain" evidence=IMP] InterPro:IPR000778 InterPro:IPR013112 InterPro:IPR013121 InterPro:IPR013130 InterPro:IPR017927 InterPro:IPR017938 Pfam:PF01794 Pfam:PF08022 Pfam:PF08030 PRINTS:PR00466 PROSITE:PS51384 GO:GO:0016021 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005506 GO:GO:0009055 GO:GO:0050660 GO:GO:0006811 GO:GO:0031969 GO:GO:0009767 SUPFAM:SSF63380 GO:GO:0000293 EMBL:AB025613 UniGene:At.29770 eggNOG:NOG264754 ProtClustDB:CLSN2690231 EMBL:AY912280 EMBL:AK227087 IPI:IPI00547178 RefSeq:NP_199785.2 UniGene:At.7122 ProteinModelPortal:Q3KTM0 STRING:Q3KTM0 PRIDE:Q3KTM0 EnsemblPlants:AT5G49740.1 GeneID:835037 KEGG:ath:AT5G49740 TAIR:At5g49740 HOGENOM:HBG316989 InParanoid:Q3KTM0 PhylomeDB:Q3KTM0 BioCyc:ARA:AT5G49740-MONOMER BioCyc:MetaCyc:AT5G49740-MONOMER BRENDA:1.16.1.7 Genevestigator:Q3KTM0 Uniprot:Q3KTM0
Leaf	Isotig01300	48	21	1.722	1.63E-06	TAIR|locus:2063354 - symbol:ACO3 "AT2G05710" species:3702 "Arabidopsis thaliana" [GO:0003994 "aconitate hydratase activity" evidence=ISS;IMP] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0006979 "response to oxidative stress" evidence=IMP;IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005829 "cytosol" evidence=RCA;NAS] [GO:0006101 "citrate metabolic process" evidence=IMP] [GO:0006102 "isocitrate metabolic process" evidence=IMP] [GO:0005524 "ATP binding" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR000573 InterPro:IPR001030 InterPro:IPR006249 InterPro:IPR015928 InterPro:IPR015931 InterPro:IPR015932 InterPro:IPR015934 InterPro:IPR015937 Pfam:PF00330 Pfam:PF00694 PRINTS:PR00415 Prosite:PS00450 GO:GO:0005829 GO:GO:0005739 GO:GO:0005524 GO:GO:0009737 GO:GO:0009570 GO:GO:0046686 GO:GO:0005774 GO:GO:0005618 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0006979 GO:GO:0005507 GO:GO:0009651 GO:GO:0051539 GO:GO:0006097 GO:GO:0006099 GO:GO:0006101 eggNOG:COG1048 HOGENOM:HBG289738 KO:K01681 ProtClustDB:PLN00070 GO:GO:0003994 GO:GO:0052632 GO:GO:0052633

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0006102 InterPro:IPR018136 Gene3D:G3DSA:3.30.499.10 Gene3D:G3DSA:3.20.19.10 Gene3D:G3DSA:3.40.1060.10 PANTHER:PTHR11670 PANTHER:PTHR11670:SF1 SUPFAM:SSF52016 SUPFAM:SSF53732 TIGRFAMs:TIGR01341 PROSITE:PS01244 EMBL:AC007170 EMBL:AY136414 EMBL:BT008809 IPI:IPI00543590 PIR:B84471 RefSeq:NP_178634.2 UniGene:At.26759 UniGene:At.67769 HSSP:P21399 ProteinModelPortal:Q9SIB9 SMR:Q9SIB9 IntAct:Q9SIB9 STRING:Q9SIB9 ANU-2DPAGE:Q9SIB9 PRIDE:Q9SIB9 EnsemblPlants:AT2G05710.1 GeneID:815120 KEGG:ath:AT2G05710 GeneFarm:4276 TAIR:At2g05710 InParanoid:Q9SIB9 OMA:IKYLVQT PhylomeDB:Q9SIB9 Genevestigator:Q9SIB9 Uniprot:Q9SIB9
Leaf	Isotig01301	47	21	1.691	2.79E-06	TAIR|locus:2063354 - symbol:ACO3 "AT2G05710" species:3702 "Arabidopsis thaliana" [GO:0003994 "aconitate hydratase activity" evidence=ISS;IMP] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0006979 "response to oxidative stress" evidence=IMP;IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005829 "cytosol" evidence=RCA;NAS] [GO:0006101 "citrate metabolic process" evidence=IMP] [GO:0006102 "isocitrate metabolic process" evidence=IMP] [GO:0005524 "ATP binding" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR000573 InterPro:IPR001030 InterPro:IPR006249 InterPro:IPR015928 InterPro:IPR015931 InterPro:IPR015932 InterPro:IPR015934 InterPro:IPR015937 Pfam:PF00330 Pfam:PF00694 PRINTS:PR00415 Prosite:PS00450 GO:GO:0005829 GO:GO:0005739 GO:GO:0005524 GO:GO:0009737 GO:GO:0009570 GO:GO:0046686 GO:GO:0005774 GO:GO:0005618 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0006979 GO:GO:0005507 GO:GO:0009651 GO:GO:0051539 GO:GO:0006097 GO:GO:0006099 GO:GO:0006101 eggNOG:COG1048 HOGENOM:HBG289738 KO:K01681 ProtClustDB:PLN00070 GO:GO:0003994 GO:GO:0052632 GO:GO:0052633 GO:GO:0006102 InterPro:IPR018136 Gene3D:G3DSA:3.30.499.10 Gene3D:G3DSA:3.20.19.10 Gene3D:G3DSA:3.40.1060.10 PANTHER:PTHR11670 PANTHER:PTHR11670:SF1 SUPFAM:SSF52016 SUPFAM:SSF53732 TIGRFAMs:TIGR01341 PROSITE:PS01244 EMBL:AC007170 EMBL:AY136414 EMBL:BT008809 IPI:IPI00543590 PIR:B84471 RefSeq:NP_178634.2 UniGene:At.26759 UniGene:At.67769 HSSP:P21399 ProteinModelPortal:Q9SIB9 SMR:Q9SIB9 IntAct:Q9SIB9 STRING:Q9SIB9 ANU-2DPAGE:Q9SIB9 PRIDE:Q9SIB9 EnsemblPlants:AT2G05710.1 GeneID:815120 KEGG:ath:AT2G05710 GeneFarm:4276 TAIR:At2g05710 InParanoid:Q9SIB9 OMA:IKYLVQT PhylomeDB:Q9SIB9 Genevestigator:Q9SIB9 Uniprot:Q9SIB9
Leaf	Isotig01302	16	4	2.529	0.000407249	TAIR|locus:2063354 - symbol:ACO3 "AT2G05710" species:3702 "Arabidopsis thaliana" [GO:0003994 "aconitate hydratase activity" evidence=ISS;IMP] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0006979 "response to oxidative stress" evidence=IMP;IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005829 "cytosol" evidence=RCA;NAS] [GO:0006101 "citrate metabolic process" evidence=IMP] [GO:0006102 "isocitrate metabolic process" evidence=IMP] [GO:0005524 "ATP binding" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR000573 InterPro:IPR001030 InterPro:IPR006249 InterPro:IPR015928 InterPro:IPR015931 InterPro:IPR015932 InterPro:IPR015934 InterPro:IPR015937 Pfam:PF00330 Pfam:PF00694 PRINTS:PR00415 Prosite:PS00450 GO:GO:0005829 GO:GO:0005739 GO:GO:0005524 GO:GO:0009737 GO:GO:0009570 GO:GO:0046686 GO:GO:0005774 GO:GO:0005618 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0006979 GO:GO:0005507 GO:GO:0009651 GO:GO:0051539 GO:GO:0006097 GO:GO:0006099 GO:GO:0006101 eggNOG:COG1048 HOGENOM:HBG289738 KO:K01681 ProtClustDB:PLN00070 GO:GO:0003994 GO:GO:0052632 GO:GO:0052633 GO:GO:0006102 InterPro:IPR018136 Gene3D:G3DSA:3.30.499.10 Gene3D:G3DSA:3.20.19.10 Gene3D:G3DSA:3.40.1060.10 PANTHER:PTHR11670 PANTHER:PTHR11670:SF1 SUPFAM:SSF52016 SUPFAM:SSF53732 TIGRFAMs:TIGR01341 PROSITE:PS01244 EMBL:AC007170 EMBL:AY136414 EMBL:BT008809 IPI:IPI00543590 PIR:B84471 RefSeq:NP_178634.2 UniGene:At.26759 UniGene:At.67769 HSSP:P21399 ProteinModelPortal:Q9SIB9 SMR:Q9SIB9 IntAct:Q9SIB9 STRING:Q9SIB9 ANU-2DPAGE:Q9SIB9 PRIDE:Q9SIB9 EnsemblPlants:AT2G05710.1 GeneID:815120 KEGG:ath:AT2G05710 GeneFarm:4276 TAIR:At2g05710 InParanoid:Q9SIB9 OMA:IKYLVQT PhylomeDB:Q9SIB9 Genevestigator:Q9SIB9 Uniprot:Q9SIB9

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig01306	43	17	1.868	1.59E-06	TAIR|locus:2161815 - symbol:HSP81-2 "AT5G56030" species:3702 "Arabidopsis thaliana" [GO:0005524 "ATP binding" evidence=ISS;IDA] [GO:0006457 "protein folding" evidence=ISS] [GO:0009408 "response to heat" evidence=IEP] [GO:0005515 "protein binding" evidence=IPI] [GO:0006952 "defense response" evidence=IMP] [GO:0009908 "flower development" evidence=IMP] [GO:0048366 "leaf development" evidence=IMP] [GO:0050821 "protein stabilization" evidence=IMP] [GO:0005618 "cell wall" evidence=IDA] [GO:0010286 "heat acclimation" evidence=IEP] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009414 "response to water deprivation" evidence=IMP] [GO:0009651 "response to salt stress" evidence=IMP] [GO:0009816 "defense response to bacterium, incompatible interaction" evidence=IMP] [GO:0016887 "ATPase activity" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0010187 "negative regulation of seed germination" evidence=IMP] [GO:0090332 "stomatal closure" evidence=IMP] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR001404 InterPro:IPR003594 InterPro:IPR019805 Pfam:PF00183 PIRSF:PIRSF002583 PROSITE:PS00298 SMART:SM00387 GO:GO:0005829 GO:GO:0005739 GO:GO:0009506 GO:GO:0005524 GO:GO:0005634 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005618 GO:GO:0006457 GO:GO:0050821 GO:GO:0051082 GO:GO:0016887 GO:GO:0009651 GO:GO:0009414 GO:GO:0010187 GO:GO:0048366 GO:GO:0010286 GO:GO:0009908 GO:GO:0009816 Gene3D:G3DSA:3.30.565.10 SUPFAM:SSF55874 InterPro:IPR020568 SUPFAM:SSF54211 EMBL:AB011476 eggNOG:COG0326 HOGENOM:HBG631012 PANTHER:PTHR11528 InterPro:IPR020575 PRINTS:PR00775 KO:K04079 ProtClustDB:CLSN2686109 EMBL:AY062750 EMBL:AY128805 EMBL:BT001944 EMBL:BT002535 IPI:IPI00537112 RefSeq:NP_200414.1 UniGene:At.25243 UniGene:At.27546 UniGene:At.45945 ProteinModelPortal:P55737 SMR:P55737 IntAct:P55737 STRING:P55737 PRIDE:P55737 EnsemblPlants:AT5G56030.1 GeneID:835701 KEGG:ath:AT5G56030 TAIR:At5g56030 InParanoid:P55737 OMA:GFSKNIK PhylomeDB:P55737 Genevestigator:P55737 GermOnline:AT5G56030 GO:GO:0090332 Uniprot:P55737
Leaf	Isotig01315	18	78	-1.587	1.59E-06	TAIR|locus:2823671 - symbol:CH1 "AT1G44446" species:3702 "Arabidopsis thaliana" [GO:0010277 "chlorophyllide a oxygenase [overall] activity" evidence=IDA;IMP] [GO:0015995 "chlorophyll biosynthetic process" evidence=IMP] [GO:0009507 "chloroplast" evidence=ISS;IDA] [GO:0009706 "chloroplast inner membrane" evidence=IDA] [GO:0042651 "thylakoid membrane" evidence=IDA] InterPro:IPR013626 InterPro:IPR015881 InterPro:IPR017941 Pfam:PF00355 Pfam:PF08417 PROSITE:PS51296 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005506 GO:GO:0009706 GO:GO:0015995 GO:GO:0051537 Gene3D:G3DSA:2.102.10.10 SUPFAM:SSF50022 GO:GO:0009535 GO:GO:0016705 EMBL:AB021316 EMBL:AF177200 EMBL:AB030565 EMBL:AC084807 EMBL:AY128357 EMBL:BT002075 IPI:IPI00519476 IPI:IPI00521014 IPI:IPI00532566 PIR:T52458 RefSeq:NP_175088.1 RefSeq:NP_973969.1 RefSeq:NP_973970.1 UniGene:At.19047 ProteinModelPortal:Q9MBA1 SMR:Q9MBA1 STRING:Q9MBA1 PRIDE:Q9MBA1 EnsemblPlants:AT1G44446.1 GeneID:841029 KEGG:ath:AT1G44446 TAIR:At1g44446 eggNOG:COG4638 HOGENOM:HBG561803 InParanoid:Q9MBA1 KO:K13600 OMA:QCATHLH PhylomeDB:Q9MBA1 ProtClustDB:PLN02281 BioCyc:ARA:AT1G44446-MONOMER BioCyc:MetaCyc:AT1G44446-MONOMER BRENDA:1.13.12.14 ArrayExpress:Q9MBA1 Genevestigator:Q9MBA1 GermOnline:AT1G44446 GO:GO:0010277 Uniprot:Q9MBA1
Leaf	Isotig01316	18	78	-1.587	1.59E-06	TAIR|locus:2823671 - symbol:CH1 "AT1G44446" species:3702 "Arabidopsis thaliana" [GO:0010277 "chlorophyllide a oxygenase [overall] activity" evidence=IDA;IMP] [GO:0015995 "chlorophyll biosynthetic process" evidence=IMP] [GO:0009507 "chloroplast" evidence=ISS;IDA] [GO:0009706 "chloroplast inner membrane" evidence=IDA] [GO:0042651 "thylakoid membrane" evidence=IDA] InterPro:IPR013626 InterPro:IPR015881 InterPro:IPR017941 Pfam:PF00355 Pfam:PF08417 PROSITE:PS51296 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005506 GO:GO:0009706 GO:GO:0015995 GO:GO:0051537 Gene3D:G3DSA:2.102.10.10 SUPFAM:SSF50022 GO:GO:0009535 GO:GO:0016705 EMBL:AB021316 EMBL:AF177200 EMBL:AB030565 EMBL:AC084807 EMBL:AY128357 EMBL:BT002075 IPI:IPI00519476 IPI:IPI00521014 IPI:IPI00532566 PIR:T52458 RefSeq:NP_175088.1 RefSeq:NP_973969.1 RefSeq:NP_973970.1 UniGene:At.19047 ProteinModelPortal:Q9MBA1 SMR:Q9MBA1 STRING:Q9MBA1 PRIDE:Q9MBA1 EnsemblPlants:AT1G44446.1 GeneID:841029 KEGG:ath:AT1G44446 TAIR:At1g44446 eggNOG:COG4638 HOGENOM:HBG561803 InParanoid:Q9MBA1 KO:K13600 OMA:QCATHLH PhylomeDB:Q9MBA1 ProtClustDB:PLN02281 BioCyc:ARA:AT1G44446-MONOMER BioCyc:MetaCyc:AT1G44446-MONOMER BRENDA:1.13.12.14 ArrayExpress:Q9MBA1 Genevestigator:Q9MBA1 GermOnline:AT1G44446 GO:GO:0010277 Uniprot:Q9MBA1

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig01317	18	79	-1.605	1.11E-06	TAIR|locus:2823671 - symbol:CH1 "AT1G44446" species:3702 "Arabidopsis thaliana" [GO:0010277 "chlorophyllide a oxygenase [overall] activity" evidence=IDA;IMP] [GO:0015995 "chlorophyll biosynthetic process" evidence=IMP] [GO:0009507 "chloroplast" evidence=ISS;IDA] [GO:0009706 "chloroplast inner membrane" evidence=IDA] [GO:0042651 "thylakoid membrane" evidence=IDA] InterPro:IPR013626 InterPro:IPR015881 InterPro:IPR017941 Pfam:PF00355 Pfam:PF08417 PROSITE:PS51296 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005506 GO:GO:0009706 GO:GO:0015995 GO:GO:0051537 Gene3D:G3DSA:2.102.10.10 SUPFAM:SSF50022 GO:GO:0009535 GO:GO:0016705 EMBL:AB021316 EMBL:AF177200 EMBL:AB030565 EMBL:AC084807 EMBL:AY128357 EMBL:BT002075 IPI:IPI00519476 IPI:IPI00521014 IPI:IPI00532566 PIR:T52458 RefSeq:NP_175088.1 RefSeq:NP_973969.1 RefSeq:NP_973970.1 UniGene:At.19047 ProteinModelPortal:Q9MBA1 SMR:Q9MBA1 STRING:Q9MBA1 PRIDE:Q9MBA1 EnsemblPlants:AT1G44446.1 GeneID:841029 KEGG:ath:AT1G44446 TAIR:At1g44446 eggNOG:COG4638 HOGENOM:HBG561803 InParanoid:Q9MBA1 KO:K13600 OMA:QCATHLH PhylomeDB:Q9MBA1 ProtClustDB:PLN02281 BioCyc:ARA:AT1G44446-MONOMER BioCyc:MetaCyc:AT1G44446-MONOMER BRENDA:1.13.12.14 ArrayExpress:Q9MBA1 Genevestigator:Q9MBA1 GermOnline:AT1G44446 GO:GO:0010277 Uniprot:Q9MBA1
Leaf	Isotig01327	89	9	3.835	6.54E-24	UNIPROTKB|P73458 - symbol:prc "Carboxyl-terminal protease" species:1111708 "Synechocystis sp. PCC 6803 substr. Kazusa" [GO:0030288 "outer membrane-bounded periplasmic space" evidence=IDA] InterPro:IPR001478 InterPro:IPR004447 InterPro:IPR005151 Pfam:PF03572 PROSITE:PS50106 SMART:SM00228 SMART:SM00245 GO:GO:0006508 GO:GO:0030288 GO:GO:0008236 SUPFAM:SSF50156 EMBL:BA000022 GenomeReviews:BA000022_GR eggNOG:COG0793 KO:K03797 TIGRFAMs:TIGR00225 HSSP:O04073 HOGENOM:HBG750030 PIR:S77395 RefSeq:NP_440818.1 ProteinModelPortal:P73458 STRING:P73458 MEROPS:S41.010 GeneID:954121 KEGG:syn:slr1751 PATRIC:23838874 OMA:RDINKHG PhylomeDB:P73458 BioCyc:SSP1148:SLR1751-MONOMER Uniprot:P73458
Leaf	Isotig01328	85	9	3.768	1.18E-22	UNIPROTKB|P73458 - symbol:prc "Carboxyl-terminal protease" species:1111708 "Synechocystis sp. PCC 6803 substr. Kazusa" [GO:0030288 "outer membrane-bounded periplasmic space" evidence=IDA] InterPro:IPR001478 InterPro:IPR004447 InterPro:IPR005151 Pfam:PF03572 PROSITE:PS50106 SMART:SM00228 SMART:SM00245 GO:GO:0006508 GO:GO:0030288 GO:GO:0008236 SUPFAM:SSF50156 EMBL:BA000022 GenomeReviews:BA000022_GR eggNOG:COG0793 KO:K03797 TIGRFAMs:TIGR00225 HSSP:O04073 HOGENOM:HBG750030 PIR:S77395 RefSeq:NP_440818.1 ProteinModelPortal:P73458 STRING:P73458 MEROPS:S41.010 GeneID:954121 KEGG:syn:slr1751 PATRIC:23838874 OMA:RDINKHG PhylomeDB:P73458 BioCyc:SSP1148:SLR1751-MONOMER Uniprot:P73458
Leaf	Isotig01329	87	9	3.802	2.77E-23	UNIPROTKB|P73458 - symbol:prc "Carboxyl-terminal protease" species:1111708 "Synechocystis sp. PCC 6803 substr. Kazusa" [GO:0030288 "outer membrane-bounded periplasmic space" evidence=IDA] InterPro:IPR001478 InterPro:IPR004447 InterPro:IPR005151 Pfam:PF03572 PROSITE:PS50106 SMART:SM00228 SMART:SM00245 GO:GO:0006508 GO:GO:0030288 GO:GO:0008236 SUPFAM:SSF50156 EMBL:BA000022 GenomeReviews:BA000022_GR eggNOG:COG0793 KO:K03797 TIGRFAMs:TIGR00225 HSSP:O04073 HOGENOM:HBG750030 PIR:S77395 RefSeq:NP_440818.1 ProteinModelPortal:P73458 STRING:P73458 MEROPS:S41.010 GeneID:954121 KEGG:syn:slr1751 PATRIC:23838874 OMA:RDINKHG PhylomeDB:P73458 BioCyc:SSP1148:SLR1751-MONOMER Uniprot:P73458
Leaf	Isotig01330	68	43	1.190	1.52E-05	TAIR|locus:2129256 - symbol:HOG1 "AT4G13940" species:3702 "Arabidopsis thaliana" [GO:0004013 "adenosylhomocysteinase activity" evidence=ISS;IMP] [GO:0006730 "one-carbon metabolic process" evidence=ISS] [GO:0009793 "embryo development ending in seed dormancy" evidence=IMP;NAS] [GO:0005773 "vacuole" evidence=IDA] [GO:0006346 "methylation-dependent chromatin silencing" evidence=IMP] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] [GO:0016441 "posttranscriptional gene silencing" evidence=IMP] InterPro:IPR000043 InterPro:IPR020082 Pfam:PF05221 PIRSF:PIRSF001109 PROSITE:PS00738 PROSITE:PS00739 SMART:SM00996 InterPro:IPR015878 Pfam:PF00670 GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005774 EMBL:Z97335 GO:GO:0005507 GO:GO:0009793 GO:GO:0006730 EMBL:AL161537 GO:GO:0006346 GO:GO:0016441 EMBL:AF059581 EMBL:AF325037 EMBL:AY042866 EMBL:AY049279 EMBL:AY081468 EMBL:AY090284 EMBL:BT002404 EMBL:AY085669 EMBL:Z97059 IPI:IPI00527713 PIR:C71400 RefSeq:NP_193130.1 UniGene:At.24056 UniGene:At.24845

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						UniGene:At.71956 UniGene:At.74987 UniGene:At.74988 ProteinModelPortal:O23255 SMR:O23255 IntAct:O23255 STRING:O23255 PRIDE:O23255 ProMEX:O23255 EnsemblPlants:AT4G13940.1 GeneID:827028 KEGG:ath:AT4G13940 TAIR:At4g13940 eggNOG:COG0499 HOGENOM:HBG352029 InParanoid:O23255 KO:K01251 OMA:ELFTKTE PhylomeDB:O23255 ProtClustDB:PLN02494 ArrayExpress:O23255 Genevestigator:O23255 GO:GO:0004013 PANTHER:PTHR23420 SMART:SM00997 TIGRFAMs:TIGR00936 Uniprot:O23255
Leaf	Isotig01331	95	64	1.099	1.62E-06	TAIR|locus:2129256 - symbol:HOG1 "AT4G13940" species:3702 "Arabidopsis thaliana" [GO:0004013 "adenosylhomocysteinase activity" evidence=ISS;IMP] [GO:0006730 "one-carbon metabolic process" evidence=ISS] [GO:0009793 "embryo development ending in seed dormancy" evidence=IMP;NAS] [GO:0005773 "vacuole" evidence=IDA] [GO:0006346 "methylation-dependent chromatin silencing" evidence=IMP] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] [GO:0016441 "posttranscriptional gene silencing" evidence=IMP] InterPro:IPR000043 InterPro:IPR020082 Pfam:PF05221 PIRSF:PIRSF001109 PROSITE:PS00738 PROSITE:PS00739 SMART:SM00996 InterPro:IPR015878 Pfam:PF00670 GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005774 EMBL:Z97335 GO:GO:0005507 GO:GO:0009793 GO:GO:0006730 EMBL:AL161537 GO:GO:0006346 GO:GO:0016441 EMBL:AF059581 EMBL:AF325037 EMBL:AY042866 EMBL:AY049279 EMBL:AY081468 EMBL:AY090284 EMBL:BT002404 EMBL:AY085669 EMBL:Z97059 IPI:IPI00527713 PIR:C71400 RefSeq:NP_193130.1 UniGene:At.24056 UniGene:At.24845 UniGene:At.71956 UniGene:At.74987 UniGene:At.74988 ProteinModelPortal:O23255 SMR:O23255 IntAct:O23255 STRING:O23255 PRIDE:O23255 ProMEX:O23255 EnsemblPlants:AT4G13940.1 GeneID:827028 KEGG:ath:AT4G13940 TAIR:At4g13940 eggNOG:COG0499 HOGENOM:HBG352029 InParanoid:O23255 KO:K01251 OMA:ELFTKTE PhylomeDB:O23255 ProtClustDB:PLN02494 ArrayExpress:O23255 Genevestigator:O23255 GO:GO:0004013 PANTHER:PTHR23420 SMART:SM00997 TIGRFAMs:TIGR00936 Uniprot:O23255
Leaf	Isotig01332	68	35	1.487	2.83E-07	TAIR|locus:2129256 - symbol:HOG1 "AT4G13940" species:3702 "Arabidopsis thaliana" [GO:0004013 "adenosylhomocysteinase activity" evidence=ISS;IMP] [GO:0006730 "one-carbon metabolic process" evidence=ISS] [GO:0009793 "embryo development ending in seed dormancy" evidence=IMP;NAS] [GO:0005773 "vacuole" evidence=IDA] [GO:0006346 "methylation-dependent chromatin silencing" evidence=IMP] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] [GO:0016441 "posttranscriptional gene silencing" evidence=IMP] InterPro:IPR000043 InterPro:IPR020082 Pfam:PF05221 PIRSF:PIRSF001109 PROSITE:PS00738 PROSITE:PS00739 SMART:SM00996 InterPro:IPR015878 Pfam:PF00670 GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005774 EMBL:Z97335 GO:GO:0005507 GO:GO:0009793 GO:GO:0006730 EMBL:AL161537 GO:GO:0006346 GO:GO:0016441 EMBL:AF059581 EMBL:AF325037 EMBL:AY042866 EMBL:AY049279 EMBL:AY081468 EMBL:AY090284 EMBL:BT002404 EMBL:AY085669 EMBL:Z97059 IPI:IPI00527713 PIR:C71400 RefSeq:NP_193130.1 UniGene:At.24056 UniGene:At.24845 UniGene:At.71956 UniGene:At.74987 UniGene:At.74988 ProteinModelPortal:O23255 SMR:O23255 IntAct:O23255 STRING:O23255 PRIDE:O23255 ProMEX:O23255 EnsemblPlants:AT4G13940.1 GeneID:827028 KEGG:ath:AT4G13940 TAIR:At4g13940 eggNOG:COG0499 HOGENOM:HBG352029 InParanoid:O23255 KO:K01251 OMA:ELFTKTE PhylomeDB:O23255 ProtClustDB:PLN02494 ArrayExpress:O23255 Genevestigator:O23255 GO:GO:0004013 PANTHER:PTHR23420 SMART:SM00997 TIGRFAMs:TIGR00936 Uniprot:O23255
Leaf	Isotig01339	33	146	-1.616	2.80E-11	TAIR|locus:2165897 - symbol:GS2 "AT5G35630" species:3702 "Arabidopsis thaliana" [GO:0004356 "glutamate-ammonia ligase activity" evidence=ISS;IDA;TAS;IPI] [GO:0007568 "aging" evidence=TAS] [GO:0009507 "chloroplast" evidence=IDA;NAS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0019676 "ammonia assimilation cycle" evidence=TAS] [GO:0009579 "thylakoid" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009651

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						"response to salt stress" evidence=IEP] [GO:0048046 "apoplast" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] InterPro:IPR008146 InterPro:IPR008147 InterPro:IPR014746 Pfam:PF00120 Pfam:PF03951 PROSITE:PS00180 PROSITE:PS00181 GO:GO:0005739 GO:GO:0005524 GO:GO:0048046 GO:GO:0009570 GO:GO:0046686 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0007568 GO:GO:0009941 GO:GO:0009651 GO:GO:0009535 GO:GO:0022626 GO:GO:0019676 eggNOG:COG0174 HOGENOM:HBG299709 KO:K01915 GO:GO:0004356 GO:GO:0006542 Gene3D:G3DSA:3.30.590.10 SUPFAM:SSF54368 EMBL:S69727 EMBL:AB015045 EMBL:AB013393 EMBL:AF428319 EMBL:AF428461 EMBL:AY081252 EMBL:AY091114 EMBL:AY122977 EMBL:AY088222 IPI:IPI00534852 PIR:S18600 RefSeq:NP_001031969.1 RefSeq:NP_001078639.1 RefSeq:NP_198413.1 UniGene:At.24218 ProteinModelPortal:Q43127 SMR:Q43127 DIP:DIP-32735N IntAct:Q43127 STRING:Q43127 SWISS-2DPAGE:Q43127 PRIDE:Q43127 EnsemblPlants:AT5G35630.1 EnsemblPlants:AT5G35630.2 EnsemblPlants:AT5G35630.3 GeneID:833535 KEGG:ath:AT5G35630 TAIR:At5g35630 InParanoid:Q43127 OMA:TLDPKPI PhylomeDB:Q43127 ProtClustDB:PLN03036 ArrayExpress:Q43127 Genevestigator:Q43127 GermOnline:AT5G35630 Uniprot:Q43127
Leaf	Isotig01340	36	151	-1.540	6.39E-11	TAIR|locus:2165897 - symbol:GS2 "AT5G35630" species:3702 "Arabidopsis thaliana" [GO:0004356 "glutamate-ammonia ligase activity" evidence=ISS;IDA;TAS;IPI] [GO:0007568 "aging" evidence=TAS] [GO:0009507 "chloroplast" evidence=IDA;NAS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0019676 "ammonia assimilation cycle" evidence=TAS] [GO:0009579 "thylakoid" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0048046 "apoplast" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] InterPro:IPR008146 InterPro:IPR008147 InterPro:IPR014746 Pfam:PF00120 Pfam:PF03951 PROSITE:PS00180 PROSITE:PS00181 GO:GO:0005739 GO:GO:0005524 GO:GO:0048046 GO:GO:0009570 GO:GO:0046686 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0007568 GO:GO:0009941 GO:GO:0009651 GO:GO:0009535 GO:GO:0022626 GO:GO:0019676 eggNOG:COG0174 HOGENOM:HBG299709 KO:K01915 GO:GO:0004356 GO:GO:0006542 Gene3D:G3DSA:3.30.590.10 SUPFAM:SSF54368 EMBL:S69727 EMBL:AB015045 EMBL:AB013393 EMBL:AF428319 EMBL:AF428461 EMBL:AY081252 EMBL:AY091114 EMBL:AY122977 EMBL:AY088222 IPI:IPI00534852 PIR:S18600 RefSeq:NP_001031969.1 RefSeq:NP_001078639.1 RefSeq:NP_198413.1 UniGene:At.24218 ProteinModelPortal:Q43127 SMR:Q43127 DIP:DIP-32735N IntAct:Q43127 STRING:Q43127 SWISS-2DPAGE:Q43127 PRIDE:Q43127 EnsemblPlants:AT5G35630.1 EnsemblPlants:AT5G35630.2 EnsemblPlants:AT5G35630.3 GeneID:833535 KEGG:ath:AT5G35630 TAIR:At5g35630 InParanoid:Q43127 OMA:TLDPKPI PhylomeDB:Q43127 ProtClustDB:PLN03036 ArrayExpress:Q43127 Genevestigator:Q43127 GermOnline:AT5G35630 Uniprot:Q43127
Leaf	Isotig01341	32	139	-1.590	1.38E-10	TAIR|locus:2165897 - symbol:GS2 "AT5G35630" species:3702 "Arabidopsis thaliana" [GO:0004356 "glutamate-ammonia ligase activity" evidence=ISS;IDA;TAS;IPI] [GO:0007568 "aging" evidence=TAS] [GO:0009507 "chloroplast" evidence=IDA;NAS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0019676 "ammonia assimilation cycle" evidence=TAS] [GO:0009579 "thylakoid" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0048046 "apoplast" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] InterPro:IPR008146 InterPro:IPR008147 InterPro:IPR014746 Pfam:PF00120 Pfam:PF03951 PROSITE:PS00180 PROSITE:PS00181 GO:GO:0005739 GO:GO:0005524 GO:GO:0048046 GO:GO:0009570 GO:GO:0046686 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0007568 GO:GO:0009941 GO:GO:0009651 GO:GO:0009535 GO:GO:0022626 GO:GO:0019676 eggNOG:COG0174 HOGENOM:HBG299709 KO:K01915 GO:GO:0004356 GO:GO:0006542 Gene3D:G3DSA:3.30.590.10 SUPFAM:SSF54368 EMBL:S69727 EMBL:AB015045 EMBL:AB013393 EMBL:AF428319 EMBL:AF428461 EMBL:AY081252 EMBL:AY091114 EMBL:AY122977 EMBL:AY088222 IPI:IPI00534852 PIR:S18600 RefSeq:NP_001031969.1 RefSeq:NP_001078639.1 RefSeq:NP_198413.1 UniGene:At.24218 ProteinModelPortal:Q43127 SMR:Q43127 DIP:DIP-32735N IntAct:Q43127 STRING:Q43127 SWISS-2DPAGE:Q43127 PRIDE:Q43127 EnsemblPlants:AT5G35630.1 EnsemblPlants:AT5G35630.2 EnsemblPlants:AT5G35630.3 GeneID:833535 KEGG:ath:AT5G35630 TAIR:At5g35630 InParanoid:Q43127

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						OMA:TLDPKPI PhylomeDB:Q43127 ProtClustDB:PLN03036 ArrayExpress:Q43127 Genevestigator:Q43127 GermOnline:AT5G35630 Uniprot:Q43127
Leaf	Isotig01348	73	282	-1.421	3.99E-17	TAIR|locus:2195366 - symbol:PRK "AT1G32060" species:3702 "Arabidopsis thaliana" [GO:0005524 "ATP binding" evidence=ISS] [GO:0008974 "phosphoribulokinase activity" evidence=ISS] [GO:0009058 "biosynthetic process" evidence=ISS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0010319 "stromule" evidence=IDA] [GO:0042742 "defense response to bacterium" evidence=IEP] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] InterPro:IPR006082 InterPro:IPR006083 Pfam:PF00485 PRINTS:PR00478 PROSITE:PS00567 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005524 GO:GO:0048046 GO:GO:0009570 GO:GO:0042742 GO:GO:0009941 GO:GO:0010319 GO:GO:0009409 GO:GO:0009535 GO:GO:0019253 eggNOG:COG0572 EMBL:AC074309 EMBL:X58149 EMBL:AY044335 EMBL:AY128355 EMBL:BT000019 EMBL:AY084576 IPI:IPI00516350 PIR:S16583 RefSeq:NP_174486.1 UniGene:At.22659 ProteinModelPortal:P25697 SMR:P25697 IntAct:P25697 STRING:P25697 SWISS-2DPAGE:P25697 World-2DPAGE:0003:P25697 PRIDE:P25697 ProMEX:P25697 EnsemblPlants:AT1G32060.1 GeneID:840098 KEGG:ath:AT1G32060 TAIR:At1g32060 HOGENOM:HBG541912 InParanoid:P25697 KO:K00855 OMA:PIYNHET PhylomeDB:P25697 ProtClustDB:PLN02348 BioCyc:ARA:AT1G32060-MONOMER BioCyc:MetaCyc:AT1G32060-MONOMER ArrayExpress:P25697 Genevestigator:P25697 GermOnline:AT1G32060 GO:GO:0008974 Uniprot:P25697
Leaf	Isotig01349	73	288	-1.451	5.70E-18	TAIR|locus:2195366 - symbol:PRK "AT1G32060" species:3702 "Arabidopsis thaliana" [GO:0005524 "ATP binding" evidence=ISS] [GO:0008974 "phosphoribulokinase activity" evidence=ISS] [GO:0009058 "biosynthetic process" evidence=ISS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0010319 "stromule" evidence=IDA] [GO:0042742 "defense response to bacterium" evidence=IEP] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] InterPro:IPR006082 InterPro:IPR006083 Pfam:PF00485 PRINTS:PR00478 PROSITE:PS00567 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005524 GO:GO:0048046 GO:GO:0009570 GO:GO:0042742 GO:GO:0009941 GO:GO:0010319 GO:GO:0009409 GO:GO:0009535 GO:GO:0019253 eggNOG:COG0572 EMBL:AC074309 EMBL:X58149 EMBL:AY044335 EMBL:AY128355 EMBL:BT000019 EMBL:AY084576 IPI:IPI00516350 PIR:S16583 RefSeq:NP_174486.1 UniGene:At.22659 ProteinModelPortal:P25697 SMR:P25697 IntAct:P25697 STRING:P25697 SWISS-2DPAGE:P25697 World-2DPAGE:0003:P25697 PRIDE:P25697 ProMEX:P25697 EnsemblPlants:AT1G32060.1 GeneID:840098 KEGG:ath:AT1G32060 TAIR:At1g32060 HOGENOM:HBG541912 InParanoid:P25697 KO:K00855 OMA:PIYNHET PhylomeDB:P25697 ProtClustDB:PLN02348 BioCyc:ARA:AT1G32060-MONOMER BioCyc:MetaCyc:AT1G32060-MONOMER ArrayExpress:P25697 Genevestigator:P25697 GermOnline:AT1G32060 GO:GO:0008974 Uniprot:P25697
Leaf	Isotig01350	37	188	-1.816	2.43E-16	TAIR|locus:2195366 - symbol:PRK "AT1G32060" species:3702 "Arabidopsis thaliana" [GO:0005524 "ATP binding" evidence=ISS] [GO:0008974 "phosphoribulokinase activity" evidence=ISS] [GO:0009058 "biosynthetic process" evidence=ISS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0010319 "stromule" evidence=IDA] [GO:0042742 "defense response to bacterium" evidence=IEP] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] InterPro:IPR006082 InterPro:IPR006083 Pfam:PF00485 PRINTS:PR00478 PROSITE:PS00567 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005524 GO:GO:0048046 GO:GO:0009570 GO:GO:0042742 GO:GO:0009941 GO:GO:0010319 GO:GO:0009409 GO:GO:0009535 GO:GO:0019253 eggNOG:COG0572 EMBL:AC074309 EMBL:X58149 EMBL:AY044335 EMBL:AY128355 EMBL:BT000019 EMBL:AY084576 IPI:IPI00516350 PIR:S16583 RefSeq:NP_174486.1 UniGene:At.22659 ProteinModelPortal:P25697 SMR:P25697 IntAct:P25697 STRING:P25697 SWISS-2DPAGE:P25697 World-2DPAGE:0003:P25697 PRIDE:P25697 ProMEX:P25697 EnsemblPlants:AT1G32060.1 GeneID:840098

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						KEGG:ath:AT1G32060 TAIR:At1g32060 HOGENOM:HBG541912 InParanoid:P25697 KO:K00855 OMA:PIYNHET PhylomeDB:P25697 ProtClustDB:PLN02348 BioCyc:ARA:AT1G32060-MONOMER BioCyc:MetaCyc:AT1G32060-MONOMER ArrayExpress:P25697 Genevestigator:P25697 GermOnline:AT1G32060 GO:GO:0008974 Uniprot:P25697
Leaf	Isotig01354	18	98	-1.916	8.41E-10	TAIR|locus:2007437 - symbol:TIC110 "translocon at the inner envelope membrane of chloroplasts 110" species:3702 "Arabidopsis thaliana" [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009658 "chloroplast organization" evidence=IMP] [GO:0031897 "Tic complex" evidence=TAS] [GO:0045037 "protein import into chloroplast stroma" evidence=IMP] [GO:0005515 "protein binding" evidence=IPI] [GO:0016020 "membrane" evidence=IDA] GO:GO:0016021 EMBL:CP002684 GO:GO:0005515 GO:GO:0009658 EMBL:AC067971 GO:GO:0031897 GO:GO:0045037 EMBL:AC011001 EMBL:AY094426 EMBL:AY099850 EMBL:AK229869 IPI:IPI00540685 PIR:B86204 RefSeq:NP_172176.1 UniGene:At.12081 IntAct:Q8LPR9 STRING:Q8LPR9 PRIDE:Q9LMI9 EnsemblPlants:AT1G06950.1 GeneID:837205 KEGG:ath:AT1G06950 TAIR:At1g06950 eggNOG:NOG259340 InParanoid:Q8LPR9 OMA:HMEIGRR PhylomeDB:Q8LPR9 ProtClustDB:CLSN2682158 ArrayExpress:Q8LPG5 Genevestigator:Q8LPR9 Uniprot:Q8LPR9
Leaf	Isotig01355	17	73	-1.573	3.92E-06	TAIR|locus:2007437 - symbol:TIC110 "translocon at the inner envelope membrane of chloroplasts 110" species:3702 "Arabidopsis thaliana" [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009658 "chloroplast organization" evidence=IMP] [GO:0031897 "Tic complex" evidence=TAS] [GO:0045037 "protein import into chloroplast stroma" evidence=IMP] [GO:0005515 "protein binding" evidence=IPI] [GO:0016020 "membrane" evidence=IDA] GO:GO:0016021 EMBL:CP002684 GO:GO:0005515 GO:GO:0009658 EMBL:AC067971 GO:GO:0031897 GO:GO:0045037 EMBL:AC011001 EMBL:AY094426 EMBL:AY099850 EMBL:AK229869 IPI:IPI00540685 PIR:B86204 RefSeq:NP_172176.1 UniGene:At.12081 IntAct:Q8LPR9 STRING:Q8LPR9 PRIDE:Q9LMI9 EnsemblPlants:AT1G06950.1 GeneID:837205 KEGG:ath:AT1G06950 TAIR:At1g06950 eggNOG:NOG259340 InParanoid:Q8LPR9 OMA:HMEIGRR PhylomeDB:Q8LPR9 ProtClustDB:CLSN2682158 ArrayExpress:Q8LPG5 Genevestigator:Q8LPR9 Uniprot:Q8LPR9
Leaf	Isotig01356	26	91	-1.278	1.05E-05	TAIR|locus:2007437 - symbol:TIC110 "translocon at the inner envelope membrane of chloroplasts 110" species:3702 "Arabidopsis thaliana" [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009658 "chloroplast organization" evidence=IMP] [GO:0031897 "Tic complex" evidence=TAS] [GO:0045037 "protein import into chloroplast stroma" evidence=IMP] [GO:0005515 "protein binding" evidence=IPI] [GO:0016020 "membrane" evidence=IDA] GO:GO:0016021 EMBL:CP002684 GO:GO:0005515 GO:GO:0009658 EMBL:AC067971 GO:GO:0031897 GO:GO:0045037 EMBL:AC011001 EMBL:AY094426 EMBL:AY099850 EMBL:AK229869 IPI:IPI00540685 PIR:B86204 RefSeq:NP_172176.1 UniGene:At.12081 IntAct:Q8LPR9 STRING:Q8LPR9 PRIDE:Q9LMI9 EnsemblPlants:AT1G06950.1 GeneID:837205 KEGG:ath:AT1G06950 TAIR:At1g06950 eggNOG:NOG259340 InParanoid:Q8LPR9 OMA:HMEIGRR PhylomeDB:Q8LPR9 ProtClustDB:CLSN2682158 ArrayExpress:Q8LPG5 Genevestigator:Q8LPR9 Uniprot:Q8LPR9
Leaf	Isotig01390	96	318	-1.199	4.69E-15	TAIR|locus:2042148 - symbol:LHCB2.1 "AT2G05100" species:3702 "Arabidopsis thaliana" [GO:0015979 "photosynthesis" evidence=ISS] [GO:0016168 "chlorophyll binding" evidence=ISS] [GO:0030076 "light-harvesting complex" evidence=ISS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009637 "response to blue light" evidence=IEP] [GO:0010114 "response to red light" evidence=IEP] [GO:0010218 "response to far red light" evidence=IEP] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR001344 Pfam:PF00504 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009941 GO:GO:0009637 GO:GO:0010218 GO:GO:0010114 GO:GO:0009535 GO:GO:0010287 HOGENOM:HBG618504 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 ProtClustDB:PLN00025 UniGene:At.48420 UniGene:At.63397 KO:K08913 EMBL:AC007443 EMBL:AY052275 EMBL:AY052348 EMBL:BT001933 IPI:IPI00535929 RefSeq:NP_178585.1 ProteinModelPortal:Q9SHR7 SMR:Q9SHR7 STRING:Q9SHR7 PRIDE:Q9SHR7 EnsemblPlants:AT2G05100.1 GeneID:815058 KEGG:ath:AT2G05100 TAIR:At2g05100 InParanoid:Q9SHR7 OMA:HQTTSFL PhylomeDB:Q9SHR7 ArrayExpress:Q9SHR7 Genevestigator:Q9SHR7 Uniprot:Q9SHR7
Leaf	Isotig01391	82	251	-1.085	1.32E-10	TAIR|locus:2005534 - symbol:PETC "AT4G03280" species:3702 "Arabidopsis thaliana" [GO:0010196 "nonphotochemical quenching" evidence=IMP] [GO:0009512 "cytochrome b6f complex" evidence=TAS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA;TAS] [GO:0009767 "photosynthetic electron transport

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						chain" evidence=TAS] [GO:0046028 "electron transporter, transferring electrons from cytochrome b6/f complex of photosystem II activity" evidence=TAS] [GO:0005515 "protein binding" evidence=IPI] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0042742 "defense response to bacterium" evidence=IEP] [GO:0016020 "membrane" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0080167 "response to karrikin" evidence=IEP] InterPro:IPR005805 InterPro:IPR014349 InterPro:IPR014909 InterPro:IPR017941 InterPro:IPR023960 Pfam:PF00355 Pfam:PF08802 PRINTS:PR00162 PROSITE:PS51296 GO:GO:0016021 GO:GO:0005886 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0042742 GO:GO:0005515 GO:GO:0046872 GO:GO:0009941 GO:GO:0080167 GO:GO:0051537 GO:GO:0009767 Gene3D:G3DSA:2.102.10.10 SUPFAM:SSF50022 GO:GO:0009535 EMBL:AL161496 GO:GO:0010196 EMBL:AC005275 GO:GO:0009512 GO:GO:0045158 GO:GO:0008121 HOGENOM:HBG668715 eggNOG:COG0723 UniGene:At.486 EMBL:AJ292972 EMBL:AJ243702 EMBL:AF370566 EMBL:AF410296 EMBL:AY093726 IPI:IPI00530995 IPI:IPI00548912 PIR:F85041 PIR:PA0041 RefSeq:NP_192237.1 RefSeq:NP_849295.1 UniGene:At.67366 ProteinModelPortal:Q9ZR03 SMR:Q9ZR03 IntAct:Q9ZR03 STRING:Q9ZR03 PRIDE:Q9ZR03 ProMEX:Q9ZR03 EnsemblPlants:AT4G03280.1 GeneID:827996 KEGG:ath:AT4G03280 GeneFarm:5037 TAIR:At4g03280 InParanoid:Q9ZR03 KO:K02636 OMA:YPVANYF PhylomeDB:Q9ZR03 ProtClustDB:CLSN2685934 ArrayExpress:Q9ZR03 Genevestigator:Q9ZR03 GermOnline:AT4G03280 GO:GO:0046028 GO:GO:0009496 PANTHER:PTHR10134 Uniprot:Q9ZR03
Leaf	Isotig01392	75	227	-1.069	1.59E-09	TAIR|locus:2005534 - symbol:PETC "AT4G03280" species:3702 "Arabidopsis thaliana" [GO:0010196 "nonphotochemical quenching" evidence=IMP] [GO:0009512 "cytochrome b6f complex" evidence=TAS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA;TAS] [GO:0009767 "photosynthetic electron transport chain" evidence=TAS] [GO:0046028 "electron transporter, transferring electrons from cytochrome b6/f complex of photosystem II activity" evidence=TAS] [GO:0005515 "protein binding" evidence=IPI] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0042742 "defense response to bacterium" evidence=IEP] [GO:0016020 "membrane" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0080167 "response to karrikin" evidence=IEP] InterPro:IPR005805 InterPro:IPR014349 InterPro:IPR014909 InterPro:IPR017941 InterPro:IPR023960 Pfam:PF00355 Pfam:PF08802 PRINTS:PR00162 PROSITE:PS51296 GO:GO:0016021 GO:GO:0005886 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0042742 GO:GO:0005515 GO:GO:0046872 GO:GO:0009941 GO:GO:0080167 GO:GO:0051537 GO:GO:0009767 Gene3D:G3DSA:2.102.10.10 SUPFAM:SSF50022 GO:GO:0009535 EMBL:AL161496 GO:GO:0010196 EMBL:AC005275 GO:GO:0009512 GO:GO:0045158 GO:GO:0008121 HOGENOM:HBG668715 eggNOG:COG0723 UniGene:At.486 EMBL:AJ292972 EMBL:AJ243702 EMBL:AF370566 EMBL:AF410296 EMBL:AY093726 IPI:IPI00530995 IPI:IPI00548912 PIR:F85041 PIR:PA0041 RefSeq:NP_192237.1 RefSeq:NP_849295.1 UniGene:At.67366 ProteinModelPortal:Q9ZR03 SMR:Q9ZR03 IntAct:Q9ZR03 STRING:Q9ZR03 PRIDE:Q9ZR03 ProMEX:Q9ZR03 EnsemblPlants:AT4G03280.1 GeneID:827996 KEGG:ath:AT4G03280 GeneFarm:5037 TAIR:At4g03280 InParanoid:Q9ZR03 KO:K02636 OMA:YPVANYF PhylomeDB:Q9ZR03 ProtClustDB:CLSN2685934 ArrayExpress:Q9ZR03 Genevestigator:Q9ZR03 GermOnline:AT4G03280 GO:GO:0046028 GO:GO:0009496 PANTHER:PTHR10134 Uniprot:Q9ZR03
Leaf	Isotig01396	57	30	1.455	3.75E-06	TAIR|locus:505006621 - symbol:RbcX2 "AT5G19855" species:3702 "Arabidopsis thaliana" [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0044183 "protein binding involved in protein folding" evidence=IDA] [GO:0061077 "chaperone-mediated protein folding" evidence=IDA] GO:GO:0009570 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0044183 GO:GO:0061077 EMBL:AY088169 EMBL:BT004014 EMBL:BT005149 IPI:IPI00527508 RefSeq:NP_568382.1 UniGene:At.31246 ProteinModelPortal:Q8L9X2 SMR:Q8L9X2 STRING:Q8L9X2 PRIDE:Q8L9X2 EnsemblPlants:AT5G19855.1 GeneID:832106 KEGG:ath:AT5G19855 TAIR:At5g19855 eggNOG:NOG14198 HOGENOM:HBG609478 InParanoid:Q8L9X2 OMA:GKRFLRA PhylomeDB:Q8L9X2 ProtClustDB:CLSN2713656 ArrayExpress:Q8L9X2 Genevestigator:Q8L9X2 InterPro:IPR003435 Pfam:PF02341 Uniprot:Q8L9X2
Leaf	Isotig01397	46	26	1.352	8.49E-05	TAIR|locus:505006621 - symbol:RbcX2 "AT5G19855" species:3702 "Arabidopsis thaliana" [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0044183 "protein binding involved in protein folding" evidence=IDA] [GO:0061077 "chaperone-mediated protein folding" evidence=IDA] GO:GO:0009570 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0044183 GO:GO:0061077 EMBL:AY088169 EMBL:BT004014

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EMBL:BT005149 IPI:IPI00527508 RefSeq:NP_568382.1 UniGene:At.31246 ProteinModelPortal:Q8L9X2 SMR:Q8L9X2 STRING:Q8L9X2 PRIDE:Q8L9X2 EnsemblPlants:AT5G19855.1 GeneID:832106 KEGG:ath:AT5G19855 TAIR:At5g19855 eggNOG:NOG14198 HOGENOM:HBG609478 InParanoid:Q8L9X2 OMA:GKRFLRA PhylomeDB:Q8L9X2 ProtClustDB:CLSN2713656 ArrayExpress:Q8L9X2 Genevestigator:Q8L9X2 InterPro:IPR003435 Pfam:PF02341 Uniprot:Q8L9X2
Leaf	Isotig01398	45	20	1.699	4.24E-06	TAIR|locus:505006621 - symbol:RbcX2 "AT5G19855" species:3702 "Arabidopsis thaliana" [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0044183 "protein binding involved in protein folding" evidence=IDA] [GO:0061077 "chaperone-mediated protein folding" evidence=IDA] GO:GO:0009570 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0044183 GO:GO:0061077 EMBL:AY088169 EMBL:BT004014 EMBL:BT005149 IPI:IPI00527508 RefSeq:NP_568382.1 UniGene:At.31246 ProteinModelPortal:Q8L9X2 SMR:Q8L9X2 STRING:Q8L9X2 PRIDE:Q8L9X2 EnsemblPlants:AT5G19855.1 GeneID:832106 KEGG:ath:AT5G19855 TAIR:At5g19855 eggNOG:NOG14198 HOGENOM:HBG609478 InParanoid:Q8L9X2 OMA:GKRFLRA PhylomeDB:Q8L9X2 ProtClustDB:CLSN2713656 ArrayExpress:Q8L9X2 Genevestigator:Q8L9X2 InterPro:IPR003435 Pfam:PF02341 Uniprot:Q8L9X2
Leaf	Isotig01411	61	214	-1.282	1.26E-11	TAIR|locus:2116485 - symbol:PDE334 "PIGMENT DEFECTIVE 334" species:3702 "Arabidopsis thaliana" [GO:0015078 "hydrogen ion transmembrane transporter activity" evidence=IEA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0042742 "defense response to bacterium" evidence=IEP] [GO:0016020 "membrane" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] InterPro:IPR002146 Pfam:PF00430 GO:GO:0016021 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0042742 GO:GO:0009941 EMBL:AL161580 GO:GO:0016787 GO:GO:0009535 EMBL:AL021811 GO:GO:0015986 GO:GO:0015078 GO:GO:0045263 KO:K02109 HOGENOM:HBG708402 OMA:DFDATLP UniGene:At.20952 EMBL:AY058101 EMBL:AY086044 EMBL:AJ245574 IPI:IPI00546026 PIR:T05402 RefSeq:NP_194953.1 ProteinModelPortal:Q42139 STRING:Q42139 PRIDE:Q42139 ProMEX:Q42139 EnsemblPlants:AT4G32260.1 GeneID:829359 KEGG:ath:AT4G32260 TAIR:At4g32260 InParanoid:Q42139 PhylomeDB:Q42139 ProtClustDB:CLSN2686027 ArrayExpress:Q42139 Genevestigator:Q42139 Uniprot:Q42139
Leaf	Isotig01412	59	205	-1.268	4.94E-11	TAIR|locus:2116485 - symbol:PDE334 "PIGMENT DEFECTIVE 334" species:3702 "Arabidopsis thaliana" [GO:0015078 "hydrogen ion transmembrane transporter activity" evidence=IEA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0042742 "defense response to bacterium" evidence=IEP] [GO:0016020 "membrane" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] InterPro:IPR002146 Pfam:PF00430 GO:GO:0016021 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0042742 GO:GO:0009941 EMBL:AL161580 GO:GO:0016787 GO:GO:0009535 EMBL:AL021811 GO:GO:0015986 GO:GO:0015078 GO:GO:0045263 KO:K02109 HOGENOM:HBG708402 OMA:DFDATLP UniGene:At.20952 EMBL:AY058101 EMBL:AY086044 EMBL:AJ245574 IPI:IPI00546026 PIR:T05402 RefSeq:NP_194953.1 ProteinModelPortal:Q42139 STRING:Q42139 PRIDE:Q42139 ProMEX:Q42139 EnsemblPlants:AT4G32260.1 GeneID:829359 KEGG:ath:AT4G32260 TAIR:At4g32260 InParanoid:Q42139 PhylomeDB:Q42139 ProtClustDB:CLSN2686027 ArrayExpress:Q42139 Genevestigator:Q42139 Uniprot:Q42139
Leaf	Isotig01413	50	180	-1.319	2.14E-10	TAIR|locus:2116485 - symbol:PDE334 "PIGMENT DEFECTIVE 334" species:3702 "Arabidopsis thaliana" [GO:0015078 "hydrogen ion transmembrane transporter activity" evidence=IEA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0042742 "defense response to bacterium" evidence=IEP] [GO:0016020 "membrane" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] InterPro:IPR002146 Pfam:PF00430 GO:GO:0016021 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0042742 GO:GO:0009941 EMBL:AL161580 GO:GO:0016787 GO:GO:0009535 EMBL:AL021811 GO:GO:0015986 GO:GO:0015078 GO:GO:0045263 KO:K02109 HOGENOM:HBG708402 OMA:DFDATLP UniGene:At.20952 EMBL:AY058101 EMBL:AY086044 EMBL:AJ245574 IPI:IPI00546026 PIR:T05402 RefSeq:NP_194953.1 ProteinModelPortal:Q42139 STRING:Q42139 PRIDE:Q42139 ProMEX:Q42139 EnsemblPlants:AT4G32260.1 GeneID:829359 KEGG:ath:AT4G32260 TAIR:At4g32260 InParanoid:Q42139 PhylomeDB:Q42139 ProtClustDB:CLSN2686027 ArrayExpress:Q42139 Genevestigator:Q42139 Uniprot:Q42139
Leaf	Isotig01414	21	7	2.114	0.000274738	TAIR|locus:2090807 - symbol:CCB1 "AT3G26710" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0009507 "chloroplast" evidence=IDA] [GO:0010190 "cytochrome b6f

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						complex assembly" evidence=IMP] GO:GO:0009507 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0010190 EMBL:AB026648 EMBL:AY087129 EMBL:AY140025 EMBL:BT006294 EMBL:AK227251 IPI:IPI00548184 RefSeq:NP_566797.1 UniGene:At.5353 STRING:Q9LSE4 PRIDE:Q9LSE4 EnsemblPlants:AT3G26710.1 GeneID:822283 KEGG:ath:AT3G26710 TAIR:At3g26710 eggNOG:NOG78978 HOGENOM:HBG412006 InParanoid:Q9LSE4 OMA:FCTCISL PhylomeDB:Q9LSE4 ProtClustDB:CLSN2688803 ArrayExpress:Q9LSE4 Genevestigator:Q9LSE4 InterPro:IPR021919 Pfam:PF12046 Uniprot:Q9LSE4
Leaf	Isotig01415	21	7	2.114	0.000274738	TAIR|locus:2090807 - symbol:CCB1 "AT3G26710" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0009507 "chloroplast" evidence=IDA] [GO:0010190 "cytochrome b6f complex assembly" evidence=IMP] GO:GO:0009507 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0010190 EMBL:AB026648 EMBL:AY087129 EMBL:AY140025 EMBL:BT006294 EMBL:AK227251 IPI:IPI00548184 RefSeq:NP_566797.1 UniGene:At.5353 STRING:Q9LSE4 PRIDE:Q9LSE4 EnsemblPlants:AT3G26710.1 GeneID:822283 KEGG:ath:AT3G26710 TAIR:At3g26710 eggNOG:NOG78978 HOGENOM:HBG412006 InParanoid:Q9LSE4 OMA:FCTCISL PhylomeDB:Q9LSE4 ProtClustDB:CLSN2688803 ArrayExpress:Q9LSE4 Genevestigator:Q9LSE4 InterPro:IPR021919 Pfam:PF12046 Uniprot:Q9LSE4
Leaf	Isotig01416	20	7	2.044	0.00051229	TAIR|locus:2090807 - symbol:CCB1 "AT3G26710" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0009507 "chloroplast" evidence=IDA] [GO:0010190 "cytochrome b6f complex assembly" evidence=IMP] GO:GO:0009507 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0010190 EMBL:AB026648 EMBL:AY087129 EMBL:AY140025 EMBL:BT006294 EMBL:AK227251 IPI:IPI00548184 RefSeq:NP_566797.1 UniGene:At.5353 STRING:Q9LSE4 PRIDE:Q9LSE4 EnsemblPlants:AT3G26710.1 GeneID:822283 KEGG:ath:AT3G26710 TAIR:At3g26710 eggNOG:NOG78978 HOGENOM:HBG412006 InParanoid:Q9LSE4 OMA:FCTCISL PhylomeDB:Q9LSE4 ProtClustDB:CLSN2688803 ArrayExpress:Q9LSE4 Genevestigator:Q9LSE4 InterPro:IPR021919 Pfam:PF12046 Uniprot:Q9LSE4
Leaf	Isotig01436	79	10	3.511	3.59E-20	TAIR|locus:2157363 - symbol:ERD1 "AT5G51070" species:3702 "Arabidopsis thaliana" [GO:0005524 "ATP binding" evidence=ISS] [GO:0009507 "chloroplast" evidence=IDA] [GO:0016887 "ATPase activity" evidence=ISS;IDA] [GO:0009570 "chloroplast stroma" evidence=IDA;TAS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0034214 "protein hexamerization" evidence=IDA] [GO:0042803 "protein homodimerization activity" evidence=IDA] InterPro:IPR001270 InterPro:IPR003593 InterPro:IPR003959 InterPro:IPR004176 InterPro:IPR013093 InterPro:IPR018368 Pfam:PF00004 Pfam:PF02861 Pfam:PF07724 PRINTS:PR00300 PROSITE:PS00870 PROSITE:PS00871 SMART:SM00382 GO:GO:0005524 GO:GO:0009570 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0042803 GO:GO:0006950 GO:GO:0009941 GO:GO:0016887 EMBL:AB017063 eggNOG:COG0542 GO:GO:0019538 InterPro:IPR023150 Gene3D:G3DSA:1.10.1780.10 HOGENOM:HBG413133 InterPro:IPR019489 Pfam:PF10431 SMART:SM01086 GO:GO:0034214 EMBL:D17582 EMBL:AB023044 EMBL:AY035112 EMBL:AY133868 IPI:IPI00535711 PIR:JN0901 RefSeq:NP_568750.1 UniGene:At.25346 UniGene:At.69453 ProteinModelPortal:P42762 SMR:P42762 IntAct:P42762 STRING:P42762 PRIDE:P42762 EnsemblPlants:AT5G51070.1 GeneID:835180 KEGG:ath:AT5G51070 GeneFarm:2731 TAIR:At5g51070 InParanoid:P42762 OMA:STKRVFE PhylomeDB:P42762 ProtClustDB:CLSN2689983 ArrayExpress:P42762 Genevestigator:P42762 GermOnline:AT5G51070 Uniprot:P42762
Leaf	Isotig01437	69	12	3.053	5.81E-16	TAIR|locus:2157363 - symbol:ERD1 "AT5G51070" species:3702 "Arabidopsis thaliana" [GO:0005524 "ATP binding" evidence=ISS] [GO:0009507 "chloroplast" evidence=IDA] [GO:0016887 "ATPase activity" evidence=ISS;IDA] [GO:0009570 "chloroplast stroma" evidence=IDA;TAS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0034214 "protein hexamerization" evidence=IDA] [GO:0042803 "protein homodimerization activity" evidence=IDA] InterPro:IPR001270 InterPro:IPR003593 InterPro:IPR003959 InterPro:IPR004176 InterPro:IPR013093 InterPro:IPR018368 Pfam:PF00004 Pfam:PF02861 Pfam:PF07724 PRINTS:PR00300 PROSITE:PS00870 PROSITE:PS00871 SMART:SM00382 GO:GO:0005524 GO:GO:0009570 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0042803 GO:GO:0006950 GO:GO:0009941 GO:GO:0016887 EMBL:AB017063 eggNOG:COG0542 GO:GO:0019538 InterPro:IPR023150 Gene3D:G3DSA:1.10.1780.10 HOGENOM:HBG413133 InterPro:IPR019489 Pfam:PF10431 SMART:SM01086 GO:GO:0034214 EMBL:D17582 EMBL:AB023044 EMBL:AY035112 EMBL:AY133868 IPI:IPI00535711 PIR:JN0901 RefSeq:NP_568750.1 UniGene:At.25346 UniGene:At.69453 ProteinModelPortal:P42762 SMR:P42762 IntAct:P42762 STRING:P42762 PRIDE:P42762 EnsemblPlants:AT5G51070.1 GeneID:835180 KEGG:ath:AT5G51070 GeneFarm:2731 TAIR:At5g51070 InParanoid:P42762 OMA:STKRVFE PhylomeDB:P42762 ProtClustDB:CLSN2689983 ArrayExpress:P42762 Genevestigator:P42762 GermOnline:AT5G51070 Uniprot:P42762

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig01438	79	10	3.511	3.59E-20	TAIR|locus:2157363 - symbol:ERD1 "AT5G51070" species:3702 "Arabidopsis thaliana" [GO:0005524 "ATP binding" evidence=ISS] [GO:0009507 "chloroplast" evidence=IDA] [GO:0016887 "ATPase activity" evidence=ISS;IDA] [GO:0009570 "chloroplast stroma" evidence=IDA;TAS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0034214 "protein hexamerization" evidence=IDA] [GO:0042803 "protein homodimerization activity" evidence=IDA] InterPro:IPR001270 InterPro:IPR003593 InterPro:IPR003959 InterPro:IPR004176 InterPro:IPR013093 InterPro:IPR018368 Pfam:PF00004 Pfam:PF02861 Pfam:PF07724 PRINTS:PR00300 PROSITE:PS00870 PROSITE:PS00871 SMART:SM00382 GO:GO:0005524 GO:GO:0009570 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0042803 GO:GO:0006950 GO:GO:0009941 GO:GO:0016887 EMBL:AB017063 eggNOG:COG0542 GO:GO:0019538 InterPro:IPR023150 Gene3D:G3DSA:1.10.1780.10 HOGENOM:HBG413133 InterPro:IPR019489 Pfam:PF10431 SMART:SM01086 GO:GO:0034214 EMBL:D17582 EMBL:AB023044 EMBL:AY035112 EMBL:AY133868 IPI:IPI00535711 PIR:JN0901 RefSeq:NP_568750.1 UniGene:At.25346 UniGene:At.69453 ProteinModelPortal:P42762 SMR:P42762 IntAct:P42762 STRING:P42762 PRIDE:P42762 EnsemblPlants:AT5G51070.1 GeneID:835180 KEGG:ath:AT5G51070 GeneFarm:2731 TAIR:At5g51070 InParanoid:P42762 OMA:STKRVFE PhylomeDB:P42762 ProtClustDB:CLSN2689983 ArrayExpress:P42762 Genevestigator:P42762 GermOnline:AT5G51070 Uniprot:P42762
Leaf	Isotig01439	69	12	3.053	5.81E-16	TAIR|locus:2157363 - symbol:ERD1 "AT5G51070" species:3702 "Arabidopsis thaliana" [GO:0005524 "ATP binding" evidence=ISS] [GO:0009507 "chloroplast" evidence=IDA] [GO:0016887 "ATPase activity" evidence=ISS;IDA] [GO:0009570 "chloroplast stroma" evidence=IDA;TAS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0034214 "protein hexamerization" evidence=IDA] [GO:0042803 "protein homodimerization activity" evidence=IDA] InterPro:IPR001270 InterPro:IPR003593 InterPro:IPR003959 InterPro:IPR004176 InterPro:IPR013093 InterPro:IPR018368 Pfam:PF00004 Pfam:PF02861 Pfam:PF07724 PRINTS:PR00300 PROSITE:PS00870 PROSITE:PS00871 SMART:SM00382 GO:GO:0005524 GO:GO:0009570 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0042803 GO:GO:0006950 GO:GO:0009941 GO:GO:0016887 EMBL:AB017063 eggNOG:COG0542 GO:GO:0019538 InterPro:IPR023150 Gene3D:G3DSA:1.10.1780.10 HOGENOM:HBG413133 InterPro:IPR019489 Pfam:PF10431 SMART:SM01086 GO:GO:0034214 EMBL:D17582 EMBL:AB023044 EMBL:AY035112 EMBL:AY133868 IPI:IPI00535711 PIR:JN0901 RefSeq:NP_568750.1 UniGene:At.25346 UniGene:At.69453 ProteinModelPortal:P42762 SMR:P42762 IntAct:P42762 STRING:P42762 PRIDE:P42762 EnsemblPlants:AT5G51070.1 GeneID:835180 KEGG:ath:AT5G51070 GeneFarm:2731 TAIR:At5g51070 InParanoid:P42762 OMA:STKRVFE PhylomeDB:P42762 ProtClustDB:CLSN2689983 ArrayExpress:P42762 Genevestigator:P42762 GermOnline:AT5G51070 Uniprot:P42762
Leaf	Isotig01444	36	10	2.377	3.10E-07	No hit
Leaf	Isotig01445	30	10	2.114	1.37E-05	No hit
Leaf	Isotig01446	25	7	2.365	2.12E-05	No hit
Leaf	Isotig01447	19	7	1.970	0.000947153	No hit
Leaf	Isotig01448	26	6	2.644	3.85E-06	TAIR|locus:2060854 - symbol:UBA1 "AT2G30110" species:3702 "Arabidopsis thaliana" [GO:0004839 "ubiquitin activating enzyme activity" evidence=ISS;IMP] [GO:0006511 "ubiquitin-dependent protein catabolic process" evidence=TAS] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0051707 "response to other organism" evidence=IMP] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0004842 "ubiquitin-protein ligase activity" evidence=IDA] [GO:0016567 "protein ubiquitination" evidence=IDA] InterPro:IPR000011 InterPro:IPR000127 InterPro:IPR000594 InterPro:IPR016040 Pfam:PF00899 Pfam:PF02134 PRINTS:PR01849 Pfam:PF10585 GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 GO:GO:0005524 GO:GO:0046686 EMBL:CP002685 GenomeReviews:CT485783_GR Gene3D:G3DSA:3.40.50.720 GO:GO:0051707 GO:GO:0004842 eggNOG:COG0476 InterPro:IPR009036 SUPFAM:SSF69572 EMBL:AC004165 HSSP:P12282 GO:GO:0008641 InterPro:IPR023280 InterPro:IPR019572 InterPro:IPR018074 Gene3D:G3DSA:1.10.3240.10 PROSITE:PS00536 PROSITE:PS00865 HOGENOM:HBG356508 KO:K03178 InterPro:IPR018965 InterPro:IPR018075 Pfam:PF09358 SMART:SM00985 TIGRFAMs:TIGR01408 OMA:GMEGLNG EMBL:U80808 EMBL:AY090248 EMBL:BT006363 IPI:IPI00545792 PIR:T00587 RefSeq:NP_565693.1 UniGene:At.21347 ProteinModelPortal:P93028 SMR:P93028 IntAct:P93028 STRING:P93028 PRIDE:P93028 EnsemblPlants:AT2G30110.1 GeneID:817562 KEGG:ath:AT2G30110 TAIR:At2g30110 InParanoid:P93028 PhylomeDB:P93028 ProtClustDB:CLSN2688565 ArrayExpress:P93028 Genevestigator:P93028 Uniprot:P93028

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig01449	23	4	3.053	2.98E-06	TAIR|locus:2060854 - symbol:UBA1 "AT2G30110" species:3702 "Arabidopsis thaliana" [GO:0004839 "ubiquitin activating enzyme activity" evidence=ISS;IMP] [GO:0006511 "ubiquitin-dependent protein catabolic process" evidence=TAS] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0051707 "response to other organism" evidence=IMP] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0004842 "ubiquitin-protein ligase activity" evidence=IDA] [GO:0016567 "protein ubiquitination" evidence=IDA] InterPro:IPR000011 InterPro:IPR000127 InterPro:IPR000594 InterPro:IPR016040 Pfam:PF00899 Pfam:PF02134 PRINTS:PR01849 Pfam:PF10585 GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 GO:GO:0005524 GO:GO:0046686 EMBL:CP002685 GenomeReviews:CT485783_GR Gene3D:G3DSA:3.40.50.720 GO:GO:0051707 GO:GO:0004842 eggNOG:COG0476 InterPro:IPR009036 SUPFAM:SSF69572 EMBL:AC004165 HSSP:P12282 GO:GO:0008641 InterPro:IPR023280 InterPro:IPR019572 InterPro:IPR018074 Gene3D:G3DSA:1.10.3240.10 PROSITE:PS00536 PROSITE:PS00865 HOGENOM:HBG356508 KO:K03178 InterPro:IPR018965 InterPro:IPR018075 Pfam:PF09358 SMART:SM00985 TIGRFAMs:TIGR01408 OMA:GMEGLNG EMBL:U80808 EMBL:AY090248 EMBL:BT006363 IPI:IPI00545792 PIR:T00587 RefSeq:NP_565693.1 UniGene:At.21347 ProteinModelPortal:P93028 SMR:P93028 IntAct:P93028 STRING:P93028 PRIDE:P93028 EnsemblPlants:AT2G30110.1 GeneID:817562 KEGG:ath:AT2G30110 TAIR:At2g30110 InParanoid:P93028 PhylomeDB:P93028 ProtClustDB:CLSN2688565 ArrayExpress:P93028 Genevestigator:P93028 Uniprot:P93028
Leaf	Isotig01450	15	3	2.851	0.000262808	TAIR|locus:2060854 - symbol:UBA1 "AT2G30110" species:3702 "Arabidopsis thaliana" [GO:0004839 "ubiquitin activating enzyme activity" evidence=ISS;IMP] [GO:0006511 "ubiquitin-dependent protein catabolic process" evidence=TAS] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0051707 "response to other organism" evidence=IMP] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0004842 "ubiquitin-protein ligase activity" evidence=IDA] [GO:0016567 "protein ubiquitination" evidence=IDA] InterPro:IPR000011 InterPro:IPR000127 InterPro:IPR000594 InterPro:IPR016040 Pfam:PF00899 Pfam:PF02134 PRINTS:PR01849 Pfam:PF10585 GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 GO:GO:0005524 GO:GO:0046686 EMBL:CP002685 GenomeReviews:CT485783_GR Gene3D:G3DSA:3.40.50.720 GO:GO:0051707 GO:GO:0004842 eggNOG:COG0476 InterPro:IPR009036 SUPFAM:SSF69572 EMBL:AC004165 HSSP:P12282 GO:GO:0008641 InterPro:IPR023280 InterPro:IPR019572 InterPro:IPR018074 Gene3D:G3DSA:1.10.3240.10 PROSITE:PS00536 PROSITE:PS00865 HOGENOM:HBG356508 KO:K03178 InterPro:IPR018965 InterPro:IPR018075 Pfam:PF09358 SMART:SM00985 TIGRFAMs:TIGR01408 OMA:GMEGLNG EMBL:U80808 EMBL:AY090248 EMBL:BT006363 IPI:IPI00545792 PIR:T00587 RefSeq:NP_565693.1 UniGene:At.21347 ProteinModelPortal:P93028 SMR:P93028 IntAct:P93028 STRING:P93028 PRIDE:P93028 EnsemblPlants:AT2G30110.1 GeneID:817562 KEGG:ath:AT2G30110 TAIR:At2g30110 InParanoid:P93028 PhylomeDB:P93028 ProtClustDB:CLSN2688565 ArrayExpress:P93028 Genevestigator:P93028 Uniprot:P93028
Leaf	Isotig01451	12	1	4.114	0.000154103	TAIR|locus:2164270 - symbol:UBA 2 "AT5G06460" species:3702 "Arabidopsis thaliana" [GO:0004839 "ubiquitin activating enzyme activity" evidence=ISS;IMP] [GO:0006511 "ubiquitin-dependent protein catabolic process" evidence=TAS] [GO:0005829 "cytosol" evidence=IDA] [GO:0004842 "ubiquitin-protein ligase activity" evidence=IDA] [GO:0005634 "nucleus" evidence=TAS] [GO:0016567 "protein ubiquitination" evidence=IDA] InterPro:IPR000011 InterPro:IPR000127 InterPro:IPR000594 InterPro:IPR016040 Pfam:PF00899 Pfam:PF02134 PRINTS:PR01849 Pfam:PF10585 GO:GO:0005829 GO:GO:0005524 GO:GO:0005634 EMBL:CP002688 GenomeReviews:BA000015_GR Gene3D:G3DSA:3.40.50.720 GO:GO:0004842 eggNOG:COG0476 InterPro:IPR009036 SUPFAM:SSF69572 EMBL:AB006700 HSSP:P12282 GO:GO:0008641 InterPro:IPR023280 InterPro:IPR019572 InterPro:IPR018074 Gene3D:G3DSA:1.10.3240.10 PROSITE:PS00536 PROSITE:PS00865 HOGENOM:HBG356508 KO:K03178 InterPro:IPR018965 InterPro:IPR018075 Pfam:PF09358 SMART:SM00985 TIGRFAMs:TIGR01408 OMA:ANGMAKN ProtClustDB:CLSN2688565 EMBL:U40566 IPI:IPI00540789 RefSeq:NP_568168.1 UniGene:At.27859 UniGene:At.65020 ProteinModelPortal:P92974 SMR:P92974 PRIDE:P92974 EnsemblPlants:AT5G06460.1 GeneID:830534 KEGG:ath:AT5G06460 TAIR:At5g06460 InParanoid:P92974 PhylomeDB:P92974 Genevestigator:P92974 Uniprot:P92974
Leaf	Isotig01468	85	42	1.546	3.48E-09	TAIR|locus:2011952 - symbol:FTSH1 "AT1G50250" species:3702 "Arabidopsis thaliana" [GO:0008237 "metallopeptidase activity" evidence=ISS] [GO:0016887 "ATPase activity" evidence=ISS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0004176 "ATP-dependent peptidase activity" evidence=ISS] [GO:0031977 "thylakoid lumen" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0010206 "photosystem II repair"

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						evidence=TAS] [GO:0010304 "PSII associated light-harvesting complex II catabolic process" evidence=TAS] [GO:0016020 "membrane" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] InterPro:IPR000642 InterPro:IPR003593 InterPro:IPR003959 InterPro:IPR003960 InterPro:IPR005936 Pfam:PF00004 Pfam:PF01434 PROSITE:PS00674 SMART:SM00382 GO:GO:0016021 GO:GO:0007275 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005524 GO:GO:0005515 GO:GO:0046872 GO:GO:0006508 GO:GO:0009941 GO:GO:0004222 GO:GO:0017111 eggNOG:COG0465 TIGRFAMs:TIGR01241 HOGENOM:HBG724153 GO:GO:0009535 GO:GO:0031977 GO:GO:0010206 EMBL:AC007980 EMBL:X99808 EMBL:AY091095 EMBL:AY123034 EMBL:Y12780 IPI:IPI00518805 PIR:G96538 RefSeq:NP_564563.1 UniGene:At.21777 ProteinModelPortal:Q39102 SMR:Q39102 STRING:Q39102 MEROPS:M41.020 PRIDE:Q39102 EnsemblPlants:AT1G50250.1 GeneID:841447 KEGG:ath:AT1G50250 GeneFarm:2667 TAIR:At1g50250 InParanoid:Q39102 KO:K03798 OMA:ASTARQM PhylomeDB:Q39102 ProtClustDB:CLSN2688633 ArrayExpress:Q39102 Genevestigator:Q39102 GermOnline:AT1G50250 GO:GO:0010304 Uniprot:Q39102
Leaf	Isotig01469	85	63	0.961	4.83E-05	TAIR|locus:2011952 - symbol:FTSH1 "AT1G50250" species:3702 "Arabidopsis thaliana" [GO:0008237 "metallopeptidase activity" evidence=ISS] [GO:0016887 "ATPase activity" evidence=ISS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0004176 "ATP-dependent peptidase activity" evidence=ISS] [GO:0031977 "thylakoid lumen" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0010206 "photosystem II repair" evidence=TAS] [GO:0010304 "PSII associated light-harvesting complex II catabolic process" evidence=TAS] [GO:0016020 "membrane" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] InterPro:IPR000642 InterPro:IPR003593 InterPro:IPR003959 InterPro:IPR003960 InterPro:IPR005936 Pfam:PF00004 Pfam:PF01434 PROSITE:PS00674 SMART:SM00382 GO:GO:0016021 GO:GO:0007275 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005524 GO:GO:0005515 GO:GO:0046872 GO:GO:0006508 GO:GO:0009941 GO:GO:0004222 GO:GO:0017111 eggNOG:COG0465 TIGRFAMs:TIGR01241 HOGENOM:HBG724153 GO:GO:0009535 GO:GO:0031977 GO:GO:0010206 EMBL:AC007980 EMBL:X99808 EMBL:AY091095 EMBL:AY123034 EMBL:Y12780 IPI:IPI00518805 PIR:G96538 RefSeq:NP_564563.1 UniGene:At.21777 ProteinModelPortal:Q39102 SMR:Q39102 STRING:Q39102 MEROPS:M41.020 PRIDE:Q39102 EnsemblPlants:AT1G50250.1 GeneID:841447 KEGG:ath:AT1G50250 GeneFarm:2667 TAIR:At1g50250 InParanoid:Q39102 KO:K03798 OMA:ASTARQM PhylomeDB:Q39102 ProtClustDB:CLSN2688633 ArrayExpress:Q39102 Genevestigator:Q39102 GermOnline:AT1G50250 GO:GO:0010304 Uniprot:Q39102
Leaf	Isotig01470	85	42	1.546	3.48E-09	TAIR|locus:2011952 - symbol:FTSH1 "AT1G50250" species:3702 "Arabidopsis thaliana" [GO:0008237 "metallopeptidase activity" evidence=ISS] [GO:0016887 "ATPase activity" evidence=ISS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0004176 "ATP-dependent peptidase activity" evidence=ISS] [GO:0031977 "thylakoid lumen" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0010206 "photosystem II repair" evidence=TAS] [GO:0010304 "PSII associated light-harvesting complex II catabolic process" evidence=TAS] [GO:0016020 "membrane" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] InterPro:IPR000642 InterPro:IPR003593 InterPro:IPR003959 InterPro:IPR003960 InterPro:IPR005936 Pfam:PF00004 Pfam:PF01434 PROSITE:PS00674 SMART:SM00382 GO:GO:0016021 GO:GO:0007275 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005524 GO:GO:0005515 GO:GO:0046872 GO:GO:0006508 GO:GO:0009941 GO:GO:0004222 GO:GO:0017111 eggNOG:COG0465 TIGRFAMs:TIGR01241 HOGENOM:HBG724153 GO:GO:0009535 GO:GO:0031977 GO:GO:0010206 EMBL:AC007980 EMBL:X99808 EMBL:AY091095 EMBL:AY123034 EMBL:Y12780 IPI:IPI00518805 PIR:G96538 RefSeq:NP_564563.1 UniGene:At.21777 ProteinModelPortal:Q39102 SMR:Q39102 STRING:Q39102 MEROPS:M41.020 PRIDE:Q39102 EnsemblPlants:AT1G50250.1 GeneID:841447 KEGG:ath:AT1G50250 GeneFarm:2667 TAIR:At1g50250 InParanoid:Q39102 KO:K03798 OMA:ASTARQM PhylomeDB:Q39102 ProtClustDB:CLSN2688633 ArrayExpress:Q39102 Genevestigator:Q39102 GermOnline:AT1G50250 GO:GO:0010304 Uniprot:Q39102
Leaf	Isotig01471	85	63	0.961	4.83E-05	TAIR|locus:2011952 - symbol:FTSH1 "AT1G50250" species:3702 "Arabidopsis thaliana" [GO:0008237 "metallopeptidase activity" evidence=ISS] [GO:0016887 "ATPase activity" evidence=ISS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0004176 "ATP-dependent peptidase activity" evidence=ISS] [GO:0031977 "thylakoid lumen" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0010206 "photosystem II repair" evidence=TAS] [GO:0010304 "PSII associated light-harvesting complex II catabolic process" evidence=TAS]

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						[GO:0016020 "membrane" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] InterPro:IPR000642 InterPro:IPR003593 InterPro:IPR003959 InterPro:IPR003960 InterPro:IPR005936 Pfam:PF00004 Pfam:PF01434 PROSITE:PS00674 SMART:SM00382 GO:GO:0016021 GO:GO:0007275 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005524 GO:GO:0005515 GO:GO:0046872 GO:GO:0006508 GO:GO:0009941 GO:GO:0004222 GO:GO:0017111 eggNOG:COG0465 TIGRFAMs:TIGR01241 HOGENOM:HBG724153 GO:GO:0009535 GO:GO:0031977 GO:GO:0010206 EMBL:AC007980 EMBL:X99808 EMBL:AY091095 EMBL:AY123034 EMBL:Y12780 IPI:IPI00518805 PIR:G96538 RefSeq:NP_564563.1 UniGene:At.21777 ProteinModelPortal:Q39102 SMR:Q39102 STRING:Q39102 MEROPS:M41.020 PRIDE:Q39102 EnsemblPlants:AT1G50250.1 GeneID:841447 KEGG:ath:AT1G50250 GeneFarm:2667 TAIR:At1g50250 InParanoid:Q39102 KO:K03798 OMA:ASTARQM PhylomeDB:Q39102 ProtClustDB:CLSN2688633 ArrayExpress:Q39102 Genevestigator:Q39102 GermOnline:AT1G50250 GO:GO:0010304 Uniprot:Q39102
Leaf	Isotig01477	17	2	3.616	1.59E-05	TAIR|locus:2116900 - symbol:XDH1 "AT4G34890" species:3702 "Arabidopsis thaliana" [GO:0004854 "xanthine dehydrogenase activity" evidence=ISS;IDA] [GO:0006145 "purine base catabolic process" evidence=IMP;TAS] [GO:0006950 "response to stress" evidence=TAS] [GO:0042554 "superoxide anion generation" evidence=IMP] [GO:0046110 "xanthine metabolic process" evidence=IMP] [GO:0000302 "response to reactive oxygen species" evidence=IMP] [GO:0009414 "response to water deprivation" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001041 InterPro:IPR002346 InterPro:IPR002888 InterPro:IPR006058 InterPro:IPR008274 InterPro:IPR016166 InterPro:IPR016167 InterPro:IPR016169 InterPro:IPR016208 Pfam:PF00111 Pfam:PF00941 Pfam:PF01799 Pfam:PF02738 PIRSF:PIRSF000127 PROSITE:PS00197 PROSITE:PS51085 PROSITE:PS51387 InterPro:IPR000674 Pfam:PF01315 GO:GO:0005829 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005506 GO:GO:0009055 GO:GO:0050660 GO:GO:0009414 GO:GO:0000302 GO:GO:0008762 Gene3D:G3DSA:3.30.43.10 SUPFAM:SSF56176 eggNOG:COG4630 GO:GO:0051537 InterPro:IPR012675 InterPro:IPR005107 Gene3D:G3DSA:1.10.150.120 Gene3D:G3DSA:3.30.365.10 Gene3D:G3DSA:3.90.1170.50 Gene3D:G3DSA:3.30.390.50 Gene3D:G3DSA:3.30.465.10 Gene3D:G3DSA:3.10.20.30 Pfam:PF03450 SMART:SM01008 SMART:SM01092 SUPFAM:SSF47741 SUPFAM:SSF56003 SUPFAM:SSF54665 SUPFAM:SSF55447 SUPFAM:SSF54292 HOGENOM:HBG386245 GO:GO:0004854 GO:GO:0006145 GO:GO:0042554 KO:K00106 HSSP:P80457 GO:GO:0046110 OMA:SGRAFNY EMBL:AY171562 IPI:IPI00529753 RefSeq:NP_195215.2 UniGene:At.27839 ProteinModelPortal:Q8GUQ8 STRING:Q8GUQ8 PRIDE:Q8GUQ8 ProMEX:Q8GUQ8 EnsemblPlants:AT4G34890.1 GeneID:829641 KEGG:ath:AT4G34890 TAIR:At4g34890 InParanoid:Q8GUQ8 PhylomeDB:Q8GUQ8 ProtClustDB:PLN02906 BRENDA:1.17.1.4 Genevestigator:Q8GUQ8 Uniprot:Q8GUQ8
Leaf	Isotig01490	9	52	-2.002	4.20E-06	TAIR|locus:2016605 - symbol:HEMA1 "AT1G58290" species:3702 "Arabidopsis thaliana" [GO:0006783 "heme biosynthetic process" evidence=IMP] [GO:0008883 "glutamyl-tRNA reductase activity" evidence=IGI;TAS] [GO:0015995 "chlorophyll biosynthetic process" evidence=IMP] [GO:0009507 "chloroplast" evidence=IDA;TAS] [GO:0005515 "protein binding" evidence=IPI] [GO:0006779 "porphyrin-containing compound biosynthetic process" evidence=TAS] [GO:0009416 "response to light stimulus" evidence=IEP] InterPro:IPR000343 InterPro:IPR015895 InterPro:IPR015896 InterPro:IPR016040 InterPro:IPR018214 Pfam:PF00745 Pfam:PF05201 PROSITE:PS00747 InterPro:IPR006151 Pfam:PF01488 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009507 GO:GO:0005515 Gene3D:G3DSA:3.40.50.720 GO:GO:0050661 EMBL:AC008051 GO:GO:0015995 GO:GO:0006783 EMBL:U03774 EMBL:AY072223 EMBL:AY096600 IPI:IPI00535419 PIR:E96616 RefSeq:NP_176125.1 UniGene:At.241 ProteinModelPortal:P42804 SMR:P42804 IntAct:P42804 STRING:P42804 PRIDE:P42804 EnsemblPlants:AT1G58290.1 GeneID:842198 KEGG:ath:AT1G58290 TAIR:At1g58290 eggNOG:COG0373 HOGENOM:HBG732626 InParanoid:P42804 KO:K02492 OMA:GPILNRL PhylomeDB:P42804 ProtClustDB:PLN00203 BioCyc:ARA:AT1G58290-MONOMER BioCyc:MetaCyc:AT1G58290-MONOMER ArrayExpress:P42804 Genevestigator:P42804 GermOnline:AT1G58290 GO:GO:0008883 SUPFAM:SSF69075 SUPFAM:SSF69742 TIGRFAMs:TIGR01035 Uniprot:P42804
Leaf	Isotig01491	9	53	-2.029	2.78E-06	TAIR|locus:2016605 - symbol:HEMA1 "AT1G58290" species:3702 "Arabidopsis thaliana" [GO:0006783 "heme biosynthetic process" evidence=IMP] [GO:0008883 "glutamyl-tRNA reductase activity" evidence=IGI;TAS] [GO:0015995 "chlorophyll biosynthetic process" evidence=IMP] [GO:0009507 "chloroplast" evidence=IDA;TAS] [GO:0005515 "protein binding" evidence=IPI] [GO:0006779 "porphyrin-containing compound biosynthetic process" evidence=TAS] [GO:0009416 "response to light stimulus" evidence=IEP] InterPro:IPR000343 InterPro:IPR015895

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						InterPro:IPR015896 InterPro:IPR016040 InterPro:IPR018214 Pfam:PF00745 Pfam:PF05201 PROSITE:PS00747 InterPro:IPR006151 Pfam:PF01488 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009507 GO:GO:0005515 Gene3D:G3DSA:3.40.50.720 GO:GO:0050661 EMBL:AC008051 GO:GO:0015995 GO:GO:0006783 EMBL:U03774 EMBL:AY072223 EMBL:AY096600 IPI:IPI00535419 PIR:E96616 RefSeq:NP_176125.1 UniGene:At.241 ProteinModelPortal:P42804 SMR:P42804 IntAct:P42804 STRING:P42804 PRIDE:P42804 EnsemblPlants:AT1G58290.1 GeneID:842198 KEGG:ath:AT1G58290 TAIR:At1g58290 eggNOG:COG0373 HOGENOM:HBG732626 InParanoid:P42804 KO:K02492 OMA:GPILNRL PhylomeDB:P42804 ProtClustDB:PLN00203 BioCyc:ARA:AT1G58290-MONOMER BioCyc:MetaCyc:AT1G58290-MONOMER ArrayExpress:P42804 Genevestigator:P42804 GermOnline:AT1G58290 GO:GO:0008883 SUPFAM:SSF69075 SUPFAM:SSF69742 TIGRFAMs:TIGR01035 Uniprot:P42804
Leaf	Isotig01500	14	58	-1.522	5.95E-05	TAIR|locus:2123797 - symbol:SQD1 "AT4G33030" species:3702 "Arabidopsis thaliana" [GO:0008146 "sulfotransferase activity" evidence=IDA] [GO:0009247 "glycolipid biosynthetic process" evidence=IDA] [GO:0046506 "sulfolipid biosynthetic process" evidence=IDA] [GO:0046507 "UDPsulfoquinovose synthase activity" evidence=IDA] [GO:0016036 "cellular response to phosphate starvation" evidence=IEP;IMP] [GO:0008270 "zinc ion binding" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] InterPro:IPR001509 InterPro:IPR016040 Pfam:PF01370 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0009507 eggNOG:COG0451 GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 GO:GO:0008270 GO:GO:0009247 GO:GO:0016036 GO:GO:0050662 EMBL:AL031804 EMBL:AL161582 GO:GO:0008146 EMBL:AF022082 EMBL:AF380641 EMBL:AY113071 IPI:IPI00524549 PIR:T05311 RefSeq:NP_195029.1 UniGene:At.2479 PDB:1I24 PDB:1I2B PDB:1I2C PDB:1QRR PDBsum:1I24 PDBsum:1I2B PDBsum:1I2C PDBsum:1QRR ProteinModelPortal:O48917 SMR:O48917 IntAct:O48917 STRING:O48917 PRIDE:O48917 ProMEX:O48917 EnsemblPlants:AT4G33030.1 GeneID:829440 KEGG:ath:AT4G33030 TAIR:At4g33030 HOGENOM:HBG285135 InParanoid:O48917 KO:K06118 OMA:VYGKGGQ PhylomeDB:O48917 ProtClustDB:PLN02572 ArrayExpress:O48917 Genevestigator:O48917 GermOnline:AT4G33030 GO:GO:0046507 Uniprot:O48917
Leaf	Isotig01501	14	55	-1.445	0.000168299	TAIR|locus:2123797 - symbol:SQD1 "AT4G33030" species:3702 "Arabidopsis thaliana" [GO:0008146 "sulfotransferase activity" evidence=IDA] [GO:0009247 "glycolipid biosynthetic process" evidence=IDA] [GO:0046506 "sulfolipid biosynthetic process" evidence=IDA] [GO:0046507 "UDPsulfoquinovose synthase activity" evidence=IDA] [GO:0016036 "cellular response to phosphate starvation" evidence=IEP;IMP] [GO:0008270 "zinc ion binding" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] InterPro:IPR001509 InterPro:IPR016040 Pfam:PF01370 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0009507 eggNOG:COG0451 GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 GO:GO:0008270 GO:GO:0009247 GO:GO:0016036 GO:GO:0050662 EMBL:AL031804 EMBL:AL161582 GO:GO:0008146 EMBL:AF022082 EMBL:AF380641 EMBL:AY113071 IPI:IPI00524549 PIR:T05311 RefSeq:NP_195029.1 UniGene:At.2479 PDB:1I24 PDB:1I2B PDB:1I2C PDB:1QRR PDBsum:1I24 PDBsum:1I2B PDBsum:1I2C PDBsum:1QRR ProteinModelPortal:O48917 SMR:O48917 IntAct:O48917 STRING:O48917 PRIDE:O48917 ProMEX:O48917 EnsemblPlants:AT4G33030.1 GeneID:829440 KEGG:ath:AT4G33030 TAIR:At4g33030 HOGENOM:HBG285135 InParanoid:O48917 KO:K06118 OMA:VYGKGGQ PhylomeDB:O48917 ProtClustDB:PLN02572 ArrayExpress:O48917 Genevestigator:O48917 GermOnline:AT4G33030 GO:GO:0046507 Uniprot:O48917
Leaf	Isotig01502	14	52	-1.364	0.000461362	TAIR|locus:2123797 - symbol:SQD1 "AT4G33030" species:3702 "Arabidopsis thaliana" [GO:0008146 "sulfotransferase activity" evidence=IDA] [GO:0009247 "glycolipid biosynthetic process" evidence=IDA] [GO:0046506 "sulfolipid biosynthetic process" evidence=IDA] [GO:0046507 "UDPsulfoquinovose synthase activity" evidence=IDA] [GO:0016036 "cellular response to phosphate starvation" evidence=IEP;IMP] [GO:0008270 "zinc ion binding" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] InterPro:IPR001509 InterPro:IPR016040 Pfam:PF01370 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0009507 eggNOG:COG0451 GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 GO:GO:0008270 GO:GO:0009247 GO:GO:0016036 GO:GO:0050662 EMBL:AL031804 EMBL:AL161582 GO:GO:0008146 EMBL:AF022082 EMBL:AF380641 EMBL:AY113071 IPI:IPI00524549 PIR:T05311 RefSeq:NP_195029.1 UniGene:At.2479 PDB:1I24 PDB:1I2B PDB:1I2C PDB:1QRR PDBsum:1I24 PDBsum:1I2B PDBsum:1I2C PDBsum:1QRR ProteinModelPortal:O48917 SMR:O48917 IntAct:O48917 STRING:O48917 PRIDE:O48917 ProMEX:O48917 EnsemblPlants:AT4G33030.1 GeneID:829440 KEGG:ath:AT4G33030 TAIR:At4g33030 HOGENOM:HBG285135 InParanoid:O48917 KO:K06118 OMA:VYGKGGQ PhylomeDB:O48917 ProtClustDB:PLN02572 ArrayExpress:O48917 Genevestigator:O48917 GermOnline:AT4G33030 GO:GO:0046507 Uniprot:O48917

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig01504	22	2	3.988	3.84E-07	TAIR|locus:2131406 - symbol:ACD1-LIKE "AT4G25650" species:3702 "Arabidopsis thaliana" [GO:0009055 "electron carrier activity" evidence=ISS] [GO:0010277 "chlorophyllide a oxygenase [overall] activity" evidence=IEA] [GO:0016491 "oxidoreductase activity" evidence=IEA] [GO:0051537 "2 iron, 2 sulfur cluster binding" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] InterPro:IPR013626 InterPro:IPR017941 Pfam:PF00355 Pfam:PF08417 PROSITE:PS51296 GO:GO:0016021 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0046872 GO:GO:0015031 EMBL:AL161563 GO:GO:0009706 GO:GO:0051537 Gene3D:G3DSA:2.102.10.10 SUPFAM:SSF50022 EMBL:AL050400 eggNOG:COG4638 GO:GO:0010277 HOGENOM:HBG748445 EMBL:AY344062 EMBL:AF424575 EMBL:AY056168 EMBL:AY062731 EMBL:BT002586 IPI:IPI00516579 PIR:T09557 RefSeq:NP_567725.1 RefSeq:NP_849444.1 UniGene:At.3350 ProteinModelPortal:Q8W496 STRING:Q8W496 PRIDE:Q93WJ7 EnsemblPlants:AT4G25650.2 GeneID:828670 KEGG:ath:AT4G25650 GeneFarm:3092 TAIR:At4g25650 InParanoid:Q8W496 OMA:LHVEERK PhylomeDB:Q8W496 ProtClustDB:CLSN2689607 Genevestigator:Q8W496 Uniprot:Q8W496
Leaf	Isotig01505	22	2	3.988	3.84E-07	TAIR|locus:2131406 - symbol:ACD1-LIKE "AT4G25650" species:3702 "Arabidopsis thaliana" [GO:0009055 "electron carrier activity" evidence=ISS] [GO:0010277 "chlorophyllide a oxygenase [overall] activity" evidence=IEA] [GO:0016491 "oxidoreductase activity" evidence=IEA] [GO:0051537 "2 iron, 2 sulfur cluster binding" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] InterPro:IPR013626 InterPro:IPR017941 Pfam:PF00355 Pfam:PF08417 PROSITE:PS51296 GO:GO:0016021 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0046872 GO:GO:0015031 EMBL:AL161563 GO:GO:0009706 GO:GO:0051537 Gene3D:G3DSA:2.102.10.10 SUPFAM:SSF50022 EMBL:AL050400 eggNOG:COG4638 GO:GO:0010277 HOGENOM:HBG748445 EMBL:AY344062 EMBL:AF424575 EMBL:AY056168 EMBL:AY062731 EMBL:BT002586 IPI:IPI00516579 PIR:T09557 RefSeq:NP_567725.1 RefSeq:NP_849444.1 UniGene:At.3350 ProteinModelPortal:Q8W496 STRING:Q8W496 PRIDE:Q93WJ7 EnsemblPlants:AT4G25650.2 GeneID:828670 KEGG:ath:AT4G25650 GeneFarm:3092 TAIR:At4g25650 InParanoid:Q8W496 OMA:LHVEERK PhylomeDB:Q8W496 ProtClustDB:CLSN2689607 Genevestigator:Q8W496 Uniprot:Q8W496
Leaf	Isotig01506	21	0	5.921	1.38E-07	TAIR|locus:2131406 - symbol:ACD1-LIKE "AT4G25650" species:3702 "Arabidopsis thaliana" [GO:0009055 "electron carrier activity" evidence=ISS] [GO:0010277 "chlorophyllide a oxygenase [overall] activity" evidence=IEA] [GO:0016491 "oxidoreductase activity" evidence=IEA] [GO:0051537 "2 iron, 2 sulfur cluster binding" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] InterPro:IPR013626 InterPro:IPR017941 Pfam:PF00355 Pfam:PF08417 PROSITE:PS51296 GO:GO:0016021 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0046872 GO:GO:0015031 EMBL:AL161563 GO:GO:0009706 GO:GO:0051537 Gene3D:G3DSA:2.102.10.10 SUPFAM:SSF50022 EMBL:AL050400 eggNOG:COG4638 GO:GO:0010277 HOGENOM:HBG748445 EMBL:AY344062 EMBL:AF424575 EMBL:AY056168 EMBL:AY062731 EMBL:BT002586 IPI:IPI00516579 PIR:T09557 RefSeq:NP_567725.1 RefSeq:NP_849444.1 UniGene:At.3350 ProteinModelPortal:Q8W496 STRING:Q8W496 PRIDE:Q93WJ7 EnsemblPlants:AT4G25650.2 GeneID:828670 KEGG:ath:AT4G25650 GeneFarm:3092 TAIR:At4g25650 InParanoid:Q8W496 OMA:LHVEERK PhylomeDB:Q8W496 ProtClustDB:CLSN2689607 Genevestigator:Q8W496 Uniprot:Q8W496
Leaf	Isotig01507	21	0	5.921	1.38E-07	TAIR|locus:2131406 - symbol:ACD1-LIKE "AT4G25650" species:3702 "Arabidopsis thaliana" [GO:0009055 "electron carrier activity" evidence=ISS] [GO:0010277 "chlorophyllide a oxygenase [overall] activity" evidence=IEA] [GO:0016491 "oxidoreductase activity" evidence=IEA] [GO:0051537 "2 iron, 2 sulfur cluster binding" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] InterPro:IPR013626 InterPro:IPR017941 Pfam:PF00355 Pfam:PF08417 PROSITE:PS51296 GO:GO:0016021 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0046872 GO:GO:0015031 EMBL:AL161563 GO:GO:0009706 GO:GO:0051537 Gene3D:G3DSA:2.102.10.10 SUPFAM:SSF50022 EMBL:AL050400 eggNOG:COG4638 GO:GO:0010277 HOGENOM:HBG748445 EMBL:AY344062 EMBL:AF424575 EMBL:AY056168 EMBL:AY062731 EMBL:BT002586 IPI:IPI00516579 PIR:T09557 RefSeq:NP_567725.1 RefSeq:NP_849444.1 UniGene:At.3350 ProteinModelPortal:Q8W496 STRING:Q8W496 PRIDE:Q93WJ7 EnsemblPlants:AT4G25650.2 GeneID:828670 KEGG:ath:AT4G25650 GeneFarm:3092 TAIR:At4g25650 InParanoid:Q8W496 OMA:LHVEERK PhylomeDB:Q8W496 ProtClustDB:CLSN2689607 Genevestigator:Q8W496 Uniprot:Q8W496

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig01524	34	4	3.616	1.03E-09	TAIR|locus:2010916 - symbol:AT1G64760 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=IEA;ISS] [GO:0005975 "carbohydrate metabolic process" evidence=IEA] [GO:0043169 "cation binding" evidence=IEA] [GO:0031225 "anchored to membrane" evidence=TAS] [GO:0046658 "anchored to plasma membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000490 InterPro:IPR013781 Pfam:PF00332 PROSITE:PS00587 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009506 GO:GO:0005618 GO:GO:0005576 GO:GO:0006952 GO:GO:0043169 InterPro:IPR017853 Gene3D:G3DSA:3.20.20.80 SUPFAM:SSF51445 GO:GO:0005975 EMBL:AC006193 GO:GO:0007047 GO:GO:0046658 CAZy:GH17 GO:GO:0042973 HSSP:O22317 HOGENOM:HBG605194 CAZy:CBM43 InterPro:IPR012946 Pfam:PF07983 SMART:SM00768 eggNOG:NOG247729 EMBL:BT012574 EMBL:AK220635 EMBL:AK176856 EMBL:AK175510 IPI:IPI00535099 PIR:G96670 RefSeq:NP_001031232.1 RefSeq:NP_176656.1 UniGene:At.50002 ProteinModelPortal:Q6NKW9 SMR:Q6NKW9 PRIDE:Q6NKW9 EnsemblPlants:AT1G64760.1 EnsemblPlants:AT1G64760.2 GeneID:842784 KEGG:ath:AT1G64760 TAIR:At1g64760 InParanoid:Q6NKW9 OMA:LYGNDNF PhylomeDB:Q6NKW9 ProtClustDB:CLSN2914646 Genevestigator:Q6NKW9 GermOnline:AT1G64760 Uniprot:Q6NKW9
Leaf	Isotig01525	34	4	3.616	1.03E-09	TAIR|locus:2010916 - symbol:AT1G64760 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=IEA;ISS] [GO:0005975 "carbohydrate metabolic process" evidence=IEA] [GO:0043169 "cation binding" evidence=IEA] [GO:0031225 "anchored to membrane" evidence=TAS] [GO:0046658 "anchored to plasma membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000490 InterPro:IPR013781 Pfam:PF00332 PROSITE:PS00587 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009506 GO:GO:0005618 GO:GO:0005576 GO:GO:0006952 GO:GO:0043169 InterPro:IPR017853 Gene3D:G3DSA:3.20.20.80 SUPFAM:SSF51445 GO:GO:0005975 EMBL:AC006193 GO:GO:0007047 GO:GO:0046658 CAZy:GH17 GO:GO:0042973 HSSP:O22317 HOGENOM:HBG605194 CAZy:CBM43 InterPro:IPR012946 Pfam:PF07983 SMART:SM00768 eggNOG:NOG247729 EMBL:BT012574 EMBL:AK220635 EMBL:AK176856 EMBL:AK175510 IPI:IPI00535099 PIR:G96670 RefSeq:NP_001031232.1 RefSeq:NP_176656.1 UniGene:At.50002 ProteinModelPortal:Q6NKW9 SMR:Q6NKW9 PRIDE:Q6NKW9 EnsemblPlants:AT1G64760.1 EnsemblPlants:AT1G64760.2 GeneID:842784 KEGG:ath:AT1G64760 TAIR:At1g64760 InParanoid:Q6NKW9 OMA:LYGNDNF PhylomeDB:Q6NKW9 ProtClustDB:CLSN2914646 Genevestigator:Q6NKW9 GermOnline:AT1G64760 Uniprot:Q6NKW9
Leaf	Isotig01526	34	4	3.616	1.03E-09	TAIR|locus:2010916 - symbol:AT1G64760 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=IEA;ISS] [GO:0005975 "carbohydrate metabolic process" evidence=IEA] [GO:0043169 "cation binding" evidence=IEA] [GO:0031225 "anchored to membrane" evidence=TAS] [GO:0046658 "anchored to plasma membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000490 InterPro:IPR013781 Pfam:PF00332 PROSITE:PS00587 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009506 GO:GO:0005618 GO:GO:0005576 GO:GO:0006952 GO:GO:0043169 InterPro:IPR017853 Gene3D:G3DSA:3.20.20.80 SUPFAM:SSF51445 GO:GO:0005975 EMBL:AC006193 GO:GO:0007047 GO:GO:0046658 CAZy:GH17 GO:GO:0042973 HSSP:O22317 HOGENOM:HBG605194 CAZy:CBM43 InterPro:IPR012946 Pfam:PF07983 SMART:SM00768 eggNOG:NOG247729 EMBL:BT012574 EMBL:AK220635 EMBL:AK176856 EMBL:AK175510 IPI:IPI00535099 PIR:G96670 RefSeq:NP_001031232.1 RefSeq:NP_176656.1 UniGene:At.50002 ProteinModelPortal:Q6NKW9 SMR:Q6NKW9 PRIDE:Q6NKW9 EnsemblPlants:AT1G64760.1 EnsemblPlants:AT1G64760.2 GeneID:842784 KEGG:ath:AT1G64760 TAIR:At1g64760 InParanoid:Q6NKW9 OMA:LYGNDNF PhylomeDB:Q6NKW9 ProtClustDB:CLSN2914646 Genevestigator:Q6NKW9 GermOnline:AT1G64760 Uniprot:Q6NKW9
Leaf	Isotig01527	34	4	3.616	1.03E-09	TAIR|locus:2010916 - symbol:AT1G64760 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=IEA;ISS] [GO:0005975 "carbohydrate metabolic process" evidence=IEA] [GO:0043169 "cation binding" evidence=IEA] [GO:0031225 "anchored to membrane" evidence=TAS] [GO:0046658 "anchored to plasma membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000490 InterPro:IPR013781 Pfam:PF00332 PROSITE:PS00587 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009506 GO:GO:0005618 GO:GO:0005576 GO:GO:0006952

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0043169 InterPro:IPR017853 Gene3D:G3DSA:3.20.20.80 SUPFAM:SSF51445 GO:GO:0005975 EMBL:AC006193 GO:GO:0007047 GO:GO:0046658 CAZy:GH17 GO:GO:0042973 HSSP:O22317 HOGENOM:HBG605194 CAZy:CBM43 InterPro:IPR012946 Pfam:PF07983 SMART:SM00768 eggNOG:NOG247729 EMBL:BT012574 EMBL:AK220635 EMBL:AK176856 EMBL:AK175510 IPI:IPI00535099 PIR:G96670 RefSeq:NP_001031232.1 RefSeq:NP_176656.1 UniGene:At.50002 ProteinModelPortal:Q6NKW9 SMR:Q6NKW9 PRIDE:Q6NKW9 EnsemblPlants:AT1G64760.1 EnsemblPlants:AT1G64760.2 GeneID:842784 KEGG:ath:AT1G64760 TAIR:At1g64760 InParanoid:Q6NKW9 OMA:LYGNDNF PhylomeDB:Q6NKW9 ProtClustDB:CLSN2914646 Genevestigator:Q6NKW9 GermOnline:AT1G64760 Uniprot:Q6NKW9
Leaf	Isotig01528	56	7	3.529	8.42E-15	TAIR|locus:2128166 - symbol:AT4G31340 "AT4G31340" species:3702 "Arabidopsis thaliana" [GO:0005783 "endoplasmic reticulum" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] GO:GO:0005783 EMBL:CP002687 GO:GO:0005774 EMBL:BT002358 EMBL:AK317035 IPI:IPI00516401 RefSeq:NP_567873.1 UniGene:At.23680 UniGene:At.34197 ProteinModelPortal:Q8GUN1 SMR:Q8GUN1 PRIDE:Q8GUN1 EnsemblPlants:AT4G31340.1 GeneID:829261 KEGG:ath:AT4G31340 TAIR:At4g31340 InParanoid:Q8GUN1 OMA:EKWAEPH PhylomeDB:Q8GUN1 ProtClustDB:CLSN2688385 Genevestigator:Q8GUN1 Uniprot:Q8GUN1
Leaf	Isotig01529	56	7	3.529	8.42E-15	TAIR|locus:2061067 - symbol:AT2G24420 "AT2G24420" species:3702 "Arabidopsis thaliana" [GO:0005783 "endoplasmic reticulum" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] GO:GO:0005783 GO:GO:0005774 EMBL:CP002685 GenomeReviews:CT485783_GR EMBL:AC006403 HSSP:P28033 UniGene:At.23666 ProtClustDB:CLSN2688385 UniGene:At.39159 EMBL:AF419562 EMBL:BT010170 EMBL:AK316670 IPI:IPI00543802 PIR:D84636 RefSeq:NP_565569.1 RefSeq:NP_850053.1 UniGene:At.67138 ProteinModelPortal:Q9ZQ26 SMR:Q9ZQ26 PRIDE:Q9ZQ26 EnsemblPlants:AT2G24420.1 EnsemblPlants:AT2G24420.2 GeneID:816978 KEGG:ath:AT2G24420 TAIR:At2g24420 HOGENOM:HBG601337 InParanoid:Q9ZQ26 OMA:AEKWAKP PhylomeDB:Q9ZQ26 ArrayExpress:Q9ZQ26 Genevestigator:Q9ZQ26 Uniprot:Q9ZQ26
Leaf	Isotig01530	56	6	3.751	2.05E-15	TAIR|locus:2128166 - symbol:AT4G31340 "AT4G31340" species:3702 "Arabidopsis thaliana" [GO:0005783 "endoplasmic reticulum" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] GO:GO:0005783 EMBL:CP002687 GO:GO:0005774 EMBL:BT002358 EMBL:AK317035 IPI:IPI00516401 RefSeq:NP_567873.1 UniGene:At.23680 UniGene:At.34197 ProteinModelPortal:Q8GUN1 SMR:Q8GUN1 PRIDE:Q8GUN1 EnsemblPlants:AT4G31340.1 GeneID:829261 KEGG:ath:AT4G31340 TAIR:At4g31340 InParanoid:Q8GUN1 OMA:EKWAEPH PhylomeDB:Q8GUN1 ProtClustDB:CLSN2688385 Genevestigator:Q8GUN1 Uniprot:Q8GUN1
Leaf	Isotig01531	56	6	3.751	2.05E-15	TAIR|locus:2061067 - symbol:AT2G24420 "AT2G24420" species:3702 "Arabidopsis thaliana" [GO:0005783 "endoplasmic reticulum" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] GO:GO:0005783 GO:GO:0005774 EMBL:CP002685 GenomeReviews:CT485783_GR EMBL:AC006403 HSSP:P28033 UniGene:At.23666 ProtClustDB:CLSN2688385 UniGene:At.39159 EMBL:AF419562 EMBL:BT010170 EMBL:AK316670 IPI:IPI00543802 PIR:D84636 RefSeq:NP_565569.1 RefSeq:NP_850053.1 UniGene:At.67138 ProteinModelPortal:Q9ZQ26 SMR:Q9ZQ26 PRIDE:Q9ZQ26 EnsemblPlants:AT2G24420.1 EnsemblPlants:AT2G24420.2 GeneID:816978 KEGG:ath:AT2G24420 TAIR:At2g24420 HOGENOM:HBG601337 InParanoid:Q9ZQ26 OMA:AEKWAKP PhylomeDB:Q9ZQ26 ArrayExpress:Q9ZQ26 Genevestigator:Q9ZQ26 Uniprot:Q9ZQ26
Leaf	Isotig01532	34	11	2.157	2.75E-06	TAIR|locus:505006696 - symbol:AT5G57655 species:3702 "Arabidopsis thaliana" [GO:0005975 "carbohydrate metabolic process" evidence=IEA;ISS] [GO:0009045 "xylose isomerase activity" evidence=IEA;ISS] [GO:0005773 "vacuole" evidence=IDA] [GO:0005783 "endoplasmic reticulum" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR001998 InterPro:IPR013452 PRINTS:PR00688 PROSITE:PS51415 Pfam:PF01261 GO:GO:0005783 GO:GO:0005774 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0006098 GO:GO:0046872 InterPro:IPR013022 InterPro:IPR012307 Gene3D:G3DSA:3.20.20.150 SUPFAM:SSF51658 EMBL:AB011482 GO:GO:0042732 EMBL:AY136469 EMBL:BT006607 IPI:IPI00535514 RefSeq:NP_568861.3 UniGene:At.20353 UniGene:At.67777 ProteinModelPortal:Q9FKK7 SMR:Q9FKK7 STRING:Q9FKK7 PRIDE:Q9FKK7 EnsemblPlants:AT5G57655.2 GeneID:835871 KEGG:ath:AT5G57655 TAIR:At5g57655 eggNOG:COG2115 HOGENOM:HBG297199 InParanoid:Q9FKK7 KO:K01805 OMA:LLGWDTD PhylomeDB:Q9FKK7 ProtClustDB:PLN02923 Genevestigator:Q9FKK7 GO:GO:0009045 TIGRFAMs:TIGR02630 Uniprot:Q9FKK7

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig01533	33	11	2.114	5.10E-06	TAIR|locus:505006696 - symbol:AT5G57655 species:3702 "Arabidopsis thaliana" [GO:0005975 "carbohydrate metabolic process" evidence=IEA;ISS] [GO:0009045 "xylose isomerase activity" evidence=IEA;ISS] [GO:0005773 "vacuole" evidence=IDA] [GO:0005783 "endoplasmic reticulum" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR001998 InterPro:IPR013452 PRINTS:PR00688 PROSITE:PS51415 Pfam:PF01261 GO:GO:0005783 GO:GO:0005774 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0006098 GO:GO:0046872 InterPro:IPR013022 InterPro:IPR012307 Gene3D:G3DSA:3.20.20.150 SUPFAM:SSF51658 EMBL:AB011482 GO:GO:0042732 EMBL:AY136469 EMBL:BT006607 IPI:IPI00535514 RefSeq:NP_568861.3 UniGene:At.20353 UniGene:At.67777 ProteinModelPortal:Q9FKK7 SMR:Q9FKK7 STRING:Q9FKK7 PRIDE:Q9FKK7 EnsemblPlants:AT5G57655.2 GeneID:835871 KEGG:ath:AT5G57655 TAIR:At5g57655 eggNOG:COG2115 HOGENOM:HBG297199 InParanoid:Q9FKK7 KO:K01805 OMA:LLGWDTD PhylomeDB:Q9FKK7 ProtClustDB:PLN02923 Genevestigator:Q9FKK7 GO:GO:0009045 TIGRFAMs:TIGR02630 Uniprot:Q9FKK7
Leaf	Isotig01534	35	11	2.199	1.48E-06	TAIR|locus:505006696 - symbol:AT5G57655 species:3702 "Arabidopsis thaliana" [GO:0005975 "carbohydrate metabolic process" evidence=IEA;ISS] [GO:0009045 "xylose isomerase activity" evidence=IEA;ISS] [GO:0005773 "vacuole" evidence=IDA] [GO:0005783 "endoplasmic reticulum" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR001998 InterPro:IPR013452 PRINTS:PR00688 PROSITE:PS51415 Pfam:PF01261 GO:GO:0005783 GO:GO:0005774 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0006098 GO:GO:0046872 InterPro:IPR013022 InterPro:IPR012307 Gene3D:G3DSA:3.20.20.150 SUPFAM:SSF51658 EMBL:AB011482 GO:GO:0042732 EMBL:AY136469 EMBL:BT006607 IPI:IPI00535514 RefSeq:NP_568861.3 UniGene:At.20353 UniGene:At.67777 ProteinModelPortal:Q9FKK7 SMR:Q9FKK7 STRING:Q9FKK7 PRIDE:Q9FKK7 EnsemblPlants:AT5G57655.2 GeneID:835871 KEGG:ath:AT5G57655 TAIR:At5g57655 eggNOG:COG2115 HOGENOM:HBG297199 InParanoid:Q9FKK7 KO:K01805 OMA:LLGWDTD PhylomeDB:Q9FKK7 ProtClustDB:PLN02923 Genevestigator:Q9FKK7 GO:GO:0009045 TIGRFAMs:TIGR02630 Uniprot:Q9FKK7
Leaf	Isotig01535	34	11	2.157	2.75E-06	TAIR|locus:505006696 - symbol:AT5G57655 species:3702 "Arabidopsis thaliana" [GO:0005975 "carbohydrate metabolic process" evidence=IEA;ISS] [GO:0009045 "xylose isomerase activity" evidence=IEA;ISS] [GO:0005773 "vacuole" evidence=IDA] [GO:0005783 "endoplasmic reticulum" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR001998 InterPro:IPR013452 PRINTS:PR00688 PROSITE:PS51415 Pfam:PF01261 GO:GO:0005783 GO:GO:0005774 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0006098 GO:GO:0046872 InterPro:IPR013022 InterPro:IPR012307 Gene3D:G3DSA:3.20.20.150 SUPFAM:SSF51658 EMBL:AB011482 GO:GO:0042732 EMBL:AY136469 EMBL:BT006607 IPI:IPI00535514 RefSeq:NP_568861.3 UniGene:At.20353 UniGene:At.67777 ProteinModelPortal:Q9FKK7 SMR:Q9FKK7 STRING:Q9FKK7 PRIDE:Q9FKK7 EnsemblPlants:AT5G57655.2 GeneID:835871 KEGG:ath:AT5G57655 TAIR:At5g57655 eggNOG:COG2115 HOGENOM:HBG297199 InParanoid:Q9FKK7 KO:K01805 OMA:LLGWDTD PhylomeDB:Q9FKK7 ProtClustDB:PLN02923 Genevestigator:Q9FKK7 GO:GO:0009045 TIGRFAMs:TIGR02630 Uniprot:Q9FKK7
Leaf	Isotig01545	8	38	-1.719	0.000388716	TAIR|locus:2063484 - symbol:AT2G35260 "AT2G35260" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] InterPro:IPR003675 Pfam:PF02517 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0016020 EMBL:AC004667 EMBL:AF361619 EMBL:AY081832 IPI:IPI00545114 PIR:D84766 RefSeq:NP_565802.1 UniGene:At.24777 STRING:O82167 PRIDE:O82167 EnsemblPlants:AT2G35260.1 GeneID:818093 KEGG:ath:AT2G35260 TAIR:At2g35260 eggNOG:NOG279687 HOGENOM:HBG593810 InParanoid:O82167 OMA:GRFICSV PhylomeDB:O82167 ProtClustDB:CLSN2688697 ArrayExpress:O82167 Genevestigator:O82167 Uniprot:O82167
Leaf	Isotig01546	7	37	-1.873	0.000203981	TAIR|locus:2063484 - symbol:AT2G35260 "AT2G35260" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] InterPro:IPR003675 Pfam:PF02517 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0016020 EMBL:AC004667 EMBL:AF361619 EMBL:AY081832 IPI:IPI00545114 PIR:D84766 RefSeq:NP_565802.1 UniGene:At.24777 STRING:O82167 PRIDE:O82167 EnsemblPlants:AT2G35260.1 GeneID:818093 KEGG:ath:AT2G35260 TAIR:At2g35260 eggNOG:NOG279687 HOGENOM:HBG593810 InParanoid:O82167 OMA:GRFICSV PhylomeDB:O82167 ProtClustDB:CLSN2688697 ArrayExpress:O82167 Genevestigator:O82167 Uniprot:O82167
Leaf	Isotig01547	5	39	-2.435	6.91E-06	TAIR|locus:2063484 - symbol:AT2G35260 "AT2G35260" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] InterPro:IPR003675

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						Pfam:PF02517 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0016020 EMBL:AC004667 EMBL:AF361619 EMBL:AY081832 IPI:IPI00545114 PIR:D84766 RefSeq:NP_565802.1 UniGene:At.24777 STRING:O82167 PRIDE:O82167 EnsemblPlants:AT2G35260.1 GeneID:818093 KEGG:ath:AT2G35260 TAIR:At2g35260 eggNOG:NOG279687 HOGENOM:HBG593810 InParanoid:O82167 OMA:GRFICSV PhylomeDB:O82167 ProtClustDB:CLSN2688697 ArrayExpress:O82167 Genevestigator:O82167 Uniprot:O82167
Leaf	Isotig01564	17	5	2.294	0.000574458	TAIR|locus:2103437 - symbol:PLC2 "phospholipase C 2" species:3702 "Arabidopsis thaliana" [GO:0006629 "lipid metabolic process" evidence=IEA] [GO:0007165 "signal transduction" evidence=IEA;ISS] [GO:0035556 "intracellular signal transduction" evidence=IEA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0004629 "phospholipase C activity" evidence=TAS] InterPro:IPR000008 InterPro:IPR000909 InterPro:IPR001192 InterPro:IPR001711 InterPro:IPR008973 InterPro:IPR011992 InterPro:IPR017946 Pfam:PF00168 Pfam:PF00387 Pfam:PF00388 PRINTS:PR00390 PROSITE:PS50007 PROSITE:PS50008 SMART:SM00148 SMART:SM00149 SMART:SM00239 GO:GO:0005886 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005509 GO:GO:0035556 GO:GO:0016042 GO:GO:0004435 Gene3D:G3DSA:3.20.20.190 SUPFAM:SSF51695 Gene3D:G3DSA:1.10.238.10 InterPro:IPR018029 SUPFAM:SSF49562 PROSITE:PS50004 GO:GO:0004871 EMBL:AC074395 eggNOG:NOG149692 InterPro:IPR015359 Pfam:PF09279 BRENDA:3.1.4.11 HSSP:P10688 HOGENOM:HBG317162 KO:K05857 EMBL:D50804 EMBL:AF360206 EMBL:AY040054 EMBL:AY084465 EMBL:AK221660 IPI:IPI00536168 PIR:S71170 RefSeq:NP_001030660.1 RefSeq:NP_187464.1 UniGene:At.20554 ProteinModelPortal:Q39033 SMR:Q39033 STRING:Q39033 PRIDE:Q39033 EnsemblPlants:AT3G08510.1 EnsemblPlants:AT3G08510.2 GeneID:819999 KEGG:ath:AT3G08510 TAIR:At3g08510 InParanoid:Q39033 OMA:VATIAQY PhylomeDB:Q39033 ProtClustDB:PLN02222 BioCyc:MetaCyc:MONOMER-1621 ArrayExpress:Q39033 Genevestigator:Q39033 Uniprot:Q39033
Leaf	Isotig01566	14	2	3.336	0.000148753	TAIR|locus:504956034 - symbol:AT2G40116 species:3702 "Arabidopsis thaliana" [GO:0004435 "phosphatidylinositol phospholipase C activity" evidence=IEA;ISS] [GO:0004629 "phospholipase C activity" evidence=IEA] [GO:0006629 "lipid metabolic process" evidence=IEA;ISS] [GO:0007165 "signal transduction" evidence=IEA;ISS] [GO:0008081 "phosphoric diester hydrolase activity" evidence=IEA] [GO:0035556 "intracellular signal transduction" evidence=IEA;ISS] InterPro:IPR000008 InterPro:IPR000909 InterPro:IPR001192 InterPro:IPR001711 InterPro:IPR008973 InterPro:IPR017946 Pfam:PF00168 Pfam:PF00387 Pfam:PF00388 PRINTS:PR00390 PROSITE:PS50007 PROSITE:PS50008 SMART:SM00148 SMART:SM00149 SMART:SM00239 GO:GO:0005886 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0035556 GO:GO:0016042 GO:GO:0004435 Gene3D:G3DSA:3.20.20.190 SUPFAM:SSF51695 InterPro:IPR018029 SUPFAM:SSF49562 PROSITE:PS50004 GO:GO:0004871 eggNOG:NOG149692 InterPro:IPR015359 Pfam:PF09279 HSSP:P10688 HOGENOM:HBG317162 KO:K05857 EMBL:BX819512 EMBL:AY150803 IPI:IPI00523149 RefSeq:NP_850327.2 UniGene:At.50126 ProteinModelPortal:Q8GV43 SMR:Q8GV43 STRING:Q8GV43 PRIDE:Q8GV43 EnsemblPlants:AT2G40116.1 GeneID:818602 KEGG:ath:AT2G40116 TAIR:At2g40116 InParanoid:Q8GV43 OMA:EVREYDM PhylomeDB:Q8GV43 ProtClustDB:PLN02952 Genevestigator:Q8GV43 Uniprot:Q8GV43
Leaf	Isotig01567	13	2	3.229	0.00031313	TAIR|locus:504956034 - symbol:AT2G40116 species:3702 "Arabidopsis thaliana" [GO:0004435 "phosphatidylinositol phospholipase C activity" evidence=IEA;ISS] [GO:0004629 "phospholipase C activity" evidence=IEA] [GO:0006629 "lipid metabolic process" evidence=IEA;ISS] [GO:0007165 "signal transduction" evidence=IEA;ISS] [GO:0008081 "phosphoric diester hydrolase activity" evidence=IEA] [GO:0035556 "intracellular signal transduction" evidence=IEA;ISS] InterPro:IPR000008 InterPro:IPR000909 InterPro:IPR001192 InterPro:IPR001711 InterPro:IPR008973 InterPro:IPR017946 Pfam:PF00168 Pfam:PF00387 Pfam:PF00388 PRINTS:PR00390 PROSITE:PS50007 PROSITE:PS50008 SMART:SM00148 SMART:SM00149 SMART:SM00239 GO:GO:0005886 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0035556 GO:GO:0016042 GO:GO:0004435 Gene3D:G3DSA:3.20.20.190 SUPFAM:SSF51695 InterPro:IPR018029 SUPFAM:SSF49562 PROSITE:PS50004 GO:GO:0004871 eggNOG:NOG149692 InterPro:IPR015359 Pfam:PF09279 HSSP:P10688 HOGENOM:HBG317162 KO:K05857 EMBL:BX819512 EMBL:AY150803 IPI:IPI00523149 RefSeq:NP_850327.2 UniGene:At.50126 ProteinModelPortal:Q8GV43 SMR:Q8GV43 STRING:Q8GV43 PRIDE:Q8GV43 EnsemblPlants:AT2G40116.1 GeneID:818602 KEGG:ath:AT2G40116 TAIR:At2g40116 InParanoid:Q8GV43 OMA:EVREYDM PhylomeDB:Q8GV43 ProtClustDB:PLN02952 Genevestigator:Q8GV43 Uniprot:Q8GV43
Leaf	Isotig01578	10	43	-1.575	0.000391523	TAIR|locus:2167225 - symbol:PSY "AT5G17230" species:3702 "Arabidopsis thaliana" [GO:0016117 "carotenoid biosynthetic process" evidence=IMP] [GO:0016767 "geranylgeranyl-diphosphate geranylgeranyltransferase activity" evidence=ISS;TAS] [GO:0046905 "phytoene synthase activity" evidence=TAS] [GO:0009507 "chloroplast"

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						evidence=IDA] InterPro:IPR002060 InterPro:IPR019845 Pfam:PF00494 PROSITE:PS01044 PROSITE:PS01045 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009507 InterPro:IPR008949 Gene3D:G3DSA:1.10.600.10 SUPFAM:SSF48576 EMBL:AB005238 eggNOG:COG1562 GO:GO:0016767 GO:GO:0046905 EMBL:L25812 EMBL:AF009954 EMBL:BT000450 EMBL:BT002084 EMBL:AY085565 IPI:IPI00527204 RefSeq:NP_001031895.1 RefSeq:NP_197225.1 UniGene:At.23726 ProteinModelPortal:P37271 SMR:P37271 STRING:P37271 PRIDE:P37271 EnsemblPlants:AT5G17230.1 EnsemblPlants:AT5G17230.2 GeneID:831587 KEGG:ath:AT5G17230 TAIR:At5g17230 HOGENOM:HBG693191 InParanoid:P37271 KO:K02291 OMA:ELKLYCY PhylomeDB:P37271 ProtClustDB:PLN02632 BioCyc:ARA:AT5G17230-MONOMER BioCyc:MetaCyc:AT5G17230-MONOMER ArrayExpress:P37271 Genevestigator:P37271 GermOnline:AT5G17230 Uniprot:P37271
Leaf	Isotig01579	10	44	-1.609	0.000271316	TAIR|locus:2167225 - symbol:PSY "AT5G17230" species:3702 "Arabidopsis thaliana" [GO:0016117 "carotenoid biosynthetic process" evidence=IMP] [GO:0016767 "geranylgeranyl-diphosphate geranylgeranyltransferase activity" evidence=ISS;TAS] [GO:0046905 "phytoene synthase activity" evidence=TAS] [GO:0009507 "chloroplast" evidence=IDA] InterPro:IPR002060 InterPro:IPR019845 Pfam:PF00494 PROSITE:PS01044 PROSITE:PS01045 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009507 InterPro:IPR008949 Gene3D:G3DSA:1.10.600.10 SUPFAM:SSF48576 EMBL:AB005238 eggNOG:COG1562 GO:GO:0016767 GO:GO:0046905 EMBL:L25812 EMBL:AF009954 EMBL:BT000450 EMBL:BT002084 EMBL:AY085565 IPI:IPI00527204 RefSeq:NP_001031895.1 RefSeq:NP_197225.1 UniGene:At.23726 ProteinModelPortal:P37271 SMR:P37271 STRING:P37271 PRIDE:P37271 EnsemblPlants:AT5G17230.1 EnsemblPlants:AT5G17230.2 GeneID:831587 KEGG:ath:AT5G17230 TAIR:At5g17230 HOGENOM:HBG693191 InParanoid:P37271 KO:K02291 OMA:ELKLYCY PhylomeDB:P37271 ProtClustDB:PLN02632 BioCyc:ARA:AT5G17230-MONOMER BioCyc:MetaCyc:AT5G17230-MONOMER ArrayExpress:P37271 Genevestigator:P37271 GermOnline:AT5G17230 Uniprot:P37271
Leaf	Isotig01580	2	19	-2.719	0.000848343	TAIR|locus:2035395 - symbol:APS2 "AT1G19920" species:3702 "Arabidopsis thaliana" [GO:0009507 "chloroplast" evidence=NAS] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0000103 "sulfate assimilation" evidence=TAS] [GO:0004781 "sulfate adenylyltransferase (ATP) activity" evidence=IMP] [GO:0009970 "cellular response to sulfate starvation" evidence=IEP] InterPro:IPR002650 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0005524 GO:GO:0009570 GO:GO:0000103 InterPro:IPR014729 Gene3D:G3DSA:3.40.50.620 HSSP:P08536 KO:K13811 ProtClustDB:CLSN2684174 GO:GO:0004781 InterPro:IPR015947 SUPFAM:SSF88697 TIGRFAMs:TIGR00339 EMBL:U06276 EMBL:X79210 EMBL:U40715 EMBL:U59737 EMBL:AC007797 EMBL:AY093049 EMBL:BT000417 EMBL:AY086101 IPI:IPI00530027 IPI:IPI01019907 PIR:S44943 RefSeq:NP_564099.1 UniGene:At.24657 ProteinModelPortal:Q43870 SMR:Q43870 IntAct:Q43870 STRING:Q43870 PRIDE:Q43870 GeneID:838580 KEGG:ath:AT1G19920 TAIR:At1g19920 eggNOG:COG2046 HOGENOM:HBG480761 InParanoid:Q43870 OMA:EGHEAVN PhylomeDB:Q43870 ArrayExpress:Q8RWJ3 Genevestigator:Q43870 GO:GO:0009970 Uniprot:Q43870
Leaf	Isotig01581	2	19	-2.719	0.000848343	TAIR|locus:2035395 - symbol:APS2 "AT1G19920" species:3702 "Arabidopsis thaliana" [GO:0009507 "chloroplast" evidence=NAS] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0000103 "sulfate assimilation" evidence=TAS] [GO:0004781 "sulfate adenylyltransferase (ATP) activity" evidence=IMP] [GO:0009970 "cellular response to sulfate starvation" evidence=IEP] InterPro:IPR002650 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0005524 GO:GO:0009570 GO:GO:0000103 InterPro:IPR014729 Gene3D:G3DSA:3.40.50.620 HSSP:P08536 KO:K13811 ProtClustDB:CLSN2684174 GO:GO:0004781 InterPro:IPR015947 SUPFAM:SSF88697 TIGRFAMs:TIGR00339 EMBL:U06276 EMBL:X79210 EMBL:U40715 EMBL:U59737 EMBL:AC007797 EMBL:AY093049 EMBL:BT000417 EMBL:AY086101 IPI:IPI00530027 IPI:IPI01019907 PIR:S44943 RefSeq:NP_564099.1 UniGene:At.24657 ProteinModelPortal:Q43870 SMR:Q43870 IntAct:Q43870 STRING:Q43870 PRIDE:Q43870 GeneID:838580 KEGG:ath:AT1G19920 TAIR:At1g19920 eggNOG:COG2046 HOGENOM:HBG480761 InParanoid:Q43870 OMA:EGHEAVN PhylomeDB:Q43870 ArrayExpress:Q8RWJ3 Genevestigator:Q43870 GO:GO:0009970 Uniprot:Q43870
Leaf	Isotig01582	2	19	-2.719	0.000848343	TAIR|locus:2035395 - symbol:APS2 "AT1G19920" species:3702 "Arabidopsis thaliana" [GO:0009507 "chloroplast" evidence=NAS] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0000103 "sulfate assimilation" evidence=TAS] [GO:0004781 "sulfate adenylyltransferase (ATP) activity"

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						evidence=IMP] [GO:0009970 "cellular response to sulfate starvation" evidence=IEP] InterPro:IPR002650 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0005524 GO:GO:0009570 GO:GO:0000103 InterPro:IPR014729 Gene3D:G3DSA:3.40.50.620 HSSP:P08536 KO:K13811 ProtClustDB:CLSN2684174 GO:GO:0004781 InterPro:IPR015947 SUPFAM:SSF88697 TIGRFAMs:TIGR00339 EMBL:U06276 EMBL:X79210 EMBL:U40715 EMBL:U59737 EMBL:AC007797 EMBL:AY093049 EMBL:BT000417 EMBL:AY086101 IPI:IPI00530027 IPI:IPI01019907 PIR:S44943 RefSeq:NP_564099.1 UniGene:At.24657 ProteinModelPortal:Q43870 SMR:Q43870 IntAct:Q43870 STRING:Q43870 PRIDE:Q43870 GeneID:838580 KEGG:ath:AT1G19920 TAIR:At1g19920 eggNOG:COG2046 HOGENOM:HBG480761 InParanoid:Q43870 OMA:EGHEAVN PhylomeDB:Q43870 ArrayExpress:Q8RWJ3 Genevestigator:Q43870 GO:GO:0009970 Uniprot:Q43870
Leaf	Isotig01583	2	19	-2.719	0.000848343	TAIR|locus:2035395 - symbol:APS2 "AT1G19920" species:3702 "Arabidopsis thaliana" [GO:0009507 "chloroplast" evidence=NAS] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0000103 "sulfate assimilation" evidence=TAS] [GO:0004781 "sulfate adenylyltransferase (ATP) activity" evidence=IMP] [GO:0009970 "cellular response to sulfate starvation" evidence=IEP] InterPro:IPR002650 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0005524 GO:GO:0009570 GO:GO:0000103 InterPro:IPR014729 Gene3D:G3DSA:3.40.50.620 HSSP:P08536 KO:K13811 ProtClustDB:CLSN2684174 GO:GO:0004781 InterPro:IPR015947 SUPFAM:SSF88697 TIGRFAMs:TIGR00339 EMBL:U06276 EMBL:X79210 EMBL:U40715 EMBL:U59737 EMBL:AC007797 EMBL:AY093049 EMBL:BT000417 EMBL:AY086101 IPI:IPI00530027 IPI:IPI01019907 PIR:S44943 RefSeq:NP_564099.1 UniGene:At.24657 ProteinModelPortal:Q43870 SMR:Q43870 IntAct:Q43870 STRING:Q43870 PRIDE:Q43870 GeneID:838580 KEGG:ath:AT1G19920 TAIR:At1g19920 eggNOG:COG2046 HOGENOM:HBG480761 InParanoid:Q43870 OMA:EGHEAVN PhylomeDB:Q43870 ArrayExpress:Q8RWJ3 Genevestigator:Q43870 GO:GO:0009970 Uniprot:Q43870
Leaf	Isotig01604	24	4	3.114	1.45E-06	TAIR|locus:2019554 - symbol:AT1G67300 "AT1G67300" species:3702 "Arabidopsis thaliana" [GO:0005351 "sugar:hydrogen symporter activity" evidence=ISS] [GO:0006810 "transport" evidence=IEA] [GO:0015144 "carbohydrate transmembrane transporter activity" evidence=ISS] [GO:0016020 "membrane" evidence=IEA;ISS] [GO:0016021 "integral to membrane" evidence=IEA] [GO:0055085 "transmembrane transport" evidence=IEA] InterPro:IPR003663 InterPro:IPR005828 InterPro:IPR005829 Pfam:PF00083 PRINTS:PR00171 PROSITE:PS00216 PROSITE:PS00217 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0031969 eggNOG:COG0477 InterPro:IPR016196 SUPFAM:SSF103473 GO:GO:0008643 InterPro:IPR020846 PROSITE:PS50850 HOGENOM:HBG744444 GO:GO:0022891 TIGRFAMs:TIGR00879 EMBL:AC002130 EMBL:AK226899 IPI:IPI00539133 PIR:F96696 RefSeq:NP_176898.1 UniGene:At.21607 UniGene:At.67017 ProteinModelPortal:Q9FYG3 EnsemblPlants:AT1G67300.1 GeneID:843050 KEGG:ath:AT1G67300 TAIR:At1g67300 InParanoid:Q9FYG3 PhylomeDB:Q9FYG3 ProtClustDB:CLSN2681973 Genevestigator:Q9FYG3 Uniprot:Q9FYG3
Leaf	Isotig01605	24	4	3.114	1.45E-06	TAIR|locus:2019554 - symbol:AT1G67300 "AT1G67300" species:3702 "Arabidopsis thaliana" [GO:0005351 "sugar:hydrogen symporter activity" evidence=ISS] [GO:0006810 "transport" evidence=IEA] [GO:0015144 "carbohydrate transmembrane transporter activity" evidence=ISS] [GO:0016020 "membrane" evidence=IEA;ISS] [GO:0016021 "integral to membrane" evidence=IEA] [GO:0055085 "transmembrane transport" evidence=IEA] InterPro:IPR003663 InterPro:IPR005828 InterPro:IPR005829 Pfam:PF00083 PRINTS:PR00171 PROSITE:PS00216 PROSITE:PS00217 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0031969 eggNOG:COG0477 InterPro:IPR016196 SUPFAM:SSF103473 GO:GO:0008643 InterPro:IPR020846 PROSITE:PS50850 HOGENOM:HBG744444 GO:GO:0022891 TIGRFAMs:TIGR00879 EMBL:AC002130 EMBL:AK226899 IPI:IPI00539133 PIR:F96696 RefSeq:NP_176898.1 UniGene:At.21607 UniGene:At.67017 ProteinModelPortal:Q9FYG3 EnsemblPlants:AT1G67300.1 GeneID:843050 KEGG:ath:AT1G67300 TAIR:At1g67300 InParanoid:Q9FYG3 PhylomeDB:Q9FYG3 ProtClustDB:CLSN2681973 Genevestigator:Q9FYG3 Uniprot:Q9FYG3
Leaf	Isotig01606	15	1	4.436	1.60E-05	TAIR|locus:2017899 - symbol:SGB1 "AT1G79820" species:3702 "Arabidopsis thaliana" [GO:0005351 "sugar:hydrogen symporter activity" evidence=ISS] [GO:0006810 "transport" evidence=IEA] [GO:0015144 "carbohydrate transmembrane transporter activity" evidence=ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0055085 "transmembrane transport" evidence=IEA] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR003663 InterPro:IPR005828 InterPro:IPR005829 Pfam:PF00083 PRINTS:PR00171 PROSITE:PS00216

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						PROSITE:PS00217 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0031969 eggNOG:COG0477 InterPro:IPR016196 SUPFAM:SSF103473 GO:GO:0008643 InterPro:IPR020846 PROSITE:PS50850 EMBL:AC010793 EMBL:AC011717 HOGENOM:HBG744444 GO:GO:0022891 TIGRFAMs:TIGR00879 UniGene:At.14743 UniGene:At.48399 EMBL:AY080624 EMBL:BT008550 EMBL:BT008693 IPI:IPI00536398 IPI:IPI00657574 IPI:IPI00810560 IPI:IPI00810565 PIR:B96829 RefSeq:NP_001031303.1 RefSeq:NP_178100.3 RefSeq:NP_850983.1 ProteinModelPortal:Q2V4B9 PRIDE:Q2V4B9 EnsemblPlants:AT1G79820.1 EnsemblPlants:AT1G79820.2 GeneID:844321 KEGG:ath:AT1G79820 TAIR:At1g79820 InParanoid:Q2V4B9 OMA:MELCVES PhylomeDB:Q2V4B9 ProtClustDB:CLSN2680669 Genevestigator:Q2V4B9 GermOnline:AT1G79820 Uniprot:Q2V4B9
Leaf	Isotig01607	15	1	4.436	1.60E-05	TAIR|locus:2017899 - symbol:SGB1 "AT1G79820" species:3702 "Arabidopsis thaliana" [GO:0005351 "sugar:hydrogen symporter activity" evidence=ISS] [GO:0006810 "transport" evidence=IEA] [GO:0015144 "carbohydrate transmembrane transporter activity" evidence=ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0055085 "transmembrane transport" evidence=IEA] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR003663 InterPro:IPR005828 InterPro:IPR005829 Pfam:PF00083 PRINTS:PR00171 PROSITE:PS00216 PROSITE:PS00217 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0031969 eggNOG:COG0477 InterPro:IPR016196 SUPFAM:SSF103473 GO:GO:0008643 InterPro:IPR020846 PROSITE:PS50850 EMBL:AC010793 EMBL:AC011717 HOGENOM:HBG744444 GO:GO:0022891 TIGRFAMs:TIGR00879 UniGene:At.14743 UniGene:At.48399 EMBL:AY080624 EMBL:BT008550 EMBL:BT008693 IPI:IPI00536398 IPI:IPI00657574 IPI:IPI00810560 IPI:IPI00810565 PIR:B96829 RefSeq:NP_001031303.1 RefSeq:NP_178100.3 RefSeq:NP_850983.1 ProteinModelPortal:Q2V4B9 PRIDE:Q2V4B9 EnsemblPlants:AT1G79820.1 EnsemblPlants:AT1G79820.2 GeneID:844321 KEGG:ath:AT1G79820 TAIR:At1g79820 InParanoid:Q2V4B9 OMA:MELCVES PhylomeDB:Q2V4B9 ProtClustDB:CLSN2680669 Genevestigator:Q2V4B9 GermOnline:AT1G79820 Uniprot:Q2V4B9
Leaf	Isotig01612	3	25	-2.530	0.000233449	TAIR|locus:2086285 - symbol:AT3G14920 "AT3G14920" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0005773 "vacuole" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0009505 "plant-type cell wall" evidence=IDA] GO:GO:0005774 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0009505 EMBL:AP000370 InterPro:IPR021102 Pfam:PF12222 eggNOG:NOG85372 HOGENOM:HBG597358 IPI:IPI00537395 RefSeq:NP_188110.1 UniGene:At.39139 PRIDE:Q9LKB2 EnsemblPlants:AT3G14920.1 GeneID:820721 KEGG:ath:AT3G14920 TAIR:At3g14920 InParanoid:Q9LKB2 OMA:CYFRNIS PhylomeDB:Q9LKB2 ProtClustDB:CLSN2915641 Genevestigator:Q9LKB2 Uniprot:Q9LKB2
Leaf	Isotig01613	3	24	-2.471	0.000374243	TAIR|locus:2086285 - symbol:AT3G14920 "AT3G14920" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0005773 "vacuole" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0009505 "plant-type cell wall" evidence=IDA] GO:GO:0005774 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0009505 EMBL:AP000370 InterPro:IPR021102 Pfam:PF12222 eggNOG:NOG85372 HOGENOM:HBG597358 IPI:IPI00537395 RefSeq:NP_188110.1 UniGene:At.39139 PRIDE:Q9LKB2 EnsemblPlants:AT3G14920.1 GeneID:820721 KEGG:ath:AT3G14920 TAIR:At3g14920 InParanoid:Q9LKB2 OMA:CYFRNIS PhylomeDB:Q9LKB2 ProtClustDB:CLSN2915641 Genevestigator:Q9LKB2 Uniprot:Q9LKB2
Leaf	Isotig01616	51	15	2.294	2.46E-09	TAIR|locus:2064965 - symbol:EULS3 "AT2G39050" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0030246 "carbohydrate binding" evidence=IDA] GO:GO:0005634 GO:GO:0005737 EMBL:CP002685 GenomeReviews:CT485783_GR InterPro:IPR000772 SUPFAM:SSF50370 PROSITE:PS50231 GO:GO:0030246 EMBL:AC005770 Pfam:PF14200 EMBL:AF411801 EMBL:AY093795 EMBL:AY087909 IPI:IPI00536641 PIR:E84812 RefSeq:NP_565899.1 UniGene:At.22599 ProteinModelPortal:Q945P1 SMR:Q945P1 PRIDE:Q945P1 EnsemblPlants:AT2G39050.1 GeneID:818491 KEGG:ath:AT2G39050 TAIR:At2g39050 eggNOG:NOG254161 HOGENOM:HBG750017 InParanoid:Q945P1 OMA:GYRTIRM PhylomeDB:Q945P1 ProtClustDB:CLSN2681741 ArrayExpress:Q945P1 Genevestigator:Q945P1 Uniprot:Q945P1
Leaf	Isotig01617	54	17	2.196	2.29E-09	TAIR|locus:2064965 - symbol:EULS3 "AT2G39050" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0030246 "carbohydrate binding" evidence=IDA] GO:GO:0005634 GO:GO:0005737 EMBL:CP002685 GenomeReviews:CT485783_GR InterPro:IPR000772 SUPFAM:SSF50370 PROSITE:PS50231

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0030246 EMBL:AC005770 Pfam:PF14200 EMBL:AF411801 EMBL:AY093795 EMBL:AY087909 IPI:IPI00536641 PIR:E84812 RefSeq:NP_565899.1 UniGene:At.22599 ProteinModelPortal:Q945P1 SMR:Q945P1 PRIDE:Q945P1 EnsemblPlants:AT2G39050.1 GeneID:818491 KEGG:ath:AT2G39050 TAIR:At2g39050 eggNOG:NOG254161 HOGENOM:HBG750017 InParanoid:Q945P1 OMA:GYRTIRM PhylomeDB:Q945P1 ProtClustDB:CLSN2681741 ArrayExpress:Q945P1 Genevestigator:Q945P1 Uniprot:Q945P1
Leaf	Isotig01618	51	15	2.294	2.46E-09	TAIR|locus:2064965 - symbol:EULS3 "AT2G39050" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0030246 "carbohydrate binding" evidence=IDA] GO:GO:0005634 GO:GO:0005737 EMBL:CP002685 GenomeReviews:CT485783_GR InterPro:IPR000772 SUPFAM:SSF50370 PROSITE:PS50231 GO:GO:0030246 EMBL:AC005770 Pfam:PF14200 EMBL:AF411801 EMBL:AY093795 EMBL:AY087909 IPI:IPI00536641 PIR:E84812 RefSeq:NP_565899.1 UniGene:At.22599 ProteinModelPortal:Q945P1 SMR:Q945P1 PRIDE:Q945P1 EnsemblPlants:AT2G39050.1 GeneID:818491 KEGG:ath:AT2G39050 TAIR:At2g39050 eggNOG:NOG254161 HOGENOM:HBG750017 InParanoid:Q945P1 OMA:GYRTIRM PhylomeDB:Q945P1 ProtClustDB:CLSN2681741 ArrayExpress:Q945P1 Genevestigator:Q945P1 Uniprot:Q945P1
Leaf	Isotig01619	54	17	2.196	2.29E-09	TAIR|locus:2064965 - symbol:EULS3 "AT2G39050" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0030246 "carbohydrate binding" evidence=IDA] GO:GO:0005634 GO:GO:0005737 EMBL:CP002685 GenomeReviews:CT485783_GR InterPro:IPR000772 SUPFAM:SSF50370 PROSITE:PS50231 GO:GO:0030246 EMBL:AC005770 Pfam:PF14200 EMBL:AF411801 EMBL:AY093795 EMBL:AY087909 IPI:IPI00536641 PIR:E84812 RefSeq:NP_565899.1 UniGene:At.22599 ProteinModelPortal:Q945P1 SMR:Q945P1 PRIDE:Q945P1 EnsemblPlants:AT2G39050.1 GeneID:818491 KEGG:ath:AT2G39050 TAIR:At2g39050 eggNOG:NOG254161 HOGENOM:HBG750017 InParanoid:Q945P1 OMA:GYRTIRM PhylomeDB:Q945P1 ProtClustDB:CLSN2681741 ArrayExpress:Q945P1 Genevestigator:Q945P1 Uniprot:Q945P1
Leaf	Isotig01640	48	462	-2.738	2.78E-61	TAIR|locus:2097608 - symbol:LHCB4.2 "AT3G08940" species:3702 "Arabidopsis thaliana" [GO:0016168 "chlorophyll binding" evidence=ISS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009637 "response to blue light" evidence=IEP] [GO:0010114 "response to red light" evidence=IEP] [GO:0010218 "response to far red light" evidence=IEP] [GO:0009534 "chloroplast thylakoid" evidence=IDA] InterPro:IPR001344 Pfam:PF00504 GO:GO:0016021 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0046872 GO:GO:0009941 GO:GO:0009637 GO:GO:0010218 GO:GO:0010114 GO:GO:0018298 EMBL:AC010871 GO:GO:0009535 HOGENOM:HBG618504 GO:GO:0009522 GO:GO:0009523 GO:GO:0016168 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 KO:K08915 ProtClustDB:PLN00187 EMBL:AF134127 EMBL:AY065140 EMBL:AY081608 IPI:IPI00521901 IPI:IPI00542269 PIR:T52317 RefSeq:NP_187506.1 RefSeq:NP_850545.1 UniGene:At.21828 UniGene:At.22485 UniGene:At.6984 ProteinModelPortal:Q9XF88 SMR:Q9XF88 STRING:Q9XF88 PRIDE:Q9XF88 ProMEX:Q9XF88 EnsemblPlants:AT3G08940.2 GeneID:820043 KEGG:ath:AT3G08940 TAIR:At3g08940 eggNOG:NOG330021 InParanoid:Q9XF88 OMA:YSNAGRI PhylomeDB:Q9XF88 ArrayExpress:Q9XF88 Genevestigator:Q9XF88 GermOnline:AT3G08940 Uniprot:Q9XF88
Leaf	Isotig01641	47	491	-2.856	7.93E-68	TAIR|locus:2149765 - symbol:LHCB4.1 "AT5G01530" species:3702 "Arabidopsis thaliana" [GO:0015979 "photosynthesis" evidence=ISS] [GO:0016168 "chlorophyll binding" evidence=ISS] [GO:0030076 "light-harvesting complex" evidence=ISS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009637 "response to blue light" evidence=IEP] [GO:0010114 "response to red light" evidence=IEP] [GO:0010218 "response to far red light" evidence=IEP] [GO:0009534 "chloroplast thylakoid" evidence=IDA] InterPro:IPR001344 Pfam:PF00504 GO:GO:0016021 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0046872 GO:GO:0009637 GO:GO:0010218 GO:GO:0010114 GO:GO:0018298 GO:GO:0009535 GO:GO:0010287 HOGENOM:HBG618504 GO:GO:0009522 GO:GO:0009523 GO:GO:0016168 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 EMBL:AL161946 eggNOG:NOG319330 KO:K08915 EMBL:X71878 EMBL:AF370474 EMBL:AY048262 EMBL:AY048300 EMBL:AY057641 EMBL:AY059861 EMBL:AY081680 EMBL:AY092980 EMBL:AY133566 EMBL:BT000363 IPI:IPI00542715 PIR:S33443 RefSeq:NP_195773.1

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						UniGene:At.23015 UniGene:At.23659 UniGene:At.23691 UniGene:At.24017 UniGene:At.75201 ProteinModelPortal:Q07473 SMR:Q07473 IntAct:Q07473 STRING:Q07473 PRIDE:Q07473 EnsemblPlants:AT5G01530.1 GeneID:830325 KEGG:ath:AT5G01530 TAIR:At5g01530 InParanoid:Q07473 OMA:HTTIIDN PhylomeDB:Q07473 ProtClustDB:PLN00187 ArrayExpress:Q07473 Genevestigator:Q07473 GermOnline:AT5G01530 Uniprot:Q07473
Leaf	Isotig01642	48	462	-2.738	2.78E-61	TAIR|locus:2097608 - symbol:LHCB4.2 "AT3G08940" species:3702 "Arabidopsis thaliana" [GO:0016168 "chlorophyll binding" evidence=ISS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009637 "response to blue light" evidence=IEP] [GO:0010114 "response to red light" evidence=IEP] [GO:0010218 "response to far red light" evidence=IEP] [GO:0009534 "chloroplast thylakoid" evidence=IDA] InterPro:IPR001344 Pfam:PF00504 GO:GO:0016021 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0046872 GO:GO:0009941 GO:GO:0009637 GO:GO:0010218 GO:GO:0010114 GO:GO:0018298 EMBL:AC010871 GO:GO:0009535 HOGENOM:HBG618504 GO:GO:0009522 GO:GO:0009523 GO:GO:0016168 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 KO:K08915 ProtClustDB:PLN00187 EMBL:AF134127 EMBL:AY065140 EMBL:AY081608 IPI:IPI00521901 IPI:IPI00542269 PIR:T52317 RefSeq:NP_187506.1 RefSeq:NP_850545.1 UniGene:At.21828 UniGene:At.22485 UniGene:At.6984 ProteinModelPortal:Q9XF88 SMR:Q9XF88 STRING:Q9XF88 PRIDE:Q9XF88 ProMEX:Q9XF88 EnsemblPlants:AT3G08940.2 GeneID:820043 KEGG:ath:AT3G08940 TAIR:At3g08940 eggNOG:NOG330021 InParanoid:Q9XF88 OMA:YSNAGRI PhylomeDB:Q9XF88 ArrayExpress:Q9XF88 Genevestigator:Q9XF88 GermOnline:AT3G08940 Uniprot:Q9XF88
Leaf	Isotig01643	47	491	-2.856	7.93E-68	TAIR|locus:2149765 - symbol:LHCB4.1 "AT5G01530" species:3702 "Arabidopsis thaliana" [GO:0015979 "photosynthesis" evidence=ISS] [GO:0016168 "chlorophyll binding" evidence=ISS] [GO:0030076 "light-harvesting complex" evidence=ISS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009637 "response to blue light" evidence=IEP] [GO:0010114 "response to red light" evidence=IEP] [GO:0010218 "response to far red light" evidence=IEP] [GO:0009534 "chloroplast thylakoid" evidence=IDA] InterPro:IPR001344 Pfam:PF00504 GO:GO:0016021 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0046872 GO:GO:0009637 GO:GO:0010218 GO:GO:0010114 GO:GO:0018298 GO:GO:0009535 GO:GO:0010287 HOGENOM:HBG618504 GO:GO:0009522 GO:GO:0009523 GO:GO:0016168 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 EMBL:AL161946 eggNOG:NOG319330 KO:K08915 EMBL:X71878 EMBL:AF370474 EMBL:AY048262 EMBL:AY048300 EMBL:AY057641 EMBL:AY059861 EMBL:AY081680 EMBL:AY092980 EMBL:AY133566 EMBL:BT000363 IPI:IPI00542715 PIR:S33443 RefSeq:NP_195773.1 UniGene:At.23015 UniGene:At.23659 UniGene:At.23691 UniGene:At.24017 UniGene:At.75201 ProteinModelPortal:Q07473 SMR:Q07473 IntAct:Q07473 STRING:Q07473 PRIDE:Q07473 EnsemblPlants:AT5G01530.1 GeneID:830325 KEGG:ath:AT5G01530 TAIR:At5g01530 InParanoid:Q07473 OMA:HTTIIDN PhylomeDB:Q07473 ProtClustDB:PLN00187 ArrayExpress:Q07473 Genevestigator:Q07473 GermOnline:AT5G01530 Uniprot:Q07473
Leaf	Isotig01646	1	17	-3.559	0.000355264	TAIR|locus:2034980 - symbol:PnsB4 "AT1G18730" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009773 "photosynthetic electron transport in photosystem I" evidence=TAS] [GO:0010598 "NAD(P)H dehydrogenase complex (plastoquinone)" evidence=NAS] EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009535 GO:GO:0009773 GO:GO:0010598 EMBL:AY080701 EMBL:AY117165 EMBL:AK226496 IPI:IPI00518157 RefSeq:NP_173308.2 UniGene:At.43083 UniGene:At.47916 STRING:Q8RXS1 PRIDE:Q8RXS1 EnsemblPlants:AT1G18730.1 GeneID:838455 KEGG:ath:AT1G18730 TAIR:At1g18730 HOGENOM:HBG319800 InParanoid:Q8RXS1 OMA:LWREELI PhylomeDB:Q8RXS1 ProtClustDB:PLN00180 ArrayExpress:Q8RXS1 Genevestigator:Q8RXS1 Uniprot:Q8RXS1
Leaf	Isotig01647	1	17	-3.559	0.000355264	TAIR|locus:2034980 - symbol:PnsB4 "AT1G18730" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009773 "photosynthetic electron transport in photosystem I" evidence=TAS] [GO:0010598 "NAD(P)H dehydrogenase complex (plastoquinone)" evidence=NAS] EMBL:CP002684

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GenomeReviews:CT485782_GR GO:GO:0009535 GO:GO:0009773 GO:GO:0010598 EMBL:AY080701 EMBL:AY117165 EMBL:AK226496 IPI:IPI00518157 RefSeq:NP_173308.2 UniGene:At.43083 UniGene:At.47916 STRING:Q8RXS1 PRIDE:Q8RXS1 EnsemblPlants:AT1G18730.1 GeneID:838455 KEGG:ath:AT1G18730 TAIR:At1g18730 HOGENOM:HBG319800 InParanoid:Q8RXS1 OMA:LWREELI PhylomeDB:Q8RXS1 ProtClustDB:PLN00180 ArrayExpress:Q8RXS1 Genevestigator:Q8RXS1 Uniprot:Q8RXS1
Leaf	Isotig01664	60	25	1.792	3.54E-08	UNIPROTKB|P80471 - symbol:P80471 "Light-induced protein, chloroplastic" species:4113 "Solanum tuberosum" [GO:0003674 "molecular_function" evidence=ND] [GO:0006950 "response to stress" evidence=IEP] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] InterPro:IPR006843 Pfam:PF04755 GO:GO:0006950 GO:GO:0005198 GO:GO:0009535 EMBL:Y15269 PIR:T07825 Uniprot:P80471
Leaf	Isotig01665	61	24	1.875	9.94E-09	UNIPROTKB|P80471 - symbol:P80471 "Light-induced protein, chloroplastic" species:4113 "Solanum tuberosum" [GO:0003674 "molecular_function" evidence=ND] [GO:0006950 "response to stress" evidence=IEP] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] InterPro:IPR006843 Pfam:PF04755 GO:GO:0006950 GO:GO:0005198 GO:GO:0009535 EMBL:Y15269 PIR:T07825 Uniprot:P80471
Leaf	Isotig01666	56	25	1.692	3.10E-07	UNIPROTKB|P80471 - symbol:P80471 "Light-induced protein, chloroplastic" species:4113 "Solanum tuberosum" [GO:0003674 "molecular_function" evidence=ND] [GO:0006950 "response to stress" evidence=IEP] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] InterPro:IPR006843 Pfam:PF04755 GO:GO:0006950 GO:GO:0005198 GO:GO:0009535 EMBL:Y15269 PIR:T07825 Uniprot:P80471
Leaf	Isotig01667	57	24	1.777	9.23E-08	UNIPROTKB|P80471 - symbol:P80471 "Light-induced protein, chloroplastic" species:4113 "Solanum tuberosum" [GO:0003674 "molecular_function" evidence=ND] [GO:0006950 "response to stress" evidence=IEP] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] InterPro:IPR006843 Pfam:PF04755 GO:GO:0006950 GO:GO:0005198 GO:GO:0009535 EMBL:Y15269 PIR:T07825 Uniprot:P80471
Leaf	Isotig01676	4	38	-2.719	2.37E-06	TAIR|locus:2825741 - symbol:Lhca5 "AT1G45474" species:3702 "Arabidopsis thaliana" [GO:0015979 "photosynthesis" evidence=ISS] [GO:0030076 "light-harvesting complex" evidence=ISS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009782 "photosystem I antenna complex" evidence=IDA] [GO:0031409 "pigment binding" evidence=IDA] [GO:0009768 "photosynthesis, light harvesting in photosystem I" evidence=IGI] [GO:0016020 "membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] InterPro:IPR001344 Pfam:PF00504 EMBL:CP002684 EMBL:AC083835 GO:GO:0009535 GO:GO:0031409 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 UniGene:At.52042 EMBL:AY062097 EMBL:AY090263 EMBL:AK221694 IPI:IPI00542586 PIR:F96510 RefSeq:NP_175137.1 RefSeq:NP_849778.1 UniGene:At.20798 ProteinModelPortal:Q9C639 SMR:Q9C639 STRING:Q9C639 PRIDE:Q9C639 EnsemblPlants:AT1G45474.1 EnsemblPlants:AT1G45474.2 GeneID:841099 KEGG:ath:AT1G45474 TAIR:At1g45474 InParanoid:Q9C639 KO:K08911 OMA:VQASVTH PhylomeDB:Q9C639 ProtClustDB:PLN00147 Genevestigator:Q9C639 GO:GO:0009782 Uniprot:Q9C639
Leaf	Isotig01677	4	37	-2.680	3.82E-06	TAIR|locus:2825741 - symbol:Lhca5 "AT1G45474" species:3702 "Arabidopsis thaliana" [GO:0015979 "photosynthesis" evidence=ISS] [GO:0030076 "light-harvesting complex" evidence=ISS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009782 "photosystem I antenna complex" evidence=IDA] [GO:0031409 "pigment binding" evidence=IDA] [GO:0009768 "photosynthesis, light harvesting in photosystem I" evidence=IGI] [GO:0016020 "membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] InterPro:IPR001344 Pfam:PF00504 EMBL:CP002684 EMBL:AC083835 GO:GO:0009535 GO:GO:0031409 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 UniGene:At.52042 EMBL:AY062097 EMBL:AY090263 EMBL:AK221694 IPI:IPI00542586 PIR:F96510 RefSeq:NP_175137.1 RefSeq:NP_849778.1 UniGene:At.20798 ProteinModelPortal:Q9C639 SMR:Q9C639 STRING:Q9C639 PRIDE:Q9C639 EnsemblPlants:AT1G45474.1 EnsemblPlants:AT1G45474.2 GeneID:841099 KEGG:ath:AT1G45474 TAIR:At1g45474 InParanoid:Q9C639 KO:K08911 OMA:VQASVTH PhylomeDB:Q9C639 ProtClustDB:PLN00147 Genevestigator:Q9C639 GO:GO:0009782 Uniprot:Q9C639
Leaf	Isotig01678	4	38	-2.719	2.37E-06	TAIR|locus:2825741 - symbol:Lhca5 "AT1G45474" species:3702 "Arabidopsis thaliana" [GO:0015979 "photosynthesis" evidence=ISS] [GO:0030076 "light-harvesting complex" evidence=ISS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009782 "photosystem I antenna complex" evidence=IDA] [GO:0031409 "pigment binding" evidence=IDA] [GO:0009768 "photosynthesis, light harvesting in photosystem I" evidence=IGI] [GO:0016020 "membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] InterPro:IPR001344 Pfam:PF00504 EMBL:CP002684 EMBL:AC083835 GO:GO:0009535 GO:GO:0031409 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						SUPFAM:SSF103511 UniGene:At.52042 EMBL:AY062097 EMBL:AY090263 EMBL:AK221694 IPI:IPI00542586 PIR:F96510 RefSeq:NP_175137.1 RefSeq:NP_849778.1 UniGene:At.20798 ProteinModelPortal:Q9C639 SMR:Q9C639 STRING:Q9C639 PRIDE:Q9C639 EnsemblPlants:AT1G45474.1 EnsemblPlants:AT1G45474.2 GeneID:841099 KEGG:ath:AT1G45474 TAIR:At1g45474 InParanoid:Q9C639 KO:K08911 OMA:VQASVTH PhylomeDB:Q9C639 ProtClustDB:PLN00147 Genevestigator:Q9C639 GO:GO:0009782 Uniprot:Q9C639
Leaf	Isotig01679	4	37	-2.680	3.82E-06	TAIR|locus:2825741 - symbol:Lhca5 "AT1G45474" species:3702 "Arabidopsis thaliana" [GO:0015979 "photosynthesis" evidence=ISS] [GO:0030076 "light-harvesting complex" evidence=ISS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009782 "photosystem I antenna complex" evidence=IDA] [GO:0031409 "pigment binding" evidence=IDA] [GO:0009768 "photosynthesis, light harvesting in photosystem I" evidence=IGI] [GO:0016020 "membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] InterPro:IPR001344 Pfam:PF00504 EMBL:CP002684 EMBL:AC083835 GO:GO:0009535 GO:GO:0031409 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 UniGene:At.52042 EMBL:AY062097 EMBL:AY090263 EMBL:AK221694 IPI:IPI00542586 PIR:F96510 RefSeq:NP_175137.1 RefSeq:NP_849778.1 UniGene:At.20798 ProteinModelPortal:Q9C639 SMR:Q9C639 STRING:Q9C639 PRIDE:Q9C639 EnsemblPlants:AT1G45474.1 EnsemblPlants:AT1G45474.2 GeneID:841099 KEGG:ath:AT1G45474 TAIR:At1g45474 InParanoid:Q9C639 KO:K08911 OMA:VQASVTH PhylomeDB:Q9C639 ProtClustDB:PLN00147 Genevestigator:Q9C639 GO:GO:0009782 Uniprot:Q9C639
Leaf	Isotig01704	13	0	5.229	3.68E-05	TAIR|locus:2161398 - symbol:DELTA-OAT "AT5G46180" species:3702 "Arabidopsis thaliana" [GO:0004587 "ornithine-oxo-acid transaminase activity" evidence=ISS;IMP] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0006561 "proline biosynthetic process" evidence=IDA;IMP] [GO:0006593 "ornithine catabolic process" evidence=IMP] [GO:0019544 "arginine catabolic process to glutamate" evidence=IMP] [GO:0008270 "zinc ion binding" evidence=IDA] [GO:0042538 "hyperosmotic salinity response" evidence=IDA] InterPro:IPR005814 InterPro:IPR010164 InterPro:IPR015421 InterPro:IPR015422 Pfam:PF00202 PROSITE:PS00600 GO:GO:0005739 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0030170 InterPro:IPR015424 Gene3D:G3DSA:3.40.640.10 Gene3D:G3DSA:3.90.1150.10 SUPFAM:SSF53383 GO:GO:0008270 GO:GO:0006561 HOGENOM:HBG725944 GO:GO:0019544 PANTHER:PTHR11986 EMBL:AB006698 GO:GO:0042538 eggNOG:COG4992 GO:GO:0006593 KO:K00819 GO:GO:0004587 PANTHER:PTHR11986:SF18 TIGRFAMs:TIGR01885 HSSP:P04181 OMA:VWDPEGK EMBL:BT023421 EMBL:BT029160 IPI:IPI00519266 RefSeq:NP_199430.1 UniGene:At.28104 ProteinModelPortal:Q9FNK4 SMR:Q9FNK4 STRING:Q9FNK4 PRIDE:Q9FNK4 EnsemblPlants:AT5G46180.1 GeneID:834660 KEGG:ath:AT5G46180 TAIR:At5g46180 InParanoid:Q9FNK4 PhylomeDB:Q9FNK4 ProtClustDB:PLN02624 Genevestigator:Q9FNK4 Uniprot:Q9FNK4
Leaf	Isotig01705	13	0	5.229	3.68E-05	TAIR|locus:2161398 - symbol:DELTA-OAT "AT5G46180" species:3702 "Arabidopsis thaliana" [GO:0004587 "ornithine-oxo-acid transaminase activity" evidence=ISS;IMP] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0006561 "proline biosynthetic process" evidence=IDA;IMP] [GO:0006593 "ornithine catabolic process" evidence=IMP] [GO:0019544 "arginine catabolic process to glutamate" evidence=IMP] [GO:0008270 "zinc ion binding" evidence=IDA] [GO:0042538 "hyperosmotic salinity response" evidence=IDA] InterPro:IPR005814 InterPro:IPR010164 InterPro:IPR015421 InterPro:IPR015422 Pfam:PF00202 PROSITE:PS00600 GO:GO:0005739 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0030170 InterPro:IPR015424 Gene3D:G3DSA:3.40.640.10 Gene3D:G3DSA:3.90.1150.10 SUPFAM:SSF53383 GO:GO:0008270 GO:GO:0006561 HOGENOM:HBG725944 GO:GO:0019544 PANTHER:PTHR11986 EMBL:AB006698 GO:GO:0042538 eggNOG:COG4992 GO:GO:0006593 KO:K00819 GO:GO:0004587 PANTHER:PTHR11986:SF18 TIGRFAMs:TIGR01885 HSSP:P04181 OMA:VWDPEGK EMBL:BT023421 EMBL:BT029160 IPI:IPI00519266 RefSeq:NP_199430.1 UniGene:At.28104 ProteinModelPortal:Q9FNK4 SMR:Q9FNK4 STRING:Q9FNK4 PRIDE:Q9FNK4 EnsemblPlants:AT5G46180.1 GeneID:834660 KEGG:ath:AT5G46180 TAIR:At5g46180 InParanoid:Q9FNK4 PhylomeDB:Q9FNK4 ProtClustDB:PLN02624 Genevestigator:Q9FNK4 Uniprot:Q9FNK4
Leaf	Isotig01706	11	1	3.988	0.000330755	TAIR|locus:2161398 - symbol:DELTA-OAT "AT5G46180" species:3702 "Arabidopsis thaliana" [GO:0004587 "ornithine-oxo-acid transaminase activity" evidence=ISS;IMP] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0006561 "proline biosynthetic process" evidence=IDA;IMP] [GO:0006593 "ornithine catabolic process" evidence=IMP] [GO:0019544 "arginine catabolic process to glutamate" evidence=IMP] [GO:0008270 "zinc ion binding" evidence=IDA] [GO:0042538 "hyperosmotic salinity response" evidence=IDA] InterPro:IPR005814 InterPro:IPR010164 InterPro:IPR015421 InterPro:IPR015422 Pfam:PF00202 PROSITE:PS00600 GO:GO:0005739 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0030170 InterPro:IPR015424

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						Gene3D:G3DSA:3.40.640.10 Gene3D:G3DSA:3.90.1150.10 SUPFAM:SSF53383 GO:GO:0008270 GO:GO:0006561 HOGENOM:HBG725944 GO:GO:0019544 PANTHER:PTHR11986 EMBL:AB006698 GO:GO:0042538 eggNOG:COG4992 GO:GO:0006593 KO:K00819 GO:GO:0004587 PANTHER:PTHR11986:SF18 TIGRFAMs:TIGR01885 HSSP:P04181 OMA:VWDPEGK EMBL:BT023421 EMBL:BT029160 IPI:IPI00519266 RefSeq:NP_199430.1 UniGene:At.28104 ProteinModelPortal:Q9FNK4 SMR:Q9FNK4 STRING:Q9FNK4 PRIDE:Q9FNK4 EnsemblPlants:AT5G46180.1 GeneID:834660 KEGG:ath:AT5G46180 TAIR:At5g46180 InParanoid:Q9FNK4 PhylomeDB:Q9FNK4 ProtClustDB:PLN02624 Genevestigator:Q9FNK4 Uniprot:Q9FNK4
Leaf	Isotig01707	11	1	3.988	0.000330755	TAIR|locus:2161398 - symbol:DELTA-OAT "AT5G46180" species:3702 "Arabidopsis thaliana" [GO:0004587 "ornithine-oxo-acid transaminase activity" evidence=ISS;IMP] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0006561 "proline biosynthetic process" evidence=IDA;IMP] [GO:0006593 "ornithine catabolic process" evidence=IMP] [GO:0019544 "arginine catabolic process to glutamate" evidence=IMP] [GO:0008270 "zinc ion binding" evidence=IDA] [GO:0042538 "hyperosmotic salinity response" evidence=IDA] InterPro:IPR005814 InterPro:IPR010164 InterPro:IPR015421 InterPro:IPR015422 Pfam:PF00202 PROSITE:PS00600 GO:GO:0005739 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0030170 InterPro:IPR015424 Gene3D:G3DSA:3.40.640.10 Gene3D:G3DSA:3.90.1150.10 SUPFAM:SSF53383 GO:GO:0008270 GO:GO:0006561 HOGENOM:HBG725944 GO:GO:0019544 PANTHER:PTHR11986 EMBL:AB006698 GO:GO:0042538 eggNOG:COG4992 GO:GO:0006593 KO:K00819 GO:GO:0004587 PANTHER:PTHR11986:SF18 TIGRFAMs:TIGR01885 HSSP:P04181 OMA:VWDPEGK EMBL:BT023421 EMBL:BT029160 IPI:IPI00519266 RefSeq:NP_199430.1 UniGene:At.28104 ProteinModelPortal:Q9FNK4 SMR:Q9FNK4 STRING:Q9FNK4 PRIDE:Q9FNK4 EnsemblPlants:AT5G46180.1 GeneID:834660 KEGG:ath:AT5G46180 TAIR:At5g46180 InParanoid:Q9FNK4 PhylomeDB:Q9FNK4 ProtClustDB:PLN02624 Genevestigator:Q9FNK4 Uniprot:Q9FNK4
Leaf	Isotig01764	14	0	5.336	1.79E-05	TAIR|locus:2093307 - symbol:AT3G15670 "AT3G15670" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0009793 "embryo development ending in seed dormancy" evidence=ISS] [GO:0005634 "nucleus" evidence=IDA] GO:GO:0005634 EMBL:CP002686 EMBL:AB017071 ProtClustDB:CLSN2679745 EMBL:AY040026 EMBL:AY054162 EMBL:AY079410 IPI:IPI00542660 RefSeq:NP_188188.1 UniGene:At.5382 STRING:Q9LW12 PRIDE:Q9LW12 ProMEX:Q9LW12 EnsemblPlants:AT3G15670.1 GeneID:820810 KEGG:ath:AT3G15670 TAIR:At3g15670 InParanoid:Q9LW12 OMA:QYTKETA PhylomeDB:Q9LW12 ArrayExpress:Q9LW12 Genevestigator:Q9LW12 Uniprot:Q9LW12
Leaf	Isotig01765	14	0	5.336	1.79E-05	TAIR|locus:2035109 - symbol:LEA7 "AT1G52690" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0009793 "embryo development ending in seed dormancy" evidence=ISS] EMBL:CP002684 EMBL:AC008016 EMBL:AF385732 EMBL:AY093968 EMBL:AY087466 EMBL:BT000737 EMBL:BT000739 EMBL:X91919 IPI:IPI00526817 PIR:H96567 RefSeq:NP_175678.1 RefSeq:NP_974009.1 UniGene:At.21275 STRING:Q96270 PRIDE:Q96270 ProMEX:Q96270 DNASU:841701 EnsemblPlants:AT1G52690.1 EnsemblPlants:AT1G52690.2 GeneID:841701 KEGG:ath:AT1G52690 TAIR:At1g52690 InParanoid:Q96270 OMA:MASHQEQ PhylomeDB:Q96270 ProtClustDB:CLSN2679745 ArrayExpress:Q96270 Genevestigator:Q96270 Uniprot:Q96270
Leaf	Isotig01766	14	0	5.336	1.79E-05	TAIR|locus:2035109 - symbol:LEA7 "AT1G52690" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0009793 "embryo development ending in seed dormancy" evidence=ISS] EMBL:CP002684 EMBL:AC008016 EMBL:AF385732 EMBL:AY093968 EMBL:AY087466 EMBL:BT000737 EMBL:BT000739 EMBL:X91919 IPI:IPI00526817 PIR:H96567 RefSeq:NP_175678.1 RefSeq:NP_974009.1 UniGene:At.21275 STRING:Q96270 PRIDE:Q96270 ProMEX:Q96270 DNASU:841701 EnsemblPlants:AT1G52690.1 EnsemblPlants:AT1G52690.2 GeneID:841701 KEGG:ath:AT1G52690 TAIR:At1g52690 InParanoid:Q96270 OMA:MASHQEQ PhylomeDB:Q96270 ProtClustDB:CLSN2679745 ArrayExpress:Q96270 Genevestigator:Q96270 Uniprot:Q96270
Leaf	Isotig01767	14	0	5.336	1.79E-05	TAIR|locus:2035109 - symbol:LEA7 "AT1G52690" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0009793 "embryo development ending in seed dormancy" evidence=ISS] EMBL:CP002684 EMBL:AC008016 EMBL:AF385732 EMBL:AY093968 EMBL:AY087466 EMBL:BT000737 EMBL:BT000739 EMBL:X91919 IPI:IPI00526817 PIR:H96567 RefSeq:NP_175678.1 RefSeq:NP_974009.1 UniGene:At.21275 STRING:Q96270 PRIDE:Q96270 ProMEX:Q96270 DNASU:841701 EnsemblPlants:AT1G52690.1 EnsemblPlants:AT1G52690.2 GeneID:841701 KEGG:ath:AT1G52690 TAIR:At1g52690 InParanoid:Q96270 OMA:MASHQEQ PhylomeDB:Q96270 ProtClustDB:CLSN2679745 ArrayExpress:Q96270 Genevestigator:Q96270 Uniprot:Q96270

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig01812	8	45	-1.963	2.38E-05	TAIR|locus:2078391 - symbol:AT3G56290 "AT3G56290" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0009658 "chloroplast organization" evidence=IMP] [GO:0045893 "positive regulation of transcription, DNA-dependent" evidence=IMP] EMBL:CP002686 GenomeReviews:BA000014_GR EMBL:AL163763 EMBL:AY062503 EMBL:AY081675 EMBL:AK228043 IPI:IPI00528653 PIR:T47746 RefSeq:NP_191188.1 UniGene:At.27406 IntAct:Q9LYL4 STRING:Q9LYL4 PRIDE:Q9LYL4 EnsemblPlants:AT3G56290.1 GeneID:824796 KEGG:ath:AT3G56290 TAIR:At3g56290 eggNOG:NOG243520 HOGENOM:HBG318089 InParanoid:Q9LYL4 OMA:KLGRYAH PhylomeDB:Q9LYL4 ProtClustDB:CLSN2684171 ArrayExpress:Q9LYL4 Genevestigator:Q9LYL4 Uniprot:Q9LYL4
Leaf	Isotig01813	8	46	-1.995	1.58E-05	TAIR|locus:2078391 - symbol:AT3G56290 "AT3G56290" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0009658 "chloroplast organization" evidence=IMP] [GO:0045893 "positive regulation of transcription, DNA-dependent" evidence=IMP] EMBL:CP002686 GenomeReviews:BA000014_GR EMBL:AL163763 EMBL:AY062503 EMBL:AY081675 EMBL:AK228043 IPI:IPI00528653 PIR:T47746 RefSeq:NP_191188.1 UniGene:At.27406 IntAct:Q9LYL4 STRING:Q9LYL4 PRIDE:Q9LYL4 EnsemblPlants:AT3G56290.1 GeneID:824796 KEGG:ath:AT3G56290 TAIR:At3g56290 eggNOG:NOG243520 HOGENOM:HBG318089 InParanoid:Q9LYL4 OMA:KLGRYAH PhylomeDB:Q9LYL4 ProtClustDB:CLSN2684171 ArrayExpress:Q9LYL4 Genevestigator:Q9LYL4 Uniprot:Q9LYL4
Leaf	Isotig01814	8	45	-1.963	2.38E-05	TAIR|locus:2078391 - symbol:AT3G56290 "AT3G56290" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0009658 "chloroplast organization" evidence=IMP] [GO:0045893 "positive regulation of transcription, DNA-dependent" evidence=IMP] EMBL:CP002686 GenomeReviews:BA000014_GR EMBL:AL163763 EMBL:AY062503 EMBL:AY081675 EMBL:AK228043 IPI:IPI00528653 PIR:T47746 RefSeq:NP_191188.1 UniGene:At.27406 IntAct:Q9LYL4 STRING:Q9LYL4 PRIDE:Q9LYL4 EnsemblPlants:AT3G56290.1 GeneID:824796 KEGG:ath:AT3G56290 TAIR:At3g56290 eggNOG:NOG243520 HOGENOM:HBG318089 InParanoid:Q9LYL4 OMA:KLGRYAH PhylomeDB:Q9LYL4 ProtClustDB:CLSN2684171 ArrayExpress:Q9LYL4 Genevestigator:Q9LYL4 Uniprot:Q9LYL4
Leaf	Isotig01815	8	46	-1.995	1.58E-05	TAIR|locus:2078391 - symbol:AT3G56290 "AT3G56290" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0009658 "chloroplast organization" evidence=IMP] [GO:0045893 "positive regulation of transcription, DNA-dependent" evidence=IMP] EMBL:CP002686 GenomeReviews:BA000014_GR EMBL:AL163763 EMBL:AY062503 EMBL:AY081675 EMBL:AK228043 IPI:IPI00528653 PIR:T47746 RefSeq:NP_191188.1 UniGene:At.27406 IntAct:Q9LYL4 STRING:Q9LYL4 PRIDE:Q9LYL4 EnsemblPlants:AT3G56290.1 GeneID:824796 KEGG:ath:AT3G56290 TAIR:At3g56290 eggNOG:NOG243520 HOGENOM:HBG318089 InParanoid:Q9LYL4 OMA:KLGRYAH PhylomeDB:Q9LYL4 ProtClustDB:CLSN2684171 ArrayExpress:Q9LYL4 Genevestigator:Q9LYL4 Uniprot:Q9LYL4
Leaf	Isotig01816	9	0	4.699	0.000718283	TAIR|locus:2040914 - symbol:AT2G34480 species:3702 "Arabidopsis thaliana" [GO:0003735 "structural constituent of ribosome" evidence=IEA;ISS] [GO:0005840 "ribosome" evidence=ISS] [GO:0006412 "translation" evidence=IEA;ISS] [GO:0042254 "ribosome biogenesis" evidence=ISS] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0022625 "cytosolic large ribosomal subunit" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR021138 InterPro:IPR023573 Pfam:PF01775 PIRSF:PIRSF002190 GO:GO:0005886 GO:GO:0005774 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0006412 GO:GO:0003735 EMBL:AC004077 EMBL:AC004481 GO:GO:0022625 eggNOG:COG2157 PANTHER:PTHR10052 EMBL:AY042803 EMBL:AY120778 EMBL:BT000076 EMBL:BT006559 EMBL:Z18039 IPI:IPI00548475 PIR:T02335 RefSeq:NP_180995.1 UniGene:At.23545 ProteinModelPortal:P51418 SMR:P51418 IntAct:P51418 STRING:P51418 PRIDE:P51418 EnsemblPlants:AT2G34480.1 GeneID:818011 KEGG:ath:AT2G34480 TAIR:At2g34480 HOGENOM:HBG319315 InParanoid:P51418 KO:K02882 OMA:KSRYWYF PhylomeDB:P51418 ProtClustDB:CLSN2683643 ArrayExpress:P51418 Genevestigator:P51418 GermOnline:AT2G34480 Uniprot:P51418
Leaf	Isotig01817	9	0	4.699	0.000718283	TAIR|locus:2040914 - symbol:AT2G34480 species:3702 "Arabidopsis thaliana" [GO:0003735 "structural constituent of ribosome" evidence=IEA;ISS] [GO:0005840 "ribosome" evidence=ISS] [GO:0006412 "translation" evidence=IEA;ISS] [GO:0042254 "ribosome biogenesis" evidence=ISS] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0022625 "cytosolic large ribosomal subunit" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR021138 InterPro:IPR023573 Pfam:PF01775 PIRSF:PIRSF002190 GO:GO:0005886

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0005774 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0006412 GO:GO:0003735 EMBL:AC004077 EMBL:AC004481 GO:GO:0022625 eggNOG:COG2157 PANTHER:PTHR10052 EMBL:AY042803 EMBL:AY120778 EMBL:BT000076 EMBL:BT006559 EMBL:Z18039 IPI:IPI00548475 PIR:T02335 RefSeq:NP_180995.1 UniGene:At.23545 ProteinModelPortal:P51418 SMR:P51418 IntAct:P51418 STRING:P51418 PRIDE:P51418 EnsemblPlants:AT2G34480.1 GeneID:818011 KEGG:ath:AT2G34480 TAIR:At2g34480 HOGENOM:HBG319315 InParanoid:P51418 KO:K02882 OMA:KSRYWYF PhylomeDB:P51418 ProtClustDB:CLSN2683643 ArrayExpress:P51418 Genevestigator:P51418 GermOnline:AT2G34480 Uniprot:P51418
Leaf	Isotig01818	9	0	4.699	0.000718283	TAIR|locus:2040914 - symbol:AT2G34480 species:3702 "Arabidopsis thaliana" [GO:0003735 "structural constituent of ribosome" evidence=IEA;ISS] [GO:0005840 "ribosome" evidence=ISS] [GO:0006412 "translation" evidence=IEA;ISS] [GO:0042254 "ribosome biogenesis" evidence=ISS] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0022625 "cytosolic large ribosomal subunit" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR021138 InterPro:IPR023573 Pfam:PF01775 PIRSF:PIRSF002190 GO:GO:0005886 GO:GO:0005774 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0006412 GO:GO:0003735 EMBL:AC004077 EMBL:AC004481 GO:GO:0022625 eggNOG:COG2157 PANTHER:PTHR10052 EMBL:AY042803 EMBL:AY120778 EMBL:BT000076 EMBL:BT006559 EMBL:Z18039 IPI:IPI00548475 PIR:T02335 RefSeq:NP_180995.1 UniGene:At.23545 ProteinModelPortal:P51418 SMR:P51418 IntAct:P51418 STRING:P51418 PRIDE:P51418 EnsemblPlants:AT2G34480.1 GeneID:818011 KEGG:ath:AT2G34480 TAIR:At2g34480 HOGENOM:HBG319315 InParanoid:P51418 KO:K02882 OMA:KSRYWYF PhylomeDB:P51418 ProtClustDB:CLSN2683643 ArrayExpress:P51418 Genevestigator:P51418 GermOnline:AT2G34480 Uniprot:P51418
Leaf	Isotig01819	9	0	4.699	0.000718283	TAIR|locus:2040914 - symbol:AT2G34480 species:3702 "Arabidopsis thaliana" [GO:0003735 "structural constituent of ribosome" evidence=IEA;ISS] [GO:0005840 "ribosome" evidence=ISS] [GO:0006412 "translation" evidence=IEA;ISS] [GO:0042254 "ribosome biogenesis" evidence=ISS] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0022625 "cytosolic large ribosomal subunit" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR021138 InterPro:IPR023573 Pfam:PF01775 PIRSF:PIRSF002190 GO:GO:0005886 GO:GO:0005774 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0006412 GO:GO:0003735 EMBL:AC004077 EMBL:AC004481 GO:GO:0022625 eggNOG:COG2157 PANTHER:PTHR10052 EMBL:AY042803 EMBL:AY120778 EMBL:BT000076 EMBL:BT006559 EMBL:Z18039 IPI:IPI00548475 PIR:T02335 RefSeq:NP_180995.1 UniGene:At.23545 ProteinModelPortal:P51418 SMR:P51418 IntAct:P51418 STRING:P51418 PRIDE:P51418 EnsemblPlants:AT2G34480.1 GeneID:818011 KEGG:ath:AT2G34480 TAIR:At2g34480 HOGENOM:HBG319315 InParanoid:P51418 KO:K02882 OMA:KSRYWYF PhylomeDB:P51418 ProtClustDB:CLSN2683643 ArrayExpress:P51418 Genevestigator:P51418 GermOnline:AT2G34480 Uniprot:P51418
Leaf	Isotig01864	59	15	2.505	1.45E-11	TAIR|locus:2074733 - symbol:AT3G11130 "AT3G11130" species:3702 "Arabidopsis thaliana" [GO:0005198 "structural molecule activity" evidence=ISS] [GO:0005773 "vacuole" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0006897 "endocytosis" evidence=IMP] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR000547 InterPro:IPR001473 InterPro:IPR011990 InterPro:IPR015348 InterPro:IPR016024 InterPro:IPR016025 Pfam:PF00637 Pfam:PF09268 SMART:SM00299 GO:GO:0009506 GO:GO:0005774 EMBL:CP002686 GO:GO:0006886 GO:GO:0005515 SUPFAM:SSF48371 GO:GO:0005198 GO:GO:0006897 Gene3D:G3DSA:1.25.40.10 EMBL:AC009991 EMBL:AC073395 GO:GO:0030130 GO:GO:0030132 EMBL:AK229443 EMBL:AK229949 IPI:IPI00527690 RefSeq:NP_187724.2 UniGene:At.17332 UniGene:At.26828 HSSP:P11442 ProteinModelPortal:Q0WNJ6 SMR:Q0WNJ6 IntAct:Q0WNJ6 STRING:Q0WNJ6 PRIDE:Q9SRM1 EnsemblPlants:AT3G11130.1 GeneID:820284 KEGG:ath:AT3G11130 TAIR:At3g11130 eggNOG:NOG314149 InParanoid:Q0WNJ6 KO:K04646 OMA:QPPVYGF PhylomeDB:Q0WNJ6 ProtClustDB:CLSN2690853 Genevestigator:Q0WNJ6 InterPro:IPR022365 InterPro:IPR016341 Gene3D:G3DSA:2.130.10.110 Pfam:PF01394 PIRSF:PIRSF002290 SUPFAM:SSF50989 Uniprot:Q0WNJ6

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig01865	54	15	2.377	3.67E-10	TAIR|locus:2074733 - symbol:AT3G11130 "AT3G11130" species:3702 "Arabidopsis thaliana" [GO:0005198 "structural molecule activity" evidence=ISS] [GO:0005773 "vacuole" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0006897 "endocytosis" evidence=IMP] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR000547 InterPro:IPR001473 InterPro:IPR011990 InterPro:IPR015348 InterPro:IPR016024 InterPro:IPR016025 Pfam:PF00637 Pfam:PF09268 SMART:SM00299 GO:GO:0009506 GO:GO:0005774 EMBL:CP002686 GO:GO:0006886 GO:GO:0005515 SUPFAM:SSF48371 GO:GO:0005198 GO:GO:0006897 Gene3D:G3DSA:1.25.40.10 EMBL:AC009991 EMBL:AC073395 GO:GO:0030130 GO:GO:0030132 EMBL:AK229443 EMBL:AK229949 IPI:IPI00527690 RefSeq:NP_187724.2 UniGene:At.17332 UniGene:At.26828 HSSP:P11442 ProteinModelPortal:Q0WNJ6 SMR:Q0WNJ6 IntAct:Q0WNJ6 STRING:Q0WNJ6 PRIDE:Q9SRM1 EnsemblPlants:AT3G11130.1 GeneID:820284 KEGG:ath:AT3G11130 TAIR:At3g11130 eggNOG:NOG314149 InParanoid:Q0WNJ6 KO:K04646 OMA:QPPVYGF PhylomeDB:Q0WNJ6 ProtClustDB:CLSN2690853 Genevestigator:Q0WNJ6 InterPro:IPR022365 InterPro:IPR016341 Gene3D:G3DSA:2.130.10.110 Pfam:PF01394 PIRSF:PIRSF002290 SUPFAM:SSF50989 Uniprot:Q0WNJ6
Leaf	Isotig01867	65	42	1.159	3.46E-05	TAIR|locus:2157383 - symbol:CLPC1 "AT5G50920" species:3702 "Arabidopsis thaliana" [GO:0005524 "ATP binding" evidence=ISS] [GO:0016887 "ATPase activity" evidence=ISS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009532 "plastid stroma" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009658 "chloroplast organization" evidence=IMP] [GO:0031897 "Tic complex" evidence=TAS] [GO:0045037 "protein import into chloroplast stroma" evidence=IMP] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0010380 "regulation of chlorophyll biosynthetic process" evidence=IMP] [GO:0045036 "protein targeting to chloroplast" evidence=IMP] [GO:0005829 "cytosol" evidence=RCA] [GO:0004176 "ATP-dependent peptidase activity" evidence=IDA] InterPro:IPR001270 InterPro:IPR001943 InterPro:IPR003593 InterPro:IPR003959 InterPro:IPR004176 InterPro:IPR013093 InterPro:IPR018368 Pfam:PF00004 Pfam:PF02151 Pfam:PF02861 Pfam:PF07724 PRINTS:PR00300 PROSITE:PS00870 PROSITE:PS00871 PROSITE:PS50151 SMART:SM00382 GO:GO:0005739 GO:GO:0005524 GO:GO:0009570 EMBL:CP002688 GO:GO:0005618 GO:GO:0003677 GO:GO:0009658 GO:GO:0010380 GO:GO:0009535 GO:GO:0004518 GO:GO:0006289 EMBL:AB017063 eggNOG:COG0542 GO:GO:0019538 InterPro:IPR023150 Gene3D:G3DSA:1.10.1780.10 GO:GO:0004176 InterPro:IPR019489 Pfam:PF10431 SMART:SM01086 HSSP:P03815 EMBL:AF022909 EMBL:AY102125 EMBL:AK227173 IPI:IPI00535976 PIR:T52292 RefSeq:NP_568746.1 UniGene:At.24774 UniGene:At.74761 UniGene:At.74764 UniGene:At.75059 ProteinModelPortal:Q9FI56 SMR:Q9FI56 IntAct:Q9FI56 STRING:Q9FI56 PRIDE:O48931 EnsemblPlants:AT5G50920.1 GeneID:835165 KEGG:ath:AT5G50920 GeneFarm:797 TAIR:At5g50920 InParanoid:Q9FI56 KO:K03696 OMA:FHQLTRD PhylomeDB:Q9FI56 ProtClustDB:CLSN2689981 Genevestigator:Q9FI56 GO:GO:0031897 GO:GO:0045037 Uniprot:Q9FI56
Leaf	Isotig01868	49	25	1.500	1.16E-05	TAIR|locus:2157383 - symbol:CLPC1 "AT5G50920" species:3702 "Arabidopsis thaliana" [GO:0005524 "ATP binding" evidence=ISS] [GO:0016887 "ATPase activity" evidence=ISS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009532 "plastid stroma" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009658 "chloroplast organization" evidence=IMP] [GO:0031897 "Tic complex" evidence=TAS] [GO:0045037 "protein import into chloroplast stroma" evidence=IMP] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0010380 "regulation of chlorophyll biosynthetic process" evidence=IMP] [GO:0045036 "protein targeting to chloroplast" evidence=IMP] [GO:0005829 "cytosol" evidence=RCA] [GO:0004176 "ATP-dependent peptidase activity" evidence=IDA] InterPro:IPR001270 InterPro:IPR001943 InterPro:IPR003593 InterPro:IPR003959 InterPro:IPR004176 InterPro:IPR013093 InterPro:IPR018368 Pfam:PF00004 Pfam:PF02151 Pfam:PF02861 Pfam:PF07724 PRINTS:PR00300 PROSITE:PS00870 PROSITE:PS00871 PROSITE:PS50151 SMART:SM00382 GO:GO:0005739 GO:GO:0005524 GO:GO:0009570 EMBL:CP002688 GO:GO:0005618 GO:GO:0003677 GO:GO:0009658 GO:GO:0010380 GO:GO:0009535 GO:GO:0004518 GO:GO:0006289 EMBL:AB017063 eggNOG:COG0542 GO:GO:0019538 InterPro:IPR023150 Gene3D:G3DSA:1.10.1780.10 GO:GO:0004176 InterPro:IPR019489 Pfam:PF10431 SMART:SM01086 HSSP:P03815 EMBL:AF022909 EMBL:AY102125 EMBL:AK227173 IPI:IPI00535976 PIR:T52292 RefSeq:NP_568746.1 UniGene:At.24774 UniGene:At.74761 UniGene:At.74764 UniGene:At.75059 ProteinModelPortal:Q9FI56 SMR:Q9FI56 IntAct:Q9FI56 STRING:Q9FI56 PRIDE:O48931 EnsemblPlants:AT5G50920.1 GeneID:835165 KEGG:ath:AT5G50920

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GeneFarm:797 TAIR:At5g50920 InParanoid:Q9FI56 KO:K03696 OMA:FHQLTRD PhylomeDB:Q9FI56 ProtClustDB:CLSN2689981 Genevestigator:Q9FI56 GO:GO:0031897 GO:GO:0045037 Uniprot:Q9FI56
Leaf	Isotig01879	292	0	9.719	1.37E-62	TAIR|locus:2063907 - symbol:P5CS1 "AT2G39800" species:3702 "Arabidopsis thaliana" [GO:0006561 "proline biosynthetic process" evidence=IMP;TAS] [GO:0009414 "response to water deprivation" evidence=IGI;IEP] [GO:0017084 "delta1-pyrroline-5-carboxylate synthetase activity" evidence=ISS] [GO:0016020 "membrane" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0006979 "response to oxidative stress" evidence=IMP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0042538 "hyperosmotic salinity response" evidence=IEP;IMP] [GO:0048364 "root development" evidence=IMP] [GO:0009269 "response to desiccation" evidence=IEP] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] InterPro:IPR000965 InterPro:IPR001048 InterPro:IPR001057 InterPro:IPR005715 InterPro:IPR005766 InterPro:IPR015590 InterPro:IPR016161 InterPro:IPR016162 InterPro:IPR016163 InterPro:IPR019797 InterPro:IPR020593 Pfam:PF00171 Pfam:PF00696 PIRSF:PIRSF036429 PRINTS:PR00474 PROSITE:PS00902 PROSITE:PS01223 GO:GO:0005524 GO:GO:0009507 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0006979 GO:GO:0016020 Gene3D:G3DSA:3.40.309.10 Gene3D:G3DSA:3.40.605.10 SUPFAM:SSF53720 GO:GO:0009414 GO:GO:0048364 GO:GO:0006561 Gene3D:G3DSA:3.40.1160.10 SUPFAM:SSF53633 GO:GO:0042538 GO:GO:0004349 EMBL:AC003000 EMBL:X89414 EMBL:X86777 EMBL:X87330 EMBL:D32138 EMBL:AF424633 EMBL:AY113046 EMBL:AY150430 IPI:IPI00529620 PIR:S66637 PIR:T50685 RefSeq:NP_001189714.1 RefSeq:NP_181510.1 UniGene:At.20482 ProteinModelPortal:P54887 SMR:P54887 IntAct:P54887 STRING:P54887 PRIDE:P54887 EnsemblPlants:AT2G39800.1 EnsemblPlants:AT2G39800.4 GeneID:818566 KEGG:ath:AT2G39800 TAIR:At2g39800 eggNOG:COG0014 HOGENOM:HBG318080 InParanoid:P54887 KO:K12657 OMA:FEARPDC PhylomeDB:P54887 ProtClustDB:PLN02418 Genevestigator:P54887 GermOnline:AT2G39800 GO:GO:0004350 TIGRFAMs:TIGR01092 TIGRFAMs:TIGR00407 TIGRFAMs:TIGR01027 Uniprot:P54887
Leaf	Isotig01880	263	0	9.568	1.02E-57	TAIR|locus:2063907 - symbol:P5CS1 "AT2G39800" species:3702 "Arabidopsis thaliana" [GO:0006561 "proline biosynthetic process" evidence=IMP;TAS] [GO:0009414 "response to water deprivation" evidence=IGI;IEP] [GO:0017084 "delta1-pyrroline-5-carboxylate synthetase activity" evidence=ISS] [GO:0016020 "membrane" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0006979 "response to oxidative stress" evidence=IMP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0042538 "hyperosmotic salinity response" evidence=IEP;IMP] [GO:0048364 "root development" evidence=IMP] [GO:0009269 "response to desiccation" evidence=IEP] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] InterPro:IPR000965 InterPro:IPR001048 InterPro:IPR001057 InterPro:IPR005715 InterPro:IPR005766 InterPro:IPR015590 InterPro:IPR016161 InterPro:IPR016162 InterPro:IPR016163 InterPro:IPR019797 InterPro:IPR020593 Pfam:PF00171 Pfam:PF00696 PIRSF:PIRSF036429 PRINTS:PR00474 PROSITE:PS00902 PROSITE:PS01223 GO:GO:0005524 GO:GO:0009507 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0006979 GO:GO:0016020 Gene3D:G3DSA:3.40.309.10 Gene3D:G3DSA:3.40.605.10 SUPFAM:SSF53720 GO:GO:0009414 GO:GO:0048364 GO:GO:0006561 Gene3D:G3DSA:3.40.1160.10 SUPFAM:SSF53633 GO:GO:0042538 GO:GO:0004349 EMBL:AC003000 EMBL:X89414 EMBL:X86777 EMBL:X87330 EMBL:D32138 EMBL:AF424633 EMBL:AY113046 EMBL:AY150430 IPI:IPI00529620 PIR:S66637 PIR:T50685 RefSeq:NP_001189714.1 RefSeq:NP_181510.1 UniGene:At.20482 ProteinModelPortal:P54887 SMR:P54887 IntAct:P54887 STRING:P54887 PRIDE:P54887 EnsemblPlants:AT2G39800.1 EnsemblPlants:AT2G39800.4 GeneID:818566 KEGG:ath:AT2G39800 TAIR:At2g39800 eggNOG:COG0014 HOGENOM:HBG318080 InParanoid:P54887 KO:K12657 OMA:FEARPDC PhylomeDB:P54887 ProtClustDB:PLN02418 Genevestigator:P54887 GermOnline:AT2G39800 GO:GO:0004350 TIGRFAMs:TIGR01092 TIGRFAMs:TIGR00407 TIGRFAMs:TIGR01027 Uniprot:P54887
Leaf	Isotig01881	230	0	9.374	5.35E-52	TAIR|locus:2063907 - symbol:P5CS1 "AT2G39800" species:3702 "Arabidopsis thaliana" [GO:0006561 "proline biosynthetic process" evidence=IMP;TAS] [GO:0009414 "response to water deprivation" evidence=IGI;IEP] [GO:0017084 "delta1-pyrroline-5-carboxylate synthetase activity" evidence=ISS] [GO:0016020 "membrane" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0006979 "response to oxidative stress" evidence=IMP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0042538 "hyperosmotic salinity response" evidence=IEP;IMP] [GO:0048364 "root development" evidence=IMP] [GO:0009269 "response to desiccation" evidence=IEP] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] InterPro:IPR000965 InterPro:IPR001048 InterPro:IPR001057 InterPro:IPR005715

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						InterPro:IPR005766 InterPro:IPR015590 InterPro:IPR016161 InterPro:IPR016162 InterPro:IPR016163 InterPro:IPR019797 InterPro:IPR020593 Pfam:PF00171 Pfam:PF00696 PIRSF:PIRSF036429 PRINTS:PR00474 PROSITE:PS00902 PROSITE:PS01223 GO:GO:0005524 GO:GO:0009507 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0006979 GO:GO:0016020 Gene3D:G3DSA:3.40.309.10 Gene3D:G3DSA:3.40.605.10 SUPFAM:SSF53720 GO:GO:0009414 GO:GO:0048364 GO:GO:0006561 Gene3D:G3DSA:3.40.1160.10 SUPFAM:SSF53633 GO:GO:0042538 GO:GO:0004349 EMBL:AC003000 EMBL:X89414 EMBL:X86777 EMBL:X87330 EMBL:D32138 EMBL:AF424633 EMBL:AY113046 EMBL:AY150430 IPI:IPI00529620 PIR:S66637 PIR:T50685 RefSeq:NP_001189714.1 RefSeq:NP_181510.1 UniGene:At.20482 ProteinModelPortal:P54887 SMR:P54887 IntAct:P54887 STRING:P54887 PRIDE:P54887 EnsemblPlants:AT2G39800.1 EnsemblPlants:AT2G39800.4 GeneID:818566 KEGG:ath:AT2G39800 TAIR:At2g39800 eggNOG:COG0014 HOGENOM:HBG318080 InParanoid:P54887 KO:K12657 OMA:FEARPDC PhylomeDB:P54887 ProtClustDB:PLN02418 Genevestigator:P54887 GermOnline:AT2G39800 GO:GO:0004350 TIGRFAMs:TIGR01092 TIGRFAMs:TIGR00407 TIGRFAMs:TIGR01027 Uniprot:P54887
Leaf	Isotig01882	210	65	2.221	1.77E-32	TAIR|locus:2170318 - symbol:ATMS1 "AT5G17920" species:3702 "Arabidopsis thaliana" [GO:0003871 "5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase activity" evidence=ISS] [GO:0005829 "cytosol" evidence=ISS;IDA] [GO:0009086 "methionine biosynthetic process" evidence=ISS] [GO:0008705 "methionine synthase activity" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0005777 "peroxisome" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0010043 "response to zinc ion" evidence=IEP] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR002629 InterPro:IPR006276 InterPro:IPR013215 Pfam:PF01717 Pfam:PF08267 PIRSF:PIRSF000382 GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 GO:GO:0048046 GO:GO:0009570 GO:GO:0046686 GO:GO:0005774 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005777 GO:GO:0010043 GO:GO:0008270 GO:GO:0005507 GO:GO:0009651 EMBL:AB011480 UniGene:At.24550 EMBL:U97200 EMBL:AF370522 EMBL:AY048201 EMBL:AY056098 EMBL:AY057499 EMBL:AY069876 EMBL:AY070771 EMBL:AY091692 IPI:IPI00522440 RefSeq:NP_001078599.1 RefSeq:NP_197294.1 UniGene:At.22340 UniGene:At.71028 PDB:1U1H PDB:1U1J PDB:1U1U PDB:1U22 PDBsum:1U1H PDBsum:1U1J PDBsum:1U1U PDBsum:1U22 ProteinModelPortal:O50008 SMR:O50008 IntAct:O50008 STRING:O50008 SWISS-2DPAGE:O50008 PRIDE:O50008 ProMEX:O50008 EnsemblPlants:AT5G17920.1 EnsemblPlants:AT5G17920.2 GeneID:831660 KEGG:ath:AT5G17920 TAIR:At5g17920 eggNOG:COG0620 HOGENOM:HBG287495 InParanoid:O50008 KO:K00549 OMA:NIWANDF PhylomeDB:O50008 ProtClustDB:PLN02475 BRENDA:2.1.1.14 Genevestigator:O50008 GermOnline:AT5G17920 GO:GO:0003871 GO:GO:0008705 TIGRFAMs:TIGR01371 Uniprot:O50008
Leaf	Isotig01883	188	59	2.201	6.03E-29	TAIR|locus:2170318 - symbol:ATMS1 "AT5G17920" species:3702 "Arabidopsis thaliana" [GO:0003871 "5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase activity" evidence=ISS] [GO:0005829 "cytosol" evidence=ISS;IDA] [GO:0009086 "methionine biosynthetic process" evidence=ISS] [GO:0008705 "methionine synthase activity" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0005777 "peroxisome" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0010043 "response to zinc ion" evidence=IEP] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR002629 InterPro:IPR006276 InterPro:IPR013215 Pfam:PF01717 Pfam:PF08267 PIRSF:PIRSF000382 GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 GO:GO:0048046 GO:GO:0009570 GO:GO:0046686 GO:GO:0005774 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005777 GO:GO:0010043 GO:GO:0008270 GO:GO:0005507 GO:GO:0009651 EMBL:AB011480 UniGene:At.24550 EMBL:U97200 EMBL:AF370522 EMBL:AY048201 EMBL:AY056098 EMBL:AY057499 EMBL:AY069876 EMBL:AY070771 EMBL:AY091692 IPI:IPI00522440 RefSeq:NP_001078599.1 RefSeq:NP_197294.1 UniGene:At.22340 UniGene:At.71028 PDB:1U1H PDB:1U1J PDB:1U1U PDB:1U22 PDBsum:1U1H PDBsum:1U1J PDBsum:1U1U PDBsum:1U22 ProteinModelPortal:O50008 SMR:O50008 IntAct:O50008 STRING:O50008 SWISS-2DPAGE:O50008 PRIDE:O50008 ProMEX:O50008 EnsemblPlants:AT5G17920.1 EnsemblPlants:AT5G17920.2

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GeneID:831660 KEGG:ath:AT5G17920 TAIR:At5g17920 eggNOG:COG0620 HOGENOM:HBG287495 InParanoid:O50008 KO:K00549 OMA:NIWANDF PhylomeDB:O50008 ProtClustDB:PLN02475 BRENDA:2.1.1.14 Genevestigator:O50008 GermOnline:AT5G17920 GO:GO:0003871 GO:GO:0008705 TIGRFAMs:TIGR01371 Uniprot:O50008
Leaf	Isotig01884	168	40	2.599	2.79E-31	TAIR|locus:2170318 - symbol:ATMS1 "AT5G17920" species:3702 "Arabidopsis thaliana" [GO:0003871 "5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase activity" evidence=ISS] [GO:0005829 "cytosol" evidence=ISS;IDA] [GO:0009086 "methionine biosynthetic process" evidence=ISS] [GO:0008705 "methionine synthase activity" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0005777 "peroxisome" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0010043 "response to zinc ion" evidence=IEP] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR002629 InterPro:IPR006276 InterPro:IPR013215 Pfam:PF01717 Pfam:PF08267 PIRSF:PIRSF000382 GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 GO:GO:0048046 GO:GO:0009570 GO:GO:0046686 GO:GO:0005774 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005777 GO:GO:0010043 GO:GO:0008270 GO:GO:0005507 GO:GO:0009651 EMBL:AB011480 UniGene:At.24550 EMBL:U97200 EMBL:AF370522 EMBL:AY048201 EMBL:AY056098 EMBL:AY057499 EMBL:AY069876 EMBL:AY070771 EMBL:AY091692 IPI:IPI00522440 RefSeq:NP_001078599.1 RefSeq:NP_197294.1 UniGene:At.22340 UniGene:At.71028 PDB:1U1H PDB:1U1J PDB:1U1U PDB:1U22 PDBsum:1U1H PDBsum:1U1J PDBsum:1U1U PDBsum:1U22 ProteinModelPortal:O50008 SMR:O50008 IntAct:O50008 STRING:O50008 SWISS-2DPAGE:O50008 PRIDE:O50008 ProMEX:O50008 EnsemblPlants:AT5G17920.1 EnsemblPlants:AT5G17920.2 GeneID:831660 KEGG:ath:AT5G17920 TAIR:At5g17920 eggNOG:COG0620 HOGENOM:HBG287495 InParanoid:O50008 KO:K00549 OMA:NIWANDF PhylomeDB:O50008 ProtClustDB:PLN02475 BRENDA:2.1.1.14 Genevestigator:O50008 GermOnline:AT5G17920 GO:GO:0003871 GO:GO:0008705 TIGRFAMs:TIGR01371 Uniprot:O50008
Leaf	Isotig01894	86	12	3.370	3.67E-21	TAIR|locus:2089270 - symbol:NiaP "AT3G13050" species:3702 "Arabidopsis thaliana" [GO:0005351 "sugar:hydrogen symporter activity" evidence=ISS] [GO:0015144 "carbohydrate transmembrane transporter activity" evidence=ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:2001142 "nicotinate transport" evidence=IDA] [GO:2001143 "N-methylnicotinate transport" evidence=IDA] InterPro:IPR005828 InterPro:IPR005829 Pfam:PF00083 PROSITE:PS00216 PROSITE:PS00217 GO:GO:0016021 GO:GO:0005886 GO:GO:0005524 EMBL:CP002686 GenomeReviews:BA000014_GR eggNOG:COG0477 InterPro:IPR016196 SUPFAM:SSF103473 InterPro:IPR020846 PROSITE:PS50850 GO:GO:0022857 EMBL:AB026645 HOGENOM:HBG715489 EMBL:AY054262 EMBL:BT004522 IPI:IPI00523791 IPI:IPI00546036 RefSeq:NP_187911.1 UniGene:At.26387 ProteinModelPortal:Q940M4 STRING:Q940M4 PRIDE:Q940M4 EnsemblPlants:AT3G13050.1 GeneID:820491 KEGG:ath:AT3G13050 TAIR:At3g13050 InParanoid:Q940M4 OMA:GRICISA PhylomeDB:Q940M4 ProtClustDB:CLSN2684648 Genevestigator:Q940M4 GO:GO:2001143 GO:GO:2001142 Uniprot:Q940M4
Leaf	Isotig01895	79	6	4.248	1.17E-22	TAIR|locus:2089270 - symbol:NiaP "AT3G13050" species:3702 "Arabidopsis thaliana" [GO:0005351 "sugar:hydrogen symporter activity" evidence=ISS] [GO:0015144 "carbohydrate transmembrane transporter activity" evidence=ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:2001142 "nicotinate transport" evidence=IDA] [GO:2001143 "N-methylnicotinate transport" evidence=IDA] InterPro:IPR005828 InterPro:IPR005829 Pfam:PF00083 PROSITE:PS00216 PROSITE:PS00217 GO:GO:0016021 GO:GO:0005886 GO:GO:0005524 EMBL:CP002686 GenomeReviews:BA000014_GR eggNOG:COG0477 InterPro:IPR016196 SUPFAM:SSF103473 InterPro:IPR020846 PROSITE:PS50850 GO:GO:0022857 EMBL:AB026645 HOGENOM:HBG715489 EMBL:AY054262 EMBL:BT004522 IPI:IPI00523791 IPI:IPI00546036 RefSeq:NP_187911.1 UniGene:At.26387 ProteinModelPortal:Q940M4 STRING:Q940M4 PRIDE:Q940M4 EnsemblPlants:AT3G13050.1 GeneID:820491 KEGG:ath:AT3G13050 TAIR:At3g13050 InParanoid:Q940M4 OMA:GRICISA PhylomeDB:Q940M4 ProtClustDB:CLSN2684648 Genevestigator:Q940M4 GO:GO:2001143 GO:GO:2001142 Uniprot:Q940M4
Leaf	Isotig01896	76	12	3.192	4.33E-18	TAIR|locus:2089270 - symbol:NiaP "AT3G13050" species:3702 "Arabidopsis thaliana" [GO:0005351 "sugar:hydrogen symporter activity" evidence=ISS] [GO:0015144 "carbohydrate transmembrane transporter activity"

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						evidence=ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:2001142 "nicotinate transport" evidence=IDA] [GO:2001143 "N-methylnicotinate transport" evidence=IDA] InterPro:IPR005828 InterPro:IPR005829 Pfam:PF00083 PROSITE:PS00216 PROSITE:PS00217 GO:GO:0016021 GO:GO:0005886 GO:GO:0005524 EMBL:CP002686 GenomeReviews:BA000014_GR eggNOG:COG0477 InterPro:IPR016196 SUPFAM:SSF103473 InterPro:IPR020846 PROSITE:PS50850 GO:GO:0022857 EMBL:AB026645 HOGENOM:HBG715489 EMBL:AY054262 EMBL:BT004522 IPI:IPI00523791 IPI:IPI00546036 RefSeq:NP_187911.1 UniGene:At.26387 ProteinModelPortal:Q940M4 STRING:Q940M4 PRIDE:Q940M4 EnsemblPlants:AT3G13050.1 GeneID:820491 KEGG:ath:AT3G13050 TAIR:At3g13050 InParanoid:Q940M4 OMA:GRICISA PhylomeDB:Q940M4 ProtClustDB:CLSN2684648 Genevestigator:Q940M4 GO:GO:2001143 GO:GO:2001142 Uniprot:Q940M4
Leaf	Isotig01897	9	44	-1.761	0.000103717	TAIR|locus:2127088 - symbol:ULP1B "UB-like protease 1B" species:3702 "Arabidopsis thaliana" [GO:0006508 "proteolysis" evidence=IEA;ISS] [GO:0008234 "cysteine-type peptidase activity" evidence=IEA;ISS] [GO:0009507 "chloroplast" evidence=IDA] InterPro:IPR003653 Pfam:PF02902 PROSITE:PS50600 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0009507 GO:GO:0006508 EMBL:AF058919 EMBL:AL161472 GO:GO:0008234 HSSP:Q02724 eggNOG:COG5160 IPI:IPI00519156 PIR:T01233 RefSeq:NP_191978.3 UniGene:At.50688 ProteinModelPortal:O65278 MEROPS:C48.A01 GeneID:828036 KEGG:ath:AT4G00690 TAIR:At4g00690 HOGENOM:HBG714709 InParanoid:O65278 PhylomeDB:O65278 ArrayExpress:O65278 Genevestigator:O65278 Uniprot:O65278
Leaf	Isotig01900	63	11	3.047	1.10E-14	TAIR|locus:2092815 - symbol:ECT2 "AT3G13460" species:3702 "Arabidopsis thaliana" [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0005829 "cytosol" evidence=IDA] GO:GO:0005829 GO:GO:0005634 EMBL:CP002686 GO:GO:0005515 EMBL:AP000603 InterPro:IPR007275 Pfam:PF04146 PROSITE:PS50882 EMBL:AY123992 IPI:IPI00538679 RefSeq:NP_187955.2 UniGene:At.23650 UniGene:At.67751 ProteinModelPortal:Q9LJE5 SMR:Q9LJE5 STRING:Q9LJE5 PRIDE:Q9LJE5 ProMEX:Q9LJE5 EnsemblPlants:AT3G13460.1 GeneID:820548 KEGG:ath:AT3G13460 TAIR:At3g13460 InParanoid:Q9LJE5 OMA:VVPDREQ PhylomeDB:Q9LJE5 ProtClustDB:CLSN2690909 Genevestigator:Q9LJE5 Uniprot:Q9LJE5
Leaf	Isotig01901	63	13	2.806	1.18E-13	TAIR|locus:2092815 - symbol:ECT2 "AT3G13460" species:3702 "Arabidopsis thaliana" [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0005829 "cytosol" evidence=IDA] GO:GO:0005829 GO:GO:0005634 EMBL:CP002686 GO:GO:0005515 EMBL:AP000603 InterPro:IPR007275 Pfam:PF04146 PROSITE:PS50882 EMBL:AY123992 IPI:IPI00538679 RefSeq:NP_187955.2 UniGene:At.23650 UniGene:At.67751 ProteinModelPortal:Q9LJE5 SMR:Q9LJE5 STRING:Q9LJE5 PRIDE:Q9LJE5 ProMEX:Q9LJE5 EnsemblPlants:AT3G13460.1 GeneID:820548 KEGG:ath:AT3G13460 TAIR:At3g13460 InParanoid:Q9LJE5 OMA:VVPDREQ PhylomeDB:Q9LJE5 ProtClustDB:CLSN2690909 Genevestigator:Q9LJE5 Uniprot:Q9LJE5
Leaf	Isotig01902	30	4	3.436	1.90E-08	TAIR|locus:2092815 - symbol:ECT2 "AT3G13460" species:3702 "Arabidopsis thaliana" [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0005829 "cytosol" evidence=IDA] GO:GO:0005829 GO:GO:0005634 EMBL:CP002686 GO:GO:0005515 EMBL:AP000603 InterPro:IPR007275 Pfam:PF04146 PROSITE:PS50882 EMBL:AY123992 IPI:IPI00538679 RefSeq:NP_187955.2 UniGene:At.23650 UniGene:At.67751 ProteinModelPortal:Q9LJE5 SMR:Q9LJE5 STRING:Q9LJE5 PRIDE:Q9LJE5 ProMEX:Q9LJE5 EnsemblPlants:AT3G13460.1 GeneID:820548 KEGG:ath:AT3G13460 TAIR:At3g13460 InParanoid:Q9LJE5 OMA:VVPDREQ PhylomeDB:Q9LJE5 ProtClustDB:CLSN2690909 Genevestigator:Q9LJE5 Uniprot:Q9LJE5
Leaf	Isotig01915	125	13	3.794	1.08E-32	TAIR|locus:2103488 - symbol:SIP2 "AT3G57520" species:3702 "Arabidopsis thaliana" [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=ISS] [GO:0006979 "response to oxidative stress" evidence=IEP] [GO:0080167 "response to karrikin" evidence=IEP] [GO:0034484 "raffinose catabolic process" evidence=IDA] [GO:0047274 "galactinol-sucrose galactosyltransferase activity" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR013785 GO:GO:0009506 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0006979 Gene3D:G3DSA:3.20.20.70 InterPro:IPR017853 SUPFAM:SSF51445 GO:GO:0080167 EMBL:AL133248 CAZy:GH36 eggNOG:NOG06986 InterPro:IPR008811 Pfam:PF05691 GO:GO:0034484 HOGENOM:HBG611539 KO:K06617 GO:GO:0047274 EMBL:AY050772 EMBL:AK226370 IPI:IPI00526258 IPI:IPI00541537 IPI:IPI00544535 PIR:T46188 RefSeq:NP_191311.1 RefSeq:NP_850715.1 UniGene:At.22207 UniGene:At.30900 ProteinModelPortal:Q94A08 STRING:Q94A08

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						PRIDE:Q94A08 EnsemblPlants:AT3G57520.1 GeneID:824919 KEGG:ath:AT3G57520 TAIR:At3g57520 InParanoid:Q9SCM1 OMA:QFMLLES PhylomeDB:Q94A08 ProtClustDB:PLN02219 BioCyc:MetaCyc:AT3G57520-MONOMER ArrayExpress:Q94A08 Uniprot:Q94A08
Leaf	Isotig01916	105	22	2.784	1.44E-21	TAIR|locus:2103488 - symbol:SIP2 "AT3G57520" species:3702 "Arabidopsis thaliana" [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=ISS] [GO:0006979 "response to oxidative stress" evidence=IEP] [GO:0080167 "response to karrikin" evidence=IEP] [GO:0034484 "raffinose catabolic process" evidence=IDA] [GO:0047274 "galactinol-sucrose galactosyltransferase activity" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR013785 GO:GO:0009506 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0006979 Gene3D:G3DSA:3.20.20.70 InterPro:IPR017853 SUPFAM:SSF51445 GO:GO:0080167 EMBL:AL133248 CAZy:GH36 eggNOG:NOG06986 InterPro:IPR008811 Pfam:PF05691 GO:GO:0034484 HOGENOM:HBG611539 KO:K06617 GO:GO:0047274 EMBL:AY050772 EMBL:AK226370 IPI:IPI00526258 IPI:IPI00541537 IPI:IPI00544535 PIR:T46188 RefSeq:NP_191311.1 RefSeq:NP_850715.1 UniGene:At.22207 UniGene:At.30900 ProteinModelPortal:Q94A08 STRING:Q94A08 PRIDE:Q94A08 EnsemblPlants:AT3G57520.1 GeneID:824919 KEGG:ath:AT3G57520 TAIR:At3g57520 InParanoid:Q9SCM1 OMA:QFMLLES PhylomeDB:Q94A08 ProtClustDB:PLN02219 BioCyc:MetaCyc:AT3G57520-MONOMER ArrayExpress:Q94A08 Uniprot:Q94A08
Leaf	Isotig01918	70	55	0.877	0.000639695	TAIR|locus:2181833 - symbol:HSC70-1 "heat shock cognate protein 70-1" species:3702 "Arabidopsis thaliana" [GO:0005524 "ATP binding" evidence=IEA] [GO:0005829 "cytosol" evidence=IDA;RCA;TAS] [GO:0006457 "protein folding" evidence=TAS] [GO:0009408 "response to heat" evidence=IEP;IMP] [GO:0005634 "nucleus" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005730 "nucleolus" evidence=IDA] [GO:0009615 "response to virus" evidence=IEP] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0042742 "defense response to bacterium" evidence=IMP] [GO:0050832 "defense response to fungus" evidence=IMP] [GO:0048046 "apoplast" evidence=IDA] [GO:0002020 "protease binding" evidence=IPI] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0010187 "negative regulation of seed germination" evidence=IMP] [GO:0090332 "stomatal closure" evidence=IMP] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR001023 PRINTS:PR00301 Pfam:PF00012 Prosite:PS00297 Prosite:PS00329 Prosite:PS01036 GO:GO:0005886 GO:GO:0009506 GO:GO:0005524 GO:GO:0048046 GO:GO:0046686 GO:GO:0005774 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005618 GO:GO:0009507 GO:GO:0042742 GO:GO:0005730 GO:GO:0050832 GO:GO:0002020 GO:GO:0009409 GO:GO:0009408 GO:GO:0009615 GO:GO:0010187 UniGene:At.23663 GO:GO:0022626 eggNOG:COG0443 HOGENOM:HBG334976 InterPro:IPR018181 InterPro:IPR013126 PANTHER:PTHR19375 EMBL:AL162971 KO:K03283 OMA:MAKSTAI GO:GO:0090332 EMBL:X74604 EMBL:AY035123 EMBL:AY057481 EMBL:AY120747 EMBL:BT002754 EMBL:M23108 EMBL:M23105 EMBL:X77199 IPI:IPI00543293 PIR:S46302 PIR:T48271 RefSeq:NP_195870.1 UniGene:At.75212 ProteinModelPortal:P22953 SMR:P22953 IntAct:P22953 STRING:P22953 TCDB:1.A.33.1.1 SWISS-2DPAGE:P22953 World-2DPAGE:0003:P22953 PRIDE:P22953 ProMEX:P22953 EnsemblPlants:AT5G02500.1 GeneID:831020 KEGG:ath:AT5G02500 TAIR:At5g02500 InParanoid:P22953 PhylomeDB:P22953 ProtClustDB:CLSN2916777 Genevestigator:P22953 GermOnline:AT5G02500 Uniprot:P22953
Leaf	Isotig01919	46	30	1.146	0.00055795	TAIR|locus:2181833 - symbol:HSC70-1 "heat shock cognate protein 70-1" species:3702 "Arabidopsis thaliana" [GO:0005524 "ATP binding" evidence=IEA] [GO:0005829 "cytosol" evidence=IDA;RCA;TAS] [GO:0006457 "protein folding" evidence=TAS] [GO:0009408 "response to heat" evidence=IEP;IMP] [GO:0005634 "nucleus" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005730 "nucleolus" evidence=IDA] [GO:0009615 "response to virus" evidence=IEP] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0042742 "defense response to bacterium" evidence=IMP] [GO:0050832 "defense response to fungus" evidence=IMP] [GO:0048046 "apoplast" evidence=IDA] [GO:0002020 "protease binding" evidence=IPI] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0010187 "negative regulation of seed germination" evidence=IMP] [GO:0090332 "stomatal closure" evidence=IMP] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR001023

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						PRINTS:PR00301 Pfam:PF00012 Prosite:PS00297 Prosite:PS00329 Prosite:PS01036 GO:GO:0005886 GO:GO:0009506 GO:GO:0005524 GO:GO:0048046 GO:GO:0046686 GO:GO:0005774 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005618 GO:GO:0009507 GO:GO:0042742 GO:GO:0005730 GO:GO:0050832 GO:GO:0002020 GO:GO:0009409 GO:GO:0009408 GO:GO:0009615 GO:GO:0010187 UniGene:At.23663 GO:GO:0022626 eggNOG:COG0443 HOGENOM:HBG334976 InterPro:IPR018181 InterPro:IPR013126 PANTHER:PTHR19375 EMBL:AL162971 KO:K03283 OMA:MAKSTAI GO:GO:0090332 EMBL:X74604 EMBL:AY035123 EMBL:AY057481 EMBL:AY120747 EMBL:BT002754 EMBL:M23108 EMBL:M23105 EMBL:X77199 IPI:IPI00543293 PIR:S46302 PIR:T48271 RefSeq:NP_195870.1 UniGene:At.75212 ProteinModelPortal:P22953 SMR:P22953 IntAct:P22953 STRING:P22953 TCDB:1.A.33.1.1 SWISS-2DPAGE:P22953 World-2DPAGE:0003:P22953 PRIDE:P22953 ProMEX:P22953 EnsemblPlants:AT5G02500.1 GeneID:831020 KEGG:ath:AT5G02500 TAIR:At5g02500 InParanoid:P22953 PhylomeDB:P22953 ProtClustDB:CLSN2916777 Genevestigator:P22953 GermOnline:AT5G02500 Uniprot:P22953
Leaf	Isotig01920	50	25	1.529	7.01E-06	TAIR|locus:2181833 - symbol:HSC70-1 "heat shock cognate protein 70-1" species:3702 "Arabidopsis thaliana" [GO:0005524 "ATP binding" evidence=IEA] [GO:0005829 "cytosol" evidence=IDA;RCA;TAS] [GO:0006457 "protein folding" evidence=TAS] [GO:0009408 "response to heat" evidence=IEP;IMP] [GO:0005634 "nucleus" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005730 "nucleolus" evidence=IDA] [GO:0009615 "response to virus" evidence=IEP] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0042742 "defense response to bacterium" evidence=IMP] [GO:0050832 "defense response to fungus" evidence=IMP] [GO:0048046 "apoplast" evidence=IDA] [GO:0002020 "protease binding" evidence=IPI] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0010187 "negative regulation of seed germination" evidence=IMP] [GO:0090332 "stomatal closure" evidence=IMP] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR001023 PRINTS:PR00301 Pfam:PF00012 Prosite:PS00297 Prosite:PS00329 Prosite:PS01036 GO:GO:0005886 GO:GO:0009506 GO:GO:0005524 GO:GO:0048046 GO:GO:0046686 GO:GO:0005774 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005618 GO:GO:0009507 GO:GO:0042742 GO:GO:0005730 GO:GO:0050832 GO:GO:0002020 GO:GO:0009409 GO:GO:0009408 GO:GO:0009615 GO:GO:0010187 UniGene:At.23663 GO:GO:0022626 eggNOG:COG0443 HOGENOM:HBG334976 InterPro:IPR018181 InterPro:IPR013126 PANTHER:PTHR19375 EMBL:AL162971 KO:K03283 OMA:MAKSTAI GO:GO:0090332 EMBL:X74604 EMBL:AY035123 EMBL:AY057481 EMBL:AY120747 EMBL:BT002754 EMBL:M23108 EMBL:M23105 EMBL:X77199 IPI:IPI00543293 PIR:S46302 PIR:T48271 RefSeq:NP_195870.1 UniGene:At.75212 ProteinModelPortal:P22953 SMR:P22953 IntAct:P22953 STRING:P22953 TCDB:1.A.33.1.1 SWISS-2DPAGE:P22953 World-2DPAGE:0003:P22953 PRIDE:P22953 ProMEX:P22953 EnsemblPlants:AT5G02500.1 GeneID:831020 KEGG:ath:AT5G02500 TAIR:At5g02500 InParanoid:P22953 PhylomeDB:P22953 ProtClustDB:CLSN2916777 Genevestigator:P22953 GermOnline:AT5G02500 Uniprot:P22953
Leaf	Isotig01924	57	36	1.192	7.33E-05	TAIR|locus:2114789 - symbol:ZDS "zeta-carotene desaturase" species:3702 "Arabidopsis thaliana" [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0016120 "carotene biosynthetic process" evidence=IDA] [GO:0016719 "carotene 7,8-desaturase activity" evidence=IDA] InterPro:IPR002937 InterPro:IPR014103 Pfam:PF01593 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0009941 GO:GO:0016117 EMBL:AC009465 GO:GO:0009509 UniGene:At.24092 UniGene:At.71000 eggNOG:COG3349 HOGENOM:HBG286164 EMBL:U38550 EMBL:AF121947 EMBL:AY059920 EMBL:AY072096 EMBL:AY096583 IPI:IPI00541621 RefSeq:NP_187138.1 RefSeq:NP_974222.1 ProteinModelPortal:Q38893 SMR:Q38893 STRING:Q38893 PRIDE:Q38893 DNASU:819647 EnsemblPlants:AT3G04870.1 EnsemblPlants:AT3G04870.2 GeneID:819647 KEGG:ath:AT3G04870 TAIR:At3g04870 InParanoid:Q38893 KO:K00514 OMA:RMWNPIA PhylomeDB:Q38893 ProtClustDB:PLN02487 BioCyc:ARA:AT3G04870-MONOMER BioCyc:MetaCyc:AT3G04870-MONOMER Genevestigator:Q38893 GO:GO:0016719 TIGRFAMs:TIGR02732 Uniprot:Q38893
Leaf	Isotig01925	53	29	1.399	1.50E-05	TAIR|locus:2114789 - symbol:ZDS "zeta-carotene desaturase" species:3702 "Arabidopsis thaliana" [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0016120 "carotene biosynthetic process" evidence=IDA] [GO:0016719 "carotene 7,8-desaturase activity" evidence=IDA] InterPro:IPR002937 InterPro:IPR014103 Pfam:PF01593 EMBL:CP002686 GenomeReviews:BA000014_GR

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0009941 GO:GO:0016117 EMBL:AC009465 GO:GO:0009509 UniGene:At.24092 UniGene:At.71000 eggNOG:COG3349 HOGENOM:HBG286164 EMBL:U38550 EMBL:AF121947 EMBL:AY059920 EMBL:AY072096 EMBL:AY096583 IPI:IPI00541621 RefSeq:NP_187138.1 RefSeq:NP_974222.1 ProteinModelPortal:Q38893 SMR:Q38893 STRING:Q38893 PRIDE:Q38893 DNASU:819647 EnsemblPlants:AT3G04870.1 EnsemblPlants:AT3G04870.2 GeneID:819647 KEGG:ath:AT3G04870 TAIR:At3g04870 InParanoid:Q38893 KO:K00514 OMA:RMWNPIA PhylomeDB:Q38893 ProtClustDB:PLN02487 BioCyc:ARA:AT3G04870-MONOMER BioCyc:MetaCyc:AT3G04870-MONOMER Genevestigator:Q38893 GO:GO:0016719 TIGRFAMs:TIGR02732 Uniprot:Q38893
Leaf	Isotig01926	49	27	1.389	3.47E-05	TAIR|locus:2114789 - symbol:ZDS "zeta-carotene desaturase" species:3702 "Arabidopsis thaliana" [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0016120 "carotene biosynthetic process" evidence=IDA] [GO:0016719 "carotene 7,8-desaturase activity" evidence=IDA] InterPro:IPR002937 InterPro:IPR014103 Pfam:PF01593 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0009941 GO:GO:0016117 EMBL:AC009465 GO:GO:0009509 UniGene:At.24092 UniGene:At.71000 eggNOG:COG3349 HOGENOM:HBG286164 EMBL:U38550 EMBL:AF121947 EMBL:AY059920 EMBL:AY072096 EMBL:AY096583 IPI:IPI00541621 RefSeq:NP_187138.1 RefSeq:NP_974222.1 ProteinModelPortal:Q38893 SMR:Q38893 STRING:Q38893 PRIDE:Q38893 DNASU:819647 EnsemblPlants:AT3G04870.1 EnsemblPlants:AT3G04870.2 GeneID:819647 KEGG:ath:AT3G04870 TAIR:At3g04870 InParanoid:Q38893 KO:K00514 OMA:RMWNPIA PhylomeDB:Q38893 ProtClustDB:PLN02487 BioCyc:ARA:AT3G04870-MONOMER BioCyc:MetaCyc:AT3G04870-MONOMER Genevestigator:Q38893 GO:GO:0016719 TIGRFAMs:TIGR02732 Uniprot:Q38893
Leaf	Isotig01927	20	5	2.529	7.73E-05	TAIR|locus:2059088 - symbol:AT2G19120 "AT2G19120" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0009506 "plasmodesma" evidence=IDA] GO:GO:0009506 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0004386 EMBL:AC002392 GO:GO:0004519 eggNOG:COG1112 IPI:IPI00542366 PIR:T00533 RefSeq:NP_179502.1 UniGene:At.52824 ProteinModelPortal:O64476 SMR:O64476 PRIDE:O64476 EnsemblPlants:AT2G19120.1 GeneID:816429 KEGG:ath:AT2G19120 TAIR:At2g19120 HOGENOM:HBG746792 InParanoid:O64476 OMA:QANESNS PhylomeDB:O64476 ProtClustDB:CLSN2683158 ArrayExpress:O64476 Genevestigator:O64476 Uniprot:O64476
Leaf	Isotig01928	19	5	2.455	0.000151807	TAIR|locus:2059088 - symbol:AT2G19120 "AT2G19120" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0009506 "plasmodesma" evidence=IDA] GO:GO:0009506 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0004386 EMBL:AC002392 GO:GO:0004519 eggNOG:COG1112 IPI:IPI00542366 PIR:T00533 RefSeq:NP_179502.1 UniGene:At.52824 ProteinModelPortal:O64476 SMR:O64476 PRIDE:O64476 EnsemblPlants:AT2G19120.1 GeneID:816429 KEGG:ath:AT2G19120 TAIR:At2g19120 HOGENOM:HBG746792 InParanoid:O64476 OMA:QANESNS PhylomeDB:O64476 ProtClustDB:CLSN2683158 ArrayExpress:O64476 Genevestigator:O64476 Uniprot:O64476
Leaf	Isotig01929	16	4	2.529	0.000407249	TAIR|locus:2059088 - symbol:AT2G19120 "AT2G19120" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0009506 "plasmodesma" evidence=IDA] GO:GO:0009506 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0004386 EMBL:AC002392 GO:GO:0004519 eggNOG:COG1112 IPI:IPI00542366 PIR:T00533 RefSeq:NP_179502.1 UniGene:At.52824 ProteinModelPortal:O64476 SMR:O64476 PRIDE:O64476 EnsemblPlants:AT2G19120.1 GeneID:816429 KEGG:ath:AT2G19120 TAIR:At2g19120 HOGENOM:HBG746792 InParanoid:O64476 OMA:QANESNS PhylomeDB:O64476 ProtClustDB:CLSN2683158 ArrayExpress:O64476 Genevestigator:O64476 Uniprot:O64476
Leaf	Isotig01933	40	19	1.603	3.18E-05	TAIR|locus:504955106 - symbol:emb1138 "embryo defective 1138" species:3702 "Arabidopsis thaliana" [GO:0003676 "nucleic acid binding" evidence=IEA] [GO:0003723 "RNA binding" evidence=IEA] [GO:0004386 "helicase activity" evidence=IEA] [GO:0005524 "ATP binding" evidence=IEA;ISS] [GO:0008026 "ATP-dependent helicase activity" evidence=IEA;ISS] [GO:0008270 "zinc ion binding" evidence=IEA] [GO:0009793 "embryo development ending in seed dormancy" evidence=NAS] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] InterPro:IPR001650 InterPro:IPR001878 InterPro:IPR011545 InterPro:IPR012562 Pfam:PF00098 Pfam:PF00270 Pfam:PF00271 Pfam:PF08152 PROSITE:PS00039 PROSITE:PS50158

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						PROSITE:PS51194 SMART:SM00343 SMART:SM00490 InterPro:IPR014001 GO:GO:0005524 GO:GO:0009570 GO:GO:0005634 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0016020 GO:GO:0008270 GO:GO:0009941 GO:GO:0003723 EMBL:AF058914 Gene3D:G3DSA:4.10.60.10 SUPFAM:SSF57756 SMART:SM00487 PROSITE:PS51192 GO:GO:0008026 eggNOG:COG0513 HOGENOM:HBG737336 InterPro:IPR014014 PROSITE:PS51195 UniGene:At.23875 EMBL:AJ010457 EMBL:AC137518 EMBL:AY080625 EMBL:AY091068 EMBL:AY094485 EMBL:AY123000 EMBL:AY128278 EMBL:BT000713 EMBL:BT002289 EMBL:BT002456 EMBL:AY102126 EMBL:BT004533 EMBL:AK229821 IPI:IPI00523172 IPI:IPI00656967 PIR:T01202 PIR:T51738 RefSeq:NP_001031943.1 RefSeq:NP_680225.2 UniGene:At.66764 ProteinModelPortal:Q8L7S8 SMR:Q8L7S8 STRING:Q8L7S8 PRIDE:Q8L7S8 EnsemblPlants:AT5G26742.2 GeneID:832713 KEGG:ath:AT5G26742 GeneFarm:1570 TAIR:At5g26742 InParanoid:Q8L7S8 OMA:EKRGITH PhylomeDB:Q8L7S8 ProtClustDB:CLSN2680279 Genevestigator:Q8L7S8 Uniprot:Q8L7S8
Leaf	Isotig01934	37	18	1.568	8.21E-05	TAIR|locus:504955106 - symbol:emb1138 "embryo defective 1138" species:3702 "Arabidopsis thaliana" [GO:0003676 "nucleic acid binding" evidence=IEA] [GO:0003723 "RNA binding" evidence=IEA] [GO:0004386 "helicase activity" evidence=IEA] [GO:0005524 "ATP binding" evidence=IEA;ISS] [GO:0008026 "ATP-dependent helicase activity" evidence=IEA;ISS] [GO:0008270 "zinc ion binding" evidence=IEA] [GO:0009793 "embryo development ending in seed dormancy" evidence=NAS] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] InterPro:IPR001650 InterPro:IPR001878 InterPro:IPR011545 InterPro:IPR012562 Pfam:PF00098 Pfam:PF00270 Pfam:PF00271 Pfam:PF08152 PROSITE:PS00039 PROSITE:PS50158 PROSITE:PS51194 SMART:SM00343 SMART:SM00490 InterPro:IPR014001 GO:GO:0005524 GO:GO:0009570 GO:GO:0005634 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0016020 GO:GO:0008270 GO:GO:0009941 GO:GO:0003723 EMBL:AF058914 Gene3D:G3DSA:4.10.60.10 SUPFAM:SSF57756 SMART:SM00487 PROSITE:PS51192 GO:GO:0008026 eggNOG:COG0513 HOGENOM:HBG737336 InterPro:IPR014014 PROSITE:PS51195 UniGene:At.23875 EMBL:AJ010457 EMBL:AC137518 EMBL:AY080625 EMBL:AY091068 EMBL:AY094485 EMBL:AY123000 EMBL:AY128278 EMBL:BT000713 EMBL:BT002289 EMBL:BT002456 EMBL:AY102126 EMBL:BT004533 EMBL:AK229821 IPI:IPI00523172 IPI:IPI00656967 PIR:T01202 PIR:T51738 RefSeq:NP_001031943.1 RefSeq:NP_680225.2 UniGene:At.66764 ProteinModelPortal:Q8L7S8 SMR:Q8L7S8 STRING:Q8L7S8 PRIDE:Q8L7S8 EnsemblPlants:AT5G26742.2 GeneID:832713 KEGG:ath:AT5G26742 GeneFarm:1570 TAIR:At5g26742 InParanoid:Q8L7S8 OMA:EKRGITH PhylomeDB:Q8L7S8 ProtClustDB:CLSN2680279 Genevestigator:Q8L7S8 Uniprot:Q8L7S8
Leaf	Isotig01936	38	6	3.192	8.77E-10	TAIR|locus:2096314 - symbol:GID1A "AT3G05120" species:3702 "Arabidopsis thaliana" [GO:0005515 "protein binding" evidence=IPI] [GO:0010325 "raffinose family oligosaccharide biosynthetic process" evidence=IGI] [GO:0009939 "positive regulation of gibberellic acid mediated signaling pathway" evidence=IGI] [GO:0048444 "floral organ morphogenesis" evidence=IGI] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0010476 "gibberellin mediated signaling pathway" evidence=IGI] [GO:0009739 "response to gibberellin stimulus" evidence=IGI;IEP] [GO:0010331 "gibberellin binding" evidence=IDA] InterPro:IPR002168 InterPro:IPR013094 Pfam:PF07859 PROSITE:PS01173 PROSITE:PS01174 GO:GO:0005634 GO:GO:0005737 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005515 GO:GO:0004872 eggNOG:COG0657 HOGENOM:HBG757640 GO:GO:0016787 EMBL:AC009177 GO:GO:0009740 PDB:2ZSH PDB:2ZSI PDBsum:2ZSH PDBsum:2ZSI EMBL:AY136305 EMBL:BT002605 IPI:IPI00527879 RefSeq:NP_187163.1 UniGene:At.18371 UniGene:At.74127 ProteinModelPortal:Q9MAA7 SMR:Q9MAA7 IntAct:Q9MAA7 STRING:Q9MAA7 PRIDE:Q9MAA7 EnsemblPlants:AT3G05120.1 GeneID:819674 KEGG:ath:AT3G05120 TAIR:At3g05120 InParanoid:Q9MAA7 KO:K14493 OMA:ATVGFYL PhylomeDB:Q9MAA7 ProtClustDB:CLSN2684300 ArrayExpress:Q9MAA7 Genevestigator:Q9MAA7 GermOnline:AT3G05120 GO:GO:0010331 GO:GO:0010325 Uniprot:Q9MAA7
Leaf	Isotig01937	38	6	3.192	8.77E-10	TAIR|locus:2096314 - symbol:GID1A "AT3G05120" species:3702 "Arabidopsis thaliana" [GO:0005515 "protein binding" evidence=IPI] [GO:0010325 "raffinose family oligosaccharide biosynthetic process" evidence=IGI] [GO:0009939 "positive regulation of gibberellic acid mediated signaling pathway" evidence=IGI] [GO:0048444 "floral organ morphogenesis" evidence=IGI] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0010476 "gibberellin mediated signaling pathway" evidence=IGI] [GO:0009739 "response to gibberellin stimulus" evidence=IGI;IEP] [GO:0010331 "gibberellin binding" evidence=IDA] InterPro:IPR002168 InterPro:IPR013094 Pfam:PF07859 PROSITE:PS01173 PROSITE:PS01174 GO:GO:0005634 GO:GO:0005737

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005515 GO:GO:0004872 eggNOG:COG0657 HOGENOM:HBG757640 GO:GO:0016787 EMBL:AC009177 GO:GO:0009740 PDB:2ZSH PDB:2ZSI PDBsum:2ZSH PDBsum:2ZSI EMBL:AY136305 EMBL:BT002605 IPI:IPI00527879 RefSeq:NP_187163.1 UniGene:At.18371 UniGene:At.74127 ProteinModelPortal:Q9MAA7 SMR:Q9MAA7 IntAct:Q9MAA7 STRING:Q9MAA7 PRIDE:Q9MAA7 EnsemblPlants:AT3G05120.1 GeneID:819674 KEGG:ath:AT3G05120 TAIR:At3g05120 InParanoid:Q9MAA7 KO:K14493 OMA:ATVGFYL PhylomeDB:Q9MAA7 ProtClustDB:CLSN2684300 ArrayExpress:Q9MAA7 Genevestigator:Q9MAA7 GermOnline:AT3G05120 GO:GO:0010331 GO:GO:0010325 Uniprot:Q9MAA7
Leaf	Isotig01938	29	6	2.802	4.91E-07	TAIR|locus:2096314 - symbol:GID1A "AT3G05120" species:3702 "Arabidopsis thaliana" [GO:0005515 "protein binding" evidence=IPI] [GO:0010325 "raffinose family oligosaccharide biosynthetic process" evidence=IGI] [GO:0009939 "positive regulation of gibberellic acid mediated signaling pathway" evidence=IGI] [GO:0048444 "floral organ morphogenesis" evidence=IGI] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0010476 "gibberellin mediated signaling pathway" evidence=IGI] [GO:0009739 "response to gibberellin stimulus" evidence=IGI;IEP] [GO:0010331 "gibberellin binding" evidence=IDA] InterPro:IPR002168 InterPro:IPR013094 Pfam:PF07859 PROSITE:PS01173 PROSITE:PS01174 GO:GO:0005634 GO:GO:0005737 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005515 GO:GO:0004872 eggNOG:COG0657 HOGENOM:HBG757640 GO:GO:0016787 EMBL:AC009177 GO:GO:0009740 PDB:2ZSH PDB:2ZSI PDBsum:2ZSH PDBsum:2ZSI EMBL:AY136305 EMBL:BT002605 IPI:IPI00527879 RefSeq:NP_187163.1 UniGene:At.18371 UniGene:At.74127 ProteinModelPortal:Q9MAA7 SMR:Q9MAA7 IntAct:Q9MAA7 STRING:Q9MAA7 PRIDE:Q9MAA7 EnsemblPlants:AT3G05120.1 GeneID:819674 KEGG:ath:AT3G05120 TAIR:At3g05120 InParanoid:Q9MAA7 KO:K14493 OMA:ATVGFYL PhylomeDB:Q9MAA7 ProtClustDB:CLSN2684300 ArrayExpress:Q9MAA7 Genevestigator:Q9MAA7 GermOnline:AT3G05120 GO:GO:0010331 GO:GO:0010325 Uniprot:Q9MAA7
Leaf	Isotig01939	16	4	2.529	0.000407249	TAIR|locus:2202700 - symbol:NAT7 "nucleobase-ascorbate transporter 7" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=IEA] [GO:0016020 "membrane" evidence=ISS] [GO:0022857 "transmembrane transporter activity" evidence=ISS] [GO:0055085 "transmembrane transport" evidence=IEA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR006043 Pfam:PF00860 PROSITE:PS01116 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005886 GO:GO:0009506 GO:GO:0055085 GO:GO:0005215 EMBL:AC005966 PANTHER:PTHR11119 eggNOG:COG2233 HOGENOM:HBG713856 EMBL:AK229125 IPI:IPI00526135 PIR:F96624 RefSeq:NP_176211.2 UniGene:At.36734 ProteinModelPortal:Q0WPE9 PRIDE:Q0WPE9 EnsemblPlants:AT1G60030.1 GeneID:842297 KEGG:ath:AT1G60030 TAIR:At1g60030 InParanoid:Q0WPE9 OMA:GAYKNTG PhylomeDB:Q0WPE9 ProtClustDB:CLSN2918389 BioCyc:MetaCyc:MONOMER-14797 Genevestigator:Q0WPE9 Uniprot:Q0WPE9
Leaf	Isotig01940	16	4	2.529	0.000407249	TAIR|locus:2202700 - symbol:NAT7 "nucleobase-ascorbate transporter 7" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=IEA] [GO:0016020 "membrane" evidence=ISS] [GO:0022857 "transmembrane transporter activity" evidence=ISS] [GO:0055085 "transmembrane transport" evidence=IEA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR006043 Pfam:PF00860 PROSITE:PS01116 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005886 GO:GO:0009506 GO:GO:0055085 GO:GO:0005215 EMBL:AC005966 PANTHER:PTHR11119 eggNOG:COG2233 HOGENOM:HBG713856 EMBL:AK229125 IPI:IPI00526135 PIR:F96624 RefSeq:NP_176211.2 UniGene:At.36734 ProteinModelPortal:Q0WPE9 PRIDE:Q0WPE9 EnsemblPlants:AT1G60030.1 GeneID:842297 KEGG:ath:AT1G60030 TAIR:At1g60030 InParanoid:Q0WPE9 OMA:GAYKNTG PhylomeDB:Q0WPE9 ProtClustDB:CLSN2918389 BioCyc:MetaCyc:MONOMER-14797 Genevestigator:Q0WPE9 Uniprot:Q0WPE9
Leaf	Isotig01941	16	4	2.529	0.000407249	TAIR|locus:2202700 - symbol:NAT7 "nucleobase-ascorbate transporter 7" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=IEA] [GO:0016020 "membrane" evidence=ISS] [GO:0022857 "transmembrane transporter activity" evidence=ISS] [GO:0055085 "transmembrane transport" evidence=IEA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR006043 Pfam:PF00860 PROSITE:PS01116 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005886 GO:GO:0009506 GO:GO:0055085 GO:GO:0005215 EMBL:AC005966 PANTHER:PTHR11119 eggNOG:COG2233 HOGENOM:HBG713856 EMBL:AK229125 IPI:IPI00526135 PIR:F96624 RefSeq:NP_176211.2 UniGene:At.36734 ProteinModelPortal:Q0WPE9 PRIDE:Q0WPE9 EnsemblPlants:AT1G60030.1 GeneID:842297

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						KEGG:ath:AT1G60030 TAIR:At1g60030 InParanoid:Q0WPE9 OMA:GAYKNTG PhylomeDB:Q0WPE9 ProtClustDB:CLSN2918389 BioCyc:MetaCyc:MONOMER-14797 Genevestigator:Q0WPE9 Uniprot:Q0WPE9
Leaf	Isotig01948	53	1	6.257	7.19E-17	TAIR|locus:2063255 - symbol:AT2G41190 "AT2G41190" species:3702 "Arabidopsis thaliana" [GO:0006865 "amino acid transport" evidence=ISS] [GO:0015171 "amino acid transmembrane transporter activity" evidence=ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0005774 "vacuolar membrane" evidence=IDA] GO:GO:0016021 GO:GO:0005774 EMBL:CP002685 GenomeReviews:CT485783_GR InterPro:IPR013057 Pfam:PF01490 EMBL:AC004261 eggNOG:COG0814 EMBL:AY039978 EMBL:AY079364 IPI:IPI00548842 PIR:T02100 RefSeq:NP_030664.1 UniGene:At.12553 ProteinModelPortal:O80668 PRIDE:O80668 EnsemblPlants:AT2G41190.1 GeneID:818718 KEGG:ath:AT2G41190 TAIR:At2g41190 HOGENOM:HBG745232 InParanoid:O80668 OMA:YGFCYSG PhylomeDB:O80668 ProtClustDB:CLSN2688858 Genevestigator:O80668 Uniprot:O80668
Leaf	Isotig01949	52	1	6.229	1.36E-16	TAIR|locus:2063255 - symbol:AT2G41190 "AT2G41190" species:3702 "Arabidopsis thaliana" [GO:0006865 "amino acid transport" evidence=ISS] [GO:0015171 "amino acid transmembrane transporter activity" evidence=ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0005774 "vacuolar membrane" evidence=IDA] GO:GO:0016021 GO:GO:0005774 EMBL:CP002685 GenomeReviews:CT485783_GR InterPro:IPR013057 Pfam:PF01490 EMBL:AC004261 eggNOG:COG0814 EMBL:AY039978 EMBL:AY079364 IPI:IPI00548842 PIR:T02100 RefSeq:NP_030664.1 UniGene:At.12553 ProteinModelPortal:O80668 PRIDE:O80668 EnsemblPlants:AT2G41190.1 GeneID:818718 KEGG:ath:AT2G41190 TAIR:At2g41190 HOGENOM:HBG745232 InParanoid:O80668 OMA:YGFCYSG PhylomeDB:O80668 ProtClustDB:CLSN2688858 Genevestigator:O80668 Uniprot:O80668
Leaf	Isotig01950	50	1	6.173	4.95E-16	TAIR|locus:2063255 - symbol:AT2G41190 "AT2G41190" species:3702 "Arabidopsis thaliana" [GO:0006865 "amino acid transport" evidence=ISS] [GO:0015171 "amino acid transmembrane transporter activity" evidence=ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0005774 "vacuolar membrane" evidence=IDA] GO:GO:0016021 GO:GO:0005774 EMBL:CP002685 GenomeReviews:CT485783_GR InterPro:IPR013057 Pfam:PF01490 EMBL:AC004261 eggNOG:COG0814 EMBL:AY039978 EMBL:AY079364 IPI:IPI00548842 PIR:T02100 RefSeq:NP_030664.1 UniGene:At.12553 ProteinModelPortal:O80668 PRIDE:O80668 EnsemblPlants:AT2G41190.1 GeneID:818718 KEGG:ath:AT2G41190 TAIR:At2g41190 HOGENOM:HBG745232 InParanoid:O80668 OMA:YGFCYSG PhylomeDB:O80668 ProtClustDB:CLSN2688858 Genevestigator:O80668 Uniprot:O80668
Leaf	Isotig01951	30	0	6.436	3.85E-10	TAIR|locus:2195563 - symbol:PUB19 "plant U-box 19" species:3702 "Arabidopsis thaliana" [GO:0000151 "ubiquitin ligase complex" evidence=IEA] [GO:0004842 "ubiquitin-protein ligase activity" evidence=IEA] [GO:0008270 "zinc ion binding" evidence=IEA] [GO:0010029 "regulation of seed germination" evidence=IGI] InterPro:IPR001841 InterPro:IPR000225 InterPro:IPR003613 InterPro:IPR011989 InterPro:IPR016024 Pfam:PF00514 Pfam:PF04564 PROSITE:PS50176 SMART:SM00184 SMART:SM00504 EMBL:CP002684 GenomeReviews:CT485782_GR SUPFAM:SSF48371 Gene3D:G3DSA:1.25.10.10 GO:GO:0008270 InterPro:IPR013083 Gene3D:G3DSA:3.30.40.10 GO:GO:0010029 GO:GO:0004842 GO:GO:0000151 EMBL:AC004473 HSSP:Q8VZ40 HOGENOM:HBG746719 eggNOG:NOG251934 ProtClustDB:CLSN2679599 IPI:IPI00530780 PIR:T02271 RefSeq:NP_176225.1 UniGene:At.66059 ProteinModelPortal:O80742 SMR:O80742 PRIDE:O80742 EnsemblPlants:AT1G60190.1 GeneID:842314 KEGG:ath:AT1G60190 TAIR:At1g60190 InParanoid:O80742 OMA:MAILAKM PhylomeDB:O80742 Genevestigator:O80742 Uniprot:O80742
Leaf	Isotig01952	33	0	6.573	5.84E-11	TAIR|locus:2195563 - symbol:PUB19 "plant U-box 19" species:3702 "Arabidopsis thaliana" [GO:0000151 "ubiquitin ligase complex" evidence=IEA] [GO:0004842 "ubiquitin-protein ligase activity" evidence=IEA] [GO:0008270 "zinc ion binding" evidence=IEA] [GO:0010029 "regulation of seed germination" evidence=IGI] InterPro:IPR001841 InterPro:IPR000225 InterPro:IPR003613 InterPro:IPR011989 InterPro:IPR016024 Pfam:PF00514 Pfam:PF04564 PROSITE:PS50176 SMART:SM00184 SMART:SM00504 EMBL:CP002684 GenomeReviews:CT485782_GR SUPFAM:SSF48371 Gene3D:G3DSA:1.25.10.10 GO:GO:0008270 InterPro:IPR013083 Gene3D:G3DSA:3.30.40.10 GO:GO:0010029 GO:GO:0004842 GO:GO:0000151 EMBL:AC004473 HSSP:Q8VZ40 HOGENOM:HBG746719 eggNOG:NOG251934 ProtClustDB:CLSN2679599 IPI:IPI00530780 PIR:T02271 RefSeq:NP_176225.1 UniGene:At.66059 ProteinModelPortal:O80742 SMR:O80742 PRIDE:O80742 EnsemblPlants:AT1G60190.1 GeneID:842314 KEGG:ath:AT1G60190 TAIR:At1g60190 InParanoid:O80742 OMA:MAILAKM PhylomeDB:O80742 Genevestigator:O80742 Uniprot:O80742
Leaf	Isotig01953	17	0	5.616	2.14E-06	TAIR|locus:2195563 - symbol:PUB19 "plant U-box 19" species:3702 "Arabidopsis thaliana" [GO:0000151 "ubiquitin ligase complex" evidence=IEA] [GO:0004842 "ubiquitin-protein ligase activity" evidence=IEA] [GO:0008270 "zinc ion binding" evidence=IEA] [GO:0010029 "regulation of seed germination" evidence=IGI] InterPro:IPR001841 InterPro:IPR000225 InterPro:IPR003613 InterPro:IPR011989 InterPro:IPR016024 Pfam:PF00514 Pfam:PF04564

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						PROSITE:PS50176 SMART:SM00184 SMART:SM00504 EMBL:CP002684 GenomeReviews:CT485782_GR SUPFAM:SSF48371 Gene3D:G3DSA:1.25.10.10 GO:GO:0008270 InterPro:IPR013083 Gene3D:G3DSA:3.30.40.10 GO:GO:0010029 GO:GO:0004842 GO:GO:0000151 EMBL:AC004473 HSSP:Q8VZ40 HOGENOM:HBG746719 eggNOG:NOG251934 ProtClustDB:CLSN2679599 IPI:IPI00530780 PIR:T02271 RefSeq:NP_176225.1 UniGene:At.66059 ProteinModelPortal:O80742 SMR:O80742 PRIDE:O80742 EnsemblPlants:AT1G60190.1 GeneID:842314 KEGG:ath:AT1G60190 TAIR:At1g60190 InParanoid:O80742 OMA:MAILAKM PhylomeDB:O80742 Genevestigator:O80742 Uniprot:O80742
Leaf	Isotig01954	59	0	7.412	1.38E-17	UNIPROTKB|Q9ZPB7 - symbol:Q9ZPB7 "Aldehyde dehydrogenase family 7 member A1" species:3750 "Malus x domestica" [GO:0004029 "aldehyde dehydrogenase (NAD) activity" evidence=ISS] [GO:0005575 "cellular_component" evidence=ND] [GO:0006081 "cellular aldehyde metabolic process" evidence=ISS] InterPro:IPR015590 InterPro:IPR016160 InterPro:IPR016161 InterPro:IPR016162 InterPro:IPR016163 Pfam:PF00171 PROSITE:PS00687 Gene3D:G3DSA:3.40.309.10 Gene3D:G3DSA:3.40.605.10 SUPFAM:SSF53720 GO:GO:0004029 GO:GO:0006081 EMBL:D88434 ProteinModelPortal:Q9ZPB7 SMR:Q9ZPB7 Uniprot:Q9ZPB7
Leaf	Isotig01955	59	0	7.412	1.38E-17	UNIPROTKB|Q9ZPB7 - symbol:Q9ZPB7 "Aldehyde dehydrogenase family 7 member A1" species:3750 "Malus x domestica" [GO:0004029 "aldehyde dehydrogenase (NAD) activity" evidence=ISS] [GO:0005575 "cellular_component" evidence=ND] [GO:0006081 "cellular aldehyde metabolic process" evidence=ISS] InterPro:IPR015590 InterPro:IPR016160 InterPro:IPR016161 InterPro:IPR016162 InterPro:IPR016163 Pfam:PF00171 PROSITE:PS00687 Gene3D:G3DSA:3.40.309.10 Gene3D:G3DSA:3.40.605.10 SUPFAM:SSF53720 GO:GO:0004029 GO:GO:0006081 EMBL:D88434 ProteinModelPortal:Q9ZPB7 SMR:Q9ZPB7 Uniprot:Q9ZPB7
Leaf	Isotig01956	52	0	7.229	7.12E-16	UNIPROTKB|Q9ZPB7 - symbol:Q9ZPB7 "Aldehyde dehydrogenase family 7 member A1" species:3750 "Malus x domestica" [GO:0004029 "aldehyde dehydrogenase (NAD) activity" evidence=ISS] [GO:0005575 "cellular_component" evidence=ND] [GO:0006081 "cellular aldehyde metabolic process" evidence=ISS] InterPro:IPR015590 InterPro:IPR016160 InterPro:IPR016161 InterPro:IPR016162 InterPro:IPR016163 Pfam:PF00171 PROSITE:PS00687 Gene3D:G3DSA:3.40.309.10 Gene3D:G3DSA:3.40.605.10 SUPFAM:SSF53720 GO:GO:0004029 GO:GO:0006081 EMBL:D88434 ProteinModelPortal:Q9ZPB7 SMR:Q9ZPB7 Uniprot:Q9ZPB7
Leaf	Isotig01963	24	82	-1.244	4.24E-05	TAIR|locus:2161620 - symbol:VTC5 "AT5G55120" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0009753 "response to jasmonic acid stimulus" evidence=IEP] [GO:0010193 "response to ozone" evidence=IEP] [GO:0010475 "galactose-1-phosphate guanylyltransferase (GDP) activity" evidence=IDA] [GO:0019853 "L-ascorbic acid biosynthetic process" evidence=IMP] [GO:0080046 "quercetin 4'-O-glucosyltransferase activity" evidence=IDA] [GO:0080048 "GDP-D-glucose phosphorylase activity" evidence=IDA] GO:GO:0005634 GO:GO:0005737 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009753 GO:GO:0000166 GO:GO:0016787 GO:GO:0010193 GO:GO:0005085 EMBL:AB010071 GO:GO:0019853 eggNOG:NOG307761 KO:K14190 ProtClustDB:PLN03103 GO:GO:0010475 GO:GO:0080048 GO:GO:0080046 EMBL:AY063788 EMBL:AY091285 IPI:IPI00537219 RefSeq:NP_200323.1 UniGene:At.21005 ProteinModelPortal:Q9FLP9 IntAct:Q9FLP9 PRIDE:Q9FLP9 EnsemblPlants:AT5G55120.1 GeneID:835603 KEGG:ath:AT5G55120 TAIR:At5g55120 InParanoid:Q9FLP9 OMA:ASEEKAW PhylomeDB:Q9FLP9 ArrayExpress:Q9FLP9 Genevestigator:Q9FLP9 Uniprot:Q9FLP9
Leaf	Isotig01964	17	82	-1.741	1.45E-07	TAIR|locus:2161620 - symbol:VTC5 "AT5G55120" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0009753 "response to jasmonic acid stimulus" evidence=IEP] [GO:0010193 "response to ozone" evidence=IEP] [GO:0010475 "galactose-1-phosphate guanylyltransferase (GDP) activity" evidence=IDA] [GO:0019853 "L-ascorbic acid biosynthetic process" evidence=IMP] [GO:0080046 "quercetin 4'-O-glucosyltransferase activity" evidence=IDA] [GO:0080048 "GDP-D-glucose phosphorylase activity" evidence=IDA] GO:GO:0005634 GO:GO:0005737 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009753 GO:GO:0000166 GO:GO:0016787 GO:GO:0010193 GO:GO:0005085 EMBL:AB010071 GO:GO:0019853 eggNOG:NOG307761 KO:K14190 ProtClustDB:PLN03103 GO:GO:0010475 GO:GO:0080048 GO:GO:0080046 EMBL:AY063788 EMBL:AY091285 IPI:IPI00537219 RefSeq:NP_200323.1 UniGene:At.21005 ProteinModelPortal:Q9FLP9 IntAct:Q9FLP9 PRIDE:Q9FLP9 EnsemblPlants:AT5G55120.1 GeneID:835603 KEGG:ath:AT5G55120 TAIR:At5g55120 InParanoid:Q9FLP9 OMA:ASEEKAW PhylomeDB:Q9FLP9 ArrayExpress:Q9FLP9 Genevestigator:Q9FLP9 Uniprot:Q9FLP9

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig01977	35	20	1.336	0.000680416	TAIR|locus:2064402 - symbol:C4H "AT2G30490" species:3702 "Arabidopsis thaliana" [GO:0009505 "plant-type cell wall" evidence=IDA] [GO:0005783 "endoplasmic reticulum" evidence=IDA;TAS] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009555 "pollen development" evidence=IMP] [GO:0009698 "phenylpropanoid metabolic process" evidence=IMP] [GO:0009808 "lignin metabolic process" evidence=IMP] [GO:0032502 "developmental process" evidence=IMP] [GO:0040007 "growth" evidence=IMP] [GO:0080167 "response to karrikin" evidence=IEP] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] [GO:0009416 "response to light stimulus" evidence=IEP] [GO:0009611 "response to wounding" evidence=IMP] [GO:0009699 "phenylpropanoid biosynthetic process" evidence=TAS] [GO:0016710 "trans-cinnamate 4-monooxygenase activity" evidence=IDA] InterPro:IPR001128 InterPro:IPR002401 InterPro:IPR017972 Pfam:PF00067 PRINTS:PR00385 PRINTS:PR00463 PROSITE:PS00086 GO:GO:0005783 GO:GO:0016021 GO:GO:0005886 GO:GO:0009506 GO:GO:0005774 GO:GO:0040007 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009055 GO:GO:0080167 GO:GO:0009555 eggNOG:COG2124 GO:GO:0020037 Gene3D:G3DSA:1.10.630.10 SUPFAM:SSF48264 GO:GO:0009505 HOGENOM:HBG749920 GO:GO:0009808 EMBL:U93215 EMBL:U71081 EMBL:U71080 EMBL:D78596 EMBL:AY065145 EMBL:BT008875 IPI:IPI00525264 PIR:A84709 RefSeq:NP_180607.1 UniGene:At.23450 ProteinModelPortal:P92994 SMR:P92994 IntAct:P92994 STRING:P92994 PRIDE:P92994 EnsemblPlants:AT2G30490.1 GeneID:817599 KEGG:ath:AT2G30490 GeneFarm:1333 TAIR:At2g30490 InParanoid:P92994 KO:K00487 OMA:GITIGRM PhylomeDB:P92994 ProtClustDB:PLN02394 ArrayExpress:P92994 Genevestigator:P92994 GermOnline:AT2G30490 GO:GO:0016710 Uniprot:P92994
Leaf	Isotig01978	8	43	-1.897	5.38E-05	TAIR|locus:2015158 - symbol:AT1G63010 species:3702 "Arabidopsis thaliana" [GO:0055085 "transmembrane transport" evidence=IEA] [GO:0000325 "plant-type vacuole" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR011701 Pfam:PF07690 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005774 EMBL:AC011000 GO:GO:0055085 GO:GO:0000325 InterPro:IPR016196 SUPFAM:SSF103473 PROSITE:PS50850 InterPro:IPR004331 Pfam:PF03105 PROSITE:PS51382 EMBL:AC010795 EMBL:AK230262 EMBL:AY035094 IPI:IPI00526268 PIR:C96655 RefSeq:NP_001077762.1 RefSeq:NP_001077763.1 RefSeq:NP_564807.2 RefSeq:NP_974073.2 UniGene:At.17751 ProteinModelPortal:Q2V4F9 PRIDE:Q2V4F9 EnsemblPlants:AT1G63010.2 GeneID:842604 KEGG:ath:AT1G63010 TAIR:At1g63010 eggNOG:NOG288227 HOGENOM:HBG318555 InParanoid:Q2V4F9 PhylomeDB:Q2V4F9 ProtClustDB:CLSN2685531 ArrayExpress:Q94C80 Genevestigator:Q2V4F9 Uniprot:Q2V4F9
Leaf	Isotig01979	8	38	-1.719	0.000388716	TAIR|locus:2015158 - symbol:AT1G63010 species:3702 "Arabidopsis thaliana" [GO:0055085 "transmembrane transport" evidence=IEA] [GO:0000325 "plant-type vacuole" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR011701 Pfam:PF07690 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005774 EMBL:AC011000 GO:GO:0055085 GO:GO:0000325 InterPro:IPR016196 SUPFAM:SSF103473 PROSITE:PS50850 InterPro:IPR004331 Pfam:PF03105 PROSITE:PS51382 EMBL:AC010795 EMBL:AK230262 EMBL:AY035094 IPI:IPI00526268 PIR:C96655 RefSeq:NP_001077762.1 RefSeq:NP_001077763.1 RefSeq:NP_564807.2 RefSeq:NP_974073.2 UniGene:At.17751 ProteinModelPortal:Q2V4F9 PRIDE:Q2V4F9 EnsemblPlants:AT1G63010.2 GeneID:842604 KEGG:ath:AT1G63010 TAIR:At1g63010 eggNOG:NOG288227 HOGENOM:HBG318555 InParanoid:Q2V4F9 PhylomeDB:Q2V4F9 ProtClustDB:CLSN2685531 ArrayExpress:Q94C80 Genevestigator:Q2V4F9 Uniprot:Q2V4F9
Leaf	Isotig01980	1	17	-3.559	0.000355264	TAIR|locus:2137075 - symbol:AT4G11810 "AT4G11810" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0055085 "transmembrane transport" evidence=IEA] InterPro:IPR011701 Pfam:PF07690 GO:GO:0016021 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0055085 InterPro:IPR016196 SUPFAM:SSF103473 EMBL:AL078606 EMBL:AL161532 PROSITE:PS50850 InterPro:IPR004331 Pfam:PF03105 PROSITE:PS51382 HOGENOM:HBG318555 ProtClustDB:CLSN2685531 IPI:IPI00546306 PIR:T09340 RefSeq:NP_192918.1 UniGene:At.54285 ProteinModelPortal:Q9T050 PRIDE:Q9T050 EnsemblPlants:AT4G11810.1 GeneID:826787 KEGG:ath:AT4G11810 TAIR:At4g11810 eggNOG:NOG295950 InParanoid:Q9T050 OMA:ERSIEEW PhylomeDB:Q9T050 Genevestigator:Q9T050 Uniprot:Q9T050
Leaf	Isotig01987	48	11	2.654	3.19E-10	TAIR|locus:2206405 - symbol:ALDH5F1 "AT1G79440" species:3702 "Arabidopsis thaliana" [GO:0004028 "3-chloroallyl aldehyde dehydrogenase activity" evidence=ISS] [GO:0004777 "succinate-semialdehyde dehydrogenase activity" evidence=ISS;IDA] [GO:0005759 "mitochondrial matrix" evidence=IDA] [GO:0006540 "glutamate decarboxylation to succinate" evidence=IMP;IDA] [GO:0009450 "gamma-aminobutyric acid catabolic process"

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						evidence=IDA] [GO:0051287 "NAD binding" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0006950 "response to stress" evidence=IMP] [GO:0009408 "response to heat" evidence=IMP] [GO:0009416 "response to light stimulus" evidence=IMP] [GO:0072593 "reactive oxygen species metabolic process" evidence=IMP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] InterPro:IPR010102 InterPro:IPR015590 InterPro:IPR016160 InterPro:IPR016161 InterPro:IPR016162 InterPro:IPR016163 Pfam:PF00171 PROSITE:PS00070 PROSITE:PS00687 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009570 GO:GO:0051287 GO:GO:0005759 eggNOG:COG1012 Gene3D:G3DSA:3.40.309.10 Gene3D:G3DSA:3.40.605.10 SUPFAM:SSF53720 HOGENOM:HBG752218 GO:GO:0005507 GO:GO:0009408 GO:GO:0009416 GO:GO:0072593 HSSP:P05091 EMBL:AC007202 GO:GO:0009450 GO:GO:0006540 KO:K00135 TIGRFAMs:TIGR01780 GO:GO:0004777 OMA:MIQNKDD EMBL:AF117335 EMBL:AF428367 EMBL:AY056147 IPI:IPI00532908 PIR:E96825 RefSeq:NP_178062.1 UniGene:At.11884 ProteinModelPortal:Q9SAK4 SMR:Q9SAK4 STRING:Q9SAK4 PRIDE:Q9SAK4 EnsemblPlants:AT1G79440.1 GeneID:844282 KEGG:ath:AT1G79440 GeneFarm:4340 TAIR:At1g79440 InParanoid:Q9SAK4 PhylomeDB:Q9SAK4 ProtClustDB:PLN02278 ArrayExpress:Q9SEK4 Genevestigator:Q9SAK4 Uniprot:Q9SAK4
Leaf	Isotig01988	45	12	2.436	6.49E-09	TAIR|locus:2206405 - symbol:ALDH5F1 "AT1G79440" species:3702 "Arabidopsis thaliana" [GO:0004028 "3-chloroallyl aldehyde dehydrogenase activity" evidence=ISS] [GO:0004777 "succinate-semialdehyde dehydrogenase activity" evidence=ISS;IDA] [GO:0005759 "mitochondrial matrix" evidence=IDA] [GO:0006540 "glutamate decarboxylation to succinate" evidence=IMP;IDA] [GO:0009450 "gamma-aminobutyric acid catabolic process" evidence=IDA] [GO:0051287 "NAD binding" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0006950 "response to stress" evidence=IMP] [GO:0009408 "response to heat" evidence=IMP] [GO:0009416 "response to light stimulus" evidence=IMP] [GO:0072593 "reactive oxygen species metabolic process" evidence=IMP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] InterPro:IPR010102 InterPro:IPR015590 InterPro:IPR016160 InterPro:IPR016161 InterPro:IPR016162 InterPro:IPR016163 Pfam:PF00171 PROSITE:PS00070 PROSITE:PS00687 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009570 GO:GO:0051287 GO:GO:0005759 eggNOG:COG1012 Gene3D:G3DSA:3.40.309.10 Gene3D:G3DSA:3.40.605.10 SUPFAM:SSF53720 HOGENOM:HBG752218 GO:GO:0005507 GO:GO:0009408 GO:GO:0009416 GO:GO:0072593 HSSP:P05091 EMBL:AC007202 GO:GO:0009450 GO:GO:0006540 KO:K00135 TIGRFAMs:TIGR01780 GO:GO:0004777 OMA:MIQNKDD EMBL:AF117335 EMBL:AF428367 EMBL:AY056147 IPI:IPI00532908 PIR:E96825 RefSeq:NP_178062.1 UniGene:At.11884 ProteinModelPortal:Q9SAK4 SMR:Q9SAK4 STRING:Q9SAK4 PRIDE:Q9SAK4 EnsemblPlants:AT1G79440.1 GeneID:844282 KEGG:ath:AT1G79440 GeneFarm:4340 TAIR:At1g79440 InParanoid:Q9SAK4 PhylomeDB:Q9SAK4 ProtClustDB:PLN02278 ArrayExpress:Q9SEK4 Genevestigator:Q9SAK4 Uniprot:Q9SAK4
Leaf	Isotig01989	48	11	2.654	3.19E-10	TAIR|locus:2206405 - symbol:ALDH5F1 "AT1G79440" species:3702 "Arabidopsis thaliana" [GO:0004028 "3-chloroallyl aldehyde dehydrogenase activity" evidence=ISS] [GO:0004777 "succinate-semialdehyde dehydrogenase activity" evidence=ISS;IDA] [GO:0005759 "mitochondrial matrix" evidence=IDA] [GO:0006540 "glutamate decarboxylation to succinate" evidence=IMP;IDA] [GO:0009450 "gamma-aminobutyric acid catabolic process" evidence=IDA] [GO:0051287 "NAD binding" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0006950 "response to stress" evidence=IMP] [GO:0009408 "response to heat" evidence=IMP] [GO:0009416 "response to light stimulus" evidence=IMP] [GO:0072593 "reactive oxygen species metabolic process" evidence=IMP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] InterPro:IPR010102 InterPro:IPR015590 InterPro:IPR016160 InterPro:IPR016161 InterPro:IPR016162 InterPro:IPR016163 Pfam:PF00171 PROSITE:PS00070 PROSITE:PS00687 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009570 GO:GO:0051287 GO:GO:0005759 eggNOG:COG1012 Gene3D:G3DSA:3.40.309.10 Gene3D:G3DSA:3.40.605.10 SUPFAM:SSF53720 HOGENOM:HBG752218 GO:GO:0005507 GO:GO:0009408 GO:GO:0009416 GO:GO:0072593 HSSP:P05091 EMBL:AC007202 GO:GO:0009450 GO:GO:0006540 KO:K00135 TIGRFAMs:TIGR01780 GO:GO:0004777 OMA:MIQNKDD EMBL:AF117335 EMBL:AF428367 EMBL:AY056147 IPI:IPI00532908 PIR:E96825 RefSeq:NP_178062.1 UniGene:At.11884 ProteinModelPortal:Q9SAK4 SMR:Q9SAK4 STRING:Q9SAK4 PRIDE:Q9SAK4 EnsemblPlants:AT1G79440.1 GeneID:844282 KEGG:ath:AT1G79440 GeneFarm:4340 TAIR:At1g79440 InParanoid:Q9SAK4 PhylomeDB:Q9SAK4 ProtClustDB:PLN02278 ArrayExpress:Q9SEK4 Genevestigator:Q9SAK4 Uniprot:Q9SAK4

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig02002	124	542	-1.599	4.03E-37	TAIR|locus:2063922 - symbol:RCA "AT2G39730" species:3702 "Arabidopsis thaliana" [GO:0009507 "chloroplast" evidence=IDA;NAS] [GO:0030234 "enzyme regulator activity" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0005524 "ATP binding" evidence=IDA] [GO:0043531 "ADP binding" evidence=IDA] [GO:0046863 "ribulose-1,5-bisphosphate carboxylase/oxygenase activator activity" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0010319 "stromule" evidence=IDA] [GO:0042742 "defense response to bacterium" evidence=IEP] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009753 "response to jasmonic acid stimulus" evidence=IEP] [GO:0010150 "leaf senescence" evidence=IMP] [GO:0009416 "response to light stimulus" evidence=IEP] InterPro:IPR003959 Pfam:PF00004 GO:GO:0005524 GO:GO:0048046 GO:GO:0005634 GO:GO:0005618 GO:GO:0042742 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009753 GO:GO:0009941 GO:GO:0043531 GO:GO:0010150 GO:GO:0010319 GO:GO:0009409 GO:GO:0009416 GO:GO:0009535 GO:GO:0010287 EMBL:AC003000 UniGene:At.25263 EMBL:X14212 EMBL:M86720 EMBL:AY052703 EMBL:AF325049 EMBL:AY056108 EMBL:BT000710 EMBL:AY088487 IPI:IPI00518163 IPI:IPI00526733 PIR:S04048 PIR:T01002 PIR:T01003 RefSeq:NP_565913.1 RefSeq:NP_850320.1 UniGene:At.25299 UniGene:At.25319 UniGene:At.47493 ProteinModelPortal:P10896 SMR:P10896 IntAct:P10896 STRING:P10896 SWISS-2DPAGE:P10896 World-2DPAGE:0003:P10896 PRIDE:P10896 ProMEX:P10896 EnsemblPlants:AT2G39730.1 GeneID:818558 KEGG:ath:AT2G39730 TAIR:At2g39730 eggNOG:NOG316327 HOGENOM:HBG320501 InParanoid:P10896 OMA:WAPTRDD PhylomeDB:P10896 ProtClustDB:PLN00020 ArrayExpress:P10896 Genevestigator:P10896 GO:GO:0046863 Uniprot:P10896
Leaf	Isotig02003	122	540	-1.617	1.44E-37	TAIR|locus:2063922 - symbol:RCA "AT2G39730" species:3702 "Arabidopsis thaliana" [GO:0009507 "chloroplast" evidence=IDA;NAS] [GO:0030234 "enzyme regulator activity" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0005524 "ATP binding" evidence=IDA] [GO:0043531 "ADP binding" evidence=IDA] [GO:0046863 "ribulose-1,5-bisphosphate carboxylase/oxygenase activator activity" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0010319 "stromule" evidence=IDA] [GO:0042742 "defense response to bacterium" evidence=IEP] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009753 "response to jasmonic acid stimulus" evidence=IEP] [GO:0010150 "leaf senescence" evidence=IMP] [GO:0009416 "response to light stimulus" evidence=IEP] InterPro:IPR003959 Pfam:PF00004 GO:GO:0005524 GO:GO:0048046 GO:GO:0005634 GO:GO:0005618 GO:GO:0042742 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009753 GO:GO:0009941 GO:GO:0043531 GO:GO:0010150 GO:GO:0010319 GO:GO:0009409 GO:GO:0009416 GO:GO:0009535 GO:GO:0010287 EMBL:AC003000 UniGene:At.25263 EMBL:X14212 EMBL:M86720 EMBL:AY052703 EMBL:AF325049 EMBL:AY056108 EMBL:BT000710 EMBL:AY088487 IPI:IPI00518163 IPI:IPI00526733 PIR:S04048 PIR:T01002 PIR:T01003 RefSeq:NP_565913.1 RefSeq:NP_850320.1 UniGene:At.25299 UniGene:At.25319 UniGene:At.47493 ProteinModelPortal:P10896 SMR:P10896 IntAct:P10896 STRING:P10896 SWISS-2DPAGE:P10896 World-2DPAGE:0003:P10896 PRIDE:P10896 ProMEX:P10896 EnsemblPlants:AT2G39730.1 GeneID:818558 KEGG:ath:AT2G39730 TAIR:At2g39730 eggNOG:NOG316327 HOGENOM:HBG320501 InParanoid:P10896 OMA:WAPTRDD PhylomeDB:P10896 ProtClustDB:PLN00020 ArrayExpress:P10896 Genevestigator:P10896 GO:GO:0046863 Uniprot:P10896
Leaf	Isotig02004	122	538	-1.612	2.89E-37	TAIR|locus:2063922 - symbol:RCA "AT2G39730" species:3702 "Arabidopsis thaliana" [GO:0009507 "chloroplast" evidence=IDA;NAS] [GO:0030234 "enzyme regulator activity" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0005524 "ATP binding" evidence=IDA] [GO:0043531 "ADP binding" evidence=IDA] [GO:0046863 "ribulose-1,5-bisphosphate carboxylase/oxygenase activator activity" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0010319 "stromule" evidence=IDA] [GO:0042742 "defense response to bacterium" evidence=IEP] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009753 "response to jasmonic acid stimulus" evidence=IEP] [GO:0010150 "leaf senescence" evidence=IMP] [GO:0009416 "response to light stimulus" evidence=IEP] InterPro:IPR003959 Pfam:PF00004 GO:GO:0005524 GO:GO:0048046

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0005634 GO:GO:0005618 GO:GO:0042742 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009753 GO:GO:0009941 GO:GO:0043531 GO:GO:0010150 GO:GO:0010319 GO:GO:0009409 GO:GO:0009416 GO:GO:0009535 GO:GO:0010287 EMBL:AC003000 UniGene:At.25263 EMBL:X14212 EMBL:M86720 EMBL:AY052703 EMBL:AF325049 EMBL:AY056108 EMBL:BT000710 EMBL:AY088487 IPI:IPI00518163 IPI:IPI00526733 PIR:S04048 PIR:T01002 PIR:T01003 RefSeq:NP_565913.1 RefSeq:NP_850320.1 UniGene:At.25299 UniGene:At.25319 UniGene:At.47493 ProteinModelPortal:P10896 SMR:P10896 IntAct:P10896 STRING:P10896 SWISS-2DPAGE:P10896 World-2DPAGE:0003:P10896 PRIDE:P10896 ProMEX:P10896 EnsemblPlants:AT2G39730.1 GeneID:818558 KEGG:ath:AT2G39730 TAIR:At2g39730 eggNOG:NOG316327 HOGENOM:HBG320501 InParanoid:P10896 OMA:WAPTRDD PhylomeDB:P10896 ProtClustDB:PLN00020 ArrayExpress:P10896 Genevestigator:P10896 GO:GO:0046863 Uniprot:P10896
Leaf	Isotig02007	42	23	1.398	0.000117424	TAIR|locus:2103040 - symbol:APY1 "AT3G04080" species:3702 "Arabidopsis thaliana" [GO:0005516 "calmodulin binding" evidence=ISS;IDA] [GO:0016887 "ATPase activity" evidence=IDA] [GO:0017110 "nucleoside-diphosphatase activity" evidence=IGI;IDA] [GO:0009846 "pollen germination" evidence=IGI] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR000407 Pfam:PF01150 PROSITE:PS01238 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0016787 EMBL:AC016829 GO:GO:0009846 eggNOG:COG5371 PANTHER:PTHR11782 OMA:MATSWGA HOGENOM:HBG444677 EMBL:AF093604 EMBL:BT029157 IPI:IPI00522459 RefSeq:NP_187058.1 UniGene:At.16940 ProteinModelPortal:Q9SQG2 SMR:Q9SQG2 STRING:Q9SQG2 PRIDE:Q9SQG2 EnsemblPlants:AT3G04080.1 GeneID:819563 KEGG:ath:AT3G04080 TAIR:At3g04080 InParanoid:Q9SQG2 KO:K14641 PhylomeDB:Q9SQG2 ProtClustDB:CLSN2684264 Genevestigator:Q9SQG2 Uniprot:Q9SQG2
Leaf	Isotig02020	32	8	2.529	5.74E-07	TAIR|locus:2037863 - symbol:MBD10 "AT1G15340" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=ISS] [GO:0008150 "biological_process" evidence=ND] [GO:0008327 "methyl-CpG binding" evidence=ISS] [GO:0005634 "nucleus" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001739 InterPro:IPR016177 Pfam:PF01429 PROSITE:PS50982 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0005634 GO:GO:0006355 GO:GO:0003677 GO:GO:0006351 EMBL:AC007591 SUPFAM:SSF54171 Gene3D:G3DSA:3.30.890.10 EMBL:AY094439 EMBL:BT020367 EMBL:AK230256 IPI:IPI00519005 IPI:IPI00785822 PIR:G86287 RefSeq:NP_001185003.1 RefSeq:NP_563971.1 UniGene:At.27594 UniGene:At.70811 ProteinModelPortal:Q9XI36 SMR:Q9XI36 STRING:Q9XI36 PRIDE:Q9XI36 ProMEX:Q9XI36 EnsemblPlants:AT1G15340.1 GeneID:838103 KEGG:ath:AT1G15340 TAIR:At1g15340 eggNOG:NOG328305 InParanoid:Q9XI36 OMA:VTTEANG PhylomeDB:Q9XI36 ProtClustDB:CLSN2917009 Genevestigator:Q9XI36 Uniprot:Q9XI36
Leaf	Isotig02021	30	8	2.436	2.15E-06	TAIR|locus:2037863 - symbol:MBD10 "AT1G15340" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=ISS] [GO:0008150 "biological_process" evidence=ND] [GO:0008327 "methyl-CpG binding" evidence=ISS] [GO:0005634 "nucleus" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001739 InterPro:IPR016177 Pfam:PF01429 PROSITE:PS50982 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0005634 GO:GO:0006355 GO:GO:0003677 GO:GO:0006351 EMBL:AC007591 SUPFAM:SSF54171 Gene3D:G3DSA:3.30.890.10 EMBL:AY094439 EMBL:BT020367 EMBL:AK230256 IPI:IPI00519005 IPI:IPI00785822 PIR:G86287 RefSeq:NP_001185003.1 RefSeq:NP_563971.1 UniGene:At.27594 UniGene:At.70811 ProteinModelPortal:Q9XI36 SMR:Q9XI36 STRING:Q9XI36 PRIDE:Q9XI36 ProMEX:Q9XI36 EnsemblPlants:AT1G15340.1 GeneID:838103 KEGG:ath:AT1G15340 TAIR:At1g15340 eggNOG:NOG328305 InParanoid:Q9XI36 OMA:VTTEANG PhylomeDB:Q9XI36 ProtClustDB:CLSN2917009 Genevestigator:Q9XI36 Uniprot:Q9XI36
Leaf	Isotig02026	19	0	5.777	5.37E-07	TAIR|locus:2172868 - symbol:AAP7 "AT5G23810" species:3702 "Arabidopsis thaliana" [GO:0015171 "amino acid transmembrane transporter activity" evidence=ISS;IDA] [GO:0006865 "amino acid transport" evidence=ISS] [GO:0016020 "membrane" evidence=ISS] GO:GO:0016021 GO:GO:0005886 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0015293 InterPro:IPR013057 Pfam:PF01490 EMBL:AB005244 EMBL:AY052209 EMBL:AY143854 EMBL:AK316999 IPI:IPI00542702 IPI:IPI00657097 RefSeq:NP_001031934.1 RefSeq:NP_197770.1 UniGene:At.26436 ProteinModelPortal:Q9FF99 IntAct:Q9FF99 PRIDE:Q9FF99 EnsemblPlants:AT5G23810.1 GeneID:832446 KEGG:ath:AT5G23810 TAIR:At5g23810 eggNOG:NOG300888 InParanoid:Q9FF99 OMA:FANACII PhylomeDB:Q9FF99 ProtClustDB:CLSN2914855 GO:GO:0006865 Uniprot:Q9FF99

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig02027	19	0	5.777	5.37E-07	TAIR|locus:2172868 - symbol:AAP7 "AT5G23810" species:3702 "Arabidopsis thaliana" [GO:0015171 "amino acid transmembrane transporter activity" evidence=ISS;IDA] [GO:0006865 "amino acid transport" evidence=ISS] [GO:0016020 "membrane" evidence=ISS] GO:GO:0016021 GO:GO:0005886 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0015293 InterPro:IPR013057 Pfam:PF01490 EMBL:AB005244 EMBL:AY052209 EMBL:AY143854 EMBL:AK316999 IPI:IPI00542702 IPI:IPI00657097 RefSeq:NP_001031934.1 RefSeq:NP_197770.1 UniGene:At.26436 ProteinModelPortal:Q9FF99 IntAct:Q9FF99 PRIDE:Q9FF99 EnsemblPlants:AT5G23810.1 GeneID:832446 KEGG:ath:AT5G23810 TAIR:At5g23810 eggNOG:NOG300888 InParanoid:Q9FF99 OMA:FANACII PhylomeDB:Q9FF99 ProtClustDB:CLSN2914855 GO:GO:0006865 Uniprot:Q9FF99
Leaf	Isotig02039	35	19	1.410	0.000400435	TAIR|locus:2120653 - symbol:BGLU3 "beta glucosidase 2" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=IEA;ISS] [GO:0005975 "carbohydrate metabolic process" evidence=IEA] [GO:0043169 "cation binding" evidence=IEA] InterPro:IPR001360 InterPro:IPR013781 InterPro:IPR018120 Pfam:PF00232 PRINTS:PR00131 PROSITE:PS00572 PROSITE:PS00653 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0043169 InterPro:IPR017853 Gene3D:G3DSA:3.20.20.80 SUPFAM:SSF51445 GO:GO:0005975 EMBL:AL022140 EMBL:AL161556 GO:GO:0008422 CAZy:GH1 eggNOG:COG2723 HOGENOM:HBG316462 PANTHER:PTHR10353 ProtClustDB:PLN02849 HSSP:P26205 IPI:IPI00518392 PIR:T49117 RefSeq:NP_193941.2 UniGene:At.32568 ProteinModelPortal:O65458 SMR:O65458 PRIDE:O65458 EnsemblPlants:AT4G22100.1 GeneID:828299 KEGG:ath:AT4G22100 TAIR:At4g22100 OMA:APWAMES PhylomeDB:O65458 ArrayExpress:O65458 Genevestigator:O65458 Uniprot:O65458
Leaf	Isotig02041	6	35	-2.015	0.000149496	TAIR|locus:2099585 - symbol:G3Pp1 "AT3G47420" species:3702 "Arabidopsis thaliana" [GO:0005351 "sugar:hydrogen symporter activity" evidence=ISS] [GO:0008643 "carbohydrate transport" evidence=ISS] [GO:0055062 "phosphate ion homeostasis" evidence=IEP] InterPro:IPR000849 InterPro:IPR011701 Pfam:PF07690 PIRSF:PIRSF002808 GO:GO:0016021 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0055085 GO:GO:0005215 InterPro:IPR016196 SUPFAM:SSF103473 GO:GO:0008643 InterPro:IPR020846 PROSITE:PS50850 GO:GO:0055062 EMBL:AL096860 eggNOG:COG2271 EMBL:AF325105 EMBL:AF360170 IPI:IPI00539535 PIR:T12997 RefSeq:NP_566891.1 UniGene:At.24003 ProteinModelPortal:Q9C5L3 STRING:Q9C5L3 PRIDE:Q9C5L3 EnsemblPlants:AT3G47420.1 GeneID:823896 KEGG:ath:AT3G47420 TAIR:At3g47420 HOGENOM:HBG384033 InParanoid:Q9C5L3 KO:K13783 OMA:TLVTHSK PhylomeDB:Q9C5L3 ProtClustDB:CLSN2682304 ArrayExpress:Q9C5L3 Genevestigator:Q9C5L3 Uniprot:Q9C5L3
Leaf	Isotig02042	6	35	-2.015	0.000149496	TAIR|locus:2099585 - symbol:G3Pp1 "AT3G47420" species:3702 "Arabidopsis thaliana" [GO:0005351 "sugar:hydrogen symporter activity" evidence=ISS] [GO:0008643 "carbohydrate transport" evidence=ISS] [GO:0055062 "phosphate ion homeostasis" evidence=IEP] InterPro:IPR000849 InterPro:IPR011701 Pfam:PF07690 PIRSF:PIRSF002808 GO:GO:0016021 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0055085 GO:GO:0005215 InterPro:IPR016196 SUPFAM:SSF103473 GO:GO:0008643 InterPro:IPR020846 PROSITE:PS50850 GO:GO:0055062 EMBL:AL096860 eggNOG:COG2271 EMBL:AF325105 EMBL:AF360170 IPI:IPI00539535 PIR:T12997 RefSeq:NP_566891.1 UniGene:At.24003 ProteinModelPortal:Q9C5L3 STRING:Q9C5L3 PRIDE:Q9C5L3 EnsemblPlants:AT3G47420.1 GeneID:823896 KEGG:ath:AT3G47420 TAIR:At3g47420 HOGENOM:HBG384033 InParanoid:Q9C5L3 KO:K13783 OMA:TLVTHSK PhylomeDB:Q9C5L3 ProtClustDB:CLSN2682304 ArrayExpress:Q9C5L3 Genevestigator:Q9C5L3 Uniprot:Q9C5L3
Leaf	Isotig02044	45	122	-0.910	0.00010812	TAIR|locus:2080560 - symbol:CRD1 "COPPER RESPONSE DEFECT 1" species:3702 "Arabidopsis thaliana" [GO:0015979 "photosynthesis" evidence=IEA] [GO:0015995 "chlorophyll biosynthetic process" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0003677 "DNA binding" evidence=TAS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009706 "chloroplast inner membrane" evidence=IDA] [GO:0048529 "magnesium-protoporphyrin IX monomethyl ester (oxidative) cyclase activity" evidence=NAS;IMP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] InterPro:IPR003251 InterPro:IPR008434 InterPro:IPR009078 Pfam:PF02915 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0003677 GO:GO:0046914 GO:GO:0009706 GO:GO:0015995 GO:GO:0009535 GO:GO:0015979 EMBL:AL138655 InterPro:IPR012347 Gene3D:G3DSA:1.20.1260.10 SUPFAM:SSF47240 EMBL:U38232 EMBL:AF236101 EMBL:AY170319 EMBL:U75599 IPI:IPI00517126 PIR:T47754 RefSeq:NP_191253.1 UniGene:At.48778 UniGene:At.70999 ProteinModelPortal:Q9M591 STRING:Q9M591 PRIDE:Q9M591 EnsemblPlants:AT3G56940.1 GeneID:824861

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						KEGG:ath:AT3G56940 TAIR:At3g56940 eggNOG:NOG10633 HOGENOM:HBG284843 InParanoid:Q9M591 KO:K04035 OMA:HGDFFDA PhylomeDB:Q9M591 ProtClustDB:PLN02508 BioCyc:ARA:AT3G56940-MONOMER BioCyc:MetaCyc:AT3G56940-MONOMER Genevestigator:Q9M591 GermOnline:AT3G56940 GO:GO:0048529 TIGRFAMs:TIGR02029 Uniprot:Q9M591
Leaf	Isotig02045	43	121	-0.964	5.22E-05	TAIR|locus:2080560 - symbol:CRD1 "COPPER RESPONSE DEFECT 1" species:3702 "Arabidopsis thaliana" [GO:0015979 "photosynthesis" evidence=IEA] [GO:0015995 "chlorophyll biosynthetic process" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0003677 "DNA binding" evidence=TAS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009706 "chloroplast inner membrane" evidence=IDA] [GO:0048529 "magnesium-protoporphyrin IX monomethyl ester (oxidative) cyclase activity" evidence=NAS;IMP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] InterPro:IPR003251 InterPro:IPR008434 InterPro:IPR009078 Pfam:PF02915 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0003677 GO:GO:0046914 GO:GO:0009706 GO:GO:0015995 GO:GO:0009535 GO:GO:0015979 EMBL:AL138655 InterPro:IPR012347 Gene3D:G3DSA:1.20.1260.10 SUPFAM:SSF47240 EMBL:U38232 EMBL:AF236101 EMBL:AY170319 EMBL:U75599 IPI:IPI00517126 PIR:T47754 RefSeq:NP_191253.1 UniGene:At.48778 UniGene:At.70999 ProteinModelPortal:Q9M591 STRING:Q9M591 PRIDE:Q9M591 EnsemblPlants:AT3G56940.1 GeneID:824861 KEGG:ath:AT3G56940 TAIR:At3g56940 eggNOG:NOG10633 HOGENOM:HBG284843 InParanoid:Q9M591 KO:K04035 OMA:HGDFFDA PhylomeDB:Q9M591 ProtClustDB:PLN02508 BioCyc:ARA:AT3G56940-MONOMER BioCyc:MetaCyc:AT3G56940-MONOMER Genevestigator:Q9M591 GermOnline:AT3G56940 GO:GO:0048529 TIGRFAMs:TIGR02029 Uniprot:Q9M591
Leaf	Isotig02046	43	121	-0.964	5.22E-05	TAIR|locus:2080560 - symbol:CRD1 "COPPER RESPONSE DEFECT 1" species:3702 "Arabidopsis thaliana" [GO:0015979 "photosynthesis" evidence=IEA] [GO:0015995 "chlorophyll biosynthetic process" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0003677 "DNA binding" evidence=TAS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009706 "chloroplast inner membrane" evidence=IDA] [GO:0048529 "magnesium-protoporphyrin IX monomethyl ester (oxidative) cyclase activity" evidence=NAS;IMP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] InterPro:IPR003251 InterPro:IPR008434 InterPro:IPR009078 Pfam:PF02915 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0003677 GO:GO:0046914 GO:GO:0009706 GO:GO:0015995 GO:GO:0009535 GO:GO:0015979 EMBL:AL138655 InterPro:IPR012347 Gene3D:G3DSA:1.20.1260.10 SUPFAM:SSF47240 EMBL:U38232 EMBL:AF236101 EMBL:AY170319 EMBL:U75599 IPI:IPI00517126 PIR:T47754 RefSeq:NP_191253.1 UniGene:At.48778 UniGene:At.70999 ProteinModelPortal:Q9M591 STRING:Q9M591 PRIDE:Q9M591 EnsemblPlants:AT3G56940.1 GeneID:824861 KEGG:ath:AT3G56940 TAIR:At3g56940 eggNOG:NOG10633 HOGENOM:HBG284843 InParanoid:Q9M591 KO:K04035 OMA:HGDFFDA PhylomeDB:Q9M591 ProtClustDB:PLN02508 BioCyc:ARA:AT3G56940-MONOMER BioCyc:MetaCyc:AT3G56940-MONOMER Genevestigator:Q9M591 GermOnline:AT3G56940 GO:GO:0048529 TIGRFAMs:TIGR02029 Uniprot:Q9M591
Leaf	Isotig02047	10	0	4.851	0.000336918	No hit
Leaf	Isotig02048	10	0	4.851	0.000336918	TAIR|locus:2024770 - symbol:SR34 "AT1G02840" species:3702 "Arabidopsis thaliana" [GO:0003723 "RNA binding" evidence=ISS] [GO:0005634 "nucleus" evidence=ISS] [GO:0035061 "interchromatin granule" evidence=IDA] [GO:0016607 "nuclear speck" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] InterPro:IPR000504 InterPro:IPR012677 Pfam:PF00076 PROSITE:PS50102 SMART:SM00360 EMBL:CP002684 GO:GO:0005515 GO:GO:0008380 GO:GO:0000166 GO:GO:0006397 Gene3D:G3DSA:3.30.70.330 GO:GO:0003723 GO:GO:0016607 EMBL:AC009525 eggNOG:COG0724 KO:K12890 EMBL:M98340 EMBL:AF001035 EMBL:AY085920 IPI:IPI00521934 IPI:IPI00538714 PIR:F86158 PIR:S71185 RefSeq:NP_563665.3 RefSeq:NP_850933.1 UniGene:At.24497 ProteinModelPortal:O22315 SMR:O22315 IntAct:O22315 STRING:O22315 PRIDE:O22315 EnsemblPlants:AT1G02840.1 EnsemblPlants:AT1G02840.3 GeneID:839262 KEGG:ath:AT1G02840 GeneFarm:4677 TAIR:At1g02840 InParanoid:O22315 OMA:MSHGRNE PhylomeDB:O22315 ProtClustDB:CLSN2690659 Genevestigator:O22315 GO:GO:0035061 Uniprot:O22315
Leaf	Isotig02062	22	96	-1.597	8.81E-08	UNIPROTKB|P49364 - symbol:GDCST "Aminomethyltransferase, mitochondrial" species:3888 "Pisum sativum" [GO:0005960 "glycine cleavage complex" evidence=IDA] InterPro:IPR006222 InterPro:IPR006223 Pfam:PF01571 PIRSF:PIRSF006487 GO:GO:0005739 GO:GO:0008483 GO:GO:0004047 GO:GO:0006546 InterPro:IPR013977 Pfam:PF08669 GO:GO:0005960 PANTHER:PTHR13847:SF5 TIGRFAMs:TIGR00528 EMBL:X74793 EMBL:Z25861

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EMBL:AJ222771 PIR:S38370 PIR:S56661 ProteinModelPortal:P49364 SMR:P49364 IntAct:P49364 PRIDE:P49364 Uniprot:P49364
Leaf	Isotig02063	19	100	-1.867	1.11E-09	UNIPROTKB|P49364 - symbol:GDCST "Aminomethyltransferase, mitochondrial" species:3888 "Pisum sativum" [GO:0005960 "glycine cleavage complex" evidence=IDA] InterPro:IPR006222 InterPro:IPR006223 Pfam:PF01571 PIRSF:PIRSF006487 GO:GO:0005739 GO:GO:0008483 GO:GO:0004047 GO:GO:0006546 InterPro:IPR013977 Pfam:PF08669 GO:GO:0005960 PANTHER:PTHR13847:SF5 TIGRFAMs:TIGR00528 EMBL:X74793 EMBL:Z25861 EMBL:AJ222771 PIR:S38370 PIR:S56661 ProteinModelPortal:P49364 SMR:P49364 IntAct:P49364 PRIDE:P49364 Uniprot:P49364
Leaf	Isotig02064	23	79	-1.251	5.39E-05	UNIPROTKB|P49364 - symbol:GDCST "Aminomethyltransferase, mitochondrial" species:3888 "Pisum sativum" [GO:0005960 "glycine cleavage complex" evidence=IDA] InterPro:IPR006222 InterPro:IPR006223 Pfam:PF01571 PIRSF:PIRSF006487 GO:GO:0005739 GO:GO:0008483 GO:GO:0004047 GO:GO:0006546 InterPro:IPR013977 Pfam:PF08669 GO:GO:0005960 PANTHER:PTHR13847:SF5 TIGRFAMs:TIGR00528 EMBL:X74793 EMBL:Z25861 EMBL:AJ222771 PIR:S38370 PIR:S56661 ProteinModelPortal:P49364 SMR:P49364 IntAct:P49364 PRIDE:P49364 Uniprot:P49364
Leaf	Isotig02079	22	78	-1.297	3.69E-05	TAIR|locus:2091642 - symbol:AT3G14420 species:3702 "Arabidopsis thaliana" [GO:0008152 "metabolic process" evidence=IEA] [GO:0008891 "glycolate oxidase activity" evidence=ISS;IMP] [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0005634 "nucleus" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005777 "peroxisome" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000262 InterPro:IPR008259 InterPro:IPR012133 InterPro:IPR013785 Pfam:PF01070 PIRSF:PIRSF000138 PROSITE:PS00557 PROSITE:PS51349 GO:GO:0009506 GO:GO:0048046 GO:GO:0009570 GO:GO:0005634 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005777 GO:GO:0016020 Gene3D:G3DSA:3.20.20.70 GO:GO:0022626 GO:GO:0010181 eggNOG:COG1304 HOGENOM:HBG517781 EMBL:AB028617 GO:GO:0008891 EMBL:AY053412 EMBL:AF428396 EMBL:AF428328 EMBL:AY065122 EMBL:AY074830 EMBL:AY081566 EMBL:AK317539 IPI:IPI00528534 IPI:IPI00656816 RefSeq:NP_001030694.1 RefSeq:NP_188060.1 RefSeq:NP_850584.1 UniGene:At.21768 UniGene:At.67007 UniGene:At.71586 ProteinModelPortal:Q9LRR9 SMR:Q9LRR9 IntAct:Q9LRR9 STRING:Q9LRR9 PRIDE:Q9LRR9 ProMEX:Q9LRR9 EnsemblPlants:AT3G14420.1 EnsemblPlants:AT3G14420.2 GeneID:820665 KEGG:ath:AT3G14420 TAIR:At3g14420 InParanoid:Q9LRR9 KO:K11517 OMA:NSGLAEY PhylomeDB:Q9LRR9 ProtClustDB:PLN02493 Genevestigator:Q9LRR9 GO:GO:0052853 GO:GO:0052854 GO:GO:0052852 GO:GO:0009854 Uniprot:Q9LRR9
Leaf	Isotig02083	59	1	6.412	1.60E-18	TAIR|locus:2090552 - symbol:AT3G17520 "AT3G17520" species:3702 "Arabidopsis thaliana" [GO:0009793 "embryo development ending in seed dormancy" evidence=ISS] Pfam:PF02987 GenomeReviews:BA000014_GR InterPro:IPR004238 EMBL:BT004128 EMBL:BT020426 IPI:IPI00525902 STRING:Q84W82 PRIDE:Q84W82 TAIR:At3g17520 eggNOG:NOG269272 ArrayExpress:Q84W82 Genevestigator:Q84W82 Uniprot:Q84W82
Leaf	Isotig02084	58	1	6.387	3.00E-18	TAIR|locus:2090552 - symbol:AT3G17520 "AT3G17520" species:3702 "Arabidopsis thaliana" [GO:0009793 "embryo development ending in seed dormancy" evidence=ISS] Pfam:PF02987 GenomeReviews:BA000014_GR InterPro:IPR004238 EMBL:BT004128 EMBL:BT020426 IPI:IPI00525902 STRING:Q84W82 PRIDE:Q84W82 TAIR:At3g17520 eggNOG:NOG269272 ArrayExpress:Q84W82 Genevestigator:Q84W82 Uniprot:Q84W82
Leaf	Isotig02085	31	0	6.483	2.05E-10	No hit
Leaf	Isotig02086	15	0	5.436	8.75E-06	TAIR|locus:2043142 - symbol:HAI3 "highly ABA-induced PP2C gene 3" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004722 "protein serine/threonine phosphatase activity" evidence=IEA;ISS] [GO:0006470 "protein dephosphorylation" evidence=IEA] [GO:0008287 "protein serine/threonine phosphatase complex" evidence=IEA] InterPro:IPR000222 InterPro:IPR001932 Pfam:PF00481 PROSITE:PS01032 SMART:SM00331 SMART:SM00332 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0006470 GO:GO:0004722 GO:GO:0046872 eggNOG:COG0631 Gene3D:G3DSA:3.60.40.10 SUPFAM:SSF81606 EMBL:AC004561 GO:GO:0008287 InterPro:IPR015655 PANTHER:PTHR13832 HSSP:P35813 HOGENOM:HBG747569 KO:K14497 ProtClustDB:CLSN2682567 EMBL:DQ056553 EMBL:BT022047 EMBL:BT023483 IPI:IPI00536276 PIR:F84695 RefSeq:NP_180499.1 UniGene:At.50109 ProteinModelPortal:Q9ZW21 SMR:Q9ZW21 DIP:DIP-48991N IntAct:Q9ZW21 PRIDE:Q9ZW21 EnsemblPlants:AT2G29380.1 GeneID:817487 KEGG:ath:AT2G29380 TAIR:At2g29380 InParanoid:Q9ZW21 OMA:CRNGKPV PhylomeDB:Q9ZW21 ArrayExpress:Q9ZW21 Genevestigator:Q9ZW21 Uniprot:Q9ZW21

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig02087	15	0	5.436	8.75E-06	TAIR|locus:2043142 - symbol:HAI3 "highly ABA-induced PP2C gene 3" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004722 "protein serine/threonine phosphatase activity" evidence=IEA;ISS] [GO:0006470 "protein dephosphorylation" evidence=IEA] [GO:0008287 "protein serine/threonine phosphatase complex" evidence=IEA] InterPro:IPR000222 InterPro:IPR001932 Pfam:PF00481 PROSITE:PS01032 SMART:SM00331 SMART:SM00332 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0006470 GO:GO:0004722 GO:GO:0046872 eggNOG:COG0631 Gene3D:G3DSA:3.60.40.10 SUPFAM:SSF81606 EMBL:AC004561 GO:GO:0008287 InterPro:IPR015655 PANTHER:PTHR13832 HSSP:P35813 HOGENOM:HBG747569 KO:K14497 ProtClustDB:CLSN2682567 EMBL:DQ056553 EMBL:BT022047 EMBL:BT023483 IPI:IPI00536276 PIR:F84695 RefSeq:NP_180499.1 UniGene:At.50109 ProteinModelPortal:Q9ZW21 SMR:Q9ZW21 DIP:DIP-48991N IntAct:Q9ZW21 PRIDE:Q9ZW21 EnsemblPlants:AT2G29380.1 GeneID:817487 KEGG:ath:AT2G29380 TAIR:At2g29380 InParanoid:Q9ZW21 OMA:CRNGKPV PhylomeDB:Q9ZW21 ArrayExpress:Q9ZW21 Genevestigator:Q9ZW21 Uniprot:Q9ZW21
Leaf	Isotig02131	8	42	-1.863	8.04E-05	TAIR|locus:2101165 - symbol:AT3G48420 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0008152 "metabolic process" evidence=IEA] [GO:0016787 "hydrolase activity" evidence=IEA;ISS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] InterPro:IPR006402 GO:GO:0009570 EMBL:CP002686 InterPro:IPR023214 Gene3D:G3DSA:3.40.50.1000 SUPFAM:SSF56784 GO:GO:0009941 GO:GO:0016787 TIGRFAMs:TIGR01509 ProtClustDB:PLN02779 EMBL:AF370250 EMBL:AY063066 EMBL:AK118118 EMBL:AK175866 EMBL:AK176795 IPI:IPI00532424 RefSeq:NP_566903.1 UniGene:At.3168 ProteinModelPortal:Q94K71 SMR:Q94K71 STRING:Q94K71 PRIDE:Q94K71 ProMEX:Q94K71 EnsemblPlants:AT3G48420.1 GeneID:824000 KEGG:ath:AT3G48420 TAIR:At3g48420 InParanoid:Q94K71 OMA:RKTELFM PhylomeDB:Q94K71 ArrayExpress:Q94K71 Genevestigator:Q94K71 Uniprot:Q94K71
Leaf	Isotig02132	8	45	-1.963	2.38E-05	TAIR|locus:2101165 - symbol:AT3G48420 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0008152 "metabolic process" evidence=IEA] [GO:0016787 "hydrolase activity" evidence=IEA;ISS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] InterPro:IPR006402 GO:GO:0009570 EMBL:CP002686 InterPro:IPR023214 Gene3D:G3DSA:3.40.50.1000 SUPFAM:SSF56784 GO:GO:0009941 GO:GO:0016787 TIGRFAMs:TIGR01509 ProtClustDB:PLN02779 EMBL:AF370250 EMBL:AY063066 EMBL:AK118118 EMBL:AK175866 EMBL:AK176795 IPI:IPI00532424 RefSeq:NP_566903.1 UniGene:At.3168 ProteinModelPortal:Q94K71 SMR:Q94K71 STRING:Q94K71 PRIDE:Q94K71 ProMEX:Q94K71 EnsemblPlants:AT3G48420.1 GeneID:824000 KEGG:ath:AT3G48420 TAIR:At3g48420 InParanoid:Q94K71 OMA:RKTELFM PhylomeDB:Q94K71 ArrayExpress:Q94K71 Genevestigator:Q94K71 Uniprot:Q94K71
Leaf	Isotig02133	8	42	-1.863	8.04E-05	TAIR|locus:2101165 - symbol:AT3G48420 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0008152 "metabolic process" evidence=IEA] [GO:0016787 "hydrolase activity" evidence=IEA;ISS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] InterPro:IPR006402 GO:GO:0009570 EMBL:CP002686 InterPro:IPR023214 Gene3D:G3DSA:3.40.50.1000 SUPFAM:SSF56784 GO:GO:0009941 GO:GO:0016787 TIGRFAMs:TIGR01509 ProtClustDB:PLN02779 EMBL:AF370250 EMBL:AY063066 EMBL:AK118118 EMBL:AK175866 EMBL:AK176795 IPI:IPI00532424 RefSeq:NP_566903.1 UniGene:At.3168 ProteinModelPortal:Q94K71 SMR:Q94K71 STRING:Q94K71 PRIDE:Q94K71 ProMEX:Q94K71 EnsemblPlants:AT3G48420.1 GeneID:824000 KEGG:ath:AT3G48420 TAIR:At3g48420 InParanoid:Q94K71 OMA:RKTELFM PhylomeDB:Q94K71 ArrayExpress:Q94K71 Genevestigator:Q94K71 Uniprot:Q94K71
Leaf	Isotig02137	9	41	-1.659	0.000326768	TAIR|locus:2093387 - symbol:ASPGB1 "AT3G16150" species:3702 "Arabidopsis thaliana" [GO:0004067 "asparaginase activity" evidence=ISS;IDA] [GO:0006516 "glycoprotein catabolic process" evidence=ISS] [GO:0033345 "asparagine catabolic process via L-aspartate" evidence=IBA] [GO:0051604 "protein maturation" evidence=IBA] InterPro:IPR000246 Pfam:PF01112 PANTHER:PTHR10188 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0006508 EMBL:AB012247 eggNOG:COG1446 KO:K13051 GO:GO:0004067 HOGENOM:HBG735787 GO:GO:0008798 ProtClustDB:PLN02689 EMBL:AK118259 EMBL:AY086130 IPI:IPI00523779 IPI:IPI00679308 RefSeq:NP_566536.1 UniGene:At.38938 ProteinModelPortal:Q8GXG1 SMR:Q8GXG1 MEROPS:T02.A02 PRIDE:Q8GXG1 EnsemblPlants:AT3G16150.1 GeneID:820860 KEGG:ath:AT3G16150 GeneFarm:1943 TAIR:At3g16150 InParanoid:Q8GXG1 OMA:VEAIAYM PhylomeDB:Q8GXG1 Genevestigator:Q8GXG1 GermOnline:AT3G16150 Uniprot:Q8GXG1

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig02138	9	41	-1.659	0.000326768	TAIR|locus:2093387 - symbol:ASPGB1 "AT3G16150" species:3702 "Arabidopsis thaliana" [GO:0004067 "asparaginase activity" evidence=ISS;IDA] [GO:0006516 "glycoprotein catabolic process" evidence=ISS] [GO:0033345 "asparagine catabolic process via L-aspartate" evidence=IBA] [GO:0051604 "protein maturation" evidence=IBA] InterPro:IPR000246 Pfam:PF01112 PANTHER:PTHR10188 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0006508 EMBL:AB012247 eggNOG:COG1446 KO:K13051 GO:GO:0004067 HOGENOM:HBG735787 GO:GO:0008798 ProtClustDB:PLN02689 EMBL:AK118259 EMBL:AY086130 IPI:IPI00523779 IPI:IPI00679308 RefSeq:NP_566536.1 UniGene:At.38938 ProteinModelPortal:Q8GXG1 SMR:Q8GXG1 MEROPS:T02.A02 PRIDE:Q8GXG1 EnsemblPlants:AT3G16150.1 GeneID:820860 KEGG:ath:AT3G16150 GeneFarm:1943 TAIR:At3g16150 InParanoid:Q8GXG1 OMA:VEAIAYM PhylomeDB:Q8GXG1 Genevestigator:Q8GXG1 GermOnline:AT3G16150 Uniprot:Q8GXG1
Leaf	Isotig02139	9	41	-1.659	0.000326768	TAIR|locus:2093387 - symbol:ASPGB1 "AT3G16150" species:3702 "Arabidopsis thaliana" [GO:0004067 "asparaginase activity" evidence=ISS;IDA] [GO:0006516 "glycoprotein catabolic process" evidence=ISS] [GO:0033345 "asparagine catabolic process via L-aspartate" evidence=IBA] [GO:0051604 "protein maturation" evidence=IBA] InterPro:IPR000246 Pfam:PF01112 PANTHER:PTHR10188 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0006508 EMBL:AB012247 eggNOG:COG1446 KO:K13051 GO:GO:0004067 HOGENOM:HBG735787 GO:GO:0008798 ProtClustDB:PLN02689 EMBL:AK118259 EMBL:AY086130 IPI:IPI00523779 IPI:IPI00679308 RefSeq:NP_566536.1 UniGene:At.38938 ProteinModelPortal:Q8GXG1 SMR:Q8GXG1 MEROPS:T02.A02 PRIDE:Q8GXG1 EnsemblPlants:AT3G16150.1 GeneID:820860 KEGG:ath:AT3G16150 GeneFarm:1943 TAIR:At3g16150 InParanoid:Q8GXG1 OMA:VEAIAYM PhylomeDB:Q8GXG1 Genevestigator:Q8GXG1 GermOnline:AT3G16150 Uniprot:Q8GXG1
Leaf	Isotig02141	101	224	-0.620	0.000169781	TAIR|locus:2207320 - symbol:PSBR "AT1G79040" species:3702 "Arabidopsis thaliana" [GO:0009523 "photosystem II" evidence=ISS] [GO:0015979 "photosynthesis" evidence=ISS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0010270 "photosystem II oxygen evolving complex assembly" evidence=IEP] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] InterPro:IPR006814 Pfam:PF04725 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005515 UniGene:At.23809 GO:GO:0009535 UniGene:At.24218 EMBL:AC002986 GO:GO:0009654 EMBL:X55970 EMBL:AY070103 EMBL:AY096544 EMBL:AY084512 EMBL:Z17693 EMBL:Z17592 IPI:IPI00528572 PIR:S17430 RefSeq:NP_178025.1 UniGene:At.317 IntAct:P27202 STRING:P27202 PRIDE:P27202 ProMEX:P27202 EnsemblPlants:AT1G79040.1 GeneID:844245 KEGG:ath:AT1G79040 TAIR:At1g79040 eggNOG:NOG266360 HOGENOM:HBG600336 InParanoid:P27202 KO:K03541 OMA:IYNENEW PhylomeDB:P27202 ProtClustDB:PLN00053 BioCyc:MetaCyc:MONOMER-1068 ArrayExpress:P27202 Genevestigator:P27202 GermOnline:AT1G79040 GO:GO:0010270 Uniprot:P27202
Leaf	Isotig02142	79	213	-0.902	3.81E-07	TAIR|locus:2207320 - symbol:PSBR "AT1G79040" species:3702 "Arabidopsis thaliana" [GO:0009523 "photosystem II" evidence=ISS] [GO:0015979 "photosynthesis" evidence=ISS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0010270 "photosystem II oxygen evolving complex assembly" evidence=IEP] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] InterPro:IPR006814 Pfam:PF04725 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005515 UniGene:At.23809 GO:GO:0009535 UniGene:At.24218 EMBL:AC002986 GO:GO:0009654 EMBL:X55970 EMBL:AY070103 EMBL:AY096544 EMBL:AY084512 EMBL:Z17693 EMBL:Z17592 IPI:IPI00528572 PIR:S17430 RefSeq:NP_178025.1 UniGene:At.317 IntAct:P27202 STRING:P27202 PRIDE:P27202 ProMEX:P27202 EnsemblPlants:AT1G79040.1 GeneID:844245 KEGG:ath:AT1G79040 TAIR:At1g79040 eggNOG:NOG266360 HOGENOM:HBG600336 InParanoid:P27202 KO:K03541 OMA:IYNENEW PhylomeDB:P27202 ProtClustDB:PLN00053 BioCyc:MetaCyc:MONOMER-1068 ArrayExpress:P27202 Genevestigator:P27202 GermOnline:AT1G79040 GO:GO:0010270 Uniprot:P27202
Leaf	Isotig02146	118	1075	-2.659	6.71E-136	TAIR|locus:2185460 - symbol:CA2 "carbonic anhydrase 2" species:3702 "Arabidopsis thaliana" [GO:0004089 "carbonate dehydratase activity" evidence=IEA;ISS] [GO:0008270 "zinc ion binding" evidence=IEA;ISS] [GO:0015976 "carbon utilization" evidence=ISS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0042742 "defense response to bacterium" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] InterPro:IPR001765 InterPro:IPR015892 Pfam:PF00484 PROSITE:PS00704 PROSITE:PS00705 SMART:SM00947 GO:GO:0005829 GO:GO:0048046 GO:GO:0009570 EMBL:CP002688 GenomeReviews:BA000015_GR

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0042742 GO:GO:0008270 GO:GO:0031969 GO:GO:0015976 GO:GO:0009535 eggNOG:COG0288 GO:GO:0004089 Gene3D:G3DSA:3.40.1050.10 PANTHER:PTHR11002 SUPFAM:SSF53056 EMBL:L18901 EMBL:AL391149 EMBL:AF324712 EMBL:AF326863 EMBL:AF339686 EMBL:AF428428 EMBL:BT000652 EMBL:BT000663 EMBL:Z26538 IPI:IPI00523587 RefSeq:NP_568303.2 RefSeq:NP_974782.1 UniGene:At.23743 ProteinModelPortal:P42737 SMR:P42737 IntAct:P42737 STRING:P42737 SWISS-2DPAGE:P42737 PRIDE:P42737 ProMEX:P42737 EnsemblPlants:AT5G14740.2 GeneID:831326 KEGG:ath:AT5G14740 TAIR:At5g14740 HOGENOM:HBG711150 InParanoid:P42737 KO:K01673 PhylomeDB:P42737 ProtClustDB:CLSN2915215 ArrayExpress:P42737 Genevestigator:P42737 Uniprot:P42737
Leaf	Isotig02147	118	1075	-2.659	6.71E-136	TAIR|locus:2185460 - symbol:CA2 "carbonic anhydrase 2" species:3702 "Arabidopsis thaliana" [GO:0004089 "carbonate dehydratase activity" evidence=IEA;ISS] [GO:0008270 "zinc ion binding" evidence=IEA;ISS] [GO:0015976 "carbon utilization" evidence=ISS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0042742 "defense response to bacterium" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] InterPro:IPR001765 InterPro:IPR015892 Pfam:PF00484 PROSITE:PS00704 PROSITE:PS00705 SMART:SM00947 GO:GO:0005829 GO:GO:0048046 GO:GO:0009570 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0042742 GO:GO:0008270 GO:GO:0031969 GO:GO:0015976 GO:GO:0009535 eggNOG:COG0288 GO:GO:0004089 Gene3D:G3DSA:3.40.1050.10 PANTHER:PTHR11002 SUPFAM:SSF53056 EMBL:L18901 EMBL:AL391149 EMBL:AF324712 EMBL:AF326863 EMBL:AF339686 EMBL:AF428428 EMBL:BT000652 EMBL:BT000663 EMBL:Z26538 IPI:IPI00523587 RefSeq:NP_568303.2 RefSeq:NP_974782.1 UniGene:At.23743 ProteinModelPortal:P42737 SMR:P42737 IntAct:P42737 STRING:P42737 SWISS-2DPAGE:P42737 PRIDE:P42737 ProMEX:P42737 EnsemblPlants:AT5G14740.2 GeneID:831326 KEGG:ath:AT5G14740 TAIR:At5g14740 HOGENOM:HBG711150 InParanoid:P42737 KO:K01673 PhylomeDB:P42737 ProtClustDB:CLSN2915215 ArrayExpress:P42737 Genevestigator:P42737 Uniprot:P42737
Leaf	Isotig02148	118	1075	-2.659	6.71E-136	TAIR|locus:2185460 - symbol:CA2 "carbonic anhydrase 2" species:3702 "Arabidopsis thaliana" [GO:0004089 "carbonate dehydratase activity" evidence=IEA;ISS] [GO:0008270 "zinc ion binding" evidence=IEA;ISS] [GO:0015976 "carbon utilization" evidence=ISS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0042742 "defense response to bacterium" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] InterPro:IPR001765 InterPro:IPR015892 Pfam:PF00484 PROSITE:PS00704 PROSITE:PS00705 SMART:SM00947 GO:GO:0005829 GO:GO:0048046 GO:GO:0009570 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0042742 GO:GO:0008270 GO:GO:0031969 GO:GO:0015976 GO:GO:0009535 eggNOG:COG0288 GO:GO:0004089 Gene3D:G3DSA:3.40.1050.10 PANTHER:PTHR11002 SUPFAM:SSF53056 EMBL:L18901 EMBL:AL391149 EMBL:AF324712 EMBL:AF326863 EMBL:AF339686 EMBL:AF428428 EMBL:BT000652 EMBL:BT000663 EMBL:Z26538 IPI:IPI00523587 RefSeq:NP_568303.2 RefSeq:NP_974782.1 UniGene:At.23743 ProteinModelPortal:P42737 SMR:P42737 IntAct:P42737 STRING:P42737 SWISS-2DPAGE:P42737 PRIDE:P42737 ProMEX:P42737 EnsemblPlants:AT5G14740.2 GeneID:831326 KEGG:ath:AT5G14740 TAIR:At5g14740 HOGENOM:HBG711150 InParanoid:P42737 KO:K01673 PhylomeDB:P42737 ProtClustDB:CLSN2915215 ArrayExpress:P42737 Genevestigator:P42737 Uniprot:P42737
Leaf	Isotig02158	30	12	1.851	6.75E-05	TAIR|locus:2174572 - symbol:XTH12 "AT5G57530" species:3702 "Arabidopsis thaliana" [GO:0016798 "hydrolase activity, acting on glycosyl bonds" evidence=ISS] [GO:0005618 "cell wall" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0010411 "xyloglucan metabolic process" evidence=IDA] [GO:0033946 "xyloglucan-specific endo-beta-1,4-glucanase activity" evidence=IDA] [GO:0080039 "xyloglucan endotransglucosylase activity" evidence=IDA] InterPro:IPR000757 InterPro:IPR008263 InterPro:IPR010713 Pfam:PF00722 Pfam:PF06955 PROSITE:PS01034 GO:GO:0048046 GO:GO:0005737 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005618 GO:GO:0004553 InterPro:IPR008985 InterPro:IPR013320 Gene3D:G3DSA:2.60.120.200 SUPFAM:SSF49899 GO:GO:0007047 GO:GO:0010411 CAZy:GH16 eggNOG:COG2273 EMBL:AB011482 HOGENOM:HBG592277 KO:K08235 GO:GO:0016762 InterPro:IPR016455 PIRSF:PIRSF005604 EMBL:AY057625 EMBL:AY113025 IPI:IPI00524409 RefSeq:NP_200561.1 UniGene:At.26243 ProteinModelPortal:Q9FKL9 SMR:Q9FKL9 STRING:Q9FKL9 PRIDE:Q9FKL9 EnsemblPlants:AT5G57530.1 GeneID:835857 KEGG:ath:AT5G57530 TAIR:At5g57530 InParanoid:Q9FKL9 OMA:RANIFES PhylomeDB:Q9FKL9

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						ProtClustDB:CLSN2685868 ArrayExpress:Q9FKL9 Genevestigator:Q9FKL9 GermOnline:AT5G57530 GO:GO:0080039 Uniprot:Q9FKL9
Leaf	Isotig02159	29	11	1.928	5.67E-05	TAIR|locus:2174572 - symbol:XTH12 "AT5G57530" species:3702 "Arabidopsis thaliana" [GO:0016798 "hydrolase activity, acting on glycosyl bonds" evidence=ISS] [GO:0005618 "cell wall" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0010411 "xyloglucan metabolic process" evidence=IDA] [GO:0033946 "xyloglucan-specific endo-beta-1,4-glucanase activity" evidence=IDA] [GO:0080039 "xyloglucan endotransglucosylase activity" evidence=IDA] InterPro:IPR000757 InterPro:IPR008263 InterPro:IPR010713 Pfam:PF00722 Pfam:PF06955 PROSITE:PS01034 GO:GO:0048046 GO:GO:0005737 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005618 GO:GO:0004553 InterPro:IPR008985 InterPro:IPR013320 Gene3D:G3DSA:2.60.120.200 SUPFAM:SSF49899 GO:GO:0007047 GO:GO:0010411 CAZy:GH16 eggNOG:COG2273 EMBL:AB011482 HOGENOM:HBG592277 KO:K08235 GO:GO:0016762 InterPro:IPR016455 PIRSF:PIRSF005604 EMBL:AY057625 EMBL:AY113025 IPI:IPI00524409 RefSeq:NP_200561.1 UniGene:At.26243 ProteinModelPortal:Q9FKL9 SMR:Q9FKL9 STRING:Q9FKL9 PRIDE:Q9FKL9 EnsemblPlants:AT5G57530.1 GeneID:835857 KEGG:ath:AT5G57530 TAIR:At5g57530 InParanoid:Q9FKL9 OMA:RANIFES PhylomeDB:Q9FKL9 ProtClustDB:CLSN2685868 ArrayExpress:Q9FKL9 Genevestigator:Q9FKL9 GermOnline:AT5G57530 GO:GO:0080039 Uniprot:Q9FKL9
Leaf	Isotig02160	29	11	1.928	5.67E-05	TAIR|locus:2174572 - symbol:XTH12 "AT5G57530" species:3702 "Arabidopsis thaliana" [GO:0016798 "hydrolase activity, acting on glycosyl bonds" evidence=ISS] [GO:0005618 "cell wall" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0010411 "xyloglucan metabolic process" evidence=IDA] [GO:0033946 "xyloglucan-specific endo-beta-1,4-glucanase activity" evidence=IDA] [GO:0080039 "xyloglucan endotransglucosylase activity" evidence=IDA] InterPro:IPR000757 InterPro:IPR008263 InterPro:IPR010713 Pfam:PF00722 Pfam:PF06955 PROSITE:PS01034 GO:GO:0048046 GO:GO:0005737 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005618 GO:GO:0004553 InterPro:IPR008985 InterPro:IPR013320 Gene3D:G3DSA:2.60.120.200 SUPFAM:SSF49899 GO:GO:0007047 GO:GO:0010411 CAZy:GH16 eggNOG:COG2273 EMBL:AB011482 HOGENOM:HBG592277 KO:K08235 GO:GO:0016762 InterPro:IPR016455 PIRSF:PIRSF005604 EMBL:AY057625 EMBL:AY113025 IPI:IPI00524409 RefSeq:NP_200561.1 UniGene:At.26243 ProteinModelPortal:Q9FKL9 SMR:Q9FKL9 STRING:Q9FKL9 PRIDE:Q9FKL9 EnsemblPlants:AT5G57530.1 GeneID:835857 KEGG:ath:AT5G57530 TAIR:At5g57530 InParanoid:Q9FKL9 OMA:RANIFES PhylomeDB:Q9FKL9 ProtClustDB:CLSN2685868 ArrayExpress:Q9FKL9 Genevestigator:Q9FKL9 GermOnline:AT5G57530 GO:GO:0080039 Uniprot:Q9FKL9
Leaf	Isotig02167	42	16	1.921	1.33E-06	TAIR|locus:2159178 - symbol:AT5G61820 "AT5G61820" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0005773 "vacuole" evidence=IDA] GO:GO:0005773 EMBL:CP002688 EMBL:AY065363 EMBL:AY117191 IPI:IPI00526914 RefSeq:NP_200990.2 UniGene:At.24832 UniGene:At.67152 STRING:Q8VZ21 PRIDE:Q8VZ21 EnsemblPlants:AT5G61820.1 GeneID:836304 KEGG:ath:AT5G61820 TAIR:At5g61820 InParanoid:Q8VZ21 OMA:GGLYCCY PhylomeDB:Q8VZ21 ProtClustDB:CLSN2690257 Genevestigator:Q8VZ21 InterPro:IPR011692 Pfam:PF07712 Uniprot:Q8VZ21
Leaf	Isotig02185	14	3	2.751	0.000536578	TAIR|locus:2050019 - symbol:AT2G21520 species:3702 "Arabidopsis thaliana" [GO:0005215 "transporter activity" evidence=IEA;ISS] [GO:0006810 "transport" evidence=IEA;ISS] InterPro:IPR001071 PRINTS:PR00180 Pfam:PF03765 EMBL:CP002685 EMBL:AC006841 GO:GO:0005215 GO:GO:0005622 InterPro:IPR001251 Gene3D:G3DSA:3.40.525.10 SUPFAM:SSF52087 PROSITE:PS50191 SMART:SM00516 InterPro:IPR011074 Gene3D:G3DSA:1.10.8.20 Pfam:PF00650 SMART:SM01100 SUPFAM:SSF46938 eggNOG:NOG309458 IPI:IPI00891831 RefSeq:NP_001118356.1 UniGene:At.43802 UniGene:At.70982 ProteinModelPortal:B3H588 SMR:B3H588 EnsemblPlants:AT2G21520.2 GeneID:816691 KEGG:ath:AT2G21520 TAIR:At2g21520 PhylomeDB:B3H588 ProtClustDB:CLSN2689833 Genevestigator:B3H588 Uniprot:B3H588
Leaf	Isotig02194	1	33	-4.515	8.84E-08	TAIR|locus:2032748 - symbol:PS2 "phosphate starvation-induced gene 2" species:3702 "Arabidopsis thaliana" [GO:0008152 "metabolic process" evidence=IEA] [GO:0004427 "inorganic diphosphatase activity" evidence=IDA] [GO:0016036 "cellular response to phosphate starvation" evidence=IEP] [GO:0016462 "pyrophosphatase activity" evidence=IDA] [GO:0051262 "protein tetramerization" evidence=IDA] InterPro:IPR006383 InterPro:IPR006384 InterPro:IPR016965 Pfam:PF06888 PIRSF:PIRSF031051 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0051262 GO:GO:0046872 InterPro:IPR023214 Gene3D:G3DSA:3.40.50.1000 SUPFAM:SSF56784 GO:GO:0016036 GO:GO:0016791 GO:GO:0004427 EMBL:AC008017 TIGRFAMs:TIGR01489

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						TIGRFAMs:TIGR01488 eggNOG:NOG331523 HOGENOM:HBG319786 EMBL:AK176548 EMBL:BT030334 EMBL:AY085944 IPI:IPI00545079 PIR:E96755 RefSeq:NP_565052.1 UniGene:At.11680 ProteinModelPortal:Q67YC0 SMR:Q67YC0 DNASU:843632 EnsemblPlants:AT1G73010.1 GeneID:843632 KEGG:ath:AT1G73010 TAIR:At1g73010 InParanoid:Q67YC0 OMA:ASVVPWE PhylomeDB:Q67YC0 ProtClustDB:CLSN2685367 ArrayExpress:Q67YC0 Genevestigator:Q67YC0 Uniprot:Q67YC0
Leaf	Isotig02195	1	33	-4.515	8.84E-08	TAIR|locus:2032748 - symbol:PS2 "phosphate starvation-induced gene 2" species:3702 "Arabidopsis thaliana" [GO:0008152 "metabolic process" evidence=IEA] [GO:0004427 "inorganic diphosphatase activity" evidence=IDA] [GO:0016036 "cellular response to phosphate starvation" evidence=IEP] [GO:0016462 "pyrophosphatase activity" evidence=IDA] [GO:0051262 "protein tetramerization" evidence=IDA] InterPro:IPR006383 InterPro:IPR006384 InterPro:IPR016965 Pfam:PF06888 PIRSF:PIRSF031051 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0051262 GO:GO:0046872 InterPro:IPR023214 Gene3D:G3DSA:3.40.50.1000 SUPFAM:SSF56784 GO:GO:0016036 GO:GO:0016791 GO:GO:0004427 EMBL:AC008017 TIGRFAMs:TIGR01489 TIGRFAMs:TIGR01488 eggNOG:NOG331523 HOGENOM:HBG319786 EMBL:AK176548 EMBL:BT030334 EMBL:AY085944 IPI:IPI00545079 PIR:E96755 RefSeq:NP_565052.1 UniGene:At.11680 ProteinModelPortal:Q67YC0 SMR:Q67YC0 DNASU:843632 EnsemblPlants:AT1G73010.1 GeneID:843632 KEGG:ath:AT1G73010 TAIR:At1g73010 InParanoid:Q67YC0 OMA:ASVVPWE PhylomeDB:Q67YC0 ProtClustDB:CLSN2685367 ArrayExpress:Q67YC0 Genevestigator:Q67YC0 Uniprot:Q67YC0
Leaf	Isotig02196	1	33	-4.515	8.84E-08	TAIR|locus:2032748 - symbol:PS2 "phosphate starvation-induced gene 2" species:3702 "Arabidopsis thaliana" [GO:0008152 "metabolic process" evidence=IEA] [GO:0004427 "inorganic diphosphatase activity" evidence=IDA] [GO:0016036 "cellular response to phosphate starvation" evidence=IEP] [GO:0016462 "pyrophosphatase activity" evidence=IDA] [GO:0051262 "protein tetramerization" evidence=IDA] InterPro:IPR006383 InterPro:IPR006384 InterPro:IPR016965 Pfam:PF06888 PIRSF:PIRSF031051 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0051262 GO:GO:0046872 InterPro:IPR023214 Gene3D:G3DSA:3.40.50.1000 SUPFAM:SSF56784 GO:GO:0016036 GO:GO:0016791 GO:GO:0004427 EMBL:AC008017 TIGRFAMs:TIGR01489 TIGRFAMs:TIGR01488 eggNOG:NOG331523 HOGENOM:HBG319786 EMBL:AK176548 EMBL:BT030334 EMBL:AY085944 IPI:IPI00545079 PIR:E96755 RefSeq:NP_565052.1 UniGene:At.11680 ProteinModelPortal:Q67YC0 SMR:Q67YC0 DNASU:843632 EnsemblPlants:AT1G73010.1 GeneID:843632 KEGG:ath:AT1G73010 TAIR:At1g73010 InParanoid:Q67YC0 OMA:ASVVPWE PhylomeDB:Q67YC0 ProtClustDB:CLSN2685367 ArrayExpress:Q67YC0 Genevestigator:Q67YC0 Uniprot:Q67YC0
Leaf	Isotig02200	25	0	6.173	9.66E-09	No hit
Leaf	Isotig02201	25	0	6.173	9.66E-09	TAIR|locus:2026869 - symbol:AT1G68660 "AT1G68660" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0030163 "protein catabolic process" evidence=IEA] InterPro:IPR003769 Pfam:PF02617 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0006508 GO:GO:0030163 EMBL:AC008075 HOGENOM:HBG644923 KO:K06891 InterPro:IPR014719 Gene3D:G3DSA:3.30.1390.10 SUPFAM:SSF54736 GO:GO:0008233 UniGene:At.66838 EMBL:AF336921 EMBL:AY045615 EMBL:AY120696 EMBL:AY085795 IPI:IPI00522034 PIR:B96711 RefSeq:NP_564937.1 UniGene:At.24277 HSSP:P75832 ProteinModelPortal:Q9SX29 SMR:Q9SX29 STRING:Q9SX29 PRIDE:Q9SX29 EnsemblPlants:AT1G68660.1 GeneID:843196 KEGG:ath:AT1G68660 TAIR:At1g68660 InParanoid:Q9SX29 OMA:ICAQADA PhylomeDB:Q9SX29 ProtClustDB:CLSN2917405 ArrayExpress:Q9SX29 Genevestigator:Q9SX29 Uniprot:Q9SX29
Leaf	Isotig02202	25	0	6.173	9.66E-09	TAIR|locus:2026869 - symbol:AT1G68660 "AT1G68660" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0030163 "protein catabolic process" evidence=IEA] InterPro:IPR003769 Pfam:PF02617 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0006508 GO:GO:0030163 EMBL:AC008075 HOGENOM:HBG644923 KO:K06891 InterPro:IPR014719 Gene3D:G3DSA:3.30.1390.10 SUPFAM:SSF54736 GO:GO:0008233 UniGene:At.66838 EMBL:AF336921 EMBL:AY045615 EMBL:AY120696 EMBL:AY085795 IPI:IPI00522034 PIR:B96711 RefSeq:NP_564937.1 UniGene:At.24277 HSSP:P75832 ProteinModelPortal:Q9SX29 SMR:Q9SX29 STRING:Q9SX29 PRIDE:Q9SX29 EnsemblPlants:AT1G68660.1 GeneID:843196 KEGG:ath:AT1G68660 TAIR:At1g68660 InParanoid:Q9SX29 OMA:ICAQADA PhylomeDB:Q9SX29 ProtClustDB:CLSN2917405 ArrayExpress:Q9SX29 Genevestigator:Q9SX29 Uniprot:Q9SX29
Leaf	Isotig02206	13	113	-2.591	2.23E-15	TAIR|locus:2008555 - symbol:PSBY "AT1G67740" species:3702 "Arabidopsis thaliana" [GO:0015979 "photosynthesis" evidence=ISS;TAS] [GO:0030095 "chloroplast photosystem II" evidence=ISS] [GO:0030145 "manganese ion binding" evidence=IEA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009523 "photosystem II" evidence=ISS] [GO:0009533 "chloroplast stromal thylakoid" evidence=IDA]

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						InterPro:IPR009388 Pfam:PF06298 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0030145 GO:GO:0009535 GO:GO:0015979 EMBL:AC008113 GO:GO:0009523 GO:GO:0009533 EMBL:AJ223306 EMBL:AF079800 EMBL:AY050391 EMBL:AY052269 EMBL:AY097348 IPI:IPI00519144 PIR:T51847 RefSeq:NP_176940.1 UniGene:At.24847 STRING:O49347 PRIDE:O49347 EnsemblPlants:AT1G67740.1 GeneID:843099 KEGG:ath:AT1G67740 TAIR:At1g67740 eggNOG:NOG245422 HOGENOM:HBG600988 InParanoid:O49347 KO:K02723 OMA:IAWVLYN PhylomeDB:O49347 ProtClustDB:PLN00063 BioCyc:MetaCyc:MONOMER-1067 ArrayExpress:O49347 Genevestigator:O49347 GermOnline:AT1G67740 Uniprot:O49347
Leaf	Isotig02207	14	106	-2.392	2.19E-13	TAIR|locus:2008555 - symbol:PSBY "AT1G67740" species:3702 "Arabidopsis thaliana" [GO:0015979 "photosynthesis" evidence=ISS;TAS] [GO:0030095 "chloroplast photosystem II" evidence=ISS] [GO:0030145 "manganese ion binding" evidence=IEA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009523 "photosystem II" evidence=ISS] [GO:0009533 "chloroplast stromal thylakoid" evidence=IDA] InterPro:IPR009388 Pfam:PF06298 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0030145 GO:GO:0009535 GO:GO:0015979 EMBL:AC008113 GO:GO:0009523 GO:GO:0009533 EMBL:AJ223306 EMBL:AF079800 EMBL:AY050391 EMBL:AY052269 EMBL:AY097348 IPI:IPI00519144 PIR:T51847 RefSeq:NP_176940.1 UniGene:At.24847 STRING:O49347 PRIDE:O49347 EnsemblPlants:AT1G67740.1 GeneID:843099 KEGG:ath:AT1G67740 TAIR:At1g67740 eggNOG:NOG245422 HOGENOM:HBG600988 InParanoid:O49347 KO:K02723 OMA:IAWVLYN PhylomeDB:O49347 ProtClustDB:PLN00063 BioCyc:MetaCyc:MONOMER-1067 ArrayExpress:O49347 Genevestigator:O49347 GermOnline:AT1G67740 Uniprot:O49347
Leaf	Isotig02208	20	98	-1.764	6.60E-09	TAIR|locus:2008555 - symbol:PSBY "AT1G67740" species:3702 "Arabidopsis thaliana" [GO:0015979 "photosynthesis" evidence=ISS;TAS] [GO:0030095 "chloroplast photosystem II" evidence=ISS] [GO:0030145 "manganese ion binding" evidence=IEA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009523 "photosystem II" evidence=ISS] [GO:0009533 "chloroplast stromal thylakoid" evidence=IDA] InterPro:IPR009388 Pfam:PF06298 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0030145 GO:GO:0009535 GO:GO:0015979 EMBL:AC008113 GO:GO:0009523 GO:GO:0009533 EMBL:AJ223306 EMBL:AF079800 EMBL:AY050391 EMBL:AY052269 EMBL:AY097348 IPI:IPI00519144 PIR:T51847 RefSeq:NP_176940.1 UniGene:At.24847 STRING:O49347 PRIDE:O49347 EnsemblPlants:AT1G67740.1 GeneID:843099 KEGG:ath:AT1G67740 TAIR:At1g67740 eggNOG:NOG245422 HOGENOM:HBG600988 InParanoid:O49347 KO:K02723 OMA:IAWVLYN PhylomeDB:O49347 ProtClustDB:PLN00063 BioCyc:MetaCyc:MONOMER-1067 ArrayExpress:O49347 Genevestigator:O49347 GermOnline:AT1G67740 Uniprot:O49347
Leaf	Isotig02218	16	4	2.529	0.000407249	TAIR|locus:2012773 - symbol:ERD9 "AT1G10370" species:3702 "Arabidopsis thaliana" [GO:0004364 "glutathione transferase activity" evidence=ISS;IDA] [GO:0005737 "cytoplasm" evidence=NAS] [GO:0009407 "toxin catabolic process" evidence=TAS] [GO:0009507 "chloroplast" evidence=IDA] [GO:0080167 "response to karrikin" evidence=IEP] [GO:0006749 "glutathione metabolic process" evidence=IMP] [GO:0009704 "de-etiolation" evidence=IMP] [GO:0048527 "lateral root development" evidence=IMP] [GO:0060416 "response to growth hormone stimulus" evidence=IEP] [GO:0009651 "response to salt stress" evidence=IMP] [GO:0080148 "negative regulation of response to water deprivation" evidence=IMP] InterPro:IPR004045 PROSITE:PS50404 InterPro:IPR004046 Pfam:PF00043 EMBL:CP002684 GO:GO:0005829 GO:GO:0009507 GO:GO:0009651 GO:GO:0080167 GO:GO:0048527 GO:GO:0009636 GO:GO:0040008 InterPro:IPR012336 Gene3D:G3DSA:3.40.30.10 SUPFAM:SSF52833 InterPro:IPR010987 Gene3D:G3DSA:1.20.1050.10 SUPFAM:SSF47616 PROSITE:PS50405 GO:GO:0060416 EMBL:AC005489 GO:GO:0006749 InterPro:IPR017933 GO:GO:0004364 GO:GO:0009407 eggNOG:NOG288793 HOGENOM:HBG749301 HSSP:O04941 EMBL:AB039930 EMBL:AF288191 EMBL:BT023743 IPI:IPI00532578 RefSeq:NP_172508.4 UniGene:At.11290 ProteinModelPortal:Q9FUS8 SMR:Q9FUS8 PRIDE:Q9FUS8 EnsemblPlants:AT1G10370.1 GeneID:837576 KEGG:ath:AT1G10370 TAIR:At1g10370 InParanoid:Q9FUS8 ProtClustDB:CLSN2679578 Genevestigator:Q9FUS8 GO:GO:0009704 GO:GO:0080148 Uniprot:Q9FUS8
Leaf	Isotig02219	18	5	2.377	0.000296328	TAIR|locus:2012773 - symbol:ERD9 "AT1G10370" species:3702 "Arabidopsis thaliana" [GO:0004364 "glutathione transferase activity" evidence=ISS;IDA] [GO:0005737 "cytoplasm" evidence=NAS] [GO:0009407 "toxin catabolic process" evidence=TAS] [GO:0009507 "chloroplast" evidence=IDA] [GO:0080167 "response to karrikin" evidence=IEP] [GO:0006749 "glutathione metabolic process" evidence=IMP] [GO:0009704 "de-etiolation"

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						evidence=IMP] [GO:0048527 "lateral root development" evidence=IMP] [GO:0060416 "response to growth hormone stimulus" evidence=IEP] [GO:0009651 "response to salt stress" evidence=IMP] [GO:0080148 "negative regulation of response to water deprivation" evidence=IMP] InterPro:IPR004045 PROSITE:PS50404 InterPro:IPR004046 Pfam:PF00043 EMBL:CP002684 GO:GO:0005829 GO:GO:0009507 GO:GO:0009651 GO:GO:0080167 GO:GO:0048527 GO:GO:0009636 GO:GO:0040008 InterPro:IPR012336 Gene3D:G3DSA:3.40.30.10 SUPFAM:SSF52833 InterPro:IPR010987 Gene3D:G3DSA:1.20.1050.10 SUPFAM:SSF47616 PROSITE:PS50405 GO:GO:0060416 EMBL:AC005489 GO:GO:0006749 InterPro:IPR017933 GO:GO:0004364 GO:GO:0009407 eggNOG:NOG288793 HOGENOM:HBG749301 HSSP:O04941 EMBL:AB039930 EMBL:AF288191 EMBL:BT023743 IPI:IPI00532578 RefSeq:NP_172508.4 UniGene:At.11290 ProteinModelPortal:Q9FUS8 SMR:Q9FUS8 PRIDE:Q9FUS8 EnsemblPlants:AT1G10370.1 GeneID:837576 KEGG:ath:AT1G10370 TAIR:At1g10370 InParanoid:Q9FUS8 ProtClustDB:CLSN2679578 Genevestigator:Q9FUS8 GO:GO:0009704 GO:GO:0080148 Uniprot:Q9FUS8
Leaf	Isotig02230	16	0	5.529	4.31E-06	No hit
Leaf	Isotig02232	13	0	5.229	3.68E-05	No hit
Leaf	Isotig02236	5	74	-3.359	3.33E-13	TAIR|locus:2040934 - symbol:LHB1B2 "AT2G34420" species:3702 "Arabidopsis thaliana" [GO:0009769 "photosynthesis, light harvesting in photosystem II" evidence=TAS] [GO:0016168 "chlorophyll binding" evidence=ISS;TAS] [GO:0030076 "light-harvesting complex" evidence=ISS] [GO:0042651 "thylakoid membrane" evidence=TAS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0015979 "photosynthesis" evidence=ISS] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR001344 Pfam:PF00504 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009535 GO:GO:0010287 EMBL:AC004077 EMBL:AC004481 HOGENOM:HBG618504 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 UniGene:At.10812 UniGene:At.24351 UniGene:At.32199 UniGene:At.66422 UniGene:At.71449 UniGene:At.71528 KO:K08912 ProtClustDB:PLN00025 UniGene:At.23647 UniGene:At.27457 UniGene:At.24888 EMBL:AF372886 EMBL:AY039561 EMBL:AY045806 EMBL:AF428397 EMBL:AF419548 EMBL:AF419587 EMBL:AY065125 EMBL:AY079101 EMBL:AY079110 EMBL:AY081587 EMBL:AY142513 EMBL:AK229627 EMBL:X64460 IPI:IPI00530785 PIR:S23546 RefSeq:NP_565786.1 UniGene:At.24064 UniGene:At.71003 UniGene:At.71384 ProteinModelPortal:Q39141 SMR:Q39141 IntAct:Q39141 STRING:Q39141 PRIDE:Q39141 EnsemblPlants:AT2G34420.1 GeneID:818005 KEGG:ath:AT2G34420 TAIR:At2g34420 InParanoid:Q39141 OMA:SILAIWG PhylomeDB:Q39141 ArrayExpress:Q39141 Genevestigator:Q39141 Uniprot:Q39141
Leaf	Isotig02237	5	75	-3.378	2.03E-13	TAIR|locus:2040934 - symbol:LHB1B2 "AT2G34420" species:3702 "Arabidopsis thaliana" [GO:0009769 "photosynthesis, light harvesting in photosystem II" evidence=TAS] [GO:0016168 "chlorophyll binding" evidence=ISS;TAS] [GO:0030076 "light-harvesting complex" evidence=ISS] [GO:0042651 "thylakoid membrane" evidence=TAS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0015979 "photosynthesis" evidence=ISS] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR001344 Pfam:PF00504 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009535 GO:GO:0010287 EMBL:AC004077 EMBL:AC004481 HOGENOM:HBG618504 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 UniGene:At.10812 UniGene:At.24351 UniGene:At.32199 UniGene:At.66422 UniGene:At.71449 UniGene:At.71528 KO:K08912 ProtClustDB:PLN00025 UniGene:At.23647 UniGene:At.27457 UniGene:At.24888 EMBL:AF372886 EMBL:AY039561 EMBL:AY045806 EMBL:AF428397 EMBL:AF419548 EMBL:AF419587 EMBL:AY065125 EMBL:AY079101 EMBL:AY079110 EMBL:AY081587 EMBL:AY142513 EMBL:AK229627 EMBL:X64460 IPI:IPI00530785 PIR:S23546 RefSeq:NP_565786.1 UniGene:At.24064 UniGene:At.71003 UniGene:At.71384 ProteinModelPortal:Q39141 SMR:Q39141 IntAct:Q39141 STRING:Q39141 PRIDE:Q39141 EnsemblPlants:AT2G34420.1 GeneID:818005 KEGG:ath:AT2G34420 TAIR:At2g34420 InParanoid:Q39141 OMA:SILAIWG PhylomeDB:Q39141 ArrayExpress:Q39141 Genevestigator:Q39141 Uniprot:Q39141
Leaf	Isotig02238	6	66	-2.930	1.04E-10	TAIR|locus:2040934 - symbol:LHB1B2 "AT2G34420" species:3702 "Arabidopsis thaliana" [GO:0009769 "photosynthesis, light harvesting in photosystem II" evidence=TAS] [GO:0016168 "chlorophyll binding"

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						evidence=ISS;TAS] [GO:0030076 "light-harvesting complex" evidence=ISS] [GO:0042651 "thylakoid membrane" evidence=TAS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0015979 "photosynthesis" evidence=ISS] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR001344 Pfam:PF00504 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009535 GO:GO:0010287 EMBL:AC004077 EMBL:AC004481 HOGENOM:HBG618504 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 UniGene:At.10812 UniGene:At.24351 UniGene:At.32199 UniGene:At.66422 UniGene:At.71449 UniGene:At.71528 KO:K08912 ProtClustDB:PLN00025 UniGene:At.23647 UniGene:At.27457 UniGene:At.24888 EMBL:AF372886 EMBL:AY039561 EMBL:AY045806 EMBL:AF428397 EMBL:AF419548 EMBL:AF419587 EMBL:AY065125 EMBL:AY079101 EMBL:AY079110 EMBL:AY081587 EMBL:AY142513 EMBL:AK229627 EMBL:X64460 IPI:IPI00530785 PIR:S23546 RefSeq:NP_565786.1 UniGene:At.24064 UniGene:At.71003 UniGene:At.71384 ProteinModelPortal:Q39141 SMR:Q39141 IntAct:Q39141 STRING:Q39141 PRIDE:Q39141 EnsemblPlants:AT2G34420.1 GeneID:818005 KEGG:ath:AT2G34420 TAIR:At2g34420 InParanoid:Q39141 OMA:SILAIWG PhylomeDB:Q39141 ArrayExpress:Q39141 Genevestigator:Q39141 Uniprot:Q39141
Leaf	Isotig02239	30	6	2.851	2.45E-07	TAIR|locus:2183740 - symbol:CBSX3 "AT5G10860" species:3702 "Arabidopsis thaliana" [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0050897 "cobalt ion binding" evidence=IDA] [GO:0045454 "cell redox homeostasis" evidence=IDA] InterPro:IPR000644 InterPro:IPR013785 Pfam:PF00571 PROSITE:PS51371 SMART:SM00116 GO:GO:0005739 EMBL:CP002688 GenomeReviews:BA000015_GR Gene3D:G3DSA:3.20.20.70 GO:GO:0003824 eggNOG:COG0517 GO:GO:0009651 GO:GO:0050897 GO:GO:0045454 EMBL:AL365234 HOGENOM:HBG739441 EMBL:AF361845 EMBL:AY066046 IPI:IPI00520382 PIR:T50795 RefSeq:NP_196647.1 UniGene:At.28210 ProteinModelPortal:Q9LEV3 SMR:Q9LEV3 STRING:Q9LEV3 PRIDE:Q9LEV3 ProMEX:Q9LEV3 EnsemblPlants:AT5G10860.1 GeneID:830953 KEGG:ath:AT5G10860 GeneFarm:1947 TAIR:At5g10860 InParanoid:Q9LEV3 OMA:TENRLRH PhylomeDB:Q9LEV3 ProtClustDB:CLSN2686434 ArrayExpress:Q9LEV3 Genevestigator:Q9LEV3 GermOnline:AT5G10860 Uniprot:Q9LEV3
Leaf	Isotig02240	29	6	2.802	4.91E-07	TAIR|locus:2183740 - symbol:CBSX3 "AT5G10860" species:3702 "Arabidopsis thaliana" [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0050897 "cobalt ion binding" evidence=IDA] [GO:0045454 "cell redox homeostasis" evidence=IDA] InterPro:IPR000644 InterPro:IPR013785 Pfam:PF00571 PROSITE:PS51371 SMART:SM00116 GO:GO:0005739 EMBL:CP002688 GenomeReviews:BA000015_GR Gene3D:G3DSA:3.20.20.70 GO:GO:0003824 eggNOG:COG0517 GO:GO:0009651 GO:GO:0050897 GO:GO:0045454 EMBL:AL365234 HOGENOM:HBG739441 EMBL:AF361845 EMBL:AY066046 IPI:IPI00520382 PIR:T50795 RefSeq:NP_196647.1 UniGene:At.28210 ProteinModelPortal:Q9LEV3 SMR:Q9LEV3 STRING:Q9LEV3 PRIDE:Q9LEV3 ProMEX:Q9LEV3 EnsemblPlants:AT5G10860.1 GeneID:830953 KEGG:ath:AT5G10860 GeneFarm:1947 TAIR:At5g10860 InParanoid:Q9LEV3 OMA:TENRLRH PhylomeDB:Q9LEV3 ProtClustDB:CLSN2686434 ArrayExpress:Q9LEV3 Genevestigator:Q9LEV3 GermOnline:AT5G10860 Uniprot:Q9LEV3
Leaf	Isotig02241	29	6	2.802	4.91E-07	TAIR|locus:2183740 - symbol:CBSX3 "AT5G10860" species:3702 "Arabidopsis thaliana" [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0050897 "cobalt ion binding" evidence=IDA] [GO:0045454 "cell redox homeostasis" evidence=IDA] InterPro:IPR000644 InterPro:IPR013785 Pfam:PF00571 PROSITE:PS51371 SMART:SM00116 GO:GO:0005739 EMBL:CP002688 GenomeReviews:BA000015_GR Gene3D:G3DSA:3.20.20.70 GO:GO:0003824 eggNOG:COG0517 GO:GO:0009651 GO:GO:0050897 GO:GO:0045454 EMBL:AL365234 HOGENOM:HBG739441 EMBL:AF361845 EMBL:AY066046 IPI:IPI00520382 PIR:T50795 RefSeq:NP_196647.1 UniGene:At.28210 ProteinModelPortal:Q9LEV3 SMR:Q9LEV3 STRING:Q9LEV3 PRIDE:Q9LEV3 ProMEX:Q9LEV3 EnsemblPlants:AT5G10860.1 GeneID:830953 KEGG:ath:AT5G10860 GeneFarm:1947 TAIR:At5g10860 InParanoid:Q9LEV3 OMA:TENRLRH PhylomeDB:Q9LEV3 ProtClustDB:CLSN2686434 ArrayExpress:Q9LEV3 Genevestigator:Q9LEV3 GermOnline:AT5G10860 Uniprot:Q9LEV3
Leaf	Isotig02242	17	5	2.294	0.000574458	TAIR|locus:2032100 - symbol:GSTU19 "AT1G78380" species:3702 "Arabidopsis thaliana" [GO:0004364 "glutathione transferase activity" evidence=ISS] [GO:0005737 "cytoplasm" evidence=NAS] [GO:0009407 "toxin catabolic process" evidence=TAS] [GO:0006979 "response to oxidative stress" evidence=IEP] [GO:0042631

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						"cellular response to water deprivation" evidence=IEP] [GO:0043295 "glutathione binding" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR004045 PROSITE:PS50404 InterPro:IPR004046 Pfam:PF00043 EMBL:CP002684 GO:GO:0005829 GO:GO:0005886 GO:GO:0009570 GO:GO:0046686 EMBL:AC013430 GO:GO:0005774 GO:GO:0006979 GO:GO:0009636 InterPro:IPR012336 Gene3D:G3DSA:3.40.30.10 SUPFAM:SSF52833 GO:GO:0004601 InterPro:IPR010987 Gene3D:G3DSA:1.20.1050.10 SUPFAM:SSF47616 PROSITE:PS50405 GO:GO:0042631 InterPro:IPR017933 GO:GO:0004364 GO:GO:0043295 HSSP:O65032 GO:GO:0009407 EMBL:AJ012571 EMBL:AF385691 EMBL:AY078012 EMBL:AY087032 IPI:IPI00655471 PIR:T51607 RefSeq:NP_565178.1 UniGene:At.25493 UniGene:At.67704 ProteinModelPortal:Q9ZRW8 SMR:Q9ZRW8 IntAct:Q9ZRW8 STRING:Q9ZRW8 PRIDE:Q8LBS1 EnsemblPlants:AT1G78380.1 GeneID:844174 KEGG:ath:AT1G78380 TAIR:At1g78380 InParanoid:Q9ZRW8 OMA:MANEVIL PhylomeDB:Q9ZRW8 Genevestigator:Q9ZRW8 Uniprot:Q9ZRW8
Leaf	Isotig02263	70	17	2.571	8.46E-14	No hit
Leaf	Isotig02265	63	13	2.806	1.18E-13	No hit
Leaf	Isotig02266	1	17	-3.559	0.000355264	TAIR|locus:2131849 - symbol:DREB1A "AT4G25480" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=ISS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS;IDA] [GO:0005634 "nucleus" evidence=ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=ISS] [GO:0009409 "response to cold" evidence=IEP;IDA;IMP;TAS] [GO:0009414 "response to water deprivation" evidence=IMP;IDA] [GO:0009631 "cold acclimation" evidence=IMP] InterPro:IPR001471 InterPro:IPR016177 Pfam:PF00847 PRINTS:PR00367 PROSITE:PS51032 SMART:SM00380 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005634 GO:GO:0003677 GO:GO:0003700 GO:GO:0006351 GO:GO:0009414 EMBL:AL022197 EMBL:AL161563 KO:K09286 Gene3D:G3DSA:3.30.730.10 SUPFAM:SSF54171 GO:GO:0009631 EMBL:AB007787 EMBL:AB013815 EMBL:AF074602 EMBL:AF076155 EMBL:AF062924 EMBL:AY667247 EMBL:AY691904 EMBL:DQ372533 EMBL:DQ415923 EMBL:BT024594 IPI:IPI00534240 PIR:D85294 PIR:JE0297 PIR:T05799 PIR:T51830 RefSeq:NP_567720.1 UniGene:At.231 ProteinModelPortal:Q9M0L0 SMR:Q9M0L0 STRING:Q9M0L0 EnsemblPlants:AT4G25480.1 GeneID:828652 KEGG:ath:AT4G25480 GeneFarm:3593 TAIR:At4g25480 eggNOG:NOG303203 InParanoid:Q9M0L0 PhylomeDB:Q9M0L0 ProtClustDB:CLSN2687445 ArrayExpress:Q9M0L0 Genevestigator:Q9M0L0 GermOnline:AT4G25480 Uniprot:Q9M0L0
Leaf	Isotig02293	1	26	-4.171	3.23E-06	TAIR|locus:2084066 - symbol:PPa4 "AT3G53620" species:3702 "Arabidopsis thaliana" [GO:0004427 "inorganic diphosphatase activity" evidence=IDA] [GO:0008152 "metabolic process" evidence=ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA] HAMAP:MF_00209 InterPro:IPR008162 Pfam:PF00719 PROSITE:PS00387 GO:GO:0005829 GO:GO:0046686 EMBL:CP002686 GO:GO:0000287 EMBL:AL132966 GO:GO:0006796 KO:K01507 GO:GO:0004427 Gene3D:G3DSA:3.90.80.10 PANTHER:PTHR10286 SUPFAM:SSF50324 ProtClustDB:PLN02373 OMA:PNDFNVI HSSP:O59570 EMBL:AK226578 IPI:IPI00524492 PIR:T45902 RefSeq:NP_190930.1 UniGene:At.19820 ProteinModelPortal:Q9LFF9 SMR:Q9LFF9 STRING:Q9LFF9 PRIDE:Q9LFF9 EnsemblPlants:AT3G53620.1 GeneID:824530 KEGG:ath:AT3G53620 TAIR:At3g53620 InParanoid:Q9LFF9 PhylomeDB:Q9LFF9 Genevestigator:Q9LFF9 Uniprot:Q9LFF9
Leaf	Isotig02294	1	24	-4.056	9.12E-06	TAIR|locus:2084066 - symbol:PPa4 "AT3G53620" species:3702 "Arabidopsis thaliana" [GO:0004427 "inorganic diphosphatase activity" evidence=IDA] [GO:0008152 "metabolic process" evidence=ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA] HAMAP:MF_00209 InterPro:IPR008162 Pfam:PF00719 PROSITE:PS00387 GO:GO:0005829 GO:GO:0046686 EMBL:CP002686 GO:GO:0000287 EMBL:AL132966 GO:GO:0006796 KO:K01507 GO:GO:0004427 Gene3D:G3DSA:3.90.80.10 PANTHER:PTHR10286 SUPFAM:SSF50324 ProtClustDB:PLN02373 OMA:PNDFNVI HSSP:O59570 EMBL:AK226578 IPI:IPI00524492 PIR:T45902 RefSeq:NP_190930.1 UniGene:At.19820 ProteinModelPortal:Q9LFF9 SMR:Q9LFF9 STRING:Q9LFF9 PRIDE:Q9LFF9 EnsemblPlants:AT3G53620.1 GeneID:824530 KEGG:ath:AT3G53620 TAIR:At3g53620 InParanoid:Q9LFF9 PhylomeDB:Q9LFF9 Genevestigator:Q9LFF9 Uniprot:Q9LFF9

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig02295	1	24	-4.056	9.12E-06	TAIR|locus:2084066 - symbol:PPa4 "AT3G53620" species:3702 "Arabidopsis thaliana" [GO:0004427 "inorganic diphosphatase activity" evidence=IDA] [GO:0008152 "metabolic process" evidence=ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA] HAMAP:MF_00209 InterPro:IPR008162 Pfam:PF00719 PROSITE:PS00387 GO:GO:0005829 GO:GO:0046686 EMBL:CP002686 GO:GO:0000287 EMBL:AL132966 GO:GO:0006796 KO:K01507 GO:GO:0004427 Gene3D:G3DSA:3.90.80.10 PANTHER:PTHR10286 SUPFAM:SSF50324 ProtClustDB:PLN02373 OMA:PNDFNVI HSSP:O59570 EMBL:AK226578 IPI:IPI00524492 PIR:T45902 RefSeq:NP_190930.1 UniGene:At.19820 ProteinModelPortal:Q9LFF9 SMR:Q9LFF9 STRING:Q9LFF9 PRIDE:Q9LFF9 EnsemblPlants:AT3G53620.1 GeneID:824530 KEGG:ath:AT3G53620 TAIR:At3g53620 InParanoid:Q9LFF9 PhylomeDB:Q9LFF9 Genevestigator:Q9LFF9 Uniprot:Q9LFF9
Leaf	Isotig02302	264	1417	-1.895	5.82E-119	TAIR|locus:2033686 - symbol:RBCS1A "AT1G67090" species:3702 "Arabidopsis thaliana" [GO:0009573 "chloroplast ribulose bisphosphate carboxylase complex" evidence=ISS] [GO:0015977 "carbon fixation" evidence=ISS] [GO:0016984 "ribulose-bisphosphate carboxylase activity" evidence=ISS] [GO:0031977 "thylakoid lumen" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009637 "response to blue light" evidence=IEP] [GO:0010114 "response to red light" evidence=IEP] [GO:0010218 "response to far red light" evidence=IEP] [GO:0015979 "photosynthesis" evidence=IMP] [GO:0080158 "chloroplast ribulose bisphosphate carboxylase complex biogenesis" evidence=IMP] InterPro:IPR000894 Pfam:PF00101 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0048046 GO:GO:0009570 GO:GO:0004497 GO:GO:0005507 GO:GO:0009409 GO:GO:0009637 GO:GO:0010218 GO:GO:0010114 GO:GO:0031969 EMBL:AC007152 GO:GO:0009853 GO:GO:0009535 GO:GO:0022626 GO:GO:0031977 EMBL:AC004146 GO:GO:0019253 UniGene:At.46639 GO:GO:0016984 UniGene:At.37531 Gene3D:G3DSA:3.30.190.10 EMBL:X13611 EMBL:AF325011 EMBL:AF325004 EMBL:AF372874 EMBL:AF410291 EMBL:AY054188 EMBL:AY054581 EMBL:AY058831 EMBL:AY059940 EMBL:AY062612 EMBL:AY062711 EMBL:AY065101 EMBL:AY093380 EMBL:AY093388 EMBL:AY097366 EMBL:BT000362 EMBL:BT002076 EMBL:X68342 IPI:IPI00539020 PIR:G96694 PIR:S03720 RefSeq:NP_176880.1 UniGene:At.12721 UniGene:At.30194 UniGene:At.49098 UniGene:At.67454 UniGene:At.68122 UniGene:At.70053 UniGene:At.75196 ProteinModelPortal:P10795 SMR:P10795 IntAct:P10795 MINT:MINT-2584041 STRING:P10795 World-2DPAGE:0003:P10795 PRIDE:P10795 ProMEX:P10795 EnsemblPlants:AT1G67090.1 GeneID:843029 KEGG:ath:AT1G67090 TAIR:At1g67090 eggNOG:COG4451 HOGENOM:HBG608223 InParanoid:P10795 KO:K01602 OMA:AFPATRK PhylomeDB:P10795 ProtClustDB:PLN02289 ArrayExpress:P10795 Genevestigator:P10795 InterPro:IPR024681 InterPro:IPR024680 Pfam:PF12338 PRINTS:PR00152 SMART:SM00961 SUPFAM:SSF55239 Uniprot:P10795
Leaf	Isotig02303	401	2248	-1.958	5.56E-196	TAIR|locus:2033686 - symbol:RBCS1A "AT1G67090" species:3702 "Arabidopsis thaliana" [GO:0009573 "chloroplast ribulose bisphosphate carboxylase complex" evidence=ISS] [GO:0015977 "carbon fixation" evidence=ISS] [GO:0016984 "ribulose-bisphosphate carboxylase activity" evidence=ISS] [GO:0031977 "thylakoid lumen" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009637 "response to blue light" evidence=IEP] [GO:0010114 "response to red light" evidence=IEP] [GO:0010218 "response to far red light" evidence=IEP] [GO:0015979 "photosynthesis" evidence=IMP] [GO:0080158 "chloroplast ribulose bisphosphate carboxylase complex biogenesis" evidence=IMP] InterPro:IPR000894 Pfam:PF00101 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0048046 GO:GO:0009570 GO:GO:0004497 GO:GO:0005507 GO:GO:0009409 GO:GO:0009637 GO:GO:0010218 GO:GO:0010114 GO:GO:0031969 EMBL:AC007152 GO:GO:0009853 GO:GO:0009535 GO:GO:0022626 GO:GO:0031977 EMBL:AC004146 GO:GO:0019253 UniGene:At.46639 GO:GO:0016984 UniGene:At.37531 Gene3D:G3DSA:3.30.190.10 EMBL:X13611 EMBL:AF325011 EMBL:AF325004 EMBL:AF372874 EMBL:AF410291 EMBL:AY054188 EMBL:AY054581 EMBL:AY058831 EMBL:AY059940 EMBL:AY062612 EMBL:AY062711 EMBL:AY065101 EMBL:AY093380 EMBL:AY093388 EMBL:AY097366 EMBL:BT000362 EMBL:BT002076 EMBL:X68342 IPI:IPI00539020 PIR:G96694

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						PIR:S03720 RefSeq:NP_176880.1 UniGene:At.12721 UniGene:At.30194 UniGene:At.49098 UniGene:At.67454 UniGene:At.68122 UniGene:At.70053 UniGene:At.75196 ProteinModelPortal:P10795 SMR:P10795 IntAct:P10795 MINT:MINT-2584041 STRING:P10795 World-2DPAGE:0003:P10795 PRIDE:P10795 ProMEX:P10795 EnsemblPlants:AT1G67090.1 GeneID:843029 KEGG:ath:AT1G67090 TAIR:At1g67090 eggNOG:COG4451 HOGENOM:HBG608223 InParanoid:P10795 KO:K01602 OMA:AFPATRK PhylomeDB:P10795 ProtClustDB:PLN02289 ArrayExpress:P10795 Genevestigator:P10795 InterPro:IPR024681 InterPro:IPR024680 Pfam:PF12338 PRINTS:PR00152 SMART:SM00961 SUPFAM:SSF55239 Uniprot:P10795
Leaf	Isotig02304	302	1646	-1.917	4.92E-140	TAIR|locus:2033686 - symbol:RBCS1A "AT1G67090" species:3702 "Arabidopsis thaliana" [GO:0009573 "chloroplast ribulose bisphosphate carboxylase complex" evidence=ISS] [GO:0015977 "carbon fixation" evidence=ISS] [GO:0016984 "ribulose-bisphosphate carboxylase activity" evidence=ISS] [GO:0031977 "thylakoid lumen" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009637 "response to blue light" evidence=IEP] [GO:0010114 "response to red light" evidence=IEP] [GO:0010218 "response to far red light" evidence=IEP] [GO:0015979 "photosynthesis" evidence=IMP] [GO:0080158 "chloroplast ribulose bisphosphate carboxylase complex biogenesis" evidence=IMP] InterPro:IPR000894 Pfam:PF00101 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0048046 GO:GO:0009570 GO:GO:0004497 GO:GO:0005507 GO:GO:0009409 GO:GO:0009637 GO:GO:0010218 GO:GO:0010114 GO:GO:0031969 EMBL:AC007152 GO:GO:0009853 GO:GO:0009535 GO:GO:0022626 GO:GO:0031977 EMBL:AC004146 GO:GO:0019253 UniGene:At.46639 GO:GO:0016984 UniGene:At.37531 Gene3D:G3DSA:3.30.190.10 EMBL:X13611 EMBL:AF325011 EMBL:AF325004 EMBL:AF372874 EMBL:AF410291 EMBL:AY054188 EMBL:AY054581 EMBL:AY058831 EMBL:AY059940 EMBL:AY062612 EMBL:AY062711 EMBL:AY065101 EMBL:AY093380 EMBL:AY093388 EMBL:AY097366 EMBL:BT000362 EMBL:BT002076 EMBL:X68342 IPI:IPI00539020 PIR:G96694 PIR:S03720 RefSeq:NP_176880.1 UniGene:At.12721 UniGene:At.30194 UniGene:At.49098 UniGene:At.67454 UniGene:At.68122 UniGene:At.70053 UniGene:At.75196 ProteinModelPortal:P10795 SMR:P10795 IntAct:P10795 MINT:MINT-2584041 STRING:P10795 World-2DPAGE:0003:P10795 PRIDE:P10795 ProMEX:P10795 EnsemblPlants:AT1G67090.1 GeneID:843029 KEGG:ath:AT1G67090 TAIR:At1g67090 eggNOG:COG4451 HOGENOM:HBG608223 InParanoid:P10795 KO:K01602 OMA:AFPATRK PhylomeDB:P10795 ProtClustDB:PLN02289 ArrayExpress:P10795 Genevestigator:P10795 InterPro:IPR024681 InterPro:IPR024680 Pfam:PF12338 PRINTS:PR00152 SMART:SM00961 SUPFAM:SSF55239 Uniprot:P10795
Leaf	Isotig02314	4	127	-4.460	1.25E-25	TAIR|locus:2033686 - symbol:RBCS1A "AT1G67090" species:3702 "Arabidopsis thaliana" [GO:0009573 "chloroplast ribulose bisphosphate carboxylase complex" evidence=ISS] [GO:0015977 "carbon fixation" evidence=ISS] [GO:0016984 "ribulose-bisphosphate carboxylase activity" evidence=ISS] [GO:0031977 "thylakoid lumen" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009637 "response to blue light" evidence=IEP] [GO:0010114 "response to red light" evidence=IEP] [GO:0010218 "response to far red light" evidence=IEP] [GO:0015979 "photosynthesis" evidence=IMP] [GO:0080158 "chloroplast ribulose bisphosphate carboxylase complex biogenesis" evidence=IMP] InterPro:IPR000894 Pfam:PF00101 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0048046 GO:GO:0009570 GO:GO:0004497 GO:GO:0005507 GO:GO:0009409 GO:GO:0009637 GO:GO:0010218 GO:GO:0010114 GO:GO:0031969 EMBL:AC007152 GO:GO:0009853 GO:GO:0009535 GO:GO:0022626 GO:GO:0031977 EMBL:AC004146 GO:GO:0019253 UniGene:At.46639 GO:GO:0016984 UniGene:At.37531 Gene3D:G3DSA:3.30.190.10 EMBL:X13611 EMBL:AF325011 EMBL:AF325004 EMBL:AF372874 EMBL:AF410291 EMBL:AY054188 EMBL:AY054581 EMBL:AY058831 EMBL:AY059940 EMBL:AY062612 EMBL:AY062711 EMBL:AY065101 EMBL:AY093380 EMBL:AY093388 EMBL:AY097366 EMBL:BT000362 EMBL:BT002076 EMBL:X68342 IPI:IPI00539020 PIR:G96694 PIR:S03720 RefSeq:NP_176880.1 UniGene:At.12721 UniGene:At.30194 UniGene:At.49098 UniGene:At.67454 UniGene:At.68122 UniGene:At.70053 UniGene:At.75196 ProteinModelPortal:P10795 SMR:P10795 IntAct:P10795 MINT:MINT-2584041 STRING:P10795 World-2DPAGE:0003:P10795 PRIDE:P10795 ProMEX:P10795

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EnsemblPlants:AT1G67090.1 GeneID:843029 KEGG:ath:AT1G67090 TAIR:At1g67090 eggNOG:COG4451 HOGENOM:HBG608223 InParanoid:P10795 KO:K01602 OMA:AFPATRK PhylomeDB:P10795 ProtClustDB:PLN02289 ArrayExpress:P10795 Genevestigator:P10795 InterPro:IPR024681 InterPro:IPR024680 Pfam:PF12338 PRINTS:PR00152 SMART:SM00961 SUPFAM:SSF55239 Uniprot:P10795
Leaf	Isotig02315	5	72	-3.319	8.96E-13	TAIR|locus:2033686 - symbol:RBCS1A "AT1G67090" species:3702 "Arabidopsis thaliana" [GO:0009573 "chloroplast ribulose bisphosphate carboxylase complex" evidence=ISS] [GO:0015977 "carbon fixation" evidence=ISS] [GO:0016984 "ribulose-bisphosphate carboxylase activity" evidence=ISS] [GO:0031977 "thylakoid lumen" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009637 "response to blue light" evidence=IEP] [GO:0010114 "response to red light" evidence=IEP] [GO:0010218 "response to far red light" evidence=IEP] [GO:0015979 "photosynthesis" evidence=IMP] [GO:0080158 "chloroplast ribulose bisphosphate carboxylase complex biogenesis" evidence=IMP] InterPro:IPR000894 Pfam:PF00101 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0048046 GO:GO:0009570 GO:GO:0004497 GO:GO:0005507 GO:GO:0009409 GO:GO:0009637 GO:GO:0010218 GO:GO:0010114 GO:GO:0031969 EMBL:AC007152 GO:GO:0009853 GO:GO:0009535 GO:GO:0022626 GO:GO:0031977 EMBL:AC004146 GO:GO:0019253 UniGene:At.46639 GO:GO:0016984 UniGene:At.37531 Gene3D:G3DSA:3.30.190.10 EMBL:X13611 EMBL:AF325011 EMBL:AF325004 EMBL:AF372874 EMBL:AF410291 EMBL:AY054188 EMBL:AY054581 EMBL:AY058831 EMBL:AY059940 EMBL:AY062612 EMBL:AY062711 EMBL:AY065101 EMBL:AY093380 EMBL:AY093388 EMBL:AY097366 EMBL:BT000362 EMBL:BT002076 EMBL:X68342 IPI:IPI00539020 PIR:G96694 PIR:S03720 RefSeq:NP_176880.1 UniGene:At.12721 UniGene:At.30194 UniGene:At.49098 UniGene:At.67454 UniGene:At.68122 UniGene:At.70053 UniGene:At.75196 ProteinModelPortal:P10795 SMR:P10795 IntAct:P10795 MINT:MINT-2584041 STRING:P10795 World-2DPAGE:0003:P10795 PRIDE:P10795 ProMEX:P10795 EnsemblPlants:AT1G67090.1 GeneID:843029 KEGG:ath:AT1G67090 TAIR:At1g67090 eggNOG:COG4451 HOGENOM:HBG608223 InParanoid:P10795 KO:K01602 OMA:AFPATRK PhylomeDB:P10795 ProtClustDB:PLN02289 ArrayExpress:P10795 Genevestigator:P10795 InterPro:IPR024681 InterPro:IPR024680 Pfam:PF12338 PRINTS:PR00152 SMART:SM00961 SUPFAM:SSF55239 Uniprot:P10795
Leaf	Isotig02316	5	123	-4.092	7.42E-24	TAIR|locus:2033686 - symbol:RBCS1A "AT1G67090" species:3702 "Arabidopsis thaliana" [GO:0009573 "chloroplast ribulose bisphosphate carboxylase complex" evidence=ISS] [GO:0015977 "carbon fixation" evidence=ISS] [GO:0016984 "ribulose-bisphosphate carboxylase activity" evidence=ISS] [GO:0031977 "thylakoid lumen" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009637 "response to blue light" evidence=IEP] [GO:0010114 "response to red light" evidence=IEP] [GO:0010218 "response to far red light" evidence=IEP] [GO:0015979 "photosynthesis" evidence=IMP] [GO:0080158 "chloroplast ribulose bisphosphate carboxylase complex biogenesis" evidence=IMP] InterPro:IPR000894 Pfam:PF00101 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0048046 GO:GO:0009570 GO:GO:0004497 GO:GO:0005507 GO:GO:0009409 GO:GO:0009637 GO:GO:0010218 GO:GO:0010114 GO:GO:0031969 EMBL:AC007152 GO:GO:0009853 GO:GO:0009535 GO:GO:0022626 GO:GO:0031977 EMBL:AC004146 GO:GO:0019253 UniGene:At.46639 GO:GO:0016984 UniGene:At.37531 Gene3D:G3DSA:3.30.190.10 EMBL:X13611 EMBL:AF325011 EMBL:AF325004 EMBL:AF372874 EMBL:AF410291 EMBL:AY054188 EMBL:AY054581 EMBL:AY058831 EMBL:AY059940 EMBL:AY062612 EMBL:AY062711 EMBL:AY065101 EMBL:AY093380 EMBL:AY093388 EMBL:AY097366 EMBL:BT000362 EMBL:BT002076 EMBL:X68342 IPI:IPI00539020 PIR:G96694 PIR:S03720 RefSeq:NP_176880.1 UniGene:At.12721 UniGene:At.30194 UniGene:At.49098 UniGene:At.67454 UniGene:At.68122 UniGene:At.70053 UniGene:At.75196 ProteinModelPortal:P10795 SMR:P10795 IntAct:P10795 MINT:MINT-2584041 STRING:P10795 World-2DPAGE:0003:P10795 PRIDE:P10795 ProMEX:P10795 EnsemblPlants:AT1G67090.1 GeneID:843029 KEGG:ath:AT1G67090 TAIR:At1g67090 eggNOG:COG4451 HOGENOM:HBG608223 InParanoid:P10795 KO:K01602 OMA:AFPATRK PhylomeDB:P10795

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						ProtClustDB:PLN02289 ArrayExpress:P10795 Genevestigator:P10795 InterPro:IPR024681 InterPro:IPR024680 Pfam:PF12338 PRINTS:PR00152 SMART:SM00961 SUPFAM:SSF55239 Uniprot:P10795
Leaf	Isotig02320	36	442	-3.089	6.21E-66	TAIR|locus:2033686 - symbol:RBCS1A "AT1G67090" species:3702 "Arabidopsis thaliana" [GO:0009573 "chloroplast ribulose bisphosphate carboxylase complex" evidence=ISS] [GO:0015977 "carbon fixation" evidence=ISS] [GO:0016984 "ribulose-bisphosphate carboxylase activity" evidence=ISS] [GO:0031977 "thylakoid lumen" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009637 "response to blue light" evidence=IEP] [GO:0010114 "response to red light" evidence=IEP] [GO:0010218 "response to far red light" evidence=IEP] [GO:0015979 "photosynthesis" evidence=IMP] [GO:0080158 "chloroplast ribulose bisphosphate carboxylase complex biogenesis" evidence=IMP] InterPro:IPR000894 Pfam:PF00101 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0048046 GO:GO:0009570 GO:GO:0004497 GO:GO:0005507 GO:GO:0009409 GO:GO:0009637 GO:GO:0010218 GO:GO:0010114 GO:GO:0031969 EMBL:AC007152 GO:GO:0009853 GO:GO:0009535 GO:GO:0022626 GO:GO:0031977 EMBL:AC004146 GO:GO:0019253 UniGene:At.46639 GO:GO:0016984 UniGene:At.37531 Gene3D:G3DSA:3.30.190.10 EMBL:X13611 EMBL:AF325011 EMBL:AF325004 EMBL:AF372874 EMBL:AF410291 EMBL:AY054188 EMBL:AY054581 EMBL:AY058831 EMBL:AY059940 EMBL:AY062612 EMBL:AY062711 EMBL:AY065101 EMBL:AY093380 EMBL:AY093388 EMBL:AY097366 EMBL:BT000362 EMBL:BT002076 EMBL:X68342 IPI:IPI00539020 PIR:G96694 PIR:S03720 RefSeq:NP_176880.1 UniGene:At.12721 UniGene:At.30194 UniGene:At.49098 UniGene:At.67454 UniGene:At.68122 UniGene:At.70053 UniGene:At.75196 ProteinModelPortal:P10795 SMR:P10795 IntAct:P10795 MINT:MINT-2584041 STRING:P10795 World-2DPAGE:0003:P10795 PRIDE:P10795 ProMEX:P10795 EnsemblPlants:AT1G67090.1 GeneID:843029 KEGG:ath:AT1G67090 TAIR:At1g67090 eggNOG:COG4451 HOGENOM:HBG608223 InParanoid:P10795 KO:K01602 OMA:AFPATRK PhylomeDB:P10795 ProtClustDB:PLN02289 ArrayExpress:P10795 Genevestigator:P10795 InterPro:IPR024681 InterPro:IPR024680 Pfam:PF12338 PRINTS:PR00152 SMART:SM00961 SUPFAM:SSF55239 Uniprot:P10795
Leaf	Isotig02321	36	442	-3.089	6.21E-66	TAIR|locus:2033686 - symbol:RBCS1A "AT1G67090" species:3702 "Arabidopsis thaliana" [GO:0009573 "chloroplast ribulose bisphosphate carboxylase complex" evidence=ISS] [GO:0015977 "carbon fixation" evidence=ISS] [GO:0016984 "ribulose-bisphosphate carboxylase activity" evidence=ISS] [GO:0031977 "thylakoid lumen" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009637 "response to blue light" evidence=IEP] [GO:0010114 "response to red light" evidence=IEP] [GO:0010218 "response to far red light" evidence=IEP] [GO:0015979 "photosynthesis" evidence=IMP] [GO:0080158 "chloroplast ribulose bisphosphate carboxylase complex biogenesis" evidence=IMP] InterPro:IPR000894 Pfam:PF00101 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0048046 GO:GO:0009570 GO:GO:0004497 GO:GO:0005507 GO:GO:0009409 GO:GO:0009637 GO:GO:0010218 GO:GO:0010114 GO:GO:0031969 EMBL:AC007152 GO:GO:0009853 GO:GO:0009535 GO:GO:0022626 GO:GO:0031977 EMBL:AC004146 GO:GO:0019253 UniGene:At.46639 GO:GO:0016984 UniGene:At.37531 Gene3D:G3DSA:3.30.190.10 EMBL:X13611 EMBL:AF325011 EMBL:AF325004 EMBL:AF372874 EMBL:AF410291 EMBL:AY054188 EMBL:AY054581 EMBL:AY058831 EMBL:AY059940 EMBL:AY062612 EMBL:AY062711 EMBL:AY065101 EMBL:AY093380 EMBL:AY093388 EMBL:AY097366 EMBL:BT000362 EMBL:BT002076 EMBL:X68342 IPI:IPI00539020 PIR:G96694 PIR:S03720 RefSeq:NP_176880.1 UniGene:At.12721 UniGene:At.30194 UniGene:At.49098 UniGene:At.67454 UniGene:At.68122 UniGene:At.70053 UniGene:At.75196 ProteinModelPortal:P10795 SMR:P10795 IntAct:P10795 MINT:MINT-2584041 STRING:P10795 World-2DPAGE:0003:P10795 PRIDE:P10795 ProMEX:P10795 EnsemblPlants:AT1G67090.1 GeneID:843029 KEGG:ath:AT1G67090 TAIR:At1g67090 eggNOG:COG4451 HOGENOM:HBG608223 InParanoid:P10795 KO:K01602 OMA:AFPATRK PhylomeDB:P10795 ProtClustDB:PLN02289 ArrayExpress:P10795 Genevestigator:P10795 InterPro:IPR024681 InterPro:IPR024680 Pfam:PF12338 PRINTS:PR00152 SMART:SM00961 SUPFAM:SSF55239 Uniprot:P10795

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig02322	29	402	-3.264	4.31E-63	TAIR|locus:2033686 - symbol:RBCS1A "AT1G67090" species:3702 "Arabidopsis thaliana" [GO:0009573 "chloroplast ribulose bisphosphate carboxylase complex" evidence=ISS] [GO:0015977 "carbon fixation" evidence=ISS] [GO:0016984 "ribulose-bisphosphate carboxylase activity" evidence=ISS] [GO:0031977 "thylakoid lumen" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009637 "response to blue light" evidence=IEP] [GO:0010114 "response to red light" evidence=IEP] [GO:0010218 "response to far red light" evidence=IEP] [GO:0015979 "photosynthesis" evidence=IMP] [GO:0080158 "chloroplast ribulose bisphosphate carboxylase complex biogenesis" evidence=IMP] InterPro:IPR000894 Pfam:PF00101 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0048046 GO:GO:0009570 GO:GO:0004497 GO:GO:0005507 GO:GO:0009409 GO:GO:0009637 GO:GO:0010218 GO:GO:0010114 GO:GO:0031969 EMBL:AC007152 GO:GO:0009853 GO:GO:0009535 GO:GO:0022626 GO:GO:0031977 EMBL:AC004146 GO:GO:0019253 UniGene:At.46639 GO:GO:0016984 UniGene:At.37531 Gene3D:G3DSA:3.30.190.10 EMBL:X13611 EMBL:AF325011 EMBL:AF325004 EMBL:AF372874 EMBL:AF410291 EMBL:AY054188 EMBL:AY054581 EMBL:AY058831 EMBL:AY059940 EMBL:AY062612 EMBL:AY062711 EMBL:AY065101 EMBL:AY093380 EMBL:AY093388 EMBL:AY097366 EMBL:BT000362 EMBL:BT002076 EMBL:X68342 IPI:IPI00539020 PIR:G96694 PIR:S03720 RefSeq:NP_176880.1 UniGene:At.12721 UniGene:At.30194 UniGene:At.49098 UniGene:At.67454 UniGene:At.68122 UniGene:At.70053 UniGene:At.75196 ProteinModelPortal:P10795 SMR:P10795 IntAct:P10795 MINT:MINT-2584041 STRING:P10795 World-2DPAGE:0003:P10795 PRIDE:P10795 ProMEX:P10795 EnsemblPlants:AT1G67090.1 GeneID:843029 KEGG:ath:AT1G67090 TAIR:At1g67090 eggNOG:COG4451 HOGENOM:HBG608223 InParanoid:P10795 KO:K01602 OMA:AFPATRK PhylomeDB:P10795 ProtClustDB:PLN02289 ArrayExpress:P10795 Genevestigator:P10795 InterPro:IPR024681 InterPro:IPR024680 Pfam:PF12338 PRINTS:PR00152 SMART:SM00961 SUPFAM:SSF55239 Uniprot:P10795
Leaf	Isotig02329	10	49	-1.764	4.10E-05	TAIR|locus:2033915 - symbol:AT1G51400 "AT1G51400" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0030095 "chloroplast photosystem II" evidence=ISS] [GO:0009543 "chloroplast thylakoid lumen" evidence=ISS] [GO:0009611 "response to wounding" evidence=IEP] [GO:0010193 "response to ozone" evidence=IEP] [GO:0010224 "response to UV-B" evidence=IEP] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] EMBL:CP002684 GO:GO:0009611 EMBL:AC024261 GO:GO:0010193 GO:GO:0009535 GO:GO:0010224 EMBL:AC006085 UniGene:At.11631 UniGene:At.66913 UniGene:At.68288 ProtClustDB:PLN00058 EMBL:AF385721 EMBL:AY050320 EMBL:AY133673 IPI:IPI00524381 PIR:B96552 RefSeq:NP_564589.1 STRING:Q9SYE2 PRIDE:Q9SYE2 EnsemblPlants:AT1G51400.1 GeneID:841564 KEGG:ath:AT1G51400 TAIR:At1g51400 InParanoid:Q9SYE2 OMA:MASVTMT PhylomeDB:Q9SYE2 Genevestigator:Q9SYE2 Uniprot:Q9SYE2
Leaf	Isotig02334	12	1	4.114	0.000154103	No hit
Leaf	Isotig02335	12	0	5.114	7.63E-05	No hit
Leaf	Isotig02336	11	0	4.988	0.000159591	No hit
Leaf	Isotig02340	13	72	-1.941	1.13E-07	No hit
Leaf	Isotig02341	14	56	-1.471	0.000119396	No hit
Leaf	Isotig02342	17	61	-1.314	0.000227416	No hit
Leaf	Isotig02351	10	56	-1.956	2.55E-06	TAIR|locus:2204207 - symbol:PSAK "AT1G30380" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0009522 "photosystem I" evidence=ISS] [GO:0015979 "photosynthesis" evidence=IEA;ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] InterPro:IPR000549 Pfam:PF01241 PROSITE:PS01026 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR EMBL:AC025295 GO:GO:0009535 GO:GO:0015979 GO:GO:0009522 UniGene:At.24759 TCDB:5.B.4.1.1 InterPro:IPR016370 PIRSF:PIRSF002912 EMBL:AJ245866 EMBL:AY039848 EMBL:AY074826 IPI:IPI00525222 PIR:B86428 RefSeq:NP_174327.1 UniGene:At.24377 UniGene:At.67254 ProteinModelPortal:Q9SUI5 SMR:Q9SUI5 STRING:Q9SUI5 PRIDE:Q9SUI5 EnsemblPlants:AT1G30380.1 GeneID:839918 KEGG:ath:AT1G30380 TAIR:At1g30380 eggNOG:NOG238582 HOGENOM:HBG600339 InParanoid:Q9SUI5 KO:K02698 OMA:DTLACGA PhylomeDB:Q9SUI5

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						ProtClustDB:PLN03070 BioCyc:MetaCyc:MONOMER-1091 ArrayExpress:Q9SUI5 Genevestigator:Q9SUI5 GermOnline:AT1G30380 InterPro:IPR017493 TIGRFAMs:TIGR03050 Uniprot:Q9SUI5
Leaf	Isotig02373	103	5	4.894	1.02E-30	TAIR|locus:2137829 - symbol:SUS3 "AT4G02280" species:3702 "Arabidopsis thaliana" [GO:0005986 "sucrose biosynthetic process" evidence=ISS] [GO:0008194 "UDP-glycosyltransferase activity" evidence=ISS] [GO:0016157 "sucrose synthase activity" evidence=ISS;IDA] [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0005982 "starch metabolic process" evidence=IMP] [GO:0005985 "sucrose metabolic process" evidence=IMP] [GO:0010431 "seed maturation" evidence=IMP] InterPro:IPR000368 InterPro:IPR001296 InterPro:IPR012820 Pfam:PF00534 Pfam:PF00862 EMBL:CP002687 GO:GO:0009058 GO:GO:0010431 CAZy:GT4 EMBL:AL161494 GO:GO:0005985 GO:GO:0005982 KO:K00695 ProtClustDB:PLN00142 GO:GO:0016157 PANTHER:PTHR12526:SF27 TIGRFAMs:TIGR02470 EMBL:AY051001 EMBL:AY056784 EMBL:AY142511 IPI:IPI00528989 PIR:B85029 RefSeq:NP_192137.1 UniGene:At.3877 ProteinModelPortal:Q9M111 SMR:Q9M111 IntAct:Q9M111 STRING:Q9M111 PRIDE:Q9M111 EnsemblPlants:AT4G02280.1 GeneID:828081 KEGG:ath:AT4G02280 TAIR:At4g02280 InParanoid:Q9M111 OMA:WKYVSKL PhylomeDB:Q9M111 Genevestigator:Q9M111 Uniprot:Q9M111
Leaf	Isotig02374	100	4	5.173	2.83E-30	TAIR|locus:2137829 - symbol:SUS3 "AT4G02280" species:3702 "Arabidopsis thaliana" [GO:0005986 "sucrose biosynthetic process" evidence=ISS] [GO:0008194 "UDP-glycosyltransferase activity" evidence=ISS] [GO:0016157 "sucrose synthase activity" evidence=ISS;IDA] [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0005982 "starch metabolic process" evidence=IMP] [GO:0005985 "sucrose metabolic process" evidence=IMP] [GO:0010431 "seed maturation" evidence=IMP] InterPro:IPR000368 InterPro:IPR001296 InterPro:IPR012820 Pfam:PF00534 Pfam:PF00862 EMBL:CP002687 GO:GO:0009058 GO:GO:0010431 CAZy:GT4 EMBL:AL161494 GO:GO:0005985 GO:GO:0005982 KO:K00695 ProtClustDB:PLN00142 GO:GO:0016157 PANTHER:PTHR12526:SF27 TIGRFAMs:TIGR02470 EMBL:AY051001 EMBL:AY056784 EMBL:AY142511 IPI:IPI00528989 PIR:B85029 RefSeq:NP_192137.1 UniGene:At.3877 ProteinModelPortal:Q9M111 SMR:Q9M111 IntAct:Q9M111 STRING:Q9M111 PRIDE:Q9M111 EnsemblPlants:AT4G02280.1 GeneID:828081 KEGG:ath:AT4G02280 TAIR:At4g02280 InParanoid:Q9M111 OMA:WKYVSKL PhylomeDB:Q9M111 Genevestigator:Q9M111 Uniprot:Q9M111
Leaf	Isotig02375	100	4	5.173	2.83E-30	TAIR|locus:2137829 - symbol:SUS3 "AT4G02280" species:3702 "Arabidopsis thaliana" [GO:0005986 "sucrose biosynthetic process" evidence=ISS] [GO:0008194 "UDP-glycosyltransferase activity" evidence=ISS] [GO:0016157 "sucrose synthase activity" evidence=ISS;IDA] [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0005982 "starch metabolic process" evidence=IMP] [GO:0005985 "sucrose metabolic process" evidence=IMP] [GO:0010431 "seed maturation" evidence=IMP] InterPro:IPR000368 InterPro:IPR001296 InterPro:IPR012820 Pfam:PF00534 Pfam:PF00862 EMBL:CP002687 GO:GO:0009058 GO:GO:0010431 CAZy:GT4 EMBL:AL161494 GO:GO:0005985 GO:GO:0005982 KO:K00695 ProtClustDB:PLN00142 GO:GO:0016157 PANTHER:PTHR12526:SF27 TIGRFAMs:TIGR02470 EMBL:AY051001 EMBL:AY056784 EMBL:AY142511 IPI:IPI00528989 PIR:B85029 RefSeq:NP_192137.1 UniGene:At.3877 ProteinModelPortal:Q9M111 SMR:Q9M111 IntAct:Q9M111 STRING:Q9M111 PRIDE:Q9M111 EnsemblPlants:AT4G02280.1 GeneID:828081 KEGG:ath:AT4G02280 TAIR:At4g02280 InParanoid:Q9M111 OMA:WKYVSKL PhylomeDB:Q9M111 Genevestigator:Q9M111 Uniprot:Q9M111
Leaf	Isotig02376	65	31	1.597	1.23E-07	TAIR|locus:2159300 - symbol:ABCF1 "AT5G60790" species:3702 "Arabidopsis thaliana" [GO:0005215 "transporter activity" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] InterPro:IPR003439 InterPro:IPR003593 InterPro:IPR017871 Pfam:PF00005 PROSITE:PS00211 PROSITE:PS50893 SMART:SM00382 GO:GO:0005886 GO:GO:0005524 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0006810 GO:GO:0016887 HOGENOM:HBG758042 EMBL:AB015472 EMBL:AY140066 EMBL:BT000946 EMBL:BT008363 EMBL:AK317570 EMBL:AK317690 IPI:IPI00540333 RefSeq:NP_200887.1 UniGene:At.9321 ProteinModelPortal:Q9FJH6 SMR:Q9FJH6 IntAct:Q9FJH6 STRING:Q9FJH6 PRIDE:Q9FJH6 EnsemblPlants:AT5G60790.1 GeneID:836200 KEGG:ath:AT5G60790 TAIR:At5g60790 eggNOG:COG0488 InParanoid:Q9FJH6 KO:K06185 OMA:YHQHLHE PhylomeDB:Q9FJH6 ProtClustDB:CLSN2686703 ArrayExpress:Q9FJH6 Genevestigator:Q9FJH6 Uniprot:Q9FJH6
Leaf	Isotig02377	65	31	1.597	1.23E-07	TAIR|locus:2159300 - symbol:ABCF1 "AT5G60790" species:3702 "Arabidopsis thaliana" [GO:0005215 "transporter activity" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] InterPro:IPR003439 InterPro:IPR003593 InterPro:IPR017871 Pfam:PF00005 PROSITE:PS00211 PROSITE:PS50893 SMART:SM00382 GO:GO:0005886 GO:GO:0005524 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0006810 GO:GO:0016887 HOGENOM:HBG758042 EMBL:AB015472 EMBL:AY140066 EMBL:BT000946 EMBL:BT008363 EMBL:AK317570

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EMBL:AK317690 IPI:IPI00540333 RefSeq:NP_200887.1 UniGene:At.9321 ProteinModelPortal:Q9FJH6 SMR:Q9FJH6 IntAct:Q9FJH6 STRING:Q9FJH6 PRIDE:Q9FJH6 EnsemblPlants:AT5G60790.1 GeneID:836200 KEGG:ath:AT5G60790 TAIR:At5g60790 eggNOG:COG0488 InParanoid:Q9FJH6 KO:K06185 OMA:YHQHLHE PhylomeDB:Q9FJH6 ProtClustDB:CLSN2686703 ArrayExpress:Q9FJH6 Genevestigator:Q9FJH6 Uniprot:Q9FJH6
Leaf	Isotig02378	65	31	1.597	1.23E-07	TAIR|locus:2159300 - symbol:ABCF1 "AT5G60790" species:3702 "Arabidopsis thaliana" [GO:0005215 "transporter activity" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] InterPro:IPR003439 InterPro:IPR003593 InterPro:IPR017871 Pfam:PF00005 PROSITE:PS00211 PROSITE:PS50893 SMART:SM00382 GO:GO:0005886 GO:GO:0005524 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0006810 GO:GO:0016887 HOGENOM:HBG758042 EMBL:AB015472 EMBL:AY140066 EMBL:BT000946 EMBL:BT008363 EMBL:AK317570 EMBL:AK317690 IPI:IPI00540333 RefSeq:NP_200887.1 UniGene:At.9321 ProteinModelPortal:Q9FJH6 SMR:Q9FJH6 IntAct:Q9FJH6 STRING:Q9FJH6 PRIDE:Q9FJH6 EnsemblPlants:AT5G60790.1 GeneID:836200 KEGG:ath:AT5G60790 TAIR:At5g60790 eggNOG:COG0488 InParanoid:Q9FJH6 KO:K06185 OMA:YHQHLHE PhylomeDB:Q9FJH6 ProtClustDB:CLSN2686703 ArrayExpress:Q9FJH6 Genevestigator:Q9FJH6 Uniprot:Q9FJH6
Leaf	Isotig02379	16	1	4.529	7.58E-06	TAIR|locus:2053205 - symbol:XBAT31 "XB3 ortholog 1 in Arabidopsis thaliana" species:3702 "Arabidopsis thaliana" [GO:0008270 "zinc ion binding" evidence=IEA] InterPro:IPR001841 InterPro:IPR002110 Pfam:PF00023 PROSITE:PS50088 PROSITE:PS50089 SMART:SM00184 SMART:SM00248 Prosite:PS00518 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0008270 eggNOG:COG0666 InterPro:IPR020683 Gene3D:G3DSA:1.25.40.20 SUPFAM:SSF48403 PROSITE:PS50297 InterPro:IPR013083 Gene3D:G3DSA:3.30.40.10 EMBL:AC005727 EMBL:DQ086863 EMBL:AF370581 EMBL:AF428301 EMBL:AY042842 EMBL:AY081458 EMBL:BT000727 EMBL:AK222223 IPI:IPI00538063 PIR:E84689 RefSeq:NP_180450.2 UniGene:At.21021 HSSP:Q60773 ProteinModelPortal:Q94B55 SMR:Q94B55 IntAct:Q94B55 STRING:Q94B55 PRIDE:Q94B55 EnsemblPlants:AT2G28840.1 GeneID:817433 KEGG:ath:AT2G28840 TAIR:At2g28840 InParanoid:Q94B55 OMA:TELCCIC PhylomeDB:Q94B55 ProtClustDB:CLSN2918121 Genevestigator:Q94B55 Uniprot:Q94B55
Leaf	Isotig02380	16	1	4.529	7.58E-06	TAIR|locus:2053205 - symbol:XBAT31 "XB3 ortholog 1 in Arabidopsis thaliana" species:3702 "Arabidopsis thaliana" [GO:0008270 "zinc ion binding" evidence=IEA] InterPro:IPR001841 InterPro:IPR002110 Pfam:PF00023 PROSITE:PS50088 PROSITE:PS50089 SMART:SM00184 SMART:SM00248 Prosite:PS00518 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0008270 eggNOG:COG0666 InterPro:IPR020683 Gene3D:G3DSA:1.25.40.20 SUPFAM:SSF48403 PROSITE:PS50297 InterPro:IPR013083 Gene3D:G3DSA:3.30.40.10 EMBL:AC005727 EMBL:DQ086863 EMBL:AF370581 EMBL:AF428301 EMBL:AY042842 EMBL:AY081458 EMBL:BT000727 EMBL:AK222223 IPI:IPI00538063 PIR:E84689 RefSeq:NP_180450.2 UniGene:At.21021 HSSP:Q60773 ProteinModelPortal:Q94B55 SMR:Q94B55 IntAct:Q94B55 STRING:Q94B55 PRIDE:Q94B55 EnsemblPlants:AT2G28840.1 GeneID:817433 KEGG:ath:AT2G28840 TAIR:At2g28840 InParanoid:Q94B55 OMA:TELCCIC PhylomeDB:Q94B55 ProtClustDB:CLSN2918121 Genevestigator:Q94B55 Uniprot:Q94B55
Leaf	Isotig02381	16	1	4.529	7.58E-06	TAIR|locus:2053205 - symbol:XBAT31 "XB3 ortholog 1 in Arabidopsis thaliana" species:3702 "Arabidopsis thaliana" [GO:0008270 "zinc ion binding" evidence=IEA] InterPro:IPR001841 InterPro:IPR002110 Pfam:PF00023 PROSITE:PS50088 PROSITE:PS50089 SMART:SM00184 SMART:SM00248 Prosite:PS00518 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0008270 eggNOG:COG0666 InterPro:IPR020683 Gene3D:G3DSA:1.25.40.20 SUPFAM:SSF48403 PROSITE:PS50297 InterPro:IPR013083 Gene3D:G3DSA:3.30.40.10 EMBL:AC005727 EMBL:DQ086863 EMBL:AF370581 EMBL:AF428301 EMBL:AY042842 EMBL:AY081458 EMBL:BT000727 EMBL:AK222223 IPI:IPI00538063 PIR:E84689 RefSeq:NP_180450.2 UniGene:At.21021 HSSP:Q60773 ProteinModelPortal:Q94B55 SMR:Q94B55 IntAct:Q94B55 STRING:Q94B55 PRIDE:Q94B55 EnsemblPlants:AT2G28840.1 GeneID:817433 KEGG:ath:AT2G28840 TAIR:At2g28840 InParanoid:Q94B55 OMA:TELCCIC PhylomeDB:Q94B55 ProtClustDB:CLSN2918121 Genevestigator:Q94B55 Uniprot:Q94B55
Leaf	Isotig02382	19	5	2.455	0.000151807	TAIR|locus:2010911 - symbol:AT1G64890 "AT1G64890" species:3702 "Arabidopsis thaliana" [GO:0005215 "transporter activity" evidence=ISS] [GO:0006810 "transport" evidence=ISS] [GO:0016020 "membrane" evidence=ISS] Pfam:PF03092 EMBL:CP002684 InterPro:IPR016196 SUPFAM:SSF103473 EMBL:AC006193 InterPro:IPR004324 EMBL:BT002319 IPI:IPI00542815 PIR:C96672 RefSeq:NP_564843.1 UniGene:At.14815 UniGene:At.71486 ProteinModelPortal:Q9XIQ7 TCDB:2.A.71.3.1 PRIDE:Q9XIQ7 EnsemblPlants:AT1G64890.1

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GeneID:842797 KEGG:ath:AT1G64890 TAIR:At1g64890 InParanoid:Q9XIQ7 OMA:QAISWLA PhylomeDB:Q9XIQ7 ProtClustDB:CLSN2689026 Genevestigator:Q9XIQ7 Uniprot:Q9XIQ7
Leaf	Isotig02383	20	3	3.266	7.04E-06	TAIR|locus:2010911 - symbol:AT1G64890 "AT1G64890" species:3702 "Arabidopsis thaliana" [GO:0005215 "transporter activity" evidence=ISS] [GO:0006810 "transport" evidence=ISS] [GO:0016020 "membrane" evidence=ISS] Pfam:PF03092 EMBL:CP002684 InterPro:IPR016196 SUPFAM:SSF103473 EMBL:AC006193 InterPro:IPR004324 EMBL:BT002319 IPI:IPI00542815 PIR:C96672 RefSeq:NP_564843.1 UniGene:At.14815 UniGene:At.71486 ProteinModelPortal:Q9XIQ7 TCDB:2.A.71.3.1 PRIDE:Q9XIQ7 EnsemblPlants:AT1G64890.1 GeneID:842797 KEGG:ath:AT1G64890 TAIR:At1g64890 InParanoid:Q9XIQ7 OMA:QAISWLA PhylomeDB:Q9XIQ7 ProtClustDB:CLSN2689026 Genevestigator:Q9XIQ7 Uniprot:Q9XIQ7
Leaf	Isotig02404	10	1	3.851	0.00071293	No hit
Leaf	Isotig02405	12	2	3.114	0.000658121	TAIR|locus:2009580 - symbol:AT1G53210 species:3702 "Arabidopsis thaliana" [GO:0005509 "calcium ion binding" evidence=IEA;ISS] [GO:0055085 "transmembrane transport" evidence=IEA] [GO:0016020 "membrane" evidence=ISS;IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0000325 "plant-type vacuole" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR002048 InterPro:IPR004837 InterPro:IPR011992 Pfam:PF01699 SMART:SM00054 Prosite:PS00018 GO:GO:0016021 EMBL:CP002684 GO:GO:0009506 GO:GO:0005774 GO:GO:0005509 InterPro:IPR018247 InterPro:IPR018249 Gene3D:G3DSA:1.10.238.10 PROSITE:PS50222 GO:GO:0055085 GO:GO:0000325 EMBL:AY099550 IPI:IPI00521295 RefSeq:NP_564623.2 UniGene:At.23754 ProteinModelPortal:Q8L636 SMR:Q8L636 PRIDE:Q8L636 EnsemblPlants:AT1G53210.1 GeneID:841755 KEGG:ath:AT1G53210 TAIR:At1g53210 InParanoid:Q8L636 OMA:CEQTYGF PhylomeDB:Q8L636 ProtClustDB:CLSN2680479 Genevestigator:Q8L636 Uniprot:Q8L636
Leaf	Isotig02415	3	30	-2.793	2.12E-05	TAIR|locus:2037435 - symbol:AT1G52220 "AT1G52220" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] EMBL:CP002684 GO:GO:0009535 EMBL:AC022354 UniGene:At.16830 InterPro:IPR025564 Pfam:PF14159 EMBL:AF410269 EMBL:AY097365 IPI:IPI00529609 PIR:B96562 RefSeq:NP_564603.1 IntAct:Q9M812 STRING:Q9M812 PRIDE:Q9M812 EnsemblPlants:AT1G52220.1 GeneID:841652 KEGG:ath:AT1G52220 TAIR:At1g52220 InParanoid:Q9M812 OMA:DKLPVIS PhylomeDB:Q9M812 ProtClustDB:CLSN2688710 Genevestigator:Q9M812 Uniprot:Q9M812
Leaf	Isotig02416	3	30	-2.793	2.12E-05	TAIR|locus:2037435 - symbol:AT1G52220 "AT1G52220" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] EMBL:CP002684 GO:GO:0009535 EMBL:AC022354 UniGene:At.16830 InterPro:IPR025564 Pfam:PF14159 EMBL:AF410269 EMBL:AY097365 IPI:IPI00529609 PIR:B96562 RefSeq:NP_564603.1 IntAct:Q9M812 STRING:Q9M812 PRIDE:Q9M812 EnsemblPlants:AT1G52220.1 GeneID:841652 KEGG:ath:AT1G52220 TAIR:At1g52220 InParanoid:Q9M812 OMA:DKLPVIS PhylomeDB:Q9M812 ProtClustDB:CLSN2688710 Genevestigator:Q9M812 Uniprot:Q9M812
Leaf	Isotig02417	3	30	-2.793	2.12E-05	TAIR|locus:2037435 - symbol:AT1G52220 "AT1G52220" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] EMBL:CP002684 GO:GO:0009535 EMBL:AC022354 UniGene:At.16830 InterPro:IPR025564 Pfam:PF14159 EMBL:AF410269 EMBL:AY097365 IPI:IPI00529609 PIR:B96562 RefSeq:NP_564603.1 IntAct:Q9M812 STRING:Q9M812 PRIDE:Q9M812 EnsemblPlants:AT1G52220.1 GeneID:841652 KEGG:ath:AT1G52220 TAIR:At1g52220 InParanoid:Q9M812 OMA:DKLPVIS PhylomeDB:Q9M812 ProtClustDB:CLSN2688710 Genevestigator:Q9M812 Uniprot:Q9M812
Leaf	Isotig02430	4	55	-3.252	5.98E-10	TAIR|locus:2055572 - symbol:SPX3 "AT2G45130" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0016036 "cellular response to phosphate starvation" evidence=IEP] [GO:0080040 "positive regulation of cellular response to phosphate starvation" evidence=IMP] EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0016036 InterPro:IPR004331 Pfam:PF03105 PROSITE:PS51382 GO:GO:0080040 EMBL:BT020235 EMBL:BT020499 IPI:IPI00520153 PIR:G84886 RefSeq:NP_182038.1 UniGene:At.50140 EnsemblPlants:AT2G45130.1 GeneID:819120 KEGG:ath:AT2G45130 TAIR:At2g45130 eggNOG:NOG290986 OMA:CGHNDEM PhylomeDB:Q5PP62 ProtClustDB:CLSN2913033 Genevestigator:Q5PP62 Uniprot:Q5PP62
Leaf	Isotig02431	4	52	-3.171	2.63E-09	TAIR|locus:2055572 - symbol:SPX3 "AT2G45130" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0016036 "cellular

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						response to phosphate starvation" evidence=IEP] [GO:0080040 "positive regulation of cellular response to phosphate starvation" evidence=IMP] EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0016036 InterPro:IPR004331 Pfam:PF03105 PROSITE:PS51382 GO:GO:0080040 EMBL:BT020235 EMBL:BT020499 IPI:IPI00520153 PIR:G84886 RefSeq:NP_182038.1 UniGene:At.50140 EnsemblPlants:AT2G45130.1 GeneID:819120 KEGG:ath:AT2G45130 TAIR:At2g45130 eggNOG:NOG290986 OMA:CGHNDEM PhylomeDB:Q5PP62 ProtClustDB:CLSN2913033 Genevestigator:Q5PP62 Uniprot:Q5PP62
Leaf	Isotig02438	40	23	1.327	0.000302514	TIGR_CMR|DET_0927 - symbol:DET_0927 "proton-translocating NADH-quinone oxidoreductase, H subunit" species:243164 "Dehalococcoides ethenogenes 195" [GO:0016655 "oxidoreductase activity, acting on NADH or NADPH, quinone or similar compound as acceptor" evidence=ISS] HAMAP:MF_01350 InterPro:IPR001694 InterPro:IPR018086 Pfam:PF00146 PROSITE:PS00667 PROSITE:PS00668 GO:GO:0016021 GO:GO:0005886 GO:GO:0048038 EMBL:CP000027 GenomeReviews:CP000027_GR HOGENOM:HBG727670 PANTHER:PTHR11432 eggNOG:COG1005 GO:GO:0050136 KO:K00337 RefSeq:YP_181652.1 STRING:Q3Z7Z7 GeneID:3229770 KEGG:det:DET0927 PATRIC:21608901 TIGR:DET0927 OMA:WNIFLQP PhylomeDB:Q3Z7Z7 ProtClustDB:CLSK837202 BioCyc:DETH243164:DET_0927-MONOMER Uniprot:Q3Z7Z7
Leaf	Isotig02449	63	14	2.699	3.61E-13	TAIR|locus:2063354 - symbol:ACO3 "AT2G05710" species:3702 "Arabidopsis thaliana" [GO:0003994 "aconitate hydratase activity" evidence=ISS;IMP] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0006979 "response to oxidative stress" evidence=IMP;IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005829 "cytosol" evidence=RCA;NAS] [GO:0006101 "citrate metabolic process" evidence=IMP] [GO:0006102 "isocitrate metabolic process" evidence=IMP] [GO:0005524 "ATP binding" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR000573 InterPro:IPR001030 InterPro:IPR006249 InterPro:IPR015928 InterPro:IPR015931 InterPro:IPR015932 InterPro:IPR015934 InterPro:IPR015937 Pfam:PF00330 Pfam:PF00694 PRINTS:PR00415 Prosite:PS00450 GO:GO:0005829 GO:GO:0005739 GO:GO:0005524 GO:GO:0009737 GO:GO:0009570 GO:GO:0046686 GO:GO:0005774 GO:GO:0005618 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0006979 GO:GO:0005507 GO:GO:0009651 GO:GO:0051539 GO:GO:0006097 GO:GO:0006099 GO:GO:0006101 eggNOG:COG1048 HOGENOM:HBG289738 KO:K01681 ProtClustDB:PLN00070 GO:GO:0003994 GO:GO:0052632 GO:GO:0052633 GO:GO:0006102 InterPro:IPR018136 Gene3D:G3DSA:3.30.499.10 Gene3D:G3DSA:3.20.19.10 Gene3D:G3DSA:3.40.1060.10 PANTHER:PTHR11670 PANTHER:PTHR11670:SF1 SUPFAM:SSF52016 SUPFAM:SSF53732 TIGRFAMs:TIGR01341 PROSITE:PS01244 EMBL:AC007170 EMBL:AY136414 EMBL:BT008809 IPI:IPI00543590 PIR:B84471 RefSeq:NP_178634.2 UniGene:At.26759 UniGene:At.67769 HSSP:P21399 ProteinModelPortal:Q9SIB9 SMR:Q9SIB9 IntAct:Q9SIB9 STRING:Q9SIB9 ANU-2DPAGE:Q9SIB9 PRIDE:Q9SIB9 EnsemblPlants:AT2G05710.1 GeneID:815120 KEGG:ath:AT2G05710 GeneFarm:4276 TAIR:At2g05710 InParanoid:Q9SIB9 OMA:IKYLVQT PhylomeDB:Q9SIB9 Genevestigator:Q9SIB9 Uniprot:Q9SIB9
Leaf	Isotig02450	63	14	2.699	3.61E-13	TAIR|locus:2063354 - symbol:ACO3 "AT2G05710" species:3702 "Arabidopsis thaliana" [GO:0003994 "aconitate hydratase activity" evidence=ISS;IMP] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0006979 "response to oxidative stress" evidence=IMP;IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005829 "cytosol" evidence=RCA;NAS] [GO:0006101 "citrate metabolic process" evidence=IMP] [GO:0006102 "isocitrate metabolic process" evidence=IMP] [GO:0005524 "ATP binding" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR000573 InterPro:IPR001030 InterPro:IPR006249 InterPro:IPR015928 InterPro:IPR015931 InterPro:IPR015932 InterPro:IPR015934 InterPro:IPR015937 Pfam:PF00330 Pfam:PF00694 PRINTS:PR00415 Prosite:PS00450 GO:GO:0005829 GO:GO:0005739 GO:GO:0005524 GO:GO:0009737 GO:GO:0009570 GO:GO:0046686 GO:GO:0005774 GO:GO:0005618 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0006979 GO:GO:0005507 GO:GO:0009651 GO:GO:0051539 GO:GO:0006097 GO:GO:0006099 GO:GO:0006101 eggNOG:COG1048 HOGENOM:HBG289738 KO:K01681 ProtClustDB:PLN00070 GO:GO:0003994 GO:GO:0052632 GO:GO:0052633 GO:GO:0006102 InterPro:IPR018136 Gene3D:G3DSA:3.30.499.10 Gene3D:G3DSA:3.20.19.10

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						Gene3D:G3DSA:3.40.1060.10 PANTHER:PTHR11670 PANTHER:PTHR11670:SF1 SUPFAM:SSF52016 SUPFAM:SSF53732 TIGRFAMs:TIGR01341 PROSITE:PS01244 EMBL:AC007170 EMBL:AY136414 EMBL:BT008809 IPI:IPI00543590 PIR:B84471 RefSeq:NP_178634.2 UniGene:At.26759 UniGene:At.67769 HSSP:P21399 ProteinModelPortal:Q9SIB9 SMR:Q9SIB9 IntAct:Q9SIB9 STRING:Q9SIB9 ANU-2DPAGE:Q9SIB9 PRIDE:Q9SIB9 EnsemblPlants:AT2G05710.1 GeneID:815120 KEGG:ath:AT2G05710 GeneFarm:4276 TAIR:At2g05710 InParanoid:Q9SIB9 OMA:IKYLVQT PhylomeDB:Q9SIB9 Genevestigator:Q9SIB9 Uniprot:Q9SIB9
Leaf	Isotig02451	0	26	-5.171	1.21E-06	TAIR|locus:2037808 - symbol:BOR4 "AT1G15460" species:3702 "Arabidopsis thaliana" [GO:0015301 "anion:anion antiporter activity" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0046713 "borate transport" evidence=IMP] [GO:0080029 "cellular response to boron-containing substance levels" evidence=IDA] [GO:0080139 "borate efflux transmembrane transporter activity" evidence=IMP] InterPro:IPR003020 InterPro:IPR011531 Pfam:PF00955 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005886 EMBL:AC007591 eggNOG:NOG268067 GO:GO:0005452 PANTHER:PTHR11453 HOGENOM:HBG318202 GO:GO:0080139 EMBL:AY069887 IPI:IPI00529094 RefSeq:NP_172999.1 UniGene:At.28440 ProteinModelPortal:Q9XI23 SMR:Q9XI23 STRING:Q9XI23 PRIDE:Q9XI23 EnsemblPlants:AT1G15460.1 GeneID:838116 KEGG:ath:AT1G15460 TAIR:At1g15460 InParanoid:Q9XI23 OMA:DIINRFT PhylomeDB:Q9XI23 ProtClustDB:CLSN2912667 Genevestigator:Q9XI23 GermOnline:AT1G15460 GO:GO:0080029 Uniprot:Q9XI23
Leaf	Isotig02452	0	26	-5.171	1.21E-06	TAIR|locus:2037808 - symbol:BOR4 "AT1G15460" species:3702 "Arabidopsis thaliana" [GO:0015301 "anion:anion antiporter activity" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0046713 "borate transport" evidence=IMP] [GO:0080029 "cellular response to boron-containing substance levels" evidence=IDA] [GO:0080139 "borate efflux transmembrane transporter activity" evidence=IMP] InterPro:IPR003020 InterPro:IPR011531 Pfam:PF00955 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005886 EMBL:AC007591 eggNOG:NOG268067 GO:GO:0005452 PANTHER:PTHR11453 HOGENOM:HBG318202 GO:GO:0080139 EMBL:AY069887 IPI:IPI00529094 RefSeq:NP_172999.1 UniGene:At.28440 ProteinModelPortal:Q9XI23 SMR:Q9XI23 STRING:Q9XI23 PRIDE:Q9XI23 EnsemblPlants:AT1G15460.1 GeneID:838116 KEGG:ath:AT1G15460 TAIR:At1g15460 InParanoid:Q9XI23 OMA:DIINRFT PhylomeDB:Q9XI23 ProtClustDB:CLSN2912667 Genevestigator:Q9XI23 GermOnline:AT1G15460 GO:GO:0080029 Uniprot:Q9XI23
Leaf	Isotig02457	30	6	2.851	2.45E-07	TAIR|locus:2171569 - symbol:AT5G47430 species:3702 "Arabidopsis thaliana" [GO:0003676 "nucleic acid binding" evidence=IEA] [GO:0008150 "biological_process" evidence=ND] [GO:0008270 "zinc ion binding" evidence=IEA] InterPro:IPR001841 InterPro:IPR001878 InterPro:IPR014891 Pfam:PF08783 PROSITE:PS51282 SMART:SM00184 SMART:SM00343 GO:GO:0005634 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0008270 GO:GO:0003676 InterPro:IPR013083 Gene3D:G3DSA:3.30.40.10 Gene3D:G3DSA:4.10.60.10 EMBL:AK316913 IPI:IPI00547250 RefSeq:NP_199554.2 UniGene:At.29893 ProteinModelPortal:B9DFV2 SMR:B9DFV2 PRIDE:B9DFV2 EnsemblPlants:AT5G47430.1 GeneID:834790 KEGG:ath:AT5G47430 TAIR:At5g47430 PhylomeDB:B9DFV2 ProtClustDB:CLSN2699121 Genevestigator:B9DFV2 Uniprot:B9DFV2
Leaf	Isotig02458	29	6	2.802	4.91E-07	TAIR|locus:2171569 - symbol:AT5G47430 species:3702 "Arabidopsis thaliana" [GO:0003676 "nucleic acid binding" evidence=IEA] [GO:0008150 "biological_process" evidence=ND] [GO:0008270 "zinc ion binding" evidence=IEA] InterPro:IPR001841 InterPro:IPR001878 InterPro:IPR014891 Pfam:PF08783 PROSITE:PS51282 SMART:SM00184 SMART:SM00343 GO:GO:0005634 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0008270 GO:GO:0003676 InterPro:IPR013083 Gene3D:G3DSA:3.30.40.10 Gene3D:G3DSA:4.10.60.10 EMBL:AK316913 IPI:IPI00547250 RefSeq:NP_199554.2 UniGene:At.29893 ProteinModelPortal:B9DFV2 SMR:B9DFV2 PRIDE:B9DFV2 EnsemblPlants:AT5G47430.1 GeneID:834790 KEGG:ath:AT5G47430 TAIR:At5g47430 PhylomeDB:B9DFV2 ProtClustDB:CLSN2699121 Genevestigator:B9DFV2 Uniprot:B9DFV2
Leaf	Isotig02459	23	6	2.468	2.91E-05	TAIR|locus:2132298 - symbol:TOC159 "AT4G02510" species:3702 "Arabidopsis thaliana" [GO:0004888 "transmembrane signaling receptor activity" evidence=IDA] [GO:0009707 "chloroplast outer membrane" evidence=IDA] [GO:0045036 "protein targeting to chloroplast" evidence=IMP;IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0009507 "chloroplast" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0003924 "GTPase activity" evidence=TAS] InterPro:IPR005690 InterPro:IPR006703 Pfam:PF04548 GO:GO:0005525 GO:GO:0016021 GO:GO:0005829 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005515 GO:GO:0046872 GO:GO:0003924 eggNOG:NOG12793 GO:GO:0045036 GO:GO:0004888 GO:GO:0009707 EMBL:AC002330 EMBL:AL161494 EMBL:AF069298 HSSP:Q41009 InterPro:IPR024283 Pfam:PF11886 TIGRFAMs:TIGR00993 EMBL:AF412063 EMBL:AY133653 EMBL:AK222164 IPI:IPI00539726 PIR:A85032 PIR:T01098

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						RefSeq:NP_567242.2 UniGene:At.24962 ProteinModelPortal:O81283 SMR:O81283 IntAct:O81283 STRING:O81283 PRIDE:O81283 EnsemblPlants:AT4G02510.1 GeneID:827934 KEGG:ath:AT4G02510 TAIR:At4g02510 InParanoid:O81283 OMA:SDEANIS PhylomeDB:O81283 ProtClustDB:CLSN2695376 ArrayExpress:O22774 Genevestigator:O81283 Uniprot:O81283
Leaf	Isotig02460	23	6	2.468	2.91E-05	TAIR|locus:2132298 - symbol:TOC159 "AT4G02510" species:3702 "Arabidopsis thaliana" [GO:0004888 "transmembrane signaling receptor activity" evidence=IDA] [GO:0009707 "chloroplast outer membrane" evidence=IDA] [GO:0045036 "protein targeting to chloroplast" evidence=IMP;IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0009507 "chloroplast" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0003924 "GTPase activity" evidence=TAS] InterPro:IPR005690 InterPro:IPR006703 Pfam:PF04548 GO:GO:0005525 GO:GO:0016021 GO:GO:0005829 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005515 GO:GO:0046872 GO:GO:0003924 eggNOG:NOG12793 GO:GO:0045036 GO:GO:0004888 GO:GO:0009707 EMBL:AC002330 EMBL:AL161494 EMBL:AF069298 HSSP:Q41009 InterPro:IPR024283 Pfam:PF11886 TIGRFAMs:TIGR00993 EMBL:AF412063 EMBL:AY133653 EMBL:AK222164 IPI:IPI00539726 PIR:A85032 PIR:T01098 RefSeq:NP_567242.2 UniGene:At.24962 ProteinModelPortal:O81283 SMR:O81283 IntAct:O81283 STRING:O81283 PRIDE:O81283 EnsemblPlants:AT4G02510.1 GeneID:827934 KEGG:ath:AT4G02510 TAIR:At4g02510 InParanoid:O81283 OMA:SDEANIS PhylomeDB:O81283 ProtClustDB:CLSN2695376 ArrayExpress:O22774 Genevestigator:O81283 Uniprot:O81283
Leaf	Isotig02474	12	46	-1.410	0.000732431	UNIPROTKB|B9RYP6 - symbol:RCOM_1312280 "Heat shock protein, putative" species:3988 "Ricinus communis" [GO:0005783 "endoplasmic reticulum" evidence=IDA] InterPro:IPR001023 PRINTS:PR00301 Pfam:PF00012 Prosite:PS00297 Prosite:PS00329 Prosite:PS01036 GO:GO:0005783 GO:GO:0005524 GO:GO:0006950 KO:K09490 InterPro:IPR018181 InterPro:IPR013126 PANTHER:PTHR19375 ProtClustDB:CLSN2713985 GO:GO:0032440 EMBL:EQ973832 RefSeq:XP_002518865.1 ProteinModelPortal:B9RYP6 GeneID:8286262 KEGG:rcu:RCOM_1312280 PhylomeDB:B9RYP6 Uniprot:B9RYP6
Leaf	Isotig02481	79	56	1.025	3.57E-05	TAIR|locus:2177547 - symbol:PAP27 "AT5G50400" species:3702 "Arabidopsis thaliana" [GO:0004722 "protein serine/threonine phosphatase activity" evidence=ISS] [GO:0008150 "biological_process" evidence=ND] [GO:0003993 "acid phosphatase activity" evidence=ISS] InterPro:IPR004843 InterPro:IPR008963 InterPro:IPR015914 Pfam:PF00149 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005576 GO:GO:0046872 GO:GO:0003993 eggNOG:COG1409 EMBL:AB012248 Gene3D:G3DSA:2.60.40.380 SUPFAM:SSF49363 HOGENOM:HBG317004 ProtClustDB:CLSN2918186 EMBL:AY842027 IPI:IPI00516545 RefSeq:NP_199851.2 UniGene:At.50715 ProteinModelPortal:Q5MAU8 SMR:Q5MAU8 PRIDE:Q5MAU8 EnsemblPlants:AT5G50400.1 GeneID:835108 KEGG:ath:AT5G50400 TAIR:At5g50400 InParanoid:Q5MAU8 OMA:FHIGDIT PhylomeDB:Q5MAU8 ArrayExpress:Q5MAU8 Genevestigator:Q5MAU8 Uniprot:Q5MAU8
Leaf	Isotig02482	73	55	0.937	0.000225647	TAIR|locus:2177547 - symbol:PAP27 "AT5G50400" species:3702 "Arabidopsis thaliana" [GO:0004722 "protein serine/threonine phosphatase activity" evidence=ISS] [GO:0008150 "biological_process" evidence=ND] [GO:0003993 "acid phosphatase activity" evidence=ISS] InterPro:IPR004843 InterPro:IPR008963 InterPro:IPR015914 Pfam:PF00149 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005576 GO:GO:0046872 GO:GO:0003993 eggNOG:COG1409 EMBL:AB012248 Gene3D:G3DSA:2.60.40.380 SUPFAM:SSF49363 HOGENOM:HBG317004 ProtClustDB:CLSN2918186 EMBL:AY842027 IPI:IPI00516545 RefSeq:NP_199851.2 UniGene:At.50715 ProteinModelPortal:Q5MAU8 SMR:Q5MAU8 PRIDE:Q5MAU8 EnsemblPlants:AT5G50400.1 GeneID:835108 KEGG:ath:AT5G50400 TAIR:At5g50400 InParanoid:Q5MAU8 OMA:FHIGDIT PhylomeDB:Q5MAU8 ArrayExpress:Q5MAU8 Genevestigator:Q5MAU8 Uniprot:Q5MAU8
Leaf	Isotig02483	20	4	2.851	2.51E-05	TAIR|locus:2098413 - symbol:HMG "AT3G28730" species:3702 "Arabidopsis thaliana" [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0005634 "nucleus" evidence=IDA] [GO:0005719 "nuclear euchromatin" evidence=IDA] [GO:0035101 "FACT complex" evidence=IDA] [GO:0010228 "vegetative to reproductive phase transition of meristem" evidence=IMP] InterPro:IPR009071 InterPro:IPR000969 Pfam:PF00505 PRINTS:PR00887 PROSITE:PS50118 SMART:SM00398 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0006355 GO:GO:0003677 GO:GO:0006260 GO:GO:0006281 GO:GO:0006351 Gene3D:G3DSA:1.10.30.10 SUPFAM:SSF47095 GO:GO:0010228 GO:GO:0005719 InterPro:IPR013719 Pfam:PF08512 eggNOG:COG5165 KO:K09272 HOGENOM:HBG592027 GO:GO:0035101 OMA:PVEVKKG EMBL:D13491 EMBL:AP002057 EMBL:BT002507 EMBL:AK318679 EMBL:AK221855 IPI:IPI00547320 IPI:IPI00931095 PIR:S35511 RefSeq:NP_189515.1 UniGene:At.21931 UniGene:At.48716

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						ProteinModelPortal:Q05153 SMR:Q05153 STRING:Q05153 PRIDE:Q05153 EnsemblPlants:AT3G28730.1 GeneID:822505 KEGG:ath:AT3G28730 TAIR:At3g28730 InParanoid:Q05153 PhylomeDB:Q05153 ProtClustDB:CLSN2684068 ArrayExpress:Q05153 Genevestigator:Q05153 GermOnline:AT3G28730 Uniprot:Q05153
Leaf	Isotig02484	20	4	2.851	2.51E-05	TAIR|locus:2098413 - symbol:HMG "AT3G28730" species:3702 "Arabidopsis thaliana" [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0005634 "nucleus" evidence=IDA] [GO:0005719 "nuclear euchromatin" evidence=IDA] [GO:0035101 "FACT complex" evidence=IDA] [GO:0010228 "vegetative to reproductive phase transition of meristem" evidence=IMP] InterPro:IPR009071 InterPro:IPR000969 Pfam:PF00505 PRINTS:PR00887 PROSITE:PS50118 SMART:SM00398 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0006355 GO:GO:0003677 GO:GO:0006260 GO:GO:0006281 GO:GO:0006351 Gene3D:G3DSA:1.10.30.10 SUPFAM:SSF47095 GO:GO:0010228 GO:GO:0005719 InterPro:IPR013719 Pfam:PF08512 eggNOG:COG5165 KO:K09272 HOGENOM:HBG592027 GO:GO:0035101 OMA:PVEVKKG EMBL:D13491 EMBL:AP002057 EMBL:BT002507 EMBL:AK318679 EMBL:AK221855 IPI:IPI00547320 IPI:IPI00931095 PIR:S35511 RefSeq:NP_189515.1 UniGene:At.21931 UniGene:At.48716 ProteinModelPortal:Q05153 SMR:Q05153 STRING:Q05153 PRIDE:Q05153 EnsemblPlants:AT3G28730.1 GeneID:822505 KEGG:ath:AT3G28730 TAIR:At3g28730 InParanoid:Q05153 PhylomeDB:Q05153 ProtClustDB:CLSN2684068 ArrayExpress:Q05153 Genevestigator:Q05153 GermOnline:AT3G28730 Uniprot:Q05153
Leaf	Isotig02485	0	19	-4.719	4.23E-05	TAIR|locus:2147890 - symbol:AT5G15070 species:3702 "Arabidopsis thaliana" [GO:0003993 "acid phosphatase activity" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0016491 "oxidoreductase activity" evidence=IEA] [GO:0046914 "transition metal ion binding" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] InterPro:IPR000560 Pfam:PF00328 PROSITE:PS00616 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0003993 eggNOG:NOG245915 HOGENOM:HBG378897 EMBL:BT001922 IPI:IPI00544492 RefSeq:NP_568308.1 UniGene:At.23566 ProteinModelPortal:Q84WW3 SMR:Q84WW3 PRIDE:Q84WW3 EnsemblPlants:AT5G15070.1 GeneID:831359 KEGG:ath:AT5G15070 TAIR:At5g15070 InParanoid:Q84WW3 OMA:NASSEME PhylomeDB:Q84WW3 ProtClustDB:CLSN2689684 Genevestigator:Q84WW3 Uniprot:Q84WW3
Leaf	Isotig02486	0	19	-4.719	4.23E-05	TAIR|locus:2147890 - symbol:AT5G15070 species:3702 "Arabidopsis thaliana" [GO:0003993 "acid phosphatase activity" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0016491 "oxidoreductase activity" evidence=IEA] [GO:0046914 "transition metal ion binding" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] InterPro:IPR000560 Pfam:PF00328 PROSITE:PS00616 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0003993 eggNOG:NOG245915 HOGENOM:HBG378897 EMBL:BT001922 IPI:IPI00544492 RefSeq:NP_568308.1 UniGene:At.23566 ProteinModelPortal:Q84WW3 SMR:Q84WW3 PRIDE:Q84WW3 EnsemblPlants:AT5G15070.1 GeneID:831359 KEGG:ath:AT5G15070 TAIR:At5g15070 InParanoid:Q84WW3 OMA:NASSEME PhylomeDB:Q84WW3 ProtClustDB:CLSN2689684 Genevestigator:Q84WW3 Uniprot:Q84WW3
Leaf	Isotig02511	33	9	2.403	8.16E-07	TAIR|locus:2198581 - symbol:SYTB "AT1G20080" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005794 "Golgi apparatus" evidence=IDA] [GO:0009306 "protein secretion" evidence=IMP] InterPro:IPR000008 InterPro:IPR008973 Pfam:PF00168 SMART:SM00239 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005794 GO:GO:0009306 InterPro:IPR018029 SUPFAM:SSF49562 PROSITE:PS50004 eggNOG:COG5038 InterPro:IPR020477 PRINTS:PR00360 EMBL:FM213366 IPI:IPI00532951 RefSeq:NP_173436.4 UniGene:At.41723 ProteinModelPortal:B6ETT4 SMR:B6ETT4 PRIDE:B6ETT4 EnsemblPlants:AT1G20080.1 GeneID:838597 KEGG:ath:AT1G20080 TAIR:At1g20080 HOGENOM:HBG316820 PhylomeDB:B6ETT4 ProtClustDB:CLSN2688294 Genevestigator:B6ETT4 Uniprot:B6ETT4
Leaf	Isotig02512	31	9	2.313	2.97E-06	TAIR|locus:2198581 - symbol:SYTB "AT1G20080" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005794 "Golgi apparatus" evidence=IDA] [GO:0009306 "protein secretion" evidence=IMP] InterPro:IPR000008 InterPro:IPR008973 Pfam:PF00168 SMART:SM00239 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005794 GO:GO:0009306 InterPro:IPR018029 SUPFAM:SSF49562 PROSITE:PS50004 eggNOG:COG5038 InterPro:IPR020477 PRINTS:PR00360 EMBL:FM213366 IPI:IPI00532951 RefSeq:NP_173436.4 UniGene:At.41723 ProteinModelPortal:B6ETT4 SMR:B6ETT4 PRIDE:B6ETT4 EnsemblPlants:AT1G20080.1 GeneID:838597 KEGG:ath:AT1G20080 TAIR:At1g20080 HOGENOM:HBG316820 PhylomeDB:B6ETT4 ProtClustDB:CLSN2688294 Genevestigator:B6ETT4 Uniprot:B6ETT4

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig02519	9	39	-1.587	0.000688545	TAIR|locus:2182270 - symbol:DiT1 "AT5G12860" species:3702 "Arabidopsis thaliana" [GO:0015367 "oxoglutarate:malate antiporter activity" evidence=ISS] [GO:0015743 "malate transport" evidence=ISS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009624 "response to nematode" evidence=IEP] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009536 "plastid" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0015131 "oxaloacetate transmembrane transporter activity" evidence=IMP] [GO:0015139 "alpha-ketoglutarate transmembrane transporter activity" evidence=IMP] InterPro:IPR001898 Pfam:PF00939 GO:GO:0005739 EMBL:CP002688 GO:GO:0016020 GO:GO:0009941 GO:GO:0009624 GO:GO:0006814 GO:GO:0009534 EMBL:AL353013 TIGRFAMs:TIGR00785 GO:GO:0015131 IPI:IPI00521860 PIR:T49900 RefSeq:NP_568283.2 UniGene:At.5282 STRING:Q9LXV3 PRIDE:Q9LXV3 EnsemblPlants:AT5G12860.1 GeneID:831126 KEGG:ath:AT5G12860 TAIR:At5g12860 InParanoid:Q9LXV3 OMA:PTIWMIA PhylomeDB:Q9LXV3 ProtClustDB:CLSN2686250 Genevestigator:Q9LXV3 GO:GO:0015139 Uniprot:Q9LXV3
Leaf	Isotig02520	9	39	-1.587	0.000688545	TAIR|locus:2182270 - symbol:DiT1 "AT5G12860" species:3702 "Arabidopsis thaliana" [GO:0015367 "oxoglutarate:malate antiporter activity" evidence=ISS] [GO:0015743 "malate transport" evidence=ISS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009624 "response to nematode" evidence=IEP] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009536 "plastid" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0015131 "oxaloacetate transmembrane transporter activity" evidence=IMP] [GO:0015139 "alpha-ketoglutarate transmembrane transporter activity" evidence=IMP] InterPro:IPR001898 Pfam:PF00939 GO:GO:0005739 EMBL:CP002688 GO:GO:0016020 GO:GO:0009941 GO:GO:0009624 GO:GO:0006814 GO:GO:0009534 EMBL:AL353013 TIGRFAMs:TIGR00785 GO:GO:0015131 IPI:IPI00521860 PIR:T49900 RefSeq:NP_568283.2 UniGene:At.5282 STRING:Q9LXV3 PRIDE:Q9LXV3 EnsemblPlants:AT5G12860.1 GeneID:831126 KEGG:ath:AT5G12860 TAIR:At5g12860 InParanoid:Q9LXV3 OMA:PTIWMIA PhylomeDB:Q9LXV3 ProtClustDB:CLSN2686250 Genevestigator:Q9LXV3 GO:GO:0015139 Uniprot:Q9LXV3
Leaf	Isotig02531	16	4	2.529	0.000407249	TAIR|locus:2063020 - symbol:GBF3 "AT2G46270" species:3702 "Arabidopsis thaliana" [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0043565 "sequence-specific DNA binding" evidence=IDA] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR004827 InterPro:IPR011616 InterPro:IPR012900 Pfam:PF00170 Pfam:PF07777 PROSITE:PS00036 PROSITE:PS50217 SMART:SM00338 GO:GO:0005829 GO:GO:0009737 GO:GO:0005634 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0043565 GO:GO:0003700 GO:GO:0006351 GO:GO:0046983 EMBL:AC005397 HOGENOM:HBG591016 KO:K09060 ProtClustDB:CLSN2683456 EMBL:U17891 EMBL:U51850 EMBL:AF370307 EMBL:AY063093 EMBL:X63896 IPI:IPI00536925 PIR:G84900 PIR:S20885 RefSeq:NP_182150.1 UniGene:At.19966 ProteinModelPortal:P42776 SMR:P42776 IntAct:P42776 STRING:P42776 PRIDE:P42776 EnsemblPlants:AT2G46270.1 GeneID:819235 KEGG:ath:AT2G46270 TAIR:At2g46270 eggNOG:NOG314709 InParanoid:P42776 OMA:PYAAVYP PhylomeDB:P42776 ArrayExpress:P42776 Genevestigator:P42776 Uniprot:P42776
Leaf	Isotig02532	16	4	2.529	0.000407249	TAIR|locus:2063020 - symbol:GBF3 "AT2G46270" species:3702 "Arabidopsis thaliana" [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0043565 "sequence-specific DNA binding" evidence=IDA] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR004827 InterPro:IPR011616 InterPro:IPR012900 Pfam:PF00170 Pfam:PF07777 PROSITE:PS00036 PROSITE:PS50217 SMART:SM00338 GO:GO:0005829 GO:GO:0009737 GO:GO:0005634 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0043565 GO:GO:0003700 GO:GO:0006351 GO:GO:0046983 EMBL:AC005397 HOGENOM:HBG591016 KO:K09060 ProtClustDB:CLSN2683456 EMBL:U17891 EMBL:U51850 EMBL:AF370307 EMBL:AY063093 EMBL:X63896 IPI:IPI00536925 PIR:G84900 PIR:S20885 RefSeq:NP_182150.1 UniGene:At.19966 ProteinModelPortal:P42776 SMR:P42776 IntAct:P42776 STRING:P42776 PRIDE:P42776 EnsemblPlants:AT2G46270.1 GeneID:819235 KEGG:ath:AT2G46270 TAIR:At2g46270 eggNOG:NOG314709 InParanoid:P42776 OMA:PYAAVYP PhylomeDB:P42776 ArrayExpress:P42776 Genevestigator:P42776 Uniprot:P42776
Leaf	Isotig02547	11	1	3.988	0.000330755	TAIR|locus:1005716273 - symbol:AT4G33625 "AT4G33625" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0005773 "vacuole" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005774 InterPro:IPR013714 Pfam:PF08507 EMBL:BT025762

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EMBL:AK118197 IPI:IPI00521335 RefSeq:NP_849487.1 UniGene:At.46078 PRIDE:Q8GXK1 EnsemblPlants:AT4G33625.1 GeneID:829503 KEGG:ath:AT4G33625 TAIR:At4g33625 HOGENOM:HBG318736 InParanoid:Q8GXK1 OMA:YLLLACG PhylomeDB:Q8GXK1 ProtClustDB:CLSN2918260 Genevestigator:Q8GXK1 Uniprot:Q8GXK1
Leaf	Isotig02548	11	1	3.988	0.000330755	TAIR|locus:1005716273 - symbol:AT4G33625 "AT4G33625" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0005773 "vacuole" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005774 InterPro:IPR013714 Pfam:PF08507 EMBL:BT025762 EMBL:AK118197 IPI:IPI00521335 RefSeq:NP_849487.1 UniGene:At.46078 PRIDE:Q8GXK1 EnsemblPlants:AT4G33625.1 GeneID:829503 KEGG:ath:AT4G33625 TAIR:At4g33625 HOGENOM:HBG318736 InParanoid:Q8GXK1 OMA:YLLLACG PhylomeDB:Q8GXK1 ProtClustDB:CLSN2918260 Genevestigator:Q8GXK1 Uniprot:Q8GXK1
Leaf	Isotig02565	28	5	3.014	2.98E-07	TAIR|locus:2075845 - symbol:SCPL49 "SERINE CARBOXYPEPTIDASE-LIKE 49" species:3702 "Arabidopsis thaliana" [GO:0004185 "serine-type carboxypeptidase activity" evidence=IEA;ISS] [GO:0006508 "proteolysis" evidence=IEA;ISS] [GO:0005773 "vacuole" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001563 InterPro:IPR018202 Pfam:PF00450 PRINTS:PR00724 PROSITE:PS00131 PROSITE:PS00560 GO:GO:0005829 GO:GO:0005773 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005576 GO:GO:0006508 EMBL:AC011560 GO:GO:0004185 eggNOG:COG2939 KO:K13289 PANTHER:PTHR11802 HOGENOM:HBG588032 ProtClustDB:CLSN2684010 EMBL:M81130 EMBL:AY091767 EMBL:AY149954 EMBL:Z25955 EMBL:Z26528 IPI:IPI00547765 RefSeq:NP_187652.1 UniGene:At.20528 UniGene:At.45878 UniGene:At.72674 ProteinModelPortal:P32826 SMR:P32826 STRING:P32826 MEROPS:S10.A45 PRIDE:P32826 EnsemblPlants:AT3G10410.1 GeneID:820205 KEGG:ath:AT3G10410 TAIR:At3g10410 InParanoid:P32826 OMA:AYPDYAL PhylomeDB:P32826 ArrayExpress:P32826 Genevestigator:P32826 GermOnline:AT3G10410 Uniprot:P32826
Leaf	Isotig02566	28	5	3.014	2.98E-07	TAIR|locus:2075845 - symbol:SCPL49 "SERINE CARBOXYPEPTIDASE-LIKE 49" species:3702 "Arabidopsis thaliana" [GO:0004185 "serine-type carboxypeptidase activity" evidence=IEA;ISS] [GO:0006508 "proteolysis" evidence=IEA;ISS] [GO:0005773 "vacuole" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001563 InterPro:IPR018202 Pfam:PF00450 PRINTS:PR00724 PROSITE:PS00131 PROSITE:PS00560 GO:GO:0005829 GO:GO:0005773 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005576 GO:GO:0006508 EMBL:AC011560 GO:GO:0004185 eggNOG:COG2939 KO:K13289 PANTHER:PTHR11802 HOGENOM:HBG588032 ProtClustDB:CLSN2684010 EMBL:M81130 EMBL:AY091767 EMBL:AY149954 EMBL:Z25955 EMBL:Z26528 IPI:IPI00547765 RefSeq:NP_187652.1 UniGene:At.20528 UniGene:At.45878 UniGene:At.72674 ProteinModelPortal:P32826 SMR:P32826 STRING:P32826 MEROPS:S10.A45 PRIDE:P32826 EnsemblPlants:AT3G10410.1 GeneID:820205 KEGG:ath:AT3G10410 TAIR:At3g10410 InParanoid:P32826 OMA:AYPDYAL PhylomeDB:P32826 ArrayExpress:P32826 Genevestigator:P32826 GermOnline:AT3G10410 Uniprot:P32826
Leaf	Isotig02605	10	1	3.851	0.00071293	TAIR|locus:2076715 - symbol:ATG6 "AT3G61710" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0006914 "autophagy" evidence=ISS] [GO:0000045 "autophagic vacuole assembly" evidence=IGI] [GO:0000407 "pre-autophagosomal structure" evidence=IDA] [GO:0006623 "protein targeting to vacuole" evidence=IGI] [GO:0009846 "pollen germination" evidence=IMP] [GO:0050832 "defense response to fungus" evidence=IEP] InterPro:IPR007243 Pfam:PF04111 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0050832 GO:GO:0000045 EMBL:AL132959 GO:GO:0006623 GO:GO:0000407 GO:GO:0009846 PANTHER:PTHR12768 EMBL:AY039613 EMBL:BT000508 IPI:IPI00521940 PIR:T47963 RefSeq:NP_567116.1 UniGene:At.958 ProteinModelPortal:Q9M367 STRING:Q9M367 PRIDE:Q9M367 EnsemblPlants:AT3G61710.1 GeneID:825344 KEGG:ath:AT3G61710 TAIR:At3g61710 eggNOG:NOG285533 HOGENOM:HBG676980 InParanoid:Q9M367 OMA:LDTQLNI PhylomeDB:Q9M367 ProtClustDB:CLSN2689306 ArrayExpress:Q9M367 Genevestigator:Q9M367 Uniprot:Q9M367
Leaf	Isotig02606	10	1	3.851	0.00071293	TAIR|locus:2076715 - symbol:ATG6 "AT3G61710" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0006914 "autophagy" evidence=ISS] [GO:0000045 "autophagic vacuole assembly" evidence=IGI] [GO:0000407 "pre-autophagosomal structure" evidence=IDA] [GO:0006623 "protein targeting to vacuole" evidence=IGI] [GO:0009846 "pollen germination" evidence=IMP] [GO:0050832 "defense response to fungus" evidence=IEP] InterPro:IPR007243 Pfam:PF04111 EMBL:CP002686

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GenomeReviews:BA000014_GR GO:GO:0050832 GO:GO:0000045 EMBL:AL132959 GO:GO:0006623 GO:GO:0000407 GO:GO:0009846 PANTHER:PTHR12768 EMBL:AY039613 EMBL:BT000508 IPI:IPI00521940 PIR:T47963 RefSeq:NP_567116.1 UniGene:At.958 ProteinModelPortal:Q9M367 STRING:Q9M367 PRIDE:Q9M367 EnsemblPlants:AT3G61710.1 GeneID:825344 KEGG:ath:AT3G61710 TAIR:At3g61710 eggNOG:NOG285533 HOGENOM:HBG676980 InParanoid:Q9M367 OMA:LDTQLNI PhylomeDB:Q9M367 ProtClustDB:CLSN2689306 ArrayExpress:Q9M367 Genevestigator:Q9M367 Uniprot:Q9M367
Leaf	Isotig02611	4	56	-3.278	3.64E-10	TAIR|locus:2178287 - symbol:CaS "AT5G23060" species:3702 "Arabidopsis thaliana" [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0071277 "cellular response to calcium ion" evidence=IMP] [GO:0090333 "regulation of stomatal closure" evidence=IMP] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0009704 "de-etiolation" evidence=IMP] Pfam:PF00581 GO:GO:0016021 GO:GO:0005739 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0071277 GO:GO:0004872 EMBL:AB006708 GO:GO:0090333 GO:GO:0009535 InterPro:IPR001763 Gene3D:G3DSA:3.40.250.10 SMART:SM00450 SUPFAM:SSF52821 PROSITE:PS50206 EMBL:AY341888 EMBL:AY045798 EMBL:AY079331 EMBL:BT000666 IPI:IPI00530400 RefSeq:NP_197697.1 UniGene:At.24421 UniGene:At.71491 UniGene:At.74783 ProteinModelPortal:Q9FN48 SMR:Q9FN48 PRIDE:Q9FN48 ProMEX:Q9FN48 EnsemblPlants:AT5G23060.1 GeneID:832370 KEGG:ath:AT5G23060 GeneFarm:3345 TAIR:At5g23060 eggNOG:NOG315676 HOGENOM:HBG316580 InParanoid:Q9FN48 OMA:PSRIIPA PhylomeDB:Q9FN48 ProtClustDB:CLSN2686105 ArrayExpress:Q9FN48 Genevestigator:Q9FN48 Uniprot:Q9FN48
Leaf	Isotig02612	4	54	-3.226	9.81E-10	TAIR|locus:2178287 - symbol:CaS "AT5G23060" species:3702 "Arabidopsis thaliana" [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0071277 "cellular response to calcium ion" evidence=IMP] [GO:0090333 "regulation of stomatal closure" evidence=IMP] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0009704 "de-etiolation" evidence=IMP] Pfam:PF00581 GO:GO:0016021 GO:GO:0005739 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0071277 GO:GO:0004872 EMBL:AB006708 GO:GO:0090333 GO:GO:0009535 InterPro:IPR001763 Gene3D:G3DSA:3.40.250.10 SMART:SM00450 SUPFAM:SSF52821 PROSITE:PS50206 EMBL:AY341888 EMBL:AY045798 EMBL:AY079331 EMBL:BT000666 IPI:IPI00530400 RefSeq:NP_197697.1 UniGene:At.24421 UniGene:At.71491 UniGene:At.74783 ProteinModelPortal:Q9FN48 SMR:Q9FN48 PRIDE:Q9FN48 ProMEX:Q9FN48 EnsemblPlants:AT5G23060.1 GeneID:832370 KEGG:ath:AT5G23060 GeneFarm:3345 TAIR:At5g23060 eggNOG:NOG315676 HOGENOM:HBG316580 InParanoid:Q9FN48 OMA:PSRIIPA PhylomeDB:Q9FN48 ProtClustDB:CLSN2686105 ArrayExpress:Q9FN48 Genevestigator:Q9FN48 Uniprot:Q9FN48
Leaf	Isotig02633	39	19	1.566	5.36E-05	TAIR|locus:2012938 - symbol:SMT2 "AT1G20330" species:3702 "Arabidopsis thaliana" [GO:0007389 "pattern specification process" evidence=IMP] [GO:0009825 "multidimensional cell growth" evidence=IMP] [GO:0005783 "endoplasmic reticulum" evidence=IDA;TAS] [GO:0010051 "xylem and phloem pattern formation" evidence=IMP] [GO:0032876 "negative regulation of DNA endoreduplication" evidence=IMP] [GO:0005829 "cytosol" evidence=RCA] [GO:0005794 "Golgi apparatus" evidence=IDA] [GO:0008757 "S-adenosylmethionine-dependent methyltransferase activity" evidence=IDA] [GO:0016126 "sterol biosynthetic process" evidence=IDA] InterPro:IPR013216 InterPro:IPR013705 Pfam:PF08241 Pfam:PF08498 GO:GO:0005783 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0016126 GO:GO:0010051 eggNOG:COG0500 GO:GO:0032876 GO:GO:0009825 HOGENOM:HBG316404 EMBL:AC026234 EMBL:X89867 EMBL:AY046042 EMBL:AF332417 EMBL:AY113961 EMBL:AY128389 EMBL:BT002093 EMBL:BT000750 EMBL:AY086699 IPI:IPI00540275 PIR:S63686 RefSeq:NP_173458.1 UniGene:At.186 UniGene:At.71890 ProteinModelPortal:Q39227 SMR:Q39227 STRING:Q39227 PRIDE:Q39227 EnsemblPlants:AT1G20330.1 GeneID:838621 KEGG:ath:AT1G20330 GeneFarm:4916 TAIR:At1g20330 InParanoid:Q39227 KO:K08242 OMA:ACHASNT PhylomeDB:Q39227 ProtClustDB:CLSN2679396 Genevestigator:Q39227 GermOnline:AT1G20330 GO:GO:0030797 Uniprot:Q39227
Leaf	Isotig02634	39	18	1.644	2.87E-05	TAIR|locus:2012938 - symbol:SMT2 "AT1G20330" species:3702 "Arabidopsis thaliana" [GO:0007389 "pattern specification process" evidence=IMP] [GO:0009825 "multidimensional cell growth" evidence=IMP] [GO:0005783 "endoplasmic reticulum" evidence=IDA;TAS] [GO:0010051 "xylem and phloem pattern formation" evidence=IMP] [GO:0032876 "negative regulation of DNA endoreduplication" evidence=IMP] [GO:0005829 "cytosol" evidence=RCA] [GO:0005794 "Golgi apparatus" evidence=IDA] [GO:0008757 "S-adenosylmethionine-dependent methyltransferase activity" evidence=IDA] [GO:0016126 "sterol biosynthetic process" evidence=IDA]

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						InterPro:IPR013216 InterPro:IPR013705 Pfam:PF08241 Pfam:PF08498 GO:GO:0005783 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0016126 GO:GO:0010051 eggNOG:COG0500 GO:GO:0032876 GO:GO:0009825 HOGENOM:HBG316404 EMBL:AC026234 EMBL:X89867 EMBL:AY046042 EMBL:AF332417 EMBL:AY113961 EMBL:AY128389 EMBL:BT002093 EMBL:BT000750 EMBL:AY086699 IPI:IPI00540275 PIR:S63686 RefSeq:NP_173458.1 UniGene:At.186 UniGene:At.71890 ProteinModelPortal:Q39227 SMR:Q39227 STRING:Q39227 PRIDE:Q39227 EnsemblPlants:AT1G20330.1 GeneID:838621 KEGG:ath:AT1G20330 GeneFarm:4916 TAIR:At1g20330 InParanoid:Q39227 KO:K08242 OMA:ACHASNT PhylomeDB:Q39227 ProtClustDB:CLSN2679396 Genevestigator:Q39227 GermOnline:AT1G20330 GO:GO:0030797 Uniprot:Q39227
Leaf	Isotig02641	13	1	4.229	7.21E-05	TAIR|locus:2198035 - symbol:PMEAMT "AT1G48600" species:3702 "Arabidopsis thaliana" [GO:0000234 "phosphoethanolamine N-methyltransferase activity" evidence=ISS] [GO:0006656 "phosphatidylcholine biosynthetic process" evidence=IGI;IDA] [GO:0052667 "phosphomethylethanolamine N-methyltransferase activity" evidence=IDA] EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005737 EMBL:AC020889 eggNOG:COG0500 GO:GO:0006656 HOGENOM:HBG320513 ProtClustDB:PLN02336 GO:GO:0000234 EMBL:AF428454 EMBL:AY063866 EMBL:AY133811 IPI:IPI00539739 PIR:F96525 RefSeq:NP_175293.1 UniGene:At.22426 ProteinModelPortal:Q944H0 SMR:Q944H0 PRIDE:Q944H0 EnsemblPlants:AT1G48600.1 GeneID:841281 KEGG:ath:AT1G48600 TAIR:At1g48600 InParanoid:Q944H0 PhylomeDB:Q944H0 ArrayExpress:Q944H0 Genevestigator:Q944H0 GO:GO:0052667 Uniprot:Q944H0
Leaf	Isotig02642	13	1	4.229	7.21E-05	TAIR|locus:2198035 - symbol:PMEAMT "AT1G48600" species:3702 "Arabidopsis thaliana" [GO:0000234 "phosphoethanolamine N-methyltransferase activity" evidence=ISS] [GO:0006656 "phosphatidylcholine biosynthetic process" evidence=IGI;IDA] [GO:0052667 "phosphomethylethanolamine N-methyltransferase activity" evidence=IDA] EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005737 EMBL:AC020889 eggNOG:COG0500 GO:GO:0006656 HOGENOM:HBG320513 ProtClustDB:PLN02336 GO:GO:0000234 EMBL:AF428454 EMBL:AY063866 EMBL:AY133811 IPI:IPI00539739 PIR:F96525 RefSeq:NP_175293.1 UniGene:At.22426 ProteinModelPortal:Q944H0 SMR:Q944H0 PRIDE:Q944H0 EnsemblPlants:AT1G48600.1 GeneID:841281 KEGG:ath:AT1G48600 TAIR:At1g48600 InParanoid:Q944H0 PhylomeDB:Q944H0 ArrayExpress:Q944H0 Genevestigator:Q944H0 GO:GO:0052667 Uniprot:Q944H0
Leaf	Isotig02649	4	26	-2.171	0.000609459	TAIR|locus:2140050 - symbol:AT4G39970 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0008152 "metabolic process" evidence=IEA] [GO:0016787 "hydrolase activity" evidence=IEA;ISS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] InterPro:IPR006402 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0009570 InterPro:IPR023214 Gene3D:G3DSA:3.40.50.1000 SUPFAM:SSF56784 GO:GO:0009941 GO:GO:0016787 TIGRFAMs:TIGR01509 eggNOG:COG0637 HOGENOM:HBG742904 EMBL:AK175831 EMBL:AK175865 EMBL:AK176082 IPI:IPI00527587 RefSeq:NP_568077.1 UniGene:At.43709 UniGene:At.68472 ProteinModelPortal:Q680K2 SMR:Q680K2 STRING:Q680K2 PRIDE:Q680K2 EnsemblPlants:AT4G39970.1 GeneID:830158 KEGG:ath:AT4G39970 TAIR:At4g39970 InParanoid:Q680K2 OMA:ANACLNS PhylomeDB:Q680K2 ProtClustDB:PLN02779 Genevestigator:Q680K2 Uniprot:Q680K2
Leaf	Isotig02650	4	25	-2.115	0.000948108	TAIR|locus:2140050 - symbol:AT4G39970 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0008152 "metabolic process" evidence=IEA] [GO:0016787 "hydrolase activity" evidence=IEA;ISS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] InterPro:IPR006402 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0009570 InterPro:IPR023214 Gene3D:G3DSA:3.40.50.1000 SUPFAM:SSF56784 GO:GO:0009941 GO:GO:0016787 TIGRFAMs:TIGR01509 eggNOG:COG0637 HOGENOM:HBG742904 EMBL:AK175831 EMBL:AK175865 EMBL:AK176082 IPI:IPI00527587 RefSeq:NP_568077.1 UniGene:At.43709 UniGene:At.68472 ProteinModelPortal:Q680K2 SMR:Q680K2 STRING:Q680K2 PRIDE:Q680K2 EnsemblPlants:AT4G39970.1 GeneID:830158 KEGG:ath:AT4G39970 TAIR:At4g39970 InParanoid:Q680K2 OMA:ANACLNS PhylomeDB:Q680K2 ProtClustDB:PLN02779 Genevestigator:Q680K2 Uniprot:Q680K2
Leaf	Isotig02651	13	2	3.229	0.00031313	TAIR|locus:2163771 - symbol:SPDS3 "AT5G53120" species:3702 "Arabidopsis thaliana" [GO:0004766 "spermidine synthase activity" evidence=ISS;IDA] [GO:0005737 "cytoplasm" evidence=TAS] [GO:0006596 "polyamine biosynthetic process" evidence=IDA] [GO:0016768 "spermine synthase activity" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] InterPro:IPR001045 Pfam:PF01564 PROSITE:PS01330 PROSITE:PS51006

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0005737 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005515 HSSP:Q9WZC2 eggNOG:COG0421 KO:K00797 GO:GO:0016768 GO:GO:0006596 PANTHER:PTHR11558 EMBL:AB025622 UniGene:At.21042 UniGene:At.49166 GO:GO:0004766 TIGRFAMs:TIGR00417 ProtClustDB:PLN02366 OMA:ELWYTEK EMBL:AF424571 EMBL:AY040013 EMBL:AY079367 EMBL:BT000742 EMBL:AK316822 EMBL:AY087226 IPI:IPI00535074 RefSeq:NP_001078748.1 RefSeq:NP_001078749.1 RefSeq:NP_568785.1 RefSeq:NP_851178.1 RefSeq:NP_851179.1 ProteinModelPortal:Q94BN2 SMR:Q94BN2 IntAct:Q94BN2 STRING:Q94BN2 PRIDE:Q94BN2 EnsemblPlants:AT5G53120.1 EnsemblPlants:AT5G53120.2 EnsemblPlants:AT5G53120.3 EnsemblPlants:AT5G53120.4 EnsemblPlants:AT5G53120.5 GeneID:835392 KEGG:ath:AT5G53120 TAIR:At5g53120 InParanoid:Q94BN2 PhylomeDB:Q94BN2 ArrayExpress:Q94BN2 Genevestigator:Q94BN2 Uniprot:Q94BN2
Leaf	Isotig02652	13	2	3.229	0.00031313	TAIR|locus:2163771 - symbol:SPDS3 "AT5G53120" species:3702 "Arabidopsis thaliana" [GO:0004766 "spermidine synthase activity" evidence=ISS;IDA] [GO:0005737 "cytoplasm" evidence=TAS] [GO:0006596 "polyamine biosynthetic process" evidence=IDA] [GO:0016768 "spermine synthase activity" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] InterPro:IPR001045 Pfam:PF01564 PROSITE:PS01330 PROSITE:PS51006 GO:GO:0005737 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005515 HSSP:Q9WZC2 eggNOG:COG0421 KO:K00797 GO:GO:0016768 GO:GO:0006596 PANTHER:PTHR11558 EMBL:AB025622 UniGene:At.21042 UniGene:At.49166 GO:GO:0004766 TIGRFAMs:TIGR00417 ProtClustDB:PLN02366 OMA:ELWYTEK EMBL:AF424571 EMBL:AY040013 EMBL:AY079367 EMBL:BT000742 EMBL:AK316822 EMBL:AY087226 IPI:IPI00535074 RefSeq:NP_001078748.1 RefSeq:NP_001078749.1 RefSeq:NP_568785.1 RefSeq:NP_851178.1 RefSeq:NP_851179.1 ProteinModelPortal:Q94BN2 SMR:Q94BN2 IntAct:Q94BN2 STRING:Q94BN2 PRIDE:Q94BN2 EnsemblPlants:AT5G53120.1 EnsemblPlants:AT5G53120.2 EnsemblPlants:AT5G53120.3 EnsemblPlants:AT5G53120.4 EnsemblPlants:AT5G53120.5 GeneID:835392 KEGG:ath:AT5G53120 TAIR:At5g53120 InParanoid:Q94BN2 PhylomeDB:Q94BN2 ArrayExpress:Q94BN2 Genevestigator:Q94BN2 Uniprot:Q94BN2
Leaf	Isotig02653	0	14	-4.278	0.000582768	TAIR|locus:2170533 - symbol:AT5G40310 species:3702 "Arabidopsis thaliana" [GO:0003676 "nucleic acid binding" evidence=IEA] [GO:0004527 "exonuclease activity" evidence=IEA;ISS] [GO:0005622 "intracellular" evidence=IEA;ISS] [GO:0008270 "zinc ion binding" evidence=IEA] Pfam:PF00096 InterPro:IPR006055 InterPro:IPR007087 InterPro:IPR012337 InterPro:IPR015880 PROSITE:PS00028 PROSITE:PS50157 SMART:SM00355 SMART:SM00479 Pfam:PF00929 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0008270 GO:GO:0003676 GO:GO:0005622 GO:GO:0004527 eggNOG:COG0847 InterPro:IPR013520 SUPFAM:SSF53098 EMBL:AB006702 HOGENOM:HBG316815 ProtClustDB:CLSN2687545 IPI:IPI00536517 RefSeq:NP_198847.1 UniGene:At.55275 ProteinModelPortal:Q9FNE7 SMR:Q9FNE7 PRIDE:Q9FNE7 EnsemblPlants:AT5G40310.1 GeneID:834029 KEGG:ath:AT5G40310 TAIR:At5g40310 InParanoid:Q9FNE7 OMA:RCQLSNV PhylomeDB:Q9FNE7 Genevestigator:Q9FNE7 Uniprot:Q9FNE7
Leaf	Isotig02654	0	14	-4.278	0.000582768	TAIR|locus:2170533 - symbol:AT5G40310 species:3702 "Arabidopsis thaliana" [GO:0003676 "nucleic acid binding" evidence=IEA] [GO:0004527 "exonuclease activity" evidence=IEA;ISS] [GO:0005622 "intracellular" evidence=IEA;ISS] [GO:0008270 "zinc ion binding" evidence=IEA] Pfam:PF00096 InterPro:IPR006055 InterPro:IPR007087 InterPro:IPR012337 InterPro:IPR015880 PROSITE:PS00028 PROSITE:PS50157 SMART:SM00355 SMART:SM00479 Pfam:PF00929 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0008270 GO:GO:0003676 GO:GO:0005622 GO:GO:0004527 eggNOG:COG0847 InterPro:IPR013520 SUPFAM:SSF53098 EMBL:AB006702 HOGENOM:HBG316815 ProtClustDB:CLSN2687545 IPI:IPI00536517 RefSeq:NP_198847.1 UniGene:At.55275 ProteinModelPortal:Q9FNE7 SMR:Q9FNE7 PRIDE:Q9FNE7 EnsemblPlants:AT5G40310.1 GeneID:834029 KEGG:ath:AT5G40310 TAIR:At5g40310 InParanoid:Q9FNE7 OMA:RCQLSNV PhylomeDB:Q9FNE7 Genevestigator:Q9FNE7 Uniprot:Q9FNE7
Leaf	Isotig02659	22	3	3.403	1.63E-06	TAIR|locus:2165106 - symbol:AT5G56840 "AT5G56840" species:3702 "Arabidopsis thaliana" [GO:0003676 "nucleic acid binding" evidence=ISS] [GO:0003677 "DNA binding" evidence=ISS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=TAS] InterPro:IPR001005 InterPro:IPR001878 InterPro:IPR009057 Pfam:PF00249 PROSITE:PS50158 SMART:SM00343 SMART:SM00717 GO:GO:0005634 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0006355 GO:GO:0003677 GO:GO:0008270 Gene3D:G3DSA:1.10.10.60 SUPFAM:SSF46689 InterPro:IPR017930 InterPro:IPR006447 TIGRFAMs:TIGR01557 PROSITE:PS51294 EMBL:AB013392 HOGENOM:HBG601503 EMBL:AY519517 EMBL:BT012528 EMBL:BT014956 IPI:IPI00548744

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						RefSeq:NP_200495.1 UniGene:At.29361 ProteinModelPortal:Q9FJS9 SMR:Q9FJS9 PRIDE:Q9FJS9 EnsemblPlants:AT5G56840.1 GeneID:835786 KEGG:ath:AT5G56840 TAIR:At5g56840 eggNOG:NOG244478 InParanoid:Q9FJS9 OMA:ESNIRPI PhylomeDB:Q9FJS9 ProtClustDB:CLSN2916792 Genevestigator:Q9FJS9 Uniprot:Q9FJS9
Leaf	Isotig02660	22	3	3.403	1.63E-06	TAIR|locus:2165106 - symbol:AT5G56840 "AT5G56840" species:3702 "Arabidopsis thaliana" [GO:0003676 "nucleic acid binding" evidence=ISS] [GO:0003677 "DNA binding" evidence=ISS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=TAS] InterPro:IPR001005 InterPro:IPR001878 InterPro:IPR009057 Pfam:PF00249 PROSITE:PS50158 SMART:SM00343 SMART:SM00717 GO:GO:0005634 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0006355 GO:GO:0003677 GO:GO:0008270 Gene3D:G3DSA:1.10.10.60 SUPFAM:SSF46689 InterPro:IPR017930 InterPro:IPR006447 TIGRFAMs:TIGR01557 PROSITE:PS51294 EMBL:AB013392 HOGENOM:HBG601503 EMBL:AY519517 EMBL:BT012528 EMBL:BT014956 IPI:IPI00548744 RefSeq:NP_200495.1 UniGene:At.29361 ProteinModelPortal:Q9FJS9 SMR:Q9FJS9 PRIDE:Q9FJS9 EnsemblPlants:AT5G56840.1 GeneID:835786 KEGG:ath:AT5G56840 TAIR:At5g56840 eggNOG:NOG244478 InParanoid:Q9FJS9 OMA:ESNIRPI PhylomeDB:Q9FJS9 ProtClustDB:CLSN2916792 Genevestigator:Q9FJS9 Uniprot:Q9FJS9
Leaf	Isotig02711	24	1	5.114	2.21E-08	TAIR|locus:2085775 - symbol:ENODL9 "early nodulin-like protein 9" species:3702 "Arabidopsis thaliana" [GO:0005507 "copper ion binding" evidence=IEA;ISS] [GO:0009055 "electron carrier activity" evidence=IEA] [GO:0031225 "anchored to membrane" evidence=TAS] InterPro:IPR003245 Pfam:PF02298 ProDom:PD003122 PROSITE:PS51485 EMBL:CP002686 GO:GO:0009055 GO:GO:0031225 GO:GO:0005507 InterPro:IPR008972 Gene3D:G3DSA:2.60.40.420 SUPFAM:SSF49503 EMBL:AP000410 UniGene:At.48682 UniGene:At.5498 HSSP:P29602 EMBL:BT009716 EMBL:AK228335 IPI:IPI00523618 RefSeq:NP_566665.1 ProteinModelPortal:Q9LJU1 SMR:Q9LJU1 STRING:Q9LJU1 PRIDE:Q9LJU1 EnsemblPlants:AT3G20570.1 GeneID:821604 KEGG:ath:AT3G20570 TAIR:At3g20570 InParanoid:Q9LJU1 OMA:SGNKDNC PhylomeDB:Q9LJU1 ProtClustDB:CLSN2718972 Genevestigator:Q9LJU1 Uniprot:Q9LJU1
Leaf	Isotig02712	24	1	5.114	2.21E-08	TAIR|locus:2085775 - symbol:ENODL9 "early nodulin-like protein 9" species:3702 "Arabidopsis thaliana" [GO:0005507 "copper ion binding" evidence=IEA;ISS] [GO:0009055 "electron carrier activity" evidence=IEA] [GO:0031225 "anchored to membrane" evidence=TAS] InterPro:IPR003245 Pfam:PF02298 ProDom:PD003122 PROSITE:PS51485 EMBL:CP002686 GO:GO:0009055 GO:GO:0031225 GO:GO:0005507 InterPro:IPR008972 Gene3D:G3DSA:2.60.40.420 SUPFAM:SSF49503 EMBL:AP000410 UniGene:At.48682 UniGene:At.5498 HSSP:P29602 EMBL:BT009716 EMBL:AK228335 IPI:IPI00523618 RefSeq:NP_566665.1 ProteinModelPortal:Q9LJU1 SMR:Q9LJU1 STRING:Q9LJU1 PRIDE:Q9LJU1 EnsemblPlants:AT3G20570.1 GeneID:821604 KEGG:ath:AT3G20570 TAIR:At3g20570 InParanoid:Q9LJU1 OMA:SGNKDNC PhylomeDB:Q9LJU1 ProtClustDB:CLSN2718972 Genevestigator:Q9LJU1 Uniprot:Q9LJU1
Leaf	Isotig02723	21	5	2.599	3.91E-05	TAIR|locus:2053144 - symbol:AT2G18110 species:3702 "Arabidopsis thaliana" [GO:0003746 "translation elongation factor activity" evidence=IEA;ISS] [GO:0005853 "eukaryotic translation elongation factor 1 complex" evidence=ISS] [GO:0006414 "translational elongation" evidence=IEA;ISS] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001326 InterPro:IPR014038 Pfam:PF00736 PROSITE:PS00824 PROSITE:PS00825 SMART:SM00888 GO:GO:0005829 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0003746 InterPro:IPR010987 Gene3D:G3DSA:1.20.1050.10 PROSITE:PS50405 EMBL:AC006201 GO:GO:0005853 eggNOG:COG2092 HOGENOM:HBG714747 KO:K03232 ProtClustDB:CLSN2683026 InterPro:IPR014717 Gene3D:G3DSA:3.30.70.60 SUPFAM:SSF54984 EMBL:AC007212 EMBL:AY065159 EMBL:AY081568 EMBL:AY087429 IPI:IPI00548124 PIR:D84560 RefSeq:NP_179402.1 UniGene:At.23357 UniGene:At.43053 ProteinModelPortal:Q9SI20 SMR:Q9SI20 IntAct:Q9SI20 STRING:Q9SI20 PRIDE:Q9SI20 EnsemblPlants:AT2G18110.1 GeneID:816323 KEGG:ath:AT2G18110 TAIR:At2g18110 InParanoid:Q9SI20 OMA:ARWYRHI PhylomeDB:Q9SI20 ArrayExpress:Q9SI20 Genevestigator:Q9SI20 GermOnline:AT2G18110 Uniprot:Q9SI20
Leaf	Isotig02724	23	5	2.731	9.89E-06	TAIR|locus:2053144 - symbol:AT2G18110 species:3702 "Arabidopsis thaliana" [GO:0003746 "translation elongation factor activity" evidence=IEA;ISS] [GO:0005853 "eukaryotic translation elongation factor 1 complex" evidence=ISS] [GO:0006414 "translational elongation" evidence=IEA;ISS] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001326 InterPro:IPR014038 Pfam:PF00736 PROSITE:PS00824 PROSITE:PS00825 SMART:SM00888 GO:GO:0005829 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0003746 InterPro:IPR010987 Gene3D:G3DSA:1.20.1050.10 PROSITE:PS50405 EMBL:AC006201 GO:GO:0005853 eggNOG:COG2092

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						HOGENOM:HBG714747 KO:K03232 ProtClustDB:CLSN2683026 InterPro:IPR014717 Gene3D:G3DSA:3.30.70.60 SUPFAM:SSF54984 EMBL:AC007212 EMBL:AY065159 EMBL:AY081568 EMBL:AY087429 IPI:IPI00548124 PIR:D84560 RefSeq:NP_179402.1 UniGene:At.23357 UniGene:At.43053 ProteinModelPortal:Q9SI20 SMR:Q9SI20 IntAct:Q9SI20 STRING:Q9SI20 PRIDE:Q9SI20 EnsemblPlants:AT2G18110.1 GeneID:816323 KEGG:ath:AT2G18110 TAIR:At2g18110 InParanoid:Q9SI20 OMA:ARWYRHI PhylomeDB:Q9SI20 ArrayExpress:Q9SI20 Genevestigator:Q9SI20 GermOnline:AT2G18110 Uniprot:Q9SI20
Leaf	Isotig02858	80	8	3.851	1.04E-21	UNIPROTKB|Q709C8 - symbol:VPS13C "Vacuolar protein sorting-associated protein 13C" species:9606 "Homo sapiens" [GO:0008104 "protein localization" evidence=IEA] InterPro:IPR009543 Pfam:PF06650 GO:GO:0008104 InterPro:IPR015412 Pfam:PF09333 eggNOG:COG5043 GeneTree:ENSGT00410000025397 HOVERGEN:HBG079736 EMBL:AJ608770 EMBL:AJ608771 EMBL:AJ626860 EMBL:AJ626861 EMBL:AB037842 EMBL:AK000143 EMBL:BC069387 IPI:IPI00412216 IPI:IPI00465428 IPI:IPI00604778 IPI:IPI00797358 RefSeq:NP_001018098.1 RefSeq:NP_060154.3 RefSeq:NP_060550.2 RefSeq:NP_065872.1 UniGene:Hs.511668 ProteinModelPortal:Q709C8 IntAct:Q709C8 STRING:Q709C8 PhosphoSite:Q709C8 DMDM:74712594 PRIDE:Q709C8 Ensembl:ENST00000261517 GeneID:54832 KEGG:hsa:54832 UCSC:uc002agz.1 UCSC:uc002aha.1 UCSC:uc002ahb.1 UCSC:uc002ahc.1 CTD:54832 GeneCards:GC15M062144 H-InvDB:HIX0020938 HGNC:HGNC:23594 HPA:HPA043356 HPA:HPA043507 MIM:608879 neXtProt:NX_Q709C8 PharmGKB:PA134990089 InParanoid:Q709C8 OMA:QPCSLFM PhylomeDB:Q709C8 NextBio:57616 ArrayExpress:Q709C8 Bgee:Q709C8 CleanEx:HS_VPS13C Genevestigator:Q709C8 GermOnline:ENSG00000129003 Uniprot:Q709C8
Leaf	Isotig02859	80	8	3.851	1.04E-21	UNIPROTKB|Q709C8 - symbol:VPS13C "Vacuolar protein sorting-associated protein 13C" species:9606 "Homo sapiens" [GO:0008104 "protein localization" evidence=IEA] InterPro:IPR009543 Pfam:PF06650 GO:GO:0008104 InterPro:IPR015412 Pfam:PF09333 eggNOG:COG5043 GeneTree:ENSGT00410000025397 HOVERGEN:HBG079736 EMBL:AJ608770 EMBL:AJ608771 EMBL:AJ626860 EMBL:AJ626861 EMBL:AB037842 EMBL:AK000143 EMBL:BC069387 IPI:IPI00412216 IPI:IPI00465428 IPI:IPI00604778 IPI:IPI00797358 RefSeq:NP_001018098.1 RefSeq:NP_060154.3 RefSeq:NP_060550.2 RefSeq:NP_065872.1 UniGene:Hs.511668 ProteinModelPortal:Q709C8 IntAct:Q709C8 STRING:Q709C8 PhosphoSite:Q709C8 DMDM:74712594 PRIDE:Q709C8 Ensembl:ENST00000261517 GeneID:54832 KEGG:hsa:54832 UCSC:uc002agz.1 UCSC:uc002aha.1 UCSC:uc002ahb.1 UCSC:uc002ahc.1 CTD:54832 GeneCards:GC15M062144 H-InvDB:HIX0020938 HGNC:HGNC:23594 HPA:HPA043356 HPA:HPA043507 MIM:608879 neXtProt:NX_Q709C8 PharmGKB:PA134990089 InParanoid:Q709C8 OMA:QPCSLFM PhylomeDB:Q709C8 NextBio:57616 ArrayExpress:Q709C8 Bgee:Q709C8 CleanEx:HS_VPS13C Genevestigator:Q709C8 GermOnline:ENSG00000129003 Uniprot:Q709C8
Leaf	Isotig02872	1751	1830	0.465	1.70E-22	TAIR|locus:2825935 - symbol:AT1G28135 "AT1G28135" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002684 GenomeReviews:CT485782_GR EMBL:BT010779 EMBL:BT014675 IPI:IPI00538576 RefSeq:NP_174135.1 UniGene:At.48243 IntAct:Q6IDD0 PRIDE:Q6IDD0 EnsemblPlants:AT1G28135.1 GeneID:839707 KEGG:ath:AT1G28135 TAIR:At1g28135 Genevestigator:Q6IDD0 Uniprot:Q6IDD0
Leaf	Isotig02873	1751	1830	0.465	1.70E-22	TAIR|locus:2825935 - symbol:AT1G28135 "AT1G28135" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002684 GenomeReviews:CT485782_GR EMBL:BT010779 EMBL:BT014675 IPI:IPI00538576 RefSeq:NP_174135.1 UniGene:At.48243 IntAct:Q6IDD0 PRIDE:Q6IDD0 EnsemblPlants:AT1G28135.1 GeneID:839707 KEGG:ath:AT1G28135 TAIR:At1g28135 Genevestigator:Q6IDD0 Uniprot:Q6IDD0
Leaf	Isotig02874	45	5	3.699	1.44E-12	TAIR|locus:2016289 - symbol:SUS2 "ABNORMAL SUSPENSOR 2" species:3702 "Arabidopsis thaliana" [GO:0000398 "nuclear mRNA splicing, via spliceosome" evidence=IEA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] InterPro:IPR000555 InterPro:IPR012591 InterPro:IPR012592 Pfam:PF01398 Pfam:PF08082 Pfam:PF08083 ProDom:PD149576 SMART:SM00232 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009507 GO:GO:0016020 EMBL:AC009322 GO:GO:0005681 GO:GO:0000398 eggNOG:COG5178 HOGENOM:HBG398200 KO:K12856 InterPro:IPR012984 InterPro:IPR021983 InterPro:IPR019581 InterPro:IPR019580 InterPro:IPR019582 Pfam:PF08084 Pfam:PF12134 Pfam:PF10598 Pfam:PF10597 Pfam:PF10596 IPI:IPI00532725 PIR:B96832 RefSeq:NP_178124.2 UniGene:At.24959 ProteinModelPortal:Q9SSD2 SMR:Q9SSD2 IntAct:Q9SSD2

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						STRING:Q9SSD2 PRIDE:Q9SSD2 EnsemblPlants:AT1G80070.1 GeneID:844347 KEGG:ath:AT1G80070 TAIR:At1g80070 InParanoid:Q9SSD2 PhylomeDB:Q9SSD2 Genevestigator:Q9SSD2 Uniprot:Q9SSD2
Leaf	Isotig02875	21	3	3.336	3.39E-06	TAIR|locus:2016289 - symbol:SUS2 "ABNORMAL SUSPENSOR 2" species:3702 "Arabidopsis thaliana" [GO:0000398 "nuclear mRNA splicing, via spliceosome" evidence=IEA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] InterPro:IPR000555 InterPro:IPR012591 InterPro:IPR012592 Pfam:PF01398 Pfam:PF08082 Pfam:PF08083 ProDom:PD149576 SMART:SM00232 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009507 GO:GO:0016020 EMBL:AC009322 GO:GO:0005681 GO:GO:0000398 eggNOG:COG5178 HOGENOM:HBG398200 KO:K12856 InterPro:IPR012984 InterPro:IPR021983 InterPro:IPR019581 InterPro:IPR019580 InterPro:IPR019582 Pfam:PF08084 Pfam:PF12134 Pfam:PF10598 Pfam:PF10597 Pfam:PF10596 IPI:IPI00532725 PIR:B96832 RefSeq:NP_178124.2 UniGene:At.24959 ProteinModelPortal:Q9SSD2 SMR:Q9SSD2 IntAct:Q9SSD2 STRING:Q9SSD2 PRIDE:Q9SSD2 EnsemblPlants:AT1G80070.1 GeneID:844347 KEGG:ath:AT1G80070 TAIR:At1g80070 InParanoid:Q9SSD2 PhylomeDB:Q9SSD2 Genevestigator:Q9SSD2 Uniprot:Q9SSD2
Leaf	Isotig02886	228	149	1.143	1.72E-14	TAIR|locus:2157383 - symbol:CLPC1 "AT5G50920" species:3702 "Arabidopsis thaliana" [GO:0005524 "ATP binding" evidence=ISS] [GO:0016887 "ATPase activity" evidence=ISS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009532 "plastid stroma" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009658 "chloroplast organization" evidence=IMP] [GO:0031897 "Tic complex" evidence=TAS] [GO:0045037 "protein import into chloroplast stroma" evidence=IMP] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0010380 "regulation of chlorophyll biosynthetic process" evidence=IMP] [GO:0045036 "protein targeting to chloroplast" evidence=IMP] [GO:0005829 "cytosol" evidence=RCA] [GO:0004176 "ATP-dependent peptidase activity" evidence=IDA] InterPro:IPR001270 InterPro:IPR001943 InterPro:IPR003593 InterPro:IPR003959 InterPro:IPR004176 InterPro:IPR013093 InterPro:IPR018368 Pfam:PF00004 Pfam:PF02151 Pfam:PF02861 Pfam:PF07724 PRINTS:PR00300 PROSITE:PS00870 PROSITE:PS00871 PROSITE:PS50151 SMART:SM00382 GO:GO:0005739 GO:GO:0005524 GO:GO:0009570 EMBL:CP002688 GO:GO:0005618 GO:GO:0003677 GO:GO:0009658 GO:GO:0010380 GO:GO:0009535 GO:GO:0004518 GO:GO:0006289 EMBL:AB017063 eggNOG:COG0542 GO:GO:0019538 InterPro:IPR023150 Gene3D:G3DSA:1.10.1780.10 GO:GO:0004176 InterPro:IPR019489 Pfam:PF10431 SMART:SM01086 HSSP:P03815 EMBL:AF022909 EMBL:AY102125 EMBL:AK227173 IPI:IPI00535976 PIR:T52292 RefSeq:NP_568746.1 UniGene:At.24774 UniGene:At.74761 UniGene:At.74764 UniGene:At.75059 ProteinModelPortal:Q9FI56 SMR:Q9FI56 IntAct:Q9FI56 STRING:Q9FI56 PRIDE:O48931 EnsemblPlants:AT5G50920.1 GeneID:835165 KEGG:ath:AT5G50920 GeneFarm:797 TAIR:At5g50920 InParanoid:Q9FI56 KO:K03696 OMA:FHQLTRD PhylomeDB:Q9FI56 ProtClustDB:CLSN2689981 Genevestigator:Q9FI56 GO:GO:0031897 GO:GO:0045037 Uniprot:Q9FI56
Leaf	Isotig02887	213	145	1.084	1.22E-12	TAIR|locus:2157383 - symbol:CLPC1 "AT5G50920" species:3702 "Arabidopsis thaliana" [GO:0005524 "ATP binding" evidence=ISS] [GO:0016887 "ATPase activity" evidence=ISS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009532 "plastid stroma" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009658 "chloroplast organization" evidence=IMP] [GO:0031897 "Tic complex" evidence=TAS] [GO:0045037 "protein import into chloroplast stroma" evidence=IMP] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0010380 "regulation of chlorophyll biosynthetic process" evidence=IMP] [GO:0045036 "protein targeting to chloroplast" evidence=IMP] [GO:0005829 "cytosol" evidence=RCA] [GO:0004176 "ATP-dependent peptidase activity" evidence=IDA] InterPro:IPR001270 InterPro:IPR001943 InterPro:IPR003593 InterPro:IPR003959 InterPro:IPR004176 InterPro:IPR013093 InterPro:IPR018368 Pfam:PF00004 Pfam:PF02151 Pfam:PF02861 Pfam:PF07724 PRINTS:PR00300 PROSITE:PS00870 PROSITE:PS00871 PROSITE:PS50151 SMART:SM00382 GO:GO:0005739 GO:GO:0005524 GO:GO:0009570 EMBL:CP002688 GO:GO:0005618 GO:GO:0003677 GO:GO:0009658 GO:GO:0010380 GO:GO:0009535 GO:GO:0004518 GO:GO:0006289 EMBL:AB017063 eggNOG:COG0542 GO:GO:0019538 InterPro:IPR023150 Gene3D:G3DSA:1.10.1780.10 GO:GO:0004176 InterPro:IPR019489 Pfam:PF10431 SMART:SM01086 HSSP:P03815 EMBL:AF022909 EMBL:AY102125 EMBL:AK227173 IPI:IPI00535976 PIR:T52292 RefSeq:NP_568746.1 UniGene:At.24774 UniGene:At.74761 UniGene:At.74764 UniGene:At.75059 ProteinModelPortal:Q9FI56 SMR:Q9FI56 IntAct:Q9FI56 STRING:Q9FI56 PRIDE:O48931 EnsemblPlants:AT5G50920.1 GeneID:835165 KEGG:ath:AT5G50920

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GeneFarm:797 TAIR:At5g50920 InParanoid:Q9FI56 KO:K03696 OMA:FHQLTRD PhylomeDB:Q9FI56 ProtClustDB:CLSN2689981 Genevestigator:Q9FI56 GO:GO:0031897 GO:GO:0045037 Uniprot:Q9FI56
Leaf	Isotig02894	55	30	1.403	9.82E-06	TAIR|locus:2199685 - symbol:GI "AT1G22770" species:3702 "Arabidopsis thaliana" [GO:0009908 "flower development" evidence=TAS] [GO:0005654 "nucleoplasm" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0005634 "nucleus" evidence=IDA] [GO:0042752 "regulation of circadian rhythm" evidence=IMP] [GO:0048578 "positive regulation of long-day photoperiodism, flowering" evidence=IMP] [GO:0009409 "response to cold" evidence=IMP] [GO:0010378 "temperature compensation of the circadian clock" evidence=IMP] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IDA] [GO:0007623 "circadian rhythm" evidence=IDA] [GO:0009637 "response to blue light" evidence=IDA] [GO:0010218 "response to far red light" evidence=IMP] [GO:0080167 "response to karrikin" evidence=IEP] [GO:0042542 "response to hydrogen peroxide" evidence=IMP] EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005654 GO:GO:0005515 GO:GO:0030154 GO:GO:0006355 GO:GO:0007623 GO:GO:0009409 GO:GO:0080167 GO:GO:0009637 GO:GO:0010218 GO:GO:0042542 GO:GO:0009908 GO:GO:0009585 GO:GO:0048578 EMBL:AC003979 GO:GO:0010378 EMBL:AJ133786 EMBL:AF105064 EMBL:AF076686 EMBL:Y12227 IPI:IPI00531066 PIR:T52575 RefSeq:NP_564180.1 UniGene:At.209 IntAct:Q9SQI2 STRING:Q9SQI2 PRIDE:Q9SQI2 EnsemblPlants:AT1G22770.1 GeneID:838883 KEGG:ath:AT1G22770 TAIR:At1g22770 eggNOG:NOG245462 HOGENOM:HBG592018 InParanoid:Q9SQI2 KO:K12124 OMA:LVCPSSE PhylomeDB:Q9SQI2 ProtClustDB:CLSN2687916 ArrayExpress:Q9SQI2 Genevestigator:Q9SQI2 GermOnline:AT1G22770 Uniprot:Q9SQI2
Leaf	Isotig02900	61	7	3.652	2.29E-16	TAIR|locus:2103488 - symbol:SIP2 "AT3G57520" species:3702 "Arabidopsis thaliana" [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=ISS] [GO:0006979 "response to oxidative stress" evidence=IEP] [GO:0080167 "response to karrikin" evidence=IEP] [GO:0034484 "raffinose catabolic process" evidence=IDA] [GO:0047274 "galactinol-sucrose galactosyltransferase activity" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR013785 GO:GO:0009506 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0006979 Gene3D:G3DSA:3.20.20.70 InterPro:IPR017853 SUPFAM:SSF51445 GO:GO:0080167 EMBL:AL133248 CAZy:GH36 eggNOG:NOG06986 InterPro:IPR008811 Pfam:PF05691 GO:GO:0034484 HOGENOM:HBG611539 KO:K06617 GO:GO:0047274 EMBL:AY050772 EMBL:AK226370 IPI:IPI00526258 IPI:IPI00541537 IPI:IPI00544535 PIR:T46188 RefSeq:NP_191311.1 RefSeq:NP_850715.1 UniGene:At.22207 UniGene:At.30900 ProteinModelPortal:Q94A08 STRING:Q94A08 PRIDE:Q94A08 EnsemblPlants:AT3G57520.1 GeneID:824919 KEGG:ath:AT3G57520 TAIR:At3g57520 InParanoid:Q9SCM1 OMA:QFMLLES PhylomeDB:Q94A08 ProtClustDB:PLN02219 BioCyc:MetaCyc:AT3G57520-MONOMER ArrayExpress:Q94A08 Uniprot:Q94A08
Leaf	Isotig02901	60	7	3.628	4.71E-16	TAIR|locus:2103488 - symbol:SIP2 "AT3G57520" species:3702 "Arabidopsis thaliana" [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=ISS] [GO:0006979 "response to oxidative stress" evidence=IEP] [GO:0080167 "response to karrikin" evidence=IEP] [GO:0034484 "raffinose catabolic process" evidence=IDA] [GO:0047274 "galactinol-sucrose galactosyltransferase activity" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR013785 GO:GO:0009506 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0006979 Gene3D:G3DSA:3.20.20.70 InterPro:IPR017853 SUPFAM:SSF51445 GO:GO:0080167 EMBL:AL133248 CAZy:GH36 eggNOG:NOG06986 InterPro:IPR008811 Pfam:PF05691 GO:GO:0034484 HOGENOM:HBG611539 KO:K06617 GO:GO:0047274 EMBL:AY050772 EMBL:AK226370 IPI:IPI00526258 IPI:IPI00541537 IPI:IPI00544535 PIR:T46188 RefSeq:NP_191311.1 RefSeq:NP_850715.1 UniGene:At.22207 UniGene:At.30900 ProteinModelPortal:Q94A08 STRING:Q94A08 PRIDE:Q94A08 EnsemblPlants:AT3G57520.1 GeneID:824919 KEGG:ath:AT3G57520 TAIR:At3g57520 InParanoid:Q9SCM1 OMA:QFMLLES PhylomeDB:Q94A08 ProtClustDB:PLN02219 BioCyc:MetaCyc:AT3G57520-MONOMER ArrayExpress:Q94A08 Uniprot:Q94A08
Leaf	Isotig02912	34	166	-1.759	4.90E-14	UNIPROTKB|Q43848 - symbol:Q43848 "Transketolase, chloroplastic" species:4113 "Solanum tuberosum" [GO:0004802 "transketolase activity" evidence=ISS] [GO:0009535 "chloroplast thylakoid membrane" evidence=ISS] InterPro:IPR005476 InterPro:IPR005478 InterPro:IPR009014 InterPro:IPR015941 Pfam:PF02780 InterPro:IPR005475 Pfam:PF00456 Pfam:PF02779 InterPro:IPR005474 GO:GO:0046872 GO:GO:0009535 SMART:SM00861 InterPro:IPR020826 Gene3D:G3DSA:3.40.50.920 SUPFAM:SSF52922 PROSITE:PS00801 PROSITE:PS00802 GO:GO:0004802 TIGRFAMs:TIGR00232 EMBL:Z50099 PIR:S58083 ProteinModelPortal:Q43848 SMR:Q43848 PRIDE:Q43848 Uniprot:Q43848

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig02913	38	135	-1.300	5.39E-08	UNIPROTKB|Q43848 - symbol:Q43848 "Transketolase, chloroplastic" species:4113 "Solanum tuberosum" [GO:0004802 "transketolase activity" evidence=ISS] [GO:0009535 "chloroplast thylakoid membrane" evidence=ISS] InterPro:IPR005476 InterPro:IPR005478 InterPro:IPR009014 InterPro:IPR015941 Pfam:PF02780 InterPro:IPR005475 Pfam:PF00456 Pfam:PF02779 InterPro:IPR005474 GO:GO:0046872 GO:GO:0009535 SMART:SM00861 InterPro:IPR020826 Gene3D:G3DSA:3.40.50.920 SUPFAM:SSF52922 PROSITE:PS00801 PROSITE:PS00802 GO:GO:0004802 TIGRFAMs:TIGR00232 EMBL:Z50099 PIR:S58083 ProteinModelPortal:Q43848 SMR:Q43848 PRIDE:Q43848 Uniprot:Q43848
Leaf	Isotig02920	104	1	7.229	3.70E-30	TAIR|locus:2063907 - symbol:P5CS1 "AT2G39800" species:3702 "Arabidopsis thaliana" [GO:0006561 "proline biosynthetic process" evidence=IMP;TAS] [GO:0009414 "response to water deprivation" evidence=IGI;IEP] [GO:0017084 "delta1-pyrroline-5-carboxylate synthetase activity" evidence=ISS] [GO:0016020 "membrane" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0006979 "response to oxidative stress" evidence=IMP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0042538 "hyperosmotic salinity response" evidence=IEP;IMP] [GO:0048364 "root development" evidence=IMP] [GO:0009269 "response to desiccation" evidence=IEP] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] InterPro:IPR000965 InterPro:IPR001048 InterPro:IPR001057 InterPro:IPR005715 InterPro:IPR005766 InterPro:IPR015590 InterPro:IPR016161 InterPro:IPR016162 InterPro:IPR016163 InterPro:IPR019797 InterPro:IPR020593 Pfam:PF00171 Pfam:PF00696 PIRSF:PIRSF036429 PRINTS:PR00474 PROSITE:PS00902 PROSITE:PS01223 GO:GO:0005524 GO:GO:0009507 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0006979 GO:GO:0016020 Gene3D:G3DSA:3.40.309.10 Gene3D:G3DSA:3.40.605.10 SUPFAM:SSF53720 GO:GO:0009414 GO:GO:0048364 GO:GO:0006561 Gene3D:G3DSA:3.40.1160.10 SUPFAM:SSF53633 GO:GO:0042538 GO:GO:0004349 EMBL:AC003000 EMBL:X89414 EMBL:X86777 EMBL:X87330 EMBL:D32138 EMBL:AF424633 EMBL:AY113046 EMBL:AY150430 IPI:IPI00529620 PIR:S66637 PIR:T50685 RefSeq:NP_001189714.1 RefSeq:NP_181510.1 UniGene:At.20482 ProteinModelPortal:P54887 SMR:P54887 IntAct:P54887 STRING:P54887 PRIDE:P54887 EnsemblPlants:AT2G39800.1 EnsemblPlants:AT2G39800.4 GeneID:818566 KEGG:ath:AT2G39800 TAIR:At2g39800 eggNOG:COG0014 HOGENOM:HBG318080 InParanoid:P54887 KO:K12657 OMA:FEARPDC PhylomeDB:P54887 ProtClustDB:PLN02418 Genevestigator:P54887 GermOnline:AT2G39800 GO:GO:0004350 TIGRFAMs:TIGR01092 TIGRFAMs:TIGR00407 TIGRFAMs:TIGR01027 Uniprot:P54887
Leaf	Isotig02921	102	1	7.201	1.15E-29	TAIR|locus:2063907 - symbol:P5CS1 "AT2G39800" species:3702 "Arabidopsis thaliana" [GO:0006561 "proline biosynthetic process" evidence=IMP;TAS] [GO:0009414 "response to water deprivation" evidence=IGI;IEP] [GO:0017084 "delta1-pyrroline-5-carboxylate synthetase activity" evidence=ISS] [GO:0016020 "membrane" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0006979 "response to oxidative stress" evidence=IMP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0042538 "hyperosmotic salinity response" evidence=IEP;IMP] [GO:0048364 "root development" evidence=IMP] [GO:0009269 "response to desiccation" evidence=IEP] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] InterPro:IPR000965 InterPro:IPR001048 InterPro:IPR001057 InterPro:IPR005715 InterPro:IPR005766 InterPro:IPR015590 InterPro:IPR016161 InterPro:IPR016162 InterPro:IPR016163 InterPro:IPR019797 InterPro:IPR020593 Pfam:PF00171 Pfam:PF00696 PIRSF:PIRSF036429 PRINTS:PR00474 PROSITE:PS00902 PROSITE:PS01223 GO:GO:0005524 GO:GO:0009507 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0006979 GO:GO:0016020 Gene3D:G3DSA:3.40.309.10 Gene3D:G3DSA:3.40.605.10 SUPFAM:SSF53720 GO:GO:0009414 GO:GO:0048364 GO:GO:0006561 Gene3D:G3DSA:3.40.1160.10 SUPFAM:SSF53633 GO:GO:0042538 GO:GO:0004349 EMBL:AC003000 EMBL:X89414 EMBL:X86777 EMBL:X87330 EMBL:D32138 EMBL:AF424633 EMBL:AY113046 EMBL:AY150430 IPI:IPI00529620 PIR:S66637 PIR:T50685 RefSeq:NP_001189714.1 RefSeq:NP_181510.1 UniGene:At.20482 ProteinModelPortal:P54887 SMR:P54887 IntAct:P54887 STRING:P54887 PRIDE:P54887 EnsemblPlants:AT2G39800.1 EnsemblPlants:AT2G39800.4 GeneID:818566 KEGG:ath:AT2G39800 TAIR:At2g39800 eggNOG:COG0014 HOGENOM:HBG318080 InParanoid:P54887 KO:K12657 OMA:FEARPDC PhylomeDB:P54887 ProtClustDB:PLN02418 Genevestigator:P54887 GermOnline:AT2G39800 GO:GO:0004350 TIGRFAMs:TIGR01092 TIGRFAMs:TIGR00407 TIGRFAMs:TIGR01027 Uniprot:P54887
Leaf	Isotig02924	17	1	4.616	3.60E-06	TAIR|locus:2155441 - symbol:EXO84B "exocyst complex component 84B" species:3702 "Arabidopsis thaliana" [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] GO:GO:0005829 GO:GO:0005886 EMBL:CP002688 GenomeReviews:BA000015_GR InterPro:IPR016159 SUPFAM:SSF74788

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						InterPro:IPR014812 Pfam:PF08700 eggNOG:NOG331886 EMBL:AB025612 EMBL:AY075643 EMBL:AY093996 IPI:IPI00533377 RefSeq:NP_199794.1 UniGene:At.29766 ProteinModelPortal:Q9LTB0 PRIDE:Q9LTB0 EnsemblPlants:AT5G49830.1 GeneID:835046 KEGG:ath:AT5G49830 TAIR:At5g49830 HOGENOM:HBG319671 InParanoid:Q9LTB0 OMA:NMQSLRP PhylomeDB:Q9LTB0 ProtClustDB:CLSN2686998 Genevestigator:Q9LTB0 Uniprot:Q9LTB0
Leaf	Isotig02925	14	3	2.751	0.000536578	TAIR|locus:2155441 - symbol:EXO84B "exocyst complex component 84B" species:3702 "Arabidopsis thaliana" [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] GO:GO:0005829 GO:GO:0005886 EMBL:CP002688 GenomeReviews:BA000015_GR InterPro:IPR016159 SUPFAM:SSF74788 InterPro:IPR014812 Pfam:PF08700 eggNOG:NOG331886 EMBL:AB025612 EMBL:AY075643 EMBL:AY093996 IPI:IPI00533377 RefSeq:NP_199794.1 UniGene:At.29766 ProteinModelPortal:Q9LTB0 PRIDE:Q9LTB0 EnsemblPlants:AT5G49830.1 GeneID:835046 KEGG:ath:AT5G49830 TAIR:At5g49830 HOGENOM:HBG319671 InParanoid:Q9LTB0 OMA:NMQSLRP PhylomeDB:Q9LTB0 ProtClustDB:CLSN2686998 Genevestigator:Q9LTB0 Uniprot:Q9LTB0
Leaf	Isotig02932	30	14	1.628	0.000268665	TAIR|locus:2163583 - symbol:AT5G45430 species:3702 "Arabidopsis thaliana" [GO:0004672 "protein kinase activity" evidence=IEA] [GO:0004674 "protein serine/threonine kinase activity" evidence=IEA] [GO:0005524 "ATP binding" evidence=IEA] [GO:0006468 "protein phosphorylation" evidence=IEA] [GO:0016301 "kinase activity" evidence=ISS] InterPro:IPR000719 InterPro:IPR002290 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 Pfam:PF00069 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 SMART:SM00220 GO:GO:0005524 EMBL:CP002688 eggNOG:COG0515 SUPFAM:SSF56112 GO:GO:0004674 HOGENOM:HBG755340 HSSP:P24941 UniGene:At.21708 EMBL:BT001210 IPI:IPI00520161 RefSeq:NP_568646.1 UniGene:At.24818 UniGene:At.72524 ProteinModelPortal:Q8H0X4 SMR:Q8H0X4 PRIDE:Q8H0X4 EnsemblPlants:AT5G45430.1 GeneID:834579 KEGG:ath:AT5G45430 TAIR:At5g45430 InParanoid:Q8H0X4 OMA:PKTNAPF PhylomeDB:Q8H0X4 ArrayExpress:Q8H0X4 Genevestigator:Q8H0X4 Uniprot:Q8H0X4
Leaf	Isotig02933	30	15	1.529	0.000500313	TAIR|locus:2163583 - symbol:AT5G45430 species:3702 "Arabidopsis thaliana" [GO:0004672 "protein kinase activity" evidence=IEA] [GO:0004674 "protein serine/threonine kinase activity" evidence=IEA] [GO:0005524 "ATP binding" evidence=IEA] [GO:0006468 "protein phosphorylation" evidence=IEA] [GO:0016301 "kinase activity" evidence=ISS] InterPro:IPR000719 InterPro:IPR002290 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 Pfam:PF00069 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 SMART:SM00220 GO:GO:0005524 EMBL:CP002688 eggNOG:COG0515 SUPFAM:SSF56112 GO:GO:0004674 HOGENOM:HBG755340 HSSP:P24941 UniGene:At.21708 EMBL:BT001210 IPI:IPI00520161 RefSeq:NP_568646.1 UniGene:At.24818 UniGene:At.72524 ProteinModelPortal:Q8H0X4 SMR:Q8H0X4 PRIDE:Q8H0X4 EnsemblPlants:AT5G45430.1 GeneID:834579 KEGG:ath:AT5G45430 TAIR:At5g45430 InParanoid:Q8H0X4 OMA:PKTNAPF PhylomeDB:Q8H0X4 ArrayExpress:Q8H0X4 Genevestigator:Q8H0X4 Uniprot:Q8H0X4
Leaf	Isotig02970	2	31	-3.425	2.03E-06	TAIR|locus:2091448 - symbol:AT3G27540 species:3702 "Arabidopsis thaliana" [GO:0006487 "protein N-linked glycosylation" evidence=IEA] [GO:0008375 "acetylglucosaminyltransferase activity" evidence=ISS] [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] InterPro:IPR006813 Pfam:PF04724 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0016020 GO:GO:0006487 EMBL:AB025626 CAZy:GT17 eggNOG:NOG85038 KO:K00737 GO:GO:0003830 PANTHER:PTHR12224 HOGENOM:HBG317367 ProtClustDB:CLSN2682029 EMBL:AY099829 EMBL:BT000311 IPI:IPI00522126 RefSeq:NP_189391.1 UniGene:At.37037 IntAct:Q9LT58 PRIDE:Q9LT58 EnsemblPlants:AT3G27540.1 GeneID:822376 KEGG:ath:AT3G27540 TAIR:At3g27540 InParanoid:Q9LT58 OMA:HYYNENV PhylomeDB:Q9LT58 ArrayExpress:Q9LT58 Genevestigator:Q9LT58 Uniprot:Q9LT58
Leaf	Isotig02971	2	31	-3.425	2.03E-06	TAIR|locus:2091448 - symbol:AT3G27540 species:3702 "Arabidopsis thaliana" [GO:0006487 "protein N-linked glycosylation" evidence=IEA] [GO:0008375 "acetylglucosaminyltransferase activity" evidence=ISS] [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] InterPro:IPR006813 Pfam:PF04724 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0016020 GO:GO:0006487 EMBL:AB025626 CAZy:GT17 eggNOG:NOG85038 KO:K00737 GO:GO:0003830 PANTHER:PTHR12224 HOGENOM:HBG317367 ProtClustDB:CLSN2682029 EMBL:AY099829 EMBL:BT000311 IPI:IPI00522126 RefSeq:NP_189391.1 UniGene:At.37037 IntAct:Q9LT58 PRIDE:Q9LT58 EnsemblPlants:AT3G27540.1 GeneID:822376

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						KEGG:ath:AT3G27540 TAIR:At3g27540 InParanoid:Q9LT58 OMA:HYYNENV PhylomeDB:Q9LT58 ArrayExpress:Q9LT58 Genevestigator:Q9LT58 Uniprot:Q9LT58
Leaf	Isotig02992	42	3	4.336	6.94E-13	TAIR|locus:2076086 - symbol:BAM1 "AT3G23920" species:3702 "Arabidopsis thaliana" [GO:0016161 "beta-amylase activity" evidence=ISS;IDA] [GO:0005983 "starch catabolic process" evidence=IMP] [GO:0005634 "nucleus" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009414 "response to water deprivation" evidence=IEP] BRENDA:3.2.1.2 InterPro:IPR001371 InterPro:IPR001554 InterPro:IPR013781 InterPro:IPR018238 Pfam:PF01373 PRINTS:PR00750 PRINTS:PR00842 PROSITE:PS00506 PROSITE:PS00679 GO:GO:0005829 GO:GO:0005634 GO:GO:0009507 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0043169 InterPro:IPR017853 Gene3D:G3DSA:3.20.20.80 SUPFAM:SSF51445 GO:GO:0009414 GO:GO:0005983 EMBL:AP001297 EMBL:AF367293 EMBL:AY074393 EMBL:AY078046 EMBL:AY096517 EMBL:AK226274 IPI:IPI00518242 RefSeq:NP_189034.1 UniGene:At.8278 HSSP:P16098 ProteinModelPortal:Q9LIR6 SMR:Q9LIR6 STRING:Q9LIR6 CAZy:GH14 PRIDE:Q9LIR6 EnsemblPlants:AT3G23920.1 GeneID:821975 KEGG:ath:AT3G23920 TAIR:At3g23920 eggNOG:NOG77898 InParanoid:Q9LIR6 KO:K01177 OMA:DKDQDLA PhylomeDB:Q9LIR6 ProtClustDB:PLN00197 ArrayExpress:Q9LIR6 Genevestigator:Q9LIR6 GO:GO:0016161 Uniprot:Q9LIR6
Leaf	Isotig02993	43	3	4.370	3.35E-13	TAIR|locus:2076086 - symbol:BAM1 "AT3G23920" species:3702 "Arabidopsis thaliana" [GO:0016161 "beta-amylase activity" evidence=ISS;IDA] [GO:0005983 "starch catabolic process" evidence=IMP] [GO:0005634 "nucleus" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009414 "response to water deprivation" evidence=IEP] BRENDA:3.2.1.2 InterPro:IPR001371 InterPro:IPR001554 InterPro:IPR013781 InterPro:IPR018238 Pfam:PF01373 PRINTS:PR00750 PRINTS:PR00842 PROSITE:PS00506 PROSITE:PS00679 GO:GO:0005829 GO:GO:0005634 GO:GO:0009507 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0043169 InterPro:IPR017853 Gene3D:G3DSA:3.20.20.80 SUPFAM:SSF51445 GO:GO:0009414 GO:GO:0005983 EMBL:AP001297 EMBL:AF367293 EMBL:AY074393 EMBL:AY078046 EMBL:AY096517 EMBL:AK226274 IPI:IPI00518242 RefSeq:NP_189034.1 UniGene:At.8278 HSSP:P16098 ProteinModelPortal:Q9LIR6 SMR:Q9LIR6 STRING:Q9LIR6 CAZy:GH14 PRIDE:Q9LIR6 EnsemblPlants:AT3G23920.1 GeneID:821975 KEGG:ath:AT3G23920 TAIR:At3g23920 eggNOG:NOG77898 InParanoid:Q9LIR6 KO:K01177 OMA:DKDQDLA PhylomeDB:Q9LIR6 ProtClustDB:PLN00197 ArrayExpress:Q9LIR6 Genevestigator:Q9LIR6 GO:GO:0016161 Uniprot:Q9LIR6
Leaf	Isotig03010	22	5	2.666	1.97E-05	No hit
Leaf	Isotig03011	22	5	2.666	1.97E-05	No hit
Leaf	Isotig03016	39	0	6.814	1.47E-12	TAIR|locus:2052045 - symbol:NADP-ME1 "AT2G19900" species:3702 "Arabidopsis thaliana" [GO:0004470 "malic enzyme activity" evidence=ISS] [GO:0006108 "malate metabolic process" evidence=ISS;IDA] [GO:0016652 "oxidoreductase activity, acting on NADH or NADPH, NAD or NADP as acceptor" evidence=ISS] [GO:0004473 "malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+) activity" evidence=IDA] [GO:0005829 "cytosol" evidence=NAS] [GO:0051260 "protein homooligomerization" evidence=IDA] InterPro:IPR001891 InterPro:IPR012301 InterPro:IPR012302 InterPro:IPR015884 InterPro:IPR016040 Pfam:PF00390 Pfam:PF03949 PIRSF:PIRSF000106 PRINTS:PR00072 PROSITE:PS00331 SMART:SM00919 GO:GO:0005829 EMBL:CP002685 GenomeReviews:CT485783_GR Gene3D:G3DSA:3.40.50.720 GO:GO:0051287 GO:GO:0046872 GO:GO:0051260 EMBL:AC005169 GO:GO:0006108 eggNOG:COG0281 HOGENOM:HBG289821 GO:GO:0016619 Gene3D:G3DSA:3.40.50.10380 KO:K00029 GO:GO:0004473 HSSP:P40927 OMA:PAFMTEE EMBL:AY062734 EMBL:BT003371 IPI:IPI00545617 PIR:E84582 RefSeq:NP_179580.1 UniGene:At.27251 ProteinModelPortal:O82191 SMR:O82191 IntAct:O82191 STRING:O82191 PRIDE:O82191 EnsemblPlants:AT2G19900.1 GeneID:816509 KEGG:ath:AT2G19900 TAIR:At2g19900 InParanoid:O82191 PhylomeDB:O82191 ProtClustDB:PLN03129 ArrayExpress:O82191 Genevestigator:O82191 Uniprot:O82191
Leaf	Isotig03017	39	0	6.814	1.47E-12	TAIR|locus:2052045 - symbol:NADP-ME1 "AT2G19900" species:3702 "Arabidopsis thaliana" [GO:0004470 "malic enzyme activity" evidence=ISS] [GO:0006108 "malate metabolic process" evidence=ISS;IDA] [GO:0016652 "oxidoreductase activity, acting on NADH or NADPH, NAD or NADP as acceptor" evidence=ISS] [GO:0004473 "malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+) activity" evidence=IDA] [GO:0005829 "cytosol" evidence=NAS] [GO:0051260 "protein homooligomerization" evidence=IDA] InterPro:IPR001891 InterPro:IPR012301 InterPro:IPR012302 InterPro:IPR015884 InterPro:IPR016040 Pfam:PF00390 Pfam:PF03949 PIRSF:PIRSF000106 PRINTS:PR00072 PROSITE:PS00331 SMART:SM00919 GO:GO:0005829 EMBL:CP002685 GenomeReviews:CT485783_GR Gene3D:G3DSA:3.40.50.720 GO:GO:0051287 GO:GO:0046872 GO:GO:0051260 EMBL:AC005169 GO:GO:0006108 eggNOG:COG0281 HOGENOM:HBG289821 GO:GO:0016619 Gene3D:G3DSA:3.40.50.10380 KO:K00029 GO:GO:0004473 HSSP:P40927 OMA:PAFMTEE EMBL:AY062734

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EMBL:BT003371 IPI:IPI00545617 PIR:E84582 RefSeq:NP_179580.1 UniGene:At.27251 ProteinModelPortal:O82191 SMR:O82191 IntAct:O82191 STRING:O82191 PRIDE:O82191 EnsemblPlants:AT2G19900.1 GeneID:816509 KEGG:ath:AT2G19900 TAIR:At2g19900 InParanoid:O82191 PhylomeDB:O82191 ProtClustDB:PLN03129 ArrayExpress:O82191 Genevestigator:O82191 Uniprot:O82191
Leaf	Isotig03018	21	7	2.114	0.000274738	TAIR|locus:2205185 - symbol:AT1G07990 "AT1G07990" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] InterPro:IPR011989 EMBL:CP002684 GO:GO:0005488 Gene3D:G3DSA:1.25.10.10 KO:K15501 InterPro:IPR007587 PANTHER:PTHR12634 Pfam:PF04499 EMBL:AY127028 EMBL:BT004535 IPI:IPI00523891 RefSeq:NP_172277.2 UniGene:At.27728 PRIDE:Q8L7T5 EnsemblPlants:AT1G07990.1 GeneID:837314 KEGG:ath:AT1G07990 TAIR:At1g07990 InParanoid:Q8L7T5 OMA:YIVEEPP PhylomeDB:Q8L7T5 ProtClustDB:CLSN2690775 Genevestigator:Q8L7T5 Uniprot:Q8L7T5
Leaf	Isotig03026	17	1	4.616	3.60E-06	TAIR|locus:2124266 - symbol:EDA9 "AT4G34200" species:3702 "Arabidopsis thaliana" [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009561 "megagametogenesis" evidence=IMP] [GO:0005524 "ATP binding" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] InterPro:IPR002912 InterPro:IPR006139 InterPro:IPR006140 InterPro:IPR006236 InterPro:IPR016040 Pfam:PF00389 Pfam:PF01842 Pfam:PF02826 PROSITE:PS00065 PROSITE:PS00670 PROSITE:PS00671 GO:GO:0005739 GO:GO:0005524 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0009570 GO:GO:0016020 Gene3D:G3DSA:3.40.50.720 GO:GO:0051287 GO:GO:0016597 EMBL:AL021961 EMBL:AL161585 GO:GO:0009561 eggNOG:COG0111 HOGENOM:HBG731446 GO:GO:0006564 KO:K00058 GO:GO:0004617 ProtClustDB:CLSN2685732 PANTHER:PTHR10996:SF20 TIGRFAMs:TIGR01327 OMA:TGVFDGY HSSP:P08328 EMBL:AY063810 EMBL:AY150462 IPI:IPI00530988 PIR:T05416 RefSeq:NP_195146.1 UniGene:At.21335 UniGene:At.74573 ProteinModelPortal:O49485 SMR:O49485 IntAct:O49485 STRING:O49485 PRIDE:O49485 ProMEX:O49485 EnsemblPlants:AT4G34200.1 GeneID:829568 KEGG:ath:AT4G34200 TAIR:At4g34200 InParanoid:O49485 PhylomeDB:O49485 Genevestigator:O49485 Uniprot:O49485
Leaf	Isotig03027	17	1	4.616	3.60E-06	TAIR|locus:2124266 - symbol:EDA9 "AT4G34200" species:3702 "Arabidopsis thaliana" [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009561 "megagametogenesis" evidence=IMP] [GO:0005524 "ATP binding" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] InterPro:IPR002912 InterPro:IPR006139 InterPro:IPR006140 InterPro:IPR006236 InterPro:IPR016040 Pfam:PF00389 Pfam:PF01842 Pfam:PF02826 PROSITE:PS00065 PROSITE:PS00670 PROSITE:PS00671 GO:GO:0005739 GO:GO:0005524 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0009570 GO:GO:0016020 Gene3D:G3DSA:3.40.50.720 GO:GO:0051287 GO:GO:0016597 EMBL:AL021961 EMBL:AL161585 GO:GO:0009561 eggNOG:COG0111 HOGENOM:HBG731446 GO:GO:0006564 KO:K00058 GO:GO:0004617 ProtClustDB:CLSN2685732 PANTHER:PTHR10996:SF20 TIGRFAMs:TIGR01327 OMA:TGVFDGY HSSP:P08328 EMBL:AY063810 EMBL:AY150462 IPI:IPI00530988 PIR:T05416 RefSeq:NP_195146.1 UniGene:At.21335 UniGene:At.74573 ProteinModelPortal:O49485 SMR:O49485 IntAct:O49485 STRING:O49485 PRIDE:O49485 ProMEX:O49485 EnsemblPlants:AT4G34200.1 GeneID:829568 KEGG:ath:AT4G34200 TAIR:At4g34200 InParanoid:O49485 PhylomeDB:O49485 Genevestigator:O49485 Uniprot:O49485
Leaf	Isotig03048	2	19	-2.719	0.000848343	No hit
Leaf	Isotig03050	31	17	1.396	0.000949097	TAIR|locus:2039064 - symbol:PI4K GAMMA 4 "AT2G46500" species:3702 "Arabidopsis thaliana" [GO:0004430 "1-phosphatidylinositol 4-kinase activity" evidence=IDA] [GO:0046854 "phosphatidylinositol phosphorylation" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR000403 InterPro:IPR000626 InterPro:IPR011009 Pfam:PF00240 Pfam:PF00454 SMART:SM00213 GO:GO:0005829 EMBL:CP002685 SUPFAM:SSF56112 EMBL:AC006526 EMBL:AC006418 InterPro:IPR019955 PROSITE:PS50053 HSSP:Q862M4 InterPro:IPR019956 PRINTS:PR00348 GO:GO:0004430 HOGENOM:HBG316610 ProtClustDB:CLSN2686321 EMBL:AF419566 EMBL:BT002694 IPI:IPI00543977 PIR:F84903 RefSeq:NP_566076.1 RefSeq:NP_973700.1 UniGene:At.27467 ProteinModelPortal:Q9ZPY9 SMR:Q9ZPY9 STRING:Q9ZPY9 EnsemblPlants:AT2G46500.1 EnsemblPlants:AT2G46500.2 GeneID:819260 KEGG:ath:AT2G46500 TAIR:At2g46500 InParanoid:Q9ZPY9 OMA:ENDGSCE PhylomeDB:Q9ZPY9 ArrayExpress:Q9ZPY9 Genevestigator:Q9ZPY9 Uniprot:Q9ZPY9
Leaf	Isotig03052	39	20	1.492	9.69E-05	TAIR|locus:2051789 - symbol:MTHFR2 "methylenetetrahydrofolate reductase 2" species:3702 "Arabidopsis thaliana" [GO:0004489 "methylenetetrahydrofolate reductase (NADPH) activity" evidence=IEA;ISS] [GO:0006555 "methionine metabolic process" evidence=IEA;ISS] [GO:0055114 "oxidation-reduction process" evidence=IEA]

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						[GO:0005829 "cytosol" evidence=IDA] InterPro:IPR003171 InterPro:IPR004621 Pfam:PF02219 GO:GO:0005829 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0006555 EMBL:AC004005 eggNOG:COG0685 HOGENOM:HBG649727 KO:K00297 GO:GO:0004489 UniGene:At.23509 ProtClustDB:PLN02540 TIGRFAMs:TIGR00677 EMBL:AJ245414 EMBL:AF181967 EMBL:AY050434 EMBL:AF370515 EMBL:AK220952 IPI:IPI00541304 PIR:T00696 RefSeq:NP_566011.1 UniGene:At.11693 ProteinModelPortal:O80585 SMR:O80585 IntAct:O80585 STRING:O80585 PRIDE:O80585 ProMEX:O80585 EnsemblPlants:AT2G44160.1 GeneID:819022 KEGG:ath:AT2G44160 GeneFarm:5158 TAIR:At2g44160 InParanoid:O80585 OMA:MIDESKI PhylomeDB:O80585 ArrayExpress:O80585 Genevestigator:O80585 GermOnline:AT2G44160 Uniprot:O80585
Leaf	Isotig03060	17	2	3.616	1.59E-05	TAIR|locus:2046079 - symbol:AT2G12400 "AT2G12400" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0009506 "plasmodesma" evidence=IDA] GO:GO:0009506 EMBL:CP002685 GenomeReviews:CT485783_GR eggNOG:NOG277729 HOGENOM:HBG319596 EMBL:BT002043 IPI:IPI00530884 RefSeq:NP_178935.2 UniGene:At.14383 PRIDE:Q8H0U2 EnsemblPlants:AT2G12400.1 GeneID:815712 KEGG:ath:AT2G12400 TAIR:At2g12400 InParanoid:Q8H0U2 OMA:MPLLCNP PhylomeDB:Q8H0U2 ProtClustDB:CLSN2690686 Genevestigator:Q8H0U2 Uniprot:Q8H0U2
Leaf	Isotig03061	17	2	3.616	1.59E-05	TAIR|locus:2046079 - symbol:AT2G12400 "AT2G12400" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0009506 "plasmodesma" evidence=IDA] GO:GO:0009506 EMBL:CP002685 GenomeReviews:CT485783_GR eggNOG:NOG277729 HOGENOM:HBG319596 EMBL:BT002043 IPI:IPI00530884 RefSeq:NP_178935.2 UniGene:At.14383 PRIDE:Q8H0U2 EnsemblPlants:AT2G12400.1 GeneID:815712 KEGG:ath:AT2G12400 TAIR:At2g12400 InParanoid:Q8H0U2 OMA:MPLLCNP PhylomeDB:Q8H0U2 ProtClustDB:CLSN2690686 Genevestigator:Q8H0U2 Uniprot:Q8H0U2
Leaf	Isotig03068	33	1	5.573	4.05E-11	TAIR|locus:2016407 - symbol:AT1G19450 "AT1G19450" species:3702 "Arabidopsis thaliana" [GO:0005351 "sugar:hydrogen symporter activity" evidence=ISS] [GO:0006810 "transport" evidence=IEA] [GO:0015144 "carbohydrate transmembrane transporter activity" evidence=ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0055085 "transmembrane transport" evidence=IEA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] InterPro:IPR003663 InterPro:IPR005828 InterPro:IPR005829 Pfam:PF00083 PRINTS:PR00171 PROSITE:PS00216 PROSITE:PS00217 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005774 eggNOG:COG0477 InterPro:IPR016196 SUPFAM:SSF103473 GO:GO:0008643 InterPro:IPR020846 PROSITE:PS50850 HOGENOM:HBG744444 GO:GO:0022891 TIGRFAMs:TIGR00879 EMBL:AC025808 EMBL:AY059848 EMBL:AY093274 IPI:IPI00534617 RefSeq:NP_173377.1 UniGene:At.22941 ProteinModelPortal:Q93YP9 IntAct:Q93YP9 PRIDE:Q93YP9 EnsemblPlants:AT1G19450.1 GeneID:838529 KEGG:ath:AT1G19450 TAIR:At1g19450 InParanoid:Q93YP9 OMA:SIGMTIS PhylomeDB:Q93YP9 ProtClustDB:CLSN2682491 ArrayExpress:Q93YP9 Genevestigator:Q93YP9 GermOnline:AT1G19450 Uniprot:Q93YP9
Leaf	Isotig03069	31	3	3.898	2.19E-09	TAIR|locus:2016407 - symbol:AT1G19450 "AT1G19450" species:3702 "Arabidopsis thaliana" [GO:0005351 "sugar:hydrogen symporter activity" evidence=ISS] [GO:0006810 "transport" evidence=IEA] [GO:0015144 "carbohydrate transmembrane transporter activity" evidence=ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0055085 "transmembrane transport" evidence=IEA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] InterPro:IPR003663 InterPro:IPR005828 InterPro:IPR005829 Pfam:PF00083 PRINTS:PR00171 PROSITE:PS00216 PROSITE:PS00217 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005774 eggNOG:COG0477 InterPro:IPR016196 SUPFAM:SSF103473 GO:GO:0008643 InterPro:IPR020846 PROSITE:PS50850 HOGENOM:HBG744444 GO:GO:0022891 TIGRFAMs:TIGR00879 EMBL:AC025808 EMBL:AY059848 EMBL:AY093274 IPI:IPI00534617 RefSeq:NP_173377.1 UniGene:At.22941 ProteinModelPortal:Q93YP9 IntAct:Q93YP9 PRIDE:Q93YP9 EnsemblPlants:AT1G19450.1 GeneID:838529 KEGG:ath:AT1G19450 TAIR:At1g19450 InParanoid:Q93YP9 OMA:SIGMTIS PhylomeDB:Q93YP9 ProtClustDB:CLSN2682491 ArrayExpress:Q93YP9 Genevestigator:Q93YP9 GermOnline:AT1G19450 Uniprot:Q93YP9
Leaf	Isotig03088	1	29	-4.329	6.86E-07	TAIR|locus:2168210 - symbol:AT5G65380 "AT5G65380" species:3702 "Arabidopsis thaliana" [GO:0005215 "transporter activity" evidence=ISS] [GO:0006855 "drug transmembrane transport" evidence=IEA] [GO:0009835 "fruit ripening" evidence=ISS] [GO:0015238 "drug transmembrane transporter activity" evidence=IEA] [GO:0015297 "antiporter activity" evidence=IEA;ISS] [GO:0016020 "membrane" evidence=IEA;ISS] [GO:0055085 "transmembrane

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						transport" evidence=IEA] InterPro:IPR002528 Pfam:PF01554 EMBL:CP002688 GenomeReviews:BA000015_GR EMBL:AB011479 GO:GO:0016020 GO:GO:0015238 GO:GO:0015297 eggNOG:COG0534 HOGENOM:HBG746942 KO:K03327 PANTHER:PTHR11206 TIGRFAMs:TIGR00797 EMBL:AF375456 EMBL:AY143960 IPI:IPI00524544 RefSeq:NP_201341.1 UniGene:At.28742 ProteinModelPortal:Q9FKQ1 PRIDE:Q9FKQ1 EnsemblPlants:AT5G65380.1 GeneID:836663 KEGG:ath:AT5G65380 TAIR:At5g65380 InParanoid:Q9FKQ1 OMA:ATISISW PhylomeDB:Q9FKQ1 ProtClustDB:CLSN2916278 Genevestigator:Q9FKQ1 Uniprot:Q9FKQ1
Leaf	Isotig03089	1	25	-4.115	5.42E-06	TAIR|locus:2168210 - symbol:AT5G65380 "AT5G65380" species:3702 "Arabidopsis thaliana" [GO:0005215 "transporter activity" evidence=ISS] [GO:0006855 "drug transmembrane transport" evidence=IEA] [GO:0009835 "fruit ripening" evidence=ISS] [GO:0015238 "drug transmembrane transporter activity" evidence=IEA] [GO:0015297 "antiporter activity" evidence=IEA;ISS] [GO:0016020 "membrane" evidence=IEA;ISS] [GO:0055085 "transmembrane transport" evidence=IEA] InterPro:IPR002528 Pfam:PF01554 EMBL:CP002688 GenomeReviews:BA000015_GR EMBL:AB011479 GO:GO:0016020 GO:GO:0015238 GO:GO:0015297 eggNOG:COG0534 HOGENOM:HBG746942 KO:K03327 PANTHER:PTHR11206 TIGRFAMs:TIGR00797 EMBL:AF375456 EMBL:AY143960 IPI:IPI00524544 RefSeq:NP_201341.1 UniGene:At.28742 ProteinModelPortal:Q9FKQ1 PRIDE:Q9FKQ1 EnsemblPlants:AT5G65380.1 GeneID:836663 KEGG:ath:AT5G65380 TAIR:At5g65380 InParanoid:Q9FKQ1 OMA:ATISISW PhylomeDB:Q9FKQ1 ProtClustDB:CLSN2916278 Genevestigator:Q9FKQ1 Uniprot:Q9FKQ1
Leaf	Isotig03092	31	9	2.313	2.97E-06	TAIR|locus:2099580 - symbol:ASN1 "AT3G47340" species:3702 "Arabidopsis thaliana" [GO:0009063 "cellular amino acid catabolic process" evidence=TAS] [GO:0043617 "cellular response to sucrose starvation" evidence=IEP] [GO:0009744 "response to sucrose stimulus" evidence=IEP] [GO:0009749 "response to glucose stimulus" evidence=IEP] [GO:0009750 "response to fructose stimulus" evidence=IEP] [GO:0009646 "response to absence of light" evidence=TAS] [GO:0004066 "asparagine synthase (glutamine-hydrolyzing) activity" evidence=ISS] InterPro:IPR001962 InterPro:IPR006426 Pfam:PF00733 PIRSF:PIRSF001589 GO:GO:0005524 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0009750 GO:GO:0009749 GO:GO:0009744 GO:GO:0009646 GO:GO:0009063 InterPro:IPR014729 Gene3D:G3DSA:3.40.50.620 GO:GO:0006529 eggNOG:COG0367 HOGENOM:HBG752912 KO:K01953 GO:GO:0004066 GO:GO:0006541 InterPro:IPR017932 TIGRFAMs:TIGR01536 PROSITE:PS51278 MEROPS:C44.974 OMA:IGTTHHE EMBL:L29083 EMBL:AL096860 EMBL:AF419557 EMBL:AY072214 EMBL:AY096592 IPI:IPI00541909 PIR:T12989 RefSeq:NP_190318.1 UniGene:At.20782 ProteinModelPortal:P49078 SMR:P49078 STRING:P49078 PRIDE:P49078 EnsemblPlants:AT3G47340.1 GeneID:823888 KEGG:ath:AT3G47340 TAIR:At3g47340 InParanoid:P49078 PhylomeDB:P49078 ProtClustDB:PLN02549 ArrayExpress:P49078 Genevestigator:P49078 GO:GO:0043617 Uniprot:P49078
Leaf	Isotig03093	31	8	2.483	1.11E-06	TAIR|locus:2099580 - symbol:ASN1 "AT3G47340" species:3702 "Arabidopsis thaliana" [GO:0009063 "cellular amino acid catabolic process" evidence=TAS] [GO:0043617 "cellular response to sucrose starvation" evidence=IEP] [GO:0009744 "response to sucrose stimulus" evidence=IEP] [GO:0009749 "response to glucose stimulus" evidence=IEP] [GO:0009750 "response to fructose stimulus" evidence=IEP] [GO:0009646 "response to absence of light" evidence=TAS] [GO:0004066 "asparagine synthase (glutamine-hydrolyzing) activity" evidence=ISS] InterPro:IPR001962 InterPro:IPR006426 Pfam:PF00733 PIRSF:PIRSF001589 GO:GO:0005524 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0009750 GO:GO:0009749 GO:GO:0009744 GO:GO:0009646 GO:GO:0009063 InterPro:IPR014729 Gene3D:G3DSA:3.40.50.620 GO:GO:0006529 eggNOG:COG0367 HOGENOM:HBG752912 KO:K01953 GO:GO:0004066 GO:GO:0006541 InterPro:IPR017932 TIGRFAMs:TIGR01536 PROSITE:PS51278 MEROPS:C44.974 OMA:IGTTHHE EMBL:L29083 EMBL:AL096860 EMBL:AF419557 EMBL:AY072214 EMBL:AY096592 IPI:IPI00541909 PIR:T12989 RefSeq:NP_190318.1 UniGene:At.20782 ProteinModelPortal:P49078 SMR:P49078 STRING:P49078 PRIDE:P49078 EnsemblPlants:AT3G47340.1 GeneID:823888 KEGG:ath:AT3G47340 TAIR:At3g47340 InParanoid:P49078 PhylomeDB:P49078 ProtClustDB:PLN02549 ArrayExpress:P49078 Genevestigator:P49078 GO:GO:0043617 Uniprot:P49078
Leaf	Isotig03112	16	2	3.529	3.35E-05	TAIR|locus:2037783 - symbol:AT1G15290 "AT1G15290" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR011990 InterPro:IPR013026 InterPro:IPR019734 PROSITE:PS50005 PROSITE:PS50293 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0005488 EMBL:AC007591 eggNOG:COG0457 Gene3D:G3DSA:1.25.40.10 HOGENOM:HBG633273 IPI:IPI00533414 PIR:B86287 ProteinModelPortal:Q9XI40 SMR:Q9XI40 STRING:Q9XI40 PRIDE:Q9XI40 TAIR:At1g15290 InParanoid:Q9XI40 PhylomeDB:Q9XI40 Genevestigator:Q9XI40 Uniprot:Q9XI40

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig03113	15	2	3.436	7.06E-05	TAIR|locus:2037783 - symbol:AT1G15290 "AT1G15290" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR011990 InterPro:IPR013026 InterPro:IPR019734 PROSITE:PS50005 PROSITE:PS50293 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0005488 EMBL:AC007591 eggNOG:COG0457 Gene3D:G3DSA:1.25.40.10 HOGENOM:HBG633273 IPI:IPI00533414 PIR:B86287 ProteinModelPortal:Q9XI40 SMR:Q9XI40 STRING:Q9XI40 PRIDE:Q9XI40 TAIR:At1g15290 InParanoid:Q9XI40 PhylomeDB:Q9XI40 Genevestigator:Q9XI40 Uniprot:Q9XI40
Leaf	Isotig03122	22	7	2.181	0.0001462	TAIR|locus:2024685 - symbol:BGLU11 "beta glucosidase 11" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=IEA;ISS] [GO:0005975 "carbohydrate metabolic process" evidence=IEA] [GO:0043169 "cation binding" evidence=IEA] InterPro:IPR001360 InterPro:IPR013781 InterPro:IPR018120 Pfam:PF00232 PRINTS:PR00131 PROSITE:PS00572 PROSITE:PS00653 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0043169 InterPro:IPR017853 Gene3D:G3DSA:3.20.20.80 SUPFAM:SSF51445 GO:GO:0005975 GO:GO:0008422 CAZy:GH1 eggNOG:COG2723 HOGENOM:HBG316462 PANTHER:PTHR10353 EMBL:AC009525 EMBL:AY049274 EMBL:AY062763 EMBL:BT001137 IPI:IPI00536257 IPI:IPI00537900 IPI:IPI00544196 IPI:IPI00890996 IPI:IPI00891207 PIR:G86158 RefSeq:NP_001117217.1 RefSeq:NP_563666.1 RefSeq:NP_849578.5 RefSeq:NP_973745.1 RefSeq:NP_973746.3 UniGene:At.26199 ProteinModelPortal:B3H5Q1 SMR:B3H5Q1 STRING:B3H5Q1 EnsemblPlants:AT1G02850.4 GeneID:839435 KEGG:ath:AT1G02850 TAIR:At1g02850 InParanoid:A8MRZ0 PhylomeDB:B3H5Q1 ProtClustDB:PLN02998 Genevestigator:B3H5Q1 Uniprot:B3H5Q1
Leaf	Isotig03123	21	7	2.114	0.000274738	TAIR|locus:2024685 - symbol:BGLU11 "beta glucosidase 11" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=IEA;ISS] [GO:0005975 "carbohydrate metabolic process" evidence=IEA] [GO:0043169 "cation binding" evidence=IEA] InterPro:IPR001360 InterPro:IPR013781 InterPro:IPR018120 Pfam:PF00232 PRINTS:PR00131 PROSITE:PS00572 PROSITE:PS00653 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0043169 InterPro:IPR017853 Gene3D:G3DSA:3.20.20.80 SUPFAM:SSF51445 GO:GO:0005975 GO:GO:0008422 CAZy:GH1 eggNOG:COG2723 HOGENOM:HBG316462 PANTHER:PTHR10353 EMBL:AC009525 EMBL:AY049274 EMBL:AY062763 EMBL:BT001137 IPI:IPI00536257 IPI:IPI00537900 IPI:IPI00544196 IPI:IPI00890996 IPI:IPI00891207 PIR:G86158 RefSeq:NP_001117217.1 RefSeq:NP_563666.1 RefSeq:NP_849578.5 RefSeq:NP_973745.1 RefSeq:NP_973746.3 UniGene:At.26199 ProteinModelPortal:B3H5Q1 SMR:B3H5Q1 STRING:B3H5Q1 EnsemblPlants:AT1G02850.4 GeneID:839435 KEGG:ath:AT1G02850 TAIR:At1g02850 InParanoid:A8MRZ0 PhylomeDB:B3H5Q1 ProtClustDB:PLN02998 Genevestigator:B3H5Q1 Uniprot:B3H5Q1
Leaf	Isotig03124	2	42	-3.863	7.44E-09	TAIR|locus:2147890 - symbol:AT5G15070 species:3702 "Arabidopsis thaliana" [GO:0003993 "acid phosphatase activity" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0016491 "oxidoreductase activity" evidence=IEA] [GO:0046914 "transition metal ion binding" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] InterPro:IPR000560 Pfam:PF00328 PROSITE:PS00616 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0003993 eggNOG:NOG245915 HOGENOM:HBG378897 EMBL:BT001922 IPI:IPI00544492 RefSeq:NP_568308.1 UniGene:At.23566 ProteinModelPortal:Q84WW3 SMR:Q84WW3 PRIDE:Q84WW3 EnsemblPlants:AT5G15070.1 GeneID:831359 KEGG:ath:AT5G15070 TAIR:At5g15070 InParanoid:Q84WW3 OMA:NASSEME PhylomeDB:Q84WW3 ProtClustDB:CLSN2689684 Genevestigator:Q84WW3 Uniprot:Q84WW3
Leaf	Isotig03125	2	41	-3.829	1.24E-08	TAIR|locus:2147890 - symbol:AT5G15070 species:3702 "Arabidopsis thaliana" [GO:0003993 "acid phosphatase activity" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0016491 "oxidoreductase activity" evidence=IEA] [GO:0046914 "transition metal ion binding" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] InterPro:IPR000560 Pfam:PF00328 PROSITE:PS00616 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0003993 eggNOG:NOG245915 HOGENOM:HBG378897 EMBL:BT001922 IPI:IPI00544492 RefSeq:NP_568308.1 UniGene:At.23566 ProteinModelPortal:Q84WW3 SMR:Q84WW3 PRIDE:Q84WW3 EnsemblPlants:AT5G15070.1 GeneID:831359 KEGG:ath:AT5G15070 TAIR:At5g15070 InParanoid:Q84WW3 OMA:NASSEME PhylomeDB:Q84WW3 ProtClustDB:CLSN2689684 Genevestigator:Q84WW3 Uniprot:Q84WW3
Leaf	Isotig03134	43	3	4.370	3.35E-13	TAIR|locus:2183720 - symbol:CIPK5 "CBL-interacting protein kinase 5" species:3702 "Arabidopsis thaliana" [GO:0004672 "protein kinase activity" evidence=IEA] [GO:0004674 "protein serine/threonine kinase activity"

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						evidence=IEA] [GO:0005524 "ATP binding" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0006468 "protein phosphorylation" evidence=IEA] [GO:0007165 "signal transduction" evidence=IEA] [GO:0016301 "kinase activity" evidence=ISS] InterPro:IPR000719 InterPro:IPR002290 InterPro:IPR004041 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 InterPro:IPR018451 Pfam:PF00069 Pfam:PF03822 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 PROSITE:PS50816 SMART:SM00220 GO:GO:0005524 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0007165 eggNOG:COG0515 SUPFAM:SSF56112 GO:GO:0004674 HOGENOM:HBG755340 HSSP:P06782 EMBL:AL365234 EMBL:AF285105 EMBL:AY062765 EMBL:BT001234 IPI:IPI00528456 PIR:T50802 RefSeq:NP_568241.2 UniGene:At.6016 ProteinModelPortal:Q9LEU7 SMR:Q9LEU7 IntAct:Q9LEU7 STRING:Q9LEU7 PRIDE:Q9LEU7 EnsemblPlants:AT5G10930.1 GeneID:830960 KEGG:ath:AT5G10930 TAIR:At5g10930 InParanoid:Q9LKF7 OMA:KTKIFFV PhylomeDB:Q9LEU7 ProtClustDB:CLSN2917712 ArrayExpress:Q8H0X3 Genevestigator:Q9LEU7 Uniprot:Q9LEU7
Leaf	Isotig03135	42	3	4.336	6.94E-13	TAIR|locus:2183720 - symbol:CIPK5 "CBL-interacting protein kinase 5" species:3702 "Arabidopsis thaliana" [GO:0004672 "protein kinase activity" evidence=IEA] [GO:0004674 "protein serine/threonine kinase activity" evidence=IEA] [GO:0005524 "ATP binding" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0006468 "protein phosphorylation" evidence=IEA] [GO:0007165 "signal transduction" evidence=IEA] [GO:0016301 "kinase activity" evidence=ISS] InterPro:IPR000719 InterPro:IPR002290 InterPro:IPR004041 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 InterPro:IPR018451 Pfam:PF00069 Pfam:PF03822 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 PROSITE:PS50816 SMART:SM00220 GO:GO:0005524 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0007165 eggNOG:COG0515 SUPFAM:SSF56112 GO:GO:0004674 HOGENOM:HBG755340 HSSP:P06782 EMBL:AL365234 EMBL:AF285105 EMBL:AY062765 EMBL:BT001234 IPI:IPI00528456 PIR:T50802 RefSeq:NP_568241.2 UniGene:At.6016 ProteinModelPortal:Q9LEU7 SMR:Q9LEU7 IntAct:Q9LEU7 STRING:Q9LEU7 PRIDE:Q9LEU7 EnsemblPlants:AT5G10930.1 GeneID:830960 KEGG:ath:AT5G10930 TAIR:At5g10930 InParanoid:Q9LKF7 OMA:KTKIFFV PhylomeDB:Q9LEU7 ProtClustDB:CLSN2917712 ArrayExpress:Q8H0X3 Genevestigator:Q9LEU7 Uniprot:Q9LEU7
Leaf	Isotig03148	13	0	5.229	3.68E-05	TAIR|locus:2116194 - symbol:AT4G34380 "AT4G34380" species:3702 "Arabidopsis thaliana" [GO:0000166 "nucleotide binding" evidence=ISS] [GO:0005834 "heterotrimeric G-protein complex" evidence=ISS] [GO:0008150 "biological_process" evidence=ND] InterPro:IPR017986 InterPro:IPR001680 InterPro:IPR015943 Pfam:PF00400 PROSITE:PS50082 PROSITE:PS50294 SMART:SM00320 EMBL:CP002687 GenomeReviews:CT486007_GR Gene3D:G3DSA:2.130.10.10 SUPFAM:SSF50978 eggNOG:COG2319 InterPro:IPR020472 PRINTS:PR00320 EMBL:AL035521 EMBL:AL161585 HOGENOM:HBG750447 ProtClustDB:CLSN2681936 EMBL:BT005888 EMBL:AK118385 IPI:IPI00526524 PIR:T04784 RefSeq:NP_195164.1 UniGene:At.31507 ProteinModelPortal:Q9SZ03 SMR:Q9SZ03 IntAct:Q9SZ03 STRING:Q9SZ03 PRIDE:Q9SZ03 EnsemblPlants:AT4G34380.1 GeneID:829588 KEGG:ath:AT4G34380 TAIR:At4g34380 InParanoid:Q9SZ03 OMA:VEEERAC PhylomeDB:Q9SZ03 Genevestigator:Q9SZ03 Uniprot:Q9SZ03
Leaf	Isotig03149	13	0	5.229	3.68E-05	TAIR|locus:2116194 - symbol:AT4G34380 "AT4G34380" species:3702 "Arabidopsis thaliana" [GO:0000166 "nucleotide binding" evidence=ISS] [GO:0005834 "heterotrimeric G-protein complex" evidence=ISS] [GO:0008150 "biological_process" evidence=ND] InterPro:IPR017986 InterPro:IPR001680 InterPro:IPR015943 Pfam:PF00400 PROSITE:PS50082 PROSITE:PS50294 SMART:SM00320 EMBL:CP002687 GenomeReviews:CT486007_GR Gene3D:G3DSA:2.130.10.10 SUPFAM:SSF50978 eggNOG:COG2319 InterPro:IPR020472 PRINTS:PR00320 EMBL:AL035521 EMBL:AL161585 HOGENOM:HBG750447 ProtClustDB:CLSN2681936 EMBL:BT005888 EMBL:AK118385 IPI:IPI00526524 PIR:T04784 RefSeq:NP_195164.1 UniGene:At.31507 ProteinModelPortal:Q9SZ03 SMR:Q9SZ03 IntAct:Q9SZ03 STRING:Q9SZ03 PRIDE:Q9SZ03 EnsemblPlants:AT4G34380.1 GeneID:829588 KEGG:ath:AT4G34380 TAIR:At4g34380 InParanoid:Q9SZ03 OMA:VEEERAC PhylomeDB:Q9SZ03 Genevestigator:Q9SZ03 Uniprot:Q9SZ03
Leaf	Isotig03156	17	0	5.616	2.14E-06	TAIR|locus:2078327 - symbol:AT3G45400 "AT3G45400" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=ISS] [GO:0008150 "biological_process" evidence=ND] [GO:0016020 "membrane" evidence=IEA;ISS] InterPro:IPR004263 Pfam:PF03016 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0016020 EMBL:AL132953 CAZy:GT47 HOGENOM:HBG320039 eggNOG:NOG308552 IPI:IPI00543011 PIR:T47480 RefSeq:NP_190126.1 UniGene:At.36041 PRIDE:Q9M3D9 EnsemblPlants:AT3G45400.1

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GeneID:823678 KEGG:ath:AT3G45400 TAIR:At3g45400 InParanoid:Q9M3D9 OMA:YPSKEGD PhylomeDB:Q9M3D9 ProtClustDB:CLSN2684651 Genevestigator:Q9M3D9 Uniprot:Q9M3D9
Leaf	Isotig03157	15	0	5.436	8.75E-06	TAIR|locus:2078327 - symbol:AT3G45400 "AT3G45400" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=ISS] [GO:0008150 "biological_process" evidence=ND] [GO:0016020 "membrane" evidence=IEA;ISS] InterPro:IPR004263 Pfam:PF03016 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0016020 EMBL:AL132953 CAZy:GT47 HOGENOM:HBG320039 eggNOG:NOG308552 IPI:IPI00543011 PIR:T47480 RefSeq:NP_190126.1 UniGene:At.36041 PRIDE:Q9M3D9 EnsemblPlants:AT3G45400.1 GeneID:823678 KEGG:ath:AT3G45400 TAIR:At3g45400 InParanoid:Q9M3D9 OMA:YPSKEGD PhylomeDB:Q9M3D9 ProtClustDB:CLSN2684651 Genevestigator:Q9M3D9 Uniprot:Q9M3D9
Leaf	Isotig03164	22	0	5.988	7.04E-08	TAIR|locus:2088857 - symbol:ERF1-3 "AT3G26618" species:3702 "Arabidopsis thaliana" [GO:0003747 "translation release factor activity" evidence=IGI;ISS] [GO:0006415 "translational termination" evidence=IGI;ISS] InterPro:IPR004403 InterPro:IPR005140 InterPro:IPR005141 InterPro:IPR005142 Pfam:PF03465 Pfam:PF03463 Pfam:PF03464 GO:GO:0005737 EMBL:CP002686 GenomeReviews:BA000014_GR EMBL:X98130 EMBL:AB028611 eggNOG:COG1503 HOGENOM:HBG497188 KO:K03265 ProtClustDB:CLSN2682479 GO:GO:0016149 InterPro:IPR024049 Gene3D:G3DSA:3.30.960.10 PANTHER:PTHR10113 SUPFAM:SSF55481 TIGRFAMs:TIGR03676 EMBL:X69375 EMBL:X97486 EMBL:AB026648 EMBL:AY050352 EMBL:AY116942 IPI:IPI00523831 PIR:S31328 RefSeq:NP_189295.3 UniGene:At.48710 ProteinModelPortal:P35614 SMR:P35614 STRING:P35614 PRIDE:P35614 EnsemblPlants:AT3G26618.1 GeneID:822273 KEGG:ath:AT3G26618 TAIR:At3g26618 InParanoid:P35614 OMA:GDYLHHE PhylomeDB:P35614 ArrayExpress:P35614 Genevestigator:P35614 GermOnline:AT3G26618 Uniprot:P35614
Leaf	Isotig03165	20	0	5.851	2.71E-07	TAIR|locus:2088857 - symbol:ERF1-3 "AT3G26618" species:3702 "Arabidopsis thaliana" [GO:0003747 "translation release factor activity" evidence=IGI;ISS] [GO:0006415 "translational termination" evidence=IGI;ISS] InterPro:IPR004403 InterPro:IPR005140 InterPro:IPR005141 InterPro:IPR005142 Pfam:PF03465 Pfam:PF03463 Pfam:PF03464 GO:GO:0005737 EMBL:CP002686 GenomeReviews:BA000014_GR EMBL:X98130 EMBL:AB028611 eggNOG:COG1503 HOGENOM:HBG497188 KO:K03265 ProtClustDB:CLSN2682479 GO:GO:0016149 InterPro:IPR024049 Gene3D:G3DSA:3.30.960.10 PANTHER:PTHR10113 SUPFAM:SSF55481 TIGRFAMs:TIGR03676 EMBL:X69375 EMBL:X97486 EMBL:AB026648 EMBL:AY050352 EMBL:AY116942 IPI:IPI00523831 PIR:S31328 RefSeq:NP_189295.3 UniGene:At.48710 ProteinModelPortal:P35614 SMR:P35614 STRING:P35614 PRIDE:P35614 EnsemblPlants:AT3G26618.1 GeneID:822273 KEGG:ath:AT3G26618 TAIR:At3g26618 InParanoid:P35614 OMA:GDYLHHE PhylomeDB:P35614 ArrayExpress:P35614 Genevestigator:P35614 GermOnline:AT3G26618 Uniprot:P35614
Leaf	Isotig03168	9	46	-1.825	4.74E-05	TAIR|locus:2193844 - symbol:ZKT "protein containing PDZ domain, a K-box domain, and a TPR region" species:3702 "Arabidopsis thaliana" [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009611 "response to wounding" evidence=IEP] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] InterPro:IPR001478 InterPro:IPR011990 InterPro:IPR013026 InterPro:IPR019734 PROSITE:PS50005 PROSITE:PS50106 PROSITE:PS50293 EMBL:CP002684 GO:GO:0009570 GO:GO:0009611 GO:GO:0005488 GO:GO:0009941 Gene3D:G3DSA:1.25.40.10 SUPFAM:SSF50156 GO:GO:0009535 EMBL:AY039926 EMBL:AY079359 EMBL:AY986818 EMBL:AB190499 IPI:IPI00548632 RefSeq:NP_564691.1 UniGene:At.19231 ProteinModelPortal:Q94BS2 SMR:Q94BS2 STRING:Q94BS2 PRIDE:Q94BS2 ProMEX:Q94BS2 EnsemblPlants:AT1G55480.1 GeneID:841995 KEGG:ath:AT1G55480 TAIR:At1g55480 InParanoid:Q94BS2 OMA:ASYNVAC PhylomeDB:Q94BS2 ProtClustDB:CLSN2688838 ArrayExpress:Q94BS2 Genevestigator:Q94BS2 Uniprot:Q94BS2
Leaf	Isotig03169	9	46	-1.825	4.74E-05	TAIR|locus:2193844 - symbol:ZKT "protein containing PDZ domain, a K-box domain, and a TPR region" species:3702 "Arabidopsis thaliana" [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009611 "response to wounding" evidence=IEP] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] InterPro:IPR001478 InterPro:IPR011990 InterPro:IPR013026 InterPro:IPR019734 PROSITE:PS50005 PROSITE:PS50106 PROSITE:PS50293 EMBL:CP002684 GO:GO:0009570 GO:GO:0009611 GO:GO:0005488 GO:GO:0009941 Gene3D:G3DSA:1.25.40.10 SUPFAM:SSF50156 GO:GO:0009535 EMBL:AY039926 EMBL:AY079359 EMBL:AY986818 EMBL:AB190499 IPI:IPI00548632 RefSeq:NP_564691.1 UniGene:At.19231 ProteinModelPortal:Q94BS2 SMR:Q94BS2 STRING:Q94BS2 PRIDE:Q94BS2 ProMEX:Q94BS2

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EnsemblPlants:AT1G55480.1 GeneID:841995 KEGG:ath:AT1G55480 TAIR:At1g55480 InParanoid:Q94BS2 OMA:ASYNVAC PhylomeDB:Q94BS2 ProtClustDB:CLSN2688838 ArrayExpress:Q94BS2 Genevestigator:Q94BS2 Uniprot:Q94BS2
Leaf	Isotig03174	8	36	-1.641	0.000834246	TAIR|locus:2033760 - symbol:PKp3 "AT1G32440" species:3702 "Arabidopsis thaliana" [GO:0004743 "pyruvate kinase activity" evidence=ISS;IDA] [GO:0006096 "glycolysis" evidence=ISS] [GO:0000287 "magnesium ion binding" evidence=IDA] [GO:0006633 "fatty acid biosynthetic process" evidence=IGI] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0030955 "potassium ion binding" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] InterPro:IPR001697 InterPro:IPR015793 InterPro:IPR015794 InterPro:IPR015806 InterPro:IPR015813 InterPro:IPR018209 Pfam:PF00224 PRINTS:PR01050 PROSITE:PS00110 Pfam:PF02887 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009570 GO:GO:0000287 GO:GO:0006633 Gene3D:G3DSA:3.20.20.60 SUPFAM:SSF51621 GO:GO:0006096 GO:GO:0030955 eggNOG:COG0469 HOGENOM:HBG734376 KO:K00873 GO:GO:0004743 InterPro:IPR011037 InterPro:IPR015795 Gene3D:G3DSA:2.40.33.10 Gene3D:G3DSA:3.40.1380.20 PANTHER:PTHR11817 SUPFAM:SSF50800 SUPFAM:SSF52935 TIGRFAMs:TIGR01064 HSSP:P14178 EMBL:AY058121 EMBL:BT001147 IPI:IPI00519857 RefSeq:NP_564402.1 UniGene:At.66798 ProteinModelPortal:Q93Z53 STRING:Q93Z53 PRIDE:Q93Z53 EnsemblPlants:AT1G32440.1 GeneID:840138 KEGG:ath:AT1G32440 TAIR:At1g32440 InParanoid:Q93Z53 OMA:KPSIVAT PhylomeDB:Q93Z53 ProtClustDB:PLN02623 Genevestigator:Q93Z53 Uniprot:Q93Z53
Leaf	Isotig03176	1	16	-3.471	0.000601166	TAIR|locus:2133012 - symbol:AT4G28080 "AT4G28080" species:3702 "Arabidopsis thaliana" [GO:0009737 "response to abscisic acid stimulus" evidence=IDA] InterPro:IPR011990 InterPro:IPR013026 InterPro:IPR019734 PROSITE:PS50005 PROSITE:PS50293 SMART:SM00028 GO:GO:0009737 GenomeReviews:CT486007_GR GO:GO:0005488 eggNOG:COG0457 Gene3D:G3DSA:1.25.40.10 EMBL:AL161572 EMBL:AL035524 IPI:IPI01019292 PIR:T02909 ProteinModelPortal:Q9SUD1 SMR:Q9SUD1 STRING:Q9SUD1 PRIDE:Q9SUD1 TAIR:At4g28080 HOGENOM:HBG633273 InParanoid:Q9SUD1 PhylomeDB:Q9SUD1 ArrayExpress:Q9SUD1 Genevestigator:Q9SUD1 Uniprot:Q9SUD1
Leaf	Isotig03186	18	5	2.377	0.000296328	TAIR|locus:2089601 - symbol:NTMC2T6.2 species:3702 "Arabidopsis thaliana" [GO:0009507 "chloroplast" evidence=IDA] InterPro:IPR000008 InterPro:IPR008973 Pfam:PF00168 SMART:SM00239 GO:GO:0009507 EMBL:CP002686 InterPro:IPR018029 SUPFAM:SSF49562 PROSITE:PS50004 eggNOG:COG5038 EMBL:AB023038 UniGene:At.39207 IPI:IPI00891324 RefSeq:NP_001118626.1 ProteinModelPortal:B3H4I1 SMR:B3H4I1 PRIDE:B3H4I1 EnsemblPlants:AT3G14590.2 GeneID:820685 KEGG:ath:AT3G14590 TAIR:At3g14590 PhylomeDB:B3H4I1 ProtClustDB:CLSN2688762 Genevestigator:B3H4I1 Uniprot:B3H4I1
Leaf	Isotig03187	16	4	2.529	0.000407249	TAIR|locus:2024912 - symbol:NTMC2T6.1 species:3702 "Arabidopsis thaliana" [GO:0005773 "vacuole" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] InterPro:IPR000008 InterPro:IPR008973 Pfam:PF00168 SMART:SM00239 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005886 GO:GO:0005773 InterPro:IPR018029 SUPFAM:SSF49562 PROSITE:PS50004 HSSP:P21707 eggNOG:COG5038 EMBL:AC018748 EMBL:AC024260 EMBL:AY054685 IPI:IPI00518774 PIR:A96576 RefSeq:NP_564637.1 UniGene:At.14917 ProteinModelPortal:Q93XX4 SMR:Q93XX4 PRIDE:Q93XX4 EnsemblPlants:AT1G53590.1 GeneID:841794 KEGG:ath:AT1G53590 TAIR:At1g53590 HOGENOM:HBG317476 InParanoid:Q93XX4 OMA:KTLSPKW Genevestigator:Q93XX4 Uniprot:Q93XX4
Leaf	Isotig03192	56	29	1.478	3.51E-06	TAIR|locus:2027186 - symbol:ALDH10A8 "AT1G74920" species:3702 "Arabidopsis thaliana" [GO:0004028 "3-chloroallyl aldehyde dehydrogenase activity" evidence=ISS] [GO:0016491 "oxidoreductase activity" evidence=IEA] [GO:0005618 "cell wall" evidence=IDA] [GO:0009414 "response to water deprivation" evidence=IMP] [GO:0009516 "leucoplast" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR015590 InterPro:IPR016160 InterPro:IPR016161 InterPro:IPR016162 InterPro:IPR016163 Pfam:PF00171 PROSITE:PS00070 PROSITE:PS00687 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0005618 GO:GO:0009507 eggNOG:COG1012 Gene3D:G3DSA:3.40.309.10 Gene3D:G3DSA:3.40.605.10 SUPFAM:SSF53720 HOGENOM:HBG752218 GO:GO:0009651 GO:GO:0009414 GO:GO:0008802 EMBL:AC008263 EMBL:AC013258 EMBL:AY093071 EMBL:BT008872 EMBL:AY087395 EMBL:AK220905 IPI:IPI00547056 PIR:H96778 RefSeq:NP_565094.1 UniGene:At.26779 ProteinModelPortal:Q9S795 SMR:Q9S795 STRING:Q9S795 PRIDE:Q9S795 EnsemblPlants:AT1G74920.1 GeneID:843831 KEGG:ath:AT1G74920 TAIR:At1g74920 InParanoid:Q9S795 KO:K00130 OMA:GEWGLDN PhylomeDB:Q9S795 ProtClustDB:PLN02467 ArrayExpress:Q9S795 Genevestigator:Q9S795 GermOnline:AT1G74920 GO:GO:0009516 Uniprot:Q9S795

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig03193	52	31	1.275	6.50E-05	TAIR|locus:2027186 - symbol:ALDH10A8 "AT1G74920" species:3702 "Arabidopsis thaliana" [GO:0004028 "3-chloroallyl aldehyde dehydrogenase activity" evidence=ISS] [GO:0016491 "oxidoreductase activity" evidence=IEA] [GO:0005618 "cell wall" evidence=IDA] [GO:0009414 "response to water deprivation" evidence=IMP] [GO:0009516 "leucoplast" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR015590 InterPro:IPR016160 InterPro:IPR016161 InterPro:IPR016162 InterPro:IPR016163 Pfam:PF00171 PROSITE:PS00070 PROSITE:PS00687 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0005618 GO:GO:0009507 eggNOG:COG1012 Gene3D:G3DSA:3.40.309.10 Gene3D:G3DSA:3.40.605.10 SUPFAM:SSF53720 HOGENOM:HBG752218 GO:GO:0009651 GO:GO:0009414 GO:GO:0008802 EMBL:AC008263 EMBL:AC013258 EMBL:AY093071 EMBL:BT008872 EMBL:AY087395 EMBL:AK220905 IPI:IPI00547056 PIR:H96778 RefSeq:NP_565094.1 UniGene:At.26779 ProteinModelPortal:Q9S795 SMR:Q9S795 STRING:Q9S795 PRIDE:Q9S795 EnsemblPlants:AT1G74920.1 GeneID:843831 KEGG:ath:AT1G74920 TAIR:At1g74920 InParanoid:Q9S795 KO:K00130 OMA:GEWGLDN PhylomeDB:Q9S795 ProtClustDB:PLN02467 ArrayExpress:Q9S795 Genevestigator:Q9S795 GermOnline:AT1G74920 GO:GO:0009516 Uniprot:Q9S795
Leaf	Isotig03195	6	33	-1.930	0.00034472	TAIR|locus:505006113 - symbol:ATP-PRT2 "AT1G09795" species:3702 "Arabidopsis thaliana" [GO:0000105 "histidine biosynthetic process" evidence=ISS;IDA] [GO:0003879 "ATP phosphoribosyltransferase activity" evidence=ISS;IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] HAMAP:MF_00079 InterPro:IPR001348 InterPro:IPR013115 InterPro:IPR013820 InterPro:IPR018198 InterPro:IPR020621 Pfam:PF01634 Pfam:PF08029 PROSITE:PS01316 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009570 GO:GO:0000287 GO:GO:0000105 InterPro:IPR011322 SUPFAM:SSF54913 InterPro:IPR015867 Gene3D:G3DSA:3.30.70.120 eggNOG:COG0040 HOGENOM:HBG391868 KO:K00765 GO:GO:0003879 PANTHER:PTHR21403 TIGRFAMs:TIGR00070 TIGRFAMs:TIGR03455 EMBL:BT002054 EMBL:BT008501 EMBL:AK118503 IPI:IPI00546445 RefSeq:NP_563853.1 UniGene:At.477 UniGene:At.49869 ProteinModelPortal:Q8GSJ1 SMR:Q8GSJ1 STRING:Q8GSJ1 PRIDE:Q8GSJ1 ProMEX:Q8GSJ1 EnsemblPlants:AT1G09795.1 GeneID:837509 KEGG:ath:AT1G09795 TAIR:At1g09795 InParanoid:Q8GSJ1 OMA:YRIVESA PhylomeDB:Q8GSJ1 ProtClustDB:PLN02245 ArrayExpress:Q8GSJ1 Genevestigator:Q8GSJ1 Uniprot:Q8GSJ1
Leaf	Isotig03196	41	23	1.363	0.000189148	TAIR|locus:2167240 - symbol:GAD "AT5G17330" species:3702 "Arabidopsis thaliana" [GO:0005516 "calmodulin binding" evidence=IDA;TAS;IPI] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA] [GO:0004351 "glutamate decarboxylase activity" evidence=IDA] InterPro:IPR002129 InterPro:IPR010107 InterPro:IPR015421 Pfam:PF00282 PROSITE:PS00392 GO:GO:0005829 GO:GO:0046686 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0030170 InterPro:IPR015424 Gene3D:G3DSA:3.40.640.10 SUPFAM:SSF53383 GO:GO:0006536 GO:GO:0005516 EMBL:AB005238 eggNOG:COG0076 PANTHER:PTHR11999 EMBL:U10034 EMBL:AY094464 EMBL:BT001047 IPI:IPI00530557 RefSeq:NP_197235.1 UniGene:At.25228 PDB:3HBX PDBsum:3HBX ProteinModelPortal:Q42521 SMR:Q42521 STRING:Q42521 PRIDE:Q42521 EnsemblPlants:AT5G17330.1 GeneID:831599 KEGG:ath:AT5G17330 TAIR:At5g17330 HOGENOM:HBG365574 InParanoid:Q42521 KO:K01580 OMA:RRWQNKM PhylomeDB:Q42521 ProtClustDB:CLSN2683665 ArrayExpress:Q42521 Genevestigator:Q42521 GermOnline:AT5G17330 GO:GO:0004351 PANTHER:PTHR11999:SF1 TIGRFAMs:TIGR01788 Uniprot:Q42521
Leaf	Isotig03197	41	21	1.494	6.32E-05	TAIR|locus:2167240 - symbol:GAD "AT5G17330" species:3702 "Arabidopsis thaliana" [GO:0005516 "calmodulin binding" evidence=IDA;TAS;IPI] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA] [GO:0004351 "glutamate decarboxylase activity" evidence=IDA] InterPro:IPR002129 InterPro:IPR010107 InterPro:IPR015421 Pfam:PF00282 PROSITE:PS00392 GO:GO:0005829 GO:GO:0046686 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0030170 InterPro:IPR015424 Gene3D:G3DSA:3.40.640.10 SUPFAM:SSF53383 GO:GO:0006536 GO:GO:0005516 EMBL:AB005238 eggNOG:COG0076 PANTHER:PTHR11999 EMBL:U10034 EMBL:AY094464 EMBL:BT001047 IPI:IPI00530557 RefSeq:NP_197235.1 UniGene:At.25228 PDB:3HBX PDBsum:3HBX ProteinModelPortal:Q42521 SMR:Q42521 STRING:Q42521 PRIDE:Q42521 EnsemblPlants:AT5G17330.1 GeneID:831599 KEGG:ath:AT5G17330 TAIR:At5g17330 HOGENOM:HBG365574 InParanoid:Q42521 KO:K01580 OMA:RRWQNKM PhylomeDB:Q42521 ProtClustDB:CLSN2683665 ArrayExpress:Q42521 Genevestigator:Q42521 GermOnline:AT5G17330 GO:GO:0004351 PANTHER:PTHR11999:SF1 TIGRFAMs:TIGR01788 Uniprot:Q42521

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig03204	2	24	-3.056	7.02E-05	TAIR|locus:2075576 - symbol:PHS2 "AT3G46970" species:3702 "Arabidopsis thaliana" [GO:0004645 "phosphorylase activity" evidence=ISS;IDA] [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0005829 "cytosol" evidence=IDA;TAS] [GO:0009414 "response to water deprivation" evidence=IMP] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] InterPro:IPR000811 InterPro:IPR011833 Pfam:PF00343 PIRSF:PIRSF000460 PROSITE:PS00102 GO:GO:0005829 GO:GO:0046686 GO:GO:0009507 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0030170 GO:GO:0005975 GO:GO:0009414 EMBL:AL133292 GO:GO:0004645 CAZy:GT35 eggNOG:COG0058 HOGENOM:HBG444050 KO:K00688 PANTHER:PTHR11468 TIGRFAMs:TIGR02093 EMBL:AY090236 EMBL:BT003012 IPI:IPI00545039 PIR:T45633 RefSeq:NP_190281.1 UniGene:At.879 ProteinModelPortal:Q9SD76 SMR:Q9SD76 STRING:Q9SD76 PRIDE:Q9SD76 EnsemblPlants:AT3G46970.1 GeneID:823850 KEGG:ath:AT3G46970 TAIR:At3g46970 InParanoid:Q9SD76 OMA:PEVNEYL PhylomeDB:Q9SD76 ProtClustDB:CLSN2684114 BRENDA:2.4.1.1 ArrayExpress:Q9SD76 Genevestigator:Q9SD76 GermOnline:AT3G46970 Uniprot:Q9SD76
Leaf	Isotig03205	2	19	-2.719	0.000848343	TAIR|locus:2075576 - symbol:PHS2 "AT3G46970" species:3702 "Arabidopsis thaliana" [GO:0004645 "phosphorylase activity" evidence=ISS;IDA] [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0005829 "cytosol" evidence=IDA;TAS] [GO:0009414 "response to water deprivation" evidence=IMP] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] InterPro:IPR000811 InterPro:IPR011833 Pfam:PF00343 PIRSF:PIRSF000460 PROSITE:PS00102 GO:GO:0005829 GO:GO:0046686 GO:GO:0009507 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0030170 GO:GO:0005975 GO:GO:0009414 EMBL:AL133292 GO:GO:0004645 CAZy:GT35 eggNOG:COG0058 HOGENOM:HBG444050 KO:K00688 PANTHER:PTHR11468 TIGRFAMs:TIGR02093 EMBL:AY090236 EMBL:BT003012 IPI:IPI00545039 PIR:T45633 RefSeq:NP_190281.1 UniGene:At.879 ProteinModelPortal:Q9SD76 SMR:Q9SD76 STRING:Q9SD76 PRIDE:Q9SD76 EnsemblPlants:AT3G46970.1 GeneID:823850 KEGG:ath:AT3G46970 TAIR:At3g46970 InParanoid:Q9SD76 OMA:PEVNEYL PhylomeDB:Q9SD76 ProtClustDB:CLSN2684114 BRENDA:2.4.1.1 ArrayExpress:Q9SD76 Genevestigator:Q9SD76 GermOnline:AT3G46970 Uniprot:Q9SD76
Leaf	Isotig03222	30	15	1.529	0.000500313	UNIPROTKB|F1PG69 - symbol:COL3A1 "Uncharacterized protein" species:9615 "Canis lupus familiaris" [GO:0005201 "extracellular matrix structural constituent" evidence=IEA] [GO:0005581 "collagen" evidence=IEA] InterPro:IPR000885 Pfam:PF01410 ProDom:PD002078 PROSITE:PS51461 SMART:SM00038 GO:GO:0005581 InterPro:IPR008160 Pfam:PF01391 GO:GO:0005201 GeneTree:ENSGT00650000092875 Ensembl:ENSCAFT00000023503 OMA:FGEEIRE Uniprot:F1PG69
Leaf	Isotig03223	28	13	1.636	0.000412977	UNIPROTKB|F1PG69 - symbol:COL3A1 "Uncharacterized protein" species:9615 "Canis lupus familiaris" [GO:0005201 "extracellular matrix structural constituent" evidence=IEA] [GO:0005581 "collagen" evidence=IEA] InterPro:IPR000885 Pfam:PF01410 ProDom:PD002078 PROSITE:PS51461 SMART:SM00038 GO:GO:0005581 InterPro:IPR008160 Pfam:PF01391 GO:GO:0005201 GeneTree:ENSGT00650000092875 Ensembl:ENSCAFT00000023503 OMA:FGEEIRE Uniprot:F1PG69
Leaf	Isotig03224	60	362	-2.064	3.07E-35	TAIR|locus:2205215 - symbol:AT1G56190 species:3702 "Arabidopsis thaliana" [GO:0004618 "phosphoglycerate kinase activity" evidence=IEA;ISS] [GO:0006096 "glycolysis" evidence=ISS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0009579 "thylakoid" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] InterPro:IPR001576 InterPro:IPR015824 InterPro:IPR015901 InterPro:IPR015911 Pfam:PF00162 PIRSF:PIRSF000724 PRINTS:PR00477 PROSITE:PS00111 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005739 GO:GO:0005524 GO:GO:0009570 GO:GO:0046686 GO:GO:0016020 GO:GO:0006096 GO:GO:0009579 EMBL:AC069159 GO:GO:0019253 EMBL:AC009894 eggNOG:COG0126 KO:K00927 GO:GO:0004618 Gene3D:G3DSA:3.40.50.1270 Gene3D:G3DSA:3.40.50.1260 PANTHER:PTHR11406 SUPFAM:SSF53748 HOGENOM:HBG453500 ProtClustDB:PLN03034 EMBL:AY056291 EMBL:AY099598 EMBL:BT000250 EMBL:U37700 IPI:IPI00530695 PIR:D96603 PIR:S71214 RefSeq:NP_176015.1 UniGene:At.11481 ProteinModelPortal:P50318 SMR:P50318 STRING:P50318 PRIDE:P50318 ProMEX:P50318 EnsemblPlants:AT1G56190.1 GeneID:842072 KEGG:ath:AT1G56190 TAIR:At1g56190 InParanoid:P50318 OMA:QDETRIL PhylomeDB:P50318 Genevestigator:P50318 Uniprot:P50318

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig03225	49	284	-2.006	4.73E-27	TAIR|locus:2205215 - symbol:AT1G56190 species:3702 "Arabidopsis thaliana" [GO:0004618 "phosphoglycerate kinase activity" evidence=IEA;ISS] [GO:0006096 "glycolysis" evidence=ISS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0009579 "thylakoid" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] InterPro:IPR001576 InterPro:IPR015824 InterPro:IPR015901 InterPro:IPR015911 Pfam:PF00162 PIRSF:PIRSF000724 PRINTS:PR00477 PROSITE:PS00111 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005739 GO:GO:0005524 GO:GO:0009570 GO:GO:0046686 GO:GO:0016020 GO:GO:0006096 GO:GO:0009579 EMBL:AC069159 GO:GO:0019253 EMBL:AC009894 eggNOG:COG0126 KO:K00927 GO:GO:0004618 Gene3D:G3DSA:3.40.50.1270 Gene3D:G3DSA:3.40.50.1260 PANTHER:PTHR11406 SUPFAM:SSF53748 HOGENOM:HBG453500 ProtClustDB:PLN03034 EMBL:AY056291 EMBL:AY099598 EMBL:BT000250 EMBL:U37700 IPI:IPI00530695 PIR:D96603 PIR:S71214 RefSeq:NP_176015.1 UniGene:At.11481 ProteinModelPortal:P50318 SMR:P50318 STRING:P50318 PRIDE:P50318 ProMEX:P50318 EnsemblPlants:AT1G56190.1 GeneID:842072 KEGG:ath:AT1G56190 TAIR:At1g56190 InParanoid:P50318 OMA:QDETRIL PhylomeDB:P50318 Genevestigator:P50318 Uniprot:P50318
Leaf	Isotig03232	7	48	-2.249	1.95E-06	TAIR|locus:2024685 - symbol:BGLU11 "beta glucosidase 11" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=IEA;ISS] [GO:0005975 "carbohydrate metabolic process" evidence=IEA] [GO:0043169 "cation binding" evidence=IEA] InterPro:IPR001360 InterPro:IPR013781 InterPro:IPR018120 Pfam:PF00232 PRINTS:PR00131 PROSITE:PS00572 PROSITE:PS00653 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0043169 InterPro:IPR017853 Gene3D:G3DSA:3.20.20.80 SUPFAM:SSF51445 GO:GO:0005975 GO:GO:0008422 CAZy:GH1 eggNOG:COG2723 HOGENOM:HBG316462 PANTHER:PTHR10353 EMBL:AC009525 EMBL:AY049274 EMBL:AY062763 EMBL:BT001137 IPI:IPI00536257 IPI:IPI00537900 IPI:IPI00544196 IPI:IPI00890996 IPI:IPI00891207 PIR:G86158 RefSeq:NP_001117217.1 RefSeq:NP_563666.1 RefSeq:NP_849578.5 RefSeq:NP_973745.1 RefSeq:NP_973746.3 UniGene:At.26199 ProteinModelPortal:B3H5Q1 SMR:B3H5Q1 STRING:B3H5Q1 EnsemblPlants:AT1G02850.4 GeneID:839435 KEGG:ath:AT1G02850 TAIR:At1g02850 InParanoid:A8MRZ0 PhylomeDB:B3H5Q1 ProtClustDB:PLN02998 Genevestigator:B3H5Q1 Uniprot:B3H5Q1
Leaf	Isotig03233	5	32	-2.149	0.000158227	TAIR|locus:2081680 - symbol:BGLU8 "beta glucosidase 8" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=IEA;ISS] [GO:0005975 "carbohydrate metabolic process" evidence=IEA] [GO:0043169 "cation binding" evidence=IEA] [GO:0005773 "vacuole" evidence=IDA] InterPro:IPR001360 InterPro:IPR013781 InterPro:IPR018120 Pfam:PF00232 PRINTS:PR00131 PROSITE:PS00572 PROSITE:PS00653 GO:GO:0005773 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0043169 InterPro:IPR017853 Gene3D:G3DSA:3.20.20.80 SUPFAM:SSF51445 GO:GO:0005975 EMBL:AL162651 GO:GO:0008422 CAZy:GH1 eggNOG:COG2723 PANTHER:PTHR10353 ProtClustDB:PLN02814 EMBL:AK175256 EMBL:AK176786 EMBL:AK176833 IPI:IPI00534420 PIR:T48064 RefSeq:NP_191834.3 UniGene:At.43830 HSSP:Q08638 ProteinModelPortal:Q67XN2 SMR:Q67XN2 STRING:Q67XN2 PRIDE:Q67XN2 EnsemblPlants:AT3G62750.1 GeneID:825450 KEGG:ath:AT3G62750 TAIR:At3g62750 InParanoid:Q67XN2 OMA:EATIFAF PhylomeDB:Q67XN2 Genevestigator:Q67XN2 Uniprot:Q67XN2
Leaf	Isotig03234	17	0	5.616	2.14E-06	TAIR|locus:2091652 - symbol:NCED3 "AT3G14440" species:3702 "Arabidopsis thaliana" [GO:0009414 "response to water deprivation" evidence=IMP] [GO:0045549 "9-cis-epoxycarotenoid dioxygenase activity" evidence=ISS;IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0009688 "abscisic acid biosynthetic process" evidence=ISS] [GO:0042538 "hyperosmotic salinity response" evidence=IMP] [GO:0006970 "response to osmotic stress" evidence=IMP] GO:GO:0009570 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0046872 GO:GO:0009414 GO:GO:0009688 GO:GO:0009535 GO:GO:0042538 eggNOG:COG3670 InterPro:IPR004294 PANTHER:PTHR10543 Pfam:PF03055 HOGENOM:HBG559594 GO:GO:0045549 KO:K09840 EMBL:AB028617 ProtClustDB:PLN02258 EMBL:AB026549 EMBL:AY056255 IPI:IPI00528622 RefSeq:NP_188062.1 UniGene:At.26346 ProteinModelPortal:Q9LRR7 SMR:Q9LRR7 STRING:Q9LRR7 PRIDE:Q9LRR7 EnsemblPlants:AT3G14440.1 GeneID:820667 KEGG:ath:AT3G14440 TAIR:At3g14440 InParanoid:Q9LRR7 OMA:KFAYLAL PhylomeDB:Q9LRR7

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						BioCyc:ARA:AT3G14440-MONOMER BioCyc:MetaCyc:AT3G14440-MONOMER ArrayExpress:Q93ZU5 Genevestigator:Q9LRR7 Uniprot:Q9LRR7
Leaf	Isotig03235	17	0	5.616	2.14E-06	TAIR|locus:2091652 - symbol:NCED3 "AT3G14440" species:3702 "Arabidopsis thaliana" [GO:0009414 "response to water deprivation" evidence=IMP] [GO:0045549 "9-cis-epoxycarotenoid dioxygenase activity" evidence=ISS;IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0009688 "abscisic acid biosynthetic process" evidence=ISS] [GO:0042538 "hyperosmotic salinity response" evidence=IMP] [GO:0006970 "response to osmotic stress" evidence=IMP] GO:GO:0009570 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0046872 GO:GO:0009414 GO:GO:0009688 GO:GO:0009535 GO:GO:0042538 eggNOG:COG3670 InterPro:IPR004294 PANTHER:PTHR10543 Pfam:PF03055 HOGENOM:HBG559594 GO:GO:0045549 KO:K09840 EMBL:AB028617 ProtClustDB:PLN02258 EMBL:AB026549 EMBL:AY056255 IPI:IPI00528622 RefSeq:NP_188062.1 UniGene:At.26346 ProteinModelPortal:Q9LRR7 SMR:Q9LRR7 STRING:Q9LRR7 PRIDE:Q9LRR7 EnsemblPlants:AT3G14440.1 GeneID:820667 KEGG:ath:AT3G14440 TAIR:At3g14440 InParanoid:Q9LRR7 OMA:KFAYLAL PhylomeDB:Q9LRR7 BioCyc:ARA:AT3G14440-MONOMER BioCyc:MetaCyc:AT3G14440-MONOMER ArrayExpress:Q93ZU5 Genevestigator:Q9LRR7 Uniprot:Q9LRR7
Leaf	Isotig03238	21	2	3.921	8.06E-07	TAIR|locus:2025087 - symbol:HAI2 "highly ABA-induced PP2C gene 2" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004722 "protein serine/threonine phosphatase activity" evidence=IEA;ISS] [GO:0006470 "protein dephosphorylation" evidence=IEA] [GO:0008287 "protein serine/threonine phosphatase complex" evidence=IEA] InterPro:IPR000222 InterPro:IPR001932 Pfam:PF00481 PROSITE:PS01032 SMART:SM00331 SMART:SM00332 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005886 GO:GO:0006470 GO:GO:0004722 GO:GO:0046872 GO:GO:0005267 EMBL:AC022464 eggNOG:COG0631 Gene3D:G3DSA:3.60.40.10 SUPFAM:SSF81606 GO:GO:0008287 InterPro:IPR015655 PANTHER:PTHR13832 HSSP:P35813 HOGENOM:HBG747569 EMBL:AY070089 EMBL:AY091341 EMBL:AY084794 IPI:IPI00521891 PIR:B86209 RefSeq:NP_172223.1 UniGene:At.28399 ProteinModelPortal:Q9LNW3 SMR:Q9LNW3 DIP:DIP-40200N IntAct:Q9LNW3 STRING:Q9LNW3 PRIDE:Q9LNW3 EnsemblPlants:AT1G07430.1 GeneID:837255 KEGG:ath:AT1G07430 TAIR:At1g07430 InParanoid:Q9LNW3 KO:K14497 OMA:ETSACES PhylomeDB:Q9LNW3 ProtClustDB:CLSN2682567 ArrayExpress:Q9LNW3 Genevestigator:Q9LNW3 Uniprot:Q9LNW3
Leaf	Isotig03239	21	2	3.921	8.06E-07	TAIR|locus:2025087 - symbol:HAI2 "highly ABA-induced PP2C gene 2" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004722 "protein serine/threonine phosphatase activity" evidence=IEA;ISS] [GO:0006470 "protein dephosphorylation" evidence=IEA] [GO:0008287 "protein serine/threonine phosphatase complex" evidence=IEA] InterPro:IPR000222 InterPro:IPR001932 Pfam:PF00481 PROSITE:PS01032 SMART:SM00331 SMART:SM00332 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005886 GO:GO:0006470 GO:GO:0004722 GO:GO:0046872 GO:GO:0005267 EMBL:AC022464 eggNOG:COG0631 Gene3D:G3DSA:3.60.40.10 SUPFAM:SSF81606 GO:GO:0008287 InterPro:IPR015655 PANTHER:PTHR13832 HSSP:P35813 HOGENOM:HBG747569 EMBL:AY070089 EMBL:AY091341 EMBL:AY084794 IPI:IPI00521891 PIR:B86209 RefSeq:NP_172223.1 UniGene:At.28399 ProteinModelPortal:Q9LNW3 SMR:Q9LNW3 DIP:DIP-40200N IntAct:Q9LNW3 STRING:Q9LNW3 PRIDE:Q9LNW3 EnsemblPlants:AT1G07430.1 GeneID:837255 KEGG:ath:AT1G07430 TAIR:At1g07430 InParanoid:Q9LNW3 KO:K14497 OMA:ETSACES PhylomeDB:Q9LNW3 ProtClustDB:CLSN2682567 ArrayExpress:Q9LNW3 Genevestigator:Q9LNW3 Uniprot:Q9LNW3
Leaf	Isotig03286	20	2	3.851	1.70E-06	TAIR|locus:2170867 - symbol:APS4 "AT5G43780" species:3702 "Arabidopsis thaliana" [GO:0004781 "sulfate adenylyltransferase (ATP) activity" evidence=ISS;IMP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0000103 "sulfate assimilation" evidence=TAS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] InterPro:IPR002650 GO:GO:0005739 GO:GO:0005524 GO:GO:0009570 EMBL:CP002688 EMBL:AB026651 GO:GO:0000103 InterPro:IPR014729 Gene3D:G3DSA:3.40.50.620 KO:K13811 ProtClustDB:CLSN2684174 GO:GO:0004781 InterPro:IPR015947 SUPFAM:SSF88697 TIGRFAMs:TIGR00339 EMBL:AF110407 EMBL:AJ012586 EMBL:AY072193 EMBL:AY117323 EMBL:AK226204 IPI:IPI00531868 PIR:T52659 RefSeq:NP_199191.1 UniGene:At.23710 UniGene:At.66691 ProteinModelPortal:Q9S7D8 SMR:Q9S7D8 STRING:Q9S7D8 PRIDE:Q9S7D8 GeneID:834400 KEGG:ath:AT5G43780 TAIR:At5g43780 InParanoid:Q9S7D8 OMA:GITPMFI PhylomeDB:Q9S7D8 ArrayExpress:Q9S7D8 Genevestigator:Q9S7D8 Uniprot:Q9S7D8
Leaf	Isotig03287	20	2	3.851	1.70E-06	TAIR|locus:2084563 - symbol:APS1 "AT3G22890" species:3702 "Arabidopsis thaliana" [GO:0001887 "selenium compound metabolic process" evidence=IMP] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0046686

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						"response to cadmium ion" evidence=IEP] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] [GO:0004781 "sulfate adenylyltransferase (ATP) activity" evidence=TAS] InterPro:IPR002650 GO:GO:0005886 GO:GO:0005524 GO:GO:0009570 GO:GO:0046686 EMBL:CP002686 EMBL:AP001300 GO:GO:0000103 InterPro:IPR014729 Gene3D:G3DSA:3.40.50.620 EMBL:U05218 EMBL:AF198964 EMBL:AF370492 EMBL:AY050869 EMBL:AY054169 EMBL:AY064648 EMBL:AY091207 EMBL:BT002538 EMBL:AK221133 EMBL:AK226559 EMBL:AY085975 EMBL:Z34534 IPI:IPI00518644 RefSeq:NP_188929.1 UniGene:At.19053 HSSP:P08536 ProteinModelPortal:Q9LIK9 SMR:Q9LIK9 STRING:Q9LIK9 PRIDE:Q9LIK9 ProMEX:Q9LIK9 GeneID:821861 KEGG:ath:AT3G22890 TAIR:At3g22890 InParanoid:Q9LIK9 KO:K13811 OMA:MRCYEIM PhylomeDB:Q9LIK9 ProtClustDB:CLSN2684174 ArrayExpress:Q9LIK9 Genevestigator:Q9LIK9 GO:GO:0004781 GO:GO:0001887 InterPro:IPR015947 SUPFAM:SSF88697 TIGRFAMs:TIGR00339 Uniprot:Q9LIK9
Leaf	Isotig03296	24	10	1.792	0.000490131	TAIR|locus:2160892 - symbol:AT5G47730 "AT5G47730" species:3702 "Arabidopsis thaliana" [GO:0005215 "transporter activity" evidence=ISS] [GO:0006810 "transport" evidence=ISS] Pfam:PF03765 EMBL:CP002688 GenomeReviews:BA000015_GR EMBL:AB016886 InterPro:IPR001251 Gene3D:G3DSA:3.40.525.10 SUPFAM:SSF52087 PROSITE:PS50191 SMART:SM00516 InterPro:IPR011074 Gene3D:G3DSA:1.10.8.20 Pfam:PF00650 SMART:SM01100 SUPFAM:SSF46938 UniGene:At.49141 UniGene:At.9393 ProtClustDB:CLSN2682676 EMBL:BT033019 IPI:IPI00529698 RefSeq:NP_199584.1 ProteinModelPortal:Q9FIK6 SMR:Q9FIK6 STRING:Q9FIK6 PRIDE:Q9FIK6 EnsemblPlants:AT5G47730.1 GeneID:834824 KEGG:ath:AT5G47730 TAIR:At5g47730 HOGENOM:HBG316946 InParanoid:Q9FIK6 OMA:PEKTNTY PhylomeDB:Q9FIK6 Genevestigator:Q9FIK6 Uniprot:Q9FIK6
Leaf	Isotig03297	24	10	1.792	0.000490131	TAIR|locus:2160892 - symbol:AT5G47730 "AT5G47730" species:3702 "Arabidopsis thaliana" [GO:0005215 "transporter activity" evidence=ISS] [GO:0006810 "transport" evidence=ISS] Pfam:PF03765 EMBL:CP002688 GenomeReviews:BA000015_GR EMBL:AB016886 InterPro:IPR001251 Gene3D:G3DSA:3.40.525.10 SUPFAM:SSF52087 PROSITE:PS50191 SMART:SM00516 InterPro:IPR011074 Gene3D:G3DSA:1.10.8.20 Pfam:PF00650 SMART:SM01100 SUPFAM:SSF46938 UniGene:At.49141 UniGene:At.9393 ProtClustDB:CLSN2682676 EMBL:BT033019 IPI:IPI00529698 RefSeq:NP_199584.1 ProteinModelPortal:Q9FIK6 SMR:Q9FIK6 STRING:Q9FIK6 PRIDE:Q9FIK6 EnsemblPlants:AT5G47730.1 GeneID:834824 KEGG:ath:AT5G47730 TAIR:At5g47730 HOGENOM:HBG316946 InParanoid:Q9FIK6 OMA:PEKTNTY PhylomeDB:Q9FIK6 Genevestigator:Q9FIK6 Uniprot:Q9FIK6
Leaf	Isotig03304	13	2	3.229	0.00031313	TAIR|locus:2090487 - symbol:CRSH "AT3G17470" species:3702 "Arabidopsis thaliana" [GO:0005509 "calcium ion binding" evidence=ISS] [GO:0015969 "guanosine tetraphosphate metabolic process" evidence=IEA] [GO:0008728 "GTP diphosphokinase activity" evidence=IGI] [GO:0009507 "chloroplast" evidence=IDA] InterPro:IPR002048 InterPro:IPR004811 InterPro:IPR007685 InterPro:IPR011992 Pfam:PF04607 SMART:SM00054 SMART:SM00954 Prosite:PS00018 GO:GO:0009507 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005509 InterPro:IPR018247 InterPro:IPR018249 Gene3D:G3DSA:1.10.238.10 PROSITE:PS50222 HSSP:P09860 eggNOG:COG0317 GO:GO:0015969 PANTHER:PTHR21262 GO:GO:0008728 EMBL:BT006180 EMBL:AK228656 IPI:IPI00528710 RefSeq:NP_188374.2 UniGene:At.38719 ProteinModelPortal:Q84R11 SMR:Q84R11 PRIDE:Q84R11 EnsemblPlants:AT3G17470.1 GeneID:821012 KEGG:ath:AT3G17470 TAIR:At3g17470 HOGENOM:HBG597952 InParanoid:Q84R11 OMA:RYKSRYS PhylomeDB:Q84R11 ProtClustDB:CLSN2679918 ArrayExpress:Q84R11 Genevestigator:Q84R11 Uniprot:Q84R11
Leaf	Isotig03305	12	2	3.114	0.000658121	TAIR|locus:2090487 - symbol:CRSH "AT3G17470" species:3702 "Arabidopsis thaliana" [GO:0005509 "calcium ion binding" evidence=ISS] [GO:0015969 "guanosine tetraphosphate metabolic process" evidence=IEA] [GO:0008728 "GTP diphosphokinase activity" evidence=IGI] [GO:0009507 "chloroplast" evidence=IDA] InterPro:IPR002048 InterPro:IPR004811 InterPro:IPR007685 InterPro:IPR011992 Pfam:PF04607 SMART:SM00054 SMART:SM00954 Prosite:PS00018 GO:GO:0009507 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005509 InterPro:IPR018247 InterPro:IPR018249 Gene3D:G3DSA:1.10.238.10 PROSITE:PS50222 HSSP:P09860 eggNOG:COG0317 GO:GO:0015969 PANTHER:PTHR21262 GO:GO:0008728 EMBL:BT006180 EMBL:AK228656 IPI:IPI00528710 RefSeq:NP_188374.2 UniGene:At.38719 ProteinModelPortal:Q84R11 SMR:Q84R11 PRIDE:Q84R11 EnsemblPlants:AT3G17470.1 GeneID:821012 KEGG:ath:AT3G17470 TAIR:At3g17470 HOGENOM:HBG597952 InParanoid:Q84R11 OMA:RYKSRYS PhylomeDB:Q84R11 ProtClustDB:CLSN2679918 ArrayExpress:Q84R11 Genevestigator:Q84R11 Uniprot:Q84R11

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig03312	12	71	-2.036	5.44E-08	TAIR|locus:2102842 - symbol:PTAC16 "plastid transcriptionally active 16" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009295 "nucleoid" evidence=IDA] [GO:0009508 "plastid chromosome" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0007623 "circadian rhythm" evidence=IEP] InterPro:IPR016040 InterPro:IPR008030 EMBL:CP002686 GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 GO:GO:0007623 GO:GO:0009941 GO:GO:0009535 EMBL:AL096859 UniGene:At.21811 Pfam:PF05368 GO:GO:0009508 IPI:IPI00542797 PIR:T12970 RefSeq:NP_566886.2 UniGene:At.21714 UniGene:At.71100 UniGene:At.71553 ProteinModelPortal:Q9STF2 SMR:Q9STF2 IntAct:Q9STF2 STRING:Q9STF2 PRIDE:Q9STF2 ProMEX:Q9STF2 EnsemblPlants:AT3G46780.1 GeneID:823831 KEGG:ath:AT3G46780 TAIR:At3g46780 InParanoid:Q9STF2 OMA:FKQETIY PhylomeDB:Q9STF2 ProtClustDB:CLSN2680891 Genevestigator:Q9STF2 Uniprot:Q9STF2
Leaf	Isotig03313	11	71	-2.161	1.63E-08	TAIR|locus:2102842 - symbol:PTAC16 "plastid transcriptionally active 16" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009295 "nucleoid" evidence=IDA] [GO:0009508 "plastid chromosome" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0007623 "circadian rhythm" evidence=IEP] InterPro:IPR016040 InterPro:IPR008030 EMBL:CP002686 GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 GO:GO:0007623 GO:GO:0009941 GO:GO:0009535 EMBL:AL096859 UniGene:At.21811 Pfam:PF05368 GO:GO:0009508 IPI:IPI00542797 PIR:T12970 RefSeq:NP_566886.2 UniGene:At.21714 UniGene:At.71100 UniGene:At.71553 ProteinModelPortal:Q9STF2 SMR:Q9STF2 IntAct:Q9STF2 STRING:Q9STF2 PRIDE:Q9STF2 ProMEX:Q9STF2 EnsemblPlants:AT3G46780.1 GeneID:823831 KEGG:ath:AT3G46780 TAIR:At3g46780 InParanoid:Q9STF2 OMA:FKQETIY PhylomeDB:Q9STF2 ProtClustDB:CLSN2680891 Genevestigator:Q9STF2 Uniprot:Q9STF2
Leaf	Isotig03314	29	0	6.387	7.28E-10	TAIR|locus:2128141 - symbol:AT4G31240 "AT4G31240" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0016209 "antioxidant activity" evidence=IEA] [GO:0016491 "oxidoreductase activity" evidence=IEA] [GO:0045454 "cell redox homeostasis" evidence=IEA] InterPro:IPR011424 Pfam:PF07649 PROSITE:PS00194 EMBL:CP002687 GenomeReviews:CT486007_GR InterPro:IPR012336 Gene3D:G3DSA:3.40.30.10 SUPFAM:SSF52833 PROSITE:PS51352 EMBL:AL161578 GO:GO:0047134 EMBL:AL021633 EMBL:AY063945 EMBL:AY096637 IPI:IPI00539142 PIR:T04491 RefSeq:NP_567869.1 RefSeq:NP_974651.1 UniGene:At.27135 HSSP:O77093 ProteinModelPortal:Q8VZQ0 SMR:Q8VZQ0 PRIDE:Q8VZQ0 EnsemblPlants:AT4G31240.1 EnsemblPlants:AT4G31240.2 GeneID:829251 KEGG:ath:AT4G31240 TAIR:At4g31240 eggNOG:NOG273116 InParanoid:Q8VZQ0 OMA:LAIPYED PhylomeDB:Q8VZQ0 ProtClustDB:CLSN2917640 Genevestigator:Q8VZQ0 Uniprot:Q8VZQ0
Leaf	Isotig03315	29	0	6.387	7.28E-10	TAIR|locus:2195623 - symbol:AT1G60420 species:3702 "Arabidopsis thaliana" [GO:0016209 "antioxidant activity" evidence=IEA] [GO:0016491 "oxidoreductase activity" evidence=IEA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0009860 "pollen tube growth" evidence=IMP] [GO:0010183 "pollen tube guidance" evidence=IMP] [GO:0080092 "regulation of pollen tube growth" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR011424 InterPro:IPR017937 Pfam:PF07649 PROSITE:PS00194 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0046686 GO:GO:0009860 InterPro:IPR012336 Gene3D:G3DSA:3.40.30.10 SUPFAM:SSF52833 GO:GO:0045454 PROSITE:PS51352 GO:GO:0080092 GO:GO:0010183 eggNOG:COG0526 GO:GO:0047134 EMBL:AC004473 EMBL:AY065433 EMBL:AY117231 EMBL:AY087396 IPI:IPI00537432 PIR:T02292 RefSeq:NP_564756.1 UniGene:At.10685 UniGene:At.64112 PDB:1V5N PDBsum:1V5N ProteinModelPortal:O80763 SMR:O80763 IntAct:O80763 PRIDE:O80763 EnsemblPlants:AT1G60420.1 GeneID:842337 KEGG:ath:AT1G60420 TAIR:At1g60420 HOGENOM:HBG594354 InParanoid:O80763 OMA:QMPWLAL PhylomeDB:O80763 ProtClustDB:CLSN2917334 ArrayExpress:O80763 Genevestigator:O80763 Uniprot:O80763
Leaf	Isotig03316	65	23	2.028	4.60E-10	TAIR|locus:2088490 - symbol:AT3G17800 "AT3G17800" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0010224 "response to UV-B" evidence=IGI;IEP] EMBL:CP002686 GO:GO:0010224 EMBL:AB019230 UniGene:At.22111 UniGene:At.71032 UniGene:At.74878 UniGene:At.74926 InterPro:IPR008479 Pfam:PF05542 ProtClustDB:CLSN2688500 EMBL:AY099554 IPI:IPI00542573 RefSeq:NP_566588.1 STRING:Q9LVJ0 PRIDE:Q9LVJ0 EnsemblPlants:AT3G17800.1 GeneID:821048

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						KEGG:ath:AT3G17800 TAIR:At3g17800 InParanoid:Q9LVJ0 OMA:RSYVMSF PhylomeDB:Q9LVJ0 Genevestigator:Q9LVJ0 Uniprot:Q9LVJ0
Leaf	Isotig03317	64	24	1.944	1.80E-09	TAIR|locus:2088490 - symbol:AT3G17800 "AT3G17800" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0010224 "response to UV-B" evidence=IGI;IEP] EMBL:CP002686 GO:GO:0010224 EMBL:AB019230 UniGene:At.22111 UniGene:At.71032 UniGene:At.74878 UniGene:At.74926 InterPro:IPR008479 Pfam:PF05542 ProtClustDB:CLSN2688500 EMBL:AY099554 IPI:IPI00542573 RefSeq:NP_566588.1 STRING:Q9LVJ0 PRIDE:Q9LVJ0 EnsemblPlants:AT3G17800.1 GeneID:821048 KEGG:ath:AT3G17800 TAIR:At3g17800 InParanoid:Q9LVJ0 OMA:RSYVMSF PhylomeDB:Q9LVJ0 Genevestigator:Q9LVJ0 Uniprot:Q9LVJ0
Leaf	Isotig03324	17	3	3.031	6.23E-05	TAIR|locus:2161258 - symbol:RPT3 "AT5G58290" species:3702 "Arabidopsis thaliana" [GO:0016887 "ATPase activity" evidence=IGI;ISS] [GO:0006511 "ubiquitin-dependent protein catabolic process" evidence=TAS] [GO:0005634 "nucleus" evidence=TAS] [GO:0005618 "cell wall" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0000502 "proteasome complex" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0008540 "proteasome regulatory particle, base subcomplex" evidence=IDA] InterPro:IPR003593 InterPro:IPR003959 InterPro:IPR003960 InterPro:IPR005937 Pfam:PF00004 PROSITE:PS00674 SMART:SM00382 GO:GO:0005829 GO:GO:0009506 GO:GO:0005524 GO:GO:0005634 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005618 GO:GO:0016020 EMBL:AB019228 GO:GO:0030163 GO:GO:0000502 GO:GO:0017111 HOGENOM:HBG724153 eggNOG:COG1222 TIGRFAMs:TIGR01242 EMBL:AF123392 EMBL:AY070466 EMBL:BT020373 IPI:IPI00537564 RefSeq:NP_200637.1 UniGene:At.45955 ProteinModelPortal:Q9SEI4 SMR:Q9SEI4 IntAct:Q9SEI4 STRING:Q9SEI4 PRIDE:Q9SEI4 EnsemblPlants:AT5G58290.1 GeneID:835941 KEGG:ath:AT5G58290 GeneFarm:1500 TAIR:At5g58290 InParanoid:Q9SEI4 KO:K03063 OMA:DQTTNVK PhylomeDB:Q9SEI4 ProtClustDB:CLSN2686094 ArrayExpress:Q9SEI4 Genevestigator:Q9SEI4 GermOnline:AT5G58290 Uniprot:Q9SEI4
Leaf	Isotig03325	16	3	2.944	0.000128177	TAIR|locus:2161258 - symbol:RPT3 "AT5G58290" species:3702 "Arabidopsis thaliana" [GO:0016887 "ATPase activity" evidence=IGI;ISS] [GO:0006511 "ubiquitin-dependent protein catabolic process" evidence=TAS] [GO:0005634 "nucleus" evidence=TAS] [GO:0005618 "cell wall" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0000502 "proteasome complex" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0008540 "proteasome regulatory particle, base subcomplex" evidence=IDA] InterPro:IPR003593 InterPro:IPR003959 InterPro:IPR003960 InterPro:IPR005937 Pfam:PF00004 PROSITE:PS00674 SMART:SM00382 GO:GO:0005829 GO:GO:0009506 GO:GO:0005524 GO:GO:0005634 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005618 GO:GO:0016020 EMBL:AB019228 GO:GO:0030163 GO:GO:0000502 GO:GO:0017111 HOGENOM:HBG724153 eggNOG:COG1222 TIGRFAMs:TIGR01242 EMBL:AF123392 EMBL:AY070466 EMBL:BT020373 IPI:IPI00537564 RefSeq:NP_200637.1 UniGene:At.45955 ProteinModelPortal:Q9SEI4 SMR:Q9SEI4 IntAct:Q9SEI4 STRING:Q9SEI4 PRIDE:Q9SEI4 EnsemblPlants:AT5G58290.1 GeneID:835941 KEGG:ath:AT5G58290 GeneFarm:1500 TAIR:At5g58290 InParanoid:Q9SEI4 KO:K03063 OMA:DQTTNVK PhylomeDB:Q9SEI4 ProtClustDB:CLSN2686094 ArrayExpress:Q9SEI4 Genevestigator:Q9SEI4 GermOnline:AT5G58290 Uniprot:Q9SEI4
Leaf	Isotig03326	34	9	2.446	4.25E-07	TAIR|locus:2175118 - symbol:AT5G60390 "AT5G60390" species:3702 "Arabidopsis thaliana" [GO:0003746 "translation elongation factor activity" evidence=ISS] [GO:0006414 "translational elongation" evidence=IEA] [GO:0005516 "calmodulin binding" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] PROSITE:PS00301 EMBL:CP002684 EMBL:U63815 EMBL:AC026875 EMBL:X16430 EMBL:AY039583 EMBL:BT000595 IPI:IPI00548618 PIR:S06724 UniGene:At.69737 UniGene:At.74830 EnsemblPlants:AT1G07940.1 EnsemblPlants:AT1G07940.2 TAIR:At1g07940 OMA:FLKAGDA GermOnline:AT1G07940 Uniprot:P0DH99
Leaf	Isotig03327	34	9	2.446	4.25E-07	TAIR|locus:2175118 - symbol:AT5G60390 "AT5G60390" species:3702 "Arabidopsis thaliana" [GO:0003746 "translation elongation factor activity" evidence=ISS] [GO:0006414 "translational elongation" evidence=IEA] [GO:0005516 "calmodulin binding" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] PROSITE:PS00301 EMBL:CP002684

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EMBL:U63815 EMBL:AC026875 EMBL:X16430 EMBL:AY039583 EMBL:BT000595 IPI:IPI00548618 PIR:S06724 UniGene:At.69737 UniGene:At.74830 EnsemblPlants:AT1G07940.1 EnsemblPlants:AT1G07940.2 TAIR:At1g07940 OMA:FLKAGDA GermOnline:AT1G07940 Uniprot:P0DH99
Leaf	Isotig03332	2	28	-3.278	9.31E-06	TAIR|locus:2087901 - symbol:Tic62 "translocon at the inner envelope membrane of chloroplasts 62" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0008152 "metabolic process" evidence=IEA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] InterPro:IPR016040 GO:GO:0009570 EMBL:CP002686 GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 GO:GO:0015031 GO:GO:0009706 GO:GO:0009535 eggNOG:COG0702 EMBL:AP002039 EMBL:BT002039 EMBL:BT008403 IPI:IPI00530638 RefSeq:NP_188519.2 UniGene:At.27605 ProteinModelPortal:Q8H0U5 SMR:Q8H0U5 STRING:Q8H0U5 PRIDE:Q8H0U5 EnsemblPlants:AT3G18890.1 GeneID:821422 KEGG:ath:AT3G18890 TAIR:At3g18890 InParanoid:Q8H0U5 OMA:CCIGASE PhylomeDB:Q8H0U5 ProtClustDB:PLN03209 ArrayExpress:Q8H0U5 Genevestigator:Q8H0U5 Uniprot:Q8H0U5
Leaf	Isotig03333	1	22	-3.930	2.59E-05	TAIR|locus:2087901 - symbol:Tic62 "translocon at the inner envelope membrane of chloroplasts 62" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0008152 "metabolic process" evidence=IEA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] InterPro:IPR016040 GO:GO:0009570 EMBL:CP002686 GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 GO:GO:0015031 GO:GO:0009706 GO:GO:0009535 eggNOG:COG0702 EMBL:AP002039 EMBL:BT002039 EMBL:BT008403 IPI:IPI00530638 RefSeq:NP_188519.2 UniGene:At.27605 ProteinModelPortal:Q8H0U5 SMR:Q8H0U5 STRING:Q8H0U5 PRIDE:Q8H0U5 EnsemblPlants:AT3G18890.1 GeneID:821422 KEGG:ath:AT3G18890 TAIR:At3g18890 InParanoid:Q8H0U5 OMA:CCIGASE PhylomeDB:Q8H0U5 ProtClustDB:PLN03209 ArrayExpress:Q8H0U5 Genevestigator:Q8H0U5 Uniprot:Q8H0U5
Leaf	Isotig03340	55	17	2.223	1.24E-09	TAIR|locus:2009759 - symbol:cICDH "AT1G65930" species:3702 "Arabidopsis thaliana" [GO:0004450 "isocitrate dehydrogenase (NADP+) activity" evidence=ISS;IMP] [GO:0008152 "metabolic process" evidence=ISS] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0048046 "apoplast" evidence=IDA] [GO:0010043 "response to zinc ion" evidence=IEP] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA;NAS] [GO:0006102 "isocitrate metabolic process" evidence=IMP] [GO:0006739 "NADP metabolic process" evidence=IMP] [GO:0042742 "defense response to bacterium" evidence=IMP] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR004790 InterPro:IPR019818 InterPro:IPR024084 Pfam:PF00180 PIRSF:PIRSF000108 PROSITE:PS00470 EMBL:CP002684 GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 GO:GO:0048046 GO:GO:0009570 GO:GO:0046686 GO:GO:0042742 GO:GO:0051287 GO:GO:0010043 GO:GO:0000287 EMBL:AC009513 GO:GO:0005507 GO:GO:0009651 GO:GO:0006099 GO:GO:0006102 Gene3D:G3DSA:3.40.718.10 KO:K00031 GO:GO:0004450 PANTHER:PTHR11822 TIGRFAMs:TIGR00127 OMA:TPDEARM GO:GO:0006739 HSSP:P33198 ProtClustDB:PLN00103 EMBL:AY045631 EMBL:AF419575 EMBL:AY097340 EMBL:BT002400 IPI:IPI00539206 PIR:F96683 RefSeq:NP_176768.1 UniGene:At.24713 ProteinModelPortal:Q9SRZ6 SMR:Q9SRZ6 IntAct:Q9SRZ6 STRING:Q9SRZ6 PRIDE:Q9SRZ6 EnsemblPlants:AT1G65930.1 GeneID:842905 KEGG:ath:AT1G65930 TAIR:At1g65930 InParanoid:Q9SRZ6 PhylomeDB:Q9SRZ6 Genevestigator:Q9SRZ6 Uniprot:Q9SRZ6
Leaf	Isotig03341	50	17	2.085	2.62E-08	TAIR|locus:2009759 - symbol:cICDH "AT1G65930" species:3702 "Arabidopsis thaliana" [GO:0004450 "isocitrate dehydrogenase (NADP+) activity" evidence=ISS;IMP] [GO:0008152 "metabolic process" evidence=ISS] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0048046 "apoplast" evidence=IDA] [GO:0010043 "response to zinc ion" evidence=IEP] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA;NAS] [GO:0006102 "isocitrate metabolic process" evidence=IMP] [GO:0006739 "NADP metabolic process" evidence=IMP] [GO:0042742 "defense response to bacterium" evidence=IMP] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR004790 InterPro:IPR019818 InterPro:IPR024084 Pfam:PF00180 PIRSF:PIRSF000108 PROSITE:PS00470 EMBL:CP002684 GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 GO:GO:0048046 GO:GO:0009570 GO:GO:0046686 GO:GO:0042742 GO:GO:0051287 GO:GO:0010043 GO:GO:0000287 EMBL:AC009513 GO:GO:0005507 GO:GO:0009651 GO:GO:0006099 GO:GO:0006102 Gene3D:G3DSA:3.40.718.10 KO:K00031 GO:GO:0004450

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						PANTHER:PTHR11822 TIGRFAMs:TIGR00127 OMA:TPDEARM GO:GO:0006739 HSSP:P33198 ProtClustDB:PLN00103 EMBL:AY045631 EMBL:AF419575 EMBL:AY097340 EMBL:BT002400 IPI:IPI00539206 PIR:F96683 RefSeq:NP_176768.1 UniGene:At.24713 ProteinModelPortal:Q9SRZ6 SMR:Q9SRZ6 IntAct:Q9SRZ6 STRING:Q9SRZ6 PRIDE:Q9SRZ6 EnsemblPlants:AT1G65930.1 GeneID:842905 KEGG:ath:AT1G65930 TAIR:At1g65930 InParanoid:Q9SRZ6 PhylomeDB:Q9SRZ6 Genevestigator:Q9SRZ6 Uniprot:Q9SRZ6
Leaf	Isotig03358	11	49	-1.626	0.000107459	UNIPROTKB|P93508 - symbol:P93508 "Calreticulin" species:3988 "Ricinus communis" [GO:0005788 "endoplasmic reticulum lumen" evidence=IDA] InterPro:IPR001580 InterPro:IPR009033 InterPro:IPR009169 InterPro:IPR018124 Pfam:PF00262 PIRSF:PIRSF002356 PRINTS:PR00626 PROSITE:PS00803 PROSITE:PS00804 PROSITE:PS00805 GO:GO:0005509 GO:GO:0006457 GO:GO:0005529 GO:GO:0051082 InterPro:IPR008985 InterPro:IPR013320 Gene3D:G3DSA:2.60.120.200 SUPFAM:SSF49899 GO:GO:0005788 PROSITE:PS00014 PANTHER:PTHR11073 SUPFAM:SSF63887 KO:K08057 EMBL:U74631 EMBL:U74630 PIR:T10172 RefSeq:XP_002512501.1 ProteinModelPortal:P93508 SMR:P93508 GeneID:8269812 KEGG:rcu:RCOM_1434770 PhylomeDB:P93508 ProtClustDB:CLSN2719690 Uniprot:P93508
Leaf	Isotig03359	11	48	-1.597	0.000155132	UNIPROTKB|P93508 - symbol:P93508 "Calreticulin" species:3988 "Ricinus communis" [GO:0005788 "endoplasmic reticulum lumen" evidence=IDA] InterPro:IPR001580 InterPro:IPR009033 InterPro:IPR009169 InterPro:IPR018124 Pfam:PF00262 PIRSF:PIRSF002356 PRINTS:PR00626 PROSITE:PS00803 PROSITE:PS00804 PROSITE:PS00805 GO:GO:0005509 GO:GO:0006457 GO:GO:0005529 GO:GO:0051082 InterPro:IPR008985 InterPro:IPR013320 Gene3D:G3DSA:2.60.120.200 SUPFAM:SSF49899 GO:GO:0005788 PROSITE:PS00014 PANTHER:PTHR11073 SUPFAM:SSF63887 KO:K08057 EMBL:U74631 EMBL:U74630 PIR:T10172 RefSeq:XP_002512501.1 ProteinModelPortal:P93508 SMR:P93508 GeneID:8269812 KEGG:rcu:RCOM_1434770 PhylomeDB:P93508 ProtClustDB:CLSN2719690 Uniprot:P93508
Leaf	Isotig03362	14	2	3.336	0.000148753	TAIR|locus:2178128 - symbol:ACT7 "AT5G09810" species:3702 "Arabidopsis thaliana" [GO:0007010 "cytoskeleton organization" evidence=TAS] [GO:0009733 "response to auxin stimulus" evidence=IEP] [GO:0009845 "seed germination" evidence=IMP] [GO:0048364 "root development" evidence=IMP] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0010053 "root epidermal cell differentiation" evidence=IMP] [GO:0048767 "root hair elongation" evidence=IMP] [GO:0051301 "cell division" evidence=IMP] [GO:0005515 "protein binding" evidence=IPI] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005200 "structural constituent of cytoskeleton" evidence=ISS] [GO:0005856 "cytoskeleton" evidence=ISS] [GO:0009416 "response to light stimulus" evidence=IEP] [GO:0009611 "response to wounding" evidence=IEP] InterPro:IPR004001 PROSITE:PS00406 PROSITE:PS00432 InterPro:IPR004000 GO:GO:0005829 GO:GO:0005739 GO:GO:0005886 GO:GO:0009506 GO:GO:0005524 GO:GO:0009570 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005618 GO:GO:0005515 GO:GO:0009733 GO:GO:0009611 GO:GO:0005730 GO:GO:0005856 GO:GO:0051301 GO:GO:0009941 EMBL:AB016893 GO:GO:0048767 GO:GO:0009845 GO:GO:0009416 HOGENOM:HBG559892 PANTHER:PTHR11937 Pfam:PF00022 PRINTS:PR00190 SMART:SM00268 KO:K10355 InterPro:IPR020902 PROSITE:PS01132 ProtClustDB:CLSN2682469 UniGene:At.23346 EMBL:U37281 EMBL:U27811 EMBL:AY062702 EMBL:AY063980 EMBL:AY096397 EMBL:AY114679 EMBL:AY120779 IPI:IPI00524611 PIR:S68107 RefSeq:NP_196543.1 UniGene:At.23605 UniGene:At.24396 ProteinModelPortal:P53492 SMR:P53492 IntAct:P53492 STRING:P53492 PRIDE:P53492 ProMEX:P53492 EnsemblPlants:AT5G09810.1 GeneID:830841 KEGG:ath:AT5G09810 TAIR:At5g09810 InParanoid:P53492 OMA:NSICVIL PhylomeDB:P53492 ArrayExpress:P53492 Genevestigator:P53492 GermOnline:AT5G09810 Uniprot:P53492
Leaf	Isotig03363	14	1	4.336	3.39E-05	TAIR|locus:2178128 - symbol:ACT7 "AT5G09810" species:3702 "Arabidopsis thaliana" [GO:0007010 "cytoskeleton organization" evidence=TAS] [GO:0009733 "response to auxin stimulus" evidence=IEP] [GO:0009845 "seed germination" evidence=IMP] [GO:0048364 "root development" evidence=IMP] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0010053 "root epidermal cell differentiation" evidence=IMP] [GO:0048767 "root hair elongation" evidence=IMP] [GO:0051301 "cell division" evidence=IMP] [GO:0005515 "protein binding" evidence=IPI] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005200 "structural constituent of cytoskeleton" evidence=ISS] [GO:0005856 "cytoskeleton" evidence=ISS] [GO:0009416 "response to

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						light stimulus" evidence=IEP] [GO:0009611 "response to wounding" evidence=IEP] InterPro:IPR004001 PROSITE:PS00406 PROSITE:PS00432 InterPro:IPR004000 GO:GO:0005829 GO:GO:0005739 GO:GO:0005886 GO:GO:0009506 GO:GO:0005524 GO:GO:0009570 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005618 GO:GO:0005515 GO:GO:0009733 GO:GO:0009611 GO:GO:0005730 GO:GO:0005856 GO:GO:0051301 GO:GO:0009941 EMBL:AB016893 GO:GO:0048767 GO:GO:0009845 GO:GO:0009416 HOGENOM:HBG559892 PANTHER:PTHR11937 Pfam:PF00022 PRINTS:PR00190 SMART:SM00268 KO:K10355 InterPro:IPR020902 PROSITE:PS01132 ProtClustDB:CLSN2682469 UniGene:At.23346 EMBL:U37281 EMBL:U27811 EMBL:AY062702 EMBL:AY063980 EMBL:AY096397 EMBL:AY114679 EMBL:AY120779 IPI:IPI00524611 PIR:S68107 RefSeq:NP_196543.1 UniGene:At.23605 UniGene:At.24396 ProteinModelPortal:P53492 SMR:P53492 IntAct:P53492 STRING:P53492 PRIDE:P53492 ProMEX:P53492 EnsemblPlants:AT5G09810.1 GeneID:830841 KEGG:ath:AT5G09810 TAIR:At5g09810 InParanoid:P53492 OMA:NSICVIL PhylomeDB:P53492 ArrayExpress:P53492 Genevestigator:P53492 GermOnline:AT5G09810 Uniprot:P53492
Leaf	Isotig03368	6	36	-2.056	9.79E-05	TAIR|locus:2031745 - symbol:LrgB "AT1G32080" species:3702 "Arabidopsis thaliana" [GO:0009706 "chloroplast inner membrane" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009658 "chloroplast organization" evidence=IMP] Pfam:PF04172 EMBL:CP002684 GO:GO:0009658 GO:GO:0009706 EMBL:AC084165 EMBL:AC074309 InterPro:IPR007300 EMBL:AY039880 EMBL:AY101515 IPI:IPI00523302 PIR:B86445 RefSeq:NP_564388.1 UniGene:At.16834 STRING:Q9FVQ4 PRIDE:Q9FVQ4 EnsemblPlants:AT1G32080.1 GeneID:840100 KEGG:ath:AT1G32080 TAIR:At1g32080 InParanoid:Q9FVQ4 OMA:PRCITVA PhylomeDB:Q9FVQ4 ProtClustDB:CLSN2688178 Genevestigator:Q9FVQ4 Uniprot:Q9FVQ4
Leaf	Isotig03369	7	33	-1.708	0.000997415	TAIR|locus:2031745 - symbol:LrgB "AT1G32080" species:3702 "Arabidopsis thaliana" [GO:0009706 "chloroplast inner membrane" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009658 "chloroplast organization" evidence=IMP] Pfam:PF04172 EMBL:CP002684 GO:GO:0009658 GO:GO:0009706 EMBL:AC084165 EMBL:AC074309 InterPro:IPR007300 EMBL:AY039880 EMBL:AY101515 IPI:IPI00523302 PIR:B86445 RefSeq:NP_564388.1 UniGene:At.16834 STRING:Q9FVQ4 PRIDE:Q9FVQ4 EnsemblPlants:AT1G32080.1 GeneID:840100 KEGG:ath:AT1G32080 TAIR:At1g32080 InParanoid:Q9FVQ4 OMA:PRCITVA PhylomeDB:Q9FVQ4 ProtClustDB:CLSN2688178 Genevestigator:Q9FVQ4 Uniprot:Q9FVQ4
Leaf	Isotig03390	4	26	-2.171	0.000609459	TAIR|locus:2124998 - symbol:TROL "thylakoid rhodanese-like" species:3702 "Arabidopsis thaliana" [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0042742 "defense response to bacterium" evidence=IEP] [GO:0005515 "protein binding" evidence=IPI] [GO:0009772 "photosynthetic electron transport in photosystem II" evidence=IMP] [GO:0009534 "chloroplast thylakoid" evidence=IDA] EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0042742 GO:GO:0005515 GO:GO:0009941 GO:GO:0009535 InterPro:IPR001763 Gene3D:G3DSA:3.40.250.10 SUPFAM:SSF52821 PROSITE:PS50206 GO:GO:0009772 EMBL:AL161491 EMBL:AF007269 EMBL:AY057701 EMBL:AY057565 EMBL:AY124870 IPI:IPI00522460 PIR:H85013 PIR:T01733 RefSeq:NP_567209.1 UniGene:At.22549 UniGene:At.70023 UniGene:At.75032 PDB:1VEE PDB:2DCQ PDBsum:1VEE PDBsum:2DCQ ProteinModelPortal:Q9M158 SMR:Q9M158 STRING:Q9M158 PRIDE:Q9M158 ProMEX:Q9M158 EnsemblPlants:AT4G01050.1 GeneID:827921 KEGG:ath:AT4G01050 TAIR:At4g01050 eggNOG:NOG274043 HOGENOM:HBG592226 InParanoid:Q9M158 OMA:LAYTEIE PhylomeDB:Q9M158 ProtClustDB:CLSN2689270 ArrayExpress:Q9M158 Genevestigator:Q9M158 GermOnline:AT4G01050 Uniprot:Q9M158
Leaf	Isotig03391	1	22	-3.930	2.59E-05	TAIR|locus:2124998 - symbol:TROL "thylakoid rhodanese-like" species:3702 "Arabidopsis thaliana" [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0042742 "defense response to bacterium" evidence=IEP] [GO:0005515 "protein binding" evidence=IPI] [GO:0009772 "photosynthetic electron transport in photosystem II" evidence=IMP] [GO:0009534 "chloroplast thylakoid" evidence=IDA] EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0042742 GO:GO:0005515 GO:GO:0009941 GO:GO:0009535 InterPro:IPR001763 Gene3D:G3DSA:3.40.250.10 SUPFAM:SSF52821 PROSITE:PS50206 GO:GO:0009772 EMBL:AL161491 EMBL:AF007269 EMBL:AY057701 EMBL:AY057565 EMBL:AY124870 IPI:IPI00522460 PIR:H85013 PIR:T01733 RefSeq:NP_567209.1 UniGene:At.22549 UniGene:At.70023 UniGene:At.75032 PDB:1VEE PDB:2DCQ

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						PDBsum:1VEE PDBsum:2DCQ ProteinModelPortal:Q9M158 SMR:Q9M158 STRING:Q9M158 PRIDE:Q9M158 ProMEX:Q9M158 EnsemblPlants:AT4G01050.1 GeneID:827921 KEGG:ath:AT4G01050 TAIR:At4g01050 eggNOG:NOG274043 HOGENOM:HBG592226 InParanoid:Q9M158 OMA:LAYTEIE PhylomeDB:Q9M158 ProtClustDB:CLSN2689270 ArrayExpress:Q9M158 Genevestigator:Q9M158 GermOnline:AT4G01050 Uniprot:Q9M158
Leaf	Isotig03392	83	17	2.817	1.44E-17	TAIR|locus:2123782 - symbol:GAMMA-VPE "AT4G32940" species:3702 "Arabidopsis thaliana" [GO:0004197 "cysteine-type endopeptidase activity" evidence=ISS;IDA] [GO:0006508 "proteolysis" evidence=ISS] [GO:0000323 "lytic vacuole" evidence=IDA] [GO:0006624 "vacuolar protein processing" evidence=ISS] InterPro:IPR001096 Pfam:PF01650 PIRSF:PIRSF019663 PRINTS:PR00776 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0004197 GO:GO:0006508 EMBL:AL031804 EMBL:AL161582 eggNOG:COG5206 PANTHER:PTHR12000 KO:K01369 HOGENOM:HBG318720 GO:GO:0000323 ProtClustDB:CLSN2682340 EMBL:D61395 EMBL:AF370160 EMBL:AF424619 EMBL:AY059104 EMBL:AY133531 IPI:IPI00537536 PIR:T05302 RefSeq:NP_195020.1 UniGene:At.21567 UniGene:At.48929 UniGene:At.75206 ProteinModelPortal:Q39119 STRING:Q39119 MEROPS:C13.006 PRIDE:Q39119 EnsemblPlants:AT4G32940.1 GeneID:829431 KEGG:ath:AT4G32940 TAIR:At4g32940 InParanoid:Q39119 OMA:ICHAYQL PhylomeDB:Q39119 Genevestigator:Q39119 Uniprot:Q39119
Leaf	Isotig03393	27	5	2.962	6.04E-07	TAIR|locus:2123782 - symbol:GAMMA-VPE "AT4G32940" species:3702 "Arabidopsis thaliana" [GO:0004197 "cysteine-type endopeptidase activity" evidence=ISS;IDA] [GO:0006508 "proteolysis" evidence=ISS] [GO:0000323 "lytic vacuole" evidence=IDA] [GO:0006624 "vacuolar protein processing" evidence=ISS] InterPro:IPR001096 Pfam:PF01650 PIRSF:PIRSF019663 PRINTS:PR00776 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0004197 GO:GO:0006508 EMBL:AL031804 EMBL:AL161582 eggNOG:COG5206 PANTHER:PTHR12000 KO:K01369 HOGENOM:HBG318720 GO:GO:0000323 ProtClustDB:CLSN2682340 EMBL:D61395 EMBL:AF370160 EMBL:AF424619 EMBL:AY059104 EMBL:AY133531 IPI:IPI00537536 PIR:T05302 RefSeq:NP_195020.1 UniGene:At.21567 UniGene:At.48929 UniGene:At.75206 ProteinModelPortal:Q39119 STRING:Q39119 MEROPS:C13.006 PRIDE:Q39119 EnsemblPlants:AT4G32940.1 GeneID:829431 KEGG:ath:AT4G32940 TAIR:At4g32940 InParanoid:Q39119 OMA:ICHAYQL PhylomeDB:Q39119 Genevestigator:Q39119 Uniprot:Q39119
Leaf	Isotig03400	23	0	6.053	3.61E-08	TAIR|locus:2184702 - symbol:AT5G09300 "AT5G09300" species:3702 "Arabidopsis thaliana" [GO:0003863 "3-methyl-2-oxobutanoate dehydrogenase (2-methylpropanoyl-transferring) activity" evidence=ISS] [GO:0008152 "metabolic process" evidence=IEA;ISS] [GO:0016624 "oxidoreductase activity, acting on the aldehyde or oxo group of donors, disulfide as acceptor" evidence=IEA] [GO:0005739 "mitochondrion" evidence=IDA] InterPro:IPR001017 Pfam:PF00676 GO:GO:0005739 EMBL:CP002688 GenomeReviews:BA000015_GR UniGene:At.32534 UniGene:At.32535 eggNOG:COG1071 KO:K00166 HSSP:P12694 HOGENOM:HBG753263 GO:GO:0016624 EMBL:BT004286 EMBL:BT005616 IPI:IPI00524357 RefSeq:NP_568209.1 ProteinModelPortal:Q84JL2 SMR:Q84JL2 STRING:Q84JL2 PRIDE:Q84JL2 EnsemblPlants:AT5G09300.1 GeneID:830789 KEGG:ath:AT5G09300 TAIR:At5g09300 InParanoid:Q84JL2 OMA:VHAVARW PhylomeDB:Q84JL2 ProtClustDB:CLSN2679722 ArrayExpress:Q84JL2 Genevestigator:Q84JL2 Uniprot:Q84JL2
Leaf	Isotig03401	17	0	5.616	2.14E-06	TAIR|locus:2184702 - symbol:AT5G09300 "AT5G09300" species:3702 "Arabidopsis thaliana" [GO:0003863 "3-methyl-2-oxobutanoate dehydrogenase (2-methylpropanoyl-transferring) activity" evidence=ISS] [GO:0008152 "metabolic process" evidence=IEA;ISS] [GO:0016624 "oxidoreductase activity, acting on the aldehyde or oxo group of donors, disulfide as acceptor" evidence=IEA] [GO:0005739 "mitochondrion" evidence=IDA] InterPro:IPR001017 Pfam:PF00676 GO:GO:0005739 EMBL:CP002688 GenomeReviews:BA000015_GR UniGene:At.32534 UniGene:At.32535 eggNOG:COG1071 KO:K00166 HSSP:P12694 HOGENOM:HBG753263 GO:GO:0016624 EMBL:BT004286 EMBL:BT005616 IPI:IPI00524357 RefSeq:NP_568209.1 ProteinModelPortal:Q84JL2 SMR:Q84JL2 STRING:Q84JL2 PRIDE:Q84JL2 EnsemblPlants:AT5G09300.1 GeneID:830789 KEGG:ath:AT5G09300 TAIR:At5g09300 InParanoid:Q84JL2 OMA:VHAVARW PhylomeDB:Q84JL2 ProtClustDB:CLSN2679722 ArrayExpress:Q84JL2 Genevestigator:Q84JL2 Uniprot:Q84JL2
Leaf	Isotig03416	45	395	-2.605	5.25E-50	TAIR|locus:2185460 - symbol:CA2 "carbonic anhydrase 2" species:3702 "Arabidopsis thaliana" [GO:0004089 "carbonate dehydratase activity" evidence=IEA;ISS] [GO:0008270 "zinc ion binding" evidence=IEA;ISS] [GO:0015976 "carbon utilization" evidence=ISS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0042742 "defense response to bacterium" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA] [GO:0009507 "chloroplast"

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] InterPro:IPR001765 InterPro:IPR015892 Pfam:PF00484 PROSITE:PS00704 PROSITE:PS00705 SMART:SM00947 GO:GO:0005829 GO:GO:0048046 GO:GO:0009570 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0042742 GO:GO:0008270 GO:GO:0031969 GO:GO:0015976 GO:GO:0009535 eggNOG:COG0288 GO:GO:0004089 Gene3D:G3DSA:3.40.1050.10 PANTHER:PTHR11002 SUPFAM:SSF53056 EMBL:L18901 EMBL:AL391149 EMBL:AF324712 EMBL:AF326863 EMBL:AF339686 EMBL:AF428428 EMBL:BT000652 EMBL:BT000663 EMBL:Z26538 IPI:IPI00523587 RefSeq:NP_568303.2 RefSeq:NP_974782.1 UniGene:At.23743 ProteinModelPortal:P42737 SMR:P42737 IntAct:P42737 STRING:P42737 SWISS-2DPAGE:P42737 PRIDE:P42737 ProMEX:P42737 EnsemblPlants:AT5G14740.2 GeneID:831326 KEGG:ath:AT5G14740 TAIR:At5g14740 HOGENOM:HBG711150 InParanoid:P42737 KO:K01673 PhylomeDB:P42737 ProtClustDB:CLSN2915215 ArrayExpress:P42737 Genevestigator:P42737 Uniprot:P42737
Leaf	Isotig03417	45	396	-2.609	3.34E-50	TAIR|locus:2185460 - symbol:CA2 "carbonic anhydrase 2" species:3702 "Arabidopsis thaliana" [GO:0004089 "carbonate dehydratase activity" evidence=IEA;ISS] [GO:0008270 "zinc ion binding" evidence=IEA;ISS] [GO:0015976 "carbon utilization" evidence=ISS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0042742 "defense response to bacterium" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] InterPro:IPR001765 InterPro:IPR015892 Pfam:PF00484 PROSITE:PS00704 PROSITE:PS00705 SMART:SM00947 GO:GO:0005829 GO:GO:0048046 GO:GO:0009570 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0042742 GO:GO:0008270 GO:GO:0031969 GO:GO:0015976 GO:GO:0009535 eggNOG:COG0288 GO:GO:0004089 Gene3D:G3DSA:3.40.1050.10 PANTHER:PTHR11002 SUPFAM:SSF53056 EMBL:L18901 EMBL:AL391149 EMBL:AF324712 EMBL:AF326863 EMBL:AF339686 EMBL:AF428428 EMBL:BT000652 EMBL:BT000663 EMBL:Z26538 IPI:IPI00523587 RefSeq:NP_568303.2 RefSeq:NP_974782.1 UniGene:At.23743 ProteinModelPortal:P42737 SMR:P42737 IntAct:P42737 STRING:P42737 SWISS-2DPAGE:P42737 PRIDE:P42737 ProMEX:P42737 EnsemblPlants:AT5G14740.2 GeneID:831326 KEGG:ath:AT5G14740 TAIR:At5g14740 HOGENOM:HBG711150 InParanoid:P42737 KO:K01673 PhylomeDB:P42737 ProtClustDB:CLSN2915215 ArrayExpress:P42737 Genevestigator:P42737 Uniprot:P42737
Leaf	Isotig03420	22	8	1.988	0.00034419	TAIR|locus:2200980 - symbol:PDH-E1 ALPHA "AT1G01090" species:3702 "Arabidopsis thaliana" [GO:0004739 "pyruvate dehydrogenase (acetyl-transferring) activity" evidence=ISS] [GO:0006096 "glycolysis" evidence=IEA] [GO:0008152 "metabolic process" evidence=IEA;ISS] [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] [GO:0009536 "plastid" evidence=ISS] InterPro:IPR001017 InterPro:IPR017597 Pfam:PF00676 EMBL:CP002684 GO:GO:0009570 GO:GO:0009941 GO:GO:0006096 GO:GO:0004739 eggNOG:COG1071 KO:K00161 TIGRFAMs:TIGR03182 HSSP:P08559 EMBL:U80185 EMBL:AY052721 EMBL:AY063724 EMBL:AK226909 IPI:IPI00525582 RefSeq:NP_171617.1 UniGene:At.20069 ProteinModelPortal:O24457 IntAct:O24457 STRING:O24457 PRIDE:O24457 ProMEX:O24457 EnsemblPlants:AT1G01090.1 GeneID:839429 KEGG:ath:AT1G01090 TAIR:At1g01090 InParanoid:O24457 OMA:SKEHHLL PhylomeDB:O24457 ProtClustDB:PLN02374 Genevestigator:O24457 Uniprot:O24457
Leaf	Isotig03421	22	8	1.988	0.00034419	TAIR|locus:2200980 - symbol:PDH-E1 ALPHA "AT1G01090" species:3702 "Arabidopsis thaliana" [GO:0004739 "pyruvate dehydrogenase (acetyl-transferring) activity" evidence=ISS] [GO:0006096 "glycolysis" evidence=IEA] [GO:0008152 "metabolic process" evidence=IEA;ISS] [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] [GO:0009536 "plastid" evidence=ISS] InterPro:IPR001017 InterPro:IPR017597 Pfam:PF00676 EMBL:CP002684 GO:GO:0009570 GO:GO:0009941 GO:GO:0006096 GO:GO:0004739 eggNOG:COG1071 KO:K00161 TIGRFAMs:TIGR03182 HSSP:P08559 EMBL:U80185 EMBL:AY052721 EMBL:AY063724 EMBL:AK226909 IPI:IPI00525582 RefSeq:NP_171617.1 UniGene:At.20069 ProteinModelPortal:O24457 IntAct:O24457 STRING:O24457 PRIDE:O24457 ProMEX:O24457 EnsemblPlants:AT1G01090.1 GeneID:839429 KEGG:ath:AT1G01090 TAIR:At1g01090 InParanoid:O24457 OMA:SKEHHLL PhylomeDB:O24457 ProtClustDB:PLN02374 Genevestigator:O24457 Uniprot:O24457
Leaf	Isotig03426	17	72	-1.554	5.58E-06	TAIR|locus:2078941 - symbol:SBPASE "AT3G55800" species:3702 "Arabidopsis thaliana" [GO:0005975 "carbohydrate metabolic process" evidence=ISS] [GO:0042578 "phosphoric ester hydrolase activity" evidence=ISS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005986

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						"sucrose biosynthetic process" evidence=IDA] [GO:0016051 "carbohydrate biosynthetic process" evidence=IDA] [GO:0019252 "starch biosynthetic process" evidence=IDA] [GO:0050278 "sedoheptulose-bisphosphatase activity" evidence=IMP] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0042742 "defense response to bacterium" evidence=IEP] [GO:0048046 "apoplast" evidence=IDA] [GO:0019253 "reductive pentose-phosphate cycle" evidence=ISS] InterPro:IPR000146 InterPro:IPR020548 Pfam:PF00316 PIRSF:PIRSF000904 PROSITE:PS00124 GO:GO:0048046 GO:GO:0009570 GO:GO:0042742 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0046872 GO:GO:0009941 GO:GO:0019252 GO:GO:0009579 GO:GO:0019253 eggNOG:COG0158 HOGENOM:HBG731261 PANTHER:PTHR11556 GO:GO:0005986 InterPro:IPR023079 PRINTS:PR01958 EMBL:AL161667 EMBL:S74719 EMBL:AY054669 EMBL:AY128737 IPI:IPI00544876 PIR:S51838 RefSeq:NP_191139.1 UniGene:At.21157 ProteinModelPortal:P46283 SMR:P46283 IntAct:P46283 STRING:P46283 SWISS-2DPAGE:P46283 World-2DPAGE:0003:P46283 PRIDE:P46283 ProMEX:P46283 EnsemblPlants:AT3G55800.1 GeneID:824746 KEGG:ath:AT3G55800 TAIR:At3g55800 InParanoid:P46283 KO:K01100 OMA:HANIVIE PhylomeDB:P46283 ProtClustDB:PLN02462 Genevestigator:P46283 GermOnline:AT3G55800 GO:GO:0050278 Uniprot:P46283
Leaf	Isotig03436	8	58	-2.329	9.16E-08	TAIR|locus:2204798 - symbol:MC1 "AT1G02170" species:3702 "Arabidopsis thaliana" [GO:0006508 "proteolysis" evidence=ISS] [GO:0004197 "cysteine-type endopeptidase activity" evidence=IDA] [GO:0043068 "positive regulation of programmed cell death" evidence=IGI;IDA] InterPro:IPR011600 Pfam:PF00656 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0006952 GO:GO:0004197 GO:GO:0006508 GO:GO:0043068 EMBL:U89959 InterPro:IPR005735 Pfam:PF06943 TIGRFAMs:TIGR01053 EMBL:AY219826 EMBL:AY322525 IPI:IPI00531085 RefSeq:NP_171719.2 UniGene:At.10711 UniGene:At.69983 ProteinModelPortal:Q7XJE6 STRING:Q7XJE6 MEROPS:C14.047 PRIDE:Q7XJE6 EnsemblPlants:AT1G02170.1 GeneID:839561 KEGG:ath:AT1G02170 TAIR:At1g02170 eggNOG:NOG68179 HOGENOM:HBG692861 InParanoid:Q7XJE6 OMA:NDAKCMR PhylomeDB:Q7XJE6 Genevestigator:Q7XJE6 Uniprot:Q7XJE6
Leaf	Isotig03437	6	45	-2.378	1.90E-06	TAIR|locus:2204798 - symbol:MC1 "AT1G02170" species:3702 "Arabidopsis thaliana" [GO:0006508 "proteolysis" evidence=ISS] [GO:0004197 "cysteine-type endopeptidase activity" evidence=IDA] [GO:0043068 "positive regulation of programmed cell death" evidence=IGI;IDA] InterPro:IPR011600 Pfam:PF00656 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0006952 GO:GO:0004197 GO:GO:0006508 GO:GO:0043068 EMBL:U89959 InterPro:IPR005735 Pfam:PF06943 TIGRFAMs:TIGR01053 EMBL:AY219826 EMBL:AY322525 IPI:IPI00531085 RefSeq:NP_171719.2 UniGene:At.10711 UniGene:At.69983 ProteinModelPortal:Q7XJE6 STRING:Q7XJE6 MEROPS:C14.047 PRIDE:Q7XJE6 EnsemblPlants:AT1G02170.1 GeneID:839561 KEGG:ath:AT1G02170 TAIR:At1g02170 eggNOG:NOG68179 HOGENOM:HBG692861 InParanoid:Q7XJE6 OMA:NDAKCMR PhylomeDB:Q7XJE6 Genevestigator:Q7XJE6 Uniprot:Q7XJE6
Leaf	Isotig03442	11	1	3.988	0.000330755	TAIR|locus:2103025 - symbol:SEC "AT3G04240" species:3702 "Arabidopsis thaliana" [GO:0006493 "protein O-linked glycosylation" evidence=ISS;IDA] [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS;IDA] InterPro:IPR001440 InterPro:IPR011990 InterPro:IPR013026 InterPro:IPR019734 Pfam:PF00515 PROSITE:PS50005 PROSITE:PS50293 SMART:SM00028 GO:GO:0007275 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005488 GO:GO:0006493 Gene3D:G3DSA:1.25.40.10 GO:GO:0016757 EMBL:AC016829 CAZy:GT41 eggNOG:COG3914 HOGENOM:HBG317910 KO:K09667 OMA:NFPDAYC EMBL:AF441079 EMBL:AY090938 EMBL:AY117340 IPI:IPI00524518 RefSeq:NP_187074.1 UniGene:At.27850 UniGene:At.71305 ProteinModelPortal:Q9M8Y0 SMR:Q9M8Y0 IntAct:Q9M8Y0 STRING:Q9M8Y0 PRIDE:Q9M8Y0 EnsemblPlants:AT3G04240.1 GeneID:819579 KEGG:ath:AT3G04240 TAIR:At3g04240 InParanoid:Q9M8Y0 PhylomeDB:Q9M8Y0 ProtClustDB:CLSN2684273 ArrayExpress:Q9M8Y0 Genevestigator:Q9M8Y0 GermOnline:AT3G04240 Uniprot:Q9M8Y0
Leaf	Isotig03443	11	1	3.988	0.000330755	TAIR|locus:2103025 - symbol:SEC "AT3G04240" species:3702 "Arabidopsis thaliana" [GO:0006493 "protein O-linked glycosylation" evidence=ISS;IDA] [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS;IDA] InterPro:IPR001440 InterPro:IPR011990 InterPro:IPR013026 InterPro:IPR019734 Pfam:PF00515 PROSITE:PS50005 PROSITE:PS50293 SMART:SM00028 GO:GO:0007275 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005488 GO:GO:0006493 Gene3D:G3DSA:1.25.40.10 GO:GO:0016757 EMBL:AC016829 CAZy:GT41 eggNOG:COG3914 HOGENOM:HBG317910 KO:K09667 OMA:NFPDAYC EMBL:AF441079 EMBL:AY090938 EMBL:AY117340 IPI:IPI00524518 RefSeq:NP_187074.1 UniGene:At.27850 UniGene:At.71305 ProteinModelPortal:Q9M8Y0 SMR:Q9M8Y0 IntAct:Q9M8Y0 STRING:Q9M8Y0 PRIDE:Q9M8Y0 EnsemblPlants:AT3G04240.1 GeneID:819579 KEGG:ath:AT3G04240 TAIR:At3g04240 InParanoid:Q9M8Y0

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						PhylomeDB:Q9M8Y0 ProtClustDB:CLSN2684273 ArrayExpress:Q9M8Y0 Genevestigator:Q9M8Y0 GermOnline:AT3G04240 Uniprot:Q9M8Y0
Leaf	Isotig03452	13	106	-2.499	5.30E-14	TAIR|locus:2204798 - symbol:MC1 "AT1G02170" species:3702 "Arabidopsis thaliana" [GO:0006508 "proteolysis" evidence=ISS] [GO:0004197 "cysteine-type endopeptidase activity" evidence=IDA] [GO:0043068 "positive regulation of programmed cell death" evidence=IGI;IDA] InterPro:IPR011600 Pfam:PF00656 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0006952 GO:GO:0004197 GO:GO:0006508 GO:GO:0043068 EMBL:U89959 InterPro:IPR005735 Pfam:PF06943 TIGRFAMs:TIGR01053 EMBL:AY219826 EMBL:AY322525 IPI:IPI00531085 RefSeq:NP_171719.2 UniGene:At.10711 UniGene:At.69983 ProteinModelPortal:Q7XJE6 STRING:Q7XJE6 MEROPS:C14.047 PRIDE:Q7XJE6 EnsemblPlants:AT1G02170.1 GeneID:839561 KEGG:ath:AT1G02170 TAIR:At1g02170 eggNOG:NOG68179 HOGENOM:HBG692861 InParanoid:Q7XJE6 OMA:NDAKCMR PhylomeDB:Q7XJE6 Genevestigator:Q7XJE6 Uniprot:Q7XJE6
Leaf	Isotig03453	13	104	-2.471	1.30E-13	TAIR|locus:2204798 - symbol:MC1 "AT1G02170" species:3702 "Arabidopsis thaliana" [GO:0006508 "proteolysis" evidence=ISS] [GO:0004197 "cysteine-type endopeptidase activity" evidence=IDA] [GO:0043068 "positive regulation of programmed cell death" evidence=IGI;IDA] InterPro:IPR011600 Pfam:PF00656 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0006952 GO:GO:0004197 GO:GO:0006508 GO:GO:0043068 EMBL:U89959 InterPro:IPR005735 Pfam:PF06943 TIGRFAMs:TIGR01053 EMBL:AY219826 EMBL:AY322525 IPI:IPI00531085 RefSeq:NP_171719.2 UniGene:At.10711 UniGene:At.69983 ProteinModelPortal:Q7XJE6 STRING:Q7XJE6 MEROPS:C14.047 PRIDE:Q7XJE6 EnsemblPlants:AT1G02170.1 GeneID:839561 KEGG:ath:AT1G02170 TAIR:At1g02170 eggNOG:NOG68179 HOGENOM:HBG692861 InParanoid:Q7XJE6 OMA:NDAKCMR PhylomeDB:Q7XJE6 Genevestigator:Q7XJE6 Uniprot:Q7XJE6
Leaf	Isotig03462	20	6	2.266	0.000209978	TAIR|locus:2063942 - symbol:TOPP4 "AT2G39840" species:3702 "Arabidopsis thaliana" [GO:0004722 "protein serine/threonine phosphatase activity" evidence=ISS;IDA] [GO:0000164 "protein phosphatase type 1 complex" evidence=ISS] [GO:0006470 "protein dephosphorylation" evidence=TAS] InterPro:IPR004843 InterPro:IPR006186 Pfam:PF00149 PRINTS:PR00114 PROSITE:PS00125 SMART:SM00156 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0006470 GO:GO:0004722 GO:GO:0046872 eggNOG:COG0639 EMBL:AC003000 HOGENOM:HBG716770 KO:K06269 OMA:YLVMESR EMBL:M93411 EMBL:BT026118 EMBL:AK229028 IPI:IPI00532673 PIR:S31088 RefSeq:NP_181514.1 UniGene:At.310 ProteinModelPortal:P48484 SMR:P48484 PRIDE:P48484 EnsemblPlants:AT2G39840.1 GeneID:818571 KEGG:ath:AT2G39840 TAIR:At2g39840 InParanoid:P48484 PhylomeDB:P48484 ProtClustDB:CLSN2683376 ArrayExpress:P48484 Genevestigator:P48484 GermOnline:AT2G39840 Uniprot:P48484
Leaf	Isotig03463	20	6	2.266	0.000209978	TAIR|locus:2063942 - symbol:TOPP4 "AT2G39840" species:3702 "Arabidopsis thaliana" [GO:0004722 "protein serine/threonine phosphatase activity" evidence=ISS;IDA] [GO:0000164 "protein phosphatase type 1 complex" evidence=ISS] [GO:0006470 "protein dephosphorylation" evidence=TAS] InterPro:IPR004843 InterPro:IPR006186 Pfam:PF00149 PRINTS:PR00114 PROSITE:PS00125 SMART:SM00156 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0006470 GO:GO:0004722 GO:GO:0046872 eggNOG:COG0639 EMBL:AC003000 HOGENOM:HBG716770 KO:K06269 OMA:YLVMESR EMBL:M93411 EMBL:BT026118 EMBL:AK229028 IPI:IPI00532673 PIR:S31088 RefSeq:NP_181514.1 UniGene:At.310 ProteinModelPortal:P48484 SMR:P48484 PRIDE:P48484 EnsemblPlants:AT2G39840.1 GeneID:818571 KEGG:ath:AT2G39840 TAIR:At2g39840 InParanoid:P48484 PhylomeDB:P48484 ProtClustDB:CLSN2683376 ArrayExpress:P48484 Genevestigator:P48484 GermOnline:AT2G39840 Uniprot:P48484
Leaf	Isotig03474	2	38	-3.719	5.73E-08	TAIR|locus:2094034 - symbol:PMT5 "AT3G18830" species:3702 "Arabidopsis thaliana" [GO:0005351 "sugar:hydrogen symporter activity" evidence=ISS;IDA] [GO:0006810 "transport" evidence=IEA] [GO:0015144 "carbohydrate transmembrane transporter activity" evidence=ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0055085 "transmembrane transport" evidence=IEA] [GO:0015145 "monosaccharide transmembrane transporter activity" evidence=IDA] [GO:0005354 "galactose transmembrane transporter activity" evidence=IDA] [GO:0005355 "glucose transmembrane transporter activity" evidence=IDA] [GO:0005365 "myo-inositol transmembrane transporter activity" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0015148 "D-xylose transmembrane transporter activity" evidence=IDA] [GO:0015168 "glycerol transmembrane transporter activity" evidence=IDA] [GO:0015575 "mannitol transmembrane transporter activity" evidence=IDA] [GO:0015576 "sorbitol transmembrane transporter activity" evidence=IDA] [GO:0015591 "D-ribose transmembrane transporter activity" evidence=IDA] InterPro:IPR003663 InterPro:IPR005828 InterPro:IPR005829 Pfam:PF00083 PRINTS:PR00171 PROSITE:PS00216 PROSITE:PS00217 GO:GO:0016021 GO:GO:0005886 EMBL:CP002686 GenomeReviews:BA000014_GR

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						eggNOG:COG0477 InterPro:IPR016196 SUPFAM:SSF103473 EMBL:AB026654 InterPro:IPR020846 PROSITE:PS50850 GO:GO:0015168 HOGENOM:HBG744444 TIGRFAMs:TIGR00879 GO:GO:0005351 GO:GO:0005355 GO:GO:0005354 GO:GO:0005365 EMBL:AY065183 EMBL:AY081618 IPI:IPI00532657 RefSeq:NP_188513.1 UniGene:At.6395 ProteinModelPortal:Q8VZ80 TCDB:2.A.1.1.34 PRIDE:Q8VZ80 EnsemblPlants:AT3G18830.1 GeneID:821416 KEGG:ath:AT3G18830 TAIR:At3g18830 InParanoid:Q8VZ80 OMA:TFLPETQ PhylomeDB:Q8VZ80 ProtClustDB:CLSN2715683 Genevestigator:Q8VZ80 GO:GO:0015591 GO:GO:0015148 GO:GO:0015575 GO:GO:0015576 Uniprot:Q8VZ80
Leaf	Isotig03475	2	38	-3.719	5.73E-08	TAIR|locus:2094034 - symbol:PMT5 "AT3G18830" species:3702 "Arabidopsis thaliana" [GO:0005351 "sugar:hydrogen symporter activity" evidence=ISS;IDA] [GO:0006810 "transport" evidence=IEA] [GO:0015144 "carbohydrate transmembrane transporter activity" evidence=ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0055085 "transmembrane transport" evidence=IEA] [GO:0015145 "monosaccharide transmembrane transporter activity" evidence=IDA] [GO:0005354 "galactose transmembrane transporter activity" evidence=IDA] [GO:0005355 "glucose transmembrane transporter activity" evidence=IDA] [GO:0005365 "myo-inositol transmembrane transporter activity" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0015148 "D-xylose transmembrane transporter activity" evidence=IDA] [GO:0015168 "glycerol transmembrane transporter activity" evidence=IDA] [GO:0015575 "mannitol transmembrane transporter activity" evidence=IDA] [GO:0015576 "sorbitol transmembrane transporter activity" evidence=IDA] [GO:0015591 "D-ribose transmembrane transporter activity" evidence=IDA] InterPro:IPR003663 InterPro:IPR005828 InterPro:IPR005829 Pfam:PF00083 PRINTS:PR00171 PROSITE:PS00216 PROSITE:PS00217 GO:GO:0016021 GO:GO:0005886 EMBL:CP002686 GenomeReviews:BA000014_GR eggNOG:COG0477 InterPro:IPR016196 SUPFAM:SSF103473 EMBL:AB026654 InterPro:IPR020846 PROSITE:PS50850 GO:GO:0015168 HOGENOM:HBG744444 TIGRFAMs:TIGR00879 GO:GO:0005351 GO:GO:0005355 GO:GO:0005354 GO:GO:0005365 EMBL:AY065183 EMBL:AY081618 IPI:IPI00532657 RefSeq:NP_188513.1 UniGene:At.6395 ProteinModelPortal:Q8VZ80 TCDB:2.A.1.1.34 PRIDE:Q8VZ80 EnsemblPlants:AT3G18830.1 GeneID:821416 KEGG:ath:AT3G18830 TAIR:At3g18830 InParanoid:Q8VZ80 OMA:TFLPETQ PhylomeDB:Q8VZ80 ProtClustDB:CLSN2715683 Genevestigator:Q8VZ80 GO:GO:0015591 GO:GO:0015148 GO:GO:0015575 GO:GO:0015576 Uniprot:Q8VZ80
Leaf	Isotig03490	47	17	1.996	1.56E-07	TAIR|locus:2120222 - symbol:RD19 "AT4G39090" species:3702 "Arabidopsis thaliana" [GO:0006508 "proteolysis" evidence=ISS] [GO:0008234 "cysteine-type peptidase activity" evidence=ISS] [GO:0009269 "response to desiccation" evidence=IEP] [GO:0006970 "response to osmotic stress" evidence=IGI] [GO:0005634 "nucleus" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0042742 "defense response to bacterium" evidence=IMP] [GO:0004197 "cysteine-type endopeptidase activity" evidence=ISS] [GO:0009414 "response to water deprivation" evidence=TAS] [GO:0009651 "response to salt stress" evidence=IEP] InterPro:IPR000668 InterPro:IPR013128 Pfam:PF00112 PRINTS:PR00705 SMART:SM00645 InterPro:IPR000169 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005634 GO:GO:0005773 GO:GO:0042742 eggNOG:COG4870 HOGENOM:HBG746690 ProtClustDB:CLSN2688311 GO:GO:0004197 GO:GO:0006508 InterPro:IPR013201 PANTHER:PTHR12411 Pfam:PF08246 SMART:SM00848 PROSITE:PS00640 PROSITE:PS00139 PROSITE:PS00639 GO:GO:0009651 EMBL:AL035679 EMBL:AL161594 MEROPS:C01.022 EMBL:D13042 EMBL:AY080598 EMBL:AY133844 IPI:IPI00544363 PIR:JN0718 RefSeq:NP_568052.1 UniGene:At.2850 UniGene:At.74924 ProteinModelPortal:P43296 SMR:P43296 STRING:P43296 PRIDE:P43296 EnsemblPlants:AT4G39090.1 GeneID:830064 KEGG:ath:AT4G39090 TAIR:At4g39090 InParanoid:P43296 OMA:EDFDWRD PhylomeDB:P43296 ArrayExpress:P43296 Genevestigator:P43296 GermOnline:AT4G39090 Uniprot:P43296
Leaf	Isotig03491	46	17	1.965	2.80E-07	TAIR|locus:2120222 - symbol:RD19 "AT4G39090" species:3702 "Arabidopsis thaliana" [GO:0006508 "proteolysis" evidence=ISS] [GO:0008234 "cysteine-type peptidase activity" evidence=ISS] [GO:0009269 "response to desiccation" evidence=IEP] [GO:0006970 "response to osmotic stress" evidence=IGI] [GO:0005634 "nucleus" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0042742 "defense response to bacterium" evidence=IMP] [GO:0004197 "cysteine-type endopeptidase activity" evidence=ISS] [GO:0009414 "response to water deprivation" evidence=TAS] [GO:0009651 "response to salt stress" evidence=IEP] InterPro:IPR000668 InterPro:IPR013128 Pfam:PF00112 PRINTS:PR00705 SMART:SM00645 InterPro:IPR000169 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005634 GO:GO:0005773 GO:GO:0042742 eggNOG:COG4870 HOGENOM:HBG746690 ProtClustDB:CLSN2688311 GO:GO:0004197 GO:GO:0006508 InterPro:IPR013201 PANTHER:PTHR12411 Pfam:PF08246 SMART:SM00848 PROSITE:PS00640 PROSITE:PS00139

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						PROSITE:PS00639 GO:GO:0009651 EMBL:AL035679 EMBL:AL161594 MEROPS:C01.022 EMBL:D13042 EMBL:AY080598 EMBL:AY133844 IPI:IPI00544363 PIR:JN0718 RefSeq:NP_568052.1 UniGene:At.2850 UniGene:At.74924 ProteinModelPortal:P43296 SMR:P43296 STRING:P43296 PRIDE:P43296 EnsemblPlants:AT4G39090.1 GeneID:830064 KEGG:ath:AT4G39090 TAIR:At4g39090 InParanoid:P43296 OMA:EDFDWRD PhylomeDB:P43296 ArrayExpress:P43296 Genevestigator:P43296 GermOnline:AT4G39090 Uniprot:P43296
Leaf	Isotig03493	13	2	3.229	0.00031313	TAIR|locus:2122063 - symbol:CPK5 "calmodulin-domain protein kinase 5" species:3702 "Arabidopsis thaliana" [GO:0004672 "protein kinase activity" evidence=IEA] [GO:0004674 "protein serine/threonine kinase activity" evidence=IEA] [GO:0004683 "calmodulin-dependent protein kinase activity" evidence=ISS] [GO:0005509 "calcium ion binding" evidence=IEA] [GO:0005524 "ATP binding" evidence=IEA] [GO:0006468 "protein phosphorylation" evidence=ISS] [GO:0016301 "kinase activity" evidence=ISS] [GO:0016020 "membrane" evidence=TAS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009737 "response to abscisic acid stimulus" evidence=IDA] InterPro:IPR000719 InterPro:IPR002048 InterPro:IPR002290 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR011992 InterPro:IPR017441 Pfam:PF00069 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 SMART:SM00054 SMART:SM00220 Prosite:PS00018 Pfam:PF00036 GO:GO:0005829 GO:GO:0005886 GO:GO:0005524 GO:GO:0009737 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005509 eggNOG:COG0515 SUPFAM:SSF56112 GO:GO:0004674 InterPro:IPR018247 InterPro:IPR018249 Gene3D:G3DSA:1.10.238.10 PROSITE:PS50222 HOGENOM:HBG755340 InterPro:IPR018248 EMBL:AL161587 EMBL:AL022604 KO:K13412 HSSP:Q06850 EMBL:U31834 EMBL:AK227104 IPI:IPI00524740 PIR:T06126 RefSeq:NP_195257.1 UniGene:At.21676 ProteinModelPortal:Q38871 SMR:Q38871 STRING:Q38871 PRIDE:Q38871 EnsemblPlants:AT4G35310.1 GeneID:829685 KEGG:ath:AT4G35310 TAIR:At4g35310 InParanoid:Q38871 OMA:NIRDIYT PhylomeDB:Q38871 ProtClustDB:CLSN2916179 ArrayExpress:Q38871 Genevestigator:Q38871 Uniprot:Q38871
Leaf	Isotig03500	16	89	-1.947	3.40E-09	TAIR|locus:2080225 - symbol:HCEF1 "AT3G54050" species:3702 "Arabidopsis thaliana" [GO:0006000 "fructose metabolic process" evidence=ISS] [GO:0042132 "fructose 1,6-bisphosphate 1-phosphatase activity" evidence=ISS;IMP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005985 "sucrose metabolic process" evidence=IMP] [GO:0015979 "photosynthesis" evidence=IMP] [GO:0030388 "fructose 1,6-bisphosphate metabolic process" evidence=IMP] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0010319 "stromule" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009773 "photosynthetic electron transport in photosystem I" evidence=IMP] InterPro:IPR000146 InterPro:IPR020548 Pfam:PF00316 PRINTS:PR00115 PROSITE:PS00124 GO:GO:0048046 GO:GO:0009570 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0046872 GO:GO:0010319 GO:GO:0009409 GO:GO:0030388 EMBL:AL132957 GO:GO:0019253 GO:GO:0042132 eggNOG:COG0158 EMBL:X58148 EMBL:AF428326 EMBL:AY039934 EMBL:AY150450 EMBL:BT000743 IPI:IPI00530130 PIR:S16582 PIR:T47564 RefSeq:NP_001190083.1 RefSeq:NP_190973.1 UniGene:At.22619 UniGene:At.51003 ProteinModelPortal:P25851 SMR:P25851 IntAct:P25851 STRING:P25851 PRIDE:P25851 ProMEX:P25851 EnsemblPlants:AT3G54050.1 EnsemblPlants:AT3G54050.2 GeneID:824572 KEGG:ath:AT3G54050 TAIR:At3g54050 HOGENOM:HBG731261 InParanoid:P25851 KO:K03841 OMA:VMVYTTG PhylomeDB:P25851 ProtClustDB:PLN02542 BioCyc:ARA:AT3G54050-MONOMER BioCyc:MetaCyc:AT3G54050-WS-MONOMER ArrayExpress:P25851 Genevestigator:P25851 GermOnline:AT3G54050 GO:GO:0009773 GO:GO:0005985 PANTHER:PTHR11556 Uniprot:P25851
Leaf	Isotig03501	17	90	-1.875	6.73E-09	TAIR|locus:2080225 - symbol:HCEF1 "AT3G54050" species:3702 "Arabidopsis thaliana" [GO:0006000 "fructose metabolic process" evidence=ISS] [GO:0042132 "fructose 1,6-bisphosphate 1-phosphatase activity" evidence=ISS;IMP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005985 "sucrose metabolic process" evidence=IMP] [GO:0015979 "photosynthesis" evidence=IMP] [GO:0030388 "fructose 1,6-bisphosphate metabolic process" evidence=IMP] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0010319 "stromule" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009773 "photosynthetic electron transport in photosystem I" evidence=IMP] InterPro:IPR000146 InterPro:IPR020548 Pfam:PF00316 PRINTS:PR00115 PROSITE:PS00124 GO:GO:0048046 GO:GO:0009570 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0046872 GO:GO:0010319 GO:GO:0009409 GO:GO:0030388 EMBL:AL132957 GO:GO:0019253 GO:GO:0042132 eggNOG:COG0158 EMBL:X58148 EMBL:AF428326 EMBL:AY039934 EMBL:AY150450 EMBL:BT000743 IPI:IPI00530130 PIR:S16582 PIR:T47564

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						RefSeq:NP_001190083.1 RefSeq:NP_190973.1 UniGene:At.22619 UniGene:At.51003 ProteinModelPortal:P25851 SMR:P25851 IntAct:P25851 STRING:P25851 PRIDE:P25851 ProMEX:P25851 EnsemblPlants:AT3G54050.1 EnsemblPlants:AT3G54050.2 GeneID:824572 KEGG:ath:AT3G54050 TAIR:At3g54050 HOGENOM:HBG731261 InParanoid:P25851 KO:K03841 OMA:VMVYTTG PhylomeDB:P25851 ProtClustDB:PLN02542 BioCyc:ARA:AT3G54050-MONOMER BioCyc:MetaCyc:AT3G54050-WS-MONOMER ArrayExpress:P25851 Genevestigator:P25851 GermOnline:AT3G54050 GO:GO:0009773 GO:GO:0005985 PANTHER:PTHR11556 Uniprot:P25851
Leaf	Isotig03504	22	90	-1.503	7.15E-07	TAIR|locus:2149099 - symbol:AT5G36790 species:3702 "Arabidopsis thaliana" [GO:0008152 "metabolic process" evidence=IEA] [GO:0008967 "phosphoglycolate phosphatase activity" evidence=ISS] [GO:0016787 "hydrolase activity" evidence=IEA] [GO:0016791 "phosphatase activity" evidence=IEA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] InterPro:IPR006349 InterPro:IPR006357 GO:GO:0048046 GO:GO:0009570 GO:GO:0005634 GO:GO:0005773 EMBL:CP002688 InterPro:IPR023214 Gene3D:G3DSA:3.40.50.1000 SUPFAM:SSF56784 GO:GO:0008967 TIGRFAMs:TIGR01460 InterPro:IPR023215 Gene3D:G3DSA:3.40.50.10410 OMA:NNSIYTP TIGRFAMs:TIGR01452 EMBL:AY094446 EMBL:AY122899 IPI:IPI00542010 RefSeq:NP_001119316.1 RefSeq:NP_001119318.1 RefSeq:NP_001190427.1 RefSeq:NP_001190428.1 RefSeq:NP_198485.2 RefSeq:NP_198495.1 UniGene:At.30537 UniGene:At.70539 ProteinModelPortal:Q8L3U4 SMR:Q8L3U4 STRING:Q8L3U4 PRIDE:Q8L3U4 DNASU:833635 EnsemblPlants:AT5G36700.1 EnsemblPlants:AT5G36700.2 EnsemblPlants:AT5G36700.4 EnsemblPlants:AT5G36790.1 EnsemblPlants:AT5G36790.2 EnsemblPlants:AT5G36790.3 GeneID:833635 GeneID:833646 KEGG:ath:AT5G36700 KEGG:ath:AT5G36790 TAIR:At5g36700 TAIR:At5g36790 InParanoid:Q8L3U4 PhylomeDB:Q8L3U4 ProtClustDB:PLN02645 Genevestigator:Q8L3U4 Uniprot:Q8L3U4
Leaf	Isotig03505	19	79	-1.527	2.63E-06	TAIR|locus:2149099 - symbol:AT5G36790 species:3702 "Arabidopsis thaliana" [GO:0008152 "metabolic process" evidence=IEA] [GO:0008967 "phosphoglycolate phosphatase activity" evidence=ISS] [GO:0016787 "hydrolase activity" evidence=IEA] [GO:0016791 "phosphatase activity" evidence=IEA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] InterPro:IPR006349 InterPro:IPR006357 GO:GO:0048046 GO:GO:0009570 GO:GO:0005634 GO:GO:0005773 EMBL:CP002688 InterPro:IPR023214 Gene3D:G3DSA:3.40.50.1000 SUPFAM:SSF56784 GO:GO:0008967 TIGRFAMs:TIGR01460 InterPro:IPR023215 Gene3D:G3DSA:3.40.50.10410 OMA:NNSIYTP TIGRFAMs:TIGR01452 EMBL:AY094446 EMBL:AY122899 IPI:IPI00542010 RefSeq:NP_001119316.1 RefSeq:NP_001119318.1 RefSeq:NP_001190427.1 RefSeq:NP_001190428.1 RefSeq:NP_198485.2 RefSeq:NP_198495.1 UniGene:At.30537 UniGene:At.70539 ProteinModelPortal:Q8L3U4 SMR:Q8L3U4 STRING:Q8L3U4 PRIDE:Q8L3U4 DNASU:833635 EnsemblPlants:AT5G36700.1 EnsemblPlants:AT5G36700.2 EnsemblPlants:AT5G36700.4 EnsemblPlants:AT5G36790.1 EnsemblPlants:AT5G36790.2 EnsemblPlants:AT5G36790.3 GeneID:833635 GeneID:833646 KEGG:ath:AT5G36700 KEGG:ath:AT5G36790 TAIR:At5g36700 TAIR:At5g36790 InParanoid:Q8L3U4 PhylomeDB:Q8L3U4 ProtClustDB:PLN02645 Genevestigator:Q8L3U4 Uniprot:Q8L3U4
Leaf	Isotig03534	31	9	2.313	2.97E-06	TAIR|locus:2062029 - symbol:UNE5 "AT2G47470" species:3702 "Arabidopsis thaliana" [GO:0009567 "double fertilization forming a zygote and endosperm" evidence=IMP] [GO:0009793 "embryo development ending in seed dormancy" evidence=IMP] [GO:0009505 "plant-type cell wall" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005783 "endoplasmic reticulum" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0003756 "protein disulfide isomerase activity" evidence=ISS] [GO:0034976 "response to endoplasmic reticulum stress" evidence=IEP] [GO:0009553 "embryo sac development" evidence=IMP] [GO:0048868 "pollen tube development" evidence=IMP] [GO:0005829 "cytosol" evidence=RCA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR005746 InterPro:IPR005788 InterPro:IPR011679 InterPro:IPR013766 InterPro:IPR017937 Pfam:PF00085 Pfam:PF07749 PRINTS:PR00421 PROSITE:PS00194 GO:GO:0005783 GO:GO:0046686 GO:GO:0005774 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009055 GO:GO:0009793 GO:GO:0009505 UniGene:At.24396 InterPro:IPR012336 Gene3D:G3DSA:3.40.30.10 SUPFAM:SSF52833 GO:GO:0009553 GO:GO:0045454 PROSITE:PS51352 GO:GO:0015035 GO:GO:0048868 GO:GO:0034976 EMBL:AC002535 GO:GO:0006662 eggNOG:COG0526 GO:GO:0009567 GO:GO:0003756 Gene3D:G3DSA:1.20.1150.12 SUPFAM:SSF47933 KO:K09584 TIGRFAMs:TIGR01126 HOGENOM:HBG523089 OMA:FFPKGST EMBL:AF083688 EMBL:AJ271470 EMBL:AY074348 EMBL:AY091388 IPI:IPI00539517

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						PIR:T00437 RefSeq:NP_182269.1 UniGene:At.66351 ProteinModelPortal:O22263 SMR:O22263 STRING:O22263 SWISS-2DPAGE:O22263 PRIDE:O22263 ProMEX:O22263 EnsemblPlants:AT2G47470.1 GeneID:819360 KEGG:ath:AT2G47470 TAIR:At2g47470 InParanoid:O22263 PhylomeDB:O22263 ProtClustDB:CLSN2683612 ArrayExpress:O22263 Genevestigator:O22263 Uniprot:O22263
Leaf	Isotig03535	31	9	2.313	2.97E-06	TAIR|locus:2062029 - symbol:UNE5 "AT2G47470" species:3702 "Arabidopsis thaliana" [GO:0009567 "double fertilization forming a zygote and endosperm" evidence=IMP] [GO:0009793 "embryo development ending in seed dormancy" evidence=IMP] [GO:0009505 "plant-type cell wall" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005783 "endoplasmic reticulum" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0003756 "protein disulfide isomerase activity" evidence=ISS] [GO:0034976 "response to endoplasmic reticulum stress" evidence=IEP] [GO:0009553 "embryo sac development" evidence=IMP] [GO:0048868 "pollen tube development" evidence=IMP] [GO:0005829 "cytosol" evidence=RCA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR005746 InterPro:IPR005788 InterPro:IPR011679 InterPro:IPR013766 InterPro:IPR017937 Pfam:PF00085 Pfam:PF07749 PRINTS:PR00421 PROSITE:PS00194 GO:GO:0005783 GO:GO:0046686 GO:GO:0005774 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009055 GO:GO:0009793 GO:GO:0009505 UniGene:At.24396 InterPro:IPR012336 Gene3D:G3DSA:3.40.30.10 SUPFAM:SSF52833 GO:GO:0009553 GO:GO:0045454 PROSITE:PS51352 GO:GO:0015035 GO:GO:0048868 GO:GO:0034976 EMBL:AC002535 GO:GO:0006662 eggNOG:COG0526 GO:GO:0009567 GO:GO:0003756 Gene3D:G3DSA:1.20.1150.12 SUPFAM:SSF47933 KO:K09584 TIGRFAMs:TIGR01126 HOGENOM:HBG523089 OMA:FFPKGST EMBL:AF083688 EMBL:AJ271470 EMBL:AY074348 EMBL:AY091388 IPI:IPI00539517 PIR:T00437 RefSeq:NP_182269.1 UniGene:At.66351 ProteinModelPortal:O22263 SMR:O22263 STRING:O22263 SWISS-2DPAGE:O22263 PRIDE:O22263 ProMEX:O22263 EnsemblPlants:AT2G47470.1 GeneID:819360 KEGG:ath:AT2G47470 TAIR:At2g47470 InParanoid:O22263 PhylomeDB:O22263 ProtClustDB:CLSN2683612 ArrayExpress:O22263 Genevestigator:O22263 Uniprot:O22263
Leaf	Isotig03538	14	0	5.336	1.79E-05	TAIR|locus:2007559 - symbol:MCCA "AT1G03090" species:3702 "Arabidopsis thaliana" [GO:0004485 "methylcrotonoyl-CoA carboxylase activity" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0006552 "leucine catabolic process" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0050897 "cobalt ion binding" evidence=IDA] InterPro:IPR005479 InterPro:IPR005481 InterPro:IPR005482 InterPro:IPR011761 InterPro:IPR011764 InterPro:IPR013815 InterPro:IPR013816 Pfam:PF00289 Pfam:PF02785 Pfam:PF02786 PROSITE:PS00866 PROSITE:PS00867 PROSITE:PS50975 PROSITE:PS50979 SMART:SM00878 InterPro:IPR013817 InterPro:IPR016185 InterPro:IPR001882 InterPro:IPR000089 Pfam:PF00364 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005524 GO:GO:0005759 GO:GO:0004075 InterPro:IPR011054 InterPro:IPR011053 Gene3D:G3DSA:3.30.1490.20 Gene3D:G3DSA:3.30.470.20 Gene3D:G3DSA:3.40.50.20 SUPFAM:SSF51230 SUPFAM:SSF52440 SUPFAM:SSF51246 PROSITE:PS00188 PROSITE:PS50968 HOGENOM:HBG535236 GO:GO:0050897 GO:GO:0022626 GO:GO:0006552 eggNOG:COG4770 EMBL:AC006550 EMBL:U12536 EMBL:AY070723 IPI:IPI00539641 IPI:IPI00544747 PIR:G86161 RefSeq:NP_563674.1 RefSeq:NP_849583.1 UniGene:At.24059 UniGene:At.75203 ProteinModelPortal:Q42523 SMR:Q42523 STRING:Q42523 PRIDE:Q42523 EnsemblPlants:AT1G03090.2 GeneID:838362 KEGG:ath:AT1G03090 TAIR:At1g03090 InParanoid:Q42523 KO:K01968 OMA:ARIYAEH PhylomeDB:Q42523 ProtClustDB:CLSN2916952 BRENDA:6.4.1.4 ArrayExpress:Q42523 Genevestigator:Q42523 GermOnline:AT1G03090 GO:GO:0004485 Uniprot:Q42523
Leaf	Isotig03540	61	232	-1.398	4.73E-14	TAIR|locus:2135054 - symbol:ATPC1 species:3702 "Arabidopsis thaliana" [GO:0009579 "thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0006754 "ATP biosynthetic process" evidence=IMP] [GO:0009772 "photosynthetic electron transport in photosystem II" evidence=IMP] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009544 "chloroplast ATP synthase complex" evidence=TAS] [GO:0015986 "ATP synthesis coupled proton transport" evidence=TAS] [GO:0030234 "enzyme regulator activity" evidence=TAS] [GO:0009534 "chloroplast thylakoid" evidence=IDA] InterPro:IPR000131 Pfam:PF00231 PRINTS:PR00126 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0030234 GO:GO:0009941 EMBL:AL161501 GO:GO:0046933 GO:GO:0046961 GO:GO:0015986 GO:GO:0045261 EMBL:M61741 EMBL:AF149414 EMBL:AF428422 EMBL:AY065199 EMBL:AY081505 EMBL:AY088438 IPI:IPI00525302 PIR:B39732 RefSeq:NP_567265.1 UniGene:At.291 ProteinModelPortal:Q01908 SMR:Q01908 IntAct:Q01908 STRING:Q01908 PRIDE:Q01908 EnsemblPlants:AT4G04640.1 GeneID:825797 KEGG:ath:AT4G04640 TAIR:At4g04640 eggNOG:COG0224

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						HOGENOM:HBG586593 InParanoid:Q01908 KO:K02115 OMA:AGNLIND PhylomeDB:Q01908 ProtClustDB:CLSN2679503 ArrayExpress:Q01908 Genevestigator:Q01908 GermOnline:AT4G04640 GO:GO:0009544 GO:GO:0009772 InterPro:IPR023632 InterPro:IPR023633 PANTHER:PTHR11693 SUPFAM:SSF52943 TIGRFAMs:TIGR01146 PROSITE:PS00153 Uniprot:Q01908
Leaf	Isotig03541	62	229	-1.356	2.53E-13	TAIR|locus:2135054 - symbol:ATPC1 species:3702 "Arabidopsis thaliana" [GO:0009579 "thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0006754 "ATP biosynthetic process" evidence=IMP] [GO:0009772 "photosynthetic electron transport in photosystem II" evidence=IMP] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009544 "chloroplast ATP synthase complex" evidence=TAS] [GO:0015986 "ATP synthesis coupled proton transport" evidence=TAS] [GO:0030234 "enzyme regulator activity" evidence=TAS] [GO:0009534 "chloroplast thylakoid" evidence=IDA] InterPro:IPR000131 Pfam:PF00231 PRINTS:PR00126 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0030234 GO:GO:0009941 EMBL:AL161501 GO:GO:0046933 GO:GO:0046961 GO:GO:0015986 GO:GO:0045261 EMBL:M61741 EMBL:AF149414 EMBL:AF428422 EMBL:AY065199 EMBL:AY081505 EMBL:AY088438 IPI:IPI00525302 PIR:B39732 RefSeq:NP_567265.1 UniGene:At.291 ProteinModelPortal:Q01908 SMR:Q01908 IntAct:Q01908 STRING:Q01908 PRIDE:Q01908 EnsemblPlants:AT4G04640.1 GeneID:825797 KEGG:ath:AT4G04640 TAIR:At4g04640 eggNOG:COG0224 HOGENOM:HBG586593 InParanoid:Q01908 KO:K02115 OMA:AGNLIND PhylomeDB:Q01908 ProtClustDB:CLSN2679503 ArrayExpress:Q01908 Genevestigator:Q01908 GermOnline:AT4G04640 GO:GO:0009544 GO:GO:0009772 InterPro:IPR023632 InterPro:IPR023633 PANTHER:PTHR11693 SUPFAM:SSF52943 TIGRFAMs:TIGR01146 PROSITE:PS00153 Uniprot:Q01908
Leaf	Isotig03542	16	75	-1.700	7.61E-07	TAIR|locus:2099222 - symbol:CSP41A "AT3G63140" species:3702 "Arabidopsis thaliana" [GO:0003729 "mRNA binding" evidence=ISS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0008266 "poly(U) RNA binding" evidence=IDA] [GO:0006364 "rRNA processing" evidence=IGI] [GO:0048046 "apoplast" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] InterPro:IPR016040 GO:GO:0048046 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0008266 eggNOG:COG0451 GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 GO:GO:0009941 GO:GO:0009534 GO:GO:0010287 GO:GO:0006364 EMBL:AL163816 UniGene:At.48804 UniGene:At.5159 HOGENOM:HBG620021 ProtClustDB:PLN00016 EMBL:AF428269 EMBL:AY059887 EMBL:AY128804 IPI:IPI00516646 PIR:T48103 RefSeq:NP_191873.1 ProteinModelPortal:Q9LYA9 SMR:Q9LYA9 STRING:Q9LYA9 PRIDE:Q9LYA9 ProMEX:Q9LYA9 EnsemblPlants:AT3G63140.1 GeneID:825489 KEGG:ath:AT3G63140 TAIR:At3g63140 InParanoid:Q9LYA9 OMA:NISHVRD PhylomeDB:Q9LYA9 ArrayExpress:Q9LYA9 Genevestigator:Q9LYA9 Uniprot:Q9LYA9
Leaf	Isotig03543	16	75	-1.700	7.61E-07	TAIR|locus:2099222 - symbol:CSP41A "AT3G63140" species:3702 "Arabidopsis thaliana" [GO:0003729 "mRNA binding" evidence=ISS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0008266 "poly(U) RNA binding" evidence=IDA] [GO:0006364 "rRNA processing" evidence=IGI] [GO:0048046 "apoplast" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] InterPro:IPR016040 GO:GO:0048046 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0008266 eggNOG:COG0451 GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 GO:GO:0009941 GO:GO:0009534 GO:GO:0010287 GO:GO:0006364 EMBL:AL163816 UniGene:At.48804 UniGene:At.5159 HOGENOM:HBG620021 ProtClustDB:PLN00016 EMBL:AF428269 EMBL:AY059887 EMBL:AY128804 IPI:IPI00516646 PIR:T48103 RefSeq:NP_191873.1 ProteinModelPortal:Q9LYA9 SMR:Q9LYA9 STRING:Q9LYA9 PRIDE:Q9LYA9 ProMEX:Q9LYA9 EnsemblPlants:AT3G63140.1 GeneID:825489 KEGG:ath:AT3G63140 TAIR:At3g63140 InParanoid:Q9LYA9 OMA:NISHVRD PhylomeDB:Q9LYA9 ArrayExpress:Q9LYA9 Genevestigator:Q9LYA9 Uniprot:Q9LYA9
Leaf	Isotig03544	77	14	2.988	2.59E-17	TAIR|locus:2088490 - symbol:AT3G17800 "AT3G17800" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0010224 "response to UV-B" evidence=IGI;IEP] EMBL:CP002686 GO:GO:0010224 EMBL:AB019230 UniGene:At.22111 UniGene:At.71032 UniGene:At.74878 UniGene:At.74926 InterPro:IPR008479 Pfam:PF05542 ProtClustDB:CLSN2688500 EMBL:AY099554 IPI:IPI00542573 RefSeq:NP_566588.1 STRING:Q9LVJ0 PRIDE:Q9LVJ0 EnsemblPlants:AT3G17800.1 GeneID:821048

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						KEGG:ath:AT3G17800 TAIR:At3g17800 InParanoid:Q9LVJ0 OMA:RSYVMSF PhylomeDB:Q9LVJ0 Genevestigator:Q9LVJ0 Uniprot:Q9LVJ0
Leaf	Isotig03545	63	14	2.699	3.61E-13	TAIR|locus:2088490 - symbol:AT3G17800 "AT3G17800" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0010224 "response to UV-B" evidence=IGI;IEP] EMBL:CP002686 GO:GO:0010224 EMBL:AB019230 UniGene:At.22111 UniGene:At.71032 UniGene:At.74878 UniGene:At.74926 InterPro:IPR008479 Pfam:PF05542 ProtClustDB:CLSN2688500 EMBL:AY099554 IPI:IPI00542573 RefSeq:NP_566588.1 STRING:Q9LVJ0 PRIDE:Q9LVJ0 EnsemblPlants:AT3G17800.1 GeneID:821048 KEGG:ath:AT3G17800 TAIR:At3g17800 InParanoid:Q9LVJ0 OMA:RSYVMSF PhylomeDB:Q9LVJ0 Genevestigator:Q9LVJ0 Uniprot:Q9LVJ0
Leaf	Isotig03546	21	69	-1.187	0.000293971	UNIPROTKB|P10933 - symbol:PETH "Ferredoxin--NADP reductase, leaf isozyme, chloroplastic" species:3888 "Pisum sativum" [GO:0005515 "protein binding" evidence=IPI] InterPro:IPR001433 InterPro:IPR001709 InterPro:IPR012146 InterPro:IPR015701 InterPro:IPR017927 InterPro:IPR017938 Pfam:PF00175 PIRSF:PIRSF000361 PRINTS:PR00371 PROSITE:PS51384 InterPro:IPR008333 Pfam:PF00970 GO:GO:0009570 GO:GO:0005515 GO:GO:0050660 GO:GO:0006810 GO:GO:0050661 GO:GO:0022900 GO:GO:0004324 SUPFAM:SSF63380 GO:GO:0009535 GO:GO:0015979 EMBL:X12446 EMBL:L15565 EMBL:L15567 EMBL:L15569 PIR:S04030 PDB:1QFY PDB:1QFZ PDB:1QG0 PDB:1QGA PDB:2XNC PDB:3MHP PDBsum:1QFY PDBsum:1QFZ PDBsum:1QG0 PDBsum:1QGA PDBsum:2XNC PDBsum:3MHP ProteinModelPortal:P10933 SMR:P10933 IntAct:P10933 PANTHER:PTHR19384:SF1 Uniprot:P10933
Leaf	Isotig03566	20	85	-1.559	7.56E-07	TAIR|locus:2163228 - symbol:RPE "D-ribulose-5-phosphate-3-epimerase" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004750 "ribulose-phosphate 3-epimerase activity" evidence=IEA;ISS] [GO:0005975 "carbohydrate metabolic process" evidence=ISS] [GO:0009793 "embryo development ending in seed dormancy" evidence=NAS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0010319 "stromule" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009624 "response to nematode" evidence=IMP] InterPro:IPR000056 InterPro:IPR011060 InterPro:IPR013785 Pfam:PF00834 PROSITE:PS01085 PROSITE:PS01086 GO:GO:0048046 GO:GO:0009570 EMBL:CP002688 Gene3D:G3DSA:3.20.20.70 GO:GO:0005975 GO:GO:0009941 GO:GO:0009624 GO:GO:0010319 GO:GO:0009409 GO:GO:0009579 HOGENOM:HBG571751 GO:GO:0004750 PANTHER:PTHR11749 SUPFAM:SSF51366 EMBL:AB010073 KO:K01783 TIGRFAMs:TIGR01163 ProtClustDB:PLN02334 EMBL:AF015274 EMBL:AY045855 EMBL:AY091381 IPI:IPI00546385 RefSeq:NP_200949.1 RefSeq:NP_851240.1 UniGene:At.25118 UniGene:At.70668 HSSP:Q43843 ProteinModelPortal:Q9SAU2 SMR:Q9SAU2 IntAct:Q9SAU2 STRING:Q9SAU2 PRIDE:Q9SAU2 EnsemblPlants:AT5G61410.1 EnsemblPlants:AT5G61410.2 GeneID:836262 KEGG:ath:AT5G61410 TAIR:At5g61410 InParanoid:Q9SAU2 OMA:APADPYL PhylomeDB:Q9SAU2 ArrayExpress:Q9SAU2 Genevestigator:Q9SAU2 Uniprot:Q9SAU2
Leaf	Isotig03567	20	92	-1.673	6.13E-08	TAIR|locus:2163228 - symbol:RPE "D-ribulose-5-phosphate-3-epimerase" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004750 "ribulose-phosphate 3-epimerase activity" evidence=IEA;ISS] [GO:0005975 "carbohydrate metabolic process" evidence=ISS] [GO:0009793 "embryo development ending in seed dormancy" evidence=NAS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0010319 "stromule" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009624 "response to nematode" evidence=IMP] InterPro:IPR000056 InterPro:IPR011060 InterPro:IPR013785 Pfam:PF00834 PROSITE:PS01085 PROSITE:PS01086 GO:GO:0048046 GO:GO:0009570 EMBL:CP002688 Gene3D:G3DSA:3.20.20.70 GO:GO:0005975 GO:GO:0009941 GO:GO:0009624 GO:GO:0010319 GO:GO:0009409 GO:GO:0009579 HOGENOM:HBG571751 GO:GO:0004750 PANTHER:PTHR11749 SUPFAM:SSF51366 EMBL:AB010073 KO:K01783 TIGRFAMs:TIGR01163 ProtClustDB:PLN02334 EMBL:AF015274 EMBL:AY045855 EMBL:AY091381 IPI:IPI00546385 RefSeq:NP_200949.1 RefSeq:NP_851240.1 UniGene:At.25118 UniGene:At.70668 HSSP:Q43843 ProteinModelPortal:Q9SAU2 SMR:Q9SAU2 IntAct:Q9SAU2 STRING:Q9SAU2 PRIDE:Q9SAU2 EnsemblPlants:AT5G61410.1 EnsemblPlants:AT5G61410.2 GeneID:836262 KEGG:ath:AT5G61410 TAIR:At5g61410 InParanoid:Q9SAU2 OMA:APADPYL PhylomeDB:Q9SAU2 ArrayExpress:Q9SAU2 Genevestigator:Q9SAU2 Uniprot:Q9SAU2

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig03572	12	61	-1.817	3.00E-06	TAIR|locus:2031103 - symbol:FBP "AT1G43670" species:3702 "Arabidopsis thaliana" [GO:0006000 "fructose metabolic process" evidence=ISS] [GO:0042132 "fructose 1,6-bisphosphate 1-phosphatase activity" evidence=ISS;IDA] [GO:0005986 "sucrose biosynthetic process" evidence=IMP] [GO:0005983 "starch catabolic process" evidence=IMP] [GO:0015979 "photosynthesis" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0009737 "response to abscisic acid stimulus" evidence=IMP] [GO:0009750 "response to fructose stimulus" evidence=IMP] [GO:0030388 "fructose 1,6-bisphosphate metabolic process" evidence=IDA] InterPro:IPR000146 InterPro:IPR020548 Pfam:PF00316 PIRSF:PIRSF000904 PRINTS:PR00115 PROSITE:PS00124 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0009737 GO:GO:0005634 GO:GO:0046872 GO:GO:0009750 GO:GO:0005983 GO:GO:0030388 GO:GO:0015979 UniGene:At.23691 GO:GO:0042132 eggNOG:COG0158 HOGENOM:HBG731261 KO:K03841 PANTHER:PTHR11556 OMA:YGSATMV EMBL:AC009526 EMBL:BT000470 EMBL:BT008732 IPI:IPI00520560 PIR:H96499 RefSeq:NP_175032.1 UniGene:At.12074 ProteinModelPortal:Q9MA79 SMR:Q9MA79 IntAct:Q9MA79 STRING:Q9MA79 PRIDE:Q9MA79 EnsemblPlants:AT1G43670.1 GeneID:840953 KEGG:ath:AT1G43670 TAIR:At1g43670 InParanoid:Q9MA79 PhylomeDB:Q9MA79 ProtClustDB:PLN02262 BioCyc:ARA:AT1G43670-MONOMER BioCyc:MetaCyc:AT1G43670-MONOMER ArrayExpress:Q9MA79 Genevestigator:Q9MA79 GermOnline:AT1G43670 GO:GO:0005986 Uniprot:Q9MA79
Leaf	Isotig03592	7	33	-1.708	0.000997415	TAIR|locus:2095203 - symbol:AT3G23700 species:3702 "Arabidopsis thaliana" [GO:0003723 "RNA binding" evidence=IEA;ISS] [GO:0005634 "nucleus" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] InterPro:IPR003029 Pfam:PF00575 PROSITE:PS50126 GO:GO:0009570 GO:GO:0005634 EMBL:CP002686 GenomeReviews:BA000014_GR EMBL:AP000377 GO:GO:0009409 GO:GO:0003723 InterPro:IPR012340 Gene3D:G3DSA:2.40.50.140 InterPro:IPR016027 SUPFAM:SSF50249 GO:GO:0005840 InterPro:IPR022967 SMART:SM00316 HSSP:P05055 UniGene:At.6667 eggNOG:COG0539 EMBL:AY049283 EMBL:AY139796 IPI:IPI00535895 RefSeq:NP_566737.1 ProteinModelPortal:Q9LK47 SMR:Q9LK47 IntAct:Q9LK47 STRING:Q9LK47 PRIDE:Q9LK47 EnsemblPlants:AT3G23700.1 GeneID:821951 KEGG:ath:AT3G23700 TAIR:At3g23700 HOGENOM:HBG560091 InParanoid:Q9LK47 OMA:LYHLTGL PhylomeDB:Q9LK47 ProtClustDB:CLSN2688704 Genevestigator:Q9LK47 Uniprot:Q9LK47
Leaf	Isotig03596	27	6	2.699	1.95E-06	TAIR|locus:2040646 - symbol:ChlAKR "AT2G37770" species:3702 "Arabidopsis thaliana" [GO:0004033 "aldo-keto reductase (NADP) activity" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0009414 "response to water deprivation" evidence=IEP] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0016229 "steroid dehydrogenase activity" evidence=IDA] [GO:0070401 "NADP+ binding" evidence=IDA] [GO:0008106 "alcohol dehydrogenase (NADP+) activity" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0055114 "oxidation-reduction process" evidence=IDA] InterPro:IPR018170 InterPro:IPR020471 PIRSF:PIRSF000097 PRINTS:PR00069 PROSITE:PS00062 PROSITE:PS00063 PROSITE:PS00798 InterPro:IPR001395 EMBL:AC004684 Pfam:PF00248 GO:GO:0009507 EMBL:CP002685 GenomeReviews:CT485783_GR eggNOG:COG0656 GO:GO:0008106 InterPro:IPR023210 Gene3D:G3DSA:3.20.20.100 PANTHER:PTHR11732 SUPFAM:SSF51430 HOGENOM:HBG605727 GO:GO:0009409 GO:GO:0009651 GO:GO:0009414 GO:GO:0009636 GO:GO:0070401 GO:GO:0016229 EMBL:DQ837654 EMBL:BX820913 EMBL:BT004098 IPI:IPI00541607 IPI:IPI00657326 PIR:T02543 RefSeq:NP_001031505.1 RefSeq:NP_181313.3 UniGene:At.12803 PDB:3H7U PDBsum:3H7U ProteinModelPortal:Q0PGJ6 SMR:Q0PGJ6 STRING:Q0PGJ6 PRIDE:Q0PGJ6 EnsemblPlants:AT2G37770.2 GeneID:818354 KEGG:ath:AT2G37770 TAIR:At2g37770 InParanoid:Q2V420 OMA:VDIPSTW PhylomeDB:Q0PGJ6 ProtClustDB:CLSN2681439 BioCyc:MetaCyc:AT2G37770-MONOMER Genevestigator:Q0PGJ6 Uniprot:Q0PGJ6
Leaf	Isotig03597	41	7	3.079	3.75E-10	TAIR|locus:2065639 - symbol:AKR4C10 "Aldo-keto reductase family 4 member C10" species:3702 "Arabidopsis thaliana" [GO:0016491 "oxidoreductase activity" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0005634 "nucleus" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR018170 InterPro:IPR020471 PIRSF:PIRSF000097 PRINTS:PR00069 PROSITE:PS00062 PROSITE:PS00063 PROSITE:PS00798 InterPro:IPR001395 Pfam:PF00248 GO:GO:0005829 GO:GO:0005634 EMBL:CP002685 GenomeReviews:CT485783_GR HSSP:P14550 eggNOG:COG0656 InterPro:IPR023210 Gene3D:G3DSA:3.20.20.100 PANTHER:PTHR11732 SUPFAM:SSF51430 GO:GO:0016491 HOGENOM:HBG605727 KO:K00011 EMBL:DQ837655 EMBL:BT005862 EMBL:AK227354 IPI:IPI00537337

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						RefSeq:NP_181315.2 UniGene:At.45953 ProteinModelPortal:Q84TF0 SMR:Q84TF0 PRIDE:Q84TF0 EnsemblPlants:AT2G37790.1 GeneID:818356 KEGG:ath:AT2G37790 TAIR:At2g37790 InParanoid:Q84TF0 OMA:GLQMGQS PhylomeDB:Q84TF0 ProtClustDB:CLSN2918196 Genevestigator:Q84TF0 Uniprot:Q84TF0
Leaf	Isotig03623	29	154	-1.880	3.05E-14	TAIR|locus:2040934 - symbol:LHB1B2 "AT2G34420" species:3702 "Arabidopsis thaliana" [GO:0009769 "photosynthesis, light harvesting in photosystem II" evidence=TAS] [GO:0016168 "chlorophyll binding" evidence=ISS;TAS] [GO:0030076 "light-harvesting complex" evidence=ISS] [GO:0042651 "thylakoid membrane" evidence=TAS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0015979 "photosynthesis" evidence=ISS] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR001344 Pfam:PF00504 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009535 GO:GO:0010287 EMBL:AC004077 EMBL:AC004481 HOGENOM:HBG618504 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 UniGene:At.10812 UniGene:At.24351 UniGene:At.32199 UniGene:At.66422 UniGene:At.71449 UniGene:At.71528 KO:K08912 ProtClustDB:PLN00025 UniGene:At.23647 UniGene:At.27457 UniGene:At.24888 EMBL:AF372886 EMBL:AY039561 EMBL:AY045806 EMBL:AF428397 EMBL:AF419548 EMBL:AF419587 EMBL:AY065125 EMBL:AY079101 EMBL:AY079110 EMBL:AY081587 EMBL:AY142513 EMBL:AK229627 EMBL:X64460 IPI:IPI00530785 PIR:S23546 RefSeq:NP_565786.1 UniGene:At.24064 UniGene:At.71003 UniGene:At.71384 ProteinModelPortal:Q39141 SMR:Q39141 IntAct:Q39141 STRING:Q39141 PRIDE:Q39141 EnsemblPlants:AT2G34420.1 GeneID:818005 KEGG:ath:AT2G34420 TAIR:At2g34420 InParanoid:Q39141 OMA:SILAIWG PhylomeDB:Q39141 ArrayExpress:Q39141 Genevestigator:Q39141 Uniprot:Q39141
Leaf	Isotig03628	4	40	-2.793	9.13E-07	TAIR|locus:2019574 - symbol:AT1G67280 species:3702 "Arabidopsis thaliana" [GO:0004462 "lactoylglutathione lyase activity" evidence=IEA;ISS] [GO:0005975 "carbohydrate metabolic process" evidence=ISS] [GO:0046872 "metal ion binding" evidence=IEA] [GO:0031977 "thylakoid lumen" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0010319 "stromule" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] InterPro:IPR004361 InterPro:IPR018146 PROSITE:PS00934 PROSITE:PS00935 Pfam:PF00903 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009570 GO:GO:0046872 GO:GO:0010319 GO:GO:0009409 GO:GO:0031977 eggNOG:COG0346 InterPro:IPR004360 EMBL:AC002130 GO:GO:0004462 EMBL:AF419551 EMBL:AY079102 EMBL:AY085148 IPI:IPI00544224 IPI:IPI00846167 PIR:E96696 RefSeq:NP_001077783.1 RefSeq:NP_176896.1 UniGene:At.22738 HSSP:Q59384 ProteinModelPortal:Q8W593 SMR:Q8W593 STRING:Q8W593 PRIDE:Q8W593 EnsemblPlants:AT1G67280.1 GeneID:843048 KEGG:ath:AT1G67280 TAIR:At1g67280 InParanoid:Q8W593 KO:K01759 OMA:GPESSHF PhylomeDB:Q8W593 ProtClustDB:PLN02300 Genevestigator:Q8W593 TIGRFAMs:TIGR00068 Uniprot:Q8W593
Leaf	Isotig03629	4	40	-2.793	9.13E-07	TAIR|locus:2019574 - symbol:AT1G67280 species:3702 "Arabidopsis thaliana" [GO:0004462 "lactoylglutathione lyase activity" evidence=IEA;ISS] [GO:0005975 "carbohydrate metabolic process" evidence=ISS] [GO:0046872 "metal ion binding" evidence=IEA] [GO:0031977 "thylakoid lumen" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0010319 "stromule" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] InterPro:IPR004361 InterPro:IPR018146 PROSITE:PS00934 PROSITE:PS00935 Pfam:PF00903 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009570 GO:GO:0046872 GO:GO:0010319 GO:GO:0009409 GO:GO:0031977 eggNOG:COG0346 InterPro:IPR004360 EMBL:AC002130 GO:GO:0004462 EMBL:AF419551 EMBL:AY079102 EMBL:AY085148 IPI:IPI00544224 IPI:IPI00846167 PIR:E96696 RefSeq:NP_001077783.1 RefSeq:NP_176896.1 UniGene:At.22738 HSSP:Q59384 ProteinModelPortal:Q8W593 SMR:Q8W593 STRING:Q8W593 PRIDE:Q8W593 EnsemblPlants:AT1G67280.1 GeneID:843048 KEGG:ath:AT1G67280 TAIR:At1g67280 InParanoid:Q8W593 KO:K01759 OMA:GPESSHF PhylomeDB:Q8W593 ProtClustDB:PLN02300 Genevestigator:Q8W593 TIGRFAMs:TIGR00068 Uniprot:Q8W593
Leaf	Isotig03634	14	3	2.751	0.000536578	TAIR|locus:505006093 - symbol:AT1G02305 species:3702 "Arabidopsis thaliana" [GO:0004197 "cysteine-type endopeptidase activity" evidence=IEA] [GO:0006508 "proteolysis" evidence=IEA;ISS] [GO:0008234 "cysteine-type peptidase activity" evidence=IEA;ISS] [GO:0050790 "regulation of catalytic activity" evidence=IEA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] InterPro:IPR000668 InterPro:IPR012599 InterPro:IPR013128 InterPro:IPR015643 Pfam:PF00112 Pfam:PF08127 PRINTS:PR00705 SMART:SM00645

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						InterPro:IPR000169 EMBL:CP002684 GO:GO:0005773 GO:GO:0004197 GO:GO:0006508 PANTHER:PTHR12411 PROSITE:PS00139 PROSITE:PS00639 GO:GO:0050790 OMA:TIPPCEH PANTHER:PTHR12411:SF16 UniGene:At.23486 UniGene:At.42610 EMBL:AY039887 EMBL:AF428337 EMBL:BT002227 IPI:IPI00524601 RefSeq:NP_563648.1 UniGene:At.43952 HSSP:P07858 ProteinModelPortal:Q93VC9 SMR:Q93VC9 IntAct:Q93VC9 STRING:Q93VC9 MEROPS:C01.049 PRIDE:Q93VC9 EnsemblPlants:AT1G02305.1 GeneID:839538 KEGG:ath:AT1G02305 TAIR:At1g02305 InParanoid:Q93VC9 PhylomeDB:Q93VC9 ProtClustDB:CLSN2687619 Genevestigator:Q93VC9 Uniprot:Q93VC9
Leaf	Isotig03648	30	120	-1.471	1.78E-08	TAIR|locus:2154870 - symbol:AT5G66530 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004034 "aldose 1-epimerase activity" evidence=ISS] [GO:0005975 "carbohydrate metabolic process" evidence=IEA] [GO:0006012 "galactose metabolic process" evidence=ISS] [GO:0016853 "isomerase activity" evidence=IEA] [GO:0030246 "carbohydrate binding" evidence=IEA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] InterPro:IPR008183 InterPro:IPR011013 InterPro:IPR014718 Pfam:PF01263 GO:GO:0048046 GO:GO:0009570 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005975 GO:GO:0016853 GO:GO:0030246 SUPFAM:SSF74650 Gene3D:G3DSA:2.70.98.10 EMBL:AB013389 eggNOG:COG0676 HOGENOM:HBG737737 InterPro:IPR025532 PIRSF:PIRSF016020 EMBL:AY120711 EMBL:BT000037 IPI:IPI00535734 RefSeq:NP_001190635.1 RefSeq:NP_201454.1 UniGene:At.19798 ProteinModelPortal:Q9FJY6 SMR:Q9FJY6 IntAct:Q9FJY6 STRING:Q9FJY6 PRIDE:Q9FJY6 EnsemblPlants:AT5G66530.1 EnsemblPlants:AT5G66530.2 GeneID:836785 KEGG:ath:AT5G66530 TAIR:At5g66530 InParanoid:Q9FJY6 OMA:CFPQFGP PhylomeDB:Q9FJY6 ProtClustDB:CLSN2686851 ArrayExpress:Q9FJY6 Genevestigator:Q9FJY6 Uniprot:Q9FJY6
Leaf	Isotig03649	26	79	-1.074	0.000350176	TAIR|locus:2154870 - symbol:AT5G66530 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004034 "aldose 1-epimerase activity" evidence=ISS] [GO:0005975 "carbohydrate metabolic process" evidence=IEA] [GO:0006012 "galactose metabolic process" evidence=ISS] [GO:0016853 "isomerase activity" evidence=IEA] [GO:0030246 "carbohydrate binding" evidence=IEA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] InterPro:IPR008183 InterPro:IPR011013 InterPro:IPR014718 Pfam:PF01263 GO:GO:0048046 GO:GO:0009570 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005975 GO:GO:0016853 GO:GO:0030246 SUPFAM:SSF74650 Gene3D:G3DSA:2.70.98.10 EMBL:AB013389 eggNOG:COG0676 HOGENOM:HBG737737 InterPro:IPR025532 PIRSF:PIRSF016020 EMBL:AY120711 EMBL:BT000037 IPI:IPI00535734 RefSeq:NP_001190635.1 RefSeq:NP_201454.1 UniGene:At.19798 ProteinModelPortal:Q9FJY6 SMR:Q9FJY6 IntAct:Q9FJY6 STRING:Q9FJY6 PRIDE:Q9FJY6 EnsemblPlants:AT5G66530.1 EnsemblPlants:AT5G66530.2 GeneID:836785 KEGG:ath:AT5G66530 TAIR:At5g66530 InParanoid:Q9FJY6 OMA:CFPQFGP PhylomeDB:Q9FJY6 ProtClustDB:CLSN2686851 ArrayExpress:Q9FJY6 Genevestigator:Q9FJY6 Uniprot:Q9FJY6
Leaf	Isotig03650	37	15	1.832	1.11E-05	TAIR|locus:2179424 - symbol:RD22 "AT5G25610" species:3702 "Arabidopsis thaliana" [GO:0009269 "response to desiccation" evidence=IEP] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] [GO:0045735 "nutrient reservoir activity" evidence=TAS] [GO:0009651 "response to salt stress" evidence=IEP] EMBL:CP002688 GenomeReviews:BA000015_GR EMBL:AC006601 GO:GO:0009651 InterPro:IPR004873 Pfam:PF03181 SMART:SM01045 PROSITE:PS51277 EMBL:D10703 EMBL:AY090244 EMBL:AY060560 EMBL:BT009697 IPI:IPI00529761 PIR:S34823 RefSeq:NP_197943.1 UniGene:At.23701 STRING:Q08298 PRIDE:Q08298 EnsemblPlants:AT5G25610.1 GeneID:832636 KEGG:ath:AT5G25610 TAIR:At5g25610 eggNOG:NOG244743 HOGENOM:HBG748351 InParanoid:Q08298 OMA:KGGVGVN PhylomeDB:Q08298 ProtClustDB:CLSN2916419 ArrayExpress:Q08298 Genevestigator:Q08298 GermOnline:AT5G25610 Uniprot:Q08298
Leaf	Isotig03651	36	15	1.792	1.96E-05	TAIR|locus:2179424 - symbol:RD22 "AT5G25610" species:3702 "Arabidopsis thaliana" [GO:0009269 "response to desiccation" evidence=IEP] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] [GO:0045735 "nutrient reservoir activity" evidence=TAS] [GO:0009651 "response to salt stress" evidence=IEP] EMBL:CP002688 GenomeReviews:BA000015_GR EMBL:AC006601 GO:GO:0009651 InterPro:IPR004873 Pfam:PF03181 SMART:SM01045 PROSITE:PS51277 EMBL:D10703 EMBL:AY090244 EMBL:AY060560 EMBL:BT009697 IPI:IPI00529761 PIR:S34823 RefSeq:NP_197943.1 UniGene:At.23701 STRING:Q08298 PRIDE:Q08298 EnsemblPlants:AT5G25610.1 GeneID:832636 KEGG:ath:AT5G25610 TAIR:At5g25610 eggNOG:NOG244743 HOGENOM:HBG748351 InParanoid:Q08298 OMA:KGGVGVN PhylomeDB:Q08298 ProtClustDB:CLSN2916419 ArrayExpress:Q08298 Genevestigator:Q08298 GermOnline:AT5G25610 Uniprot:Q08298

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig03656	17	1	4.616	3.60E-06	TAIR|locus:2061231 - symbol:AT2G40010 "AT2G40010" species:3702 "Arabidopsis thaliana" [GO:0003735 "structural constituent of ribosome" evidence=ISS] [GO:0005840 "ribosome" evidence=ISS] [GO:0006412 "translation" evidence=ISS] [GO:0006414 "translational elongation" evidence=IEA;ISS] [GO:0042254 "ribosome biogenesis" evidence=IEA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR001790 InterPro:IPR001813 Pfam:PF00428 Pfam:PF00466 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0005515 GO:GO:0003735 GO:GO:0022626 GO:GO:0042254 EMBL:AF002109 GO:GO:0006414 eggNOG:COG0244 EMBL:BT001919 IPI:IPI00525504 PIR:B84824 RefSeq:NP_181530.1 UniGene:At.28353 UniGene:At.49578 ProteinModelPortal:O04204 SMR:O04204 IntAct:O04204 STRING:O04204 PRIDE:O04204 EnsemblPlants:AT2G40010.1 GeneID:818589 KEGG:ath:AT2G40010 TAIR:At2g40010 HOGENOM:HBG601294 InParanoid:O04204 KO:K02941 OMA:DYEKLLP PhylomeDB:O04204 ProtClustDB:CLSN2683388 ArrayExpress:O04204 Genevestigator:O04204 GermOnline:AT2G40010 Uniprot:O04204
Leaf	Isotig03657	17	1	4.616	3.60E-06	TAIR|locus:2061231 - symbol:AT2G40010 "AT2G40010" species:3702 "Arabidopsis thaliana" [GO:0003735 "structural constituent of ribosome" evidence=ISS] [GO:0005840 "ribosome" evidence=ISS] [GO:0006412 "translation" evidence=ISS] [GO:0006414 "translational elongation" evidence=IEA;ISS] [GO:0042254 "ribosome biogenesis" evidence=IEA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR001790 InterPro:IPR001813 Pfam:PF00428 Pfam:PF00466 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0005515 GO:GO:0003735 GO:GO:0022626 GO:GO:0042254 EMBL:AF002109 GO:GO:0006414 eggNOG:COG0244 EMBL:BT001919 IPI:IPI00525504 PIR:B84824 RefSeq:NP_181530.1 UniGene:At.28353 UniGene:At.49578 ProteinModelPortal:O04204 SMR:O04204 IntAct:O04204 STRING:O04204 PRIDE:O04204 EnsemblPlants:AT2G40010.1 GeneID:818589 KEGG:ath:AT2G40010 TAIR:At2g40010 HOGENOM:HBG601294 InParanoid:O04204 KO:K02941 OMA:DYEKLLP PhylomeDB:O04204 ProtClustDB:CLSN2683388 ArrayExpress:O04204 Genevestigator:O04204 GermOnline:AT2G40010 Uniprot:O04204
Leaf	Isotig03664	8	36	-1.641	0.000834246	TAIR|locus:2047072 - symbol:TIM "AT2G21170" species:3702 "Arabidopsis thaliana" [GO:0004807 "triose-phosphate isomerase activity" evidence=ISS;IDA] [GO:0009507 "chloroplast" evidence=ISS;IDA] [GO:0019253 "reductive pentose-phosphate cycle" evidence=ISS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0006642 "triglyceride mobilization" evidence=IMP] [GO:0009658 "chloroplast organization" evidence=IMP] [GO:0019563 "glycerol catabolic process" evidence=IMP] [GO:0032504 "multicellular organism reproduction" evidence=IMP] [GO:0046166 "glyceraldehyde-3-phosphate biosynthetic process" evidence=IDA] [GO:0080022 "primary root development" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR000652 InterPro:IPR013785 InterPro:IPR020861 InterPro:IPR022896 Pfam:PF00121 PROSITE:PS00171 PROSITE:PS51440 GO:GO:0005829 GO:GO:0005739 GO:GO:0048046 GO:GO:0009570 EMBL:CP002685 GenomeReviews:CT485783_GR Gene3D:G3DSA:3.20.20.70 GO:GO:0009941 GO:GO:0009658 GO:GO:0009579 GO:GO:0080022 GO:GO:0032504 UniGene:At.24668 GO:GO:0019253 EMBL:AC006264 GO:GO:0019563 GO:GO:0006642 EMBL:AF247559 EMBL:AF378898 EMBL:AY052748 EMBL:AY087893 IPI:IPI00524641 PIR:A84598 RefSeq:NP_179713.1 UniGene:At.31909 ProteinModelPortal:Q9SKP6 SMR:Q9SKP6 IntAct:Q9SKP6 STRING:Q9SKP6 World-2DPAGE:0003:Q9SKP6 PRIDE:Q9SKP6 ProMEX:Q9SKP6 EnsemblPlants:AT2G21170.1 GeneID:816652 KEGG:ath:AT2G21170 TAIR:At2g21170 eggNOG:COG0149 HOGENOM:HBG708281 InParanoid:Q9SKP6 KO:K01803 OMA:VCVGETQ PhylomeDB:Q9SKP6 ProtClustDB:PLN02429 ArrayExpress:Q9SKP6 Genevestigator:Q9SKP6 GermOnline:AT2G21170 GO:GO:0004807 GO:GO:0046166 PANTHER:PTHR21139 SUPFAM:SSF51351 TIGRFAMs:TIGR00419 Uniprot:Q9SKP6
Leaf	Isotig03712	18	5	2.377	0.000296328	TAIR|locus:2082642 - symbol:PIP2;5 "plasma membrane intrinsic protein 2;5" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=IEA;ISS] [GO:0015250 "water channel activity" evidence=ISS] [GO:0016020 "membrane" evidence=IEA;ISS] [GO:0016021 "integral to membrane" evidence=IEA] [GO:0055085 "transmembrane transport" evidence=IEA] [GO:0005515 "protein binding" evidence=IPI] InterPro:IPR000425 InterPro:IPR012269 InterPro:IPR022357 Pfam:PF00230 PRINTS:PR00783 PROSITE:PS00221 GO:GO:0016021 GO:GO:0005886 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005515 EMBL:AL049655 GO:GO:0055085 GO:GO:0005215 GO:GO:0006833 InterPro:IPR023271 Gene3D:G3DSA:1.20.1080.10 SUPFAM:SSF81338 eggNOG:COG0580 HOGENOM:HBG705794 PANTHER:PTHR19139 TIGRFAMs:TIGR00861 KO:K09872

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EMBL:AF370351 EMBL:AY062981 EMBL:BT000670 EMBL:AY084843 IPI:IPI00520414 PIR:T06738 RefSeq:NP_191042.1 UniGene:At.3117 ProteinModelPortal:Q9SV31 SMR:Q9SV31 IntAct:Q9SV31 PRIDE:Q9SV31 ProMEX:Q9SV31 EnsemblPlants:AT3G54820.1 GeneID:824647 KEGG:ath:AT3G54820 GeneFarm:4870 TAIR:At3g54820 InParanoid:Q9SV31 OMA:FIVHLAT PhylomeDB:Q9SV31 ProtClustDB:CLSN2915746 ArrayExpress:Q9SV31 Genevestigator:Q9SV31 GermOnline:AT3G54820 Uniprot:Q9SV31
Leaf	Isotig03713	19	6	2.192	0.000400191	TAIR|locus:2082642 - symbol:PIP2;5 "plasma membrane intrinsic protein 2;5" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=IEA;ISS] [GO:0015250 "water channel activity" evidence=ISS] [GO:0016020 "membrane" evidence=IEA;ISS] [GO:0016021 "integral to membrane" evidence=IEA] [GO:0055085 "transmembrane transport" evidence=IEA] [GO:0005515 "protein binding" evidence=IPI] InterPro:IPR000425 InterPro:IPR012269 InterPro:IPR022357 Pfam:PF00230 PRINTS:PR00783 PROSITE:PS00221 GO:GO:0016021 GO:GO:0005886 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005515 EMBL:AL049655 GO:GO:0055085 GO:GO:0005215 GO:GO:0006833 InterPro:IPR023271 Gene3D:G3DSA:1.20.1080.10 SUPFAM:SSF81338 eggNOG:COG0580 HOGENOM:HBG705794 PANTHER:PTHR19139 TIGRFAMs:TIGR00861 KO:K09872 EMBL:AF370351 EMBL:AY062981 EMBL:BT000670 EMBL:AY084843 IPI:IPI00520414 PIR:T06738 RefSeq:NP_191042.1 UniGene:At.3117 ProteinModelPortal:Q9SV31 SMR:Q9SV31 IntAct:Q9SV31 PRIDE:Q9SV31 ProMEX:Q9SV31 EnsemblPlants:AT3G54820.1 GeneID:824647 KEGG:ath:AT3G54820 GeneFarm:4870 TAIR:At3g54820 InParanoid:Q9SV31 OMA:FIVHLAT PhylomeDB:Q9SV31 ProtClustDB:CLSN2915746 ArrayExpress:Q9SV31 Genevestigator:Q9SV31 GermOnline:AT3G54820 Uniprot:Q9SV31
Leaf	Isotig03736	20	6	2.266	0.000209978	TAIR|locus:2010499 - symbol:AT1G28140 "AT1G28140" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0009507 "chloroplast" evidence=IDA] EMBL:CP002684 GO:GO:0009507 EMBL:AC021044 EMBL:AY054483 EMBL:AY093287 IPI:IPI00540331 PIR:C86407 RefSeq:NP_564300.1 UniGene:At.22956 IntAct:Q9FZ88 STRING:Q9FZ88 PRIDE:Q9FZ88 EnsemblPlants:AT1G28140.1 GeneID:839708 KEGG:ath:AT1G28140 TAIR:At1g28140 InParanoid:Q9FZ88 OMA:IGDKSVF PhylomeDB:Q9FZ88 ProtClustDB:CLSN2688046 ArrayExpress:Q9FZ88 Genevestigator:Q9FZ88 InterPro:IPR019275 Pfam:PF10063 Uniprot:Q9FZ88
Leaf	Isotig03737	22	6	2.403	5.66E-05	TAIR|locus:2010499 - symbol:AT1G28140 "AT1G28140" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0009507 "chloroplast" evidence=IDA] EMBL:CP002684 GO:GO:0009507 EMBL:AC021044 EMBL:AY054483 EMBL:AY093287 IPI:IPI00540331 PIR:C86407 RefSeq:NP_564300.1 UniGene:At.22956 IntAct:Q9FZ88 STRING:Q9FZ88 PRIDE:Q9FZ88 EnsemblPlants:AT1G28140.1 GeneID:839708 KEGG:ath:AT1G28140 TAIR:At1g28140 InParanoid:Q9FZ88 OMA:IGDKSVF PhylomeDB:Q9FZ88 ProtClustDB:CLSN2688046 ArrayExpress:Q9FZ88 Genevestigator:Q9FZ88 InterPro:IPR019275 Pfam:PF10063 Uniprot:Q9FZ88
Leaf	Isotig03748	22	68	-1.099	0.000728775	TAIR|locus:2183254 - symbol:AT5G19760 "AT5G19760" species:3702 "Arabidopsis thaliana" [GO:0005743 "mitochondrial inner membrane" evidence=ISS] [GO:0006810 "transport" evidence=ISS] [GO:0006839 "mitochondrial transport" evidence=ISS] [GO:0017077 "oxidative phosphorylation uncoupler activity" evidence=ISS] [GO:0005310 "dicarboxylic acid transmembrane transporter activity" evidence=IDA] [GO:0006835 "dicarboxylic acid transport" evidence=IDA] [GO:0015142 "tricarboxylic acid transmembrane transporter activity" evidence=IDA] [GO:0035674 "tricarboxylic acid transmembrane transport" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR002067 PRINTS:PR00926 Pfam:PF00153 GO:GO:0016021 GO:GO:0009506 GO:GO:0005774 EMBL:CP002688 GO:GO:0005618 GO:GO:0005488 GO:GO:0005743 GO:GO:0009941 InterPro:IPR018108 InterPro:IPR023395 Gene3D:G3DSA:1.50.40.10 SUPFAM:SSF103506 PROSITE:PS50920 GO:GO:0005310 KO:K15104 UniGene:At.24504 EMBL:AF360153 EMBL:AY056307 EMBL:AY085901 EMBL:AK226470 EMBL:AJ311780 IPI:IPI00545483 RefSeq:NP_197477.1 UniGene:At.24857 UniGene:At.49038 ProteinModelPortal:Q9C5M0 SMR:Q9C5M0 STRING:Q9C5M0 PRIDE:Q9C5M0 ProMEX:Q9C5M0 DNASU:832096 EnsemblPlants:AT5G19760.1 GeneID:832096 KEGG:ath:AT5G19760 TAIR:At5g19760 InParanoid:Q9C5M0 OMA:LRQAVYT PhylomeDB:Q9C5M0 ProtClustDB:CLSN2687170 ArrayExpress:Q9C5M0 Genevestigator:Q9C5M0 GO:GO:0015142 Uniprot:Q9C5M0
Leaf	Isotig03749	21	67	-1.145	0.000529115	TAIR|locus:2183254 - symbol:AT5G19760 "AT5G19760" species:3702 "Arabidopsis thaliana" [GO:0005743 "mitochondrial inner membrane" evidence=ISS] [GO:0006810 "transport" evidence=ISS] [GO:0006839

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						"mitochondrial transport" evidence=ISS] [GO:0017077 "oxidative phosphorylation uncoupler activity" evidence=ISS] [GO:0005310 "dicarboxylic acid transmembrane transporter activity" evidence=IDA] [GO:0006835 "dicarboxylic acid transport" evidence=IDA] [GO:0015142 "tricarboxylic acid transmembrane transporter activity" evidence=IDA] [GO:0035674 "tricarboxylic acid transmembrane transport" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR002067 PRINTS:PR00926 Pfam:PF00153 GO:GO:0016021 GO:GO:0009506 GO:GO:0005774 EMBL:CP002688 GO:GO:0005618 GO:GO:0005488 GO:GO:0005743 GO:GO:0009941 InterPro:IPR018108 InterPro:IPR023395 Gene3D:G3DSA:1.50.40.10 SUPFAM:SSF103506 PROSITE:PS50920 GO:GO:0005310 KO:K15104 UniGene:At.24504 EMBL:AF360153 EMBL:AY056307 EMBL:AY085901 EMBL:AK226470 EMBL:AJ311780 IPI:IPI00545483 RefSeq:NP_197477.1 UniGene:At.24857 UniGene:At.49038 ProteinModelPortal:Q9C5M0 SMR:Q9C5M0 STRING:Q9C5M0 PRIDE:Q9C5M0 ProMEX:Q9C5M0 DNASU:832096 EnsemblPlants:AT5G19760.1 GeneID:832096 KEGG:ath:AT5G19760 TAIR:At5g19760 InParanoid:Q9C5M0 OMA:LRQAVYT PhylomeDB:Q9C5M0 ProtClustDB:CLSN2687170 ArrayExpress:Q9C5M0 Genevestigator:Q9C5M0 GO:GO:0015142 Uniprot:Q9C5M0
Leaf	Isotig03760	144	23	3.175	1.09E-32	TAIR|locus:2034369 - symbol:ERD10 "AT1G20450" species:3702 "Arabidopsis thaliana" [GO:0006950 "response to stress" evidence=ISS] [GO:0009409 "response to cold" evidence=IEP;IDA;IMP] [GO:0009415 "response to water" evidence=ISS] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0009631 "cold acclimation" evidence=IGI] [GO:0016020 "membrane" evidence=IDA] [GO:0005634 "nucleus" evidence=ISS] [GO:0003779 "actin binding" evidence=IDA] [GO:0009414 "response to water deprivation" evidence=IEP;IMP] [GO:0010029 "regulation of seed germination" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000167 Pfam:PF00257 PROSITE:PS00315 PROSITE:PS00823 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0009506 GO:GO:0009737 GO:GO:0003779 GO:GO:0016020 EMBL:AC027665 GO:GO:0009414 GO:GO:0010029 GO:GO:0009631 HOGENOM:HBG593091 ProtClustDB:CLSN2679400 EMBL:D17714 EMBL:X90958 EMBL:AF360351 EMBL:AY136407 EMBL:AY142491 EMBL:BT002131 EMBL:AY048208 EMBL:X77614 EMBL:AF083731 IPI:IPI00548649 PIR:S60480 RefSeq:NP_850947.1 UniGene:At.24491 UniGene:At.67298 IntAct:P42759 STRING:P42759 PRIDE:P42759 EnsemblPlants:AT1G20450.1 GeneID:838633 KEGG:ath:AT1G20450 TAIR:At1g20450 eggNOG:NOG281319 InParanoid:P42759 OMA:TLASEFE PhylomeDB:P42759 ArrayExpress:P42759 Genevestigator:P42759 Uniprot:P42759
Leaf	Isotig03761	135	16	3.606	5.72E-34	TAIR|locus:2034369 - symbol:ERD10 "AT1G20450" species:3702 "Arabidopsis thaliana" [GO:0006950 "response to stress" evidence=ISS] [GO:0009409 "response to cold" evidence=IEP;IDA;IMP] [GO:0009415 "response to water" evidence=ISS] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0009631 "cold acclimation" evidence=IGI] [GO:0016020 "membrane" evidence=IDA] [GO:0005634 "nucleus" evidence=ISS] [GO:0003779 "actin binding" evidence=IDA] [GO:0009414 "response to water deprivation" evidence=IEP;IMP] [GO:0010029 "regulation of seed germination" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000167 Pfam:PF00257 PROSITE:PS00315 PROSITE:PS00823 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0009506 GO:GO:0009737 GO:GO:0003779 GO:GO:0016020 EMBL:AC027665 GO:GO:0009414 GO:GO:0010029 GO:GO:0009631 HOGENOM:HBG593091 ProtClustDB:CLSN2679400 EMBL:D17714 EMBL:X90958 EMBL:AF360351 EMBL:AY136407 EMBL:AY142491 EMBL:BT002131 EMBL:AY048208 EMBL:X77614 EMBL:AF083731 IPI:IPI00548649 PIR:S60480 RefSeq:NP_850947.1 UniGene:At.24491 UniGene:At.67298 IntAct:P42759 STRING:P42759 PRIDE:P42759 EnsemblPlants:AT1G20450.1 GeneID:838633 KEGG:ath:AT1G20450 TAIR:At1g20450 eggNOG:NOG281319 InParanoid:P42759 OMA:TLASEFE PhylomeDB:P42759 ArrayExpress:P42759 Genevestigator:P42759 Uniprot:P42759
Leaf	Isotig03776	12	2	3.114	0.000658121	TAIR|locus:2148027 - symbol:AT5G11200 species:3702 "Arabidopsis thaliana" [GO:0003676 "nucleic acid binding" evidence=IEA] [GO:0004386 "helicase activity" evidence=IEA] [GO:0005524 "ATP binding" evidence=IEA] [GO:0008026 "ATP-dependent helicase activity" evidence=IEA;ISS] [GO:0008150 "biological_process" evidence=ND] [GO:0005618 "cell wall" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR001650 InterPro:IPR011545 Pfam:PF00270 Pfam:PF00271 PROSITE:PS00039 PROSITE:PS51194 SMART:SM00490 InterPro:IPR014001 GO:GO:0009506 GO:GO:0005524

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0005634 EMBL:CP002688 GO:GO:0005618 GO:GO:0008380 GO:GO:0006397 GO:GO:0003723 SMART:SM00487 PROSITE:PS51192 GO:GO:0051028 GO:GO:0008026 EMBL:AL360314 eggNOG:COG0513 HOGENOM:HBG737336 InterPro:IPR014014 PROSITE:PS51195 IPI:IPI00760344 RefSeq:NP_568244.2 RefSeq:NP_568245.1 UniGene:At.49007 UniGene:At.73904 EnsemblPlants:AT5G11170.1 EnsemblPlants:AT5G11200.1 GeneID:830986 GeneID:830990 KEGG:ath:AT5G11170 KEGG:ath:AT5G11200 ProtClustDB:CLSN2689601 EMBL:AF378868 EMBL:AY059168 ProteinModelPortal:Q9LFN6 SMR:Q9LFN6 PRIDE:Q9LFN6 GeneFarm:1035 TAIR:At5g11200 InParanoid:Q9LFN6 PhylomeDB:Q9LFN6 Genevestigator:Q9LFN6 GermOnline:AT5G11200 Uniprot:Q9LFN6
Leaf	Isotig03780	13	53	-1.499	0.000147829	TAIR|locus:2179142 - symbol:RSR4 "AT5G01410" species:3702 "Arabidopsis thaliana" [GO:0010224 "response to UV-B" evidence=IGI] [GO:0005829 "cytosol" evidence=IDA] [GO:0042819 "vitamin B6 biosynthetic process" evidence=IGI] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0006950 "response to stress" evidence=IMP] [GO:0006979 "response to oxidative stress" evidence=IMP] [GO:0006982 "response to lipid hydroperoxide" evidence=IMP] [GO:0008615 "pyridoxine biosynthetic process" evidence=IGI] [GO:0012505 "endomembrane system" evidence=IDA] [GO:0042538 "hyperosmotic salinity response" evidence=IMP] [GO:0005515 "protein binding" evidence=IPI] [GO:0006520 "cellular amino acid metabolic process" evidence=IMP] [GO:0015994 "chlorophyll metabolic process" evidence=IMP] [GO:0042803 "protein homodimerization activity" evidence=IPI] [GO:0046982 "protein heterodimerization activity" evidence=IPI] [GO:0009651 "response to salt stress" evidence=IMP] [GO:0010335 "response to non-ionic osmotic stress" evidence=IMP] InterPro:IPR001852 InterPro:IPR011060 InterPro:IPR013785 Pfam:PF01680 PIRSF:PIRSF029271 PROSITE:PS01235 PROSITE:PS51129 GO:GO:0005829 GO:GO:0005886 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0042803 Gene3D:G3DSA:3.20.20.70 GO:GO:0003824 GO:GO:0012505 GO:GO:0006520 SUPFAM:SSF51366 GO:GO:0006982 GO:GO:0042538 EMBL:AL161746 GO:GO:0008615 GO:GO:0042823 eggNOG:COG0214 HOGENOM:HBG292342 KO:K06215 ProtClustDB:CLSN2683112 PANTHER:PTHR22854:SF9 TIGRFAMs:TIGR00343 EMBL:AY972813 EMBL:AF428298 EMBL:AF446352 EMBL:AY097428 EMBL:AY088650 EMBL:AK227197 IPI:IPI00544908 PIR:T48163 RefSeq:NP_195761.1 UniGene:At.23386 ProteinModelPortal:Q8L940 SMR:Q8L940 IntAct:Q8L940 STRING:Q8L940 PRIDE:Q8L940 ProMEX:Q8L940 DNASU:831738 EnsemblPlants:AT5G01410.1 GeneID:831738 KEGG:ath:AT5G01410 TAIR:At5g01410 InParanoid:Q8L940 OMA:RIWEGAA PhylomeDB:Q8L940 ArrayExpress:Q8L940 Genevestigator:Q8L940 GermOnline:AT5G01410 GO:GO:0015994 GO:GO:0010335 Uniprot:Q8L940
Leaf	Isotig03818	29	7	2.580	1.49E-06	TAIR|locus:2076244 - symbol:PAL4 "phenylalanine ammonia-lyase 4" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0005737 "cytoplasm" evidence=IEA] [GO:0006559 "L-phenylalanine catabolic process" evidence=IEA] [GO:0009058 "biosynthetic process" evidence=IEA] [GO:0016841 "ammonia-lyase activity" evidence=IEA] InterPro:IPR001106 InterPro:IPR005922 InterPro:IPR008948 InterPro:IPR022313 Pfam:PF00221 PROSITE:PS00488 GO:GO:0005737 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0009698 GO:GO:0009058 SUPFAM:SSF48557 GO:GO:0006559 InterPro:IPR024083 Gene3D:G3DSA:1.10.275.10 EMBL:AC009400 eggNOG:COG2986 HOGENOM:HBG318028 KO:K10775 ProtClustDB:PLN02457 BRENDA:4.3.1.24 InterPro:IPR023144 Gene3D:G3DSA:1.10.274.20 TIGRFAMs:TIGR01226 GO:GO:0016841 EMBL:AY303130 EMBL:AY099657 EMBL:BT000252 IPI:IPI00533524 RefSeq:NP_187645.1 UniGene:At.18429 UniGene:At.67148 ProteinModelPortal:Q9SS45 SMR:Q9SS45 IntAct:Q9SS45 STRING:Q9SS45 PRIDE:Q9SS45 EnsemblPlants:AT3G10340.1 GeneID:820196 KEGG:ath:AT3G10340 TAIR:At3g10340 InParanoid:Q9SS45 OMA:GERQATQ PhylomeDB:Q9SS45 ArrayExpress:Q9SS45 Genevestigator:Q9SS45 GermOnline:AT3G10340 Uniprot:Q9SS45
Leaf	Isotig03822	2	32	-3.471	1.22E-06	TAIR|locus:2149254 - symbol:SPX1 "AT5G20150" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005634 "nucleus" evidence=IDA] [GO:0016036 "cellular response to phosphate starvation" evidence=IEP] [GO:0080040 "positive regulation of cellular response to phosphate starvation" evidence=IMP] GO:GO:0005634 EMBL:CP002688 GenomeReviews:BA000015_GR EMBL:AF296825 InterPro:IPR004331 Pfam:PF03105 PROSITE:PS51382 EMBL:AY075605 EMBL:BT000868 EMBL:AY087206 IPI:IPI00537462 RefSeq:NP_197515.1 UniGene:At.19659 IntAct:Q8LBH4 STRING:Q8LBH4 PRIDE:Q8LBH4 DNASU:832137 EnsemblPlants:AT5G20150.1 GeneID:832137 KEGG:ath:AT5G20150 TAIR:At5g20150 eggNOG:NOG289536 InParanoid:Q8RY68 OMA:NGLDETW PhylomeDB:Q8LBH4 ProtClustDB:CLSN2683415 Genevestigator:Q8LBH4 Uniprot:Q8LBH4

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig03823	4	37	-2.680	3.82E-06	TAIR|locus:2043844 - symbol:SPX2 "AT2G26660" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005634 "nucleus" evidence=IDA] [GO:0016036 "cellular response to phosphate starvation" evidence=IEP] GO:GO:0005634 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0016036 EMBL:AC003105 InterPro:IPR004331 Pfam:PF03105 PROSITE:PS51382 ProtClustDB:CLSN2683415 EMBL:AK118537 EMBL:BT003688 IPI:IPI00529925 PIR:C84663 RefSeq:NP_180234.1 UniGene:At.38863 PRIDE:O48781 EnsemblPlants:AT2G26660.1 GeneID:817207 KEGG:ath:AT2G26660 TAIR:At2g26660 eggNOG:NOG311509 HOGENOM:HBG593729 InParanoid:O48781 OMA:EMINIKK PhylomeDB:O48781 Genevestigator:O48781 Uniprot:O48781
Leaf	Isotig03828	1	22	-3.930	2.59E-05	TAIR|locus:2178590 - symbol:BOU "A BOUT DE SOUFFLE" species:3702 "Arabidopsis thaliana" [GO:0005215 "transporter activity" evidence=IEA] [GO:0005743 "mitochondrial inner membrane" evidence=ISS] [GO:0006810 "transport" evidence=ISS] [GO:0006839 "mitochondrial transport" evidence=ISS;IDA] [GO:0015822 "ornithine transport" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009536 "plastid" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] Pfam:PF00153 GO:GO:0016021 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009507 GO:GO:0005743 InterPro:IPR018108 InterPro:IPR023395 Gene3D:G3DSA:1.50.40.10 SUPFAM:SSF103506 PROSITE:PS50920 GO:GO:0006839 EMBL:AB016882 HOGENOM:HBG735918 eggNOG:NOG245605 KO:K15109 EMBL:AJ277732 EMBL:AY136374 EMBL:BT000165 IPI:IPI00545279 RefSeq:NP_568670.1 UniGene:At.23694 UniGene:At.74120 ProteinModelPortal:Q93XM7 SMR:Q93XM7 STRING:Q93XM7 PRIDE:Q93XM7 EnsemblPlants:AT5G46800.1 GeneID:834724 KEGG:ath:AT5G46800 GeneFarm:3828 TAIR:At5g46800 InParanoid:Q93XM7 OMA:VLFTVRG PhylomeDB:Q93XM7 ProtClustDB:CLSN2689945 ArrayExpress:Q93XM7 Genevestigator:Q93XM7 GermOnline:AT5G46800 GO:GO:0015822 Uniprot:Q93XM7
Leaf	Isotig03829	1	22	-3.930	2.59E-05	TAIR|locus:2178590 - symbol:BOU "A BOUT DE SOUFFLE" species:3702 "Arabidopsis thaliana" [GO:0005215 "transporter activity" evidence=IEA] [GO:0005743 "mitochondrial inner membrane" evidence=ISS] [GO:0006810 "transport" evidence=ISS] [GO:0006839 "mitochondrial transport" evidence=ISS;IDA] [GO:0015822 "ornithine transport" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009536 "plastid" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] Pfam:PF00153 GO:GO:0016021 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009507 GO:GO:0005743 InterPro:IPR018108 InterPro:IPR023395 Gene3D:G3DSA:1.50.40.10 SUPFAM:SSF103506 PROSITE:PS50920 GO:GO:0006839 EMBL:AB016882 HOGENOM:HBG735918 eggNOG:NOG245605 KO:K15109 EMBL:AJ277732 EMBL:AY136374 EMBL:BT000165 IPI:IPI00545279 RefSeq:NP_568670.1 UniGene:At.23694 UniGene:At.74120 ProteinModelPortal:Q93XM7 SMR:Q93XM7 STRING:Q93XM7 PRIDE:Q93XM7 EnsemblPlants:AT5G46800.1 GeneID:834724 KEGG:ath:AT5G46800 GeneFarm:3828 TAIR:At5g46800 InParanoid:Q93XM7 OMA:VLFTVRG PhylomeDB:Q93XM7 ProtClustDB:CLSN2689945 ArrayExpress:Q93XM7 Genevestigator:Q93XM7 GermOnline:AT5G46800 GO:GO:0015822 Uniprot:Q93XM7
Leaf	Isotig03836	5329	3722	1.047	4.89E-265	UNIPROTKB|P16033 - symbol:psbA2 "Photosystem Q(B) protein 2" species:1111708 "Synechocystis sp. PCC 6803 substr. Kazusa" [GO:0030096 "plasma membrane-derived thylakoid photosystem II" evidence=IDA] HAMAP:MF_01379 InterPro:IPR000484 InterPro:IPR005867 Pfam:PF00124 PRINTS:PR00256 PROSITE:PS00244 GO:GO:0016021 GO:GO:0009635 GO:GO:0046872 GO:GO:0006810 GO:GO:0016491 EMBL:BA000022 GenomeReviews:BA000022_GR GO:GO:0042651 GO:GO:0009772 GO:GO:0030096 TCDB:3.E.2.2.2 GO:GO:0045156 EMBL:X56000 EMBL:X13547 PIR:S13112 RefSeq:NP_439906.1 RefSeq:NP_441550.1 ProteinModelPortal:P16033 SMR:P16033 IntAct:P16033 STRING:P16033 GeneID:951890 GeneID:953105 KEGG:syn:sll1867 KEGG:syn:slr1311 PATRIC:23836870 eggNOG:NOG04871 HOGENOM:HBG284766 KO:K02703 OMA:GIWFTSM PhylomeDB:P16033 ProtClustDB:CLSK892431 BioCyc:SSP1148:SLL1867-MONOMER BioCyc:SSP1148:SLR1311-MONOMER GO:GO:0030076 Gene3D:G3DSA:1.20.85.10 SUPFAM:SSF81483 TIGRFAMs:TIGR01151 Uniprot:P16033
Leaf	Isotig03837	1974	1298	1.134	6.72E-112	UNIPROTKB|P16033 - symbol:psbA2 "Photosystem Q(B) protein 2" species:1111708 "Synechocystis sp. PCC 6803 substr. Kazusa" [GO:0030096 "plasma membrane-derived thylakoid photosystem II" evidence=IDA] HAMAP:MF_01379 InterPro:IPR000484 InterPro:IPR005867 Pfam:PF00124 PRINTS:PR00256 PROSITE:PS00244 GO:GO:0016021 GO:GO:0009635 GO:GO:0046872 GO:GO:0006810 GO:GO:0016491 EMBL:BA000022 GenomeReviews:BA000022_GR GO:GO:0042651 GO:GO:0009772 GO:GO:0030096 TCDB:3.E.2.2.2 GO:GO:0045156 EMBL:X56000 EMBL:X13547 PIR:S13112 RefSeq:NP_439906.1 RefSeq:NP_441550.1 ProteinModelPortal:P16033 SMR:P16033 IntAct:P16033 STRING:P16033 GeneID:951890 GeneID:953105

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						KEGG:syn:sll1867 KEGG:syn:slr1311 PATRIC:23836870 eggNOG:NOG04871 HOGENOM:HBG284766 KO:K02703 OMA:GIWFTSM PhylomeDB:P16033 ProtClustDB:CLSK892431 BioCyc:SSP1148:SLL1867-MONOMER BioCyc:SSP1148:SLR1311-MONOMER GO:GO:0030076 Gene3D:G3DSA:1.20.85.10 SUPFAM:SSF81483 TIGRFAMs:TIGR01151 Uniprot:P16033
Leaf	Isotig03842	34	111	-1.178	5.02E-06	TAIR|locus:2015616 - symbol:ACR11 "ACT domain repeats 11" species:3702 "Arabidopsis thaliana" [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0010319 "stromule" evidence=IDA] [GO:0009416 "response to light stimulus" evidence=IEP] [GO:0009744 "response to sucrose stimulus" evidence=IEP] EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009570 GO:GO:0009941 GO:GO:0010319 GO:GO:0009409 GO:GO:0009744 GO:GO:0009416 GO:GO:0009535 EMBL:AC051629 GO:GO:0016779 UniGene:At.19280 UniGene:At.16052 UniGene:At.24697 EMBL:AF386988 EMBL:BT006317 EMBL:JF797176 IPI:IPI00517825 PIR:B86304 RefSeq:NP_564010.1 ProteinModelPortal:Q9FZ47 SMR:Q9FZ47 STRING:Q9FZ47 PRIDE:Q9FZ47 ProMEX:Q9FZ47 EnsemblPlants:AT1G16880.1 GeneID:838259 KEGG:ath:AT1G16880 TAIR:At1g16880 eggNOG:NOG288292 HOGENOM:HBG589584 InParanoid:Q9FZ47 OMA:ATIVEIT PhylomeDB:Q9FZ47 ProtClustDB:CLSN2687834 Genevestigator:Q9FZ47 Uniprot:Q9FZ47
Leaf	Isotig03843	29	116	-1.471	3.07E-08	TAIR|locus:2015616 - symbol:ACR11 "ACT domain repeats 11" species:3702 "Arabidopsis thaliana" [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0010319 "stromule" evidence=IDA] [GO:0009416 "response to light stimulus" evidence=IEP] [GO:0009744 "response to sucrose stimulus" evidence=IEP] EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009570 GO:GO:0009941 GO:GO:0010319 GO:GO:0009409 GO:GO:0009744 GO:GO:0009416 GO:GO:0009535 EMBL:AC051629 GO:GO:0016779 UniGene:At.19280 UniGene:At.16052 UniGene:At.24697 EMBL:AF386988 EMBL:BT006317 EMBL:JF797176 IPI:IPI00517825 PIR:B86304 RefSeq:NP_564010.1 ProteinModelPortal:Q9FZ47 SMR:Q9FZ47 STRING:Q9FZ47 PRIDE:Q9FZ47 ProMEX:Q9FZ47 EnsemblPlants:AT1G16880.1 GeneID:838259 KEGG:ath:AT1G16880 TAIR:At1g16880 eggNOG:NOG288292 HOGENOM:HBG589584 InParanoid:Q9FZ47 OMA:ATIVEIT PhylomeDB:Q9FZ47 ProtClustDB:CLSN2687834 Genevestigator:Q9FZ47 Uniprot:Q9FZ47
Leaf	Isotig03844	15	4	2.436	0.000806142	TAIR|locus:2098257 - symbol:AT3G51730 "AT3G51730" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0006629 "lipid metabolic process" evidence=IEA] [GO:0005773 "vacuole" evidence=IDA] InterPro:IPR007856 Pfam:PF05184 GO:GO:0005773 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0006629 InterPro:IPR008138 InterPro:IPR011001 InterPro:IPR008139 Gene3D:G3DSA:1.10.225.10 Pfam:PF03489 SMART:SM00741 SUPFAM:SSF47862 PROSITE:PS50015 EMBL:AL132968 eggNOG:NOG302685 HOGENOM:HBG750185 EMBL:AY088736 EMBL:AY125518 EMBL:AY143821 IPI:IPI00544606 PIR:T46069 RefSeq:NP_190741.1 UniGene:At.43655 ProteinModelPortal:Q9SCT5 SMR:Q9SCT5 STRING:Q9SCT5 PRIDE:Q9SCT5 EnsemblPlants:AT3G51730.1 GeneID:824336 KEGG:ath:AT3G51730 TAIR:At3g51730 InParanoid:Q9SCT5 OMA:CEEFASQ PhylomeDB:Q9SCT5 ProtClustDB:CLSN2915460 Genevestigator:Q9SCT5 Uniprot:Q9SCT5
Leaf	Isotig03858	15	1	4.436	1.60E-05	TAIR|locus:2118929 - symbol:OST1 "AT4G33950" species:3702 "Arabidopsis thaliana" [GO:0016301 "kinase activity" evidence=ISS;IDA] [GO:0009414 "response to water deprivation" evidence=IGI;IMP] [GO:0009737 "response to abscisic acid stimulus" evidence=IDA;IMP] [GO:0010119 "regulation of stomatal movement" evidence=IMP] [GO:0004672 "protein kinase activity" evidence=IDA;TAS] [GO:0009931 "calcium-dependent protein serine/threonine kinase activity" evidence=ISS] [GO:0009738 "abscisic acid mediated signaling pathway" evidence=TAS] [GO:2000377 "regulation of reactive oxygen species metabolic process" evidence=IMP] [GO:0006970 "response to osmotic stress" evidence=IGI;IDA] [GO:0009651 "response to salt stress" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0010118 "stomatal movement" evidence=IMP] [GO:0042742 "defense response to bacterium" evidence=IMP] [GO:0005829 "cytosol" evidence=RCA;IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0005985 "sucrose metabolic process" evidence=IMP] [GO:0006636 "unsaturated fatty acid biosynthetic process" evidence=IMP] [GO:0019432 "triglyceride biosynthetic process" evidence=IMP] [GO:0040007 "growth" evidence=IMP] [GO:0048366 "leaf development" evidence=IMP] InterPro:IPR000719 InterPro:IPR002290 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 Pfam:PF00069 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 SMART:SM00220

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0005829 GO:GO:0005524 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005634 GO:GO:0040007 GO:GO:0042742 GO:GO:0009738 GO:GO:0010119 eggNOG:COG0515 SUPFAM:SSF56112 GO:GO:0004674 HOGENOM:HBG755340 GO:GO:0009651 GO:GO:0009414 GO:GO:0010118 GO:GO:0019432 GO:GO:0048366 GO:GO:0006636 EMBL:AL031032 EMBL:AL161584 GO:GO:0019903 GO:GO:0010359 GO:GO:0005985 GO:GO:2000377 KO:K14498 EMBL:AJ316009 EMBL:AY054624 EMBL:AY081538 IPI:IPI00547757 IPI:IPI00900499 PIR:T05223 RefSeq:NP_567945.1 UniGene:At.2399 PDB:3UC4 PDB:3UDB PDB:3ZUT PDB:3ZUU PDBsum:3UC4 PDBsum:3UDB PDBsum:3ZUT PDBsum:3ZUU ProteinModelPortal:Q940H6 SMR:Q940H6 DIP:DIP-36705N IntAct:Q940H6 MINT:MINT-7260107 STRING:Q940H6 PRIDE:Q940H6 EnsemblPlants:AT4G33950.1 GeneID:829541 KEGG:ath:AT4G33950 TAIR:At4g33950 InParanoid:Q940H6 OMA:QYEEPEQ PhylomeDB:Q940H6 ProtClustDB:CLSN2917660 Genevestigator:Q940H6 Uniprot:Q940H6
Leaf	Isotig03866	14	0	5.336	1.79E-05	TAIR|locus:2097623 - symbol:PYD4 "PYRIMIDINE 4" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0008453 "alanine-glyoxylate transaminase activity" evidence=ISS] [GO:0008483 "transaminase activity" evidence=IEA] [GO:0030170 "pyridoxal phosphate binding" evidence=IEA] [GO:0043562 "cellular response to nitrogen levels" evidence=IEP] InterPro:IPR005814 InterPro:IPR015421 InterPro:IPR015422 Pfam:PF00202 PROSITE:PS00600 GO:GO:0005739 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0030170 InterPro:IPR015424 Gene3D:G3DSA:3.40.640.10 Gene3D:G3DSA:3.90.1150.10 SUPFAM:SSF53383 eggNOG:COG0160 HOGENOM:HBG725944 KO:K00827 ProtClustDB:CLSN2683116 GO:GO:0008453 GO:GO:0009853 PANTHER:PTHR11986 EMBL:AC010871 EMBL:AY099816 IPI:IPI00525395 RefSeq:NP_187498.1 UniGene:At.19925 ProteinModelPortal:Q9SR86 SMR:Q9SR86 STRING:Q9SR86 PRIDE:Q9SR86 EnsemblPlants:AT3G08860.1 GeneID:820034 KEGG:ath:AT3G08860 GeneFarm:5079 TAIR:At3g08860 InParanoid:Q9SR86 OMA:NWKFNVV PhylomeDB:Q9SR86 ArrayExpress:Q9SR86 Genevestigator:Q9SR86 GermOnline:AT3G08860 GO:GO:0043562 Uniprot:Q9SR86
Leaf	Isotig03868	19	3	3.192	1.46E-05	TAIR|locus:2165765 - symbol:AT5G42050 "AT5G42050" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] EMBL:CP002688 GenomeReviews:BA000015_GR InterPro:IPR013989 Pfam:PF10539 SMART:SM00767 PROSITE:PS51222 EMBL:AY080773 EMBL:AY114057 EMBL:AY088465 IPI:IPI00517664 RefSeq:NP_568600.1 UniGene:At.21438 STRING:Q8RXN8 PRIDE:Q8RXN8 EnsemblPlants:AT5G42050.1 GeneID:834210 KEGG:ath:AT5G42050 TAIR:At5g42050 eggNOG:NOG301088 HOGENOM:HBG185259 InParanoid:Q8RXN8 OMA:SLNDSIW PhylomeDB:Q8RXN8 ProtClustDB:CLSN2917728 ArrayExpress:Q8RXN8 Genevestigator:Q8RXN8 Uniprot:Q8RXN8
Leaf	Isotig03869	15	3	2.851	0.000262808	TAIR|locus:2165765 - symbol:AT5G42050 "AT5G42050" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] EMBL:CP002688 GenomeReviews:BA000015_GR InterPro:IPR013989 Pfam:PF10539 SMART:SM00767 PROSITE:PS51222 EMBL:AY080773 EMBL:AY114057 EMBL:AY088465 IPI:IPI00517664 RefSeq:NP_568600.1 UniGene:At.21438 STRING:Q8RXN8 PRIDE:Q8RXN8 EnsemblPlants:AT5G42050.1 GeneID:834210 KEGG:ath:AT5G42050 TAIR:At5g42050 eggNOG:NOG301088 HOGENOM:HBG185259 InParanoid:Q8RXN8 OMA:SLNDSIW PhylomeDB:Q8RXN8 ProtClustDB:CLSN2917728 ArrayExpress:Q8RXN8 Genevestigator:Q8RXN8 Uniprot:Q8RXN8
Leaf	Isotig03876	8	37	-1.680	0.000570683	TAIR|locus:2095375 - symbol:AT3G19970 "AT3G19970" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002686 GenomeReviews:BA000014_GR EMBL:AP002050 eggNOG:NOG241561 InterPro:IPR008547 PANTHER:PTHR12265 Pfam:PF05705 ProtClustDB:CLSN2688226 EMBL:AY039875 EMBL:BT006339 IPI:IPI00543702 RefSeq:NP_566652.1 UniGene:At.5939 ProteinModelPortal:Q9LHE8 STRING:Q9LHE8 PRIDE:Q9LHE8 EnsemblPlants:AT3G19970.1 GeneID:821535 KEGG:ath:AT3G19970 TAIR:At3g19970 HOGENOM:HBG748505 InParanoid:Q9LHE8 OMA:SYQVGGK PhylomeDB:Q9LHE8 Genevestigator:Q9LHE8 Uniprot:Q9LHE8
Leaf	Isotig03896	1	28	-4.278	1.15E-06	TAIR|locus:2175831 - symbol:PIP2;4 "AT5G60660" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=ISS] [GO:0015250 "water channel activity" evidence=ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0080170 "hydrogen peroxide transmembrane transport" evidence=IDA] [GO:0009737 "response to abscisic acid stimulus" evidence=IDA] [GO:0048767 "root hair elongation" evidence=IMP] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000425 InterPro:IPR012269 InterPro:IPR022357 Pfam:PF00230 PRINTS:PR00783 PROSITE:PS00221 GO:GO:0016021 GO:GO:0005886 GO:GO:0009506 GO:GO:0009737 EMBL:CP002688 GenomeReviews:BA000015_GR EMBL:AB005246 GO:GO:0005215 GO:GO:0048767 GO:GO:0006833 InterPro:IPR023271 Gene3D:G3DSA:1.20.1080.10 SUPFAM:SSF81338 eggNOG:COG0580

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						HOGENOM:HBG705794 PANTHER:PTHR19139 TIGRFAMs:TIGR00861 GO:GO:0080170 KO:K09872 EMBL:AK228720 EMBL:AY087245 IPI:IPI00525248 RefSeq:NP_200874.1 UniGene:At.22996 ProteinModelPortal:Q9FF53 SMR:Q9FF53 PRIDE:Q9FF53 EnsemblPlants:AT5G60660.1 GeneID:836187 KEGG:ath:AT5G60660 GeneFarm:4869 TAIR:At5g60660 InParanoid:Q9FF53 OMA:CIGHISG PhylomeDB:Q9FF53 ProtClustDB:CLSN2916407 ArrayExpress:Q9FF53 Genevestigator:Q9FF53 GermOnline:AT5G60660 Uniprot:Q9FF53
Leaf	Isotig03897	1	27	-4.226	1.93E-06	TAIR|locus:2175831 - symbol:PIP2;4 "AT5G60660" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=ISS] [GO:0015250 "water channel activity" evidence=ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0080170 "hydrogen peroxide transmembrane transport" evidence=IDA] [GO:0009737 "response to abscisic acid stimulus" evidence=IDA] [GO:0048767 "root hair elongation" evidence=IMP] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000425 InterPro:IPR012269 InterPro:IPR022357 Pfam:PF00230 PRINTS:PR00783 PROSITE:PS00221 GO:GO:0016021 GO:GO:0005886 GO:GO:0009506 GO:GO:0009737 EMBL:CP002688 GenomeReviews:BA000015_GR EMBL:AB005246 GO:GO:0005215 GO:GO:0048767 GO:GO:0006833 InterPro:IPR023271 Gene3D:G3DSA:1.20.1080.10 SUPFAM:SSF81338 eggNOG:COG0580 HOGENOM:HBG705794 PANTHER:PTHR19139 TIGRFAMs:TIGR00861 GO:GO:0080170 KO:K09872 EMBL:AK228720 EMBL:AY087245 IPI:IPI00525248 RefSeq:NP_200874.1 UniGene:At.22996 ProteinModelPortal:Q9FF53 SMR:Q9FF53 PRIDE:Q9FF53 EnsemblPlants:AT5G60660.1 GeneID:836187 KEGG:ath:AT5G60660 GeneFarm:4869 TAIR:At5g60660 InParanoid:Q9FF53 OMA:CIGHISG PhylomeDB:Q9FF53 ProtClustDB:CLSN2916407 ArrayExpress:Q9FF53 Genevestigator:Q9FF53 GermOnline:AT5G60660 Uniprot:Q9FF53
Leaf	Isotig03902	15	0	5.436	8.75E-06	No hit
Leaf	Isotig03903	14	0	5.336	1.79E-05	No hit
Leaf	Isotig03930	14	0	5.336	1.79E-05	TAIR|locus:2043142 - symbol:HAI3 "highly ABA-induced PP2C gene 3" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004722 "protein serine/threonine phosphatase activity" evidence=IEA;ISS] [GO:0006470 "protein dephosphorylation" evidence=IEA] [GO:0008287 "protein serine/threonine phosphatase complex" evidence=IEA] InterPro:IPR000222 InterPro:IPR001932 Pfam:PF00481 PROSITE:PS01032 SMART:SM00331 SMART:SM00332 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0006470 GO:GO:0004722 GO:GO:0046872 eggNOG:COG0631 Gene3D:G3DSA:3.60.40.10 SUPFAM:SSF81606 EMBL:AC004561 GO:GO:0008287 InterPro:IPR015655 PANTHER:PTHR13832 HSSP:P35813 HOGENOM:HBG747569 KO:K14497 ProtClustDB:CLSN2682567 EMBL:DQ056553 EMBL:BT022047 EMBL:BT023483 IPI:IPI00536276 PIR:F84695 RefSeq:NP_180499.1 UniGene:At.50109 ProteinModelPortal:Q9ZW21 SMR:Q9ZW21 DIP:DIP-48991N IntAct:Q9ZW21 PRIDE:Q9ZW21 EnsemblPlants:AT2G29380.1 GeneID:817487 KEGG:ath:AT2G29380 TAIR:At2g29380 InParanoid:Q9ZW21 OMA:CRNGKPV PhylomeDB:Q9ZW21 ArrayExpress:Q9ZW21 Genevestigator:Q9ZW21 Uniprot:Q9ZW21
Leaf	Isotig03931	13	0	5.229	3.68E-05	TAIR|locus:2168449 - symbol:HAI1 "AT5G59220" species:3702 "Arabidopsis thaliana" [GO:0004722 "protein serine/threonine phosphatase activity" evidence=IGI;ISS] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] [GO:0009414 "response to water deprivation" evidence=IEP] [GO:0010118 "stomatal movement" evidence=IMP] [GO:0010150 "leaf senescence" evidence=IMP] [GO:0033106 "cis-Golgi network membrane" evidence=IDA] [GO:0009658 "chloroplast organization" evidence=IMP] InterPro:IPR001932 Pfam:PF00481 PROSITE:PS01032 SMART:SM00331 SMART:SM00332 GO:GO:0009737 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0004722 GO:GO:0046872 GO:GO:0010150 GO:GO:0009414 GO:GO:0010118 eggNOG:COG0631 Gene3D:G3DSA:3.60.40.10 SUPFAM:SSF81606 GO:GO:0033106 EMBL:AB016890 InterPro:IPR015655 PANTHER:PTHR13832 HSSP:P35813 KO:K14497 EMBL:AF428395 EMBL:AY054163 EMBL:AY074555 IPI:IPI00524327 RefSeq:NP_200730.1 UniGene:At.22149 ProteinModelPortal:Q9FIF5 SMR:Q9FIF5 DIP:DIP-48992N IntAct:Q9FIF5 STRING:Q9FIF5 PRIDE:Q9FIF5 EnsemblPlants:AT5G59220.1 GeneID:836040 KEGG:ath:AT5G59220 TAIR:At5g59220 InParanoid:Q9FIF5 OMA:RMEIRRF PhylomeDB:Q9FIF5 ProtClustDB:CLSN2914857 Genevestigator:Q9FIF5 Uniprot:Q9FIF5
Leaf	Isotig03944	53	158	-1.047	7.40E-07	TAIR|locus:2040934 - symbol:LHB1B2 "AT2G34420" species:3702 "Arabidopsis thaliana" [GO:0009769 "photosynthesis, light harvesting in photosystem II" evidence=TAS] [GO:0016168 "chlorophyll binding" evidence=ISS;TAS] [GO:0030076 "light-harvesting complex" evidence=ISS] [GO:0042651 "thylakoid membrane" evidence=TAS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0015979 "photosynthesis" evidence=ISS] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009507

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						"chloroplast" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR001344 Pfam:PF00504 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009535 GO:GO:0010287 EMBL:AC004077 EMBL:AC004481 HOGENOM:HBG618504 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 UniGene:At.10812 UniGene:At.24351 UniGene:At.32199 UniGene:At.66422 UniGene:At.71449 UniGene:At.71528 KO:K08912 ProtClustDB:PLN00025 UniGene:At.23647 UniGene:At.27457 UniGene:At.24888 EMBL:AF372886 EMBL:AY039561 EMBL:AY045806 EMBL:AF428397 EMBL:AF419548 EMBL:AF419587 EMBL:AY065125 EMBL:AY079101 EMBL:AY079110 EMBL:AY081587 EMBL:AY142513 EMBL:AK229627 EMBL:X64460 IPI:IPI00530785 PIR:S23546 RefSeq:NP_565786.1 UniGene:At.24064 UniGene:At.71003 UniGene:At.71384 ProteinModelPortal:Q39141 SMR:Q39141 IntAct:Q39141 STRING:Q39141 PRIDE:Q39141 EnsemblPlants:AT2G34420.1 GeneID:818005 KEGG:ath:AT2G34420 TAIR:At2g34420 InParanoid:Q39141 OMA:SILAIWG PhylomeDB:Q39141 ArrayExpress:Q39141 Genevestigator:Q39141 Uniprot:Q39141
Leaf	Isotig03945	73	182	-0.789	2.82E-05	TAIR|locus:2040934 - symbol:LHB1B2 "AT2G34420" species:3702 "Arabidopsis thaliana" [GO:0009769 "photosynthesis, light harvesting in photosystem II" evidence=TAS] [GO:0016168 "chlorophyll binding" evidence=ISS;TAS] [GO:0030076 "light-harvesting complex" evidence=ISS] [GO:0042651 "thylakoid membrane" evidence=TAS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0015979 "photosynthesis" evidence=ISS] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR001344 Pfam:PF00504 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009535 GO:GO:0010287 EMBL:AC004077 EMBL:AC004481 HOGENOM:HBG618504 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 UniGene:At.10812 UniGene:At.24351 UniGene:At.32199 UniGene:At.66422 UniGene:At.71449 UniGene:At.71528 KO:K08912 ProtClustDB:PLN00025 UniGene:At.23647 UniGene:At.27457 UniGene:At.24888 EMBL:AF372886 EMBL:AY039561 EMBL:AY045806 EMBL:AF428397 EMBL:AF419548 EMBL:AF419587 EMBL:AY065125 EMBL:AY079101 EMBL:AY079110 EMBL:AY081587 EMBL:AY142513 EMBL:AK229627 EMBL:X64460 IPI:IPI00530785 PIR:S23546 RefSeq:NP_565786.1 UniGene:At.24064 UniGene:At.71003 UniGene:At.71384 ProteinModelPortal:Q39141 SMR:Q39141 IntAct:Q39141 STRING:Q39141 PRIDE:Q39141 EnsemblPlants:AT2G34420.1 GeneID:818005 KEGG:ath:AT2G34420 TAIR:At2g34420 InParanoid:Q39141 OMA:SILAIWG PhylomeDB:Q39141 ArrayExpress:Q39141 Genevestigator:Q39141 Uniprot:Q39141
Leaf	Isotig03948	1	17	-3.559	0.000355264	TAIR|locus:2116987 - symbol:TIP1;3 "AT4G01470" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=ISS] [GO:0015250 "water channel activity" evidence=ISS;IDA] [GO:0016020 "membrane" evidence=ISS] [GO:0006833 "water transport" evidence=IDA] [GO:0015204 "urea transmembrane transporter activity" evidence=IDA] [GO:0015840 "urea transport" evidence=IDA] InterPro:IPR000425 InterPro:IPR022357 Pfam:PF00230 PRINTS:PR00783 PROSITE:PS00221 GO:GO:0016021 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005774 GO:GO:0006950 InterPro:IPR023271 Gene3D:G3DSA:1.20.1080.10 SUPFAM:SSF81338 HOGENOM:HBG705794 PANTHER:PTHR19139 GO:GO:0015250 EMBL:AF096370 EMBL:AL161492 GO:GO:0015204 KO:K09873 ProtClustDB:PLN00027 EMBL:DQ446793 EMBL:DQ653172 IPI:IPI00524657 PIR:T01947 RefSeq:NP_192056.1 UniGene:At.65315 ProteinModelPortal:O82598 SMR:O82598 STRING:O82598 TCDB:1.A.8.10.6 PRIDE:O82598 EnsemblPlants:AT4G01470.1 GeneID:828051 KEGG:ath:AT4G01470 GeneFarm:4856 TAIR:At4g01470 eggNOG:NOG312454 InParanoid:O82598 OMA:IGSNGHE PhylomeDB:O82598 ArrayExpress:O82598 Genevestigator:O82598 Uniprot:O82598
Leaf	Isotig03949	1	17	-3.559	0.000355264	TAIR|locus:2116987 - symbol:TIP1;3 "AT4G01470" species:3702 "Arabidopsis thaliana" [GO:0006810 "transport" evidence=ISS] [GO:0015250 "water channel activity" evidence=ISS;IDA] [GO:0016020 "membrane" evidence=ISS] [GO:0006833 "water transport" evidence=IDA] [GO:0015204 "urea transmembrane transporter activity" evidence=IDA] [GO:0015840 "urea transport" evidence=IDA] InterPro:IPR000425 InterPro:IPR022357 Pfam:PF00230 PRINTS:PR00783 PROSITE:PS00221 GO:GO:0016021 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005774 GO:GO:0006950 InterPro:IPR023271 Gene3D:G3DSA:1.20.1080.10 SUPFAM:SSF81338 HOGENOM:HBG705794 PANTHER:PTHR19139 GO:GO:0015250 EMBL:AF096370 EMBL:AL161492 GO:GO:0015204 KO:K09873 ProtClustDB:PLN00027

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EMBL:DQ446793 EMBL:DQ653172 IPI:IPI00524657 PIR:T01947 RefSeq:NP_192056.1 UniGene:At.65315 ProteinModelPortal:O82598 SMR:O82598 STRING:O82598 TCDB:1.A.8.10.6 PRIDE:O82598 EnsemblPlants:AT4G01470.1 GeneID:828051 KEGG:ath:AT4G01470 GeneFarm:4856 TAIR:At4g01470 eggNOG:NOG312454 InParanoid:O82598 OMA:IGSNGHE PhylomeDB:O82598 ArrayExpress:O82598 Genevestigator:O82598 Uniprot:O82598
Leaf	Isotig03950	1	20	-3.793	7.36E-05	TAIR|locus:2169150 - symbol:AT5G37360 "AT5G37360" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009535 EMBL:AY058859 EMBL:AY103300 IPI:IPI00538544 RefSeq:NP_198552.1 UniGene:At.21463 STRING:Q93Z11 PRIDE:Q93Z11 EnsemblPlants:AT5G37360.1 GeneID:833710 KEGG:ath:AT5G37360 TAIR:At5g37360 eggNOG:NOG276204 HOGENOM:HBG316765 InParanoid:Q93Z11 OMA:QYANDNA PhylomeDB:Q93Z11 ProtClustDB:CLSN2686903 Genevestigator:Q93Z11 Uniprot:Q93Z11
Leaf	Isotig03951	1	20	-3.793	7.36E-05	TAIR|locus:2169150 - symbol:AT5G37360 "AT5G37360" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009535 EMBL:AY058859 EMBL:AY103300 IPI:IPI00538544 RefSeq:NP_198552.1 UniGene:At.21463 STRING:Q93Z11 PRIDE:Q93Z11 EnsemblPlants:AT5G37360.1 GeneID:833710 KEGG:ath:AT5G37360 TAIR:At5g37360 eggNOG:NOG276204 HOGENOM:HBG316765 InParanoid:Q93Z11 OMA:QYANDNA PhylomeDB:Q93Z11 ProtClustDB:CLSN2686903 Genevestigator:Q93Z11 Uniprot:Q93Z11
Leaf	Isotig03958	44	235	-1.888	4.88E-21	TAIR|locus:2082717 - symbol:LHCA1 "AT3G54890" species:3702 "Arabidopsis thaliana" [GO:0015979 "photosynthesis" evidence=ISS] [GO:0016168 "chlorophyll binding" evidence=ISS] [GO:0030076 "light-harvesting complex" evidence=ISS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009768 "photosynthesis, light harvesting in photosystem I" evidence=IMP] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009637 "response to blue light" evidence=IEP] [GO:0010114 "response to red light" evidence=IEP] [GO:0010218 "response to far red light" evidence=IEP] [GO:0009534 "chloroplast thylakoid" evidence=IDA] InterPro:IPR001344 Pfam:PF00504 GO:GO:0016021 EMBL:CP002686 GenomeReviews:BA000014_GR EMBL:AL049655 GO:GO:0046872 GO:GO:0009941 GO:GO:0009637 GO:GO:0010218 GO:GO:0010114 GO:GO:0018298 GO:GO:0009535 GO:GO:0010287 HOGENOM:HBG618504 GO:GO:0009522 GO:GO:0009523 GO:GO:0016168 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 EMBL:M85150 EMBL:X56062 EMBL:AF324692 EMBL:AF325016 EMBL:AF326866 EMBL:AF339688 EMBL:AF361847 EMBL:AY070473 EMBL:AY094437 EMBL:BT000852 EMBL:AK317555 IPI:IPI00516813 PIR:S25435 RefSeq:NP_191049.1 UniGene:At.23982 UniGene:At.67867 PDB:2O01 PDB:2WSC PDB:2WSE PDB:2WSF PDBsum:2O01 PDBsum:2WSC PDBsum:2WSE PDBsum:2WSF ProteinModelPortal:Q01667 SMR:Q01667 DIP:DIP-59003N STRING:Q01667 PRIDE:Q01667 ProMEX:Q01667 EnsemblPlants:AT3G54890.1 GeneID:824654 KEGG:ath:AT3G54890 TAIR:At3g54890 eggNOG:NOG263751 InParanoid:Q01667 KO:K08907 OMA:FCVQQSA PhylomeDB:Q01667 ProtClustDB:PLN00099 ArrayExpress:Q01667 Genevestigator:Q01667 GO:GO:0009768 Uniprot:Q01667
Leaf	Isotig03959	34	200	-2.027	8.98E-20	TAIR|locus:2082717 - symbol:LHCA1 "AT3G54890" species:3702 "Arabidopsis thaliana" [GO:0015979 "photosynthesis" evidence=ISS] [GO:0016168 "chlorophyll binding" evidence=ISS] [GO:0030076 "light-harvesting complex" evidence=ISS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009768 "photosynthesis, light harvesting in photosystem I" evidence=IMP] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009637 "response to blue light" evidence=IEP] [GO:0010114 "response to red light" evidence=IEP] [GO:0010218 "response to far red light" evidence=IEP] [GO:0009534 "chloroplast thylakoid" evidence=IDA] InterPro:IPR001344 Pfam:PF00504 GO:GO:0016021 EMBL:CP002686 GenomeReviews:BA000014_GR EMBL:AL049655 GO:GO:0046872 GO:GO:0009941 GO:GO:0009637 GO:GO:0010218 GO:GO:0010114 GO:GO:0018298 GO:GO:0009535 GO:GO:0010287 HOGENOM:HBG618504 GO:GO:0009522 GO:GO:0009523 GO:GO:0016168 InterPro:IPR022796

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 EMBL:M85150 EMBL:X56062 EMBL:AF324692 EMBL:AF325016 EMBL:AF326866 EMBL:AF339688 EMBL:AF361847 EMBL:AY070473 EMBL:AY094437 EMBL:BT000852 EMBL:AK317555 IPI:IPI00516813 PIR:S25435 RefSeq:NP_191049.1 UniGene:At.23982 UniGene:At.67867 PDB:2O01 PDB:2WSC PDB:2WSE PDB:2WSF PDBsum:2O01 PDBsum:2WSC PDBsum:2WSE PDBsum:2WSF ProteinModelPortal:Q01667 SMR:Q01667 DIP:DIP-59003N STRING:Q01667 PRIDE:Q01667 ProMEX:Q01667 EnsemblPlants:AT3G54890.1 GeneID:824654 KEGG:ath:AT3G54890 TAIR:At3g54890 eggNOG:NOG263751 InParanoid:Q01667 KO:K08907 OMA:FCVQQSA PhylomeDB:Q01667 ProtClustDB:PLN00099 ArrayExpress:Q01667 Genevestigator:Q01667 GO:GO:0009768 Uniprot:Q01667
Leaf	Isotig03962	3	23	-2.410	0.000598058	TAIR|locus:2202150 - symbol:Lhca6 "AT1G19150" species:3702 "Arabidopsis thaliana" [GO:0015979 "photosynthesis" evidence=ISS] [GO:0016168 "chlorophyll binding" evidence=ISS] [GO:0030076 "light-harvesting complex" evidence=ISS] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009637 "response to blue light" evidence=IEP] [GO:0010114 "response to red light" evidence=IEP] [GO:0010218 "response to far red light" evidence=IEP] InterPro:IPR001344 Pfam:PF00504 EMBL:CP002684 GO:GO:0009507 GO:GO:0016020 GO:GO:0009637 GO:GO:0010218 GO:GO:0010114 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 EMBL:AY086461 EMBL:BT020322 EMBL:BT020554 IPI:IPI00532569 RefSeq:NP_173349.1 UniGene:At.359 ProteinModelPortal:Q8LCQ4 SMR:Q8LCQ4 STRING:Q8LCQ4 PRIDE:Q8LCQ4 DNASU:838498 EnsemblPlants:AT1G19150.1 GeneID:838498 KEGG:ath:AT1G19150 TAIR:At1g19150 InParanoid:Q8LCQ4 KO:K08908 OMA:WFAQAEL PhylomeDB:Q8LCQ4 ProtClustDB:PLN00098 Genevestigator:Q8LCQ4 Uniprot:Q8LCQ4
Leaf	Isotig03963	3	24	-2.471	0.000374243	TAIR|locus:2202150 - symbol:Lhca6 "AT1G19150" species:3702 "Arabidopsis thaliana" [GO:0015979 "photosynthesis" evidence=ISS] [GO:0016168 "chlorophyll binding" evidence=ISS] [GO:0030076 "light-harvesting complex" evidence=ISS] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009637 "response to blue light" evidence=IEP] [GO:0010114 "response to red light" evidence=IEP] [GO:0010218 "response to far red light" evidence=IEP] InterPro:IPR001344 Pfam:PF00504 EMBL:CP002684 GO:GO:0009507 GO:GO:0016020 GO:GO:0009637 GO:GO:0010218 GO:GO:0010114 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 EMBL:AY086461 EMBL:BT020322 EMBL:BT020554 IPI:IPI00532569 RefSeq:NP_173349.1 UniGene:At.359 ProteinModelPortal:Q8LCQ4 SMR:Q8LCQ4 STRING:Q8LCQ4 PRIDE:Q8LCQ4 DNASU:838498 EnsemblPlants:AT1G19150.1 GeneID:838498 KEGG:ath:AT1G19150 TAIR:At1g19150 InParanoid:Q8LCQ4 KO:K08908 OMA:WFAQAEL PhylomeDB:Q8LCQ4 ProtClustDB:PLN00098 Genevestigator:Q8LCQ4 Uniprot:Q8LCQ4
Leaf	Isotig03964	13	2	3.229	0.00031313	TAIR|locus:2075054 - symbol:SYP71 "AT3G09740" species:3702 "Arabidopsis thaliana" [GO:0006886 "intracellular protein transport" evidence=TAS] [GO:0008565 "protein transporter activity" evidence=TAS] [GO:0016021 "integral to membrane" evidence=TAS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0006612 "protein targeting to membrane" evidence=IDA] [GO:0005783 "endoplasmic reticulum" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000727 InterPro:IPR006012 Pfam:PF05739 PROSITE:PS00914 PROSITE:PS50192 GO:GO:0005783 GO:GO:0016021 GO:GO:0005886 GO:GO:0009506 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0006612 GO:GO:0008565 EMBL:AC016661 GO:GO:0005484 EMBL:AF355757 EMBL:AY090358 IPI:IPI00523840 RefSeq:NP_566354.1 UniGene:At.20899 UniGene:At.66500 ProteinModelPortal:Q9SF29 SMR:Q9SF29 STRING:Q9SF29 PRIDE:Q9SF29 EnsemblPlants:AT3G09740.1 GeneID:820132 KEGG:ath:AT3G09740 GeneFarm:3895 TAIR:At3g09740 eggNOG:NOG71047 HOGENOM:HBG317868 InParanoid:Q9SF29 KO:K08506 OMA:MTVIDIL PhylomeDB:Q9SF29 ProtClustDB:CLSN2688218 ArrayExpress:Q9SF29 Genevestigator:Q9SF29 GermOnline:AT3G09740 Uniprot:Q9SF29
Leaf	Isotig03965	13	2	3.229	0.00031313	TAIR|locus:2075054 - symbol:SYP71 "AT3G09740" species:3702 "Arabidopsis thaliana" [GO:0006886 "intracellular protein transport" evidence=TAS] [GO:0008565 "protein transporter activity" evidence=TAS] [GO:0016021 "integral to membrane" evidence=TAS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0006612 "protein targeting to membrane" evidence=IDA] [GO:0005783 "endoplasmic reticulum" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000727 InterPro:IPR006012 Pfam:PF05739 PROSITE:PS00914 PROSITE:PS50192 GO:GO:0005783 GO:GO:0016021 GO:GO:0005886 GO:GO:0009506 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0006612 GO:GO:0008565 EMBL:AC016661 GO:GO:0005484 EMBL:AF355757 EMBL:AY090358 IPI:IPI00523840 RefSeq:NP_566354.1 UniGene:At.20899 UniGene:At.66500

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						ProteinModelPortal:Q9SF29 SMR:Q9SF29 STRING:Q9SF29 PRIDE:Q9SF29 EnsemblPlants:AT3G09740.1 GeneID:820132 KEGG:ath:AT3G09740 GeneFarm:3895 TAIR:At3g09740 eggNOG:NOG71047 HOGENOM:HBG317868 InParanoid:Q9SF29 KO:K08506 OMA:MTVIDIL PhylomeDB:Q9SF29 ProtClustDB:CLSN2688218 ArrayExpress:Q9SF29 Genevestigator:Q9SF29 GermOnline:AT3G09740 Uniprot:Q9SF29
Leaf	Isotig03991	31	16	1.483	0.000541208	TAIR|locus:2118314 - symbol:AT4G29260 species:3702 "Arabidopsis thaliana" [GO:0003993 "acid phosphatase activity" evidence=IEA;ISS] [GO:0008150 "biological_process" evidence=ND] [GO:0005773 "vacuole" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR005519 InterPro:IPR010028 Pfam:PF03767 GO:GO:0005829 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005774 InterPro:IPR023214 Gene3D:G3DSA:3.40.50.1000 SUPFAM:SSF56784 GO:GO:0003993 EMBL:AL161574 HOGENOM:HBG599685 InterPro:IPR014403 PIRSF:PIRSF002674 TIGRFAMs:TIGR01675 eggNOG:NOG41277 ProtClustDB:CLSN2685345 EMBL:AY050945 EMBL:AY091175 IPI:IPI00548735 PIR:T13437 RefSeq:NP_194655.1 UniGene:At.4537 UniGene:At.48918 ProteinModelPortal:Q9M0F5 PRIDE:Q9M0F5 DNASU:829047 EnsemblPlants:AT4G29260.1 GeneID:829047 KEGG:ath:AT4G29260 TAIR:At4g29260 InParanoid:Q9M0F5 OMA:SFDEWVD PhylomeDB:Q9M0F5 Genevestigator:Q9M0F5 Uniprot:Q9M0F5
Leaf	Isotig04004	15	88	-2.024	1.65E-09	TAIR|locus:2099906 - symbol:TPI "AT3G55440" species:3702 "Arabidopsis thaliana" [GO:0004807 "triose-phosphate isomerase activity" evidence=ISS;IDA] [GO:0005829 "cytosol" evidence=ISS;IDA] [GO:0008152 "metabolic process" evidence=ISS] [GO:0006096 "glycolysis" evidence=IC] [GO:0044262 "cellular carbohydrate metabolic process" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0010043 "response to zinc ion" evidence=IEP] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR000652 InterPro:IPR013785 InterPro:IPR020861 InterPro:IPR022896 Pfam:PF00121 PROSITE:PS00171 PROSITE:PS51440 GO:GO:0005829 GO:GO:0005739 GO:GO:0005886 GO:GO:0009506 GO:GO:0048046 GO:GO:0009570 GO:GO:0046686 GO:GO:0005774 GO:GO:0005618 EMBL:CP002686 GenomeReviews:BA000014_GR Gene3D:G3DSA:3.20.20.70 GO:GO:0010043 GO:GO:0006098 GO:GO:0005507 GO:GO:0006094 GO:GO:0009651 GO:GO:0006096 EMBL:AL132975 eggNOG:COG0149 HOGENOM:HBG708281 KO:K01803 GO:GO:0004807 PANTHER:PTHR21139 SUPFAM:SSF51351 TIGRFAMs:TIGR00419 EMBL:U02949 EMBL:AF375426 EMBL:AY074822 IPI:IPI00549121 PIR:T47683 PIR:T50646 RefSeq:NP_191104.1 UniGene:At.24563 UniGene:At.31873 ProteinModelPortal:P48491 SMR:P48491 IntAct:P48491 STRING:P48491 SWISS-2DPAGE:P48491 World-2DPAGE:0003:P48491 PRIDE:P48491 ProMEX:P48491 EnsemblPlants:AT3G55440.1 GeneID:824710 KEGG:ath:AT3G55440 TAIR:At3g55440 InParanoid:P48491 OMA:ISGQWPR PhylomeDB:P48491 ProtClustDB:PLN02561 BioCyc:ARA:AT3G55440-MONOMER BioCyc:MetaCyc:AT3G55440-MONOMER ArrayExpress:P48491 Genevestigator:P48491 GermOnline:AT3G55440 Uniprot:P48491
Leaf	Isotig04005	19	88	-1.683	1.05E-07	TAIR|locus:2099906 - symbol:TPI "AT3G55440" species:3702 "Arabidopsis thaliana" [GO:0004807 "triose-phosphate isomerase activity" evidence=ISS;IDA] [GO:0005829 "cytosol" evidence=ISS;IDA] [GO:0008152 "metabolic process" evidence=ISS] [GO:0006096 "glycolysis" evidence=IC] [GO:0044262 "cellular carbohydrate metabolic process" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0010043 "response to zinc ion" evidence=IEP] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR000652 InterPro:IPR013785 InterPro:IPR020861 InterPro:IPR022896 Pfam:PF00121 PROSITE:PS00171 PROSITE:PS51440 GO:GO:0005829 GO:GO:0005739 GO:GO:0005886 GO:GO:0009506 GO:GO:0048046 GO:GO:0009570 GO:GO:0046686 GO:GO:0005774 GO:GO:0005618 EMBL:CP002686 GenomeReviews:BA000014_GR Gene3D:G3DSA:3.20.20.70 GO:GO:0010043 GO:GO:0006098 GO:GO:0005507 GO:GO:0006094 GO:GO:0009651 GO:GO:0006096 EMBL:AL132975

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						eggNOG:COG0149 HOGENOM:HBG708281 KO:K01803 GO:GO:0004807 PANTHER:PTHR21139 SUPFAM:SSF51351 TIGRFAMs:TIGR00419 EMBL:U02949 EMBL:AF375426 EMBL:AY074822 IPI:IPI00549121 PIR:T47683 PIR:T50646 RefSeq:NP_191104.1 UniGene:At.24563 UniGene:At.31873 ProteinModelPortal:P48491 SMR:P48491 IntAct:P48491 STRING:P48491 SWISS-2DPAGE:P48491 World-2DPAGE:0003:P48491 PRIDE:P48491 ProMEX:P48491 EnsemblPlants:AT3G55440.1 GeneID:824710 KEGG:ath:AT3G55440 TAIR:At3g55440 InParanoid:P48491 OMA:ISGQWPR PhylomeDB:P48491 ProtClustDB:PLN02561 BioCyc:ARA:AT3G55440-MONOMER BioCyc:MetaCyc:AT3G55440-MONOMER ArrayExpress:P48491 Genevestigator:P48491 GermOnline:AT3G55440 Uniprot:P48491
Leaf	Isotig04020	12	0	5.114	7.63E-05	TAIR|locus:2047695 - symbol:AT2G19390 "AT2G19390" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002685 GenomeReviews:CT485783_GR EMBL:AC003058 IPI:IPI00541161 PIR:T01287 RefSeq:NP_565452.1 UniGene:At.26637 PRIDE:O64572 EnsemblPlants:AT2G19390.1 GeneID:816458 KEGG:ath:AT2G19390 TAIR:At2g19390 eggNOG:NOG248195 HOGENOM:HBG597217 InParanoid:O64572 OMA:NEANSEY PhylomeDB:O64572 ProtClustDB:CLSN2685390 Genevestigator:O64572 Uniprot:O64572
Leaf	Isotig04026	19	1	4.777	8.26E-07	TAIR|locus:2078481 - symbol:FER3 "AT3G56090" species:3702 "Arabidopsis thaliana" [GO:0006826 "iron ion transport" evidence=IGI;ISS] [GO:0006879 "cellular iron ion homeostasis" evidence=ISS] [GO:0008199 "ferric iron binding" evidence=IEA;ISS] [GO:0016491 "oxidoreductase activity" evidence=IEA] [GO:0046914 "transition metal ion binding" evidence=IEA] [GO:0009507 "chloroplast" evidence=ISS;IDA] [GO:0010039 "response to iron ion" evidence=IEP] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0000302 "response to reactive oxygen species" evidence=IGI] [GO:0009908 "flower development" evidence=IGI] [GO:0015979 "photosynthesis" evidence=IGI] [GO:0048366 "leaf development" evidence=IGI] [GO:0055072 "iron ion homeostasis" evidence=IGI] [GO:0009570 "chloroplast stroma" evidence=IDA] InterPro:IPR001519 InterPro:IPR008331 InterPro:IPR009078 Pfam:PF00210 GO:GO:0009570 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0016020 GO:GO:0009941 GO:GO:0006879 GO:GO:0010039 eggNOG:COG1528 HOGENOM:HBG750128 GO:GO:0008199 GO:GO:0004322 GO:GO:0006826 InterPro:IPR009040 InterPro:IPR012347 Gene3D:G3DSA:1.20.1260.10 PANTHER:PTHR11431 SUPFAM:SSF47240 PROSITE:PS50905 EMBL:AL163763 InterPro:IPR014034 PROSITE:PS00540 PROSITE:PS00204 KO:K00522 ProtClustDB:CLSN2683400 EMBL:AJ312190 EMBL:AY072221 EMBL:AY122951 IPI:IPI00526405 PIR:T47726 RefSeq:NP_191168.1 UniGene:At.20042 UniGene:At.67841 ProteinModelPortal:Q9LYN2 SMR:Q9LYN2 STRING:Q9LYN2 PRIDE:Q9LYN2 EnsemblPlants:AT3G56090.1 GeneID:824775 KEGG:ath:AT3G56090 TAIR:At3g56090 InParanoid:Q9LYN2 OMA:QEEMTHA PhylomeDB:Q9LYN2 ArrayExpress:Q9LYN2 Genevestigator:Q9LYN2 GermOnline:AT3G56090 Uniprot:Q9LYN2
Leaf	Isotig04027	23	2	4.053	1.83E-07	TAIR|locus:2063104 - symbol:FER4 "AT2G40300" species:3702 "Arabidopsis thaliana" [GO:0006826 "iron ion transport" evidence=IGI;ISS] [GO:0006879 "cellular iron ion homeostasis" evidence=ISS] [GO:0008199 "ferric iron binding" evidence=IEA;ISS] [GO:0016491 "oxidoreductase activity" evidence=IEA] [GO:0046914 "transition metal ion binding" evidence=IEA] [GO:0009507 "chloroplast" evidence=ISS;IDA] [GO:0010039 "response to iron ion" evidence=IEP] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0000302 "response to reactive oxygen species" evidence=IGI] [GO:0009908 "flower development" evidence=IGI] [GO:0015979 "photosynthesis" evidence=IGI] [GO:0048366 "leaf development" evidence=IGI] [GO:0055072 "iron ion homeostasis" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0071214 "cellular response to abiotic stimulus" evidence=IMP] InterPro:IPR001519 InterPro:IPR008331 InterPro:IPR009078 Pfam:PF00210 GO:GO:0005739 GO:GO:0009570 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009941 GO:GO:0006879 EMBL:AF085279 GO:GO:0010039 eggNOG:COG1528 HOGENOM:HBG750128 GO:GO:0008199 GO:GO:0004322 GO:GO:0006826 InterPro:IPR009040 InterPro:IPR012347 Gene3D:G3DSA:1.20.1260.10 PANTHER:PTHR11431 SUPFAM:SSF47240 PROSITE:PS50905 EMBL:AC007020 UniGene:At.27228 InterPro:IPR014034 PROSITE:PS00540 PROSITE:PS00204 KO:K00522 ProtClustDB:CLSN2683400 EMBL:AJ312191 EMBL:AY062795 EMBL:AY081615 IPI:IPI00534160 PIR:G84827 RefSeq:NP_181559.1 UniGene:At.69019 ProteinModelPortal:Q9S756 SMR:Q9S756 STRING:Q9S756 PRIDE:Q9S756 EnsemblPlants:AT2G40300.1 GeneID:818622 KEGG:ath:AT2G40300 TAIR:At2g40300 InParanoid:Q9S756 OMA:AMAYHFD PhylomeDB:Q9S756 ArrayExpress:Q9S756 Genevestigator:Q9S756 GermOnline:AT2G40300 Uniprot:Q9S756

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig04032	14	1	4.336	3.39E-05	TAIR|locus:2019858 - symbol:SYP52 "AT1G79590" species:3702 "Arabidopsis thaliana" [GO:0005484 "SNAP receptor activity" evidence=TAS] [GO:0010008 "endosome membrane" evidence=NAS;TAS] [GO:0016192 "vesicle-mediated transport" evidence=TAS] [GO:0005773 "vacuole" evidence=IDA] InterPro:IPR000727 InterPro:IPR006012 Pfam:PF05739 PROSITE:PS00914 PROSITE:PS50192 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005773 GO:GO:0006886 GO:GO:0005794 GO:GO:0031902 GO:GO:0016192 EMBL:AC010793 GO:GO:0005484 eggNOG:NOG259218 HOGENOM:HBG562798 KO:K08503 ProtClustDB:CLSN2687826 EMBL:AF355756 EMBL:BT003941 EMBL:BT006106 EMBL:AY086285 IPI:IPI00532229 PIR:C96827 RefSeq:NP_001031301.1 RefSeq:NP_565213.1 UniGene:At.19840 ProteinModelPortal:Q94KK7 SMR:Q94KK7 STRING:Q94KK7 PRIDE:Q94KK7 EnsemblPlants:AT1G79590.1 EnsemblPlants:AT1G79590.2 GeneID:844297 KEGG:ath:AT1G79590 GeneFarm:3889 TAIR:At1g79590 InParanoid:Q94KK7 OMA:MALINID PhylomeDB:Q94KK7 ArrayExpress:Q94KK7 Genevestigator:Q94KK7 GermOnline:AT1G79590 Uniprot:Q94KK7
Leaf	Isotig04033	13	1	4.229	7.21E-05	TAIR|locus:2019858 - symbol:SYP52 "AT1G79590" species:3702 "Arabidopsis thaliana" [GO:0005484 "SNAP receptor activity" evidence=TAS] [GO:0010008 "endosome membrane" evidence=NAS;TAS] [GO:0016192 "vesicle-mediated transport" evidence=TAS] [GO:0005773 "vacuole" evidence=IDA] InterPro:IPR000727 InterPro:IPR006012 Pfam:PF05739 PROSITE:PS00914 PROSITE:PS50192 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005773 GO:GO:0006886 GO:GO:0005794 GO:GO:0031902 GO:GO:0016192 EMBL:AC010793 GO:GO:0005484 eggNOG:NOG259218 HOGENOM:HBG562798 KO:K08503 ProtClustDB:CLSN2687826 EMBL:AF355756 EMBL:BT003941 EMBL:BT006106 EMBL:AY086285 IPI:IPI00532229 PIR:C96827 RefSeq:NP_001031301.1 RefSeq:NP_565213.1 UniGene:At.19840 ProteinModelPortal:Q94KK7 SMR:Q94KK7 STRING:Q94KK7 PRIDE:Q94KK7 EnsemblPlants:AT1G79590.1 EnsemblPlants:AT1G79590.2 GeneID:844297 KEGG:ath:AT1G79590 GeneFarm:3889 TAIR:At1g79590 InParanoid:Q94KK7 OMA:MALINID PhylomeDB:Q94KK7 ArrayExpress:Q94KK7 Genevestigator:Q94KK7 GermOnline:AT1G79590 Uniprot:Q94KK7
Leaf	Isotig04037	107	86	0.844	4.37E-05	TAIR|locus:2153529 - symbol:PRX52 "AT5G05340" species:3702 "Arabidopsis thaliana" [GO:0004601 "peroxidase activity" evidence=ISS] [GO:0006979 "response to oxidative stress" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0005618 "cell wall" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0005829 "cytosol" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR000823 InterPro:IPR002016 InterPro:IPR010255 InterPro:IPR019793 InterPro:IPR019794 Pfam:PF00141 PRINTS:PR00458 PRINTS:PR00461 PROSITE:PS00435 PROSITE:PS00436 PROSITE:PS50873 GO:GO:0005829 GO:GO:0048046 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005618 GO:GO:0005515 GO:GO:0020037 GO:GO:0004601 GO:GO:0042744 HOGENOM:HBG597790 SUPFAM:SSF48113 EMBL:AB010692 KO:K00430 EMBL:AY065270 IPI:IPI00527468 RefSeq:NP_196153.1 UniGene:At.28537 ProteinModelPortal:Q9FLC0 SMR:Q9FLC0 IntAct:Q9FLC0 STRING:Q9FLC0 PeroxiBase:218 PRIDE:Q9FLC0 EnsemblPlants:AT5G05340.1 GeneID:830416 KEGG:ath:AT5G05340 GeneFarm:1905 TAIR:At5g05340 eggNOG:NOG298084 InParanoid:Q9FLC0 OMA:TNFRARI PhylomeDB:Q9FLC0 ProtClustDB:CLSN2916362 ArrayExpress:Q9FLC0 Genevestigator:Q9FLC0 GermOnline:AT5G05340 Uniprot:Q9FLC0
Leaf	Isotig04041	2	29	-3.329	5.61E-06	TAIR|locus:2099362 - symbol:SWEET2 "AT3G14770" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0016020 "membrane" evidence=IEA;ISS] [GO:0016021 "integral to membrane" evidence=IEA] [GO:0005887 "integral to plasma membrane" evidence=ISS] [GO:0051119 "sugar transmembrane transporter activity" evidence=ISS] InterPro:IPR004316 Pfam:PF03083 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005887 EMBL:AP002061 GO:GO:0051119 PANTHER:PTHR10791 KO:K15382 OMA:EPLIVSY EMBL:AY054229 EMBL:AY066044 EMBL:AK230146 IPI:IPI00534203 RefSeq:NP_566493.1 UniGene:At.26391 EnsemblPlants:AT3G14770.1 GeneID:820705 KEGG:ath:AT3G14770 TAIR:At3g14770 eggNOG:NOG304578 InParanoid:Q9LH79 PhylomeDB:Q9LH79 ProtClustDB:CLSN2688384 Genevestigator:Q9LH79 Uniprot:Q9LH79
Leaf	Isotig04044	46	0	7.053	2.29E-14	TAIR|locus:2093307 - symbol:AT3G15670 "AT3G15670" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0009793 "embryo development ending in seed dormancy" evidence=ISS] [GO:0005634 "nucleus" evidence=IDA] GO:GO:0005634 EMBL:CP002686 EMBL:AB017071 ProtClustDB:CLSN2679745 EMBL:AY040026 EMBL:AY054162 EMBL:AY079410 IPI:IPI00542660 RefSeq:NP_188188.1 UniGene:At.5382 STRING:Q9LW12 PRIDE:Q9LW12 ProMEX:Q9LW12 EnsemblPlants:AT3G15670.1 GeneID:820810 KEGG:ath:AT3G15670 TAIR:At3g15670 InParanoid:Q9LW12 OMA:QYTKETA PhylomeDB:Q9LW12 ArrayExpress:Q9LW12 Genevestigator:Q9LW12 Uniprot:Q9LW12

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig04045	46	0	7.053	2.29E-14	TAIR|locus:2093307 - symbol:AT3G15670 "AT3G15670" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0009793 "embryo development ending in seed dormancy" evidence=ISS] [GO:0005634 "nucleus" evidence=IDA] GO:GO:0005634 EMBL:CP002686 EMBL:AB017071 ProtClustDB:CLSN2679745 EMBL:AY040026 EMBL:AY054162 EMBL:AY079410 IPI:IPI00542660 RefSeq:NP_188188.1 UniGene:At.5382 STRING:Q9LW12 PRIDE:Q9LW12 ProMEX:Q9LW12 EnsemblPlants:AT3G15670.1 GeneID:820810 KEGG:ath:AT3G15670 TAIR:At3g15670 InParanoid:Q9LW12 OMA:QYTKETA PhylomeDB:Q9LW12 ArrayExpress:Q9LW12 Genevestigator:Q9LW12 Uniprot:Q9LW12
Leaf	Isotig04064	21	66	-1.123	0.000706272	TAIR|locus:2164265 - symbol:2-Cys Prx B "AT5G06290" species:3702 "Arabidopsis thaliana" [GO:0016209 "antioxidant activity" evidence=ISS] [GO:0051920 "peroxiredoxin activity" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0010319 "stromule" evidence=IDA] [GO:0042742 "defense response to bacterium" evidence=IEP] [GO:0048046 "apoplast" evidence=IDA] InterPro:IPR000866 InterPro:IPR019479 Pfam:PF00578 Pfam:PF10417 GO:GO:0048046 GO:GO:0009570 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0042742 GO:GO:0010319 GO:GO:0009409 InterPro:IPR012336 Gene3D:G3DSA:3.40.30.10 SUPFAM:SSF52833 HOGENOM:HBG493509 PROSITE:PS51352 eggNOG:COG0450 KO:K03386 GO:GO:0004601 GO:GO:0051920 InterPro:IPR024706 PIRSF:PIRSF000239 ProtClustDB:CLSN2716862 EMBL:AB006700 EMBL:AF324689 EMBL:AF326871 EMBL:AF339693 EMBL:AY054621 EMBL:AY081503 IPI:IPI00539263 RefSeq:NP_568166.1 UniGene:At.7277 HSSP:P32119 ProteinModelPortal:Q9C5R8 SMR:Q9C5R8 IntAct:Q9C5R8 STRING:Q9C5R8 PeroxiBase:4361 PRIDE:Q9C5R8 EnsemblPlants:AT5G06290.1 GeneID:830517 KEGG:ath:AT5G06290 TAIR:At5g06290 InParanoid:Q9C5R8 PhylomeDB:Q9C5R8 ArrayExpress:Q9FED5 Genevestigator:Q9C5R8 Uniprot:Q9C5R8
Leaf	Isotig04066	14	1	4.336	3.39E-05	TAIR|locus:2171417 - symbol:AT5G16550 "AT5G16550" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002688 EMBL:AB005242 UniGene:At.66763 IPI:IPI00527710 RefSeq:NP_568333.1 PRIDE:Q9FFC9 EnsemblPlants:AT5G16550.1 GeneID:831517 KEGG:ath:AT5G16550 TAIR:At5g16550 InParanoid:Q9FFC9 OMA:REVNIES PhylomeDB:Q9FFC9 ProtClustDB:CLSN2689715 Genevestigator:Q9FFC9 Uniprot:Q9FFC9
Leaf	Isotig04067	14	1	4.336	3.39E-05	TAIR|locus:2171417 - symbol:AT5G16550 "AT5G16550" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002688 EMBL:AB005242 UniGene:At.66763 IPI:IPI00527710 RefSeq:NP_568333.1 PRIDE:Q9FFC9 EnsemblPlants:AT5G16550.1 GeneID:831517 KEGG:ath:AT5G16550 TAIR:At5g16550 InParanoid:Q9FFC9 OMA:REVNIES PhylomeDB:Q9FFC9 ProtClustDB:CLSN2689715 Genevestigator:Q9FFC9 Uniprot:Q9FFC9
Leaf	Isotig04106	14	0	5.336	1.79E-05	TAIR|locus:2158735 - symbol:AT5G44310 "AT5G44310" species:3702 "Arabidopsis thaliana" [GO:0009793 "embryo development ending in seed dormancy" evidence=ISS] EMBL:CP002688 EMBL:AB011475 IPI:IPI00522827 RefSeq:NP_199244.1 UniGene:At.43190 PRIDE:Q9FKV7 EnsemblPlants:AT5G44310.2 GeneID:834454 KEGG:ath:AT5G44310 TAIR:At5g44310 InParanoid:Q9FKV7 OMA:NEGASRA ProtClustDB:CLSN2687244 Genevestigator:Q9FKV7 Uniprot:Q9FKV7
Leaf	Isotig04112	1	24	-4.056	9.12E-06	TAIR|locus:2194065 - symbol:AT1G18170 "AT1G18170" species:3702 "Arabidopsis thaliana" [GO:0000413 "protein peptidyl-prolyl isomerization" evidence=IBA] [GO:0003755 "peptidyl-prolyl cis-trans isomerase activity" evidence=ISS;IBA] [GO:0005528 "FK506 binding" evidence=ISS;IBA] [GO:0018208 "peptidyl-proline modification" evidence=IBA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] InterPro:IPR001179 Pfam:PF00254 PROSITE:PS50059 PANTHER:PTHR10516 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0006457 GO:GO:0009535 EMBL:AC034107 EMBL:AC069551 GO:GO:0003755 GO:GO:0009543 eggNOG:COG0545 InterPro:IPR023566 EMBL:AF334381 EMBL:AY088153 IPI:IPI00545630 RefSeq:NP_564048.1 UniGene:At.20994 HSSP:Q9SCY2 ProteinModelPortal:Q9LDY5 SMR:Q9LDY5 STRING:Q9LDY5 PRIDE:Q9LDY5 EnsemblPlants:AT1G18170.1 GeneID:838396 KEGG:ath:AT1G18170 TAIR:At1g18170 HOGENOM:HBG608110 InParanoid:Q9LDY5 OMA:ALVMGSR PhylomeDB:Q9LDY5 ProtClustDB:CLSN2687851 ArrayExpress:Q9LDY5 Genevestigator:Q9LDY5 Uniprot:Q9LDY5
Leaf	Isotig04113	2	23	-2.995	0.000115946	TAIR|locus:2194065 - symbol:AT1G18170 "AT1G18170" species:3702 "Arabidopsis thaliana" [GO:0000413 "protein peptidyl-prolyl isomerization" evidence=IBA] [GO:0003755 "peptidyl-prolyl cis-trans isomerase activity" evidence=ISS;IBA] [GO:0005528 "FK506 binding" evidence=ISS;IBA] [GO:0018208 "peptidyl-proline modification" evidence=IBA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] InterPro:IPR001179 Pfam:PF00254 PROSITE:PS50059 PANTHER:PTHR10516 EMBL:CP002684

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GenomeReviews:CT485782_GR GO:GO:0006457 GO:GO:0009535 EMBL:AC034107 EMBL:AC069551 GO:GO:0003755 GO:GO:0009543 eggNOG:COG0545 InterPro:IPR023566 EMBL:AF334381 EMBL:AY088153 IPI:IPI00545630 RefSeq:NP_564048.1 UniGene:At.20994 HSSP:Q9SCY2 ProteinModelPortal:Q9LDY5 SMR:Q9LDY5 STRING:Q9LDY5 PRIDE:Q9LDY5 EnsemblPlants:AT1G18170.1 GeneID:838396 KEGG:ath:AT1G18170 TAIR:At1g18170 HOGENOM:HBG608110 InParanoid:Q9LDY5 OMA:ALVMGSR PhylomeDB:Q9LDY5 ProtClustDB:CLSN2687851 ArrayExpress:Q9LDY5 Genevestigator:Q9LDY5 Uniprot:Q9LDY5
Leaf	Isotig04118	1	16	-3.471	0.000601166	TAIR|locus:2011671 - symbol:AT1G76550 "AT1G76550" species:3702 "Arabidopsis thaliana" [GO:0006096 "glycolysis" evidence=ISS] [GO:0010317 "pyrophosphate-dependent phosphofructokinase complex, alpha-subunit complex" evidence=ISS] [GO:0047334 "diphosphate-fructose-6-phosphate 1-phosphotransferase activity" evidence=ISS;IMP] [GO:0015979 "photosynthesis" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR000023 InterPro:IPR011183 InterPro:IPR013981 Pfam:PF00365 PIRSF:PIRSF005677 EMBL:CP002684 GO:GO:0005524 GO:GO:0006096 GO:GO:0015979 EMBL:AC015450 GO:GO:0005945 GO:GO:0003872 SUPFAM:SSF53784 HSSP:P70826 GO:GO:0047334 Gene3D:G3DSA:1.10.10.480 TIGRFAMs:TIGR02477 KO:K00895 IPI:IPI00538921 PIR:E96793 RefSeq:NP_177781.1 UniGene:At.23436 UniGene:At.67125 ProteinModelPortal:Q9C9K3 SMR:Q9C9K3 STRING:Q9C9K3 PRIDE:Q9C9K3 EnsemblPlants:AT1G76550.1 GeneID:843988 KEGG:ath:AT1G76550 TAIR:At1g76550 InParanoid:Q9C9K3 OMA:DMLGRTK PhylomeDB:Q9C9K3 ProtClustDB:PLN03028 Genevestigator:Q9C9K3 Uniprot:Q9C9K3
Leaf	Isotig04119	1	16	-3.471	0.000601166	TAIR|locus:2011671 - symbol:AT1G76550 "AT1G76550" species:3702 "Arabidopsis thaliana" [GO:0006096 "glycolysis" evidence=ISS] [GO:0010317 "pyrophosphate-dependent phosphofructokinase complex, alpha-subunit complex" evidence=ISS] [GO:0047334 "diphosphate-fructose-6-phosphate 1-phosphotransferase activity" evidence=ISS;IMP] [GO:0015979 "photosynthesis" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR000023 InterPro:IPR011183 InterPro:IPR013981 Pfam:PF00365 PIRSF:PIRSF005677 EMBL:CP002684 GO:GO:0005524 GO:GO:0006096 GO:GO:0015979 EMBL:AC015450 GO:GO:0005945 GO:GO:0003872 SUPFAM:SSF53784 HSSP:P70826 GO:GO:0047334 Gene3D:G3DSA:1.10.10.480 TIGRFAMs:TIGR02477 KO:K00895 IPI:IPI00538921 PIR:E96793 RefSeq:NP_177781.1 UniGene:At.23436 UniGene:At.67125 ProteinModelPortal:Q9C9K3 SMR:Q9C9K3 STRING:Q9C9K3 PRIDE:Q9C9K3 EnsemblPlants:AT1G76550.1 GeneID:843988 KEGG:ath:AT1G76550 TAIR:At1g76550 InParanoid:Q9C9K3 OMA:DMLGRTK PhylomeDB:Q9C9K3 ProtClustDB:PLN03028 Genevestigator:Q9C9K3 Uniprot:Q9C9K3
Leaf	Isotig04122	55	7	3.503	1.73E-14	TAIR|locus:2140411 - symbol:AT4G19390 "AT4G19390" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0009941 "chloroplast envelope" evidence=IDA] EMBL:CP002687 GO:GO:0009941 InterPro:IPR005134 Pfam:PF03350 EMBL:AF378856 IPI:IPI00545210 RefSeq:NP_567583.1 UniGene:At.19094 PRIDE:Q94JM4 EnsemblPlants:AT4G19390.1 GeneID:827680 KEGG:ath:AT4G19390 TAIR:At4g19390 InParanoid:Q94JM4 OMA:LCFIKGC PhylomeDB:Q94JM4 ProtClustDB:CLSN2917585 Genevestigator:Q94JM4 InterPro:IPR016804 PIRSF:PIRSF022348 Uniprot:Q94JM4
Leaf	Isotig04123	47	5	3.762	3.35E-13	TAIR|locus:2140411 - symbol:AT4G19390 "AT4G19390" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0009941 "chloroplast envelope" evidence=IDA] EMBL:CP002687 GO:GO:0009941 InterPro:IPR005134 Pfam:PF03350 EMBL:AF378856 IPI:IPI00545210 RefSeq:NP_567583.1 UniGene:At.19094 PRIDE:Q94JM4 EnsemblPlants:AT4G19390.1 GeneID:827680 KEGG:ath:AT4G19390 TAIR:At4g19390 InParanoid:Q94JM4 OMA:LCFIKGC PhylomeDB:Q94JM4 ProtClustDB:CLSN2917585 Genevestigator:Q94JM4 InterPro:IPR016804 PIRSF:PIRSF022348 Uniprot:Q94JM4
Leaf	Isotig04130	5	31	-2.103	0.000244415	TAIR|locus:2075522 - symbol:TRXF1 "AT3G02730" species:3702 "Arabidopsis thaliana" [GO:0008047 "enzyme activator activity" evidence=IDA] [GO:0043085 "positive regulation of catalytic activity" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0004857 "enzyme inhibitor activity" evidence=IDA] [GO:0006109 "regulation of carbohydrate metabolic process" evidence=IDA] [GO:0043086 "negative regulation of catalytic activity" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] InterPro:IPR005746 InterPro:IPR013766 InterPro:IPR017937 Pfam:PF00085 PRINTS:PR00421 PROSITE:PS00194 GO:GO:0009570 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0006109 GO:GO:0009055 GO:GO:0006810 GO:GO:0004857 GO:GO:0022900 InterPro:IPR012336 Gene3D:G3DSA:3.40.30.10 SUPFAM:SSF52833 HOGENOM:HBG493509 GO:GO:0045454 PROSITE:PS51352 GO:GO:0015035 GO:GO:0008047 GO:GO:0009534 EMBL:AC018363 GO:GO:0006662 PANTHER:PTHR10438 eggNOG:COG0526 EMBL:AF144385 EMBL:AY065391 EMBL:AY096721 EMBL:AY084778 IPI:IPI00518514 RefSeq:NP_186922.1 UniGene:At.20211 UniGene:At.46169 ProteinModelPortal:Q9XFH8 SMR:Q9XFH8 STRING:Q9XFH8

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						PRIDE:Q9XFH8 ProMEX:Q9XFH8 EnsemblPlants:AT3G02730.1 GeneID:821260 KEGG:ath:AT3G02730 GeneFarm:2480 TAIR:At3g02730 InParanoid:Q9XFH8 OMA:CRIPYSG PhylomeDB:Q9XFH8 ProtClustDB:CLSN2685211 ArrayExpress:Q9XFH8 Genevestigator:Q9XFH8 GermOnline:AT3G02730 Uniprot:Q9XFH8
Leaf	Isotig04140	110	14	3.503	2.08E-27	TIGR_CMR|BA_4858 - symbol:BA_4858 "thioesterase family protein" species:198094 "Bacillus anthracis str. Ames" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] InterPro:IPR000524 InterPro:IPR000644 Pfam:PF00392 Pfam:PF00571 PROSITE:PS51371 SMART:SM00116 InterPro:IPR006683 Pfam:PF03061 EMBL:AE016879 EMBL:AE017334 EMBL:AE017225 GenomeReviews:AE016879_GR GenomeReviews:AE017225_GR GenomeReviews:AE017334_GR GO:GO:0003700 InterPro:IPR011991 Gene3D:G3DSA:1.10.10.10 GO:GO:0005622 InterPro:IPR010766 Pfam:PF07085 HOGENOM:HBG314023 OMA:PIISTSY ProtClustDB:CLSK873528 RefSeq:NP_847059.1 RefSeq:YP_021501.1 RefSeq:YP_030753.1 ProteinModelPortal:Q81KX8 DNASU:1084014 EnsemblBacteria:EBBACT00000012784 EnsemblBacteria:EBBACT00000018567 EnsemblBacteria:EBBACT00000019988 GeneID:1084014 GeneID:2818548 GeneID:2850363 KEGG:ban:BA_4858 KEGG:bar:GBAA_4858 KEGG:bat:BAS4505 TIGR:BA_4858 TIGR:GBAA4858 Uniprot:Q81KX8
Leaf	Isotig04141	106	14	3.450	3.60E-26	TIGR_CMR|BA_4858 - symbol:BA_4858 "thioesterase family protein" species:198094 "Bacillus anthracis str. Ames" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] InterPro:IPR000524 InterPro:IPR000644 Pfam:PF00392 Pfam:PF00571 PROSITE:PS51371 SMART:SM00116 InterPro:IPR006683 Pfam:PF03061 EMBL:AE016879 EMBL:AE017334 EMBL:AE017225 GenomeReviews:AE016879_GR GenomeReviews:AE017225_GR GenomeReviews:AE017334_GR GO:GO:0003700 InterPro:IPR011991 Gene3D:G3DSA:1.10.10.10 GO:GO:0005622 InterPro:IPR010766 Pfam:PF07085 HOGENOM:HBG314023 OMA:PIISTSY ProtClustDB:CLSK873528 RefSeq:NP_847059.1 RefSeq:YP_021501.1 RefSeq:YP_030753.1 ProteinModelPortal:Q81KX8 DNASU:1084014 EnsemblBacteria:EBBACT00000012784 EnsemblBacteria:EBBACT00000018567 EnsemblBacteria:EBBACT00000019988 GeneID:1084014 GeneID:2818548 GeneID:2850363 KEGG:ban:BA_4858 KEGG:bar:GBAA_4858 KEGG:bat:BAS4505 TIGR:BA_4858 TIGR:GBAA4858 Uniprot:Q81KX8
Leaf	Isotig04161	16	0	5.529	4.31E-06	TAIR|locus:2044641 - symbol:COR413-PM1 "AT2G15970" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005886 "plasma membrane" evidence=ISS] [GO:0009631 "cold acclimation" evidence=IEP] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] [GO:0042631 "cellular response to water deprivation" evidence=IEP] [GO:0005773 "vacuole" evidence=IDA] GO:GO:0009737 GO:GO:0005773 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0042631 GO:GO:0009631 EMBL:AC006438 UniGene:At.22305 HOGENOM:HBG595418 ProtClustDB:CLSN2717102 InterPro:IPR008892 Pfam:PF05562 eggNOG:NOG267474 EMBL:AF283004 EMBL:AY093767 EMBL:AY088558 EMBL:AY143813 EMBL:AB044404 IPI:IPI00547690 PIR:C84535 RefSeq:NP_179196.1 UniGene:At.24347 STRING:Q9XIM7 PRIDE:Q9XIM7 EnsemblPlants:AT2G15970.1 GeneID:816092 KEGG:ath:AT2G15970 TAIR:At2g15970 InParanoid:Q9XIM7 OMA:GTTFLEW PhylomeDB:Q9XIM7 ArrayExpress:Q9XIM7 Genevestigator:Q9XIM7 Uniprot:Q9XIM7
Leaf	Isotig04166	16	1	4.529	7.58E-06	TAIR|locus:2828343 - symbol:AT2G07741 species:3702 "Arabidopsis thaliana" [GO:0015078 "hydrogen ion transmembrane transporter activity" evidence=IEA] [GO:0015986 "ATP synthesis coupled proton transport" evidence=IEA] [GO:0015992 "proton transport" evidence=ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0045263 "proton-transporting ATP synthase complex, coupling factor F(o)" evidence=IEA] [GO:0046933 "hydrogen ion transporting ATP synthase activity, rotational mechanism" evidence=ISS] InterPro:IPR000568 Pfam:PF00119 PRINTS:PR00123 GO:GO:0016021 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0005743 EMBL:AC006225 GO:GO:0015986 GO:GO:0015078 GO:GO:0045263 EMBL:Y08501 EMBL:JF729200 EMBL:JF729201 EMBL:JF729202 EMBL:EF488888 EMBL:EF488889 IPI:IPI00544815 IPI:IPI01019875 RefSeq:NP_085503.1 RefSeq:NP_178810.1 UniGene:At.70276 ProteinModelPortal:P93298 IntAct:P93298 STRING:P93298 PRIDE:P93298 GeneID:814588 GeneID:815413 GenomeReviews:Y08501_GR KEGG:ath:ArthMp035 KEGG:ath:AT2G07741 TAIR:AtMg00410 eggNOG:COG0356 HOGENOM:HBG734175 InParanoid:P93298 KO:K02126 PhylomeDB:P93298 ProtClustDB:CLSN2683503 Genevestigator:P93298 GermOnline:ATMG00410 InterPro:IPR023011 Gene3D:G3DSA:1.20.120.220 PANTHER:PTHR11410 SUPFAM:SSF81336 TIGRFAMs:TIGR01131 PROSITE:PS00449 Uniprot:P93298
Leaf	Isotig04167	10	0	4.851	0.000336918	No hit

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig04170	10	1	3.851	0.00071293	TAIR|locus:2206265 - symbol:AT1G65320 "AT1G65320" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0005773 "vacuole" evidence=IDA] InterPro:IPR000644 Pfam:PF00571 PROSITE:PS51371 SMART:SM00116 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005774 EMBL:AC004512 EMBL:AK117112 IPI:IPI00524279 PIR:T02355 RefSeq:NP_176711.1 UniGene:At.35899 UniGene:At.67954 ProteinModelPortal:Q8GZA4 SMR:Q8GZA4 PRIDE:Q8GZA4 EnsemblPlants:AT1G65320.1 GeneID:842840 KEGG:ath:AT1G65320 TAIR:At1g65320 eggNOG:NOG311373 HOGENOM:HBG320396 InParanoid:Q8GZA4 OMA:KLWKCDY PhylomeDB:Q8GZA4 ProtClustDB:CLSN2679616 Genevestigator:Q8GZA4 Uniprot:Q8GZA4
Leaf	Isotig04171	10	1	3.851	0.00071293	TAIR|locus:2206265 - symbol:AT1G65320 "AT1G65320" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0005773 "vacuole" evidence=IDA] InterPro:IPR000644 Pfam:PF00571 PROSITE:PS51371 SMART:SM00116 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005774 EMBL:AC004512 EMBL:AK117112 IPI:IPI00524279 PIR:T02355 RefSeq:NP_176711.1 UniGene:At.35899 UniGene:At.67954 ProteinModelPortal:Q8GZA4 SMR:Q8GZA4 PRIDE:Q8GZA4 EnsemblPlants:AT1G65320.1 GeneID:842840 KEGG:ath:AT1G65320 TAIR:At1g65320 eggNOG:NOG311373 HOGENOM:HBG320396 InParanoid:Q8GZA4 OMA:KLWKCDY PhylomeDB:Q8GZA4 ProtClustDB:CLSN2679616 Genevestigator:Q8GZA4 Uniprot:Q8GZA4
Leaf	Isotig04175	1	17	-3.559	0.000355264	TAIR|locus:2185193 - symbol:OHP "AT5G02120" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009644 "response to high light intensity" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009644 GO:GO:0009535 EMBL:AL162508 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 SUPFAM:SSF103511 EMBL:AF054617 EMBL:AY062846 EMBL:AY081584 IPI:IPI00526059 PIR:T48233 RefSeq:NP_195832.1 UniGene:At.23559 ProteinModelPortal:O81208 SMR:O81208 STRING:O81208 PRIDE:O81208 EnsemblPlants:AT5G02120.1 GeneID:831799 KEGG:ath:AT5G02120 TAIR:At5g02120 eggNOG:NOG146316 HOGENOM:HBG750329 InParanoid:O81208 OMA:QTAEIWN PhylomeDB:O81208 ProtClustDB:CLSN2916752 ArrayExpress:O81208 Genevestigator:O81208 Uniprot:O81208
Leaf	Isotig04227	3	26	-2.587	0.000145202	TAIR|locus:2064097 - symbol:AT2G38610 "AT2G38610" species:3702 "Arabidopsis thaliana" [GO:0003676 "nucleic acid binding" evidence=ISS] [GO:0003723 "RNA binding" evidence=IEA] [GO:0008150 "biological_process" evidence=ND] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR004087 InterPro:IPR004088 Pfam:PF00013 PROSITE:PS50084 SMART:SM00322 GO:GO:0005829 GO:GO:0005634 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0003723 EMBL:AC005499 eggNOG:COG5176 HSSP:Q32NN2 HOGENOM:HBG319392 EMBL:AY042804 EMBL:AY064682 EMBL:AY065112 EMBL:BT000084 IPI:IPI00520364 PIR:B84807 RefSeq:NP_181395.1 RefSeq:NP_850296.1 UniGene:At.23456 ProteinModelPortal:Q9ZVI3 SMR:Q9ZVI3 IntAct:Q9ZVI3 PRIDE:Q9ZVI3 EnsemblPlants:AT2G38610.1 EnsemblPlants:AT2G38610.2 GeneID:818443 KEGG:ath:AT2G38610 TAIR:At2g38610 InParanoid:Q9ZVI3 OMA:ANIVDMR PhylomeDB:Q9ZVI3 ProtClustDB:CLSN2683215 ArrayExpress:Q9ZVI3 Genevestigator:Q9ZVI3 Uniprot:Q9ZVI3
Leaf	Isotig04232	8	45	-1.963	2.38E-05	TAIR|locus:2084898 - symbol:EMB3119 "EMBRYO DEFECTIVE 3119" species:3702 "Arabidopsis thaliana" [GO:0004751 "ribose-5-phosphate isomerase activity" evidence=IEA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0042742 "defense response to bacterium" evidence=IEP] [GO:0019253 "reductive pentose-phosphate cycle" evidence=NAS] HAMAP:MF_00170 InterPro:IPR004788 InterPro:IPR020672 Pfam:PF06026 GO:GO:0009570 GO:GO:0042742 EMBL:CP002686 GO:GO:0009941 EMBL:AC009465 GO:GO:0009535 EMBL:AC011437 GO:GO:0019253 GO:GO:0009052 KO:K01807 GO:GO:0004751 PANTHER:PTHR11934 TIGRFAMs:TIGR00021 HSSP:O50083 EMBL:AY045785 EMBL:AY142600 IPI:IPI00539339 RefSeq:NP_187130.1 UniGene:At.24856 UniGene:At.75161 UniGene:At.75369 ProteinModelPortal:Q9S726 SMR:Q9S726 STRING:Q9S726 PRIDE:Q9S726 ProMEX:Q9S726 EnsemblPlants:AT3G04790.1 GeneID:819639 KEGG:ath:AT3G04790 TAIR:At3g04790 InParanoid:Q9S726 OMA:NLSLYVD PhylomeDB:Q9S726 ProtClustDB:CLSN2719924 ArrayExpress:Q9S726 Genevestigator:Q9S726 Uniprot:Q9S726
Leaf	Isotig04233	8	45	-1.963	2.38E-05	TAIR|locus:2084898 - symbol:EMB3119 "EMBRYO DEFECTIVE 3119" species:3702 "Arabidopsis thaliana" [GO:0004751 "ribose-5-phosphate isomerase activity" evidence=IEA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA]

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						[GO:0042742 "defense response to bacterium" evidence=IEP] [GO:0019253 "reductive pentose-phosphate cycle" evidence=NAS] HAMAP:MF_00170 InterPro:IPR004788 InterPro:IPR020672 Pfam:PF06026 GO:GO:0009570 GO:GO:0042742 EMBL:CP002686 GO:GO:0009941 EMBL:AC009465 GO:GO:0009535 EMBL:AC011437 GO:GO:0019253 GO:GO:0009052 KO:K01807 GO:GO:0004751 PANTHER:PTHR11934 TIGRFAMs:TIGR00021 HSSP:O50083 EMBL:AY045785 EMBL:AY142600 IPI:IPI00539339 RefSeq:NP_187130.1 UniGene:At.24856 UniGene:At.75161 UniGene:At.75369 ProteinModelPortal:Q9S726 SMR:Q9S726 STRING:Q9S726 PRIDE:Q9S726 ProMEX:Q9S726 EnsemblPlants:AT3G04790.1 GeneID:819639 KEGG:ath:AT3G04790 TAIR:At3g04790 InParanoid:Q9S726 OMA:NLSLYVD PhylomeDB:Q9S726 ProtClustDB:CLSN2719924 ArrayExpress:Q9S726 Genevestigator:Q9S726 Uniprot:Q9S726
Leaf	Isotig04244	8	68	-2.559	1.01E-09	TAIR|locus:2040934 - symbol:LHB1B2 "AT2G34420" species:3702 "Arabidopsis thaliana" [GO:0009769 "photosynthesis, light harvesting in photosystem II" evidence=TAS] [GO:0016168 "chlorophyll binding" evidence=ISS;TAS] [GO:0030076 "light-harvesting complex" evidence=ISS] [GO:0042651 "thylakoid membrane" evidence=TAS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0015979 "photosynthesis" evidence=ISS] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR001344 Pfam:PF00504 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009535 GO:GO:0010287 EMBL:AC004077 EMBL:AC004481 HOGENOM:HBG618504 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 UniGene:At.10812 UniGene:At.24351 UniGene:At.32199 UniGene:At.66422 UniGene:At.71449 UniGene:At.71528 KO:K08912 ProtClustDB:PLN00025 UniGene:At.23647 UniGene:At.27457 UniGene:At.24888 EMBL:AF372886 EMBL:AY039561 EMBL:AY045806 EMBL:AF428397 EMBL:AF419548 EMBL:AF419587 EMBL:AY065125 EMBL:AY079101 EMBL:AY079110 EMBL:AY081587 EMBL:AY142513 EMBL:AK229627 EMBL:X64460 IPI:IPI00530785 PIR:S23546 RefSeq:NP_565786.1 UniGene:At.24064 UniGene:At.71003 UniGene:At.71384 ProteinModelPortal:Q39141 SMR:Q39141 IntAct:Q39141 STRING:Q39141 PRIDE:Q39141 EnsemblPlants:AT2G34420.1 GeneID:818005 KEGG:ath:AT2G34420 TAIR:At2g34420 InParanoid:Q39141 OMA:SILAIWG PhylomeDB:Q39141 ArrayExpress:Q39141 Genevestigator:Q39141 Uniprot:Q39141
Leaf	Isotig04245	1	33	-4.515	8.84E-08	TAIR|locus:2040934 - symbol:LHB1B2 "AT2G34420" species:3702 "Arabidopsis thaliana" [GO:0009769 "photosynthesis, light harvesting in photosystem II" evidence=TAS] [GO:0016168 "chlorophyll binding" evidence=ISS;TAS] [GO:0030076 "light-harvesting complex" evidence=ISS] [GO:0042651 "thylakoid membrane" evidence=TAS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0015979 "photosynthesis" evidence=ISS] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR001344 Pfam:PF00504 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009535 GO:GO:0010287 EMBL:AC004077 EMBL:AC004481 HOGENOM:HBG618504 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 UniGene:At.10812 UniGene:At.24351 UniGene:At.32199 UniGene:At.66422 UniGene:At.71449 UniGene:At.71528 KO:K08912 ProtClustDB:PLN00025 UniGene:At.23647 UniGene:At.27457 UniGene:At.24888 EMBL:AF372886 EMBL:AY039561 EMBL:AY045806 EMBL:AF428397 EMBL:AF419548 EMBL:AF419587 EMBL:AY065125 EMBL:AY079101 EMBL:AY079110 EMBL:AY081587 EMBL:AY142513 EMBL:AK229627 EMBL:X64460 IPI:IPI00530785 PIR:S23546 RefSeq:NP_565786.1 UniGene:At.24064 UniGene:At.71003 UniGene:At.71384 ProteinModelPortal:Q39141 SMR:Q39141 IntAct:Q39141 STRING:Q39141 PRIDE:Q39141 EnsemblPlants:AT2G34420.1 GeneID:818005 KEGG:ath:AT2G34420 TAIR:At2g34420 InParanoid:Q39141 OMA:SILAIWG PhylomeDB:Q39141 ArrayExpress:Q39141 Genevestigator:Q39141 Uniprot:Q39141
Leaf	Isotig04246	10	0	4.851	0.000336918	TAIR|locus:2168988 - symbol:TDT "AT5G47560" species:3702 "Arabidopsis thaliana" [GO:0006814 "sodium ion transport" evidence=ISS] [GO:0006835 "dicarboxylic acid transport" evidence=ISS] [GO:0017153 "sodium:dicarboxylate symporter activity" evidence=ISS] [GO:0005773 "vacuole" evidence=IDA] [GO:0015140 "malate transmembrane transporter activity" evidence=IMP;IDA] [GO:0015743 "malate transport" evidence=TAS] [GO:0051453 "regulation of intracellular pH" evidence=TAS] InterPro:IPR001898 Pfam:PF00939 GO:GO:0016021 GO:GO:0005774 EMBL:CP002688 GenomeReviews:BA000015_GR EMBL:AB025628 GO:GO:0006814 GO:GO:0015140 GO:GO:0051453 eggNOG:COG0471 TIGRFAMs:TIGR00785 KO:K14445

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						HOGENOM:HBG616159 EMBL:AJ223445 EMBL:AB043024 EMBL:AY072145 EMBL:AY133792 EMBL:AY084408 IPI:IPI00534224 RefSeq:NP_199567.1 UniGene:At.21038 UniGene:At.68515 UniGene:At.71618 STRING:Q8LG88 TCDB:2.A.47.1.6 PRIDE:Q8LG88 EnsemblPlants:AT5G47560.1 GeneID:834806 KEGG:ath:AT5G47560 GeneFarm:4980 TAIR:At5g47560 InParanoid:Q8LG88 OMA:TECMPLA PhylomeDB:Q8LG88 ProtClustDB:CLSN2686388 ArrayExpress:Q9MAW4 Genevestigator:Q8LG88 GermOnline:AT5G47560 Uniprot:Q8LG88
Leaf	Isotig04247	10	0	4.851	0.000336918	TAIR|locus:2168988 - symbol:TDT "AT5G47560" species:3702 "Arabidopsis thaliana" [GO:0006814 "sodium ion transport" evidence=ISS] [GO:0006835 "dicarboxylic acid transport" evidence=ISS] [GO:0017153 "sodium:dicarboxylate symporter activity" evidence=ISS] [GO:0005773 "vacuole" evidence=IDA] [GO:0015140 "malate transmembrane transporter activity" evidence=IMP;IDA] [GO:0015743 "malate transport" evidence=TAS] [GO:0051453 "regulation of intracellular pH" evidence=TAS] InterPro:IPR001898 Pfam:PF00939 GO:GO:0016021 GO:GO:0005774 EMBL:CP002688 GenomeReviews:BA000015_GR EMBL:AB025628 GO:GO:0006814 GO:GO:0015140 GO:GO:0051453 eggNOG:COG0471 TIGRFAMs:TIGR00785 KO:K14445 HOGENOM:HBG616159 EMBL:AJ223445 EMBL:AB043024 EMBL:AY072145 EMBL:AY133792 EMBL:AY084408 IPI:IPI00534224 RefSeq:NP_199567.1 UniGene:At.21038 UniGene:At.68515 UniGene:At.71618 STRING:Q8LG88 TCDB:2.A.47.1.6 PRIDE:Q8LG88 EnsemblPlants:AT5G47560.1 GeneID:834806 KEGG:ath:AT5G47560 GeneFarm:4980 TAIR:At5g47560 InParanoid:Q8LG88 OMA:TECMPLA PhylomeDB:Q8LG88 ProtClustDB:CLSN2686388 ArrayExpress:Q9MAW4 Genevestigator:Q8LG88 GermOnline:AT5G47560 Uniprot:Q8LG88
Leaf	Isotig04252	12	0	5.114	7.63E-05	UNIPROTKB|Q41050 - symbol:OEP16 "Outer envelope pore protein 16, chloroplastic" species:3888 "Pisum sativum" [GO:0042803 "protein homodimerization activity" evidence=IDA] [GO:0045037 "protein import into chloroplast stroma" evidence=IDA] InterPro:IPR003397 Pfam:PF02466 GO:GO:0016021 GO:GO:0042803 GO:GO:0045037 EMBL:Z73553 PIR:T06471 TCDB:1.B.30.1.1 Uniprot:Q41050
Leaf	Isotig04253	12	0	5.114	7.63E-05	UNIPROTKB|Q41050 - symbol:OEP16 "Outer envelope pore protein 16, chloroplastic" species:3888 "Pisum sativum" [GO:0042803 "protein homodimerization activity" evidence=IDA] [GO:0045037 "protein import into chloroplast stroma" evidence=IDA] InterPro:IPR003397 Pfam:PF02466 GO:GO:0016021 GO:GO:0042803 GO:GO:0045037 EMBL:Z73553 PIR:T06471 TCDB:1.B.30.1.1 Uniprot:Q41050
Leaf	Isotig04302	18	2	3.699	7.53E-06	TAIR|locus:2122189 - symbol:AT4G36130 species:3702 "Arabidopsis thaliana" [GO:0003735 "structural constituent of ribosome" evidence=IEA;ISS] [GO:0005840 "ribosome" evidence=ISS] [GO:0006412 "translation" evidence=IEA;ISS] [GO:0005773 "vacuole" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0022625 "cytosolic large ribosomal subunit" evidence=IDA] InterPro:IPR002171 InterPro:IPR022666 InterPro:IPR022669 InterPro:IPR022671 InterPro:IPR023672 Pfam:PF00181 Pfam:PF03947 PIRSF:PIRSF002158 PROSITE:PS00467 GO:GO:0005886 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005773 GO:GO:0006412 GO:GO:0003723 EMBL:AL161588 GO:GO:0003735 InterPro:IPR012340 Gene3D:G3DSA:2.40.50.140 InterPro:IPR016027 SUPFAM:SSF50249 EMBL:AL022141 EMBL:AL022373 InterPro:IPR014722 Gene3D:G3DSA:2.30.30.30 InterPro:IPR008991 SUPFAM:SSF50104 GO:GO:0022625 KO:K02938 InterPro:IPR014726 Gene3D:G3DSA:4.10.950.10 PANTHER:PTHR13691 eggNOG:COG0090 HOGENOM:HBG748739 ProtClustDB:CLSN2683927 EMBL:AF361610 EMBL:AF367335 EMBL:AY058221 EMBL:Z25971 IPI:IPI00523186 PIR:T04582 RefSeq:NP_195336.1 UniGene:At.2119 UniGene:At.72399 ProteinModelPortal:Q42064 SMR:Q42064 STRING:Q42064 PRIDE:Q42064 EnsemblPlants:AT4G36130.1 GeneID:829770 KEGG:ath:AT4G36130 GeneFarm:407 TAIR:At4g36130 InParanoid:Q42064 OMA:DNDTSRI PhylomeDB:Q42064 Genevestigator:Q42064 GermOnline:AT4G36130 Uniprot:Q42064
Leaf	Isotig04303	18	2	3.699	7.53E-06	TAIR|locus:2122189 - symbol:AT4G36130 species:3702 "Arabidopsis thaliana" [GO:0003735 "structural constituent of ribosome" evidence=IEA;ISS] [GO:0005840 "ribosome" evidence=ISS] [GO:0006412 "translation" evidence=IEA;ISS] [GO:0005773 "vacuole" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0022625 "cytosolic large ribosomal subunit" evidence=IDA] InterPro:IPR002171 InterPro:IPR022666 InterPro:IPR022669 InterPro:IPR022671 InterPro:IPR023672 Pfam:PF00181 Pfam:PF03947 PIRSF:PIRSF002158 PROSITE:PS00467 GO:GO:0005886 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005773 GO:GO:0006412 GO:GO:0003723 EMBL:AL161588 GO:GO:0003735 InterPro:IPR012340 Gene3D:G3DSA:2.40.50.140 InterPro:IPR016027 SUPFAM:SSF50249 EMBL:AL022141 EMBL:AL022373 InterPro:IPR014722 Gene3D:G3DSA:2.30.30.30 InterPro:IPR008991

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						SUPFAM:SSF50104 GO:GO:0022625 KO:K02938 InterPro:IPR014726 Gene3D:G3DSA:4.10.950.10 PANTHER:PTHR13691 eggNOG:COG0090 HOGENOM:HBG748739 ProtClustDB:CLSN2683927 EMBL:AF361610 EMBL:AF367335 EMBL:AY058221 EMBL:Z25971 IPI:IPI00523186 PIR:T04582 RefSeq:NP_195336.1 UniGene:At.2119 UniGene:At.72399 ProteinModelPortal:Q42064 SMR:Q42064 STRING:Q42064 PRIDE:Q42064 EnsemblPlants:AT4G36130.1 GeneID:829770 KEGG:ath:AT4G36130 GeneFarm:407 TAIR:At4g36130 InParanoid:Q42064 OMA:DNDTSRI PhylomeDB:Q42064 Genevestigator:Q42064 GermOnline:AT4G36130 Uniprot:Q42064
Leaf	Isotig04310	25	1	5.173	1.09E-08	TAIR|locus:2168479 - symbol:AT5G59240 "AT5G59240" species:3702 "Arabidopsis thaliana" [GO:0000462 "maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)" evidence=IBA] [GO:0003735 "structural constituent of ribosome" evidence=ISS;IBA] [GO:0005840 "ribosome" evidence=ISS] [GO:0006412 "translation" evidence=ISS] [GO:0006414 "translational elongation" evidence=IBA] [GO:0042254 "ribosome biogenesis" evidence=ISS] [GO:0022627 "cytosolic small ribosomal subunit" evidence=ISS;IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] InterPro:IPR001047 InterPro:IPR018283 PROSITE:PS01193 Pfam:PF01201 PANTHER:PTHR10394 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0016020 GO:GO:0006412 GO:GO:0003735 EMBL:AB016890 GO:GO:0022627 eggNOG:COG2007 InterPro:IPR022309 HOGENOM:HBG745393 KO:K02995 ProtClustDB:CLSN2687206 TIGRFAMs:TIGR00307 EMBL:BT004603 IPI:IPI00519779 RefSeq:NP_200732.2 UniGene:At.29238 ProteinModelPortal:Q9FIF3 SMR:Q9FIF3 STRING:Q9FIF3 PRIDE:Q9FIF3 EnsemblPlants:AT5G59240.1 GeneID:836042 KEGG:ath:AT5G59240 TAIR:At5g59240 InParanoid:Q9FIF3 OMA:KNCIVLV PhylomeDB:Q9FIF3 ArrayExpress:Q9FIF3 Genevestigator:Q9FIF3 GermOnline:AT5G59240 Uniprot:Q9FIF3
Leaf	Isotig04311	25	1	5.173	1.09E-08	TAIR|locus:2168479 - symbol:AT5G59240 "AT5G59240" species:3702 "Arabidopsis thaliana" [GO:0000462 "maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)" evidence=IBA] [GO:0003735 "structural constituent of ribosome" evidence=ISS;IBA] [GO:0005840 "ribosome" evidence=ISS] [GO:0006412 "translation" evidence=ISS] [GO:0006414 "translational elongation" evidence=IBA] [GO:0042254 "ribosome biogenesis" evidence=ISS] [GO:0022627 "cytosolic small ribosomal subunit" evidence=ISS;IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] InterPro:IPR001047 InterPro:IPR018283 PROSITE:PS01193 Pfam:PF01201 PANTHER:PTHR10394 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0016020 GO:GO:0006412 GO:GO:0003735 EMBL:AB016890 GO:GO:0022627 eggNOG:COG2007 InterPro:IPR022309 HOGENOM:HBG745393 KO:K02995 ProtClustDB:CLSN2687206 TIGRFAMs:TIGR00307 EMBL:BT004603 IPI:IPI00519779 RefSeq:NP_200732.2 UniGene:At.29238 ProteinModelPortal:Q9FIF3 SMR:Q9FIF3 STRING:Q9FIF3 PRIDE:Q9FIF3 EnsemblPlants:AT5G59240.1 GeneID:836042 KEGG:ath:AT5G59240 TAIR:At5g59240 InParanoid:Q9FIF3 OMA:KNCIVLV PhylomeDB:Q9FIF3 ArrayExpress:Q9FIF3 Genevestigator:Q9FIF3 GermOnline:AT5G59240 Uniprot:Q9FIF3
Leaf	Isotig04316	2	20	-2.793	0.00051744	TAIR|locus:2049597 - symbol:AT2G01610 species:3702 "Arabidopsis thaliana" [GO:0004857 "enzyme inhibitor activity" evidence=IEA] [GO:0008150 "biological_process" evidence=ND] [GO:0030599 "pectinesterase activity" evidence=IEA] [GO:0046910 "pectinesterase inhibitor activity" evidence=ISS] InterPro:IPR006501 Pfam:PF04043 SMART:SM00856 EMBL:CP002685 GO:GO:0004857 EMBL:AC006069 EMBL:AC005560 GO:GO:0030599 Gene3D:G3DSA:1.20.140.40 SUPFAM:SSF101148 TIGRFAMs:TIGR01614 EMBL:BT030064 IPI:IPI00526890 PIR:H84426 RefSeq:NP_178270.1 UniGene:At.42477 ProteinModelPortal:Q9ZNU5 PRIDE:Q9ZNU5 EnsemblPlants:AT2G01610.1 GeneID:814690 KEGG:ath:AT2G01610 TAIR:At2g01610 InParanoid:Q9ZNU5 OMA:EDTCTDG PhylomeDB:Q9ZNU5 ProtClustDB:CLSN2913127 Genevestigator:Q9ZNU5 Uniprot:Q9ZNU5
Leaf	Isotig04317	1	19	-3.719	0.000124272	TAIR|locus:2049597 - symbol:AT2G01610 species:3702 "Arabidopsis thaliana" [GO:0004857 "enzyme inhibitor activity" evidence=IEA] [GO:0008150 "biological_process" evidence=ND] [GO:0030599 "pectinesterase activity" evidence=IEA] [GO:0046910 "pectinesterase inhibitor activity" evidence=ISS] InterPro:IPR006501 Pfam:PF04043 SMART:SM00856 EMBL:CP002685 GO:GO:0004857 EMBL:AC006069 EMBL:AC005560 GO:GO:0030599 Gene3D:G3DSA:1.20.140.40 SUPFAM:SSF101148 TIGRFAMs:TIGR01614 EMBL:BT030064 IPI:IPI00526890 PIR:H84426 RefSeq:NP_178270.1 UniGene:At.42477 ProteinModelPortal:Q9ZNU5 PRIDE:Q9ZNU5 EnsemblPlants:AT2G01610.1 GeneID:814690 KEGG:ath:AT2G01610 TAIR:At2g01610 InParanoid:Q9ZNU5 OMA:EDTCTDG PhylomeDB:Q9ZNU5 ProtClustDB:CLSN2913127 Genevestigator:Q9ZNU5 Uniprot:Q9ZNU5

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig04318	34	131	-1.417	1.05E-08	UNIPROTKB|P83522 - symbol:P83522 "Ferredoxin" species:4513 "Hordeum vulgare" [GO:0006124 "ferredoxin metabolic process" evidence=TAS] [GO:0009055 "electron carrier activity" evidence=TAS] InterPro:IPR001041 InterPro:IPR006058 InterPro:IPR010241 Pfam:PF00111 PROSITE:PS00197 PROSITE:PS51085 GO:GO:0009507 GO:GO:0009055 GO:GO:0046872 GO:GO:0006810 GO:GO:0022900 GO:GO:0051537 InterPro:IPR012675 Gene3D:G3DSA:3.10.20.30 SUPFAM:SSF54292 TIGRFAMs:TIGR02008 GO:GO:0006124 ProteinModelPortal:P83522 SMR:P83522 Gramene:P83522 Genevestigator:P83522 Uniprot:P83522
Leaf	Isotig04319	21	124	-2.033	7.07E-13	UNIPROTKB|P83522 - symbol:P83522 "Ferredoxin" species:4513 "Hordeum vulgare" [GO:0006124 "ferredoxin metabolic process" evidence=TAS] [GO:0009055 "electron carrier activity" evidence=TAS] InterPro:IPR001041 InterPro:IPR006058 InterPro:IPR010241 Pfam:PF00111 PROSITE:PS00197 PROSITE:PS51085 GO:GO:0009507 GO:GO:0009055 GO:GO:0046872 GO:GO:0006810 GO:GO:0022900 GO:GO:0051537 InterPro:IPR012675 Gene3D:G3DSA:3.10.20.30 SUPFAM:SSF54292 TIGRFAMs:TIGR02008 GO:GO:0006124 ProteinModelPortal:P83522 SMR:P83522 Gramene:P83522 Genevestigator:P83522 Uniprot:P83522
Leaf	Isotig04332	14	0	5.336	1.79E-05	TAIR|locus:2152815 - symbol:AT5G06060 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0008152 "metabolic process" evidence=IEA] [GO:0016491 "oxidoreductase activity" evidence=IEA;ISS] [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR002198 InterPro:IPR016040 InterPro:IPR020904 PRINTS:PR00080 PROSITE:PS00061 InterPro:IPR002347 GO:GO:0005829 EMBL:CP002688 GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 GO:GO:0016491 PRINTS:PR00081 EMBL:AP002030 HSSP:P50162 KO:K08081 EMBL:BT002894 EMBL:BT004454 IPI:IPI00526603 RefSeq:NP_196225.1 UniGene:At.32907 UniGene:At.9505 ProteinModelPortal:Q9LHT0 SMR:Q9LHT0 IntAct:Q9LHT0 PRIDE:Q9LHT0 EnsemblPlants:AT5G06060.1 GeneID:830493 KEGG:ath:AT5G06060 TAIR:At5g06060 InParanoid:Q9LHT0 OMA:TVEYSSE PhylomeDB:Q9LHT0 ProtClustDB:CLSN2916397 ArrayExpress:Q9LHT0 Genevestigator:Q9LHT0 Uniprot:Q9LHT0
Leaf	Isotig04333	12	0	5.114	7.63E-05	TAIR|locus:2152815 - symbol:AT5G06060 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0008152 "metabolic process" evidence=IEA] [GO:0016491 "oxidoreductase activity" evidence=IEA;ISS] [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR002198 InterPro:IPR016040 InterPro:IPR020904 PRINTS:PR00080 PROSITE:PS00061 InterPro:IPR002347 GO:GO:0005829 EMBL:CP002688 GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 GO:GO:0016491 PRINTS:PR00081 EMBL:AP002030 HSSP:P50162 KO:K08081 EMBL:BT002894 EMBL:BT004454 IPI:IPI00526603 RefSeq:NP_196225.1 UniGene:At.32907 UniGene:At.9505 ProteinModelPortal:Q9LHT0 SMR:Q9LHT0 IntAct:Q9LHT0 PRIDE:Q9LHT0 EnsemblPlants:AT5G06060.1 GeneID:830493 KEGG:ath:AT5G06060 TAIR:At5g06060 InParanoid:Q9LHT0 OMA:TVEYSSE PhylomeDB:Q9LHT0 ProtClustDB:CLSN2916397 ArrayExpress:Q9LHT0 Genevestigator:Q9LHT0 Uniprot:Q9LHT0
Leaf	Isotig04356	30	91	-1.072	0.000128183	TAIR|locus:2140255 - symbol:PSAD-1 "AT4G02770" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0009538 "photosystem I reaction center" evidence=ISS] [GO:0015979 "photosynthesis" evidence=IEA;ISS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] InterPro:IPR003685 Pfam:PF02531 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0009941 EMBL:AL161495 GO:GO:0009535 GO:GO:0010287 GO:GO:0015979 EMBL:AC004044 UniGene:At.22672 UniGene:At.23628 EMBL:AJ245906 EMBL:AF324675 EMBL:AF326887 EMBL:AF389290 EMBL:AY062512 EMBL:AY081671 EMBL:AY102159 EMBL:AY113939 EMBL:AY088533 IPI:IPI00523129 PIR:C85035 RefSeq:NP_192186.1 UniGene:At.20829 ProteinModelPortal:Q9S7H1 SMR:Q9S7H1 IntAct:Q9S7H1 STRING:Q9S7H1 PRIDE:Q9S7H1 EnsemblPlants:AT4G02770.1 GeneID:828183 KEGG:ath:AT4G02770 TAIR:At4g02770 eggNOG:NOG06294 HOGENOM:HBG286318 InParanoid:Q9S7H1 KO:K02692 OMA:YLARKEQ PhylomeDB:Q9S7H1 ProtClustDB:PLN00041 BioCyc:MetaCyc:MONOMER-1098 ArrayExpress:Q9S7H1 Genevestigator:Q9S7H1 GermOnline:AT4G02770 GO:GO:0009538 Gene3D:G3DSA:3.30.1470.10 SUPFAM:SSF64234 Uniprot:Q9S7H1
Leaf	Isotig04357	30	97	-1.164	2.38E-05	TAIR|locus:2140255 - symbol:PSAD-1 "AT4G02770" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0009538 "photosystem I reaction center" evidence=ISS] [GO:0015979 "photosynthesis" evidence=IEA;ISS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0009941

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						"chloroplast envelope" evidence=IDA] InterPro:IPR003685 Pfam:PF02531 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0009941 EMBL:AL161495 GO:GO:0009535 GO:GO:0010287 GO:GO:0015979 EMBL:AC004044 UniGene:At.22672 UniGene:At.23628 EMBL:AJ245906 EMBL:AF324675 EMBL:AF326887 EMBL:AF389290 EMBL:AY062512 EMBL:AY081671 EMBL:AY102159 EMBL:AY113939 EMBL:AY088533 IPI:IPI00523129 PIR:C85035 RefSeq:NP_192186.1 UniGene:At.20829 ProteinModelPortal:Q9S7H1 SMR:Q9S7H1 IntAct:Q9S7H1 STRING:Q9S7H1 PRIDE:Q9S7H1 EnsemblPlants:AT4G02770.1 GeneID:828183 KEGG:ath:AT4G02770 TAIR:At4g02770 eggNOG:NOG06294 HOGENOM:HBG286318 InParanoid:Q9S7H1 KO:K02692 OMA:YLARKEQ PhylomeDB:Q9S7H1 ProtClustDB:PLN00041 BioCyc:MetaCyc:MONOMER-1098 ArrayExpress:Q9S7H1 Genevestigator:Q9S7H1 GermOnline:AT4G02770 GO:GO:0009538 Gene3D:G3DSA:3.30.1470.10 SUPFAM:SSF64234 Uniprot:Q9S7H1
Leaf	Isotig04366	10	0	4.851	0.000336918	TAIR|locus:2222687 - symbol:AT5G14680 "AT5G14680" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0006950 "response to stress" evidence=IEA;ISS] InterPro:IPR006016 Pfam:PF00582 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0006950 InterPro:IPR014729 Gene3D:G3DSA:3.40.50.620 EMBL:AL163792 eggNOG:COG0589 InterPro:IPR006015 PRINTS:PR01438 HOGENOM:HBG316424 ProtClustDB:CLSN2687240 EMBL:BT011776 EMBL:BT015743 IPI:IPI00537310 PIR:T48641 RefSeq:NP_196972.1 UniGene:At.31897 ProteinModelPortal:Q9LYJ2 SMR:Q9LYJ2 STRING:Q9LYJ2 PRIDE:Q9LYJ2 EnsemblPlants:AT5G14680.1 GeneID:831320 KEGG:ath:AT5G14680 TAIR:At5g14680 InParanoid:Q9LYJ2 OMA:CPVITIK PhylomeDB:Q9LYJ2 Genevestigator:Q9LYJ2 Uniprot:Q9LYJ2
Leaf	Isotig04368	17	5	2.294	0.000574458	TAIR|locus:2089383 - symbol:AT3G16780 species:3702 "Arabidopsis thaliana" [GO:0003735 "structural constituent of ribosome" evidence=IEA;ISS] [GO:0005840 "ribosome" evidence=ISS] [GO:0006412 "translation" evidence=IEA;ISS] [GO:0042254 "ribosome biogenesis" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0022625 "cytosolic large ribosomal subunit" evidence=IDA] InterPro:IPR000196 InterPro:IPR015972 InterPro:IPR015974 Pfam:PF01280 GO:GO:0005886 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0006412 GO:GO:0003735 EMBL:AB022217 GO:GO:0022625 eggNOG:COG2147 HOGENOM:HBG748852 KO:K02885 ProtClustDB:CLSN2679603 InterPro:IPR023638 Gene3D:G3DSA:1.10.1650.10 Gene3D:G3DSA:1.10.1200.60 SUPFAM:SSF48140 PROSITE:PS00526 EMBL:AY045610 EMBL:AY090335 IPI:IPI00538939 RefSeq:NP_188300.1 UniGene:At.21317 UniGene:At.5836 ProteinModelPortal:Q9LUQ6 SMR:Q9LUQ6 STRING:Q9LUQ6 PRIDE:Q9LUQ6 EnsemblPlants:AT3G16780.1 GeneID:820931 KEGG:ath:AT3G16780 GeneFarm:247 TAIR:At3g16780 InParanoid:Q9LUQ6 OMA:MAKGGAF PhylomeDB:Q9LUQ6 ArrayExpress:Q9LUQ6 Genevestigator:Q9LUQ6 GermOnline:AT3G16780 Uniprot:Q9LUQ6
Leaf	Isotig04369	17	5	2.294	0.000574458	TAIR|locus:2089383 - symbol:AT3G16780 species:3702 "Arabidopsis thaliana" [GO:0003735 "structural constituent of ribosome" evidence=IEA;ISS] [GO:0005840 "ribosome" evidence=ISS] [GO:0006412 "translation" evidence=IEA;ISS] [GO:0042254 "ribosome biogenesis" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0022625 "cytosolic large ribosomal subunit" evidence=IDA] InterPro:IPR000196 InterPro:IPR015972 InterPro:IPR015974 Pfam:PF01280 GO:GO:0005886 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0006412 GO:GO:0003735 EMBL:AB022217 GO:GO:0022625 eggNOG:COG2147 HOGENOM:HBG748852 KO:K02885 ProtClustDB:CLSN2679603 InterPro:IPR023638 Gene3D:G3DSA:1.10.1650.10 Gene3D:G3DSA:1.10.1200.60 SUPFAM:SSF48140 PROSITE:PS00526 EMBL:AY045610 EMBL:AY090335 IPI:IPI00538939 RefSeq:NP_188300.1 UniGene:At.21317 UniGene:At.5836 ProteinModelPortal:Q9LUQ6 SMR:Q9LUQ6 STRING:Q9LUQ6 PRIDE:Q9LUQ6 EnsemblPlants:AT3G16780.1 GeneID:820931 KEGG:ath:AT3G16780 GeneFarm:247 TAIR:At3g16780 InParanoid:Q9LUQ6 OMA:MAKGGAF PhylomeDB:Q9LUQ6 ArrayExpress:Q9LUQ6 Genevestigator:Q9LUQ6 GermOnline:AT3G16780 Uniprot:Q9LUQ6
Leaf	Isotig04378	9	0	4.699	0.000718283	No hit
Leaf	Isotig04379	9	0	4.699	0.000718283	No hit
Leaf	Isotig04384	9	0	4.699	0.000718283	TAIR|locus:2034995 - symbol:NRP2 "AT1G18800" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=ISS] [GO:0005634 "nucleus" evidence=ISS;IDA] [GO:0006334 "nucleosome assembly" evidence=ISS] [GO:0003682 "chromatin binding" evidence=IPI] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0008283 "cell proliferation" evidence=IGI] [GO:0010311 "lateral root formation" evidence=IGI] [GO:0030154 "cell differentiation" evidence=IGI] [GO:0042393 "histone binding" evidence=IPI] InterPro:IPR002164 Pfam:PF00956 EMBL:CP002684 GO:GO:0005634 GO:GO:0005737 GO:GO:0030154 GO:GO:0008283 GO:GO:0003682 GO:GO:0010311 GO:GO:0042393 GO:GO:0006334 PANTHER:PTHR11875 KO:K11290

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						ProtClustDB:CLSN2682258 EMBL:AY086761 IPI:IPI00521079 RefSeq:NP_564063.1 UniGene:At.28227 ProteinModelPortal:Q8LC68 SMR:Q8LC68 STRING:Q8LC68 PRIDE:Q8LC68 EnsemblPlants:AT1G18800.1 GeneID:838462 KEGG:ath:AT1G18800 TAIR:At1g18800 InParanoid:Q8LC68 OMA:TIPDFWL PhylomeDB:Q8LC68 Genevestigator:Q8LC68 Uniprot:Q8LC68
Leaf	Isotig04385	16	0	5.529	4.31E-06	TAIR|locus:2034995 - symbol:NRP2 "AT1G18800" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=ISS] [GO:0005634 "nucleus" evidence=ISS;IDA] [GO:0006334 "nucleosome assembly" evidence=ISS] [GO:0003682 "chromatin binding" evidence=IPI] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0008283 "cell proliferation" evidence=IGI] [GO:0010311 "lateral root formation" evidence=IGI] [GO:0030154 "cell differentiation" evidence=IGI] [GO:0042393 "histone binding" evidence=IPI] InterPro:IPR002164 Pfam:PF00956 EMBL:CP002684 GO:GO:0005634 GO:GO:0005737 GO:GO:0030154 GO:GO:0008283 GO:GO:0003682 GO:GO:0010311 GO:GO:0042393 GO:GO:0006334 PANTHER:PTHR11875 KO:K11290 ProtClustDB:CLSN2682258 EMBL:AY086761 IPI:IPI00521079 RefSeq:NP_564063.1 UniGene:At.28227 ProteinModelPortal:Q8LC68 SMR:Q8LC68 STRING:Q8LC68 PRIDE:Q8LC68 EnsemblPlants:AT1G18800.1 GeneID:838462 KEGG:ath:AT1G18800 TAIR:At1g18800 InParanoid:Q8LC68 OMA:TIPDFWL PhylomeDB:Q8LC68 Genevestigator:Q8LC68 Uniprot:Q8LC68
Leaf	Isotig04398	2	23	-2.995	0.000115946	TAIR|locus:2132323 - symbol:AT4G02530 "AT4G02530" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0009543 "chloroplast thylakoid lumen" evidence=IDA] [GO:0031977 "thylakoid lumen" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0009570 GO:GO:0009941 GO:GO:0009535 EMBL:AC002330 EMBL:AL161494 GO:GO:0009543 EMBL:AY039885 EMBL:AY081737 EMBL:AY088583 EMBL:AK226276 IPI:IPI00525823 PIR:T01096 RefSeq:NP_192162.1 UniGene:At.22175 STRING:O22773 PRIDE:O22773 ProMEX:O22773 EnsemblPlants:AT4G02530.1 GeneID:827927 KEGG:ath:AT4G02530 GeneFarm:3264 TAIR:At4g02530 eggNOG:NOG258803 HOGENOM:HBG744204 InParanoid:O22773 OMA:QAIDNND PhylomeDB:O22773 ProtClustDB:CLSN2916016 Genevestigator:O22773 GermOnline:AT4G02530 Uniprot:O22773
Leaf	Isotig04420	16	1	4.529	7.58E-06	No hit
Leaf	Isotig04421	14	1	4.336	3.39E-05	UNIPROTKB|F1PBA6 - symbol:HIVEP1 "Uncharacterized protein" species:9615 "Canis lupus familiaris" [GO:0003676 "nucleic acid binding" evidence=IEA] [GO:0005622 "intracellular" evidence=IEA] [GO:0008270 "zinc ion binding" evidence=IEA] InterPro:IPR007087 InterPro:IPR013087 InterPro:IPR015880 PROSITE:PS00028 PROSITE:PS50157 SMART:SM00355 GO:GO:0008270 GO:GO:0003676 Gene3D:G3DSA:3.30.160.60 GO:GO:0005622 GeneTree:ENSGT00530000063161 OMA:IFKDSFQ Ensembl:ENSCAFT00000015544 Uniprot:F1PBA6
Leaf	Isotig04426	0	17	-4.559	0.00011959	TAIR|locus:2204798 - symbol:MC1 "AT1G02170" species:3702 "Arabidopsis thaliana" [GO:0006508 "proteolysis" evidence=ISS] [GO:0004197 "cysteine-type endopeptidase activity" evidence=IDA] [GO:0043068 "positive regulation of programmed cell death" evidence=IGI;IDA] InterPro:IPR011600 Pfam:PF00656 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0006952 GO:GO:0004197 GO:GO:0006508 GO:GO:0043068 EMBL:U89959 InterPro:IPR005735 Pfam:PF06943 TIGRFAMs:TIGR01053 EMBL:AY219826 EMBL:AY322525 IPI:IPI00531085 RefSeq:NP_171719.2 UniGene:At.10711 UniGene:At.69983 ProteinModelPortal:Q7XJE6 STRING:Q7XJE6 MEROPS:C14.047 PRIDE:Q7XJE6 EnsemblPlants:AT1G02170.1 GeneID:839561 KEGG:ath:AT1G02170 TAIR:At1g02170 eggNOG:NOG68179 HOGENOM:HBG692861 InParanoid:Q7XJE6 OMA:NDAKCMR PhylomeDB:Q7XJE6 Genevestigator:Q7XJE6 Uniprot:Q7XJE6
Leaf	Isotig04427	0	19	-4.719	4.23E-05	TAIR|locus:2204798 - symbol:MC1 "AT1G02170" species:3702 "Arabidopsis thaliana" [GO:0006508 "proteolysis" evidence=ISS] [GO:0004197 "cysteine-type endopeptidase activity" evidence=IDA] [GO:0043068 "positive regulation of programmed cell death" evidence=IGI;IDA] InterPro:IPR011600 Pfam:PF00656 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0006952 GO:GO:0004197 GO:GO:0006508 GO:GO:0043068 EMBL:U89959 InterPro:IPR005735 Pfam:PF06943 TIGRFAMs:TIGR01053 EMBL:AY219826 EMBL:AY322525 IPI:IPI00531085 RefSeq:NP_171719.2 UniGene:At.10711 UniGene:At.69983 ProteinModelPortal:Q7XJE6 STRING:Q7XJE6 MEROPS:C14.047 PRIDE:Q7XJE6 EnsemblPlants:AT1G02170.1 GeneID:839561 KEGG:ath:AT1G02170 TAIR:At1g02170 eggNOG:NOG68179 HOGENOM:HBG692861 InParanoid:Q7XJE6 OMA:NDAKCMR PhylomeDB:Q7XJE6 Genevestigator:Q7XJE6 Uniprot:Q7XJE6

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig04432	12	0	5.114	7.63E-05	UNIPROTKB|B2C7Y6 - symbol:NRIP1 "Chloroplast N receptor-interacting protein 1" species:4100 "Nicotiana benthamiana" [GO:0005515 "protein binding" evidence=IPI] Pfam:PF00581 GO:GO:0005515 GO:GO:0004872 InterPro:IPR001763 Gene3D:G3DSA:3.40.250.10 SMART:SM00450 SUPFAM:SSF52821 PROSITE:PS50206 EMBL:EU332890 EMBL:EU332891 ProteinModelPortal:B2C7Y6 SMR:B2C7Y6 IntAct:B2C7Y6 Uniprot:B2C7Y6
Leaf	Isotig04433	12	0	5.114	7.63E-05	UNIPROTKB|B2C7Y6 - symbol:NRIP1 "Chloroplast N receptor-interacting protein 1" species:4100 "Nicotiana benthamiana" [GO:0005515 "protein binding" evidence=IPI] Pfam:PF00581 GO:GO:0005515 GO:GO:0004872 InterPro:IPR001763 Gene3D:G3DSA:3.40.250.10 SMART:SM00450 SUPFAM:SSF52821 PROSITE:PS50206 EMBL:EU332890 EMBL:EU332891 ProteinModelPortal:B2C7Y6 SMR:B2C7Y6 IntAct:B2C7Y6 Uniprot:B2C7Y6
Leaf	Isotig04442	13	1	4.229	7.21E-05	TAIR|locus:2013668 - symbol:AT1G29680 "AT1G29680" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0005515 "protein binding" evidence=IPI] EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005515 EMBL:AC068667 UniGene:At.48247 UniGene:At.71163 ProtClustDB:CLSN2682014 InterPro:IPR010686 Pfam:PF06884 HOGENOM:HBG473015 EMBL:BT005255 EMBL:AK118004 IPI:IPI00523169 PIR:B86420 RefSeq:NP_174261.1 IntAct:Q9C7N3 PRIDE:Q9C7N3 DNASU:839845 EnsemblPlants:AT1G29680.1 GeneID:839845 KEGG:ath:AT1G29680 TAIR:At1g29680 eggNOG:NOG295567 InParanoid:Q9C7N3 OMA:AGSTIMQ PhylomeDB:Q9C7N3 Genevestigator:Q9C7N3 Uniprot:Q9C7N3
Leaf	Isotig04474	21	8	1.921	0.000629135	TAIR|locus:2041839 - symbol:AT2G15220 "AT2G15220" species:3702 "Arabidopsis thaliana" [GO:0006952 "defense response" evidence=ISS] Pfam:PF04450 EMBL:CP002685 GenomeReviews:CT485783_GR EMBL:AC006298 InterPro:IPR007541 eggNOG:NOG83661 EMBL:AF345341 EMBL:AY090375 IPI:IPI00528646 PIR:D84526 RefSeq:NP_565369.1 UniGene:At.13396 PRIDE:Q9SKL6 EnsemblPlants:AT2G15220.1 GeneID:816011 KEGG:ath:AT2G15220 TAIR:At2g15220 HOGENOM:HBG319630 InParanoid:Q9SKL6 OMA:MENGDGV PhylomeDB:Q9SKL6 ProtClustDB:CLSN2683478 Genevestigator:Q9SKL6 Uniprot:Q9SKL6
Leaf	Isotig04475	21	6	2.336	0.000109395	TAIR|locus:2041839 - symbol:AT2G15220 "AT2G15220" species:3702 "Arabidopsis thaliana" [GO:0006952 "defense response" evidence=ISS] Pfam:PF04450 EMBL:CP002685 GenomeReviews:CT485783_GR EMBL:AC006298 InterPro:IPR007541 eggNOG:NOG83661 EMBL:AF345341 EMBL:AY090375 IPI:IPI00528646 PIR:D84526 RefSeq:NP_565369.1 UniGene:At.13396 PRIDE:Q9SKL6 EnsemblPlants:AT2G15220.1 GeneID:816011 KEGG:ath:AT2G15220 TAIR:At2g15220 HOGENOM:HBG319630 InParanoid:Q9SKL6 OMA:MENGDGV PhylomeDB:Q9SKL6 ProtClustDB:CLSN2683478 Genevestigator:Q9SKL6 Uniprot:Q9SKL6
Leaf	Isotig04476	48	3	4.529	8.89E-15	TAIR|locus:2094354 - symbol:ELIP1 "AT3G22840" species:3702 "Arabidopsis thaliana" [GO:0016168 "chlorophyll binding" evidence=ISS] [GO:0009409 "response to cold" evidence=IEP] [GO:0080167 "response to karrikin" evidence=IEP] Pfam:PF00504 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0009409 GO:GO:0080167 InterPro:IPR022796 InterPro:IPR023329 SUPFAM:SSF103511 EMBL:AB022223 EMBL:U89014 EMBL:AY057560 EMBL:AY075672 EMBL:AY097423 EMBL:AY085317 IPI:IPI00518629 RefSeq:NP_188923.1 UniGene:At.20776 ProteinModelPortal:P93735 SMR:P93735 STRING:P93735 PRIDE:P93735 EnsemblPlants:AT3G22840.1 GeneID:821855 KEGG:ath:AT3G22840 TAIR:At3g22840 eggNOG:NOG260229 HOGENOM:HBG562551 InParanoid:P93735 OMA:GVRCMAE PhylomeDB:P93735 ProtClustDB:CLSN2684167 Genevestigator:P93735 Uniprot:P93735
Leaf	Isotig04477	48	3	4.529	8.89E-15	TAIR|locus:2094354 - symbol:ELIP1 "AT3G22840" species:3702 "Arabidopsis thaliana" [GO:0016168 "chlorophyll binding" evidence=ISS] [GO:0009409 "response to cold" evidence=IEP] [GO:0080167 "response to karrikin" evidence=IEP] Pfam:PF00504 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0009409 GO:GO:0080167 InterPro:IPR022796 InterPro:IPR023329 SUPFAM:SSF103511 EMBL:AB022223 EMBL:U89014 EMBL:AY057560 EMBL:AY075672 EMBL:AY097423 EMBL:AY085317 IPI:IPI00518629 RefSeq:NP_188923.1 UniGene:At.20776 ProteinModelPortal:P93735 SMR:P93735 STRING:P93735 PRIDE:P93735 EnsemblPlants:AT3G22840.1 GeneID:821855 KEGG:ath:AT3G22840 TAIR:At3g22840 eggNOG:NOG260229 HOGENOM:HBG562551 InParanoid:P93735 OMA:GVRCMAE PhylomeDB:P93735 ProtClustDB:CLSN2684167 Genevestigator:P93735 Uniprot:P93735
Leaf	Isotig04488	11	1	3.988	0.000330755	No hit
Leaf	Isotig04510	20	7	2.044	0.00051229	TAIR|locus:2007176 - symbol:ELF5A-3 "eukaryotic elongation factor 5A-3" species:3702 "Arabidopsis thaliana" [GO:0003723 "RNA binding" evidence=IEA] [GO:0003743 "translation initiation factor activity" evidence=ISS] [GO:0003746 "translation elongation factor activity" evidence=IEA] [GO:0006413 "translational initiation" evidence=ISS] [GO:0006452 "translational frameshifting" evidence=IEA] [GO:0008612 "peptidyl-lysine modification to hypusine" evidence=IEA] [GO:0043022 "ribosome binding" evidence=IEA] [GO:0045901 "positive regulation of

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						translational elongation" evidence=IEA] [GO:0045905 "positive regulation of translational termination" evidence=IEA] InterPro:IPR001884 InterPro:IPR019769 InterPro:IPR020189 Pfam:PF01287 PIRSF:PIRSF003025 PROSITE:PS00302 Pfam:PF00467 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0043022 GO:GO:0003746 EMBL:AC018364 GO:GO:0003743 EMBL:AC073178 InterPro:IPR012340 Gene3D:G3DSA:2.40.50.140 InterPro:IPR016027 SUPFAM:SSF50249 InterPro:IPR014722 Gene3D:G3DSA:2.30.30.30 GO:GO:0008612 GO:GO:0045901 eggNOG:COG0231 InterPro:IPR008991 SUPFAM:SSF50104 InterPro:IPR005824 HOGENOM:HBG526951 KO:K03263 ProtClustDB:PLN03107 GO:GO:0045905 GO:GO:0006452 PANTHER:PTHR11673 TIGRFAMs:TIGR00037 EMBL:AF372933 EMBL:AY060530 EMBL:AY087040 IPI:IPI00527220 RefSeq:NP_177100.1 UniGene:At.47614 ProteinModelPortal:Q9C505 SMR:Q9C505 STRING:Q9C505 PRIDE:Q9C505 EnsemblPlants:AT1G69410.1 GeneID:843273 KEGG:ath:AT1G69410 TAIR:At1g69410 InParanoid:Q9C505 OMA:CALKEVG PhylomeDB:Q9C505 ArrayExpress:Q9C505 Genevestigator:Q9C505 GermOnline:AT1G69410 Uniprot:Q9C505
Leaf	Isotig04566	1	23	-3.995	1.53E-05	TAIR|locus:505006299 - symbol:AT2G36145 "AT2G36145" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] GO:GO:0009570 EMBL:CP002685 GO:GO:0009535 EMBL:AC007135 EMBL:AY074366 EMBL:AY117291 EMBL:AY084343 EMBL:AK220614 IPI:IPI00542177 RefSeq:NP_565835.1 UniGene:At.37584 IntAct:Q8VXY0 STRING:Q8VXY0 PRIDE:Q8VXY0 EnsemblPlants:AT2G36145.1 GeneID:818187 KEGG:ath:AT2G36145 TAIR:At2g36145 InParanoid:Q8VXY0 OMA:NSLCQGA PhylomeDB:Q8VXY0 ProtClustDB:CLSN2688721 Genevestigator:Q8VXY0 Uniprot:Q8VXY0
Leaf	Isotig04567	1	21	-3.863	4.36E-05	TAIR|locus:505006299 - symbol:AT2G36145 "AT2G36145" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] GO:GO:0009570 EMBL:CP002685 GO:GO:0009535 EMBL:AC007135 EMBL:AY074366 EMBL:AY117291 EMBL:AY084343 EMBL:AK220614 IPI:IPI00542177 RefSeq:NP_565835.1 UniGene:At.37584 IntAct:Q8VXY0 STRING:Q8VXY0 PRIDE:Q8VXY0 EnsemblPlants:AT2G36145.1 GeneID:818187 KEGG:ath:AT2G36145 TAIR:At2g36145 InParanoid:Q8VXY0 OMA:NSLCQGA PhylomeDB:Q8VXY0 ProtClustDB:CLSN2688721 Genevestigator:Q8VXY0 Uniprot:Q8VXY0
Leaf	Isotig04618	11	1	3.988	0.000330755	UNIPROTKB|Q8W3Z4 - symbol:CASBPX1 "Cycloartenol synthase" species:78630 "Betula platyphylla" [GO:0010686 "tetracyclic triterpenoid biosynthetic process" evidence=IDA] [GO:0016871 "cycloartenol synthase activity" evidence=IDA] InterPro:IPR001330 InterPro:IPR002365 InterPro:IPR018333 Pfam:PF00432 PROSITE:PS01074 InterPro:IPR008930 SUPFAM:SSF48239 TIGRFAMs:TIGR01787 GO:GO:0010686 GO:GO:0016871 EMBL:AB055509 ProteinModelPortal:Q8W3Z4 Uniprot:Q8W3Z4
Leaf	Isotig04619	11	1	3.988	0.000330755	TAIR|locus:2060121 - symbol:CAS1 "AT2G07050" species:3702 "Arabidopsis thaliana" [GO:0019745 "pentacyclic triterpenoid biosynthetic process" evidence=ISS;IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0009555 "pollen development" evidence=IMP] [GO:0010027 "thylakoid membrane organization" evidence=IMP] [GO:0016871 "cycloartenol synthase activity" evidence=IDA] InterPro:IPR001330 InterPro:IPR002365 InterPro:IPR018333 Pfam:PF00432 PROSITE:PS01074 GO:GO:0005773 EMBL:CP002685 GenomeReviews:CT485783_GR InterPro:IPR008930 SUPFAM:SSF48239 GO:GO:0009555 GO:GO:0010027 GO:GO:0019745 TIGRFAMs:TIGR01787 eggNOG:COG1657 HOGENOM:HBG750669 EMBL:U02555 EMBL:AC005171 EMBL:AY094394 EMBL:BT001118 IPI:IPI00535551 PIR:A49398 PIR:H84481 RefSeq:NP_178722.1 UniGene:At.10550 ProteinModelPortal:P38605 SMR:P38605 STRING:P38605 PRIDE:P38605 EnsemblPlants:AT2G07050.1 GeneID:815275 KEGG:ath:AT2G07050 TAIR:At2g07050 InParanoid:P38605 KO:K01853 OMA:YLPMAYC PhylomeDB:P38605 ProtClustDB:CLSN2913056 BioCyc:ARA:AT2G07050-MONOMER BioCyc:MetaCyc:AT2G07050-MONOMER BRENDA:5.4.99.8 ArrayExpress:P38605 Genevestigator:P38605 GermOnline:AT2G07050 GO:GO:0016871 Uniprot:P38605
Leaf	Isotig04636	18	1	4.699	1.72E-06	TAIR|locus:2132090 - symbol:ISU1 "AT4G22220" species:3702 "Arabidopsis thaliana" [GO:0016226 "iron-sulfur cluster assembly" evidence=IGI;ISS] [GO:0005198 "structural molecule activity" evidence=ISS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] InterPro:IPR002871 InterPro:IPR011339 Pfam:PF01592 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005506 GO:GO:0005759 GO:GO:0016226 EMBL:AL161556 GO:GO:0051537 EMBL:AL021712 eggNOG:COG0822 HOGENOM:HBG584215 OMA:SSMVTEM TIGRFAMs:TIGR01999 EMBL:AJ866966 EMBL:AF361579 EMBL:AY081721 EMBL:AY088584

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						IPI:IPI00516740 PIR:T04903 RefSeq:NP_193953.1 UniGene:At.43669 HSSP:Q57074 ProteinModelPortal:O49627 SMR:O49627 IntAct:O49627 STRING:O49627 PRIDE:O49627 EnsemblPlants:AT4G22220.1 GeneID:828316 KEGG:ath:AT4G22220 TAIR:At4g22220 InParanoid:O49627 PhylomeDB:O49627 ProtClustDB:CLSN2684974 ArrayExpress:O49627 Genevestigator:O49627 Uniprot:O49627
Leaf	Isotig04637	19	1	4.777	8.26E-07	TAIR|locus:2132090 - symbol:ISU1 "AT4G22220" species:3702 "Arabidopsis thaliana" [GO:0016226 "iron-sulfur cluster assembly" evidence=IGI;ISS] [GO:0005198 "structural molecule activity" evidence=ISS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] InterPro:IPR002871 InterPro:IPR011339 Pfam:PF01592 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005506 GO:GO:0005759 GO:GO:0016226 EMBL:AL161556 GO:GO:0051537 EMBL:AL021712 eggNOG:COG0822 HOGENOM:HBG584215 OMA:SSMVTEM TIGRFAMs:TIGR01999 EMBL:AJ866966 EMBL:AF361579 EMBL:AY081721 EMBL:AY088584 IPI:IPI00516740 PIR:T04903 RefSeq:NP_193953.1 UniGene:At.43669 HSSP:Q57074 ProteinModelPortal:O49627 SMR:O49627 IntAct:O49627 STRING:O49627 PRIDE:O49627 EnsemblPlants:AT4G22220.1 GeneID:828316 KEGG:ath:AT4G22220 TAIR:At4g22220 InParanoid:O49627 PhylomeDB:O49627 ProtClustDB:CLSN2684974 ArrayExpress:O49627 Genevestigator:O49627 Uniprot:O49627
Leaf	Isotig04670	9	0	4.699	0.000718283	TAIR|locus:2057407 - symbol:PYL2 "AT2G26040" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0005515 "protein binding" evidence=IPI] [GO:0009738 "abscisic acid mediated signaling pathway" evidence=IGI;IDA] [GO:0004872 "receptor activity" evidence=IDA] [GO:0042803 "protein homodimerization activity" evidence=IDA] GO:GO:0005634 GO:GO:0005737 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0042803 GO:GO:0009738 GO:GO:0004872 InterPro:IPR023393 Gene3D:G3DSA:3.30.530.20 EMBL:AC004747 GO:GO:0010427 PDB:3KB3 PDB:3NMT PDBsum:3KB3 PDBsum:3NMT PDB:3NMV PDBsum:3NMV KO:K14496 InterPro:IPR019587 Pfam:PF10604 HOGENOM:HBG598713 IPI:IPI00546194 PIR:T02619 RefSeq:NP_180174.1 UniGene:At.66246 PDB:3KAZ PDB:3KB0 PDB:3KDH PDB:3KDI PDB:3KL1 PDB:3NJ0 PDB:3NJ1 PDB:3NMH PDB:3NMP PDB:3NR4 PDB:3NS2 PDBsum:3KAZ PDBsum:3KB0 PDBsum:3KDH PDBsum:3KDI PDBsum:3KL1 PDBsum:3NJ0 PDBsum:3NJ1 PDBsum:3NMH PDBsum:3NMP PDBsum:3NR4 PDBsum:3NS2 ProteinModelPortal:O80992 SMR:O80992 DIP:DIP-48582N IntAct:O80992 STRING:O80992 PRIDE:O80992 EnsemblPlants:AT2G26040.1 GeneID:817145 KEGG:ath:AT2G26040 TAIR:At2g26040 eggNOG:NOG299178 InParanoid:O80992 OMA:IPEGNTE PhylomeDB:O80992 ProtClustDB:CLSN2683286 ArrayExpress:O80992 Genevestigator:O80992 Uniprot:O80992
Leaf	Isotig04671	9	0	4.699	0.000718283	TAIR|locus:2057407 - symbol:PYL2 "AT2G26040" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0005515 "protein binding" evidence=IPI] [GO:0009738 "abscisic acid mediated signaling pathway" evidence=IGI;IDA] [GO:0004872 "receptor activity" evidence=IDA] [GO:0042803 "protein homodimerization activity" evidence=IDA] GO:GO:0005634 GO:GO:0005737 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0042803 GO:GO:0009738 GO:GO:0004872 InterPro:IPR023393 Gene3D:G3DSA:3.30.530.20 EMBL:AC004747 GO:GO:0010427 PDB:3KB3 PDB:3NMT PDBsum:3KB3 PDBsum:3NMT PDB:3NMV PDBsum:3NMV KO:K14496 InterPro:IPR019587 Pfam:PF10604 HOGENOM:HBG598713 IPI:IPI00546194 PIR:T02619 RefSeq:NP_180174.1 UniGene:At.66246 PDB:3KAZ PDB:3KB0 PDB:3KDH PDB:3KDI PDB:3KL1 PDB:3NJ0 PDB:3NJ1 PDB:3NMH PDB:3NMP PDB:3NR4 PDB:3NS2 PDBsum:3KAZ PDBsum:3KB0 PDBsum:3KDH PDBsum:3KDI PDBsum:3KL1 PDBsum:3NJ0 PDBsum:3NJ1 PDBsum:3NMH PDBsum:3NMP PDBsum:3NR4 PDBsum:3NS2 ProteinModelPortal:O80992 SMR:O80992 DIP:DIP-48582N IntAct:O80992 STRING:O80992 PRIDE:O80992 EnsemblPlants:AT2G26040.1 GeneID:817145 KEGG:ath:AT2G26040 TAIR:At2g26040 eggNOG:NOG299178 InParanoid:O80992 OMA:IPEGNTE PhylomeDB:O80992 ProtClustDB:CLSN2683286 ArrayExpress:O80992 Genevestigator:O80992 Uniprot:O80992
Leaf	Isotig04686	0	14	-4.278	0.000582768	TAIR|locus:2150119 - symbol:AT5G01260 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA;ISS] [GO:0005575 "cellular_component" evidence=ND] [GO:0005975 "carbohydrate metabolic process" evidence=IEA;ISS] [GO:0030246 "carbohydrate binding" evidence=IEA] InterPro:IPR002044 InterPro:IPR013784 Pfam:PF00686 PROSITE:PS51166 SMART:SM01065 EMBL:CP002688 InterPro:IPR013783 Gene3D:G3DSA:2.60.40.10 InterPro:IPR015902 PANTHER:PTHR10357 SUPFAM:SSF49452 EMBL:AL137189 CAZy:CBM20 GO:GO:2001070 IPI:IPI00540149 PIR:T45966 RefSeq:NP_974720.1 UniGene:At.26244 ProteinModelPortal:Q9LFB0 SMR:Q9LFB0 PRIDE:Q9LFB0 EnsemblPlants:AT5G01260.2 GeneID:831794 KEGG:ath:AT5G01260 TAIR:At5g01260 InParanoid:Q9LFB0 OMA:TIRICED PhylomeDB:Q9LFB0 ProtClustDB:CLSN2689357 Genevestigator:Q9LFB0 Uniprot:Q9LFB0
Leaf	Isotig04720	12	2	3.114	0.000658121	No hit

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig04721	12	1	4.114	0.000154103	No hit
Leaf	Isotig04722	35	158	-1.646	2.31E-12	TAIR|locus:2164371 - symbol:PSAN "AT5G64040" species:3702 "Arabidopsis thaliana" [GO:0009522 "photosystem I" evidence=TAS] [GO:0009773 "photosynthetic electron transport in photosystem I" evidence=TAS] [GO:0030093 "chloroplast photosystem I" evidence=IPI] [GO:0009543 "chloroplast thylakoid lumen" evidence=IDA] [GO:0005516 "calmodulin binding" evidence=TAS;IPI] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] InterPro:IPR008796 Pfam:PF05479 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005516 GO:GO:0009535 GO:GO:0015979 GO:GO:0009522 EMBL:AB008266 EMBL:U32176 EMBL:AY062835 EMBL:AY081594 IPI:IPI00547610 IPI:IPI00895629 RefSeq:NP_201209.1 UniGene:At.21476 ProteinModelPortal:P49107 SMR:P49107 IntAct:P49107 STRING:P49107 PRIDE:P49107 EnsemblPlants:AT5G64040.1 GeneID:836525 KEGG:ath:AT5G64040 GeneFarm:2295 TAIR:At5g64040 eggNOG:NOG284850 HOGENOM:HBG589689 InParanoid:P49107 KO:K02701 OMA:SCKFPEN PhylomeDB:P49107 ProtClustDB:PLN00054 BioCyc:MetaCyc:MONOMER-1095 ArrayExpress:P49107 Genevestigator:P49107 Uniprot:P49107
Leaf	Isotig04723	28	149	-1.883	7.45E-14	TAIR|locus:2164371 - symbol:PSAN "AT5G64040" species:3702 "Arabidopsis thaliana" [GO:0009522 "photosystem I" evidence=TAS] [GO:0009773 "photosynthetic electron transport in photosystem I" evidence=TAS] [GO:0030093 "chloroplast photosystem I" evidence=IPI] [GO:0009543 "chloroplast thylakoid lumen" evidence=IDA] [GO:0005516 "calmodulin binding" evidence=TAS;IPI] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] InterPro:IPR008796 Pfam:PF05479 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005516 GO:GO:0009535 GO:GO:0015979 GO:GO:0009522 EMBL:AB008266 EMBL:U32176 EMBL:AY062835 EMBL:AY081594 IPI:IPI00547610 IPI:IPI00895629 RefSeq:NP_201209.1 UniGene:At.21476 ProteinModelPortal:P49107 SMR:P49107 IntAct:P49107 STRING:P49107 PRIDE:P49107 EnsemblPlants:AT5G64040.1 GeneID:836525 KEGG:ath:AT5G64040 GeneFarm:2295 TAIR:At5g64040 eggNOG:NOG284850 HOGENOM:HBG589689 InParanoid:P49107 KO:K02701 OMA:SCKFPEN PhylomeDB:P49107 ProtClustDB:PLN00054 BioCyc:MetaCyc:MONOMER-1095 ArrayExpress:P49107 Genevestigator:P49107 Uniprot:P49107
Leaf	Isotig04752	9	0	4.699	0.000718283	TAIR|locus:2018605 - symbol:RP1 "ribosomal protein 1" species:3702 "Arabidopsis thaliana" [GO:0003735 "structural constituent of ribosome" evidence=IEA;ISS] [GO:0005840 "ribosome" evidence=ISS] [GO:0006412 "translation" evidence=ISS] [GO:0009793 "embryo development ending in seed dormancy" evidence=NAS] [GO:0005773 "vacuole" evidence=IDA] [GO:0005730 "nucleolus" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0022625 "cytosolic large ribosomal subunit" evidence=IDA;TAS] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR000597 Pfam:PF00297 EMBL:CP002684 GO:GO:0005886 GO:GO:0009506 GO:GO:0005774 GO:GO:0005618 GO:GO:0005730 GO:GO:0006412 GO:GO:0003735 InterPro:IPR009000 SUPFAM:SSF50447 GO:GO:0022625 UniGene:At.48973 EMBL:AC005687 eggNOG:COG0087 InterPro:IPR019926 PROSITE:PS00474 EMBL:M32654 EMBL:AY057487 EMBL:AF327421 EMBL:AF361101 EMBL:AF361809 EMBL:AY039544 EMBL:AY052743 EMBL:Z25950 IPI:IPI00540778 PIR:E96498 PIR:JQ0771 RefSeq:NP_001031146.1 RefSeq:NP_001185148.1 RefSeq:NP_001185149.1 RefSeq:NP_001185150.1 RefSeq:NP_001185151.1 RefSeq:NP_001185152.1 RefSeq:NP_175009.1 RefSeq:NP_973966.1 UniGene:At.21634 UniGene:At.24630 UniGene:At.7195 ProteinModelPortal:P17094 SMR:P17094 STRING:P17094 PRIDE:P17094 EnsemblPlants:AT1G43170.1 EnsemblPlants:AT1G43170.2 EnsemblPlants:AT1G43170.3 EnsemblPlants:AT1G43170.5 EnsemblPlants:AT1G43170.6 EnsemblPlants:AT1G43170.7 EnsemblPlants:AT1G43170.8 EnsemblPlants:AT1G43170.9 GeneID:840916 KEGG:ath:AT1G43170 GeneFarm:274 TAIR:At1g43170 InParanoid:P17094 KO:K02925 OMA:WGTKKLP PhylomeDB:P17094 ProtClustDB:CLSN2679512 Genevestigator:P17094 GermOnline:AT1G43170 Uniprot:P17094
Leaf	Isotig04790	0	13	-4.171	0.000994782	TAIR|locus:2008041 - symbol:AT1G50450 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0008152 "metabolic process" evidence=IEA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] InterPro:IPR005097 InterPro:IPR016040 Pfam:PF03435 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 GO:GO:0016491

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						eggNOG:COG1748 GO:GO:0009534 EMBL:AY039543 EMBL:AY097361 IPI:IPI00520569 RefSeq:NP_564570.1 UniGene:At.38025 UniGene:At.48296 ProteinModelPortal:Q94BZ0 SMR:Q94BZ0 IntAct:Q94BZ0 STRING:Q94BZ0 PRIDE:Q94BZ0 EnsemblPlants:AT1G50450.1 GeneID:841467 KEGG:ath:AT1G50450 TAIR:At1g50450 HOGENOM:HBG710841 InParanoid:Q94BZ0 OMA:TVMRTTF PhylomeDB:Q94BZ0 ProtClustDB:CLSN2688642 Genevestigator:Q94BZ0 Uniprot:Q94BZ0
Leaf	Isotig04791	0	13	-4.171	0.000994782	TAIR|locus:2008041 - symbol:AT1G50450 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0008152 "metabolic process" evidence=IEA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] InterPro:IPR005097 InterPro:IPR016040 Pfam:PF03435 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 GO:GO:0016491 eggNOG:COG1748 GO:GO:0009534 EMBL:AY039543 EMBL:AY097361 IPI:IPI00520569 RefSeq:NP_564570.1 UniGene:At.38025 UniGene:At.48296 ProteinModelPortal:Q94BZ0 SMR:Q94BZ0 IntAct:Q94BZ0 STRING:Q94BZ0 PRIDE:Q94BZ0 EnsemblPlants:AT1G50450.1 GeneID:841467 KEGG:ath:AT1G50450 TAIR:At1g50450 HOGENOM:HBG710841 InParanoid:Q94BZ0 OMA:TVMRTTF PhylomeDB:Q94BZ0 ProtClustDB:CLSN2688642 Genevestigator:Q94BZ0 Uniprot:Q94BZ0
Leaf	Isotig04800	11	66	-2.056	1.33E-07	UNIPROTKB|P83522 - symbol:P83522 "Ferredoxin" species:4513 "Hordeum vulgare" [GO:0006124 "ferredoxin metabolic process" evidence=TAS] [GO:0009055 "electron carrier activity" evidence=TAS] InterPro:IPR001041 InterPro:IPR006058 InterPro:IPR010241 Pfam:PF00111 PROSITE:PS00197 PROSITE:PS51085 GO:GO:0009507 GO:GO:0009055 GO:GO:0046872 GO:GO:0006810 GO:GO:0022900 GO:GO:0051537 InterPro:IPR012675 Gene3D:G3DSA:3.10.20.30 SUPFAM:SSF54292 TIGRFAMs:TIGR02008 GO:GO:0006124 ProteinModelPortal:P83522 SMR:P83522 Gramene:P83522 Genevestigator:P83522 Uniprot:P83522
Leaf	Isotig04801	11	65	-2.034	2.01E-07	UNIPROTKB|P83522 - symbol:P83522 "Ferredoxin" species:4513 "Hordeum vulgare" [GO:0006124 "ferredoxin metabolic process" evidence=TAS] [GO:0009055 "electron carrier activity" evidence=TAS] InterPro:IPR001041 InterPro:IPR006058 InterPro:IPR010241 Pfam:PF00111 PROSITE:PS00197 PROSITE:PS51085 GO:GO:0009507 GO:GO:0009055 GO:GO:0046872 GO:GO:0006810 GO:GO:0022900 GO:GO:0051537 InterPro:IPR012675 Gene3D:G3DSA:3.10.20.30 SUPFAM:SSF54292 TIGRFAMs:TIGR02008 GO:GO:0006124 ProteinModelPortal:P83522 SMR:P83522 Gramene:P83522 Genevestigator:P83522 Uniprot:P83522
Leaf	Isotig04842	0	13	-4.171	0.000994782	TAIR|locus:2135287 - symbol:PnsL4 "AT4G39710" species:3702 "Arabidopsis thaliana" [GO:0000413 "protein peptidyl-prolyl isomerization" evidence=IBA] [GO:0003755 "peptidyl-prolyl cis-trans isomerase activity" evidence=ISS;IBA] [GO:0005528 "FK506 binding" evidence=ISS;IBA] [GO:0018208 "peptidyl-proline modification" evidence=IBA] [GO:0009543 "chloroplast thylakoid lumen" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0031679 "NADH dehydrogenase (plastoquinone) activity" evidence=IMP] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0010598 "NAD(P)H dehydrogenase complex (plastoquinone)" evidence=IDA] InterPro:IPR001179 Pfam:PF00254 PROSITE:PS50059 PANTHER:PTHR10516 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0006457 GO:GO:0005515 EMBL:AL022605 EMBL:AL161595 GO:GO:0009535 GO:GO:0003755 eggNOG:COG0545 HOGENOM:HBG731200 InterPro:IPR023566 EMBL:AJ242481 EMBL:AY052226 IPI:IPI00538271 PIR:T05008 RefSeq:NP_568067.1 UniGene:At.693 ProteinModelPortal:Q9SCY3 SMR:Q9SCY3 IntAct:Q9SCY3 STRING:Q9SCY3 PRIDE:Q9SCY3 EnsemblPlants:AT4G39710.1 GeneID:830126 KEGG:ath:AT4G39710 TAIR:At4g39710 InParanoid:Q9SCY3 OMA:HYTARFA PhylomeDB:Q9SCY3 ProtClustDB:CLSN2689844 ArrayExpress:O65658 Genevestigator:Q9SCY3 GermOnline:AT4G39710 GO:GO:0010598 Uniprot:Q9SCY3
Leaf	Isotig04878	45	30	1.114	0.000845792	TAIR|locus:2093307 - symbol:AT3G15670 "AT3G15670" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0009793 "embryo development ending in seed dormancy" evidence=ISS] [GO:0005634 "nucleus" evidence=IDA] GO:GO:0005634 EMBL:CP002686 EMBL:AB017071 ProtClustDB:CLSN2679745 EMBL:AY040026 EMBL:AY054162 EMBL:AY079410 IPI:IPI00542660 RefSeq:NP_188188.1 UniGene:At.5382 STRING:Q9LW12 PRIDE:Q9LW12 ProMEX:Q9LW12 EnsemblPlants:AT3G15670.1 GeneID:820810 KEGG:ath:AT3G15670 TAIR:At3g15670 InParanoid:Q9LW12 OMA:QYTKETA PhylomeDB:Q9LW12 ArrayExpress:Q9LW12 Genevestigator:Q9LW12 Uniprot:Q9LW12
Leaf	Isotig04879	44	28	1.181	0.00054333	TAIR|locus:2093307 - symbol:AT3G15670 "AT3G15670" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0009793 "embryo development ending in seed dormancy" evidence=ISS] [GO:0005634 "nucleus" evidence=IDA] GO:GO:0005634 EMBL:CP002686 EMBL:AB017071 ProtClustDB:CLSN2679745 EMBL:AY040026 EMBL:AY054162 EMBL:AY079410 IPI:IPI00542660

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						RefSeq:NP_188188.1 UniGene:At.5382 STRING:Q9LW12 PRIDE:Q9LW12 ProMEX:Q9LW12 EnsemblPlants:AT3G15670.1 GeneID:820810 KEGG:ath:AT3G15670 TAIR:At3g15670 InParanoid:Q9LW12 OMA:QYTKETA PhylomeDB:Q9LW12 ArrayExpress:Q9LW12 Genevestigator:Q9LW12 Uniprot:Q9LW12
Leaf	Isotig04918	9	0	4.699	0.000718283	TAIR|locus:2206629 - symbol:AtLEA4-1 "AT1G32560" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0009793 "embryo development ending in seed dormancy" evidence=ISS] [GO:0006970 "response to osmotic stress" evidence=IMP] [GO:0009414 "response to water deprivation" evidence=IMP] [GO:0048316 "seed development" evidence=IMP] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR005513 Pfam:PF03760 ProDom:PD005538 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009506 GO:GO:0009790 GO:GO:0009414 GO:GO:0006970 GO:GO:0048316 EMBL:AC055769 EMBL:AY063826 EMBL:AY096424 EMBL:X89505 IPI:IPI00545826 PIR:S71249 RefSeq:NP_174534.1 UniGene:At.5386 STRING:Q39138 PRIDE:Q39138 EnsemblPlants:AT1G32560.1 GeneID:840150 KEGG:ath:AT1G32560 TAIR:At1g32560 eggNOG:NOG312967 InParanoid:Q39138 OMA:HAEDKLM PhylomeDB:Q39138 ProtClustDB:CLSN2720625 ArrayExpress:Q39138 Genevestigator:Q39138 Uniprot:Q39138
Leaf	Isotig04919	9	0	4.699	0.000718283	TAIR|locus:2206629 - symbol:AtLEA4-1 "AT1G32560" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0009793 "embryo development ending in seed dormancy" evidence=ISS] [GO:0006970 "response to osmotic stress" evidence=IMP] [GO:0009414 "response to water deprivation" evidence=IMP] [GO:0048316 "seed development" evidence=IMP] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR005513 Pfam:PF03760 ProDom:PD005538 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009506 GO:GO:0009790 GO:GO:0009414 GO:GO:0006970 GO:GO:0048316 EMBL:AC055769 EMBL:AY063826 EMBL:AY096424 EMBL:X89505 IPI:IPI00545826 PIR:S71249 RefSeq:NP_174534.1 UniGene:At.5386 STRING:Q39138 PRIDE:Q39138 EnsemblPlants:AT1G32560.1 GeneID:840150 KEGG:ath:AT1G32560 TAIR:At1g32560 eggNOG:NOG312967 InParanoid:Q39138 OMA:HAEDKLM PhylomeDB:Q39138 ProtClustDB:CLSN2720625 ArrayExpress:Q39138 Genevestigator:Q39138 Uniprot:Q39138
Leaf	Isotig04928	11	1	3.988	0.000330755	TAIR|locus:2168118 - symbol:AT5G59850 "AT5G59850" species:3702 "Arabidopsis thaliana" [GO:0003735 "structural constituent of ribosome" evidence=ISS] [GO:0006412 "translation" evidence=ISS] [GO:0022627 "cytosolic small ribosomal subunit" evidence=ISS;IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR000630 Pfam:PF00410 PROSITE:PS00053 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005886 GO:GO:0009506 GO:GO:0005774 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005618 GO:GO:0006412 GO:GO:0003735 EMBL:AB015475 EMBL:AC007583 GO:GO:0022627 EMBL:L27461 EMBL:AF001412 EMBL:AF332447 EMBL:AF360284 EMBL:AF386922 EMBL:AY042830 EMBL:AY051040 EMBL:AY081472 EMBL:AY081689 EMBL:AY035157 EMBL:AY063028 EMBL:BT000671 EMBL:AY088335 EMBL:AY087576 IPI:IPI00529697 PIR:B86213 RefSeq:NP_172256.1 RefSeq:NP_200793.1 RefSeq:NP_973783.1 UniGene:At.21259 UniGene:At.23585 UniGene:At.57582 UniGene:At.6667 ProteinModelPortal:P42798 SMR:P42798 IntAct:P42798 STRING:P42798 PRIDE:P42798 EnsemblPlants:AT1G07770.1 EnsemblPlants:AT1G07770.2 EnsemblPlants:AT5G59850.1 GeneID:836107 GeneID:837291 KEGG:ath:AT1G07770 KEGG:ath:AT5G59850 TAIR:At1g07770 TAIR:At5g59850 eggNOG:COG0096 HOGENOM:HBG735443 InParanoid:P42798 KO:K02957 OMA:KVIVKFL PhylomeDB:P42798 ProtClustDB:PLN00146 ArrayExpress:P42798 Genevestigator:P42798 GermOnline:AT1G07770 PANTHER:PTHR11758 SUPFAM:SSF56047 Uniprot:P42798
Leaf	Isotig04929	11	1	3.988	0.000330755	TAIR|locus:2168118 - symbol:AT5G59850 "AT5G59850" species:3702 "Arabidopsis thaliana" [GO:0003735 "structural constituent of ribosome" evidence=ISS] [GO:0006412 "translation" evidence=ISS] [GO:0022627 "cytosolic small ribosomal subunit" evidence=ISS;IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR000630 Pfam:PF00410 PROSITE:PS00053 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005886 GO:GO:0009506 GO:GO:0005774 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005618 GO:GO:0006412 GO:GO:0003735 EMBL:AB015475 EMBL:AC007583 GO:GO:0022627 EMBL:L27461 EMBL:AF001412 EMBL:AF332447 EMBL:AF360284 EMBL:AF386922 EMBL:AY042830 EMBL:AY051040 EMBL:AY081472 EMBL:AY081689 EMBL:AY035157 EMBL:AY063028 EMBL:BT000671 EMBL:AY088335 EMBL:AY087576 IPI:IPI00529697 PIR:B86213 RefSeq:NP_172256.1 RefSeq:NP_200793.1 RefSeq:NP_973783.1 UniGene:At.21259 UniGene:At.23585 UniGene:At.57582 UniGene:At.6667 ProteinModelPortal:P42798 SMR:P42798 IntAct:P42798 STRING:P42798 PRIDE:P42798

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EnsemblPlants:AT1G07770.1 EnsemblPlants:AT1G07770.2 EnsemblPlants:AT5G59850.1 GeneID:836107 GeneID:837291 KEGG:ath:AT1G07770 KEGG:ath:AT5G59850 TAIR:At1g07770 TAIR:At5g59850 eggNOG:COG0096 HOGENOM:HBG735443 InParanoid:P42798 KO:K02957 OMA:KVIVKFL PhylomeDB:P42798 ProtClustDB:PLN00146 ArrayExpress:P42798 Genevestigator:P42798 GermOnline:AT1G07770 PANTHER:PTHR11758 SUPFAM:SSF56047 Uniprot:P42798
Leaf	Isotig04934	11	0	4.988	0.000159591	TAIR|locus:2156937 - symbol:STR16 "AT5G66040" species:3702 "Arabidopsis thaliana" [GO:0007568 "aging" evidence=ISS] [GO:0004792 "thiosulfate sulfurtransferase activity" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] PROSITE:PS00683 Pfam:PF00581 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009507 EMBL:AB011474 InterPro:IPR001763 Gene3D:G3DSA:3.40.250.10 SMART:SM00450 SUPFAM:SSF52821 PROSITE:PS50206 eggNOG:COG0607 HOGENOM:HBG743107 GO:GO:0004792 EMBL:X89036 EMBL:AY049302 EMBL:BT000864 EMBL:AY084763 IPI:IPI00531957 PIR:S58275 RefSeq:NP_851278.1 UniGene:At.23333 PDB:1TQ1 PDBsum:1TQ1 ProteinModelPortal:Q39129 SMR:Q39129 STRING:Q39129 PRIDE:Q39129 EnsemblPlants:AT5G66040.1 GeneID:836734 KEGG:ath:AT5G66040 GeneFarm:4731 TAIR:At5g66040 InParanoid:Q39129 OMA:ELCSAGF PhylomeDB:Q39129 BRENDA:2.8.1.1 ArrayExpress:Q39129 Genevestigator:Q39129 Uniprot:Q39129
Leaf	Isotig04935	13	0	5.229	3.68E-05	TAIR|locus:2156937 - symbol:STR16 "AT5G66040" species:3702 "Arabidopsis thaliana" [GO:0007568 "aging" evidence=ISS] [GO:0004792 "thiosulfate sulfurtransferase activity" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] PROSITE:PS00683 Pfam:PF00581 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009507 EMBL:AB011474 InterPro:IPR001763 Gene3D:G3DSA:3.40.250.10 SMART:SM00450 SUPFAM:SSF52821 PROSITE:PS50206 eggNOG:COG0607 HOGENOM:HBG743107 GO:GO:0004792 EMBL:X89036 EMBL:AY049302 EMBL:BT000864 EMBL:AY084763 IPI:IPI00531957 PIR:S58275 RefSeq:NP_851278.1 UniGene:At.23333 PDB:1TQ1 PDBsum:1TQ1 ProteinModelPortal:Q39129 SMR:Q39129 STRING:Q39129 PRIDE:Q39129 EnsemblPlants:AT5G66040.1 GeneID:836734 KEGG:ath:AT5G66040 GeneFarm:4731 TAIR:At5g66040 InParanoid:Q39129 OMA:ELCSAGF PhylomeDB:Q39129 BRENDA:2.8.1.1 ArrayExpress:Q39129 Genevestigator:Q39129 Uniprot:Q39129
Leaf	Isotig04946	19	5	2.455	0.000151807	UNIPROTKB|Q84N29 - symbol:LTP3 "Probable non-specific lipid-transfer protein 3" species:4565 "Triticum aestivum" [GO:0009611 "response to wounding" evidence=IDA] [GO:0009723 "response to ethylene stimulus" evidence=IDA] [GO:0009751 "response to salicylic acid stimulus" evidence=IDA] [GO:0042542 "response to hydrogen peroxide" evidence=IDA] InterPro:IPR000528 InterPro:IPR013770 PRINTS:PR00382 PROSITE:PS00597 Pfam:PF00234 GO:GO:0009611 InterPro:IPR016140 SMART:SM00499 SUPFAM:SSF47699 GO:GO:0006869 GO:GO:0009723 GO:GO:0009751 GO:GO:0042542 GO:GO:0008289 Gene3D:G3DSA:1.10.110.10 EMBL:AY226580 UniGene:Ta.50482 HSSP:P19656 ProteinModelPortal:Q84N29 SMR:Q84N29 Gramene:Q84N29 Uniprot:Q84N29
Leaf	Isotig04947	20	5	2.529	7.73E-05	UNIPROTKB|Q84N29 - symbol:LTP3 "Probable non-specific lipid-transfer protein 3" species:4565 "Triticum aestivum" [GO:0009611 "response to wounding" evidence=IDA] [GO:0009723 "response to ethylene stimulus" evidence=IDA] [GO:0009751 "response to salicylic acid stimulus" evidence=IDA] [GO:0042542 "response to hydrogen peroxide" evidence=IDA] InterPro:IPR000528 InterPro:IPR013770 PRINTS:PR00382 PROSITE:PS00597 Pfam:PF00234 GO:GO:0009611 InterPro:IPR016140 SMART:SM00499 SUPFAM:SSF47699 GO:GO:0006869 GO:GO:0009723 GO:GO:0009751 GO:GO:0042542 GO:GO:0008289 Gene3D:G3DSA:1.10.110.10 EMBL:AY226580 UniGene:Ta.50482 HSSP:P19656 ProteinModelPortal:Q84N29 SMR:Q84N29 Gramene:Q84N29 Uniprot:Q84N29
Leaf	Isotig04986	10	1	3.851	0.00071293	TAIR|locus:2078491 - symbol:AT3G56340 species:3702 "Arabidopsis thaliana" [GO:0003735 "structural constituent of ribosome" evidence=IEA;ISS] [GO:0005840 "ribosome" evidence=ISS] [GO:0006412 "translation" evidence=IEA;ISS] [GO:0042254 "ribosome biogenesis" evidence=ISS] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0022627 "cytosolic small ribosomal subunit" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] InterPro:IPR000892 Pfam:PF01283 PROSITE:PS00733 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0016020 GO:GO:0006412 GO:GO:0003735 EMBL:AL163763 GO:GO:0022627 eggNOG:COG4830 HOGENOM:HBG744826 KO:K02976 ProtClustDB:PLN00186 PANTHER:PTHR12538 EMBL:AY039886 EMBL:AY133664 IPI:IPI00546882 PIR:T47751 RefSeq:NP_191193.1 UniGene:At.5076 ProteinModelPortal:Q9LYK9 SMR:Q9LYK9 STRING:Q9LYK9 PRIDE:Q9LYK9 EnsemblPlants:AT3G56340.1 GeneID:824801 KEGG:ath:AT3G56340 TAIR:At3g56340

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						InParanoid:Q9LYK9 OMA:RRTNCAR PhylomeDB:Q9LYK9 Genevestigator:Q9LYK9 GermOnline:AT3G56340 Uniprot:Q9LYK9
Leaf	Isotig04987	10	1	3.851	0.00071293	TAIR|locus:2078491 - symbol:AT3G56340 species:3702 "Arabidopsis thaliana" [GO:0003735 "structural constituent of ribosome" evidence=IEA;ISS] [GO:0005840 "ribosome" evidence=ISS] [GO:0006412 "translation" evidence=IEA;ISS] [GO:0042254 "ribosome biogenesis" evidence=ISS] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0022627 "cytosolic small ribosomal subunit" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] InterPro:IPR000892 Pfam:PF01283 PROSITE:PS00733 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0016020 GO:GO:0006412 GO:GO:0003735 EMBL:AL163763 GO:GO:0022627 eggNOG:COG4830 HOGENOM:HBG744826 KO:K02976 ProtClustDB:PLN00186 PANTHER:PTHR12538 EMBL:AY039886 EMBL:AY133664 IPI:IPI00546882 PIR:T47751 RefSeq:NP_191193.1 UniGene:At.5076 ProteinModelPortal:Q9LYK9 SMR:Q9LYK9 STRING:Q9LYK9 PRIDE:Q9LYK9 EnsemblPlants:AT3G56340.1 GeneID:824801 KEGG:ath:AT3G56340 TAIR:At3g56340 InParanoid:Q9LYK9 OMA:RRTNCAR PhylomeDB:Q9LYK9 Genevestigator:Q9LYK9 GermOnline:AT3G56340 Uniprot:Q9LYK9
Leaf	Isotig05024	11	0	4.988	0.000159591	TAIR|locus:2116762 - symbol:AT4G31830 "AT4G31830" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002687 GenomeReviews:CT486007_GR EMBL:AL161579 EMBL:AL049607 EMBL:BT010813 EMBL:BT011290 IPI:IPI00539008 PIR:T06305 RefSeq:NP_194911.1 UniGene:At.31710 IntAct:Q9SZ50 PRIDE:Q9SZ50 EnsemblPlants:AT4G31830.1 GeneID:829312 KEGG:ath:AT4G31830 TAIR:At4g31830 eggNOG:NOG287408 HOGENOM:HBG748438 InParanoid:Q9SZ50 OMA:THKMSPE PhylomeDB:Q9SZ50 ProtClustDB:CLSN2685982 ArrayExpress:Q9SZ50 Genevestigator:Q9SZ50 Uniprot:Q9SZ50
Leaf	Isotig05025	11	0	4.988	0.000159591	TAIR|locus:2116762 - symbol:AT4G31830 "AT4G31830" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002687 GenomeReviews:CT486007_GR EMBL:AL161579 EMBL:AL049607 EMBL:BT010813 EMBL:BT011290 IPI:IPI00539008 PIR:T06305 RefSeq:NP_194911.1 UniGene:At.31710 IntAct:Q9SZ50 PRIDE:Q9SZ50 EnsemblPlants:AT4G31830.1 GeneID:829312 KEGG:ath:AT4G31830 TAIR:At4g31830 eggNOG:NOG287408 HOGENOM:HBG748438 InParanoid:Q9SZ50 OMA:THKMSPE PhylomeDB:Q9SZ50 ProtClustDB:CLSN2685982 ArrayExpress:Q9SZ50 Genevestigator:Q9SZ50 Uniprot:Q9SZ50
Leaf	Isotig05134	19	5	2.455	0.000151807	TAIR|locus:2079924 - symbol:UBQ1 "AT3G52590" species:3702 "Arabidopsis thaliana" [GO:0009793 "embryo development ending in seed dormancy" evidence=NAS] [GO:0003735 "structural constituent of ribosome" evidence=ISS] [GO:0016567 "protein ubiquitination" evidence=TAS] InterPro:IPR000626 Pfam:PF00240 SMART:SM00213 Prosite:PS00299 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005634 GO:GO:0005737 EMBL:AL161503 InterPro:IPR019955 PROSITE:PS50053 UniGene:At.48785 InterPro:IPR019954 eggNOG:COG5272 EMBL:AC012392 InterPro:IPR019956 PRINTS:PR00348 UniGene:At.23108 KO:K08770 EMBL:L05361 EMBL:AY139999 EMBL:BT000701 IPI:IPI00520650 IPI:IPI00895605 RefSeq:NP_001118922.1 RefSeq:NP_849292.1 RefSeq:NP_849299.4 RefSeq:NP_849301.4 RefSeq:NP_974516.4 UniGene:At.24970 UniGene:At.25274 UniGene:At.47590 UniGene:At.74401 ProteinModelPortal:Q8H159 SMR:Q8H159 EnsemblPlants:AT4G05320.2 EnsemblPlants:AT4G05320.4 GeneID:825880 GeneID:828148 KEGG:ath:AT4G02890 KEGG:ath:AT4G05320 TAIR:At4g05320 PhylomeDB:Q8H159 ProtClustDB:CLSN2692469 Uniprot:Q8H159
Leaf	Isotig05135	21	6	2.336	0.000109395	TAIR|locus:2079924 - symbol:UBQ1 "AT3G52590" species:3702 "Arabidopsis thaliana" [GO:0009793 "embryo development ending in seed dormancy" evidence=NAS] [GO:0003735 "structural constituent of ribosome" evidence=ISS] [GO:0016567 "protein ubiquitination" evidence=TAS] InterPro:IPR000626 Pfam:PF00240 SMART:SM00213 Prosite:PS00299 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005634 GO:GO:0005737 EMBL:AL161503 InterPro:IPR019955 PROSITE:PS50053 UniGene:At.48785 InterPro:IPR019954 eggNOG:COG5272 EMBL:AC012392 InterPro:IPR019956 PRINTS:PR00348 UniGene:At.23108 KO:K08770 EMBL:L05361 EMBL:AY139999 EMBL:BT000701 IPI:IPI00520650 IPI:IPI00895605 RefSeq:NP_001118922.1 RefSeq:NP_849292.1 RefSeq:NP_849299.4 RefSeq:NP_849301.4 RefSeq:NP_974516.4 UniGene:At.24970 UniGene:At.25274 UniGene:At.47590 UniGene:At.74401 ProteinModelPortal:Q8H159 SMR:Q8H159 EnsemblPlants:AT4G05320.2 EnsemblPlants:AT4G05320.4 GeneID:825880 GeneID:828148

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						KEGG:ath:AT4G02890 KEGG:ath:AT4G05320 TAIR:At4g05320 PhylomeDB:Q8H159 ProtClustDB:CLSN2692469 Uniprot:Q8H159
Leaf	Isotig05160	12	0	5.114	7.63E-05	TAIR|locus:2078107 - symbol:AT3G05560 species:3702 "Arabidopsis thaliana" [GO:0003735 "structural constituent of ribosome" evidence=IEA] [GO:0005840 "ribosome" evidence=ISS] [GO:0006412 "translation" evidence=IEA] [GO:0005730 "nucleolus" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0022625 "cytosolic large ribosomal subunit" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR002671 Pfam:PF01776 GO:GO:0005886 GO:GO:0009506 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005730 GO:GO:0006412 GO:GO:0003735 EMBL:AC011620 GO:GO:0022625 eggNOG:NOG260326 HOGENOM:HBG716459 KO:K02891 ProtClustDB:CLSN2679607 PANTHER:PTHR10064 OMA:KYLKKQQ EMBL:AY065359 EMBL:AY096581 EMBL:BT002469 EMBL:BT006523 EMBL:AY088594 IPI:IPI00546577 RefSeq:NP_001078112.1 RefSeq:NP_187207.1 RefSeq:NP_974229.1 UniGene:At.28518 STRING:Q9M9W1 PRIDE:Q9M9W1 EnsemblPlants:AT3G05560.1 EnsemblPlants:AT3G05560.2 EnsemblPlants:AT3G05560.3 GeneID:819722 KEGG:ath:AT3G05560 GeneFarm:254 TAIR:At3g05560 InParanoid:Q9M9W1 PhylomeDB:Q9M9W1 ArrayExpress:Q9M9W1 Genevestigator:Q9M9W1 GermOnline:AT3G05560 Uniprot:Q9M9W1
Leaf	Isotig05161	12	0	5.114	7.63E-05	TAIR|locus:2078107 - symbol:AT3G05560 species:3702 "Arabidopsis thaliana" [GO:0003735 "structural constituent of ribosome" evidence=IEA] [GO:0005840 "ribosome" evidence=ISS] [GO:0006412 "translation" evidence=IEA] [GO:0005730 "nucleolus" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0022625 "cytosolic large ribosomal subunit" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR002671 Pfam:PF01776 GO:GO:0005886 GO:GO:0009506 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005730 GO:GO:0006412 GO:GO:0003735 EMBL:AC011620 GO:GO:0022625 eggNOG:NOG260326 HOGENOM:HBG716459 KO:K02891 ProtClustDB:CLSN2679607 PANTHER:PTHR10064 OMA:KYLKKQQ EMBL:AY065359 EMBL:AY096581 EMBL:BT002469 EMBL:BT006523 EMBL:AY088594 IPI:IPI00546577 RefSeq:NP_001078112.1 RefSeq:NP_187207.1 RefSeq:NP_974229.1 UniGene:At.28518 STRING:Q9M9W1 PRIDE:Q9M9W1 EnsemblPlants:AT3G05560.1 EnsemblPlants:AT3G05560.2 EnsemblPlants:AT3G05560.3 GeneID:819722 KEGG:ath:AT3G05560 GeneFarm:254 TAIR:At3g05560 InParanoid:Q9M9W1 PhylomeDB:Q9M9W1 ArrayExpress:Q9M9W1 Genevestigator:Q9M9W1 GermOnline:AT3G05560 Uniprot:Q9M9W1
Leaf	Isotig05172	22	127	-2.000	6.56E-13	TAIR|locus:2012928 - symbol:DRT112 "DNA-DAMAGE-REPAIR/TOLERATION PROTEIN 112" species:3702 "Arabidopsis thaliana" [GO:0005507 "copper ion binding" evidence=IEA] [GO:0009055 "electron carrier activity" evidence=IEA] [GO:0009543 "chloroplast thylakoid lumen" evidence=IDA] [GO:0031977 "thylakoid lumen" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0046688 "response to copper ion" evidence=IEP] [GO:0055070 "copper ion homeostasis" evidence=IMP] [GO:0017148 "negative regulation of translation" evidence=IMP] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0009411 "response to UV" evidence=IGI] [GO:0042221 "response to chemical stimulus" evidence=IGI] InterPro:IPR000923 InterPro:IPR001235 InterPro:IPR002387 Pfam:PF00127 PRINTS:PR00156 PRINTS:PR00157 PROSITE:PS00196 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009570 GO:GO:0009411 GO:GO:0017148 GO:GO:0009055 GO:GO:0006810 GO:GO:0005507 GO:GO:0046688 GO:GO:0022900 HOGENOM:HBG653810 InterPro:IPR008972 Gene3D:G3DSA:2.60.40.420 SUPFAM:SSF49503 GO:GO:0055070 GO:GO:0009543 EMBL:AC026234 eggNOG:COG3794 KO:K02638 ProtClustDB:CLSN2679397 TIGRFAMs:TIGR02656 EMBL:M98456 EMBL:AJ271355 EMBL:AF324702 EMBL:AF326879 EMBL:AF334383 EMBL:AF361853 EMBL:BT001030 EMBL:AY086284 EMBL:AY374308 IPI:IPI00520177 PIR:B86337 PIR:PA0004 PIR:S33707 RefSeq:NP_173459.1 UniGene:At.24399 UniGene:At.71481 UniGene:At.71708 UniGene:At.72031 ProteinModelPortal:P42699 SMR:P42699 STRING:P42699 PRIDE:P42699 ProMEX:P42699 EnsemblPlants:AT1G20340.1 GeneID:838622 KEGG:ath:AT1G20340 TAIR:At1g20340 InParanoid:P42699 OMA:WEETFSE PhylomeDB:P42699 ArrayExpress:P42699 Genevestigator:P42699 GermOnline:AT1G20340 Uniprot:P42699
Leaf	Isotig05286	12	0	5.114	7.63E-05	POMBASE|SPAPB18E9.04c - symbol:SPAPB18E9.04c "sequence orphan" species:4896 "Schizosaccharomyces pombe" [GO:0009986 "cell surface" evidence=TAS] [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] PomBase:SPAPB18E9.04c GO:GO:0005576 GO:GO:0009986 EMBL:CU329670 eggNOG:NOG12793 RefSeq:NP_001018272.1 EnsemblFungi:SPAPB18E9.04c.1 GeneID:3361427 KEGG:spo:SPAPB18E9.04c OMA:TTNCTTS ArrayExpress:Q8TFG4 Uniprot:Q8TFG4

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig05287	12	0	5.114	7.63E-05	No hit
Leaf	Isotig05296	21	2	3.921	8.06E-07	UNIPROTKB|Q5A109 - symbol:UBI3 "Ubiquitin-ribosomal protein fusion S27a" species:237561 "Candida albicans SC5314" [GO:0003735 "structural constituent of ribosome" evidence=IGI] [GO:0005576 "extracellular region" evidence=IDA] [GO:0016567 "protein ubiquitination" evidence=IGI] [GO:0031386 "protein tag" evidence=IGI] [GO:0042254 "ribosome biogenesis" evidence=IGI] InterPro:IPR000626 InterPro:IPR002906 Pfam:PF00240 Pfam:PF01599 SMART:SM00213 CGD:CAL0001506 Prosite:PS00299 GO:GO:0005576 GO:GO:0006412 GO:GO:0016567 GO:GO:0003735 InterPro:IPR019955 PROSITE:PS50053 GO:GO:0005840 GO:GO:0042254 GO:GO:0031386 InterPro:IPR019954 EMBL:AACQ01000086 EMBL:AACQ01000085 InterPro:IPR019956 PRINTS:PR00348 KO:K02977 RefSeq:XP_715397.1 RefSeq:XP_715467.1 ProteinModelPortal:Q5A109 SMR:Q5A109 STRING:Q5A109 GeneID:3642848 GeneID:3642934 KEGG:cal:CaO19.10599 KEGG:cal:CaO19.3087 PhylomeDB:Q5A109 Uniprot:Q5A109
Leaf	Isotig05297	21	2	3.921	8.06E-07	UNIPROTKB|Q5A109 - symbol:UBI3 "Ubiquitin-ribosomal protein fusion S27a" species:237561 "Candida albicans SC5314" [GO:0003735 "structural constituent of ribosome" evidence=IGI] [GO:0005576 "extracellular region" evidence=IDA] [GO:0016567 "protein ubiquitination" evidence=IGI] [GO:0031386 "protein tag" evidence=IGI] [GO:0042254 "ribosome biogenesis" evidence=IGI] InterPro:IPR000626 InterPro:IPR002906 Pfam:PF00240 Pfam:PF01599 SMART:SM00213 CGD:CAL0001506 Prosite:PS00299 GO:GO:0005576 GO:GO:0006412 GO:GO:0016567 GO:GO:0003735 InterPro:IPR019955 PROSITE:PS50053 GO:GO:0005840 GO:GO:0042254 GO:GO:0031386 InterPro:IPR019954 EMBL:AACQ01000086 EMBL:AACQ01000085 InterPro:IPR019956 PRINTS:PR00348 KO:K02977 RefSeq:XP_715397.1 RefSeq:XP_715467.1 ProteinModelPortal:Q5A109 SMR:Q5A109 STRING:Q5A109 GeneID:3642848 GeneID:3642934 KEGG:cal:CaO19.10599 KEGG:cal:CaO19.3087 PhylomeDB:Q5A109 Uniprot:Q5A109
Leaf	Isotig05302	0	16	-4.471	0.000202082	No hit
Leaf	Isotig05303	1194	1307	0.399	3.05E-12	UNIPROTKB|P12154 - symbol:psaA "Photosystem I P700 chlorophyll a apoprotein A1" species:3055 "Chlamydomonas reinhardtii" [GO:0005515 "protein binding" evidence=IPI] HAMAP:MF_00458 InterPro:IPR001280 InterPro:IPR006243 Pfam:PF00223 PIRSF:PIRSF002905 PRINTS:PR00257 GO:GO:0016021 GO:GO:0005515 GO:GO:0046872 GO:GO:0006810 GO:GO:0016491 GO:GO:0051539 GO:GO:0022900 GO:GO:0018298 GO:GO:0009535 GO:GO:0015979 GO:GO:0009522 GO:GO:0016168 EMBL:X05845 EMBL:X05846 EMBL:X05847 EMBL:FJ423446 EMBL:AB044419 EMBL:BK000554 PIR:A28341 RefSeq:NP_958375.1 ProteinModelPortal:P12154 SMR:P12154 DIP:DIP-34985N IntAct:P12154 PRIDE:P12154 GeneID:2717000 KEGG:cre:ChreCp019 KO:K02689 ProtClustDB:CHL00056 BioCyc:CHLAMY:CHRECP019-MONOMER BioCyc:MetaCyc:CHRECP019-MONOMER InterPro:IPR020586 Gene3D:G3DSA:1.20.1130.10 TIGRFAMs:TIGR01335 PROSITE:PS00419 Uniprot:P12154
Leaf	Isotig05304	121	104	0.747	9.11E-05	UNIPROTKB|Q6H8M0 - symbol:petA "Apocytochrome f" species:1168 "Nostoc sp. PCC 7119" [GO:0005515 "protein binding" evidence=IPI] HAMAP:MF_00610 InterPro:IPR002325 Pfam:PF01333 PRINTS:PR00610 PROSITE:PS51010 GO:GO:0005515 GO:GO:0009055 GO:GO:0006810 GO:GO:0020037 InterPro:IPR011054 SUPFAM:SSF51246 GO:GO:0022900 GO:GO:0015979 GO:GO:0031361 InterPro:IPR024058 InterPro:IPR024094 Gene3D:G3DSA:2.60.40.830 Gene3D:G3DSA:1.20.5.700 SUPFAM:SSF49441 SUPFAM:SSF103431 EMBL:AJ749608 ProteinModelPortal:Q6H8M0 SMR:Q6H8M0 IntAct:Q6H8M0 Uniprot:Q6H8M0
Leaf	Isotig05305	40	3	4.266	2.99E-12	UNIPROTKB|G4N6L6 - symbol:MGG_06537 "Vacuolar protein sorting-associated protein 13" species:242507 "Magnaporthe oryzae 70-15" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] InterPro:IPR009543 Pfam:PF06650 GO:GO:0008104 EMBL:CM001234 InterPro:IPR015412 Pfam:PF09333 InterPro:IPR017148 PIRSF:PIRSF037235 Uniprot:G4N6L6
Leaf	Isotig05306	10	51	-1.822	1.88E-05	TAIR|locus:2205005 - symbol:RLP7 "AT1G47890" species:3702 "Arabidopsis thaliana" [GO:0006952 "defense response" evidence=ISS] [GO:0016301 "kinase activity" evidence=ISS] [GO:0007165 "signal transduction" evidence=IC] Pfam:PF00560 InterPro:IPR001611 PROSITE:PS51450 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0004872 eggNOG:COG4886 HOGENOM:HBG755340 HSSP:P25147 InterPro:IPR013210 Pfam:PF08263 EMBL:AC079679 ProtClustDB:CLSN2681899 IPI:IPI00518642 PIR:C96519 RefSeq:NP_175225.1 UniGene:At.52064 ProteinModelPortal:Q9C699 SMR:Q9C699 PRIDE:Q9C699 EnsemblPlants:AT1G47890.1 GeneID:841206 KEGG:ath:AT1G47890 TAIR:At1g47890 InParanoid:Q9C699 OMA:NTHNANE PhylomeDB:Q9C699 Genevestigator:Q9C699 Uniprot:Q9C699
Leaf	Isotig05309	27	10	1.962	8.47E-05	TAIR|locus:2097925 - symbol:AT3G48060 species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=IEA;ISS] [GO:0005634 "nucleus" evidence=IEA] [GO:0006351 "transcription, DNA-dependent" evidence=IEA] InterPro:IPR001025 InterPro:IPR003617 InterPro:IPR017923 Pfam:PF01426 Pfam:PF08711

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						PROSITE:PS51038 PROSITE:PS51319 SMART:SM00439 SMART:SM00509 GO:GO:0005634 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0003677 GO:GO:0006351 EMBL:AL049658 Gene3D:G3DSA:1.20.930.10 SUPFAM:SSF47676 HOGENOM:HBG745173 IPI:IPI00534352 PIR:T06677 RefSeq:NP_190389.1 UniGene:At.19774 UniGene:At.48751 ProteinModelPortal:Q9SU69 SMR:Q9SU69 STRING:Q9SU69 PRIDE:Q9SU69 EnsemblPlants:AT3G48060.1 GeneID:823961 KEGG:ath:AT3G48060 TAIR:At3g48060 eggNOG:NOG298939 InParanoid:Q9SU69 OMA:LENIEIM PhylomeDB:Q9SU69 ProtClustDB:CLSN2684022 Genevestigator:Q9SU69 Uniprot:Q9SU69
Leaf	Isotig05313	21	6	2.336	0.000109395	TAIR|locus:2089678 - symbol:BTS "BRUTUS" species:3702 "Arabidopsis thaliana" [GO:0008270 "zinc ion binding" evidence=IEA;ISS] [GO:0009793 "embryo development ending in seed dormancy" evidence=NAS] [GO:0010106 "cellular response to iron ion starvation" evidence=IEP] InterPro:IPR001841 InterPro:IPR008913 Pfam:PF05495 PROSITE:PS50089 PROSITE:PS51266 SMART:SM00184 InterPro:IPR004039 Pfam:PF01814 EMBL:CP002686 GO:GO:0008270 InterPro:IPR013083 Gene3D:G3DSA:3.30.40.10 GO:GO:0010106 Gene3D:G3DSA:2.20.28.10 InterPro:IPR012312 InterPro:IPR017921 PROSITE:PS51270 EMBL:AY094471 EMBL:BT005819 IPI:IPI00527325 RefSeq:NP_188457.1 UniGene:At.43728 UniGene:At.69146 ProteinModelPortal:Q8LPQ5 SMR:Q8LPQ5 STRING:Q8LPQ5 PRIDE:Q8LPQ5 EnsemblPlants:AT3G18290.1 GeneID:821357 KEGG:ath:AT3G18290 TAIR:At3g18290 InParanoid:Q8LPQ5 OMA:HKAISKD PhylomeDB:Q8LPQ5 ProtClustDB:CLSN2684371 Genevestigator:Q8LPQ5 Uniprot:Q8LPQ5
Leaf	Isotig05314	25	9	2.003	0.000126076	TAIR|locus:2175579 - symbol:ACA8 "AT5G57110" species:3702 "Arabidopsis thaliana" [GO:0005388 "calcium-transporting ATPase activity" evidence=ISS;IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005516 "calmodulin binding" evidence=TAS] [GO:0043621 "protein self-association" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0009624 "response to nematode" evidence=IEP] [GO:0016020 "membrane" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000695 InterPro:IPR001757 InterPro:IPR005834 InterPro:IPR006408 InterPro:IPR008250 InterPro:IPR024750 Pfam:PF00122 Pfam:PF00702 Pfam:PF12515 PRINTS:PR00119 PRINTS:PR00120 InterPro:IPR018303 InterPro:IPR004014 InterPro:IPR006068 Pfam:PF00690 Pfam:PF00689 Prosite:PS00154 GO:GO:0016021 GO:GO:0005886 GO:GO:0009506 GO:GO:0005524 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0046872 InterPro:IPR023214 SUPFAM:SSF56784 GO:GO:0006754 GO:GO:0009624 GO:GO:0005516 GO:GO:0043621 eggNOG:COG0474 HOGENOM:HBG456486 GO:GO:0005388 InterPro:IPR023300 InterPro:IPR023299 InterPro:IPR023298 Gene3D:G3DSA:2.70.150.10 Gene3D:G3DSA:3.40.1110.10 Gene3D:G3DSA:1.20.1110.10 SMART:SM00831 TIGRFAMs:TIGR01517 TIGRFAMs:TIGR01494 EMBL:AJ249352 EMBL:AB023042 EMBL:AY069869 IPI:IPI00540817 PIR:T52654 RefSeq:NP_200521.3 RefSeq:NP_851200.1 UniGene:At.9676 ProteinModelPortal:Q9LF79 SMR:Q9LF79 IntAct:Q9LF79 TCDB:3.A.3.2.10 PRIDE:Q9LF79 EnsemblPlants:AT5G57110.1 EnsemblPlants:AT5G57110.2 GeneID:835815 KEGG:ath:AT5G57110 TAIR:At5g57110 InParanoid:Q9LF79 OMA:VAFVGAC PhylomeDB:Q9LF79 ProtClustDB:CLSN2685405 ArrayExpress:Q9LF79 Genevestigator:Q9LF79 GermOnline:AT5G57110 Uniprot:Q9LF79
Leaf	Isotig05317	22	5	2.666	1.97E-05	TAIR|locus:2032382 - symbol:SNL3 "SIN3-like 3" species:3702 "Arabidopsis thaliana" [GO:0005634 "nucleus" evidence=IEA;ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=ISS] [GO:0009737 "response to abscisic acid stimulus" evidence=IMP] [GO:0045892 "negative regulation of transcription, DNA-dependent" evidence=IEP;IDA] InterPro:IPR003822 Pfam:PF02671 PROSITE:PS51477 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009737 GO:GO:0005634 GO:GO:0045892 GO:GO:0006351 EMBL:AC002396 Gene3D:G3DSA:1.20.1160.11 SUPFAM:SSF47762 eggNOG:COG5602 KO:K11644 InterPro:IPR013194 Pfam:PF08295 SMART:SM00761 HSSP:Q62141 EMBL:AK227621 IPI:IPI00540414 PIR:T00649 RefSeq:NP_173829.3 UniGene:At.47999 ProteinModelPortal:O48686 SMR:O48686 STRING:O48686 PRIDE:O48686 EnsemblPlants:AT1G24190.1 GeneID:839032 KEGG:ath:AT1G24190 TAIR:At1g24190 HOGENOM:HBG316427 InParanoid:O48686 OMA:LIKYSCA ProtClustDB:CLSN2680720 Genevestigator:O48686 Uniprot:O48686
Leaf	Isotig05318	20	7	2.044	0.00051229	TAIR|locus:2041329 - symbol:SPL1 "AT2G47070" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=ISS] [GO:0005634 "nucleus" evidence=IEA;ISS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=TAS] InterPro:IPR002110 InterPro:IPR004333 Pfam:PF03110 PROSITE:PS51141 SMART:SM00248 GO:GO:0005634 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0006355 GO:GO:0046872 GO:GO:0003677 InterPro:IPR020683 Gene3D:G3DSA:1.25.40.20 SUPFAM:SSF48403 GO:GO:0006351

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EMBL:AC004411 Gene3D:G3DSA:4.10.1100.10 SUPFAM:SSF103612 eggNOG:NOG266915 HOGENOM:HBG318155 ProtClustDB:CLSN2685028 EMBL:AJ011577 EMBL:AJ011628 EMBL:AJ011629 EMBL:AK230269 IPI:IPI00519879 PIR:T02179 PIR:T02180 PIR:T52601 PIR:T52602 RefSeq:NP_850468.1 UniGene:At.12581 ProteinModelPortal:Q9SMX9 SMR:Q9SMX9 STRING:Q9SMX9 PRIDE:Q9SMX9 EnsemblPlants:AT2G47070.1 GeneID:819321 KEGG:ath:AT2G47070 GeneFarm:4762 TAIR:At2g47070 InParanoid:Q9SMX9 OMA:SEIRILE PhylomeDB:Q9SMX9 ArrayExpress:O80717 Genevestigator:Q9SMX9 GermOnline:AT2G47070 Uniprot:Q9SMX9
Leaf	Isotig05320	12	1	4.114	0.000154103	TAIR|locus:2030432 - symbol:AT1G20760 species:3702 "Arabidopsis thaliana" [GO:0005509 "calcium ion binding" evidence=IEA;ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] InterPro:IPR000261 InterPro:IPR002048 InterPro:IPR011992 PROSITE:PS50031 SMART:SM00027 SMART:SM00054 EMBL:CP002684 GO:GO:0005886 GO:GO:0005509 InterPro:IPR018249 Gene3D:G3DSA:1.10.238.10 PROSITE:PS50222 EMBL:AC069251 HSSP:O54916 UniGene:At.27660 EMBL:AK226951 IPI:IPI00529733 RefSeq:NP_173499.1 ProteinModelPortal:Q9LM78 SMR:Q9LM78 PRIDE:Q9LM78 EnsemblPlants:AT1G20760.1 GeneID:838666 KEGG:ath:AT1G20760 TAIR:At1g20760 InParanoid:Q9LM78 OMA:RFDSINS PhylomeDB:Q9LM78 ProtClustDB:CLSN2914684 Genevestigator:Q9LM78 Uniprot:Q9LM78
Leaf	Isotig05332	25	6	2.588	7.60E-06	ZFIN|ZDB-GENE-030131-1473 - symbol:ubr3 "ubiquitin protein ligase E3 component n-recognin 3" species:7955 "Danio rerio" [GO:0008270 "zinc ion binding" evidence=IEA] [GO:0046872 "metal ion binding" evidence=IEA] InterPro:IPR001841 PROSITE:PS50089 SMART:SM00184 ZFIN:ZDB-GENE-030131-1473 GO:GO:0008270 InterPro:IPR013083 Gene3D:G3DSA:3.30.40.10 GeneTree:ENSGT00530000063055 EMBL:CU639483 EMBL:CU986282 EMBL:FP089512 IPI:IPI00897370 Ensembl:ENSDART00000129091 Bgee:F1QJX5 Uniprot:F1QJX5
Leaf	Isotig05338	8	112	-3.278	7.62E-19	TAIR|locus:2086315 - symbol:PPC3 "AT3G14940" species:3702 "Arabidopsis thaliana" [GO:0006099 "tricarboxylic acid cycle" evidence=ISS] [GO:0008964 "phosphoenolpyruvate carboxylase activity" evidence=ISS;IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR015813 InterPro:IPR018129 InterPro:IPR021135 InterPro:IPR022805 Pfam:PF00311 PRINTS:PR00150 PROSITE:PS00393 PROSITE:PS00781 GO:GO:0005829 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0006099 SUPFAM:SSF51621 GO:GO:0015979 EMBL:AP000370 eggNOG:COG2352 HOGENOM:HBG351035 KO:K01595 ProtClustDB:CLSN2679806 BRENDA:4.1.1.31 GO:GO:0008964 GO:GO:0015977 EMBL:AF071788 EMBL:AJ131710 EMBL:BT004642 EMBL:AK227556 IPI:IPI00522131 PIR:T52186 RefSeq:NP_188112.1 UniGene:At.24126 UniGene:At.74839 ProteinModelPortal:Q84VW9 SMR:Q84VW9 STRING:Q84VW9 PRIDE:Q84VW9 EnsemblPlants:AT3G14940.1 GeneID:820723 KEGG:ath:AT3G14940 GeneFarm:5062 TAIR:At3g14940 InParanoid:Q84VW9 OMA:QIENLMF PhylomeDB:Q84VW9 BioCyc:ARA:AT3G14940-MONOMER BioCyc:MetaCyc:AT3G14940-MONOMER Genevestigator:Q84VW9 GermOnline:AT3G14940 Uniprot:Q84VW9
Leaf	Isotig05340	14	3	2.751	0.000536578	TAIR|locus:2051809 - symbol:AT2G43900 "AT2G43900" species:3702 "Arabidopsis thaliana" [GO:0004445 "inositol-polyphosphate 5-phosphatase activity" evidence=ISS] [GO:0008150 "biological_process" evidence=ND] [GO:0080008 "CUL4 RING ubiquitin ligase complex" evidence=ISS] InterPro:IPR000300 InterPro:IPR001680 InterPro:IPR015943 PROSITE:PS50082 PROSITE:PS50294 SMART:SM00128 SMART:SM00320 Pfam:PF03372 EMBL:CP002685 GenomeReviews:CT485783_GR Gene3D:G3DSA:2.130.10.10 PROSITE:PS00678 GO:GO:0046872 EMBL:AC004005 InterPro:IPR005135 SUPFAM:SSF56219 GO:GO:0046854 GO:GO:0052659 GO:GO:0052658 GO:GO:0004445 eggNOG:COG5411 HSSP:O43001 EMBL:AY761187 EMBL:AY761191 EMBL:AJ277884 IPI:IPI00534495 IPI:IPI00919332 PIR:T00670 RefSeq:NP_181918.4 UniGene:At.36825 ProteinModelPortal:O80560 SMR:O80560 STRING:O80560 PRIDE:O80560 GeneID:818994 KEGG:ath:AT2G43900 GeneFarm:3134 TAIR:At2g43900 HOGENOM:HBG319261 InParanoid:O80560 OMA:SKKSDGD PhylomeDB:O80560 Genevestigator:O80560 Uniprot:O80560
Leaf	Isotig05346	35	12	2.073	3.50E-06	TAIR|locus:2026694 - symbol:AT1G63770 "AT1G63770" species:3702 "Arabidopsis thaliana" [GO:0006508 "proteolysis" evidence=ISS] [GO:0008237 "metallopeptidase activity" evidence=IEA] [GO:0008270 "zinc ion binding" evidence=IEA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001930 InterPro:IPR012779 InterPro:IPR014782 Pfam:PF01433 PRINTS:PR00756 EMBL:CP002684 GO:GO:0005829 GO:GO:0005886 GO:GO:0048046

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0009570 GO:GO:0005773 GO:GO:0046686 GO:GO:0008270 GO:GO:0006508 GO:GO:0009941 GO:GO:0008237 eggNOG:COG0308 PANTHER:PTHR11533 InterPro:IPR024601 Gene3D:G3DSA:1.25.50.10 PANTHER:PTHR11533:SF8 Pfam:PF11940 TIGRFAMs:TIGR02414 MEROPS:M01.005 KO:K01256 EMBL:AC010852 IPI:IPI00545384 RefSeq:NP_974083.1 UniGene:At.45960 UniGene:At.73057 ProteinModelPortal:B3H621 STRING:B3H621 PRIDE:B3H621 EnsemblPlants:AT1G63770.2 GeneID:842681 KEGG:ath:AT1G63770 TAIR:At1g63770 OMA:IGGFCGS ProtClustDB:CLSN2915193 Genevestigator:B3H621 Uniprot:B3H621
Leaf	Isotig05349	15	4	2.436	0.000806142	TAIR|locus:2101452 - symbol:ABCC9 "AT3G60160" species:3702 "Arabidopsis thaliana" [GO:0042626 "ATPase activity, coupled to transmembrane movement of substances" evidence=ISS] [GO:0009624 "response to nematode" evidence=IEP] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR001140 InterPro:IPR003439 InterPro:IPR003593 InterPro:IPR011527 InterPro:IPR017871 Pfam:PF00005 Pfam:PF00664 PROSITE:PS00211 PROSITE:PS50893 SMART:SM00382 GO:GO:0016021 GO:GO:0009506 GO:GO:0005524 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0009624 eggNOG:COG1132 HOGENOM:HBG758042 InterPro:IPR017940 SUPFAM:SSF90123 PROSITE:PS50929 GO:GO:0008559 EMBL:AL138658 IPI:IPI00519552 IPI:IPI01020062 PIR:T47840 RefSeq:NP_191575.2 UniGene:At.34346 ProteinModelPortal:Q9M1C7 PRIDE:Q9M1C7 GeneID:825186 KEGG:ath:AT3G60160 TAIR:At3g60160 InParanoid:Q9M1C7 OMA:SHARREK PhylomeDB:Q9M1C7 ProtClustDB:CLSN2685033 Genevestigator:Q9M1C7 GermOnline:AT3G60160 Uniprot:Q9M1C7
Leaf	Isotig05354	19	2	3.777	3.57E-06	TAIR|locus:2121884 - symbol:MOS1 "AT4G24680" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0040029 "regulation of gene expression, epigenetic" evidence=IMP] EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0016568 EMBL:AL035356 EMBL:AL161562 eggNOG:NOG12793 GO:GO:0040029 EMBL:HM208348 EMBL:AY062548 EMBL:AY093339 IPI:IPI00969741 PIR:T05566 RefSeq:NP_194199.4 UniGene:At.2541 IntAct:Q9SB63 PRIDE:Q9SB63 GeneID:828570 KEGG:ath:AT4G24680 TAIR:At4g24680 InParanoid:Q9SB63 PhylomeDB:Q9SB63 Genevestigator:Q9SB63 Uniprot:Q9SB63
Leaf	Isotig05363	9	0	4.699	0.000718283	TAIR|locus:2027109 - symbol:AT1G62310 "AT1G62310" species:3702 "Arabidopsis thaliana" [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0008270 "zinc ion binding" evidence=IEA] InterPro:IPR001841 InterPro:IPR003347 Pfam:PF02373 PROSITE:PS50089 PROSITE:PS51184 SMART:SM00184 SMART:SM00558 InterPro:IPR014710 Gene3D:G3DSA:2.60.120.10 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0008270 InterPro:IPR013129 eggNOG:NOG305537 ProtClustDB:CLSN2914506 EMBL:AB493515 IPI:IPI00545153 RefSeq:NP_176421.1 UniGene:At.36279 UniGene:At.68585 ProteinModelPortal:C0SV12 SMR:C0SV12 PRIDE:C0SV12 EnsemblPlants:AT1G62310.1 GeneID:842529 KEGG:ath:AT1G62310 TAIR:At1g62310 OMA:LANCEVE Genevestigator:C0SV12 Uniprot:C0SV12
Leaf	Isotig05365	17	4	2.616	0.000204438	DICTYBASE|DDB_G0278661 - symbol:DDB_G0278661 "WD40 repeat-containing protein" species:44689 "Dictyostelium discoideum" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] InterPro:IPR017986 InterPro:IPR001680 InterPro:IPR015943 Pfam:PF00400 PROSITE:PS50082 PROSITE:PS50294 SMART:SM00320 dictyBase:DDB_G0278661 InterPro:IPR019775 Gene3D:G3DSA:2.130.10.10 PROSITE:PS00678 EMBL:AAFI02000023 RefSeq:XP_642289.1 ProteinModelPortal:Q54YB3 EnsemblProtists:DDB0233463 GeneID:8621496 KEGG:ddi:DDB_G0278661 eggNOG:NOG82536 InParanoid:Q54YB3 Uniprot:Q54YB3
Leaf	Isotig05368	60	10	3.114	2.59E-14	TAIR|locus:2096915 - symbol:LOX2 "AT3G45140" species:3702 "Arabidopsis thaliana" [GO:0005515 "protein binding" evidence=IPI] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0009507 "chloroplast" evidence=ISS;IDA;TAS] [GO:0009611 "response to wounding" evidence=IEP] [GO:0080027 "response to herbivore" evidence=IEP] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009753 "response to jasmonic acid stimulus" evidence=IEP] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0009617 "response to bacterium" evidence=IEP] [GO:0016165 "lipoxygenase activity" evidence=IMP;IDA] [GO:0009620 "response to fungus" evidence=IEP] [GO:0009695 "jasmonic acid biosynthetic process" evidence=IMP;TAS] [GO:0009414 "response to water deprivation" evidence=TAS] [GO:0051707 "response to other organism" evidence=TAS] InterPro:IPR000907 InterPro:IPR001024 InterPro:IPR001246 InterPro:IPR013819 InterPro:IPR020833 InterPro:IPR020834 Pfam:PF00305 Pfam:PF01477 PRINTS:PR00087 PRINTS:PR00468 PROSITE:PS00081 PROSITE:PS00711 PROSITE:PS50095 PROSITE:PS51393 SMART:SM00308 GO:GO:0009570 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0009617 GO:GO:0005515

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0009753 GO:GO:0009611 GO:GO:0005506 GO:GO:0009695 GO:GO:0009941 GO:GO:0009620 GO:GO:0080027 GO:GO:0009535 InterPro:IPR008976 Gene3D:G3DSA:2.60.60.20 SUPFAM:SSF49723 EMBL:AL138649 GO:GO:0016165 PANTHER:PTHR11771 SUPFAM:SSF48484 eggNOG:NOG69653 HOGENOM:HBG749429 EMBL:L23968 EMBL:AY062611 EMBL:AK119093 EMBL:AK222075 EMBL:AK230124 IPI:IPI00548522 PIR:JQ2391 PIR:T47454 RefSeq:NP_566875.1 UniGene:At.22079 UniGene:At.75027 ProteinModelPortal:P38418 SMR:P38418 IntAct:P38418 STRING:P38418 SWISS-2DPAGE:P38418 PRIDE:P38418 ProMEX:P38418 EnsemblPlants:AT3G45140.1 GeneID:823650 KEGG:ath:AT3G45140 TAIR:At3g45140 InParanoid:P38418 KO:K00454 OMA:YGGYFPN PhylomeDB:P38418 ProtClustDB:CLSN2917374 ArrayExpress:P38418 Genevestigator:P38418 GermOnline:AT3G45140 Uniprot:P38418
Leaf	Isotig05369	63	28	1.699	5.27E-08	TAIR|locus:2120217 - symbol:VHA-A3 "AT4G39080" species:3702 "Arabidopsis thaliana" [GO:0016887 "ATPase activity" evidence=ISS] [GO:0005773 "vacuole" evidence=IDA] [GO:0009705 "plant-type vacuole membrane" evidence=IDA] [GO:0000325 "plant-type vacuole" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009678 "hydrogen-translocating pyrophosphatase activity" evidence=IDA] [GO:0015986 "ATP synthesis coupled proton transport" evidence=IDA] [GO:0031669 "cellular response to nutrient levels" evidence=IGI] [GO:0071472 "cellular response to salt stress" evidence=IGI] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR002490 Pfam:PF01496 GO:GO:0005886 EMBL:CP002687 GO:GO:0009941 GO:GO:0009705 GO:GO:0015991 GO:GO:0015986 GO:GO:0015078 GO:GO:0009678 GO:GO:0031669 KO:K02154 PANTHER:PTHR11629 GO:GO:0033177 OMA:HVSQHAP ProtClustDB:CLSN2683585 EMBL:AY060557 EMBL:BT002615 EMBL:AK227321 IPI:IPI00525158 RefSeq:NP_568051.1 UniGene:At.10101 UniGene:At.70994 STRING:Q8W4S4 PRIDE:Q8W4S4 EnsemblPlants:AT4G39080.1 GeneID:830063 KEGG:ath:AT4G39080 TAIR:At4g39080 InParanoid:Q8W4S4 PhylomeDB:Q8W4S4 Genevestigator:Q8W4S4 Uniprot:Q8W4S4
Leaf	Isotig05376	24	3	3.529	3.76E-07	TAIR|locus:2133298 - symbol:AT4G02480 species:3702 "Arabidopsis thaliana" [GO:0000166 "nucleotide binding" evidence=IEA] [GO:0005524 "ATP binding" evidence=IEA] [GO:0016887 "ATPase activity" evidence=ISS] [GO:0017111 "nucleoside-triphosphatase activity" evidence=IEA] InterPro:IPR000253 InterPro:IPR003593 InterPro:IPR003959 InterPro:IPR003960 InterPro:IPR008984 Pfam:PF00004 PROSITE:PS00674 SMART:SM00382 GO:GO:0005524 EMBL:CP002687 Gene3D:G3DSA:2.60.200.20 SUPFAM:SSF49879 GO:GO:0017111 ProtClustDB:CLSN2690660 EMBL:AK229937 IPI:IPI00540740 RefSeq:NP_567238.2 UniGene:At.27891 UniGene:At.54098 ProteinModelPortal:Q0WM93 SMR:Q0WM93 STRING:Q0WM93 PRIDE:Q0WM93 EnsemblPlants:AT4G02480.1 GeneID:827979 KEGG:ath:AT4G02480 TAIR:At4g02480 InParanoid:Q0WM93 OMA:LKVQANI PhylomeDB:Q0WM93 Genevestigator:Q0WM93 Uniprot:Q0WM93
Leaf	Isotig05379	2	32	-3.471	1.22E-06	TAIR|locus:2025067 - symbol:AT1G07280 "AT1G07280" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] InterPro:IPR011990 InterPro:IPR013026 PROSITE:PS50293 EMBL:CP002684 GO:GO:0005488 Gene3D:G3DSA:1.25.40.10 EMBL:AY065061 EMBL:AY133574 IPI:IPI00540005 RefSeq:NP_001030984.1 RefSeq:NP_001117242.1 RefSeq:NP_172208.2 UniGene:At.20235 UniGene:At.28743 ProteinModelPortal:Q8VZC8 SMR:Q8VZC8 PRIDE:Q8VZC8 EnsemblPlants:AT1G07280.1 EnsemblPlants:AT1G07280.2 EnsemblPlants:AT1G07280.3 GeneID:837239 KEGG:ath:AT1G07280 TAIR:At1g07280 InParanoid:Q8VZC8 OMA:EETYLEA PhylomeDB:Q8VZC8 ProtClustDB:CLSN2688551 Genevestigator:Q8VZC8 Uniprot:Q8VZC8
Leaf	Isotig05382	22	1	4.988	9.32E-08	TAIR|locus:2075346 - symbol:HERK1 "AT3G46290" species:3702 "Arabidopsis thaliana" [GO:0016301 "kinase activity" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0004672 "protein kinase activity" evidence=IDA] [GO:0009742 "brassinosteroid mediated signaling pathway" evidence=IGI] [GO:0009791 "post-embryonic development" evidence=IGI] [GO:0051510 "regulation of unidimensional cell growth" evidence=IGI] [GO:0009741 "response to brassinosteroid stimulus" evidence=IGI] [GO:0009826 "unidimensional cell growth" evidence=IGI] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000719 InterPro:IPR001245 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 Pfam:PF07714 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 GO:GO:0016021 GO:GO:0005886 GO:GO:0009506 GO:GO:0005524 GO:GO:0009742 EMBL:CP002686 GenomeReviews:BA000014_GR eggNOG:COG0515 GO:GO:0004872 SUPFAM:SSF56112 GO:GO:0004674 HOGENOM:HBG755340 GO:GO:0009826 GO:GO:0009791 InterPro:IPR024788 Pfam:PF12819 GO:GO:0051510 EMBL:AL355775 EMBL:AL133298 IPI:IPI00517099 PIR:T45686 PIR:T49270 RefSeq:NP_190214.1 UniGene:At.546 UniGene:At.69879 ProteinModelPortal:Q9LX66

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						SMR:Q9LX66 PRIDE:Q9LX66 EnsemblPlants:AT3G46290.1 GeneID:823774 KEGG:ath:AT3G46290 GeneFarm:2116 TAIR:At3g46290 InParanoid:Q9LX66 OMA:PELDQTH PhylomeDB:Q9LX66 ProtClustDB:CLSN2684820 Genevestigator:Q9LX66 Uniprot:Q9LX66
Leaf	Isotig05398	18	2	3.699	7.53E-06	TAIR|locus:2148216 - symbol:XPO1A "AT5G17020" species:3702 "Arabidopsis thaliana" [GO:0000059 "protein import into nucleus, docking" evidence=ISS] [GO:0005634 "nucleus" evidence=ISS;TAS] [GO:0005643 "nuclear pore" evidence=ISS] [GO:0005737 "cytoplasm" evidence=ISS] [GO:0008565 "protein transporter activity" evidence=ISS] [GO:0004872 "receptor activity" evidence=ISS] [GO:0005515 "protein binding" evidence=IPI] [GO:0006611 "protein export from nucleus" evidence=ISS] [GO:0009553 "embryo sac development" evidence=IGI] [GO:0009555 "pollen development" evidence=IGI] [GO:0009846 "pollen germination" evidence=IGI] [GO:0009860 "pollen tube growth" evidence=IGI] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001494 InterPro:IPR011989 InterPro:IPR016024 Pfam:PF03810 PROSITE:PS50166 SMART:SM00913 GO:GO:0005829 GO:GO:0005634 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0006886 GO:GO:0005515 SUPFAM:SSF48371 Gene3D:G3DSA:1.25.10.10 GO:GO:0008565 GO:GO:0009555 GO:GO:0009860 GO:GO:0009553 GO:GO:0009846 EMBL:AL391141 InterPro:IPR013598 Pfam:PF08389 HOGENOM:HBG315058 KO:K14290 OMA:PANMEKE InterPro:IPR014877 Pfam:PF08767 SMART:SM01102 EMBL:AY056126 EMBL:AY096633 EMBL:Y18470 EMBL:Y18469 IPI:IPI00544899 PIR:T51557 PIR:T52638 RefSeq:NP_197204.1 UniGene:At.492 ProteinModelPortal:Q9SMV6 SMR:Q9SMV6 IntAct:Q9SMV6 STRING:Q9SMV6 PRIDE:Q9SMV6 ProMEX:Q9SMV6 EnsemblPlants:AT5G17020.1 GeneID:831565 KEGG:ath:AT5G17020 TAIR:At5g17020 InParanoid:Q9SMV6 PhylomeDB:Q9SMV6 ProtClustDB:CLSN2686313 ArrayExpress:Q9SMV6 Genevestigator:Q9SMV6 Uniprot:Q9SMV6
Leaf	Isotig05399	40	21	1.459	0.00010398	TAIR|locus:2155894 - symbol:SUS2 "AT5G49190" species:3702 "Arabidopsis thaliana" [GO:0005986 "sucrose biosynthetic process" evidence=ISS] [GO:0008194 "UDP-glycosyltransferase activity" evidence=ISS] [GO:0016157 "sucrose synthase activity" evidence=ISS;IMP] [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0001666 "response to hypoxia" evidence=IEP] [GO:0009505 "plant-type cell wall" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0005982 "starch metabolic process" evidence=IMP] [GO:0005985 "sucrose metabolic process" evidence=IMP] [GO:0010431 "seed maturation" evidence=IMP] InterPro:IPR000368 InterPro:IPR001296 InterPro:IPR012820 Pfam:PF00534 Pfam:PF00862 GO:GO:0005829 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0016020 GO:GO:0001666 GO:GO:0009058 GO:GO:0009505 eggNOG:COG0438 GO:GO:0010431 CAZy:GT4 EMBL:AB016872 GO:GO:0005985 GO:GO:0005982 HOGENOM:HBG286768 GO:GO:0016157 PANTHER:PTHR12526:SF27 TIGRFAMs:TIGR02470 EMBL:X60987 IPI:IPI00539012 PIR:S19125 RefSeq:NP_199730.1 UniGene:At.8597 ProteinModelPortal:Q00917 STRING:Q00917 PRIDE:Q00917 GeneID:834978 KEGG:ath:AT5G49190 TAIR:At5g49190 InParanoid:Q00917 PhylomeDB:Q00917 ArrayExpress:Q00917 Genevestigator:Q00917 GermOnline:AT5G49190 Uniprot:Q00917
Leaf	Isotig05400	18	2	3.699	7.53E-06	TAIR|locus:2196045 - symbol:AT1G02660 species:3702 "Arabidopsis thaliana" [GO:0004806 "triglyceride lipase activity" evidence=IEA;ISS] [GO:0006629 "lipid metabolic process" evidence=IEA;ISS] InterPro:IPR002921 Pfam:PF01764 GO:GO:0004806 GO:GO:0006629 EMBL:AY139797 IPI:IPI00544599 ProteinModelPortal:Q8L739 SMR:Q8L739 TAIR:At1g02660 HOGENOM:HBG590898 InParanoid:Q8L739 PhylomeDB:Q8L739 Genevestigator:Q8L739 Uniprot:Q8L739
Leaf	Isotig05419	30	10	2.114	1.37E-05	TAIR|locus:2016364 - symbol:HSP91 "AT1G79930" species:3702 "Arabidopsis thaliana" [GO:0006457 "protein folding" evidence=ISS] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0005634 "nucleus" evidence=ISS;IDA] [GO:0005524 "ATP binding" evidence=ISS] [GO:0009408 "response to heat" evidence=IEP] InterPro:IPR001023 PRINTS:PR00301 Pfam:PF00012 Prosite:PS00297 Prosite:PS00329 Prosite:PS01036 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0005886 GO:GO:0005524 GO:GO:0005634 GO:GO:0046686 GO:GO:0006950 GO:GO:0009408 EMBL:AC009322 EMBL:AC011717 HSSP:P19120 eggNOG:COG0443 InterPro:IPR013126 PANTHER:PTHR19375 OMA:QAPFNIE EMBL:Z70314 EMBL:AY079015 EMBL:BT002625 EMBL:AK226836 IPI:IPI00516239 IPI:IPI00657023 IPI:IPI00944283 PIR:E96830 PIR:S74252 RefSeq:NP_001031305.1 RefSeq:NP_178111.1 UniGene:At.28629 UniGene:At.74735 ProteinModelPortal:Q9S7C0 SMR:Q9S7C0 STRING:Q9S7C0 PRIDE:Q96269 ProMEX:Q9S7C0 EnsemblPlants:AT1G79930.1 GeneID:844333 KEGG:ath:AT1G79930 TAIR:At1g79930 InParanoid:Q9S7C0 PhylomeDB:Q9S7C0 ProtClustDB:CLSN2681875 Genevestigator:Q9S7C0 Uniprot:Q9S7C0

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig05425	23	7	2.245	7.72E-05	TAIR|locus:2121894 - symbol:ATR1 "AT4G24520" species:3702 "Arabidopsis thaliana" [GO:0009737 "response to abscisic acid stimulus" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0003958 "NADPH-hemoprotein reductase activity" evidence=IDA] [GO:0005783 "endoplasmic reticulum" evidence=IDA] [GO:0009698 "phenylpropanoid metabolic process" evidence=IDA] [GO:0006979 "response to oxidative stress" evidence=IEP] InterPro:IPR001094 InterPro:IPR001433 InterPro:IPR001709 InterPro:IPR003097 InterPro:IPR008254 InterPro:IPR017927 InterPro:IPR017938 InterPro:IPR023173 InterPro:IPR023208 Pfam:PF00175 Pfam:PF00258 Pfam:PF00667 PIRSF:PIRSF000208 PRINTS:PR00369 PRINTS:PR00371 PROSITE:PS50902 PROSITE:PS51384 GO:GO:0005829 GO:GO:0009737 EMBL:CP002687 GO:GO:0006979 GO:GO:0005789 GO:GO:0005506 GO:GO:0009698 EMBL:AL161561 EMBL:AL035356 SUPFAM:SSF63380 GO:GO:0010181 Gene3D:G3DSA:1.20.990.10 OMA:KIQPRYY HSSP:P00388 GO:GO:0003958 KO:K00327 EMBL:AY054688 EMBL:BT008426 IPI:IPI00541592 PIR:T05582 RefSeq:NP_194183.1 UniGene:At.144 UniGene:At.70123 ProteinModelPortal:Q9SB48 SMR:Q9SB48 STRING:Q9SB48 PRIDE:Q9SB48 EnsemblPlants:AT4G24520.1 GeneID:828554 KEGG:ath:AT4G24520 TAIR:At4g24520 InParanoid:Q9SB48 PhylomeDB:Q9SB48 ProtClustDB:CLSN2685426 ArrayExpress:Q9SB48 Genevestigator:Q9SB48 Uniprot:Q9SB48
Leaf	Isotig05427	42	0	6.921	2.43E-13	TAIR|locus:2024522 - symbol:DAA1 "DUO1-activated ATPase 1" species:3702 "Arabidopsis thaliana" [GO:0000166 "nucleotide binding" evidence=IEA] [GO:0005524 "ATP binding" evidence=IEA] [GO:0016887 "ATPase activity" evidence=ISS] [GO:0017111 "nucleoside-triphosphatase activity" evidence=IEA] [GO:0048235 "pollen sperm cell differentiation" evidence=IEP] InterPro:IPR003593 InterPro:IPR003959 InterPro:IPR003960 Pfam:PF00004 PROSITE:PS00674 SMART:SM00382 EMBL:CP002684 GO:GO:0005524 eggNOG:COG0464 GO:GO:0017111 GO:GO:0048235 EMBL:AC007764 IPI:IPI00891776 RefSeq:NP_001117544.1 UniGene:At.16450 ProteinModelPortal:B3H7I9 SMR:B3H7I9 PRIDE:B3H7I9 EnsemblPlants:AT1G64110.3 GeneID:842716 KEGG:ath:AT1G64110 TAIR:At1g64110 PhylomeDB:B3H7I9 ProtClustDB:CLSN2689017 Genevestigator:B3H7I9 Uniprot:B3H7I9
Leaf	Isotig05431	22	8	1.988	0.00034419	TAIR|locus:2144608 - symbol:SBE2.2 "starch branching enzyme 2.2" species:3702 "Arabidopsis thaliana" [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0003844 "1,4-alpha-glucan branching enzyme activity" evidence=ISS;IDA] [GO:0005982 "starch metabolic process" evidence=IMP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0010021 "amylopectin biosynthetic process" evidence=TAS] InterPro:IPR004193 InterPro:IPR006047 InterPro:IPR006048 InterPro:IPR006407 InterPro:IPR013780 InterPro:IPR013781 Pfam:PF00128 Pfam:PF02806 Pfam:PF02922 PIRSF:PIRSF000463 GO:GO:0009570 EMBL:CP002688 InterPro:IPR013783 Gene3D:G3DSA:2.60.40.10 GO:GO:0071333 GO:GO:0043169 InterPro:IPR017853 Gene3D:G3DSA:3.20.20.80 SUPFAM:SSF51445 CAZy:GH13 InterPro:IPR015902 Gene3D:G3DSA:2.60.40.1180 PANTHER:PTHR10357 GO:GO:0004553 CAZy:CBM48 InterPro:IPR014756 SUPFAM:SSF81296 GO:GO:0071329 GO:GO:0005978 EMBL:AL162506 GO:GO:0003844 GO:GO:0071482 GO:GO:0009501 UniGene:At.24317 HSSP:P07762 eggNOG:COG0296 KO:K00700 ProtClustDB:PLN02447 GO:GO:0010021 GO:GO:0071332 EMBL:AJ005130 EMBL:U22428 EMBL:AK117729 IPI:IPI00518558 PIR:S65046 PIR:T48392 RefSeq:NP_195985.3 UniGene:At.4765 ProteinModelPortal:Q9LZS3 SMR:Q9LZS3 STRING:Q9LZS3 PRIDE:Q8GYC4 EnsemblPlants:AT5G03650.1 GeneID:831769 KEGG:ath:AT5G03650 TAIR:At5g03650 InParanoid:Q9LZS3 PhylomeDB:Q9LZS3 Genevestigator:Q9LZS3 Uniprot:Q9LZS3
Leaf	Isotig05450	26	6	2.644	3.85E-06	TAIR|locus:2204227 - symbol:ERD4 "early-responsive to dehydration 4" species:3702 "Arabidopsis thaliana" [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR003864 Pfam:PF02714 EMBL:CP002684 GO:GO:0005886 GO:GO:0009506 GO:GO:0005774 GO:GO:0009941 EMBL:AC025295 EMBL:AY035092 EMBL:AY063056 IPI:IPI00526219 PIR:H86427 RefSeq:NP_564354.1 UniGene:At.25329 PRIDE:Q9C8G5 ProMEX:Q9C8G5 EnsemblPlants:AT1G30360.1 GeneID:839916 KEGG:ath:AT1G30360 TAIR:At1g30360 InParanoid:Q9C8G5 OMA:YESYGRM PhylomeDB:Q9C8G5 ProtClustDB:CLSN2917110 ArrayExpress:Q9C8G5 Genevestigator:Q9C8G5 Uniprot:Q9C8G5
Leaf	Isotig05453	21	3	3.336	3.39E-06	TAIR|locus:2125964 - symbol:LKR species:3702 "Arabidopsis thaliana" [GO:0047130 "saccharopine dehydrogenase (NADP+, L-lysine-forming) activity" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0019477 "L-lysine catabolic process" evidence=IMP] [GO:0004753 "saccharopine dehydrogenase activity" evidence=IDA] InterPro:IPR005097 InterPro:IPR016040 Pfam:PF03435 PROSITE:PS00836 PROSITE:PS00837

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
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Leaf	Isotig05454	21	0	5.921	1.38E-07	TAIR|locus:2131488 - symbol:CPSUFE "AT4G26500" species:3702 "Arabidopsis thaliana" [GO:0009793 "embryo development ending in seed dormancy" evidence=NAS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0008047 "enzyme activator activity" evidence=IGI;IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0016226 "iron-sulfur cluster assembly" evidence=IGI] [GO:0009570 "chloroplast stroma" evidence=IDA] Pfam:PF02657 GO:GO:0005739 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0009570 GO:GO:0016226 EMBL:AL161565 eggNOG:COG0271 InterPro:IPR002634 Gene3D:G3DSA:3.30.300.90 PANTHER:PTHR12735 Pfam:PF01722 SUPFAM:SSF82657 GO:GO:0008047 EMBL:AL022223 EMBL:BT004190 EMBL:BT021125 EMBL:AY084591 IPI:IPI00524714 PIR:T05054 RefSeq:NP_194380.1 UniGene:At.32175 HSSP:Q9D8S9 ProteinModelPortal:Q84W65 SMR:Q84W65 STRING:Q84W65 PRIDE:Q84W65 ProMEX:Q84W65 EnsemblPlants:AT4G26500.1 GeneID:828756 KEGG:ath:AT4G26500 TAIR:At4g26500 HOGENOM:HBG597984 InParanoid:Q84W65 OMA:IVKLFQS PhylomeDB:Q84W65 ProtClustDB:CLSN2686029 Genevestigator:Q84W65 GermOnline:AT4G26500 InterPro:IPR003808 Uniprot:Q84W65
Leaf	Isotig05458	218	55	2.516	1.03E-38	SGD|S000028422 - symbol:TAR1 "Mitochondrial protein potentially involved in respiratory metabolism" species:4932 "Saccharomyces cerevisiae" [GO:0003674 "molecular_function" evidence=ND] [GO:0043457 "regulation of cellular respiration" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IEA;IMP] SGD:S000028422 GO:GO:0005739 EMBL:BK006945 EMBL:U53879 GO:GO:0043457 EMBL:Z73326 EMBL:AF479964 RefSeq:NP_690845.1 ProteinModelPortal:Q8TGM6 STRING:Q8TGM6 EnsemblFungi:YLR154W-C GeneID:1466405 KEGG:sce:YLR154W-C CYGD:YLR154w-c eggNOG:NOG79861 OMA:SCSKEHR OrthoDB:EOG466ZX8 NextBio:967146 Genevestigator:Q8TGM6 GermOnline:YLR154W-C Uniprot:Q8TGM6
Leaf	Isotig05459	34	10	2.294	1.12E-06	TAIR|locus:2085136 - symbol:VSR1 "AT3G52850" species:3702 "Arabidopsis thaliana" [GO:0005887 "integral to plasma membrane" evidence=ISS] [GO:0006623 "protein targeting to vacuole" evidence=IGI;ISS;IMP;TAS] [GO:0005886 "plasma membrane" evidence=ISS;IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] [GO:0005802 "trans-Golgi network" evidence=IDA;TAS] [GO:0009940 "amino-terminal vacuolar sorting propeptide binding" evidence=IDA] [GO:0017119 "Golgi transport complex" evidence=IPI] [GO:0007034 "vacuolar transport" evidence=IMP] [GO:0005515 "protein binding" evidence=IPI] [GO:0006896 "Golgi to vacuole transport" evidence=ISS;IDA] InterPro:IPR001881 InterPro:IPR018097 Pfam:PF07645 PROSITE:PS01187 PROSITE:PS50026 InterPro:IPR003137 Pfam:PF02225 GO:GO:0016021 GO:GO:0005886 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005509 GO:GO:0005515 GO:GO:0000139 GO:GO:0031902 PROSITE:PS00022 PROSITE:PS01186 PROSITE:PS00010 GO:GO:0030665 GO:GO:0006896 GO:GO:0006623 EMBL:AL132969 EMBL:U86700 EMBL:U79959 EMBL:Y07917 EMBL:AY048289 IPI:IPI00520575 PIR:T47542 RefSeq:NP_190853.1 UniGene:At.24701 UniGene:At.60941 ProteinModelPortal:P93026 SMR:P93026 IntAct:P93026 STRING:P93026 PRIDE:P93026 EnsemblPlants:AT3G52850.1 GeneID:824451 KEGG:ath:AT3G52850 TAIR:At3g52850 eggNOG:NOG286724 HOGENOM:HBG319221 InParanoid:P93026 OMA:YSACVDD PhylomeDB:P93026 ProtClustDB:CLSN2682336 Genevestigator:P93026 GermOnline:AT3G52850 GO:GO:0009940 Uniprot:P93026
Leaf	Isotig05461	17	5	2.294	0.000574458	TAIR|locus:2132377 - symbol:CUL1 "AT4G02570" species:3702 "Arabidopsis thaliana" [GO:0007049 "cell cycle" evidence=ISS] [GO:0000151 "ubiquitin ligase complex" evidence=IPI] [GO:0009733 "response to auxin stimulus" evidence=IMP] [GO:0009793 "embryo development ending in seed dormancy" evidence=IMP] [GO:0005634 "nucleus" evidence=IDA] [GO:0005819 "spindle" evidence=IDA] [GO:0009524 "phragmoplast" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0000794 "condensed nuclear chromosome" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0009753 "response to jasmonic acid stimulus" evidence=IMP] [GO:0009867 "jasmonic acid mediated signaling pathway" evidence=TAS] [GO:0010265 "SCF complex assembly" evidence=IPI] [GO:0042752 "regulation of circadian rhythm" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001373 InterPro:IPR016157 InterPro:IPR016158 InterPro:IPR019559 Pfam:PF00888 Pfam:PF10557

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<tr><th>Tissue</th><th>Identification</th><th># of reads (stress)</th><th># of reads (control)</th><th>Fold Change</th><th>p-value</th><th>Description</th></tr>
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<tr><td>Leaf</td><td>Isotig05463</td><td>11</td><td>0</td><td>4.988</td><td>0.000159591</td><td>TAIR|locus:2151948 - symbol:AT5G55040 "AT5G55040" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=ISS] [GO:0008150 "biological_process" evidence=ND] InterPro:IPR001487 Pfam:PF00439 PRINTS:PR00503 PROSITE:PS50014 SMART:SM00297 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0003677 Gene3D:G3DSA:1.20.920.10 SUPFAM:SSF47370 PROSITE:PS00633 eggNOG:COG5076 InterPro:IPR018359 KO:K11723 HSSP:Q03330 EMBL:AY074282 EMBL:AY096621 IPI:IPI00526129 RefSeq:NP_001119438.1 RefSeq:NP_200315.2 UniGene:At.48079 ProteinModelPortal:Q8VY17 SMR:Q8VY17 PRIDE:Q8VY17 EnsemblPlants:AT5G55040.1 EnsemblPlants:AT5G55040.2 GeneID:835595 KEGG:ath:AT5G55040 TAIR:At5g55040 HOGENOM:HBG317093 InParanoid:Q8VY17 PhylomeDB:Q8VY17 ProtClustDB:CLSN2708557 ArrayExpress:Q8VY17 Genevestigator:Q8VY17 Uniprot:Q8VY17</td></tr>
<tr><td>Leaf</td><td>Isotig05472</td><td>17</td><td>3</td><td>3.031</td><td>6.23E-05</td><td>TAIR|locus:2180867 - symbol:DND1 "AT5G15410" species:3702 "Arabidopsis thaliana" [GO:0005261 "cation channel activity" evidence=ISS] [GO:0030551 "cyclic nucleotide binding" evidence=ISS] [GO:0005242 "inward rectifier potassium channel activity" evidence=IGI] [GO:0005221 "intracellular cyclic nucleotide activated cation channel activity" evidence=IMP] [GO:0006952 "defense response" evidence=TAS] [GO:0009626 "plant-type hypersensitive response" evidence=IMP] [GO:0005516 "calmodulin binding" evidence=TAS] [GO:0005222 "intracellular cAMP activated cation channel activity" evidence=IDA] [GO:0005262 "calcium channel activity" evidence=IMP] [GO:0007263 "nitric oxide mediated signal transduction" evidence=IMP] PROSITE:PS50096 InterPro:IPR000595 Pfam:PF00027 InterPro:IPR014710 Gene3D:G3DSA:2.60.120.10 GO:GO:0016021 GO:GO:0005886 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005262 GO:GO:0005516 GO:GO:0009626 GO:GO:0007263 InterPro:IPR018490 SMART:SM00100 SUPFAM:SSF51206 PROSITE:PS00888 PROSITE:PS00889 PROSITE:PS50042 EMBL:AL391143 GO:GO:0030552 GO:GO:0030553 HOGENOM:HBG599469 KO:K05391 GO:GO:0005222 EMBL:Y16328 EMBL:AF067798 EMBL:AF280939 IPI:IPI00517917 PIR:T51519 RefSeq:NP_197045.1 UniGene:At.20813 UniGene:At.74751 ProteinModelPortal:O65718 SMR:O65718 STRING:O65718 TCDB:1.A.1.5.6 EnsemblPlants:AT5G15410.1 GeneID:831393 KEGG:ath:AT5G15410 GeneFarm:2464 TAIR:At5g15410 eggNOG:NOG261665 InParanoid:O65718 OMA:IQRVASC PhylomeDB:O65718 ProtClustDB:CLSN2687460 ArrayExpress:O65718 Genevestigator:O65718 Uniprot:O65718</td></tr>
<tr><td>Leaf</td><td>Isotig05482</td><td>24</td><td>6</td><td>2.529</td><td>1.49E-05</td><td>TAIR|locus:2124261 - symbol:PAB2 "AT4G34110" species:3702 "Arabidopsis thaliana" [GO:0003723 "RNA binding" evidence=ISS] [GO:0003743 "translation initiation factor activity" evidence=ISS] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA] [GO:0006413 "translational initiation" evidence=ISS] InterPro:IPR000504 InterPro:IPR002004 InterPro:IPR002343 InterPro:IPR006515 InterPro:IPR012677 Pfam:PF00076 Pfam:PF00658 PRINTS:PR00961 PROSITE:PS50102 PROSITE:PS51309 SMART:SM00360 SMART:SM00517 GO:GO:0005829 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0000166 Gene3D:G3DSA:3.30.70.330 GO:GO:0009651 GO:GO:0003723 EMBL:AL021961 EMBL:AL161584 eggNOG:COG0724 HOGENOM:HBG756718 KO:K13126 Gene3D:G3DSA:1.10.1900.10 SUPFAM:SSF63570 TIGRFAMs:TIGR01628 EMBL:L19418 EMBL:BT002354 IPI:IPI00532109 PIR:T05425 RefSeq:NP_195137.5 UniGene:At.25252 ProteinModelPortal:P42731 SMR:P42731 IntAct:P42731 STRING:P42731 PRIDE:P42731 ProMEX:P42731 EnsemblPlants:AT4G34110.1 GeneID:829557 KEGG:ath:AT4G34110 TAIR:At4g34110 InParanoid:P42731 PhylomeDB:P42731 ProtClustDB:CLSN2714507 Genevestigator:P42731 GermOnline:AT4G34110 Uniprot:P42731</td></tr>
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Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
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Leaf	Isotig05485	29	14	1.580	0.000457445	TAIR|locus:2050019 - symbol:AT2G21520 species:3702 "Arabidopsis thaliana" [GO:0005215 "transporter activity" evidence=IEA;ISS] [GO:0006810 "transport" evidence=IEA;ISS] InterPro:IPR001071 PRINTS:PR00180 Pfam:PF03765 EMBL:CP002685 EMBL:AC006841 GO:GO:0005215 GO:GO:0005622 InterPro:IPR001251 Gene3D:G3DSA:3.40.525.10 SUPFAM:SSF52087 PROSITE:PS50191 SMART:SM00516 InterPro:IPR011074 Gene3D:G3DSA:1.10.8.20 Pfam:PF00650 SMART:SM01100 SUPFAM:SSF46938 eggNOG:NOG309458 IPI:IPI00891831 RefSeq:NP_001118356.1 UniGene:At.43802 UniGene:At.70982 ProteinModelPortal:B3H588 SMR:B3H588 EnsemblPlants:AT2G21520.2 GeneID:816691 KEGG:ath:AT2G21520 TAIR:At2g21520 PhylomeDB:B3H588 ProtClustDB:CLSN2689833 Genevestigator:B3H588 Uniprot:B3H588
Leaf	Isotig05486	8	50	-2.115	2.94E-06	TAIR|locus:2026177 - symbol:AT1G62660 species:3702 "Arabidopsis thaliana" [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=IEA;ISS] [GO:0071370 "cellular response to gibberellin stimulus" evidence=IEP] [GO:0000325 "plant-type vacuole" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0009617 "response to bacterium" evidence=IEP] InterPro:IPR001362 InterPro:IPR018053 InterPro:IPR021792 Pfam:PF11837 PROSITE:PS00609 SMART:SM00640 EMBL:CP002684 GO:GO:0005975 InterPro:IPR008985 SUPFAM:SSF49899 InterPro:IPR023296 SUPFAM:SSF75005 CAZy:GH32 KO:K01193 GO:GO:0004575 InterPro:IPR013189 InterPro:IPR013148 Pfam:PF08244 Pfam:PF00251 ProtClustDB:CLSN2687777 EMBL:AY048269 EMBL:AY062481 EMBL:AY063904 EMBL:AY114066 EMBL:X99111 IPI:IPI00517592 PIR:S71268 RefSeq:NP_564798.1 UniGene:At.24113 UniGene:At.67066 ProteinModelPortal:Q43348 SMR:Q43348 STRING:Q43348 PRIDE:Q43348 ProMEX:Q43348 EnsemblPlants:AT1G62660.1 GeneID:842563 KEGG:ath:AT1G62660 TAIR:At1g62660 InParanoid:Q43348 OMA:HSIVEGF PhylomeDB:Q43348 ArrayExpress:Q43348 Genevestigator:Q43348 Uniprot:Q43348
Leaf	Isotig05488	26	3	3.644	8.65E-08	TAIR|locus:2142414 - symbol:MSL2 "AT5G10490" species:3702 "Arabidopsis thaliana" [GO:0016020 "membrane" evidence=ISS] [GO:0005216 "ion channel activity" evidence=IGI] [GO:0009526 "plastid envelope" evidence=IDA] [GO:0009657 "plastid organization" evidence=IGI] [GO:0009507 "chloroplast" evidence=IDA] [GO:0010020 "chloroplast fission" evidence=IGI] InterPro:IPR006685 Pfam:PF00924 GO:GO:0016021 EMBL:CP002688 GenomeReviews:BA000015_GR EMBL:AL353995 GO:GO:0031969 GO:GO:0005216 GO:GO:0010020 InterPro:IPR010920 SUPFAM:SSF50182 eggNOG:COG0668 EMBL:AK221831 EMBL:AK230015 EMBL:AK317509 IPI:IPI00533775 IPI:IPI00846450 IPI:IPI00991346 PIR:T49990 RefSeq:NP_001078567.1 RefSeq:NP_001190278.1 RefSeq:NP_568230.2 UniGene:At.48016 ProteinModelPortal:Q56X46 TCDB:1.A.23.7.1 PRIDE:Q9LXA1 EnsemblPlants:AT5G10490.1 GeneID:830913 KEGG:ath:AT5G10490 TAIR:At5g10490 HOGENOM:HBG746763 InParanoid:Q56X46 OMA:SHHEEYL PhylomeDB:Q56X46 ProtClustDB:CLSN2680522 Genevestigator:Q56X46 Uniprot:Q56X46
Leaf	Isotig05498	17	5	2.294	0.000574458	TAIR|locus:2041549 - symbol:AT2G42520 species:3702 "Arabidopsis thaliana" [GO:0003676 "nucleic acid binding" evidence=IEA] [GO:0004386 "helicase activity" evidence=IEA] [GO:0005524 "ATP binding" evidence=IEA] [GO:0008026 "ATP-dependent helicase activity" evidence=IEA;ISS] [GO:0005777 "peroxisome" evidence=IDA] InterPro:IPR001650 InterPro:IPR011545 Pfam:PF00270 Pfam:PF00271 PROSITE:PS00039 PROSITE:PS51194 SMART:SM00490 InterPro:IPR014001 GO:GO:0005524 EMBL:AC007087 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0005777 GO:GO:0003723 SMART:SM00487 PROSITE:PS51192 GO:GO:0008026 eggNOG:COG0513 HOGENOM:HBG737336 InterPro:IPR014014 PROSITE:PS51195 KO:K11594 ProtClustDB:CLSN2683925 EMBL:BT004111 IPI:IPI00545939 PIR:H84854 RefSeq:NP_181780.1 UniGene:At.43442 ProteinModelPortal:Q84W89 SMR:Q84W89 PRIDE:Q84W89 EnsemblPlants:AT2G42520.1 GeneID:818852 KEGG:ath:AT2G42520 GeneFarm:1013 TAIR:At2g42520 InParanoid:Q84W89 OMA:DYLERYL PhylomeDB:Q84W89 Genevestigator:Q84W89 GermOnline:AT2G42520 Uniprot:Q84W89

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig05504	16	2	3.529	3.35E-05	TAIR|locus:2005614 - symbol:XRN3 "AT1G75660" species:3702 "Arabidopsis thaliana" [GO:0004534 "5'-3' exoribonuclease activity" evidence=IGI;ISS] [GO:0005634 "nucleus" evidence=IDA] [GO:0010587 "miRNA catabolic process" evidence=IMP] InterPro:IPR001878 InterPro:IPR004859 InterPro:IPR017151 Pfam:PF00098 Pfam:PF03159 PIRSF:PIRSF037239 PROSITE:PS50158 SMART:SM00343 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005634 GO:GO:0008270 GO:GO:0006397 GO:GO:0003676 Gene3D:G3DSA:4.10.60.10 GO:GO:0010587 EMBL:AC006434 eggNOG:COG5049 GO:GO:0004534 HOGENOM:HBG592534 KO:K12619 EMBL:AF286719 EMBL:AY136383 EMBL:BT000175 IPI:IPI00542756 IPI:IPI00903453 PIR:D96786 RefSeq:NP_565114.1 UniGene:At.23685 ProteinModelPortal:Q9FQ03 SMR:Q9FQ03 STRING:Q9FQ03 PRIDE:Q9FQ03 EnsemblPlants:AT1G75660.1 GeneID:843900 KEGG:ath:AT1G75660 TAIR:At1g75660 InParanoid:Q9FQ03 OMA:ILREVVY PhylomeDB:Q9FQ03 ArrayExpress:Q8L7A3 Genevestigator:Q9FQ03 Uniprot:Q9FQ03
Leaf	Isotig05510	33	2	4.573	1.17E-10	TAIR|locus:2185500 - symbol:FDH "formate dehydrogenase" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0016616 "oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor" evidence=IEA] [GO:0048037 "cofactor binding" evidence=IEA] [GO:0051287 "NAD binding" evidence=IEA] [GO:0005739 "mitochondrion" evidence=IDA;TAS] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009611 "response to wounding" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] InterPro:IPR006139 InterPro:IPR006140 InterPro:IPR016040 Pfam:PF00389 Pfam:PF02826 PROSITE:PS00065 PROSITE:PS00670 PROSITE:PS00671 GO:GO:0005739 GO:GO:0046686 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009507 Gene3D:G3DSA:3.40.50.720 GO:GO:0051287 GO:GO:0009579 GO:GO:0016616 EMBL:AL391149 eggNOG:COG1052 HOGENOM:HBG328050 KO:K00122 OMA:DCELEKH GO:GO:0008863 EMBL:AB023897 EMBL:AF208028 EMBL:AF208029 EMBL:AF217195 EMBL:AY054285 EMBL:AY039609 EMBL:AY081734 IPI:IPI00534642 PIR:T51423 RefSeq:NP_196982.1 UniGene:At.23637 UniGene:At.6781 PDB:3JTM PDB:3N7U PDB:3NAQ PDBsum:3JTM PDBsum:3N7U PDBsum:3NAQ ProteinModelPortal:Q9S7E4 SMR:Q9S7E4 IntAct:Q9S7E4 STRING:Q9S7E4 PRIDE:Q9S7E4 EnsemblPlants:AT5G14780.1 GeneID:831330 KEGG:ath:AT5G14780 TAIR:At5g14780 InParanoid:Q9S7E4 PhylomeDB:Q9S7E4 ProtClustDB:PLN03139 ArrayExpress:Q9S7E4 Genevestigator:Q9S7E4 GermOnline:AT5G14780 Uniprot:Q9S7E4
Leaf	Isotig05514	20	3	3.266	7.04E-06	TAIR|locus:2125314 - symbol:PLDDELTA "AT4G35790" species:3702 "Arabidopsis thaliana" [GO:0004630 "phospholipase D activity" evidence=ISS;IMP;IDA] [GO:0046473 "phosphatidic acid metabolic process" evidence=IMP] [GO:0012501 "programmed cell death" evidence=IMP] [GO:0009409 "response to cold" evidence=IEP;IMP] [GO:0005773 "vacuole" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000008 InterPro:IPR001736 InterPro:IPR008973 InterPro:IPR011402 Pfam:PF00168 Pfam:PF00614 PIRSF:PIRSF036470 PROSITE:PS50035 SMART:SM00155 SMART:SM00239 GO:GO:0005886 GO:GO:0009506 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005773 GO:GO:0005509 GO:GO:0046470 GO:GO:0016042 GO:GO:0009409 InterPro:IPR018029 SUPFAM:SSF49562 PROSITE:PS50004 EMBL:AL031986 EMBL:AL161588 GO:GO:0012501 eggNOG:COG1502 InterPro:IPR015679 PANTHER:PTHR18896 GO:GO:0070290 GO:GO:0004630 GO:GO:0046473 KO:K01115 HOGENOM:HBG748198 InterPro:IPR024632 Pfam:PF12357 EMBL:AF322228 EMBL:AF274239 EMBL:AF306345 EMBL:AB031047 EMBL:AF424632 EMBL:AK227213 IPI:IPI00520107 IPI:IPI00541650 RefSeq:NP_567989.1 RefSeq:NP_849501.1 UniGene:At.22959 ProteinModelPortal:Q9C5Y0 SMR:Q9C5Y0 STRING:Q9C5Y0 PRIDE:Q9C5Y0 EnsemblPlants:AT4G35790.1 GeneID:829733 KEGG:ath:AT4G35790 TAIR:At4g35790 InParanoid:Q9C5Y0 OMA:GRISWIL PhylomeDB:Q9C5Y0 ProtClustDB:PLN03008 ArrayExpress:Q9C5Y0 Genevestigator:Q9C5Y0 Uniprot:Q9C5Y0
Leaf	Isotig05515	671	649	0.577	2.23E-13	No hit
Leaf	Isotig05524	2	23	-2.995	0.000115946	TAIR|locus:2100464 - symbol:AT3G48200 "AT3G48200" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002686 GenomeReviews:BA000014_GR eggNOG:NOG12793 EMBL:AK226883 IPI:IPI00534200 RefSeq:NP_566899.1 UniGene:At.26147 STRING:Q0WV86 PRIDE:Q0WV86 EnsemblPlants:AT3G48200.1 GeneID:823977 KEGG:ath:AT3G48200 TAIR:At3g48200 HOGENOM:HBG317921 InParanoid:Q0WV86 OMA:FIRTANS PhylomeDB:Q0WV86 ProtClustDB:CLSN2689049 Genevestigator:Q0WV86 Uniprot:Q0WV86
Leaf	Isotig05530	34	14	1.809	2.96E-05	TAIR|locus:2137594 - symbol:PCK1 "AT4G37870" species:3702 "Arabidopsis thaliana" [GO:0004612 "phosphoenolpyruvate carboxykinase (ATP) activity" evidence=ISS;IMP] [GO:0005524 "ATP binding" evidence=ISS]

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						[GO:0006094 "gluconeogenesis" evidence=ISS] [GO:0005730 "nucleolus" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0016036 "cellular response to phosphate starvation" evidence=IEP] [GO:0016020 "membrane" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009817 "defense response to fungus, incompatible interaction" evidence=IDA] InterPro:IPR001272 InterPro:IPR008210 InterPro:IPR013035 InterPro:IPR015994 Pfam:PF01293 PROSITE:PS00532 GO:GO:0005829 GO:GO:0005524 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0046686 EMBL:AL035709 EMBL:AL161592 GO:GO:0005730 GO:GO:0016020 GO:GO:0006094 GO:GO:0009817 GO:GO:0016036 EMBL:AF372922 EMBL:AY078035 IPI:IPI00526152 PIR:T06034 RefSeq:NP_195500.1 UniGene:At.22897 ProteinModelPortal:Q9T074 SMR:Q9T074 IntAct:Q9T074 STRING:Q9T074 PRIDE:Q9T074 EnsemblPlants:AT4G37870.1 GeneID:829943 KEGG:ath:AT4G37870 TAIR:At4g37870 eggNOG:COG1866 HOGENOM:HBG293387 InParanoid:Q9T074 KO:K01610 OMA:VYNPSYE PhylomeDB:Q9T074 ProtClustDB:PLN02597 BioCyc:MetaCyc:AT4G37870-MONOMER ArrayExpress:Q9T074 Genevestigator:Q9T074 GO:GO:0004612 Gene3D:G3DSA:3.90.228.20 Gene3D:G3DSA:3.40.449.10 SUPFAM:SSF68923 TIGRFAMs:TIGR00224 Uniprot:Q9T074
Leaf	Isotig05549	14	3	2.751	0.000536578	TAIR|locus:2173373 - symbol:GCH "AT5G64300" species:3702 "Arabidopsis thaliana" [GO:0003935 "GTP cyclohydrolase II activity" evidence=IGI;ISS] [GO:0008686 "3,4-dihydroxy-2-butanone-4-phosphate synthase activity" evidence=IGI;ISS] [GO:0009231 "riboflavin biosynthetic process" evidence=IGI;ISS] [GO:0016020 "membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] InterPro:IPR000422 InterPro:IPR000926 Pfam:PF00925 Pfam:PF00926 GO:GO:0005525 GO:GO:0009570 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0016020 GO:GO:0046872 EMBL:AB008268 GO:GO:0009231 InterPro:IPR017945 Gene3D:G3DSA:3.90.870.10 SUPFAM:SSF55821 HOGENOM:HBG735778 GO:GO:0003935 TIGRFAMs:TIGR00505 eggNOG:COG0108 GO:GO:0008686 TIGRFAMs:TIGR00506 EMBL:AJ000053 EMBL:D45165 IPI:IPI00522822 PIR:JC4209 RefSeq:NP_201235.4 UniGene:At.49217 ProteinModelPortal:P47924 SMR:P47924 STRING:P47924 PRIDE:P47924 EnsemblPlants:AT5G64300.1 GeneID:836551 KEGG:ath:AT5G64300 GeneFarm:2299 TAIR:At5g64300 InParanoid:P47924 KO:K14652 OMA:RCDCRMQ PhylomeDB:P47924 ProtClustDB:PLN02831 BioCyc:ARA:AT5G64300-MONOMER BioCyc:MetaCyc:AT5G64300-MONOMER ArrayExpress:P47924 Genevestigator:P47924 GermOnline:AT5G64300 InterPro:IPR016299 Uniprot:P47924
Leaf	Isotig05551	15	61	-1.495	4.83E-05	TAIR|locus:2016605 - symbol:HEMA1 "AT1G58290" species:3702 "Arabidopsis thaliana" [GO:0006783 "heme biosynthetic process" evidence=IMP] [GO:0008883 "glutamyl-tRNA reductase activity" evidence=IGI;TAS] [GO:0015995 "chlorophyll biosynthetic process" evidence=IMP] [GO:0009507 "chloroplast" evidence=IDA;TAS] [GO:0005515 "protein binding" evidence=IPI] [GO:0006779 "porphyrin-containing compound biosynthetic process" evidence=TAS] [GO:0009416 "response to light stimulus" evidence=IEP] InterPro:IPR000343 InterPro:IPR015895 InterPro:IPR015896 InterPro:IPR016040 InterPro:IPR018214 Pfam:PF00745 Pfam:PF05201 PROSITE:PS00747 InterPro:IPR006151 Pfam:PF01488 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009507 GO:GO:0005515 Gene3D:G3DSA:3.40.50.720 GO:GO:0050661 EMBL:AC008051 GO:GO:0015995 GO:GO:0006783 EMBL:U03774 EMBL:AY072223 EMBL:AY096600 IPI:IPI00535419 PIR:E96616 RefSeq:NP_176125.1 UniGene:At.241 ProteinModelPortal:P42804 SMR:P42804 IntAct:P42804 STRING:P42804 PRIDE:P42804 EnsemblPlants:AT1G58290.1 GeneID:842198 KEGG:ath:AT1G58290 TAIR:At1g58290 eggNOG:COG0373 HOGENOM:HBG732626 InParanoid:P42804 KO:K02492 OMA:GPILNRL PhylomeDB:P42804 ProtClustDB:PLN00203 BioCyc:ARA:AT1G58290-MONOMER BioCyc:MetaCyc:AT1G58290-MONOMER ArrayExpress:P42804 Genevestigator:P42804 GermOnline:AT1G58290 GO:GO:0008883 SUPFAM:SSF69075 SUPFAM:SSF69742 TIGRFAMs:TIGR01035 Uniprot:P42804
Leaf	Isotig05563	4	25	-2.115	0.000948108	TAIR|locus:2026177 - symbol:AT1G62660 species:3702 "Arabidopsis thaliana" [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=IEA;ISS] [GO:0071370 "cellular response to gibberellin stimulus" evidence=IEP] [GO:0000325 "plant-type vacuole" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0009617 "response to bacterium" evidence=IEP] InterPro:IPR001362 InterPro:IPR018053 InterPro:IPR021792 Pfam:PF11837 PROSITE:PS00609 SMART:SM00640 EMBL:CP002684 GO:GO:0005975 InterPro:IPR008985 SUPFAM:SSF49899 InterPro:IPR023296 SUPFAM:SSF75005 CAZy:GH32 KO:K01193 GO:GO:0004575 InterPro:IPR013189 InterPro:IPR013148 Pfam:PF08244 Pfam:PF00251 ProtClustDB:CLSN2687777 EMBL:AY048269 EMBL:AY062481 EMBL:AY063904 EMBL:AY114066 EMBL:X99111 IPI:IPI00517592 PIR:S71268 RefSeq:NP_564798.1 UniGene:At.24113 UniGene:At.67066 ProteinModelPortal:Q43348 SMR:Q43348

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						STRING:Q43348 PRIDE:Q43348 ProMEX:Q43348 EnsemblPlants:AT1G62660.1 GeneID:842563 KEGG:ath:AT1G62660 TAIR:At1g62660 InParanoid:Q43348 OMA:HSIVEGF PhylomeDB:Q43348 ArrayExpress:Q43348 Genevestigator:Q43348 Uniprot:Q43348
Leaf	Isotig05566	12	69	-1.995	1.23E-07	TAIR|locus:2016605 - symbol:HEMA1 "AT1G58290" species:3702 "Arabidopsis thaliana" [GO:0006783 "heme biosynthetic process" evidence=IMP] [GO:0008883 "glutamyl-tRNA reductase activity" evidence=IGI;TAS] [GO:0015995 "chlorophyll biosynthetic process" evidence=IMP] [GO:0009507 "chloroplast" evidence=IDA;TAS] [GO:0005515 "protein binding" evidence=IPI] [GO:0006779 "porphyrin-containing compound biosynthetic process" evidence=TAS] [GO:0009416 "response to light stimulus" evidence=IEP] InterPro:IPR000343 InterPro:IPR015895 InterPro:IPR015896 InterPro:IPR016040 InterPro:IPR018214 Pfam:PF00745 Pfam:PF05201 PROSITE:PS00747 InterPro:IPR006151 Pfam:PF01488 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009507 GO:GO:0005515 Gene3D:G3DSA:3.40.50.720 GO:GO:0050661 EMBL:AC008051 GO:GO:0015995 GO:GO:0006783 EMBL:U03774 EMBL:AY072223 EMBL:AY096600 IPI:IPI00535419 PIR:E96616 RefSeq:NP_176125.1 UniGene:At.241 ProteinModelPortal:P42804 SMR:P42804 IntAct:P42804 STRING:P42804 PRIDE:P42804 EnsemblPlants:AT1G58290.1 GeneID:842198 KEGG:ath:AT1G58290 TAIR:At1g58290 eggNOG:COG0373 HOGENOM:HBG732626 InParanoid:P42804 KO:K02492 OMA:GPILNRL PhylomeDB:P42804 ProtClustDB:PLN00203 BioCyc:ARA:AT1G58290-MONOMER BioCyc:MetaCyc:AT1G58290-MONOMER ArrayExpress:P42804 Genevestigator:P42804 GermOnline:AT1G58290 GO:GO:0008883 SUPFAM:SSF69075 SUPFAM:SSF69742 TIGRFAMs:TIGR01035 Uniprot:P42804
Leaf	Isotig05569	16	2	3.529	3.35E-05	TAIR|locus:2197379 - symbol:SNRK2.4 "AT1G10940" species:3702 "Arabidopsis thaliana" [GO:0016301 "kinase activity" evidence=ISS;IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0006970 "response to osmotic stress" evidence=IGI;IDA] [GO:0009651 "response to salt stress" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0009737 "response to abscisic acid stimulus" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR000719 InterPro:IPR002290 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 Pfam:PF00069 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 SMART:SM00220 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0005524 GO:GO:0009737 GO:GO:0005634 GO:GO:0005515 eggNOG:COG0515 SUPFAM:SSF56112 GO:GO:0004674 HOGENOM:HBG755340 BRENDA:2.7.11.1 GO:GO:0009651 EMBL:U95973 EMBL:M91548 EMBL:AY093130 EMBL:BT008850 EMBL:AY084221 IPI:IPI00522193 PIR:S36944 RefSeq:NP_172563.1 UniGene:At.23750 ProteinModelPortal:P43291 SMR:P43291 IntAct:P43291 STRING:P43291 PRIDE:P43291 ProMEX:P43291 EnsemblPlants:AT1G10940.1 GeneID:837637 KEGG:ath:AT1G10940 TAIR:At1g10940 InParanoid:P43291 KO:K14498 OMA:LAIAMEY PhylomeDB:P43291 ProtClustDB:CLSN2681826 ArrayExpress:P43291 Genevestigator:P43291 GermOnline:AT1G10940 Uniprot:P43291
Leaf	Isotig05574	5	36	-2.319	2.69E-05	TAIR|locus:2060236 - symbol:AT2G32560 "AT2G32560" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] InterPro:IPR001810 Pfam:PF00646 PROSITE:PS50181 SMART:SM00256 EMBL:CP002685 GenomeReviews:CT485783_GR SUPFAM:SSF81383 EMBL:AC004681 eggNOG:NOG247418 HOGENOM:HBG319167 ProtClustDB:CLSN2679978 EMBL:AY074536 EMBL:AY096469 EMBL:AY085567 IPI:IPI00518201 PIR:T02555 RefSeq:NP_850191.1 UniGene:At.27709 ProteinModelPortal:Q8RY82 SMR:Q8RY82 PRIDE:Q8RY82 DNASU:817817 EnsemblPlants:AT2G32560.1 GeneID:817817 KEGG:ath:AT2G32560 TAIR:At2g32560 InParanoid:Q8RY82 OMA:CKEEIAM PhylomeDB:Q8RY82 Genevestigator:Q8RY82 Uniprot:Q8RY82
Leaf	Isotig05579	21	6	2.336	0.000109395	TAIR|locus:2012166 - symbol:NQR species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0008152 "metabolic process" evidence=ISS] [GO:0008270 "zinc ion binding" evidence=IEA;ISS] [GO:0016491 "oxidoreductase activity" evidence=IEA;ISS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0005777 "peroxisome" evidence=IDA] [GO:0006979 "response to oxidative stress" evidence=IGI;IEP] InterPro:IPR002085 InterPro:IPR002198 InterPro:IPR002364 InterPro:IPR013149 InterPro:IPR013154 InterPro:IPR016040 InterPro:IPR020904 Pfam:PF00106 Pfam:PF00107 Pfam:PF08240 PRINTS:PR00080 PROSITE:PS00061 PROSITE:PS01162 InterPro:IPR002347 EMBL:CP002684 GO:GO:0005739 GO:GO:0006979 GO:GO:0005777 GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 GO:GO:0008270 GO:GO:0016491 PRINTS:PR00081 InterPro:IPR011032 PANTHER:PTHR11695 SUPFAM:SSF50129 EMBL:AC011807 KO:K07119 HSSP:P96202 EMBL:AY062728 EMBL:AY072306 EMBL:AY093342 EMBL:BT008393 IPI:IPI00529233 PIR:D96533 RefSeq:NP_175390.2 UniGene:At.91 ProteinModelPortal:Q9FX95 SMR:Q9FX95 PRIDE:Q9FX95 EnsemblPlants:AT1G49670.1 GeneID:841391 KEGG:ath:AT1G49670 TAIR:At1g49670 InParanoid:Q9FX95

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						OMA:LAKSQTV PhylomeDB:Q9FX95 ProtClustDB:CLSN2690451 ArrayExpress:Q9FX95 Genevestigator:Q9FX95 Uniprot:Q9FX95
Leaf	Isotig05584	15	81	-1.904	2.76E-08	TAIR|locus:2016605 - symbol:HEMA1 "AT1G58290" species:3702 "Arabidopsis thaliana" [GO:0006783 "heme biosynthetic process" evidence=IMP] [GO:0008883 "glutamyl-tRNA reductase activity" evidence=IGI;TAS] [GO:0015995 "chlorophyll biosynthetic process" evidence=IMP] [GO:0009507 "chloroplast" evidence=IDA;TAS] [GO:0005515 "protein binding" evidence=IPI] [GO:0006779 "porphyrin-containing compound biosynthetic process" evidence=TAS] [GO:0009416 "response to light stimulus" evidence=IEP] InterPro:IPR000343 InterPro:IPR015895 InterPro:IPR015896 InterPro:IPR016040 InterPro:IPR018214 Pfam:PF00745 Pfam:PF05201 PROSITE:PS00747 InterPro:IPR006151 Pfam:PF01488 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009507 GO:GO:0005515 Gene3D:G3DSA:3.40.50.720 GO:GO:0050661 EMBL:AC008051 GO:GO:0015995 GO:GO:0006783 EMBL:U03774 EMBL:AY072223 EMBL:AY096600 IPI:IPI00535419 PIR:E96616 RefSeq:NP_176125.1 UniGene:At.241 ProteinModelPortal:P42804 SMR:P42804 IntAct:P42804 STRING:P42804 PRIDE:P42804 EnsemblPlants:AT1G58290.1 GeneID:842198 KEGG:ath:AT1G58290 TAIR:At1g58290 eggNOG:COG0373 HOGENOM:HBG732626 InParanoid:P42804 KO:K02492 OMA:GPILNRL PhylomeDB:P42804 ProtClustDB:PLN00203 BioCyc:ARA:AT1G58290-MONOMER BioCyc:MetaCyc:AT1G58290-MONOMER ArrayExpress:P42804 Genevestigator:P42804 GermOnline:AT1G58290 GO:GO:0008883 SUPFAM:SSF69075 SUPFAM:SSF69742 TIGRFAMs:TIGR01035 Uniprot:P42804
Leaf	Isotig05592	23	100	-1.591	5.12E-08	TAIR|locus:2165306 - symbol:ACS12 "AT5G51690" species:3702 "Arabidopsis thaliana" [GO:0009693 "ethylene biosynthetic process" evidence=ISS] [GO:0016847 "1-aminocyclopropane-1-carboxylate synthase activity" evidence=ISS;IDA] [GO:0004069 "L-aspartate:2-oxoglutarate aminotransferase activity" evidence=IGI] [GO:0006520 "cellular amino acid metabolic process" evidence=IGI] [GO:0008793 "aromatic-amino-acid:2-oxoglutarate aminotransferase activity" evidence=IGI] InterPro:IPR001176 InterPro:IPR004838 InterPro:IPR004839 InterPro:IPR015421 InterPro:IPR015422 Pfam:PF00155 PRINTS:PR00753 PROSITE:PS00105 EMBL:CP002688 GenomeReviews:BA000015_GR eggNOG:COG0436 HOGENOM:HBG317030 KO:K14270 ProtClustDB:CLSN2715434 GO:GO:0016847 GO:GO:0008793 GO:GO:0004069 GO:GO:0030170 InterPro:IPR015424 Gene3D:G3DSA:3.40.640.10 Gene3D:G3DSA:3.90.1150.10 SUPFAM:SSF53383 EMBL:AB010074 EMBL:AF336920 EMBL:BT000463 EMBL:BT002111 EMBL:AK117323 IPI:IPI00538212 RefSeq:NP_199982.2 UniGene:At.18827 UniGene:At.75220 PDB:2GEA PDBsum:2GEA ProteinModelPortal:Q8GYY0 SMR:Q8GYY0 STRING:Q8GYY0 PRIDE:Q8GYY0 EnsemblPlants:AT5G51690.1 GeneID:835243 KEGG:ath:AT5G51690 TAIR:At5g51690 InParanoid:Q8GYY0 OMA:CLEFAHR PhylomeDB:Q8GYY0 ArrayExpress:Q8GYY0 Genevestigator:Q8GYY0 GermOnline:AT5G51690 Uniprot:Q8GYY0
Leaf	Isotig05604	11	0	4.988	0.000159591	No hit
Leaf	Isotig05608	16	3	2.944	0.000128177	TAIR|locus:2091618 - symbol:AT3G22270 "AT3G22270" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] GenomeReviews:BA000014_GR HOGENOM:HBG318375 EMBL:AK228960 IPI:IPI00533404 ProteinModelPortal:Q0WPV0 PRIDE:Q0WPV0 TAIR:At3g22270 eggNOG:NOG323978 InParanoid:Q0WPV0 PhylomeDB:Q0WPV0 Genevestigator:Q0WPV0 Uniprot:Q0WPV0
Leaf	Isotig05611	15	3	2.851	0.000262808	TAIR|locus:2057386 - symbol:ftsh4 "FTSH protease 4" species:3702 "Arabidopsis thaliana" [GO:0006508 "proteolysis" evidence=IEA] [GO:0008237 "metallopeptidase activity" evidence=ISS] [GO:0016887 "ATPase activity" evidence=ISS] [GO:0030163 "protein catabolic process" evidence=IEA] [GO:0004176 "ATP-dependent peptidase activity" evidence=ISS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009536 "plastid" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] InterPro:IPR000642 InterPro:IPR003593 InterPro:IPR003959 InterPro:IPR003960 InterPro:IPR005936 Pfam:PF00004 Pfam:PF01434 PROSITE:PS00674 SMART:SM00382 GO:GO:0016021 GO:GO:0005524 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0005743 GO:GO:0046872 GO:GO:0006508 GO:GO:0030163 GO:GO:0004222 GO:GO:0017111 HSSP:Q9WZ49 eggNOG:COG0465 TIGRFAMs:TIGR01241 HOGENOM:HBG724153 EMBL:AC004747 GO:GO:0009536 EMBL:AK220842 IPI:IPI00534293 PIR:T02610 RefSeq:NP_565616.1 UniGene:At.23415 ProteinModelPortal:O80983 SMR:O80983 STRING:O80983 PRIDE:O80983 EnsemblPlants:AT2G26140.1 GeneID:817154 KEGG:ath:AT2G26140 GeneFarm:2508 TAIR:At2g26140 InParanoid:O80983 OMA:NGKSMST PhylomeDB:O80983 ProtClustDB:CLSN2688437 ArrayExpress:O80983 Genevestigator:O80983 Uniprot:O80983
Leaf	Isotig05616	24	1	5.114	2.21E-08	TAIR|locus:2185515 - symbol:AT5G14880 species:3702 "Arabidopsis thaliana" [GO:0006813 "potassium ion transport" evidence=IEA;ISS] [GO:0015079 "potassium ion transmembrane transporter activity" evidence=ISS]

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						[GO:0016020 "membrane" evidence=IEA] InterPro:IPR003855 Pfam:PF02705 GO:GO:0016021 GO:GO:0005886 EMBL:CP002688 GenomeReviews:BA000015_GR EMBL:AL391149 GO:GO:0015079 eggNOG:COG3158 TIGRFAMs:TIGR00794 OMA:AVYPSLI HOGENOM:HBG606427 ProtClustDB:PLN00149 EMBL:AF129483 IPI:IPI00532645 PIR:T51433 RefSeq:NP_196992.1 UniGene:At.31871 ProteinModelPortal:Q9M7J9 PRIDE:Q9M7J9 EnsemblPlants:AT5G14880.1 GeneID:831340 KEGG:ath:AT5G14880 TAIR:At5g14880 InParanoid:Q9M7J9 PhylomeDB:Q9M7J9 ArrayExpress:Q9M7J9 Genevestigator:Q9M7J9 GermOnline:AT5G14880 Uniprot:Q9M7J9
Leaf	Isotig05623	16	4	2.529	0.000407249	TAIR|locus:2087433 - symbol:AT3G63460 "AT3G63460" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0016020 "membrane" evidence=IDA] [GO:0080008 "CUL4 RING ubiquitin ligase complex" evidence=ISS] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR017986 InterPro:IPR001680 InterPro:IPR015943 Pfam:PF00400 PROSITE:PS50082 PROSITE:PS50294 SMART:SM00320 GO:GO:0005829 GO:GO:0009506 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0016020 InterPro:IPR019775 Gene3D:G3DSA:2.130.10.10 SUPFAM:SSF50978 PROSITE:PS00678 KO:K14005 InterPro:IPR009917 Pfam:PF07304 OMA:NGEDFFN EMBL:AY099702 EMBL:BT008435 IPI:IPI00547111 RefSeq:NP_851024.1 UniGene:At.22771 UniGene:At.67091 ProteinModelPortal:Q8L611 SMR:Q8L611 IntAct:Q8L611 STRING:Q8L611 PRIDE:Q8L611 ProMEX:Q8L611 EnsemblPlants:AT3G63460.1 GeneID:825521 KEGG:ath:AT3G63460 TAIR:At3g63460 InParanoid:Q8L611 PhylomeDB:Q8L611 ProtClustDB:CLSN2680494 ArrayExpress:Q8L611 Genevestigator:Q8L611 Uniprot:Q8L611
Leaf	Isotig05626	25	8	2.173	5.38E-05	TAIR|locus:2042902 - symbol:FAC1 "AT2G38280" species:3702 "Arabidopsis thaliana" [GO:0003876 "AMP deaminase activity" evidence=IGI;ISS] [GO:0009168 "purine ribonucleoside monophosphate biosynthetic process" evidence=ISS] [GO:0009793 "embryo development ending in seed dormancy" evidence=IMP] [GO:0005792 "microsome" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0043424 "protein histidine kinase binding" evidence=IPI] [GO:0009737 "response to abscisic acid stimulus" evidence=IDA] InterPro:IPR001365 InterPro:IPR006329 InterPro:IPR006650 Pfam:PF00962 PROSITE:PS00485 GO:GO:0005783 GO:GO:0005792 GO:GO:0016021 GO:GO:0005829 GO:GO:0005524 GO:GO:0009737 GO:GO:0005634 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0043424 GO:GO:0046872 GO:GO:0009793 eggNOG:COG1816 HOGENOM:HBG713563 GO:GO:0003876 KO:K01490 GO:GO:0006188 PANTHER:PTHR11359 TIGRFAMs:TIGR01429 EMBL:AC003028 EMBL:AY056301 EMBL:AY133852 EMBL:AK316943 EMBL:AK221552 IPI:IPI00546126 PIR:T01259 RefSeq:NP_565886.1 RefSeq:NP_850294.1 UniGene:At.12466 PDB:2A3L PDBsum:2A3L ProteinModelPortal:O80452 SMR:O80452 IntAct:O80452 STRING:O80452 PRIDE:O80452 EnsemblPlants:AT2G38280.1 EnsemblPlants:AT2G38280.2 GeneID:818408 KEGG:ath:AT2G38280 TAIR:At2g38280 InParanoid:O80452 OMA:TIDPASH PhylomeDB:O80452 ProtClustDB:PLN02768 ArrayExpress:O80452 Genevestigator:O80452 GermOnline:AT2G38280 Uniprot:O80452
Leaf	Isotig05656	11	0	4.988	0.000159591	TAIR|locus:2076487 - symbol:BIG "BIG" species:3702 "Arabidopsis thaliana" [GO:0004842 "ubiquitin-protein ligase activity" evidence=IEA] [GO:0008270 "zinc ion binding" evidence=IEA] [GO:0048283 "indeterminate inflorescence morphogenesis" evidence=IMP] [GO:0009733 "response to auxin stimulus" evidence=IMP] [GO:0009926 "auxin polar transport" evidence=IDA] [GO:0010311 "lateral root formation" evidence=IMP] [GO:0048364 "root development" evidence=IMP] [GO:0016020 "membrane" evidence=IDA] [GO:0009826 "unidimensional cell growth" evidence=IMP] [GO:0048281 "inflorescence morphogenesis" evidence=IMP] [GO:0009620 "response to fungus" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0009640 "photomorphogenesis" evidence=IMP] InterPro:IPR000433 InterPro:IPR003126 InterPro:IPR015943 Pfam:PF00569 Pfam:PF02207 PROSITE:PS01357 PROSITE:PS01360 PROSITE:PS50135 PROSITE:PS50865 PROSITE:PS51157 SMART:SM00291 GO:GO:0016021 GO:GO:0005829 GO:GO:0009506 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0009734 GO:GO:0009926 Gene3D:G3DSA:2.130.10.10 GO:GO:0008270 GO:GO:0009640 GO:GO:0009826 GO:GO:0009620 GO:GO:0010311 EMBL:AC009755 GO:GO:0004842 EMBL:AF507018 IPI:IPI00528496 RefSeq:NP_186875.2 UniGene:At.46446 STRING:Q9SRU2 PRIDE:Q9SRU2 GeneID:820398 KEGG:ath:AT3G02260 TAIR:At3g02260 eggNOG:NOG236675 HOGENOM:HBG317487 InParanoid:Q9SRU2 KO:K10691 Genevestigator:Q9SRU2 GO:GO:0048281 Uniprot:Q9SRU2
Leaf	Isotig05661	15	1	4.436	1.60E-05	TAIR|locus:2148171 - symbol:CSLD2 "AT5G16910" species:3702 "Arabidopsis thaliana" [GO:0000271 "polysaccharide biosynthetic process" evidence=ISS] [GO:0009832 "plant-type cell wall biogenesis" evidence=ISS] [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0016759 "cellulose synthase activity" evidence=ISS] [GO:0005794 "Golgi apparatus" evidence=IDA] [GO:0005886 "plasma membrane"

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						evidence=IDA] [GO:0030173 "integral to Golgi membrane" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0048767 "root hair elongation" evidence=IMP] InterPro:IPR005150 Pfam:PF03552 GO:GO:0005886 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0030173 GO:GO:0009409 GO:GO:0048767 InterPro:IPR013083 Gene3D:G3DSA:3.30.40.10 GO:GO:0007047 CAZy:GT2 eggNOG:COG1215 GO:GO:0016760 GO:GO:0030244 HOGENOM:HBG744549 ProtClustDB:PLN02248 EMBL:AL391141 IPI:IPI00532872 PIR:T51546 RefSeq:NP_197193.1 UniGene:At.20318 ProteinModelPortal:Q9LFL0 SMR:Q9LFL0 PRIDE:Q9LFL0 EnsemblPlants:AT5G16910.1 GeneID:831554 KEGG:ath:AT5G16910 TAIR:At5g16910 InParanoid:Q9LFL0 OMA:WRIKHQN PhylomeDB:Q9LFL0 Genevestigator:Q9LFL0 Uniprot:Q9LFL0
Leaf	Isotig05665	10	1	3.851	0.00071293	TAIR|locus:2011671 - symbol:AT1G76550 "AT1G76550" species:3702 "Arabidopsis thaliana" [GO:0006096 "glycolysis" evidence=ISS] [GO:0010317 "pyrophosphate-dependent phosphofructokinase complex, alpha-subunit complex" evidence=ISS] [GO:0047334 "diphosphate-fructose-6-phosphate 1-phosphotransferase activity" evidence=ISS;IMP] [GO:0015979 "photosynthesis" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR000023 InterPro:IPR011183 InterPro:IPR013981 Pfam:PF00365 PIRSF:PIRSF005677 EMBL:CP002684 GO:GO:0005524 GO:GO:0006096 GO:GO:0015979 EMBL:AC015450 GO:GO:0005945 GO:GO:0003872 SUPFAM:SSF53784 HSSP:P70826 GO:GO:0047334 Gene3D:G3DSA:1.10.10.480 TIGRFAMs:TIGR02477 KO:K00895 IPI:IPI00538921 PIR:E96793 RefSeq:NP_177781.1 UniGene:At.23436 UniGene:At.67125 ProteinModelPortal:Q9C9K3 SMR:Q9C9K3 STRING:Q9C9K3 PRIDE:Q9C9K3 EnsemblPlants:AT1G76550.1 GeneID:843988 KEGG:ath:AT1G76550 TAIR:At1g76550 InParanoid:Q9C9K3 OMA:DMLGRTK PhylomeDB:Q9C9K3 ProtClustDB:PLN03028 Genevestigator:Q9C9K3 Uniprot:Q9C9K3
Leaf	Isotig05672	12	0	5.114	7.63E-05	TAIR|locus:2206330 - symbol:GTB1 "global transcription factor group B1" species:3702 "Arabidopsis thaliana" [GO:0003723 "RNA binding" evidence=IEA] [GO:0006333 "chromatin assembly or disassembly" evidence=ISS] [GO:0006352 "transcription initiation, DNA-dependent" evidence=ISS] [GO:0016788 "hydrolase activity, acting on ester bonds" evidence=IEA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000980 InterPro:IPR003029 InterPro:IPR006641 InterPro:IPR017072 PIRSF:PIRSF036947 PROSITE:PS50126 SMART:SM00252 SMART:SM00732 EMBL:CP002684 GO:GO:0005829 GO:GO:0009506 Gene3D:G3DSA:3.30.505.10 GO:GO:0006357 GO:GO:0003746 GO:GO:0016788 InterPro:IPR012340 Gene3D:G3DSA:2.40.50.140 InterPro:IPR016027 SUPFAM:SSF50249 GO:GO:0006139 InterPro:IPR022967 SMART:SM00316 EMBL:AC010795 GO:GO:0032784 eggNOG:COG2183 KO:K11292 InterPro:IPR023323 InterPro:IPR023097 Gene3D:G3DSA:1.10.150.310 Gene3D:G3DSA:1.10.3500.10 PANTHER:PTHR10145 IPI:IPI00846769 RefSeq:NP_176723.3 UniGene:At.20510 ProteinModelPortal:A8MS85 SMR:A8MS85 PRIDE:A8MS85 EnsemblPlants:AT1G65440.1 GeneID:842855 KEGG:ath:AT1G65440 TAIR:At1g65440 InParanoid:A8MS85 OMA:WGSESGG PhylomeDB:A8MS85 ProtClustDB:CLSN2682387 Genevestigator:A8MS85 Uniprot:A8MS85
Leaf	Isotig05673	13	1	4.229	7.21E-05	TAIR|locus:2013688 - symbol:PUB17 "AT1G29340" species:3702 "Arabidopsis thaliana" [GO:0004842 "ubiquitin-protein ligase activity" evidence=IDA] [GO:0009626 "plant-type hypersensitive response" evidence=IGI] [GO:0009814 "defense response, incompatible interaction" evidence=IMP] [GO:0009817 "defense response to fungus, incompatible interaction" evidence=IGI] [GO:0016567 "protein ubiquitination" evidence=IDA] InterPro:IPR000225 InterPro:IPR003613 InterPro:IPR011989 InterPro:IPR016024 Pfam:PF00514 Pfam:PF04564 PROSITE:PS50176 SMART:SM00185 SMART:SM00504 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005488 SUPFAM:SSF48371 Gene3D:G3DSA:1.25.10.10 GO:GO:0009817 InterPro:IPR013083 Gene3D:G3DSA:3.30.40.10 GO:GO:0004842 UniGene:At.17411 EMBL:AC068667 GO:GO:0000151 HSSP:Q8VZ40 HOGENOM:HBG746719 EMBL:AY064045 EMBL:AY150512 IPI:IPI00523315 PIR:A86416 RefSeq:NP_174228.1 UniGene:At.27415 ProteinModelPortal:Q9C7R6 SMR:Q9C7R6 IntAct:Q9C7R6 STRING:Q9C7R6 PRIDE:Q9C7R6 EnsemblPlants:AT1G29340.1 GeneID:839808 KEGG:ath:AT1G29340 TAIR:At1g29340 eggNOG:NOG329430 InParanoid:Q9C7R6 OMA:ENRAYIA PhylomeDB:Q9C7R6 ProtClustDB:CLSN2679704 Genevestigator:Q9C7R6 Uniprot:Q9C7R6
Leaf	Isotig05681	24	11	1.654	0.000979975	TAIR|locus:2088262 - symbol:RSH2 "AT3G14050" species:3702 "Arabidopsis thaliana" [GO:0008728 "GTP diphosphokinase activity" evidence=IGI] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009611 "response to wounding" evidence=IEP] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] InterPro:IPR003607 InterPro:IPR004811 InterPro:IPR007685 Pfam:PF04607 SMART:SM00471 SMART:SM00954 GO:GO:0009737 GO:GO:0009507 EMBL:CP002686 GO:GO:0009611 GO:GO:0016301 EMBL:AB019229 eggNOG:COG0317 GO:GO:0015969 PANTHER:PTHR21262 GO:GO:0008728 IPI:IPI00520491 RefSeq:NP_188021.1

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						UniGene:At.25183 ProteinModelPortal:Q9LVJ3 SMR:Q9LVJ3 STRING:Q9LVJ3 PRIDE:Q9LVJ3 EnsemblPlants:AT3G14050.1 GeneID:820619 KEGG:ath:AT3G14050 TAIR:At3g14050 InParanoid:Q9LVJ3 OMA:CKYSSFV PhylomeDB:Q9LVJ3 ProtClustDB:CLSN2684912 Genevestigator:Q9LVJ3 Uniprot:Q9LVJ3
Leaf	Isotig05684	10	0	4.851	0.000336918	TAIR|locus:2080310 - symbol:RGD3 "ROOT GROWTH DEFECTIVE 3" species:3702 "Arabidopsis thaliana" [GO:0003676 "nucleic acid binding" evidence=IEA] [GO:0003677 "DNA binding" evidence=IEA;ISS] [GO:0004386 "helicase activity" evidence=IEA;ISS] [GO:0005524 "ATP binding" evidence=IEA;ISS] InterPro:IPR000330 InterPro:IPR001650 InterPro:IPR011989 InterPro:IPR016024 Pfam:PF00176 Pfam:PF00271 PROSITE:PS51194 SMART:SM00490 InterPro:IPR014001 GO:GO:0005524 EMBL:CP002686 SUPFAM:SSF48371 Gene3D:G3DSA:1.25.10.10 GO:GO:0003677 GO:GO:0004386 eggNOG:COG0553 SMART:SM00487 PROSITE:PS51192 KO:K15192 InterPro:IPR022707 Pfam:PF12054 EMBL:AB440793 IPI:IPI00548573 RefSeq:NP_190996.3 UniGene:At.35125 STRING:B5BT18 PRIDE:B5BT18 EnsemblPlants:AT3G54280.1 GeneID:824595 KEGG:ath:AT3G54280 TAIR:At3g54280 PhylomeDB:B5BT18 Genevestigator:B5BT18 Uniprot:B5BT18
Leaf	Isotig05686	200	181	0.673	4.45E-06	TAIR|locus:2094473 - symbol:AT3G25570 species:3702 "Arabidopsis thaliana" [GO:0004014 "adenosylmethionine decarboxylase activity" evidence=IEA;ISS] [GO:0005575 "cellular_component" evidence=ND] [GO:0006597 "spermine biosynthetic process" evidence=IEA] [GO:0008295 "spermidine biosynthetic process" evidence=IEA] InterPro:IPR001985 InterPro:IPR016067 InterPro:IPR018166 InterPro:IPR018167 Pfam:PF01536 PIRSF:PIRSF001355 PROSITE:PS01336 EMBL:CP002686 GenomeReviews:BA000014_GR eggNOG:NOG77566 HOGENOM:HBG610629 KO:K01611 ProtClustDB:PLN02524 GO:GO:0004014 GO:GO:0008295 GO:GO:0006597 Gene3D:G3DSA:3.60.90.10 PANTHER:PTHR11570 SUPFAM:SSF56276 TIGRFAMs:TIGR00535 HSSP:P17707 OMA:TSELLMY EMBL:AB025639 EMBL:BT012654 IPI:IPI00546639 RefSeq:NP_001189972.1 RefSeq:NP_189184.1 UniGene:At.49653 ProteinModelPortal:Q9LSU6 SMR:Q9LSU6 STRING:Q9LSU6 PRIDE:Q9LSU6 EnsemblPlants:AT3G25570.1 EnsemblPlants:AT3G25570.2 GeneID:822144 KEGG:ath:AT3G25570 TAIR:At3g25570 InParanoid:Q9LSU6 PhylomeDB:Q9LSU6 Genevestigator:Q9LSU6 Uniprot:Q9LSU6
Leaf	Isotig05701	23	4	3.053	2.98E-06	TAIR|locus:2012161 - symbol:PAB8 "AT1G49760" species:3702 "Arabidopsis thaliana" [GO:0003723 "RNA binding" evidence=ISS] [GO:0003743 "translation initiation factor activity" evidence=ISS] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR000504 InterPro:IPR002004 InterPro:IPR006515 InterPro:IPR012677 Pfam:PF00076 Pfam:PF00658 PROSITE:PS50102 PROSITE:PS51309 SMART:SM00360 SMART:SM00517 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0046686 GO:GO:0000166 Gene3D:G3DSA:3.30.70.330 GO:GO:0003723 EMBL:AC011807 eggNOG:COG0724 HOGENOM:HBG756718 KO:K13126 Gene3D:G3DSA:1.10.1900.10 SUPFAM:SSF63570 TIGRFAMs:TIGR01628 HSSP:P11940 ProtClustDB:CLSN2714507 EMBL:AF370517 EMBL:AY064622 IPI:IPI00535850 PIR:C96534 RefSeq:NP_001185184.1 RefSeq:NP_564554.1 UniGene:At.21584 UniGene:At.67107 UniGene:At.67318 ProteinModelPortal:Q9FXA2 SMR:Q9FXA2 IntAct:Q9FXA2 STRING:Q9FXA2 PRIDE:Q9FXA2 ProMEX:Q9FXA2 EnsemblPlants:AT1G49760.1 EnsemblPlants:AT1G49760.2 GeneID:841399 KEGG:ath:AT1G49760 TAIR:At1g49760 InParanoid:Q9FXA2 OMA:LHADITE PhylomeDB:Q9FXA2 Genevestigator:Q9FXA2 Uniprot:Q9FXA2
Leaf	Isotig05707	25	9	2.003	0.000126076	TAIR|locus:2078623 - symbol:MPPBETA "AT3G02090" species:3702 "Arabidopsis thaliana" [GO:0004222 "metalloendopeptidase activity" evidence=ISS] [GO:0006508 "proteolysis" evidence=IEA;ISS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0005741 "mitochondrial outer membrane" evidence=IDA] [GO:0005743 "mitochondrial inner membrane" evidence=IDA] [GO:0005758 "mitochondrial intermembrane space" evidence=IDA] [GO:0005759 "mitochondrial matrix" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005750 "mitochondrial respiratory chain complex III" evidence=IDA] [GO:0008270 "zinc ion binding" evidence=IDA] InterPro:IPR001431 InterPro:IPR007863 InterPro:IPR011237 InterPro:IPR011249 InterPro:IPR011765 Pfam:PF00675 Pfam:PF05193 PROSITE:PS00143 GO:GO:0005774 GO:GO:0005618 GO:GO:0009507 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005730 GO:GO:0005741 GO:GO:0005758 GO:GO:0005759 GO:GO:0008270 GO:GO:0016491 GO:GO:0006508 GO:GO:0004222 EMBL:AC011664 Gene3D:G3DSA:3.30.830.10 SUPFAM:SSF63411 GO:GO:0005750 eggNOG:COG0612 KO:K01412 EMBL:AY126990 EMBL:BT000830 EMBL:BT000662 EMBL:BT001915 EMBL:Z35354 IPI:IPI00530627 IPI:IPI00539775 RefSeq:NP_186858.1 RefSeq:NP_850500.1

<table>
<tr><th>Tissue</th><th>Identification</th><th># of reads (stress)</th><th># of reads (control)</th><th>Fold Change</th><th>p-value</th><th>Description</th></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td></td><td>UniGene:At.23364 UniGene:At.69050 UniGene:At.74786 ProteinModelPortal:Q42290 SMR:Q42290 IntAct:Q42290 MINT:MINT-4330335 STRING:Q42290 PRIDE:Q42290 EnsemblPlants:AT3G02090.1 GeneID:821084 KEGG:ath:AT3G02090 GeneFarm:2127 TAIR:At3g02090 HOGENOM:HBG476859 InParanoid:Q42290 OMA:IPLMVAN PhylomeDB:Q42290 ProtClustDB:CLSN2685188 Genevestigator:Q42290 GermOnline:AT3G02090 Uniprot:Q42290</td></tr>
<tr><td>Leaf</td><td>Isotig05723</td><td>10</td><td>0</td><td>4.851</td><td>0.000336918</td><td>TAIR|locus:2028275 - symbol:AT1G45150 "AT1G45150" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002684 GenomeReviews:CT485782_GR EMBL:BT008320 EMBL:AK227318 IPI:IPI00523041 RefSeq:NP_175129.3 UniGene:At.38729 PRIDE:Q7Y231 EnsemblPlants:AT1G45150.1 GeneID:841083 KEGG:ath:AT1G45150 TAIR:At1g45150 eggNOG:NOG119415 HOGENOM:HBG320113 InParanoid:Q7Y231 OMA:LQYRISP PhylomeDB:Q7Y231 ProtClustDB:CLSN2680742 Genevestigator:Q7Y231 InterPro:IPR025150 Pfam:PF13320 Uniprot:Q7Y231</td></tr>
<tr><td>Leaf</td><td>Isotig05725</td><td>15</td><td>1</td><td>4.436</td><td>1.60E-05</td><td>No hit</td></tr>
<tr><td>Leaf</td><td>Isotig05731</td><td>16</td><td>3</td><td>2.944</td><td>0.000128177</td><td>TAIR|locus:2028466 - symbol:AT1G49050 species:3702 "Arabidopsis thaliana" [GO:0004190 "aspartic-type endopeptidase activity" evidence=IEA] [GO:0006508 "proteolysis" evidence=IEA;ISS] InterPro:IPR001461 InterPro:IPR001969 InterPro:IPR009007 Pfam:PF00026 PROSITE:PS00141 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0006508 EMBL:AC016041 GO:GO:0004190 InterPro:IPR021109 SUPFAM:SSF50630 Gene3D:G3DSA:2.40.70.10 PANTHER:PTHR13683 HOGENOM:HBG318733 EMBL:AF360182 EMBL:AY039998 IPI:IPI00528863 RefSeq:NP_564539.1 UniGene:At.20904 ProteinModelPortal:Q9M9A8 STRING:Q9M9A8 MEROPS:A01.A25 PRIDE:Q9M9A8 EnsemblPlants:AT1G49050.1 GeneID:841328 KEGG:ath:AT1G49050 TAIR:At1g49050 InParanoid:Q9M9A8 OMA:SSYTYFP PhylomeDB:Q9M9A8 ProtClustDB:CLSN2917196 ArrayExpress:Q9M9A8 Genevestigator:Q9M9A8 Uniprot:Q9M9A8</td></tr>
<tr><td>Leaf</td><td>Isotig05735</td><td>16</td><td>4</td><td>2.529</td><td>0.000407249</td><td>TAIR|locus:2065279 - symbol:CAND1 "AT2G02560" species:3702 "Arabidopsis thaliana" [GO:0009733 "response to auxin stimulus" evidence=IMP] [GO:0005515 "protein binding" evidence=IPI] [GO:0010228 "vegetative to reproductive phase transition of meristem" evidence=IMP] [GO:0005618 "cell wall" evidence=IDA] [GO:0010051 "xylem and phloem pattern formation" evidence=IMP] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR011989 InterPro:IPR016024 GO:GO:0005829 GO:GO:0005886 GO:GO:0005618 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0005515 GO:GO:0009733 SUPFAM:SSF48371 Gene3D:G3DSA:1.25.10.10 PROSITE:PS50077 GO:GO:0006355 GO:GO:0006351 GO:GO:0010051 GO:GO:0010228 EMBL:AC004136 EMBL:AY099857 EMBL:BT010134 IPI:IPI00524474 IPI:IPI00656867 PIR:T00607 RefSeq:NP_001030954.1 RefSeq:NP_178360.2 UniGene:At.41482 ProteinModelPortal:Q8L5Y6 SMR:Q8L5Y6 DIP:DIP-33719N IntAct:Q8L5Y6 STRING:Q8L5Y6 PRIDE:Q8L5Y6 EnsemblPlants:AT2G02560.1 GeneID:814786 KEGG:ath:AT2G02560 TAIR:At2g02560 eggNOG:NOG278162 HOGENOM:HBG560547 InParanoid:Q8L5Y6 OMA:EGSRNVV PhylomeDB:Q8L5Y6 ProtClustDB:CLSN2690104 Genevestigator:Q8L5Y6 InterPro:IPR013932 Pfam:PF08623 Uniprot:Q8L5Y6</td></tr>
<tr><td>Leaf</td><td>Isotig05740</td><td>19</td><td>6</td><td>2.192</td><td>0.000400191</td><td>TAIR|locus:2183359 - symbol:Tudor1 "AT5G07350" species:3702 "Arabidopsis thaliana" [GO:0003676 "nucleic acid binding" evidence=ISS] [GO:0004518 "nuclease activity" evidence=ISS] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0003723 "RNA binding" evidence=TAS] [GO:0005635 "nuclear envelope" evidence=IDA] [GO:0005783 "endoplasmic reticulum" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0006950 "response to stress" evidence=IGI] [GO:0009306 "protein secretion" evidence=IGI] InterPro:IPR006021 InterPro:IPR016071 InterPro:IPR016685 Pfam:PF00565 PIRSF:PIRSF017179 PROSITE:PS50830 SMART:SM00318 InterPro:IPR002999 GO:GO:0005783 GO:GO:0005829 GO:GO:0005886 GO:GO:0046686 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005618 GO:GO:0009507 GO:GO:0006950 GO:GO:0009306 GO:GO:0003723 GO:GO:0005635 GO:GO:0016788 GO:GO:0031047 GO:GO:0016442 Pfam:PF00567 SMART:SM00333 PROSITE:PS50304 Gene3D:G3DSA:2.40.50.90 eggNOG:COG1525 SUPFAM:SSF50199 OMA:VITEYLN HSSP:P00644 EMBL:AY064975 IPI:IPI00541332 RefSeq:NP_196352.2 UniGene:At.5224 ProteinModelPortal:Q8VZG7 SMR:Q8VZG7 PRIDE:Q8VZG7 ProMEX:Q8VZG7 EnsemblPlants:AT5G07350.1 GeneID:830626 KEGG:ath:AT5G07350 TAIR:At5g07350 InParanoid:Q8VZG7 PhylomeDB:Q8VZG7 ProtClustDB:CLSN2686944 Genevestigator:Q8VZG7 Uniprot:Q8VZG7</td></tr>
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Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
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Leaf	Isotig05792	12	0	5.114	7.63E-05	TAIR|locus:2130165 - symbol:AT4G16180 "AT4G16180" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0005886 "plasma membrane" evidence=IDA] GO:GO:0005886 EMBL:CP002687 GenomeReviews:CT486007_GR EMBL:AY800635 IPI:IPI00540178 RefSeq:NP_193353.2 UniGene:At.43288 STRING:Q5Q0B6 PRIDE:Q5Q0B6 EnsemblPlants:AT4G16180.1 GeneID:827310 KEGG:ath:AT4G16180 TAIR:At4g16180 HOGENOM:HBG318402 InParanoid:Q5Q0B6 OMA:ITQRTEE PhylomeDB:Q5Q0B6 ProtClustDB:CLSN2718481 Genevestigator:Q5Q0B6 Uniprot:Q5Q0B6
Leaf	Isotig05820	25	7	2.365	2.12E-05	TAIR|locus:2099277 - symbol:emb2738 "embryo defective 2738" species:3702 "Arabidopsis thaliana" [GO:0005525 "GTP binding" evidence=IEA;ISS] [GO:0009793 "embryo development ending in seed dormancy" evidence=NAS] [GO:0009507 "chloroplast" evidence=IDA] HAMAP:MF_00195 InterPro:IPR005225 InterPro:IPR006073 InterPro:IPR016484 Pfam:PF01926 PRINTS:PR00326 GO:GO:0005525 TIGRFAMs:TIGR00231 GO:GO:0009507 EMBL:CP002686 GenomeReviews:BA000014_GR eggNOG:COG1160 HOGENOM:HBG592135 OMA:LAVNKCE InterPro:IPR015946 Gene3D:G3DSA:3.30.300.20 PANTHER:PTHR11649:SF5 TIGRFAMs:TIGR03594 EMBL:BT046184 IPI:IPI00529367 RefSeq:NP_187815.2 UniGene:At.21430 ProteinModelPortal:B5X565 SMR:B5X565 STRING:B5X565 PRIDE:B5X565 EnsemblPlants:AT3G12080.1 GeneID:820382 KEGG:ath:AT3G12080 TAIR:At3g12080 PhylomeDB:B5X565 ProtClustDB:CLSN2918072 Genevestigator:B5X565 Uniprot:B5X565
Leaf	Isotig05826	14	0	5.336	1.79E-05	No hit
Leaf	Isotig05829	27	3	3.699	4.15E-08	TAIR|locus:2121209 - symbol:VAB2 "AT4G38510" species:3702 "Arabidopsis thaliana" [GO:0046933 "hydrogen ion transporting ATP synthase activity, rotational mechanism" evidence=ISS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0030835 "negative regulation of actin filament depolymerization" evidence=IDA] [GO:0051015 "actin filament binding" evidence=IDA] [GO:0051017 "actin filament bundle assembly" evidence=IDA] [GO:0051693 "actin filament capping" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR000194 InterPro:IPR000793 InterPro:IPR004100 InterPro:IPR005723 InterPro:IPR020003 Pfam:PF00006 Pfam:PF00306 Pfam:PF02874 PROSITE:PS00152 GO:GO:0005524 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005774 GO:GO:0009941 GO:GO:0015991 GO:GO:0046933 GO:GO:0046961 EMBL:AL161593 EMBL:AL035540 TCDB:3.A.2.2.5 GO:GO:0033180 eggNOG:COG1156 KO:K02147 ProtClustDB:CLSN2682718 InterPro:IPR022879 TIGRFAMs:TIGR01040 EMBL:AY039518 EMBL:AY045609 EMBL:AY059167 EMBL:AY090334 EMBL:AK317281 EMBL:AK317596 EMBL:AK222158 IPI:IPI00533962 PIR:T05679 RefSeq:NP_001031807.1 RefSeq:NP_001031808.1 RefSeq:NP_195563.1 RefSeq:NP_974707.1 UniGene:At.48961 UniGene:At.71095 ProteinModelPortal:Q9SZN1 SMR:Q9SZN1 IntAct:Q9SZN1 STRING:Q9SZN1 PRIDE:Q9SZN1 EnsemblPlants:AT4G38510.1 EnsemblPlants:AT4G38510.2 EnsemblPlants:AT4G38510.3 EnsemblPlants:AT4G38510.4 GeneID:830008 KEGG:ath:AT4G38510

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						TAIR:At4g38510 InParanoid:Q9SZN1 OMA:VVFINLA PhylomeDB:Q9SZN1 ArrayExpress:Q9SZN1 Genevestigator:Q9SZN1 Uniprot:Q9SZN1
Leaf	Isotig05840	16	0	5.529	4.31E-06	TAIR|locus:2078302 - symbol:IVD "AT3G45300" species:3702 "Arabidopsis thaliana" [GO:0008470 "isovaleryl-CoA dehydrogenase activity" evidence=ISS;IDA] [GO:0005759 "mitochondrial matrix" evidence=IDA] [GO:0006552 "leucine catabolic process" evidence=IMP;IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0005524 "ATP binding" evidence=IDA] [GO:0009083 "branched chain family amino acid catabolic process" evidence=IMP] InterPro:IPR006089 InterPro:IPR006090 InterPro:IPR006091 InterPro:IPR006092 InterPro:IPR009075 InterPro:IPR009100 InterPro:IPR013786 Pfam:PF00441 Pfam:PF02770 Pfam:PF02771 PROSITE:PS00072 PROSITE:PS00073 GO:GO:0005524 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0050660 GO:GO:0005759 eggNOG:COG1960 Gene3D:G3DSA:2.40.110.10 Gene3D:G3DSA:1.10.540.10 Gene3D:G3DSA:1.20.140.10 SUPFAM:SSF56645 SUPFAM:SSF47203 HOGENOM:HBG699365 GO:GO:0008470 EMBL:AL132953 GO:GO:0006552 EMBL:Y12695 EMBL:AF160729 EMBL:AY062567 EMBL:AY128799 EMBL:AY087286 IPI:IPI00541942 PIR:T47470 RefSeq:NP_190116.1 UniGene:At.428 ProteinModelPortal:Q9SWG0 SMR:Q9SWG0 STRING:Q9SWG0 PRIDE:Q9SWG0 EnsemblPlants:AT3G45300.1 GeneID:823668 KEGG:ath:AT3G45300 GeneFarm:4384 TAIR:At3g45300 InParanoid:Q9SWG0 KO:K00253 OMA:KCGMRAS PhylomeDB:Q9SWG0 ProtClustDB:PLN02519 ArrayExpress:Q9SWG0 Genevestigator:Q9SWG0 GermOnline:AT3G45300 Uniprot:Q9SWG0
Leaf	Isotig05848	29	6	2.802	4.91E-07	TAIR|locus:2201036 - symbol:NTMC2T2.1 "AT1G05500" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0012505 "endomembrane system" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000008 InterPro:IPR008973 Pfam:PF00168 SMART:SM00239 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005886 GO:GO:0009506 GO:GO:0012505 InterPro:IPR018029 SUPFAM:SSF49562 PROSITE:PS50004 eggNOG:COG5038 InterPro:IPR020477 PRINTS:PR00360 HSSP:P04410 ProtClustDB:CLSN2697228 EMBL:AY140038 EMBL:BT008907 EMBL:AK228581 IPI:IPI00548718 RefSeq:NP_172041.2 UniGene:At.27942 ProteinModelPortal:Q8L706 SMR:Q8L706 PRIDE:Q8L706 EnsemblPlants:AT1G05500.1 GeneID:837052 KEGG:ath:AT1G05500 TAIR:At1g05500 HOGENOM:HBG320331 InParanoid:Q8L706 PhylomeDB:Q8L706 ArrayExpress:Q8L706 Genevestigator:Q8L706 Uniprot:Q8L706
Leaf	Isotig05852	13	0	5.229	3.68E-05	TAIR|locus:2054346 - symbol:AT2G41790 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004222 "metalloendopeptidase activity" evidence=IEA;ISS] [GO:0005575 "cellular_component" evidence=ND] [GO:0006508 "proteolysis" evidence=IEA;ISS] [GO:0008270 "zinc ion binding" evidence=IEA] [GO:0046872 "metal ion binding" evidence=IEA] InterPro:IPR001431 InterPro:IPR007863 InterPro:IPR011237 InterPro:IPR011249 InterPro:IPR011765 Pfam:PF00675 Pfam:PF05193 PROSITE:PS00143 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0005777 GO:GO:0008270 GO:GO:0006508 EMBL:AC002339 GO:GO:0004222 eggNOG:COG1025 Gene3D:G3DSA:3.30.830.10 SUPFAM:SSF63411 KO:K01408 HOGENOM:HBG328356 OMA:IYYLALL EMBL:AK226643 IPI:IPI00537903 PIR:B84846 RefSeq:NP_181710.1 UniGene:At.28081 ProteinModelPortal:O22941 SMR:O22941 IntAct:O22941 MEROPS:M16.A02 PRIDE:O22941 EnsemblPlants:AT2G41790.1 GeneID:818778 KEGG:ath:AT2G41790 TAIR:At2g41790 InParanoid:O22941 PhylomeDB:O22941 ProtClustDB:CLSN2913246 ArrayExpress:O22941 Genevestigator:O22941 Uniprot:O22941
Leaf	Isotig05857	18	6	2.114	0.000756754	TAIR|locus:2148368 - symbol:ORP3C "AT5G59420" species:3702 "Arabidopsis thaliana" [GO:0008142 "oxysterol binding" evidence=ISS] [GO:0008202 "steroid metabolic process" evidence=IEA;ISS] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR000648 INTERPRO:IPR018494 GO:GO:0005829 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0006869 EMBL:AB025604 GO:GO:0008289 PANTHER:PTHR10972 Pfam:PF01237 PROSITE:PS01013 eggNOG:NOG281324 HOGENOM:HBG412870 ProtClustDB:CLSN2685127 EMBL:AY054473 EMBL:BT000115 IPI:IPI00523641 RefSeq:NP_200750.1 UniGene:At.24458 ProteinModelPortal:Q93Y40 STRING:Q93Y40 PRIDE:Q93Y40 DNASU:836061 EnsemblPlants:AT5G59420.1 GeneID:836061 KEGG:ath:AT5G59420 TAIR:At5g59420 InParanoid:Q93Y40 OMA:ERDSYWK PhylomeDB:Q93Y40 Genevestigator:Q93Y40 Uniprot:Q93Y40
Leaf	Isotig05858	19	4	2.777	5.07E-05	TAIR|locus:2059247 - symbol:EIL1 "AT2G27050" species:3702 "Arabidopsis thaliana" [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS;TAS] [GO:0009723 "response to ethylene stimulus" evidence=IMP] [GO:0009873 "ethylene mediated signaling pathway" evidence=TAS] [GO:0042742 "defense response to bacterium" evidence=IGI] [GO:0071281 "cellular response to iron ion" evidence=IEP] InterPro:IPR006957 InterPro:IPR023278 Pfam:PF04873 GO:GO:0005634 GO:GO:0042742 EMBL:CP002685

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GenomeReviews:CT485783_GR GO:GO:0071281 GO:GO:0009873 GO:GO:0003677 GO:GO:0003700 GO:GO:0006351 EMBL:AC005623 EMBL:AF004213 EMBL:AY065191 EMBL:BT003344 IPI:IPI00524389 PIR:B84668 RefSeq:NP_180273.1 UniGene:At.10809 ProteinModelPortal:Q9SLH0 SMR:Q9SLH0 IntAct:Q9SLH0 STRING:Q9SLH0 EnsemblPlants:AT2G27050.1 GeneID:817247 KEGG:ath:AT2G27050 GeneFarm:2366 TAIR:At2g27050 eggNOG:NOG331197 HOGENOM:HBG594100 InParanoid:Q9SLH0 KO:K14514 OMA:INDCSEY PhylomeDB:Q9SLH0 ProtClustDB:CLSN2913078 ArrayExpress:Q9SLH0 Genevestigator:Q9SLH0 GermOnline:AT2G27050 Gene3D:G3DSA:1.10.3180.10 SUPFAM:SSF116768 Uniprot:Q9SLH0
Leaf	Isotig05869	1	16	-3.471	0.000601166	TAIR|locus:2007412 - symbol:AT1G07200 "AT1G07200" species:3702 "Arabidopsis thaliana" [GO:0005524 "ATP binding" evidence=ISS] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0016787 EMBL:AC067971 InterPro:IPR023150 Gene3D:G3DSA:1.10.1780.10 HOGENOM:HBG589559 ProtClustDB:CLSN2688559 IPI:IPI00542322 PIR:B86207 RefSeq:NP_001077474.1 UniGene:At.27670 ProteinModelPortal:Q9LML2 PRIDE:Q9LML2 EnsemblPlants:AT1G07200.2 GeneID:837231 KEGG:ath:AT1G07200 TAIR:At1g07200 PhylomeDB:Q9LML2 Genevestigator:Q9LML2 Uniprot:Q9LML2
Leaf	Isotig05885	5	29	-2.007	0.000576639	ZFIN|ZDB-GENE-090610-2 - symbol:zgc:172109 "zgc:172109" species:7955 "Danio rerio" [GO:0005575 "cellular_component" evidence=ND] [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] ZFIN:ZDB-GENE-090610-2 InterPro:IPR023307 Gene3D:G3DSA:2.170.15.10 eggNOG:NOG296306 GeneTree:ENSGT00390000003194 HOGENOM:HBG446882 HOVERGEN:HBG104923 OrthoDB:EOG4HQDKV EMBL:CR759816 EMBL:CT573481 EMBL:CU019647 EMBL:BC154534 IPI:IPI00877422 RefSeq:NP_001103876.1 UniGene:Dr.115589 ProteinModelPortal:A8WG08 Ensembl:ENSDART00000090862 GeneID:795922 KEGG:dre:795922 Bgee:A8WG08 Uniprot:A8WG08
Leaf	Isotig05894	10	1	3.851	0.00071293	TAIR|locus:2042689 - symbol:PAP10 "AT2G16430" species:3702 "Arabidopsis thaliana" [GO:0004722 "protein serine/threonine phosphatase activity" evidence=ISS] [GO:0008150 "biological_process" evidence=ND] [GO:0003993 "acid phosphatase activity" evidence=ISS] [GO:0005618 "cell wall" evidence=IDA] [GO:0009505 "plant-type cell wall" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR004843 InterPro:IPR008963 InterPro:IPR015914 Pfam:PF00149 GO:GO:0005829 GO:GO:0009506 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0005576 GO:GO:0046872 GO:GO:0009505 GO:GO:0003993 eggNOG:COG1409 EMBL:AC007047 Gene3D:G3DSA:2.60.40.380 SUPFAM:SSF49363 EMBL:AF492662 EMBL:AY090893 EMBL:AY093236 EMBL:BT008761 IPI:IPI00530753 IPI:IPI00539645 PIR:B84540 RefSeq:NP_179235.1 RefSeq:NP_849960.1 UniGene:At.14307 HSSP:P80366 ProteinModelPortal:Q9SIV9 SMR:Q9SIV9 STRING:Q9SIV9 PRIDE:Q9SIV9 EnsemblPlants:AT2G16430.2 GeneID:816141 KEGG:ath:AT2G16430 TAIR:At2g16430 HOGENOM:HBG316723 InParanoid:Q9SIV9 OMA:QSYDSNI PhylomeDB:Q9SIV9 ProtClustDB:CLSN2913228 ArrayExpress:Q9SIV9 Genevestigator:Q9SIV9 Uniprot:Q9SIV9
Leaf	Isotig05907	57	320	-1.960	2.05E-29	TAIR|locus:2122794 - symbol:LHCB5 "AT4G10340" species:3702 "Arabidopsis thaliana" [GO:0009533 "chloroplast stromal thylakoid" evidence=IDA] [GO:0015979 "photosynthesis" evidence=ISS;IMP] [GO:0016168 "chlorophyll binding" evidence=ISS] [GO:0030076 "light-harvesting complex" evidence=ISS] [GO:0009783 "photosystem II antenna complex" evidence=IMP] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0010196 "nonphotochemical quenching" evidence=IMP] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009637 "response to blue light" evidence=IEP] [GO:0010114 "response to red light" evidence=IEP] [GO:0010218 "response to far red light" evidence=IEP] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0009517 "PSII associated light-harvesting complex II" evidence=IDA] InterPro:IPR001344 Pfam:PF00504 GO:GO:0016021 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0046872 GO:GO:0009637 GO:GO:0010218 GO:GO:0010114 GO:GO:0018298 GO:GO:0010287 EMBL:AL049488 EMBL:AL161517 HOGENOM:HBG618504 GO:GO:0009522 GO:GO:0016168 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 EMBL:AF134129 EMBL:AF326900 EMBL:AF339718 EMBL:AF424597 EMBL:AF380631 EMBL:AY054126 EMBL:AY087939 IPI:IPI00535216 PIR:T04049 RefSeq:NP_192772.1 UniGene:At.23060 ProteinModelPortal:Q9XF89 SMR:Q9XF89 DIP:DIP-59004N STRING:Q9XF89 PRIDE:Q9XF89 EnsemblPlants:AT4G10340.1 GeneID:826626 KEGG:ath:AT4G10340 TAIR:At4g10340 eggNOG:NOG321165 InParanoid:Q9XF89 KO:K08916 OMA:EGPVENL PhylomeDB:Q9XF89

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						ProtClustDB:CLSN2685679 ArrayExpress:Q9XF89 Genevestigator:Q9XF89 GermOnline:AT4G10340 GO:GO:0009783 GO:GO:0009517 GO:GO:0010196 Uniprot:Q9XF89
Leaf	Isotig05913	14	1	4.336	3.39E-05	TAIR|locus:2062754 - symbol:HB-7 "homeobox 7" species:3702 "Arabidopsis thaliana" [GO:0005634 "nucleus" evidence=IEA;ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=ISS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0045893 "positive regulation of transcription, DNA-dependent" evidence=IDA] [GO:0009414 "response to water deprivation" evidence=IEP] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] [GO:0009738 "abscisic acid mediated signaling pathway" evidence=IGI] InterPro:IPR000047 InterPro:IPR001356 InterPro:IPR003106 InterPro:IPR009057 InterPro:IPR017970 Pfam:PF00046 Pfam:PF02183 PRINTS:PR00031 PROSITE:PS00027 PROSITE:PS50071 SMART:SM00389 GO:GO:0005634 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0045893 GO:GO:0009738 GO:GO:0003700 GO:GO:0006351 GO:GO:0009414 Gene3D:G3DSA:1.10.10.60 SUPFAM:SSF46689 GO:GO:0000976 eggNOG:NOG252905 HOGENOM:HBG593038 ProtClustDB:CLSN2683559 EMBL:X67032 EMBL:AC005819 EMBL:AY045826 EMBL:AY091364 IPI:IPI00544746 PIR:H84905 PIR:S47137 RefSeq:NP_182191.1 UniGene:At.136 ProteinModelPortal:P46897 SMR:P46897 STRING:P46897 EnsemblPlants:AT2G46680.1 GeneID:819280 KEGG:ath:AT2G46680 GeneFarm:3966 TAIR:At2g46680 InParanoid:P46897 OMA:ALVIQLQ PhylomeDB:P46897 ArrayExpress:P46897 Genevestigator:P46897 Uniprot:P46897
Leaf	Isotig05923	27	1	5.284	2.63E-09	TAIR|locus:2100449 - symbol:ALDH10A9 "AT3G48170" species:3702 "Arabidopsis thaliana" [GO:0004028 "3-chloroallyl aldehyde dehydrogenase activity" evidence=ISS] [GO:0005777 "peroxisome" evidence=IDA] [GO:0004029 "aldehyde dehydrogenase (NAD) activity" evidence=IDA] [GO:0008802 "betaine-aldehyde dehydrogenase activity" evidence=IDA] [GO:0009414 "response to water deprivation" evidence=IEP] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] [GO:0055114 "oxidation-reduction process" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] InterPro:IPR015590 InterPro:IPR016160 InterPro:IPR016161 InterPro:IPR016162 InterPro:IPR016163 Pfam:PF00171 PROSITE:PS00070 PROSITE:PS00687 GO:GO:0005739 GO:GO:0009737 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005777 eggNOG:COG1012 Gene3D:G3DSA:3.40.309.10 Gene3D:G3DSA:3.40.605.10 SUPFAM:SSF53720 HOGENOM:HBG752218 GO:GO:0009414 HSSP:P05091 GO:GO:0008802 EMBL:AL096856 KO:K00130 ProtClustDB:PLN02467 EMBL:AF370333 EMBL:AY062987 EMBL:Z29888 IPI:IPI00545825 PIR:T13006 RefSeq:NP_190400.1 UniGene:At.1613 ProteinModelPortal:Q9STS1 SMR:Q9STS1 STRING:Q9STS1 PRIDE:Q9STS1 EnsemblPlants:AT3G48170.1 GeneID:823972 KEGG:ath:AT3G48170 TAIR:At3g48170 InParanoid:Q9STS1 OMA:MEIWREE PhylomeDB:Q9STS1 BioCyc:MetaCyc:AT3G48170-MONOMER ArrayExpress:Q9STS1 Genevestigator:Q9STS1 GermOnline:AT3G48170 Uniprot:Q9STS1
Leaf	Isotig05924	1499	1702	0.346	7.54E-12	UNIPROTKB|Q95F11 - symbol:rbcL "Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit" species:123678 "Fendlerella utahensis" [GO:0016021 "integral to membrane" evidence=NAS] [GO:0016339 "calcium-dependent cell-cell adhesion" evidence=NAS] HAMAP:MF_01338 InterPro:IPR000685 InterPro:IPR017443 InterPro:IPR017444 InterPro:IPR020878 InterPro:IPR020888 Pfam:PF00016 Pfam:PF02788 PROSITE:PS00157 GO:GO:0016021 GO:GO:0009507 GO:GO:0000287 GO:GO:0016339 GO:GO:0015979 GO:GO:0015977 GO:GO:0016984 Gene3D:G3DSA:3.20.20.110 SUPFAM:SSF51649 Gene3D:G3DSA:3.30.70.150 SUPFAM:SSF54966 EMBL:AF323198 HSSP:P00875 ProteinModelPortal:Q95F11 Uniprot:Q95F11
Leaf	Isotig05928	2	72	-4.641	1.93E-15	TAIR|locus:2150059 - symbol:SQD2 "AT5G01220" species:3702 "Arabidopsis thaliana" [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0008194 "UDP-glycosyltransferase activity" evidence=IDA] [GO:0009247 "glycolipid biosynthetic process" evidence=IDA] [GO:0016036 "cellular response to phosphate starvation" evidence=IMP] [GO:0046506 "sulfolipid biosynthetic process" evidence=TAS] [GO:0046510 "UDP-sulfoquinovose:DAG sulfoquinovosyltransferase activity" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] InterPro:IPR001296 Pfam:PF00534 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009247 GO:GO:0009941 eggNOG:COG0438 CAZy:GT4 HOGENOM:HBG726846 GO:GO:0008194 EMBL:AF454354 EMBL:BT005796 IPI:IPI00548055 RefSeq:NP_568085.2 UniGene:At.47995 ProteinModelPortal:Q8S4F6 STRING:Q8S4F6 PRIDE:Q8S4F6 EnsemblPlants:AT5G01220.1 GeneID:831888 KEGG:ath:AT5G01220 TAIR:At5g01220 InParanoid:Q8S4F6 KO:K06119 OMA:LCTSTAM PhylomeDB:Q8S4F6 ProtClustDB:PLN02871 Genevestigator:Q8S4F6 Uniprot:Q8S4F6
Leaf	Isotig05929	15	2	3.436	7.06E-05	TAIR|locus:2156794 - symbol:AT5G05180 "AT5G05180" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] EMBL:CP002688 EMBL:AB018111 IPI:IPI00547028 RefSeq:NP_196137.1

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						UniGene:At.33024 ProteinModelPortal:Q9FHK5 PRIDE:Q9FHK5 EnsemblPlants:AT5G05180.1 GeneID:830400 KEGG:ath:AT5G05180 TAIR:At5g05180 OMA:DMLMAEK PhylomeDB:Q9FHK5 ProtClustDB:CLSN2686471 Genevestigator:Q9FHK5 Uniprot:Q9FHK5
Leaf	Isotig05941	15	2	3.436	7.06E-05	TAIR|locus:2181047 - symbol:CIPK15 "AT5G01810" species:3702 "Arabidopsis thaliana" [GO:0016301 "kinase activity" evidence=ISS] [GO:0004672 "protein kinase activity" evidence=ISS;TAS] [GO:0009738 "abscisic acid mediated signaling pathway" evidence=TAS] [GO:0009788 "negative regulation of abscisic acid mediated signaling pathway" evidence=IMP] InterPro:IPR000719 InterPro:IPR002290 InterPro:IPR004041 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 InterPro:IPR018451 Pfam:PF00069 Pfam:PF03822 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 PROSITE:PS50816 SMART:SM00220 GO:GO:0005524 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009738 eggNOG:COG0515 SUPFAM:SSF56112 GO:GO:0004674 HOGENOM:HBG755340 GO:GO:0009788 EMBL:AL162351 EMBL:D30622 EMBL:AF302111 EMBL:AF339144 EMBL:AK228889 EMBL:BT028964 IPI:IPI00543368 PIR:T48202 RefSeq:NP_001031820.1 RefSeq:NP_195801.1 UniGene:At.20284 ProteinModelPortal:P92937 SMR:P92937 IntAct:P92937 STRING:P92937 PRIDE:P92937 EnsemblPlants:AT5G01810.1 EnsemblPlants:AT5G01810.2 GeneID:830556 KEGG:ath:AT5G01810 TAIR:At5g01810 InParanoid:P92937 OMA:REASEIT PhylomeDB:P92937 ProtClustDB:CLSN2687142 ArrayExpress:P92937 Genevestigator:P92937 GermOnline:AT5G01810 Uniprot:P92937
Leaf	Isotig05945	54	22	1.824	1.20E-07	TAIR|locus:2090614 - symbol:AT3G19390 species:3702 "Arabidopsis thaliana" [GO:0004197 "cysteine-type endopeptidase activity" evidence=IEA] [GO:0006508 "proteolysis" evidence=IEA] [GO:0008234 "cysteine-type peptidase activity" evidence=IEA;ISS] InterPro:IPR000668 InterPro:IPR013128 Pfam:PF00112 PRINTS:PR00705 SMART:SM00645 InterPro:IPR000169 EMBL:CP002686 GenomeReviews:BA000014_GR eggNOG:COG4870 HOGENOM:HBG746690 GO:GO:0004197 GO:GO:0006508 InterPro:IPR013201 PANTHER:PTHR12411 Pfam:PF08246 SMART:SM00848 PROSITE:PS00640 PROSITE:PS00139 PROSITE:PS00639 EMBL:AB025624 HSSP:O65039 MEROPS:C01.029 InterPro:IPR000118 Pfam:PF00396 SMART:SM00277 EMBL:AY062725 EMBL:AY093350 IPI:IPI00520189 RefSeq:NP_566633.1 UniGene:At.27473 ProteinModelPortal:Q9LT78 SMR:Q9LT78 IntAct:Q9LT78 STRING:Q9LT78 PRIDE:Q9LT78 EnsemblPlants:AT3G19390.1 GeneID:821473 KEGG:ath:AT3G19390 TAIR:At3g19390 InParanoid:Q9LT78 OMA:RSKMERT PhylomeDB:Q9LT78 ProtClustDB:CLSN2917188 Genevestigator:Q9LT78 Uniprot:Q9LT78
Leaf	Isotig05952	23	4	3.053	2.98E-06	TAIR|locus:2137015 - symbol:HMGS "AT4G11820" species:3702 "Arabidopsis thaliana" [GO:0019287 "isopentenyl diphosphate biosynthetic process, mevalonate pathway" evidence=TAS] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0003985 "acetyl-CoA C-acetyltransferase activity" evidence=IGI] [GO:0004421 "hydroxymethylglutaryl-CoA synthase activity" evidence=IGI;ISS] InterPro:IPR000590 InterPro:IPR010122 InterPro:IPR013528 InterPro:IPR013746 InterPro:IPR016038 InterPro:IPR016039 Pfam:PF01154 Pfam:PF08540 PROSITE:PS01226 GO:GO:0005829 GO:GO:0009506 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0016126 EMBL:AL078606 EMBL:AL161532 Gene3D:G3DSA:3.40.47.10 SUPFAM:SSF53901 GO:GO:0019287 eggNOG:COG3425 HOGENOM:HBG578402 KO:K01641 BRENDA:2.3.3.10 GO:GO:0004421 TIGRFAMs:TIGR01833 OMA:DTVNACY EMBL:X83882 EMBL:U79160 EMBL:U79161 EMBL:AY140008 EMBL:BT008492 IPI:IPI00530283 IPI:IPI00533922 PIR:T09341 RefSeq:NP_192919.1 RefSeq:NP_849361.1 UniGene:At.5362 ProteinModelPortal:P54873 SMR:P54873 STRING:P54873 PRIDE:P54873 EnsemblPlants:AT4G11820.2 GeneID:826788 KEGG:ath:AT4G11820 TAIR:At4g11820 InParanoid:P54873 PhylomeDB:P54873 ProtClustDB:PLN02577 BioCyc:ARA:AT4G11820-MONOMER BioCyc:MetaCyc:AT4G11820-MONOMER ArrayExpress:P54873 Genevestigator:P54873 GermOnline:AT4G11820 Uniprot:P54873
Leaf	Isotig05963	1	33	-4.515	8.84E-08	TAIR|locus:2150059 - symbol:SQD2 "AT5G01220" species:3702 "Arabidopsis thaliana" [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0008194 "UDP-glycosyltransferase activity" evidence=IDA] [GO:0009247 "glycolipid biosynthetic process" evidence=IDA] [GO:0016036 "cellular response to phosphate starvation" evidence=IMP] [GO:0046506 "sulfolipid biosynthetic process" evidence=TAS] [GO:0046510 "UDP-sulfoquinovose:DAG sulfoquinovosyltransferase activity" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] InterPro:IPR001296 Pfam:PF00534 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009247 GO:GO:0009941 eggNOG:COG0438 CAZy:GT4 HOGENOM:HBG726846 GO:GO:0008194 EMBL:AF454354 EMBL:BT005796 IPI:IPI00548055 RefSeq:NP_568085.2 UniGene:At.47995 ProteinModelPortal:Q8S4F6 STRING:Q8S4F6 PRIDE:Q8S4F6 EnsemblPlants:AT5G01220.1 GeneID:831888 KEGG:ath:AT5G01220 TAIR:At5g01220 InParanoid:Q8S4F6 KO:K06119 OMA:LCTSTAM PhylomeDB:Q8S4F6 ProtClustDB:PLN02871 Genevestigator:Q8S4F6 Uniprot:Q8S4F6

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig05969	15	3	2.851	0.000262808	TAIR|locus:2096049 - symbol:AT3G62360 species:3702 "Arabidopsis thaliana" [GO:0030246 "carbohydrate binding" evidence=IEA] [GO:0009505 "plant-type cell wall" evidence=IDA] [GO:0005783 "endoplasmic reticulum" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] GO:GO:0005783 GO:GO:0005774 EMBL:CP002686 InterPro:IPR013783 Gene3D:G3DSA:2.60.40.10 GO:GO:0009505 InterPro:IPR008970 SUPFAM:SSF49478 EMBL:AL162507 OMA:NGYYFIP IPI:IPI00518326 PIR:T48028 RefSeq:NP_191795.1 UniGene:At.27742 ProteinModelPortal:Q9LZQ4 SMR:Q9LZQ4 STRING:Q9LZQ4 PRIDE:Q9LZQ4 EnsemblPlants:AT3G62360.1 GeneID:825409 KEGG:ath:AT3G62360 TAIR:At3g62360 InParanoid:Q9LZQ4 PhylomeDB:Q9LZQ4 ProtClustDB:CLSN2684130 Genevestigator:Q9LZQ4 Uniprot:Q9LZQ4
Leaf	Isotig05976	27	2	4.284	9.49E-09	TAIR|locus:2124102 - symbol:MRH1 "morphogenesis of root hair 1" species:3702 "Arabidopsis thaliana" [GO:0004672 "protein kinase activity" evidence=IEA] [GO:0004674 "protein serine/threonine kinase activity" evidence=ISS] [GO:0005524 "ATP binding" evidence=IEA;ISS] [GO:0006468 "protein phosphorylation" evidence=ISS] [GO:0007169 "transmembrane receptor protein tyrosine kinase signaling pathway" evidence=ISS] [GO:0048765 "root hair cell differentiation" evidence=IMP] InterPro:IPR000719 InterPro:IPR001245 InterPro:IPR011009 Pfam:PF07714 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 GO:GO:0016021 GO:GO:0005524 EMBL:CP002687 GenomeReviews:CT486007_GR EMBL:AL161549 GO:GO:0004872 SUPFAM:SSF56112 GO:GO:0004674 GO:GO:0048765 InterPro:IPR013210 Pfam:PF08263 EMBL:AL035526 EMBL:FJ708745 IPI:IPI00526838 PIR:T04856 RefSeq:NP_193599.3 UniGene:At.32880 ProteinModelPortal:C0LGQ4 SMR:C0LGQ4 STRING:C0LGQ4 PRIDE:C0LGQ4 EnsemblPlants:AT4G18640.1 GeneID:827598 KEGG:ath:AT4G18640 GeneFarm:2334 TAIR:At4g18640 eggNOG:NOG271462 HOGENOM:HBG749254 InParanoid:Q9M0L9 PhylomeDB:C0LGQ4 ProtClustDB:CLSN2719097 ArrayExpress:Q9M0L9 Uniprot:C0LGQ4
Leaf	Isotig05982	6	45	-2.378	1.90E-06	TAIR|locus:2040934 - symbol:LHB1B2 "AT2G34420" species:3702 "Arabidopsis thaliana" [GO:0009769 "photosynthesis, light harvesting in photosystem II" evidence=TAS] [GO:0016168 "chlorophyll binding" evidence=ISS;TAS] [GO:0030076 "light-harvesting complex" evidence=ISS] [GO:0042651 "thylakoid membrane" evidence=TAS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0015979 "photosynthesis" evidence=ISS] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR001344 Pfam:PF00504 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009535 GO:GO:0010287 EMBL:AC004077 EMBL:AC004481 HOGENOM:HBG618504 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 UniGene:At.10812 UniGene:At.24351 UniGene:At.32199 UniGene:At.66422 UniGene:At.71449 UniGene:At.71528 KO:K08912 ProtClustDB:PLN00025 UniGene:At.23647 UniGene:At.27457 UniGene:At.24888 EMBL:AF372886 EMBL:AY039561 EMBL:AY045806 EMBL:AF428397 EMBL:AF419548 EMBL:AF419587 EMBL:AY065125 EMBL:AY079101 EMBL:AY079110 EMBL:AY081587 EMBL:AY142513 EMBL:AK229627 EMBL:X64460 IPI:IPI00530785 PIR:S23546 RefSeq:NP_565786.1 UniGene:At.24064 UniGene:At.71003 UniGene:At.71384 ProteinModelPortal:Q39141 SMR:Q39141 IntAct:Q39141 STRING:Q39141 PRIDE:Q39141 EnsemblPlants:AT2G34420.1 GeneID:818005 KEGG:ath:AT2G34420 TAIR:At2g34420 InParanoid:Q39141 OMA:SILAIWG PhylomeDB:Q39141 ArrayExpress:Q39141 Genevestigator:Q39141 Uniprot:Q39141
Leaf	Isotig05983	9	0	4.699	0.000718283	TAIR|locus:2135237 - symbol:AGT2 "AT4G39660" species:3702 "Arabidopsis thaliana" [GO:0008453 "alanine-glyoxylate transaminase activity" evidence=ISS;IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0019544 "arginine catabolic process to glutamate" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0008270 "zinc ion binding" evidence=IDA] InterPro:IPR005814 InterPro:IPR015421 InterPro:IPR015422 Pfam:PF00202 PROSITE:PS00600 GO:GO:0005739 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0046686 GO:GO:0005774 GO:GO:0030170 InterPro:IPR015424 Gene3D:G3DSA:3.40.640.10 Gene3D:G3DSA:3.90.1150.10 SUPFAM:SSF53383 GO:GO:0008270 EMBL:AF166351 EMBL:AL022605 EMBL:AL161595 EMBL:AY054264 EMBL:BT002306 IPI:IPI00519673 PIR:T05003 RefSeq:NP_568064.1 UniGene:At.22488 ProteinModelPortal:Q940M2 SMR:Q940M2 STRING:Q940M2 PRIDE:Q940M2 EnsemblPlants:AT4G39660.1 GeneID:830120 KEGG:ath:AT4G39660 GeneFarm:5077 TAIR:At4g39660 eggNOG:COG0160 HOGENOM:HBG725944 InParanoid:Q940M2 KO:K00827 OMA:GIVTVSC PhylomeDB:Q940M2

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						ProtClustDB:CLSN2683116 ArrayExpress:Q9SU41 Genevestigator:Q940M2 GermOnline:AT4G39660 GO:GO:0008453 GO:GO:0019544 GO:GO:0009853 PANTHER:PTHR11986 Uniprot:Q940M2
Leaf	Isotig06000	39	8	2.814	5.03E-09	TAIR|locus:2044641 - symbol:COR413-PM1 "AT2G15970" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005886 "plasma membrane" evidence=ISS] [GO:0009631 "cold acclimation" evidence=IEP] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] [GO:0042631 "cellular response to water deprivation" evidence=IEP] [GO:0005773 "vacuole" evidence=IDA] GO:GO:0009737 GO:GO:0005773 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0042631 GO:GO:0009631 EMBL:AC006438 UniGene:At.22305 HOGENOM:HBG595418 ProtClustDB:CLSN2717102 InterPro:IPR008892 Pfam:PF05562 eggNOG:NOG267474 EMBL:AF283004 EMBL:AY093767 EMBL:AY088558 EMBL:AY143813 EMBL:AB044404 IPI:IPI00547690 PIR:C84535 RefSeq:NP_179196.1 UniGene:At.24347 STRING:Q9XIM7 PRIDE:Q9XIM7 EnsemblPlants:AT2G15970.1 GeneID:816092 KEGG:ath:AT2G15970 TAIR:At2g15970 InParanoid:Q9XIM7 OMA:GTTFLEW PhylomeDB:Q9XIM7 ArrayExpress:Q9XIM7 Genevestigator:Q9XIM7 Uniprot:Q9XIM7
Leaf	Isotig06017	24	3	3.529	3.76E-07	TAIR|locus:2169985 - symbol:NFS1 "AT5G65720" species:3702 "Arabidopsis thaliana" [GO:0008483 "transaminase activity" evidence=ISS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0031071 "cysteine desulfurase activity" evidence=IDA] [GO:0005524 "ATP binding" evidence=IDA] [GO:0016226 "iron-sulfur cluster assembly" evidence=IDA] [GO:0008270 "zinc ion binding" evidence=IDA] InterPro:IPR000192 InterPro:IPR010240 InterPro:IPR015421 InterPro:IPR015422 Pfam:PF00266 GO:GO:0005739 GO:GO:0005524 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0030170 InterPro:IPR015424 Gene3D:G3DSA:3.40.640.10 Gene3D:G3DSA:3.90.1150.10 SUPFAM:SSF53383 EMBL:AB010075 EMBL:AL021684 GO:GO:0008270 GO:GO:0016226 HOGENOM:HBG635316 GO:GO:0031071 GO:GO:0006534 eggNOG:COG1104 KO:K04487 OMA:CIHHVKR InterPro:IPR016454 PIRSF:PIRSF005572 TIGRFAMs:TIGR02006 EMBL:AJ243393 EMBL:AF229854 EMBL:AY050874 EMBL:AY096358 IPI:IPI00545655 PIR:T05896 RefSeq:NP_201373.1 UniGene:At.696 ProteinModelPortal:O49543 SMR:O49543 STRING:O49543 PRIDE:O49543 EnsemblPlants:AT5G65720.1 GeneID:836701 KEGG:ath:AT5G65720 TAIR:At5g65720 InParanoid:O49543 PhylomeDB:O49543 ProtClustDB:PLN02651 BRENDA:2.8.1.6 ArrayExpress:O49543 Genevestigator:O49543 GermOnline:AT5G65720 Uniprot:O49543
Leaf	Isotig06019	20	0	5.851	2.71E-07	TAIR|locus:2127510 - symbol:TPPG "trehalose-6-phosphate phosphatase G" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004805 "trehalose-phosphatase activity" evidence=ISS] [GO:0005992 "trehalose biosynthetic process" evidence=IEA;ISS] [GO:0008152 "metabolic process" evidence=IEA] InterPro:IPR003337 InterPro:IPR006379 Pfam:PF02358 EMBL:CP002687 GenomeReviews:CT486007_GR InterPro:IPR023214 Gene3D:G3DSA:3.40.50.1000 SUPFAM:SSF56784 GO:GO:0016787 EMBL:AL161557 EMBL:AL033545 GO:GO:0005992 TIGRFAMs:TIGR01484 eggNOG:COG1877 HOGENOM:HBG686849 TIGRFAMs:TIGR00685 ProtClustDB:PLN02580 EMBL:AK221933 EMBL:AK316702 IPI:IPI00544426 PIR:T05453 RefSeq:NP_193990.1 UniGene:At.2505 ProteinModelPortal:Q9SUW0 SMR:Q9SUW0 PRIDE:Q9SUW0 EnsemblPlants:AT4G22590.1 GeneID:828355 KEGG:ath:AT4G22590 TAIR:At4g22590 InParanoid:Q9SUW0 OMA:NIEIAPE PhylomeDB:Q9SUW0 ArrayExpress:Q9SUW0 Genevestigator:Q9SUW0 Uniprot:Q9SUW0
Leaf	Isotig06023	10	1	3.851	0.00071293	TAIR|locus:2017552 - symbol:UBP6 "AT1G51710" species:3702 "Arabidopsis thaliana" [GO:0004843 "ubiquitin-specific protease activity" evidence=IGI;ISS] [GO:0005516 "calmodulin binding" evidence=IDA] [GO:0016579 "protein deubiquitination" evidence=TAS] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000626 InterPro:IPR001394 InterPro:IPR018200 Pfam:PF00240 Pfam:PF00443 PROSITE:PS00972 PROSITE:PS00973 PROSITE:PS50235 SMART:SM00213 Prosite:PS00299 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009506 EMBL:AC025294 GO:GO:0005516 GO:GO:0006511 InterPro:IPR019955 PROSITE:PS50053 GO:GO:0004843 GO:GO:0016579 InterPro:IPR019954 GO:GO:0004221 HSSP:P54578 eggNOG:NOG286607 KO:K11843 HOGENOM:HBG524155 EMBL:AF302660 EMBL:AY050817 EMBL:AY114081 EMBL:BT000658 EMBL:AY084730 EMBL:AK221019 IPI:IPI00519355 PIR:A96556 RefSeq:NP_564596.1 UniGene:At.16941 ProteinModelPortal:Q949Y0 SMR:Q949Y0 MINT:MINT-1351065 STRING:Q949Y0 MEROPS:C19.094 PRIDE:Q949Y0 DNASU:841596 EnsemblPlants:AT1G51710.1 GeneID:841596 KEGG:ath:AT1G51710 TAIR:At1g51710 InParanoid:Q949Y0 OMA:TVQCLKS PhylomeDB:Q949Y0 ProtClustDB:CLSN2688687 ArrayExpress:Q949Y0 Genevestigator:Q949Y0 Uniprot:Q949Y0
Leaf	Isotig06024	11	0	4.988	0.000159591	TAIR|locus:2160170 - symbol:PDC2 "pyruvate decarboxylase-2" species:3702 "Arabidopsis thaliana" [GO:0000287 "magnesium ion binding" evidence=IEA] [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004737 "pyruvate

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						decarboxylase activity" evidence=ISS] [GO:0016831 "carboxy-lyase activity" evidence=IEA] [GO:0030976 "thiamine pyrophosphate binding" evidence=IEA] [GO:0001666 "response to hypoxia" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR011766 InterPro:IPR012000 InterPro:IPR012001 InterPro:IPR012110 Pfam:PF00205 Pfam:PF02775 Pfam:PF02776 PIRSF:PIRSF036565 GO:GO:0005829 EMBL:CP002688 GO:GO:0000287 GO:GO:0001666 GO:GO:0030976 PANTHER:PTHR18968:SF4 EMBL:AB005232 GO:GO:0016831 HSSP:P06169 KO:K01568 OMA:FIEVIAH ProtClustDB:PLN02573 IPI:IPI00516480 RefSeq:NP_200307.1 UniGene:At.47515 UniGene:At.71484 ProteinModelPortal:Q9FFT4 SMR:Q9FFT4 STRING:Q9FFT4 PRIDE:Q9FFT4 EnsemblPlants:AT5G54960.1 GeneID:835587 KEGG:ath:AT5G54960 TAIR:At5g54960 InParanoid:Q9FFT4 PhylomeDB:Q9FFT4 Genevestigator:Q9FFT4 Uniprot:Q9FFT4
Leaf	Isotig06025	35	10	2.336	5.90E-07	TAIR|locus:2125657 - symbol:VTE1 "AT4G32770" species:3702 "Arabidopsis thaliana" [GO:0009507 "chloroplast" evidence=ISS;IDA] [GO:0009706 "chloroplast inner membrane" evidence=TAS] [GO:0009976 "tocopherol cyclase activity" evidence=IMP;IDA] [GO:0010189 "vitamin E biosynthetic process" evidence=IDA] [GO:0006979 "response to oxidative stress" evidence=IEP] [GO:0009644 "response to high light intensity" evidence=IEP] [GO:0006631 "fatty acid metabolic process" evidence=IGI] [GO:0015994 "chlorophyll metabolic process" evidence=IGI] [GO:0016122 "xanthophyll metabolic process" evidence=IMP] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0009266 "response to temperature stimulus" evidence=IMP] [GO:0009915 "phloem sucrose loading" evidence=IMP] [GO:0031347 "regulation of defense response" evidence=IMP] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0006979 GO:GO:0006631 GO:GO:0009706 GO:GO:0009644 EMBL:AL022537 GO:GO:0009534 GO:GO:0010287 GO:GO:0009266 EMBL:AL161582 GO:GO:0009915 GO:GO:0031347 GO:GO:0010189 GO:GO:0015994 EMBL:AF302188 IPI:IPI00540321 RefSeq:NP_567906.1 UniGene:At.22259 STRING:Q94FY7 PRIDE:Q94FY7 EnsemblPlants:AT4G32770.1 GeneID:829413 KEGG:ath:AT4G32770 TAIR:At4g32770 eggNOG:NOG05806 HOGENOM:HBG284910 InParanoid:Q94FY7 KO:K09834 OMA:FFEGWYY PhylomeDB:Q94FY7 ProtClustDB:PLN02818 ArrayExpress:Q94FY7 Genevestigator:Q94FY7 GermOnline:AT4G32770 GO:GO:0009976 GO:GO:0016122 Uniprot:Q94FY7
Leaf	Isotig06036	12	0	5.114	7.63E-05	TAIR|locus:2156652 - symbol:LTI65 "AT5G52300" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0009738 "abscisic acid mediated signaling pathway" evidence=IEP] [GO:0009414 "response to water deprivation" evidence=IEP] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] [GO:0010150 "leaf senescence" evidence=IMP] [GO:0009409 "response to cold" evidence=IEP] EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009738 GO:GO:0010150 GO:GO:0009409 GO:GO:0009651 GO:GO:0009414 EMBL:AB019226 EMBL:X67670 EMBL:D13044 EMBL:AY081282 EMBL:AY128731 EMBL:Z34014 IPI:IPI00526103 PIR:S30153 RefSeq:NP_200043.2 UniGene:At.43012 STRING:Q04980 PRIDE:Q04980 EnsemblPlants:AT5G52300.1 GeneID:835306 KEGG:ath:AT5G52300 TAIR:At5g52300 eggNOG:NOG281420 HOGENOM:HBG027913 InParanoid:Q04980 OMA:APVYESS PhylomeDB:Q04980 ProtClustDB:PLN03021 ArrayExpress:Q04980 Genevestigator:Q04980 InterPro:IPR012418 Pfam:PF07918 Uniprot:Q04980
Leaf	Isotig06038	9	0	4.699	0.000718283	TAIR|locus:2119886 - symbol:AT4G29090 species:3702 "Arabidopsis thaliana" [GO:0003676 "nucleic acid binding" evidence=IEA] [GO:0003723 "RNA binding" evidence=ISS] [GO:0003964 "RNA-directed DNA polymerase activity" evidence=ISS] [GO:0006278 "RNA-dependent DNA replication" evidence=ISS] InterPro:IPR012337 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0003676 SUPFAM:SSF53098 GO:GO:0003964 EMBL:AL078470 EMBL:AL161574 ProtClustDB:CLSN2683532 EMBL:DQ056660 IPI:IPI00548066 PIR:T08964 RefSeq:NP_194638.1 UniGene:At.54541 ProteinModelPortal:Q9SZD8 PRIDE:Q9SZD8 EnsemblPlants:AT4G29090.1 GeneID:829030 KEGG:ath:AT4G29090 TAIR:At4g29090 eggNOG:NOG253635 InParanoid:Q9SZD8 OMA:KESACIR PhylomeDB:Q9SZD8 ArrayExpress:Q9SZD8 Genevestigator:Q9SZD8 Uniprot:Q9SZD8
Leaf	Isotig06039	10	1	3.851	0.00071293	TAIR|locus:2091606 - symbol:ATBFRUCT1 "AT3G13790" species:3702 "Arabidopsis thaliana" [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=ISS] [GO:0004564 "beta-fructofuranosidase activity" evidence=IMP;IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0009611 "response to wounding" evidence=IMP] [GO:0080167 "response to karrikin" evidence=IEP] InterPro:IPR001362 InterPro:IPR018053 PROSITE:PS00609 SMART:SM00640 GO:GO:0048046 GO:GO:0005618 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0009611 GO:GO:0080167 EMBL:AP001307 InterPro:IPR008985

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						SUPFAM:SSF49899 InterPro:IPR023296 Gene3D:G3DSA:2.115.10.20 SUPFAM:SSF75005 EMBL:X74514 EMBL:X74515 EMBL:AY045776 EMBL:AY079422 IPI:IPI00518427 PIR:S37212 RefSeq:NP_001189881.1 RefSeq:NP_566464.1 UniGene:At.24308 PDB:2AC1 PDB:2OXB PDB:2QQU PDB:2QQV PDB:2QQW PDB:2XQR PDBsum:2AC1 PDBsum:2OXB PDBsum:2QQU PDBsum:2QQV PDBsum:2QQW PDBsum:2XQR ProteinModelPortal:Q43866 SMR:Q43866 DIP:DIP-59391N STRING:Q43866 CAZy:GH32 PRIDE:Q43866 EnsemblPlants:AT3G13790.1 GeneID:820591 KEGG:ath:AT3G13790 TAIR:At3g13790 eggNOG:COG1621 HOGENOM:HBG317462 InParanoid:Q43866 KO:K01193 OMA:CIANPPK PhylomeDB:Q43866 ProtClustDB:CLSN2914992 ArrayExpress:Q43866 Genevestigator:Q43866 GO:GO:0004575 InterPro:IPR013189 InterPro:IPR013148 Pfam:PF08244 Pfam:PF00251 Uniprot:Q43866
Leaf	Isotig06049	13	1	4.229	7.21E-05	TAIR|locus:505006580 - symbol:AT5G03555 species:3702 "Arabidopsis thaliana" [GO:0015205 "nucleobase transmembrane transporter activity" evidence=IEA;ISS] [GO:0015931 "nucleobase-containing compound transport" evidence=IEA] [GO:0055085 "transmembrane transport" evidence=IEA] [GO:0016020 "membrane" evidence=ISS] InterPro:IPR001248 Pfam:PF02133 EMBL:CP002688 EMBL:AL162751 GO:GO:0016020 GO:GO:0015205 KO:K03457 OMA:KWHITAL IPI:IPI00522899 PIR:T48383 RefSeq:NP_568122.2 UniGene:At.4879 ProteinModelPortal:Q9LZD0 SMR:Q9LZD0 STRING:Q9LZD0 PRIDE:Q9LZD0 EnsemblPlants:AT5G03555.1 GeneID:831791 KEGG:ath:AT5G03555 TAIR:At5g03555 InParanoid:Q9LZD0 PhylomeDB:Q9LZD0 ProtClustDB:CLSN2681024 Genevestigator:Q9LZD0 Uniprot:Q9LZD0
Leaf	Isotig06063	25	10	1.851	0.000275191	TAIR|locus:2088237 - symbol:EIF4A1 "AT3G13920" species:3702 "Arabidopsis thaliana" [GO:0003743 "translation initiation factor activity" evidence=ISS] [GO:0008026 "ATP-dependent helicase activity" evidence=ISS] [GO:0006413 "translational initiation" evidence=ISS] [GO:0005515 "protein binding" evidence=IPI] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0016020 "membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR000629 InterPro:IPR001650 InterPro:IPR011545 Pfam:PF00270 Pfam:PF00271 PROSITE:PS00039 PROSITE:PS51194 SMART:SM00490 InterPro:IPR014001 GO:GO:0005829 GO:GO:0009506 GO:GO:0005524 GO:GO:0046686 GO:GO:0005618 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005515 GO:GO:0005730 GO:GO:0016020 GO:GO:0003743 EMBL:AB019229 SMART:SM00487 PROSITE:PS51192 GO:GO:0008026 eggNOG:COG0513 HOGENOM:HBG737336 InterPro:IPR014014 PROSITE:PS51195 EMBL:X65052 EMBL:AJ298137 EMBL:AJ298138 EMBL:AY050957 EMBL:AY052344 EMBL:AY081287 EMBL:AY091304 EMBL:AY098962 EMBL:AY139981 EMBL:BT000655 EMBL:AK226414 EMBL:AY086907 IPI:IPI00530767 PIR:JC1452 RefSeq:NP_566469.1 UniGene:At.23558 UniGene:At.28184 ProteinModelPortal:P41376 SMR:P41376 IntAct:P41376 STRING:P41376 PRIDE:P41376 EnsemblPlants:AT3G13920.1 GeneID:820605 KEGG:ath:AT3G13920 GeneFarm:909 TAIR:At3g13920 InParanoid:P41376 PhylomeDB:P41376 ProtClustDB:CLSN2679594 Genevestigator:P41376 Uniprot:P41376
Leaf	Isotig06079	24	8	2.114	0.000100566	TAIR|locus:2088150 - symbol:AT3G13340 "AT3G13340" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005834 "heterotrimeric G-protein complex" evidence=ISS] [GO:0008150 "biological_process" evidence=ND] [GO:0080008 "CUL4 RING ubiquitin ligase complex" evidence=ISS] InterPro:IPR017986 InterPro:IPR001680 InterPro:IPR015943 Pfam:PF00400 PROSITE:PS50082 PROSITE:PS50294 SMART:SM00320 EMBL:CP002686 GenomeReviews:BA000014_GR Gene3D:G3DSA:2.130.10.10 eggNOG:COG2319 OMA:MYYEFRR HOGENOM:HBG320064 EMBL:AY048298 EMBL:AY139803 IPI:IPI00546104 RefSeq:NP_001189878.1 RefSeq:NP_566453.1 UniGene:At.24087 ProteinModelPortal:Q94AB4 SMR:Q94AB4 STRING:Q94AB4 PRIDE:Q94AB4 EnsemblPlants:AT3G13340.1 EnsemblPlants:AT3G13340.2 GeneID:820534 KEGG:ath:AT3G13340 TAIR:At3g13340 InParanoid:Q94AB4 PhylomeDB:Q94AB4 ProtClustDB:CLSN2688345 Genevestigator:Q94AB4 Uniprot:Q94AB4
Leaf	Isotig06080	15	2	3.436	7.06E-05	TAIR|locus:2127565 - symbol:ORP2A "AT4G22540" species:3702 "Arabidopsis thaliana" [GO:0008142 "oxysterol binding" evidence=ISS] [GO:0008202 "steroid metabolic process" evidence=ISS] [GO:0007165 "signal transduction" evidence=ISS] [GO:0035091 "phosphatidylinositol binding" evidence=ISS] Pfam:PF00169 InterPro:IPR001849 PROSITE:PS50003 SMART:SM00233 InterPro:IPR000648 EMBL:CP002687 GenomeReviews:CT486007_GR InterPro:IPR011993 Gene3D:G3DSA:2.30.29.30 GO:GO:0006869 GO:GO:0008289 EMBL:AL161557 EMBL:AL033545 PANTHER:PTHR10972 Pfam:PF01237 PROSITE:PS01013 eggNOG:NOG281324 HOGENOM:HBG445378 EMBL:AK229811 EMBL:AY052361 EMBL:BT001093 EMBL:AK222178 IPI:IPI00520502 IPI:IPI00527612 PIR:T05448 RefSeq:NP_001031698.1 RefSeq:NP_001190800.1 RefSeq:NP_567662.1

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						RefSeq:NP_974592.1 UniGene:At.23326 ProteinModelPortal:Q940Y1 SMR:Q940Y1 IntAct:Q940Y1 PRIDE:Q940Y1 EnsemblPlants:AT4G22540.1 GeneID:828349 KEGG:ath:AT4G22540 TAIR:At4g22540 InParanoid:Q940Y1 OMA:KECEQIM PhylomeDB:Q940Y1 ProtClustDB:CLSN2689556 ArrayExpress:Q9SUW5 Genevestigator:Q940Y1 Uniprot:Q940Y1
Leaf	Isotig06088	9	100	-2.945	1.55E-15	TAIR|locus:2131513 - symbol:AT4G26530 "AT4G26530" species:3702 "Arabidopsis thaliana" [GO:0004332 "fructose-bisphosphate aldolase activity" evidence=ISS;NAS] [GO:0006096 "glycolysis" evidence=IEA;ISS] [GO:0008152 "metabolic process" evidence=IEA] [GO:0009507 "chloroplast" evidence=IDA] InterPro:IPR000741 InterPro:IPR013785 Pfam:PF00274 PROSITE:PS00158 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0009507 Gene3D:G3DSA:3.20.20.70 GO:GO:0006096 EMBL:AL161565 eggNOG:COG3588 HOGENOM:HBG559178 KO:K01623 GO:GO:0004332 PANTHER:PTHR11627 OMA:LHRSKAN EMBL:AL022223 ProtClustDB:PLN02455 EMBL:AY087376 EMBL:BT002006 EMBL:BT008844 IPI:IPI00548350 PIR:T05051 RefSeq:NP_001031721.1 RefSeq:NP_194383.1 UniGene:At.57980 HSSP:P00883 ProteinModelPortal:O65581 SMR:O65581 IntAct:O65581 STRING:O65581 PRIDE:O65581 ProMEX:O65581 EnsemblPlants:AT4G26530.1 EnsemblPlants:AT4G26530.2 GeneID:828759 KEGG:ath:AT4G26530 TAIR:At4g26530 InParanoid:O65581 PhylomeDB:O65581 Genevestigator:O65581 Uniprot:O65581
Leaf	Isotig06099	19	4	2.777	5.07E-05	TAIR|locus:2163847 - symbol:AT5G42620 species:3702 "Arabidopsis thaliana" [GO:0004222 "metalloendopeptidase activity" evidence=IEA] [GO:0006508 "proteolysis" evidence=IEA] [GO:0007155 "cell adhesion" evidence=IEA] [GO:0008270 "zinc ion binding" evidence=IEA] [GO:0016020 "membrane" evidence=IEA] InterPro:IPR000742 InterPro:IPR001577 InterPro:IPR006210 Pfam:PF01457 PRINTS:PR00782 PROSITE:PS50026 SMART:SM00181 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0016020 GO:GO:0008270 GO:GO:0006508 GO:GO:0007155 InterPro:IPR013032 PROSITE:PS00022 GO:GO:0004222 PROSITE:PS01186 InterPro:IPR013111 Pfam:PF07974 PANTHER:PTHR10942 eggNOG:NOG279222 OMA:GAYHCNT EMBL:AK176188 EMBL:AK221227 EMBL:AK230319 IPI:IPI00535811 RefSeq:NP_568608.2 UniGene:At.22770 ProteinModelPortal:Q67ZD0 SMR:Q67ZD0 STRING:Q67ZD0 MEROPS:M08.A01 PRIDE:Q67ZD0 EnsemblPlants:AT5G42620.1 GeneID:834269 KEGG:ath:AT5G42620 TAIR:At5g42620 HOGENOM:HBG595021 InParanoid:Q67ZD0 KO:K01404 PhylomeDB:Q67ZD0 ProtClustDB:CLSN2681086 ArrayExpress:Q67ZD0 Genevestigator:Q67ZD0 Uniprot:Q67ZD0
Leaf	Isotig06111	16	2	3.529	3.35E-05	TAIR|locus:2012808 - symbol:MPK1 "AT1G10210" species:3702 "Arabidopsis thaliana" [GO:0016301 "kinase activity" evidence=ISS] [GO:0004707 "MAP kinase activity" evidence=ISS;IDA] [GO:0007165 "signal transduction" evidence=IC] [GO:0009734 "auxin mediated signaling pathway" evidence=TAS] InterPro:IPR000719 InterPro:IPR002290 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 Pfam:PF00069 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS01351 PROSITE:PS50011 SMART:SM00220 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005524 GO:GO:0009734 eggNOG:COG0515 SUPFAM:SSF56112 HOGENOM:HBG755340 EMBL:AC005489 BRENDA:2.7.11.24 KO:K04371 GO:GO:0004707 ProtClustDB:CLSN2679557 EMBL:D14713 EMBL:AY059937 EMBL:BT000062 IPI:IPI00538718 PIR:F86236 RefSeq:NP_001031017.1 RefSeq:NP_172492.1 UniGene:At.261 ProteinModelPortal:Q39021 SMR:Q39021 IntAct:Q39021 STRING:Q39021 PRIDE:Q39021 EnsemblPlants:AT1G10210.1 EnsemblPlants:AT1G10210.2 GeneID:837559 KEGG:ath:AT1G10210 GeneFarm:855 TAIR:At1g10210 InParanoid:Q39021 OMA:IKEIGHG PhylomeDB:Q39021 ArrayExpress:Q39021 Genevestigator:Q39021 GermOnline:AT1G10210 Uniprot:Q39021
Leaf	Isotig06113	19	3	3.192	1.46E-05	TAIR|locus:2081675 - symbol:AUD1 "AT3G62830" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=ISS] [GO:0009225 "nucleotide-sugar metabolic process" evidence=ISS] [GO:0008460 "dTDP-glucose 4,6-dehydratase activity" evidence=ISS] [GO:0019305 "dTDP-rhamnose biosynthetic process" evidence=ISS] [GO:0016020 "membrane" evidence=TAS] [GO:0042732 "D-xylose metabolic process" evidence=IDA] [GO:0048040 "UDP-glucuronate decarboxylase activity" evidence=IDA] [GO:0000139 "Golgi membrane" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR001509 InterPro:IPR016040 Pfam:PF01370 GO:GO:0005886 EMBL:CP002686 GO:GO:0000139 GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 EMBL:AL162651 GO:GO:0050662 GO:GO:0042732 GO:GO:0048040 OMA:EMVEPLR UniGene:At.23561 UniGene:At.27002 UniGene:At.63633 ProtClustDB:PLN02206 EMBL:AY143897 IPI:IPI00539694 PIR:T48072 RefSeq:NP_001118893.1 RefSeq:NP_191842.1 ProteinModelPortal:Q9LZI2 SMR:Q9LZI2 PRIDE:Q9LZI2 EnsemblPlants:AT3G62830.1 EnsemblPlants:AT3G62830.2 GeneID:825458 KEGG:ath:AT3G62830 TAIR:At3g62830 InParanoid:Q9LZI2 PhylomeDB:Q9LZI2 Genevestigator:Q9LZI2 Uniprot:Q9LZI2

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig06118	11	0	4.988	0.000159591	TAIR|locus:2011271 - symbol:AT1G19140 "AT1G19140" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0006744 "ubiquinone biosynthetic process" evidence=IEA] [GO:0005739 "mitochondrion" evidence=IDA] InterPro:IPR012762 EMBL:CP002684 GO:GO:0005739 GO:GO:0006744 EMBL:AC069143 InterPro:IPR013718 Pfam:PF08511 TIGRFAMs:TIGR02396 IPI:IPI00529372 PIR:G86324 RefSeq:NP_564074.1 UniGene:At.15082 ProteinModelPortal:Q9LMB2 STRING:Q9LMB2 PRIDE:Q9LMB2 EnsemblPlants:AT1G19140.1 GeneID:838497 KEGG:ath:AT1G19140 TAIR:At1g19140 InParanoid:Q9LMB2 PhylomeDB:Q9LMB2 ProtClustDB:CLSN2687864 Genevestigator:Q9LMB2 Uniprot:Q9LMB2
Leaf	Isotig06124	28	10	2.014	4.65E-05	TAIR|locus:2831859 - symbol:RABC2A "AT5G03530" species:3702 "Arabidopsis thaliana" [GO:0005525 "GTP binding" evidence=ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0007264 "small GTPase mediated signal transduction" evidence=IEA] [GO:0015031 "protein transport" evidence=IEA] [GO:0005515 "protein binding" evidence=IPI] [GO:0005777 "peroxisome" evidence=IDA] [GO:0030742 "GTP-dependent protein binding" evidence=IPI] [GO:0080115 "myosin XI tail binding" evidence=IPI] InterPro:IPR001806 InterPro:IPR002078 InterPro:IPR003579 InterPro:IPR005225 Pfam:PF00071 PRINTS:PR00449 SMART:SM00175 GO:GO:0005525 TIGRFAMs:TIGR00231 GO:GO:0005886 GO:GO:0005524 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0008134 EMBL:AL162751 GO:GO:0005777 GO:GO:0006355 GO:GO:0015031 GO:GO:0007264 PROSITE:PS51419 eggNOG:COG1100 HOGENOM:HBG745225 GO:GO:0030742 PROSITE:PS00675 KO:K07976 HSSP:P07560 OMA:FAKRHRT GO:GO:0080115 EMBL:D89824 EMBL:AK119027 EMBL:BT006101 IPI:IPI00545141 PIR:T48379 RefSeq:NP_568121.1 UniGene:At.346 ProteinModelPortal:O49841 SMR:O49841 IntAct:O49841 STRING:O49841 PRIDE:O49841 EnsemblPlants:AT5G03530.1 GeneID:831810 KEGG:ath:AT5G03530 TAIR:At5g03530 InParanoid:O49841 PhylomeDB:O49841 ProtClustDB:PLN03118 ArrayExpress:O49841 Genevestigator:O49841 Uniprot:O49841
Leaf	Isotig06150	10	1	3.851	0.00071293	TAIR|locus:2222607 - symbol:AT5G14520 "AT5G14520" species:3702 "Arabidopsis thaliana" [GO:0003713 "transcription coactivator activity" evidence=ISS] [GO:0005622 "intracellular" evidence=IEA;ISS] [GO:0005730 "nucleolus" evidence=IEA] [GO:0008283 "cell proliferation" evidence=IEA] InterPro:IPR001357 InterPro:IPR010613 Pfam:PF00533 Pfam:PF06732 PROSITE:PS50172 SMART:SM00292 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005730 SUPFAM:SSF52113 GO:GO:0006364 EMBL:AL163792 eggNOG:COG5163 HOGENOM:HBG410102 KO:K14843 OMA:SIKGVYY HSSP:P18887 IPI:IPI00522738 PIR:T48625 RefSeq:NP_196956.1 UniGene:At.50457 ProteinModelPortal:Q9LYK7 SMR:Q9LYK7 STRING:Q9LYK7 PRIDE:Q9LYK7 EnsemblPlants:AT5G14520.1 GeneID:831303 KEGG:ath:AT5G14520 TAIR:At5g14520 InParanoid:Q9LYK7 PhylomeDB:Q9LYK7 ProtClustDB:CLSN2687226 Genevestigator:Q9LYK7 Uniprot:Q9LYK7
Leaf	Isotig06153	16	2	3.529	3.35E-05	TAIR|locus:2121234 - symbol:AT4G38520 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004722 "protein serine/threonine phosphatase activity" evidence=IEA;ISS] [GO:0006470 "protein dephosphorylation" evidence=IEA] [GO:0008287 "protein serine/threonine phosphatase complex" evidence=IEA] InterPro:IPR000222 InterPro:IPR001932 Pfam:PF00481 PROSITE:PS01032 SMART:SM00331 SMART:SM00332 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0006470 GO:GO:0004722 GO:GO:0046872 EMBL:AL161593 eggNOG:COG0631 Gene3D:G3DSA:3.60.40.10 SUPFAM:SSF81606 GO:GO:0008287 InterPro:IPR015655 PANTHER:PTHR13832 EMBL:AL035540 HOGENOM:HBG317284 EMBL:AY062454 EMBL:BT020368 EMBL:BT021094 IPI:IPI00546484 PIR:T05680 RefSeq:NP_195564.2 RefSeq:NP_974708.1 UniGene:At.47543 ProteinModelPortal:Q5PNS9 SMR:Q5PNS9 PRIDE:Q5PNS9 EnsemblPlants:AT4G38520.1 EnsemblPlants:AT4G38520.2 GeneID:830009 KEGG:ath:AT4G38520 TAIR:At4g38520 InParanoid:Q5PNS9 OMA:YLKRSEF PhylomeDB:Q5PNS9 ProtClustDB:CLSN2915065 ArrayExpress:Q9SZN2 Genevestigator:Q5PNS9 Uniprot:Q5PNS9
Leaf	Isotig06177	1	23	-3.995	1.53E-05	TAIR|locus:2034476 - symbol:CYP97A3 "AT1G31800" species:3702 "Arabidopsis thaliana" [GO:0019825 "oxygen binding" evidence=ISS] [GO:0010291 "carotene beta-ring hydroxylase activity" evidence=IMP] [GO:0016117 "carotenoid biosynthetic process" evidence=IMP] [GO:0016123 "xanthophyll biosynthetic process" evidence=IGI] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] InterPro:IPR001128 InterPro:IPR002401 InterPro:IPR017972 Pfam:PF00067 PRINTS:PR00385 PRINTS:PR00463 PROSITE:PS00086 EMBL:CP002684 GO:GO:0009055 EMBL:AC079041 GO:GO:0031969 GO:GO:0020037 Gene3D:G3DSA:1.10.630.10 SUPFAM:SSF48264 GO:GO:0016117 GO:GO:0010291 GO:GO:0016705 HSSP:P14779 UniGene:At.48254 UniGene:At.71094 EMBL:AY056446 EMBL:AY058173 EMBL:AY142017 IPI:IPI00522598 PIR:F86441 RefSeq:NP_564384.1 ProteinModelPortal:Q93VK5 PRIDE:Q93VK5 EnsemblPlants:AT1G31800.1 GeneID:840067 KEGG:ath:AT1G31800 GeneFarm:1344 TAIR:At1g31800

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						InParanoid:Q93VK5 KO:K15747 OMA:DPSIAKH PhylomeDB:Q93VK5 ProtClustDB:PLN02738 Genevestigator:Q93VK5 Uniprot:Q93VK5
Leaf	Isotig06190	11	0	4.988	0.000159591	TAIR|locus:2025502 - symbol:EDA10 "AT1G01960" species:3702 "Arabidopsis thaliana" [GO:0005085 "guanyl-nucleotide exchange factor activity" evidence=ISS] [GO:0005086 "ARF guanyl-nucleotide exchange factor activity" evidence=IEA;IBA] [GO:0016192 "vesicle-mediated transport" evidence=IBA] [GO:0050790 "regulation of catalytic activity" evidence=IBA] [GO:0009561 "megagametogenesis" evidence=IMP] [GO:0005634 "nucleus" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR000904 InterPro:IPR011989 InterPro:IPR016024 Pfam:PF01369 PROSITE:PS50190 SMART:SM00222 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0005634 GO:GO:0005488 SUPFAM:SSF48371 Gene3D:G3DSA:1.25.10.10 GO:GO:0009561 EMBL:AC020622 UniGene:At.17002 UniGene:At.66839 eggNOG:COG5307 GO:GO:0005086 GO:GO:0032012 InterPro:IPR015403 InterPro:IPR023394 Gene3D:G3DSA:1.10.1000.11 Pfam:PF09324 SUPFAM:SSF48425 HSSP:Q99418 OMA:QKNLMEQ HOGENOM:HBG413465 IPI:IPI00547943 PIR:E86151 RefSeq:NP_171698.1 UniGene:At.69285 ProteinModelPortal:Q9LPC5 SMR:Q9LPC5 STRING:Q9LPC5 PRIDE:Q9LPC5 ProMEX:Q9LPC5 EnsemblPlants:AT1G01960.1 GeneID:839301 KEGG:ath:AT1G01960 TAIR:At1g01960 InParanoid:Q9LPC5 PhylomeDB:Q9LPC5 ProtClustDB:PLN03076 Genevestigator:Q9LPC5 Uniprot:Q9LPC5
Leaf	Isotig06220	37	6	3.153	1.79E-09	TAIR|locus:2007943 - symbol:HAB2 "homology to ABI2" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004722 "protein serine/threonine phosphatase activity" evidence=IEA;ISS] [GO:0006470 "protein dephosphorylation" evidence=IEA] InterPro:IPR000222 InterPro:IPR001932 Pfam:PF00481 PROSITE:PS01032 SMART:SM00331 SMART:SM00332 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0006470 GO:GO:0009738 GO:GO:0004722 GO:GO:0046872 EMBL:AC022492 eggNOG:COG0631 Gene3D:G3DSA:3.60.40.10 SUPFAM:SSF81606 GO:GO:0008287 InterPro:IPR015655 PANTHER:PTHR13832 HSSP:P35813 HOGENOM:HBG747569 KO:K14497 EMBL:AK118656 IPI:IPI00532752 RefSeq:NP_173199.2 UniGene:At.41827 ProteinModelPortal:Q9LNP9 SMR:Q9LNP9 DIP:DIP-48989N PRIDE:Q9LNP9 EnsemblPlants:AT1G17550.1 GeneID:838330 KEGG:ath:AT1G17550 TAIR:At1g17550 InParanoid:Q8GWS8 OMA:RRILAWH PhylomeDB:Q9LNP9 ProtClustDB:CLSN2679602 Genevestigator:Q9LNP9 Uniprot:Q9LNP9
Leaf	Isotig06224	15	4	2.436	0.000806142	TAIR|locus:2012206 - symbol:ABF1 "AT1G49720" species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=ISS;IDA] [GO:0006950 "response to stress" evidence=TAS] [GO:0045893 "positive regulation of transcription, DNA-dependent" evidence=IDA] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS;TAS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=TAS] [GO:0005634 "nucleus" evidence=TAS] [GO:0009738 "abscisic acid mediated signaling pathway" evidence=TAS] [GO:0005515 "protein binding" evidence=IPI] [GO:0009737 "response to abscisic acid stimulus" evidence=IDA] InterPro:IPR004827 InterPro:IPR011616 Pfam:PF00170 PROSITE:PS00036 PROSITE:PS50217 SMART:SM00338 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005634 GO:GO:0009738 GO:GO:0043565 GO:GO:0003700 GO:GO:0006351 GO:GO:0046983 KO:K14432 EMBL:AF093544 EMBL:AC011807 EMBL:BT008575 EMBL:BT008647 EMBL:AK226983 IPI:IPI00544556 PIR:G96533 RefSeq:NP_564551.1 UniGene:At.46187 UniGene:At.48293 ProteinModelPortal:Q9M7Q5 SMR:Q9M7Q5 IntAct:Q9M7Q5 STRING:Q9M7Q5 PRIDE:Q9M7Q5 EnsemblPlants:AT1G49720.1 GeneID:841395 KEGG:ath:AT1G49720 TAIR:At1g49720 eggNOG:NOG290553 InParanoid:Q9M7Q5 OMA:FYANNGA PhylomeDB:Q9M7Q5 ProtClustDB:CLSN2688558 ArrayExpress:Q9M7Q5 Genevestigator:Q9M7Q5 Uniprot:Q9M7Q5
Leaf	Isotig06243	12	2	3.114	0.000658121	TAIR|locus:2044440 - symbol:HPT1 "AT2G18950" species:3702 "Arabidopsis thaliana" [GO:0010189 "vitamin E biosynthetic process" evidence=IMP;TAS] [GO:0004659 "prenyltransferase activity" evidence=IDA] [GO:0009507 "chloroplast" evidence=ISS] [GO:0010176 "homogentisate phytyltransferase activity" evidence=IMP;IDA] [GO:0042362 "fat-soluble vitamin biosynthetic process" evidence=TAS] [GO:0009266 "response to temperature stimulus" evidence=IMP] [GO:0009915 "phloem sucrose loading" evidence=IMP] [GO:0031347 "regulation of defense response" evidence=IMP] [GO:0006636 "unsaturated fatty acid biosynthetic process" evidence=IMP] [GO:0007047 "cellular cell wall organization" evidence=IMP] InterPro:IPR000537 Pfam:PF01040 GO:GO:0016021 EMBL:CP002685 GenomeReviews:CT485783_GR eggNOG:COG0382 GO:GO:0006636 EMBL:AC003673 GO:GO:0007047 GO:GO:0009535 GO:GO:0009266 GO:GO:0009915 GO:GO:0031347 GO:GO:0010189 EMBL:AF324344 EMBL:AY089963 EMBL:GU198365 EMBL:AY063893 EMBL:AY113993 IPI:IPI00546170 PIR:T01623 RefSeq:NP_849984.1 UniGene:At.27152 STRING:Q8VWJ1 PRIDE:Q8VWJ1 GeneID:816412 KEGG:ath:AT2G18950 TAIR:At2g18950 HOGENOM:HBG618562 InParanoid:Q8VWJ1 KO:K09833 OMA:YQFIWKL PhylomeDB:Q8VWJ1 ProtClustDB:PLN02878 Genevestigator:Q8VWJ1 GO:GO:0010176 Uniprot:Q8VWJ1

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig06248	11	0	4.988	0.000159591	TAIR|locus:2081277 - symbol:AT3G59350 species:3702 "Arabidopsis thaliana" [GO:0004672 "protein kinase activity" evidence=IEA] [GO:0004713 "protein tyrosine kinase activity" evidence=IEA] [GO:0005524 "ATP binding" evidence=IEA] [GO:0006468 "protein phosphorylation" evidence=IEA] [GO:0016301 "kinase activity" evidence=ISS] [GO:0019901 "protein kinase binding" evidence=IPI] [GO:0005886 "plasma membrane" evidence=IDA] InterPro:IPR000719 InterPro:IPR001245 InterPro:IPR008266 InterPro:IPR011009 InterPro:IPR017441 Pfam:PF07714 PROSITE:PS00107 PROSITE:PS00109 PROSITE:PS50011 GO:GO:0005886 GO:GO:0005524 EMBL:CP002686 GenomeReviews:BA000014_GR eggNOG:COG0515 SUPFAM:SSF56112 GO:GO:0019901 HOGENOM:HBG755340 GO:GO:0004715 EMBL:AL356014 EMBL:AY054639 EMBL:BT008449 EMBL:AK316761 EMBL:AK317695 IPI:IPI00518930 IPI:IPI00522951 PIR:T49003 RefSeq:NP_001030893.1 RefSeq:NP_567082.2 RefSeq:NP_850720.1 UniGene:At.1517 ProteinModelPortal:B9DFG5 SMR:B9DFG5 IntAct:B9DFG5 STRING:B9DFG5 PRIDE:B9DFG5 EnsemblPlants:AT3G59350.1 EnsemblPlants:AT3G59350.3 GeneID:825104 KEGG:ath:AT3G59350 GeneFarm:1786 TAIR:At3g59350 InParanoid:Q9LX36 OMA:SKLKHDN PhylomeDB:B9DFG5 ProtClustDB:CLSN2680456 Genevestigator:B9DFG5 Uniprot:B9DFG5
Leaf	Isotig06257	37	204	-1.934	5.06E-19	TAIR|locus:2120192 - symbol:FBA2 "fructose-bisphosphate aldolase 2" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004332 "fructose-bisphosphate aldolase activity" evidence=IEA] [GO:0006098 "pentose-phosphate shunt" evidence=TAS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0009579 "thylakoid" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] InterPro:IPR000741 InterPro:IPR013785 Pfam:PF00274 PROSITE:PS00158 GO:GO:0009737 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0048046 GO:GO:0046686 GO:GO:0016020 Gene3D:G3DSA:3.20.20.70 GO:GO:0009941 GO:GO:0006096 GO:GO:0009579 HSSP:P05062 eggNOG:COG3588 HOGENOM:HBG559178 KO:K01623 GO:GO:0004332 PANTHER:PTHR11627 UniGene:At.21716 GO:GO:0010287 EMBL:AL035679 EMBL:AL161594 EMBL:AF428455 EMBL:BT015870 EMBL:AK226247 IPI:IPI00541448 PIR:T06057 RefSeq:NP_568049.1 UniGene:At.24925 UniGene:At.75329 ProteinModelPortal:Q944G9 SMR:Q944G9 STRING:Q944G9 PRIDE:Q944G9 ProMEX:Q944G9 GeneID:830052 KEGG:ath:AT4G38970 TAIR:At4g38970 InParanoid:Q944G9 PhylomeDB:Q944G9 ProtClustDB:CLSN2917687 ArrayExpress:Q9SVJ6 Genevestigator:Q944G9 Uniprot:Q944G9
Leaf	Isotig06266	9	0	4.699	0.000718283	TAIR|locus:2058001 - symbol:GSL8 "AT2G36850" species:3702 "Arabidopsis thaliana" [GO:0000148 "1,3-beta-D-glucan synthase complex" evidence=ISS] [GO:0003843 "1,3-beta-D-glucan synthase activity" evidence=ISS] [GO:0006075 "(1->3)-beta-D-glucan biosynthetic process" evidence=ISS] [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009555 "pollen development" evidence=IMP] [GO:0009556 "microsporogenesis" evidence=IMP] [GO:0048589 "developmental growth" evidence=IMP] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR003440 Pfam:PF02364 GO:GO:0016021 GO:GO:0009506 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0008360 EMBL:AC006922 GO:GO:0048589 GO:GO:0007047 CAZy:GT48 GO:GO:0000148 GO:GO:0003843 HOGENOM:HBG316390 GO:GO:0006075 GO:GO:0009556 EMBL:GQ373182 EMBL:AK229594 IPI:IPI00532489 IPI:IPI01020464 PIR:E84785 RefSeq:NP_850271.5 UniGene:At.37496 STRING:Q9SJM0 PRIDE:Q9SJM0 GeneID:818258 KEGG:ath:AT2G36850 TAIR:At2g36850 eggNOG:NOG324784 PhylomeDB:Q9SJM0 ProtClustDB:CLSN2704898 ArrayExpress:Q9SJM0 Genevestigator:Q9SJM0 Uniprot:Q9SJM0
Leaf	Isotig06285	10	72	-2.319	2.90E-09	TAIR|locus:2078941 - symbol:SBPASE "AT3G55800" species:3702 "Arabidopsis thaliana" [GO:0005975 "carbohydrate metabolic process" evidence=ISS] [GO:0042578 "phosphoric ester hydrolase activity" evidence=ISS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005986 "sucrose biosynthetic process" evidence=IDA] [GO:0016051 "carbohydrate biosynthetic process" evidence=IDA] [GO:0019252 "starch biosynthetic process" evidence=IDA] [GO:0050278 "sedoheptulose-bisphosphatase activity" evidence=IMP] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0042742 "defense response to bacterium" evidence=IEP] [GO:0048046 "apoplast" evidence=IDA] [GO:0019253 "reductive pentose-phosphate cycle" evidence=ISS] InterPro:IPR000146 InterPro:IPR020548 Pfam:PF00316 PIRSF:PIRSF000904 PROSITE:PS00124 GO:GO:0048046 GO:GO:0009570 GO:GO:0042742 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0046872 GO:GO:0009941 GO:GO:0019252 GO:GO:0009579 GO:GO:0019253 eggNOG:COG0158 HOGENOM:HBG731261 PANTHER:PTHR11556 GO:GO:0005986

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						InterPro:IPR023079 PRINTS:PR01958 EMBL:AL161667 EMBL:S74719 EMBL:AY054669 EMBL:AY128737 IPI:IPI00544876 PIR:S51838 RefSeq:NP_191139.1 UniGene:At.21157 ProteinModelPortal:P46283 SMR:P46283 IntAct:P46283 STRING:P46283 SWISS-2DPAGE:P46283 World-2DPAGE:0003:P46283 PRIDE:P46283 ProMEX:P46283 EnsemblPlants:AT3G55800.1 GeneID:824746 KEGG:ath:AT3G55800 TAIR:At3g55800 InParanoid:P46283 KO:K01100 OMA:HANIVIE PhylomeDB:P46283 ProtClustDB:PLN02462 Genevestigator:P46283 GermOnline:AT3G55800 GO:GO:0050278 Uniprot:P46283
Leaf	Isotig06288	25	1	5.173	1.09E-08	TAIR|locus:2197379 - symbol:SNRK2.4 "AT1G10940" species:3702 "Arabidopsis thaliana" [GO:0016301 "kinase activity" evidence=ISS;IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0006970 "response to osmotic stress" evidence=IGI;IDA] [GO:0009651 "response to salt stress" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0009737 "response to abscisic acid stimulus" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR000719 InterPro:IPR002290 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 Pfam:PF00069 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 SMART:SM00220 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0005524 GO:GO:0009737 GO:GO:0005634 GO:GO:0005515 eggNOG:COG0515 SUPFAM:SSF56112 GO:GO:0004674 HOGENOM:HBG755340 BRENDA:2.7.11.1 GO:GO:0009651 EMBL:U95973 EMBL:M91548 EMBL:AY093130 EMBL:BT008850 EMBL:AY084221 IPI:IPI00522193 PIR:S36944 RefSeq:NP_172563.1 UniGene:At.23750 ProteinModelPortal:P43291 SMR:P43291 IntAct:P43291 STRING:P43291 PRIDE:P43291 ProMEX:P43291 EnsemblPlants:AT1G10940.1 GeneID:837637 KEGG:ath:AT1G10940 TAIR:At1g10940 InParanoid:P43291 KO:K14498 OMA:LAIAMEY PhylomeDB:P43291 ProtClustDB:CLSN2681826 ArrayExpress:P43291 Genevestigator:P43291 GermOnline:AT1G10940 Uniprot:P43291
Leaf	Isotig06290	36	204	-1.974	1.70E-19	TAIR|locus:2120192 - symbol:FBA2 "fructose-bisphosphate aldolase 2" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004332 "fructose-bisphosphate aldolase activity" evidence=IEA] [GO:0006098 "pentose-phosphate shunt" evidence=TAS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0009579 "thylakoid" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] InterPro:IPR000741 InterPro:IPR013785 Pfam:PF00274 PROSITE:PS00158 GO:GO:0009737 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0048046 GO:GO:0046686 GO:GO:0016020 Gene3D:G3DSA:3.20.20.70 GO:GO:0009941 GO:GO:0006096 GO:GO:0009579 HSSP:P05062 eggNOG:COG3588 HOGENOM:HBG559178 KO:K01623 GO:GO:0004332 PANTHER:PTHR11627 UniGene:At.21716 GO:GO:0010287 EMBL:AL035679 EMBL:AL161594 EMBL:AF428455 EMBL:BT015870 EMBL:AK226247 IPI:IPI00541448 PIR:T06057 RefSeq:NP_568049.1 UniGene:At.24925 UniGene:At.75329 ProteinModelPortal:Q944G9 SMR:Q944G9 STRING:Q944G9 PRIDE:Q944G9 ProMEX:Q944G9 GeneID:830052 KEGG:ath:AT4G38970 TAIR:At4g38970 InParanoid:Q944G9 PhylomeDB:Q944G9 ProtClustDB:CLSN2917687 ArrayExpress:Q9SVJ6 Genevestigator:Q944G9 Uniprot:Q944G9
Leaf	Isotig06291	28	170	-2.073	1.72E-17	TAIR|locus:2120192 - symbol:FBA2 "fructose-bisphosphate aldolase 2" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004332 "fructose-bisphosphate aldolase activity" evidence=IEA] [GO:0006098 "pentose-phosphate shunt" evidence=TAS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0009579 "thylakoid" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] InterPro:IPR000741 InterPro:IPR013785 Pfam:PF00274 PROSITE:PS00158 GO:GO:0009737 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0048046 GO:GO:0046686 GO:GO:0016020 Gene3D:G3DSA:3.20.20.70 GO:GO:0009941 GO:GO:0006096 GO:GO:0009579 HSSP:P05062 eggNOG:COG3588 HOGENOM:HBG559178 KO:K01623 GO:GO:0004332 PANTHER:PTHR11627 UniGene:At.21716 GO:GO:0010287 EMBL:AL035679 EMBL:AL161594 EMBL:AF428455 EMBL:BT015870 EMBL:AK226247 IPI:IPI00541448 PIR:T06057 RefSeq:NP_568049.1 UniGene:At.24925 UniGene:At.75329 ProteinModelPortal:Q944G9 SMR:Q944G9 STRING:Q944G9 PRIDE:Q944G9 ProMEX:Q944G9 GeneID:830052 KEGG:ath:AT4G38970 TAIR:At4g38970 InParanoid:Q944G9 PhylomeDB:Q944G9 ProtClustDB:CLSN2917687 ArrayExpress:Q9SVJ6 Genevestigator:Q944G9 Uniprot:Q944G9
Leaf	Isotig06299	9	0	4.699	0.000718283	TAIR|locus:2036303 - symbol:STOP1 "AT1G34370" species:3702 "Arabidopsis thaliana" [GO:0003676 "nucleic acid binding" evidence=ISS] [GO:0008270 "zinc ion binding" evidence=ISS] [GO:0003700 "sequence-specific DNA

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						binding transcription factor activity" evidence=ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IMP;TAS] [GO:0005634 "nucleus" evidence=ISS;IDA] [GO:0010044 "response to aluminum ion" evidence=IMP] [GO:0010447 "response to acidity" evidence=IMP] Pfam:PF00096 InterPro:IPR007087 InterPro:IPR013087 InterPro:IPR015880 PROSITE:PS00028 PROSITE:PS50157 SMART:SM00355 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005634 GO:GO:0006355 GO:GO:0010044 GO:GO:0008270 GO:GO:0006351 GO:GO:0003676 Gene3D:G3DSA:3.30.160.60 GO:GO:0010447 EMBL:AC023913 EMBL:AB300236 EMBL:AB300237 EMBL:AB300238 EMBL:AB300239 EMBL:AB300240 EMBL:AB300241 EMBL:AB300242 EMBL:AB300243 EMBL:AB300244 EMBL:AB300245 EMBL:AB300246 EMBL:AB300247 EMBL:AK227128 EMBL:AY087985 IPI:IPI00542277 PIR:A86468 RefSeq:NP_174697.1 RefSeq:NP_849746.1 UniGene:At.39746 UniGene:At.64018 UniGene:At.74453 ProteinModelPortal:Q9C8N5 SMR:Q9C8N5 IntAct:Q9C8N5 STRING:Q9C8N5 PRIDE:Q9C8N5 EnsemblPlants:AT1G34370.1 EnsemblPlants:AT1G34370.2 GeneID:840339 KEGG:ath:AT1G34370 TAIR:At1g34370 eggNOG:NOG266871 InParanoid:Q9C8N5 OMA:CKRNKEH PhylomeDB:Q9C8N5 ProtClustDB:CLSN2679604 Genevestigator:Q9C8N5 Uniprot:Q9C8N5
Leaf	Isotig06306	15	2	3.436	7.06E-05	TAIR|locus:2074464 - symbol:ATSK12 "AT3G05840" species:3702 "Arabidopsis thaliana" [GO:0004672 "protein kinase activity" evidence=ISS] [GO:0009933 "meristem structural organization" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] [GO:0004674 "protein serine/threonine kinase activity" evidence=ISS;IDA] [GO:0046777 "protein autophosphorylation" evidence=IDA] [GO:0016310 "phosphorylation" evidence=IDA] InterPro:IPR000719 InterPro:IPR002290 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 Pfam:PF00069 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 SMART:SM00220 GO:GO:0005829 GO:GO:0005524 EMBL:CP002686 GenomeReviews:BA000014_GR eggNOG:COG0515 SUPFAM:SSF56112 GO:GO:0004674 GO:GO:0046777 HOGENOM:HBG755340 GO:GO:0009933 EMBL:AC012393 BRENDA:2.7.11.26 ProtClustDB:CLSN2679358 UniGene:At.132 EMBL:X75431 EMBL:Y12710 EMBL:AY093347 EMBL:AY062713 EMBL:AY085752 IPI:IPI00543479 PIR:S41597 RefSeq:NP_187235.1 RefSeq:NP_850520.1 UniGene:At.20895 ProteinModelPortal:P43289 SMR:P43289 IntAct:P43289 STRING:P43289 EnsemblPlants:AT3G05840.1 EnsemblPlants:AT3G05840.2 GeneID:819753 KEGG:ath:AT3G05840 GeneFarm:581 TAIR:At3g05840 InParanoid:P43289 OMA:QDDKEME PhylomeDB:P43289 ArrayExpress:P43289 Genevestigator:P43289 GermOnline:AT3G05840 Uniprot:P43289
Leaf	Isotig06309	10	1	3.851	0.00071293	TAIR|locus:2101906 - symbol:AT3G60860 "AT3G60860" species:3702 "Arabidopsis thaliana" [GO:0005085 "guanyl-nucleotide exchange factor activity" evidence=ISS] [GO:0005086 "ARF guanyl-nucleotide exchange factor activity" evidence=IEA;IBA] [GO:0005737 "cytoplasm" evidence=IBA] [GO:0016192 "vesicle-mediated transport" evidence=IBA] [GO:0050790 "regulation of catalytic activity" evidence=IBA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR000904 InterPro:IPR011989 InterPro:IPR016024 Pfam:PF01369 PROSITE:PS50190 SMART:SM00222 GO:GO:0005829 EMBL:CP002686 GO:GO:0005488 SUPFAM:SSF48371 Gene3D:G3DSA:1.25.10.10 EMBL:AL162295 GO:GO:0005086 GO:GO:0032012 InterPro:IPR015403 InterPro:IPR023394 Gene3D:G3DSA:1.10.1000.11 Pfam:PF09324 SUPFAM:SSF48425 HSSP:Q99418 ProtClustDB:PLN03076 IPI:IPI00544005 PIR:T47897 RefSeq:NP_191645.1 UniGene:At.34364 ProteinModelPortal:Q9LZX8 SMR:Q9LZX8 PRIDE:Q9LZX8 EnsemblPlants:AT3G60860.1 GeneID:825257 KEGG:ath:AT3G60860 TAIR:At3g60860 InParanoid:Q9LZX8 OMA:IAHGYIR PhylomeDB:Q9LZX8 Genevestigator:Q9LZX8 Uniprot:Q9LZX8
Leaf	Isotig06315	6	32	-1.886	0.000520383	TAIR|locus:2013164 - symbol:AT1G19660 species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=IEA] [GO:0004518 "nuclease activity" evidence=IEA] [GO:0006289 "nucleotide-excision repair" evidence=IEA] [GO:0009611 "response to wounding" evidence=ISS] InterPro:IPR001943 Pfam:PF02151 EMBL:CP002684 GO:GO:0003677 GO:GO:0004518 GO:GO:0006289 InterPro:IPR003729 Pfam:PF02577 SUPFAM:SSF103256 EMBL:AY035016 EMBL:AY059082 EMBL:AK317508 IPI:IPI00546371 RefSeq:NP_001031068.1 RefSeq:NP_564093.1 UniGene:At.16184 ProteinModelPortal:Q93VH2 SMR:Q93VH2 STRING:Q93VH2 PRIDE:Q93VH2 EnsemblPlants:AT1G19660.1 EnsemblPlants:AT1G19660.2 GeneID:838553 KEGG:ath:AT1G19660 TAIR:At1g19660 InParanoid:Q93VH2 OMA:TRVHEAY PhylomeDB:Q93VH2 ProtClustDB:CLSN2682514 ArrayExpress:Q93VH2 Genevestigator:Q93VH2 Uniprot:Q93VH2
Leaf	Isotig06347	17	5	2.294	0.000574458	ZFIN|ZDB-GENE-030131-2182 - symbol:pa2g4b "proliferation-associated 2G4, b" species:7955 "Danio rerio" [GO:0009987 "cellular process" evidence=IEA] [GO:0016787 "hydrolase activity" evidence=IEA] InterPro:IPR000994 Pfam:PF00557 ZFIN:ZDB-GENE-030131-2182 InterPro:IPR011991 Gene3D:G3DSA:1.10.10.10 eggNOG:COG0024 Gene3D:G3DSA:3.90.230.10 SUPFAM:SSF55920 GO:GO:0009987 InterPro:IPR018349

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						PROSITE:PS01202 GeneTree:ENSGT00530000063220 HOGENOM:HBG629020 OMA:AHTFVVG InterPro:IPR004545 TIGRFAMs:TIGR00495 MEROPS:M24.973 HOVERGEN:HBG053117 OrthoDB:EOG4J6RR6 EMBL:CR382340 EMBL:BC056591 EMBL:BC071536 IPI:IPI00482363 RefSeq:NP_997806.1 UniGene:Dr.76539 ProteinModelPortal:Q6PHD8 SMR:Q6PHD8 PRIDE:Q6PHD8 Ensembl:ENSDART00000016248 GeneID:323462 KEGG:dre:323462 CTD:323462 InParanoid:Q6PHD8 PhylomeDB:Q6PHD8 ArrayExpress:Q6PHD8 Bgee:Q6PHD8 Uniprot:Q6PHD8
Leaf	Isotig06391	19	0	5.777	5.37E-07	TAIR|locus:2032367 - symbol:IAR4 "AT1G24180" species:3702 "Arabidopsis thaliana" [GO:0004739 "pyruvate dehydrogenase (acetyl-transferring) activity" evidence=ISS] [GO:0008152 "metabolic process" evidence=ISS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0005634 "nucleus" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0008270 "zinc ion binding" evidence=IDA] [GO:0050897 "cobalt ion binding" evidence=IDA] InterPro:IPR001017 InterPro:IPR017597 Pfam:PF00676 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0005634 GO:GO:0005759 GO:GO:0008270 GO:GO:0009651 GO:GO:0050897 GO:GO:0006096 GO:GO:0004739 EMBL:AC002396 eggNOG:COG1071 HOGENOM:HBG753263 KO:K00161 ProtClustDB:PLN02269 TIGRFAMs:TIGR03182 EMBL:AY135561 EMBL:AF360215 EMBL:AY051018 EMBL:AY088101 IPI:IPI00540928 PIR:T00648 RefSeq:NP_173828.1 UniGene:At.24830 HSSP:P08559 ProteinModelPortal:Q8H1Y0 SMR:Q8H1Y0 STRING:Q8H1Y0 PRIDE:Q8H1Y0 ProMEX:Q8H1Y0 EnsemblPlants:AT1G24180.1 GeneID:839031 KEGG:ath:AT1G24180 GeneFarm:4373 TAIR:At1g24180 InParanoid:Q8H1Y0 OMA:TEFAINY PhylomeDB:Q8H1Y0 ArrayExpress:O48685 Genevestigator:Q8H1Y0 Uniprot:Q8H1Y0
Leaf	Isotig06409	11	0	4.988	0.000159591	TAIR|locus:2121884 - symbol:MOS1 "AT4G24680" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0040029 "regulation of gene expression, epigenetic" evidence=IMP] EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0016568 EMBL:AL035356 EMBL:AL161562 eggNOG:NOG12793 GO:GO:0040029 EMBL:HM208348 EMBL:AY062548 EMBL:AY093339 IPI:IPI00969741 PIR:T05566 RefSeq:NP_194199.4 UniGene:At.2541 IntAct:Q9SB63 PRIDE:Q9SB63 GeneID:828570 KEGG:ath:AT4G24680 TAIR:At4g24680 InParanoid:Q9SB63 PhylomeDB:Q9SB63 Genevestigator:Q9SB63 Uniprot:Q9SB63
Leaf	Isotig06443	18	6	2.114	0.000756754	TAIR|locus:2013880 - symbol:GSR2 "AT1G66200" species:3702 "Arabidopsis thaliana" [GO:0004356 "glutamate-ammonia ligase activity" evidence=ISS;IDA] [GO:0005829 "cytosol" evidence=IDA;TAS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0042128 "nitrate assimilation" evidence=TAS] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0048046 "apoplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] InterPro:IPR008146 InterPro:IPR008147 InterPro:IPR014746 Pfam:PF00120 Pfam:PF03951 PROSITE:PS00180 PROSITE:PS00181 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005524 GO:GO:0048046 GO:GO:0009570 GO:GO:0005773 EMBL:AC026480 GO:GO:0009941 GO:GO:0005507 GO:GO:0009651 GO:GO:0022626 GO:GO:0042128 GO:GO:0009399 eggNOG:COG0174 HOGENOM:HBG299709 ProtClustDB:PLN02284 GO:GO:0004356 GO:GO:0006542 Gene3D:G3DSA:3.30.590.10 Gene3D:G3DSA:3.10.20.70 SUPFAM:SSF54368 EMBL:AY091101 EMBL:AY122962 EMBL:AY086653 IPI:IPI00532772 PIR:H96686 PIR:S18602 RefSeq:NP_176794.1 UniGene:At.47484 UniGene:At.74857 ProteinModelPortal:Q8LCE1 SMR:Q8LCE1 IntAct:Q8LCE1 STRING:Q8LCE1 PRIDE:Q8LCE1 ProMEX:Q8LCE1 DNASU:842935 EnsemblPlants:AT1G66200.1 GeneID:842935 KEGG:ath:AT1G66200 TAIR:At1g66200 InParanoid:Q8LCE1 OMA:HICVYDP PhylomeDB:Q8LCE1 ArrayExpress:Q9C8C7 Genevestigator:Q8LCE1 Uniprot:Q8LCE1
Leaf	Isotig06451	13	1	4.229	7.21E-05	TAIR|locus:2172472 - symbol:AT5G43960 species:3702 "Arabidopsis thaliana" [GO:0000166 "nucleotide binding" evidence=IEA] [GO:0003676 "nucleic acid binding" evidence=IEA] [GO:0003723 "RNA binding" evidence=ISS] [GO:0005622 "intracellular" evidence=IEA] [GO:0006810 "transport" evidence=IEA] [GO:0006913 "nucleocytoplasmic transport" evidence=ISS] InterPro:IPR000504 InterPro:IPR002075 InterPro:IPR012677 Pfam:PF02136 PROSITE:PS50102 SMART:SM00360 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0000166 GO:GO:0006810 Gene3D:G3DSA:3.30.70.330 GO:GO:0003676 GO:GO:0005622 EMBL:AB006703 InterPro:IPR018222 PROSITE:PS50177 HOGENOM:HBG592577 EMBL:AY080755 EMBL:AY114017 IPI:IPI00523493 RefSeq:NP_199209.1 UniGene:At.24860 ProteinModelPortal:Q9FND0 SMR:Q9FND0 IntAct:Q9FND0 STRING:Q9FND0 PRIDE:Q9FND0 EnsemblPlants:AT5G43960.1 GeneID:834419

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						KEGG:ath:AT5G43960 TAIR:At5g43960 eggNOG:NOG295220 InParanoid:Q9FND0 OMA:EAPRGRF PhylomeDB:Q9FND0 ProtClustDB:CLSN2686872 ArrayExpress:Q9FND0 Genevestigator:Q9FND0 Uniprot:Q9FND0
Leaf	Isotig06457	25	3	3.588	1.80E-07	TAIR|locus:2175118 - symbol:AT5G60390 "AT5G60390" species:3702 "Arabidopsis thaliana" [GO:0003746 "translation elongation factor activity" evidence=ISS] [GO:0006414 "translational elongation" evidence=IEA] [GO:0005516 "calmodulin binding" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] PROSITE:PS00301 EMBL:CP002684 EMBL:U63815 EMBL:AC026875 EMBL:X16430 EMBL:AY039583 EMBL:BT000595 IPI:IPI00548618 PIR:S06724 UniGene:At.69737 UniGene:At.74830 EnsemblPlants:AT1G07940.1 EnsemblPlants:AT1G07940.2 TAIR:At1g07940 OMA:FLKAGDA GermOnline:AT1G07940 Uniprot:P0DH99
Leaf	Isotig06471	26	100	-1.414	5.96E-07	TAIR|locus:2028563 - symbol:AT1G48900 species:3702 "Arabidopsis thaliana" [GO:0000166 "nucleotide binding" evidence=IEA] [GO:0003729 "mRNA binding" evidence=ISS] [GO:0005525 "GTP binding" evidence=IEA;ISS] [GO:0005786 "signal recognition particle, endoplasmic reticulum targeting" evidence=ISS] [GO:0006614 "SRP-dependent cotranslational protein targeting to membrane" evidence=IEA] [GO:0006617 "SRP-dependent cotranslational protein targeting to membrane, signal sequence recognition" evidence=ISS] [GO:0008312 "7S RNA binding" evidence=IEA;ISS] [GO:0017111 "nucleoside-triphosphatase activity" evidence=IEA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR000897 InterPro:IPR003593 InterPro:IPR004125 InterPro:IPR006325 InterPro:IPR013822 Pfam:PF00448 Pfam:PF02881 Pfam:PF02978 PROSITE:PS00300 SMART:SM00382 SMART:SM00962 SMART:SM00963 GO:GO:0005525 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0017111 EMBL:AC084414 HOGENOM:HBG562580 GO:GO:0006614 Gene3D:G3DSA:1.20.120.140 SUPFAM:SSF47364 GO:GO:0008312 GO:GO:0005786 eggNOG:COG0541 KO:K03106 ProtClustDB:CLSN2686827 Gene3D:G3DSA:1.10.260.30 SUPFAM:SSF47446 TIGRFAMs:TIGR01425 EMBL:U12127 EMBL:AY054273 EMBL:AY052331 EMBL:AF446864 IPI:IPI00531486 PIR:G96526 RefSeq:NP_564535.1 UniGene:At.23838 ProteinModelPortal:P49967 SMR:P49967 STRING:P49967 PRIDE:P49967 EnsemblPlants:AT1G48900.1 GeneID:841312 KEGG:ath:AT1G48900 GeneFarm:1889 TAIR:At1g48900 InParanoid:P49967 OMA:SKKEHII PhylomeDB:P49967 ArrayExpress:P49967 Genevestigator:P49967 GermOnline:AT1G48900 Uniprot:P49967
Leaf	Isotig06472	17	4	2.616	0.000204438	TAIR|locus:2074403 - symbol:ACX4 "AT3G51840" species:3702 "Arabidopsis thaliana" [GO:0016491 "oxidoreductase activity" evidence=ISS] [GO:0003997 "acyl-CoA oxidase activity" evidence=IMP;IDA] [GO:0005777 "peroxisome" evidence=IDA] [GO:0006635 "fatty acid beta-oxidation" evidence=IMP;IDA] [GO:0009793 "embryo development ending in seed dormancy" evidence=IGI] [GO:0046459 "short-chain fatty acid metabolic process" evidence=TAS] [GO:0005829 "cytosol" evidence=RCA] InterPro:IPR006089 InterPro:IPR006090 InterPro:IPR006091 InterPro:IPR006092 InterPro:IPR009075 InterPro:IPR009100 InterPro:IPR013786 Pfam:PF00441 Pfam:PF02770 Pfam:PF02771 PROSITE:PS00072 PROSITE:PS00073 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0050660 GO:GO:0009514 GO:GO:0009793 eggNOG:COG1960 GO:GO:0003995 Gene3D:G3DSA:2.40.110.10 Gene3D:G3DSA:1.10.540.10 Gene3D:G3DSA:1.20.140.10 SUPFAM:SSF56645 SUPFAM:SSF47203 HOGENOM:HBG699365 GO:GO:0006635 KO:K00232 GO:GO:0003997 GO:GO:0046459 BRENDA:1.3.3.6 EMBL:U72505 EMBL:AB017643 EMBL:AF049236 EMBL:AY094441 EMBL:AY125536 EMBL:AY087793 IPI:IPI00544713 PIR:T46895 RefSeq:NP_190752.1 UniGene:At.21620 PDB:2IX5 PDB:2IX6 PDBsum:2IX5 PDBsum:2IX6 ProteinModelPortal:Q96329 SMR:Q96329 STRING:Q96329 PRIDE:Q96329 ProMEX:Q96329 EnsemblPlants:AT3G51840.1 GeneID:824347 KEGG:ath:AT3G51840 GeneFarm:4887 TAIR:At3g51840 InParanoid:Q96329 OMA:IFARNTT PhylomeDB:Q96329 ProtClustDB:PLN02526 Genevestigator:Q96329 GermOnline:AT3G51840 Uniprot:Q96329
Leaf	Isotig06478	26	155	-2.047	7.59E-16	TAIR|locus:2203028 - symbol:CRB "chloroplast RNA binding" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0050662 "coenzyme binding" evidence=IEA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0010319 "stromule" evidence=IDA] [GO:0042742 "defense response to bacterium" evidence=IEP] [GO:0016020 "membrane" evidence=IDA] [GO:0007623 "circadian rhythm" evidence=IEP;IMP] [GO:0009658 "chloroplast organization" evidence=IMP] [GO:0005777 "peroxisome" evidence=IDA] [GO:0005840 "ribosome" evidence=IDA] [GO:0006364 "rRNA processing" evidence=IGI]

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						[GO:0048046 "apoplast" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR016040 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009506 GO:GO:0048046 GO:GO:0005773 GO:GO:0042742 GO:GO:0005777 GO:GO:0016020 eggNOG:COG0451 GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 GO:GO:0007623 GO:GO:0009941 GO:GO:0010319 GO:GO:0009409 GO:GO:0009658 GO:GO:0010287 GO:GO:0005840 GO:GO:0006364 EMBL:AC006416 UniGene:At.50307 EMBL:Y10557 EMBL:Y15382 EMBL:AY070022 EMBL:AF428282 EMBL:AY035050 EMBL:AF325043 EMBL:AY062570 EMBL:AY087609 IPI:IPI00548101 PIR:E86226 PIR:T51863 PIR:T52072 RefSeq:NP_172405.1 UniGene:At.21708 ProteinModelPortal:Q9SA52 SMR:Q9SA52 STRING:Q9SA52 PRIDE:Q9SA52 ProMEX:Q9SA52 EnsemblPlants:AT1G09340.1 GeneID:837455 KEGG:ath:AT1G09340 TAIR:At1g09340 HOGENOM:HBG620021 InParanoid:Q9SA52 OMA:PTYIYGP PhylomeDB:Q9SA52 ProtClustDB:PLN00016 ArrayExpress:Q9SA52 Genevestigator:Q9SA52 Uniprot:Q9SA52
Leaf	Isotig06481	23	3	3.468	7.83E-07	TAIR|locus:2174799 - symbol:MGT9 "magnesium transporter 9" species:3702 "Arabidopsis thaliana" [GO:0016020 "membrane" evidence=IEA;ISS] [GO:0030001 "metal ion transport" evidence=IEA;ISS] [GO:0046873 "metal ion transmembrane transporter activity" evidence=ISS] [GO:0055085 "transmembrane transport" evidence=IEA] [GO:0015095 "magnesium ion transmembrane transporter activity" evidence=IDA] InterPro:IPR002523 Pfam:PF01544 GO:GO:0016021 EMBL:CP002688 GenomeReviews:BA000015_GR EMBL:AB010076 GO:GO:0015095 eggNOG:NOG284534 HOGENOM:HBG316327 EMBL:AJ297817 EMBL:AY150287 EMBL:AY065449 EMBL:AY096449 EMBL:AY084382 IPI:IPI00520870 IPI:IPI00548395 RefSeq:NP_201261.2 RefSeq:NP_851269.1 UniGene:At.9122 ProteinModelPortal:Q9FLG2 IntAct:Q9FLG2 PRIDE:Q9FLG2 EnsemblPlants:AT5G64560.1 GeneID:836577 KEGG:ath:AT5G64560 TAIR:At5g64560 InParanoid:Q9FLG2 OMA:IPYTWND PhylomeDB:Q9FLG2 ProtClustDB:CLSN2680613 ArrayExpress:Q9FLG2 Genevestigator:Q9FLG2 Uniprot:Q9FLG2
Leaf	Isotig06483	4	25	-2.115	0.000948108	TAIR|locus:2016605 - symbol:HEMA1 "AT1G58290" species:3702 "Arabidopsis thaliana" [GO:0006783 "heme biosynthetic process" evidence=IMP] [GO:0008883 "glutamyl-tRNA reductase activity" evidence=IGI;TAS] [GO:0015995 "chlorophyll biosynthetic process" evidence=IMP] [GO:0009507 "chloroplast" evidence=IDA;TAS] [GO:0005515 "protein binding" evidence=IPI] [GO:0006779 "porphyrin-containing compound biosynthetic process" evidence=TAS] [GO:0009416 "response to light stimulus" evidence=IEP] InterPro:IPR000343 InterPro:IPR015895 InterPro:IPR015896 InterPro:IPR016040 InterPro:IPR018214 Pfam:PF00745 Pfam:PF05201 PROSITE:PS00747 InterPro:IPR006151 Pfam:PF01488 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009507 GO:GO:0005515 Gene3D:G3DSA:3.40.50.720 GO:GO:0050661 EMBL:AC008051 GO:GO:0015995 GO:GO:0006783 EMBL:U03774 EMBL:AY072223 EMBL:AY096600 IPI:IPI00535419 PIR:E96616 RefSeq:NP_176125.1 UniGene:At.241 ProteinModelPortal:P42804 SMR:P42804 IntAct:P42804 STRING:P42804 PRIDE:P42804 EnsemblPlants:AT1G58290.1 GeneID:842198 KEGG:ath:AT1G58290 TAIR:At1g58290 eggNOG:COG0373 HOGENOM:HBG732626 InParanoid:P42804 KO:K02492 OMA:GPILNRL PhylomeDB:P42804 ProtClustDB:PLN00203 BioCyc:ARA:AT1G58290-MONOMER BioCyc:MetaCyc:AT1G58290-MONOMER ArrayExpress:P42804 Genevestigator:P42804 GermOnline:AT1G58290 GO:GO:0008883 SUPFAM:SSF69075 SUPFAM:SSF69742 TIGRFAMs:TIGR01035 Uniprot:P42804
Leaf	Isotig06486	24	0	6.114	1.86E-08	TAIR|locus:2174582 - symbol:XTH13 "xyloglucan endotransglucosylase/hydrolase 13" species:3702 "Arabidopsis thaliana" [GO:0005618 "cell wall" evidence=IEA] [GO:0016798 "hydrolase activity, acting on glycosyl bonds" evidence=ISS] [GO:0048046 "apoplast" evidence=IEA] [GO:0010411 "xyloglucan metabolic process" evidence=IDA] [GO:0033946 "xyloglucan-specific endo-beta-1,4-glucanase activity" evidence=IDA] [GO:0080039 "xyloglucan endotransglucosylase activity" evidence=IDA] InterPro:IPR000757 InterPro:IPR008263 InterPro:IPR008264 InterPro:IPR010713 Pfam:PF00722 Pfam:PF06955 PRINTS:PR00737 PROSITE:PS01034 GO:GO:0048046 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005618 GO:GO:0004553 InterPro:IPR008985 InterPro:IPR013320 Gene3D:G3DSA:2.60.120.200 SUPFAM:SSF49899 GO:GO:0007047 GO:GO:0010411 CAZy:GH16 eggNOG:COG2273 EMBL:AB011482 HOGENOM:HBG592277 KO:K08235 GO:GO:0016762 InterPro:IPR016455 PIRSF:PIRSF005604 ProtClustDB:CLSN2685868 GO:GO:0080039 IPI:IPI00529293 RefSeq:NP_200562.1 UniGene:At.55604 ProteinModelPortal:Q9FKL8 SMR:Q9FKL8 STRING:Q9FKL8 PRIDE:Q9FKL8 EnsemblPlants:AT5G57540.1 GeneID:835858 KEGG:ath:AT5G57540 TAIR:At5g57540 InParanoid:Q9FKL8 OMA:PLECTAT PhylomeDB:Q9FKL8 ArrayExpress:Q9FKL8 Genevestigator:Q9FKL8 GermOnline:AT5G57540 Uniprot:Q9FKL8

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig06495	31	0	6.483	2.05E-10	TAIR|locus:2026545 - symbol:AT1G07750 "AT1G07750" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0045735 "nutrient reservoir activity" evidence=ISS] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0008270 "zinc ion binding" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR006044 InterPro:IPR006045 Pfam:PF00190 PRINTS:PR00439 SMART:SM00835 GO:GO:0045735 InterPro:IPR011051 InterPro:IPR014710 Gene3D:G3DSA:2.60.120.10 SUPFAM:SSF51182 EMBL:CP002684 GO:GO:0005829 GO:GO:0009506 GO:GO:0008270 GO:GO:0005507 EMBL:AC007583 EMBL:AF334728 EMBL:AF410308 EMBL:BT001038 IPI:IPI00528478 PIR:A86213 RefSeq:NP_172255.1 UniGene:At.22153 ProteinModelPortal:Q9LQQ3 SMR:Q9LQQ3 PRIDE:Q9LQQ3 EnsemblPlants:AT1G07750.1 GeneID:837290 KEGG:ath:AT1G07750 TAIR:At1g07750 InParanoid:Q9LQQ3 OMA:LETHIKA PhylomeDB:Q9LQQ3 ProtClustDB:CLSN2682742 ArrayExpress:Q9LQQ3 Genevestigator:Q9LQQ3 Uniprot:Q9LQQ3
Leaf	Isotig06500	11	94	-2.566	6.36E-13	TAIR|locus:2131513 - symbol:AT4G26530 "AT4G26530" species:3702 "Arabidopsis thaliana" [GO:0004332 "fructose-bisphosphate aldolase activity" evidence=ISS;NAS] [GO:0006096 "glycolysis" evidence=IEA;ISS] [GO:0008152 "metabolic process" evidence=IEA] [GO:0009507 "chloroplast" evidence=IDA] InterPro:IPR000741 InterPro:IPR013785 Pfam:PF00274 PROSITE:PS00158 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0009507 Gene3D:G3DSA:3.20.20.70 GO:GO:0006096 EMBL:AL161565 eggNOG:COG3588 HOGENOM:HBG559178 KO:K01623 GO:GO:0004332 PANTHER:PTHR11627 OMA:LHRSKAN EMBL:AL022223 ProtClustDB:PLN02455 EMBL:AY087376 EMBL:BT002006 EMBL:BT008844 IPI:IPI00548350 PIR:T05051 RefSeq:NP_001031721.1 RefSeq:NP_194383.1 UniGene:At.57980 HSSP:P00883 ProteinModelPortal:O65581 SMR:O65581 IntAct:O65581 STRING:O65581 PRIDE:O65581 ProMEX:O65581 EnsemblPlants:AT4G26530.1 EnsemblPlants:AT4G26530.2 GeneID:828759 KEGG:ath:AT4G26530 TAIR:At4g26530 InParanoid:O65581 PhylomeDB:O65581 Genevestigator:O65581 Uniprot:O65581
Leaf	Isotig06510	15	0	5.436	8.75E-06	TAIR|locus:2025237 - symbol:ADH1 "AT1G77120" species:3702 "Arabidopsis thaliana" [GO:0045333 "cellular respiration" evidence=TAS] [GO:0006970 "response to osmotic stress" evidence=IGI] [GO:0001666 "response to hypoxia" evidence=IEP] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] [GO:0004022 "alcohol dehydrogenase (NAD) activity" evidence=ISS;IMP] InterPro:IPR002085 InterPro:IPR002328 InterPro:IPR013149 InterPro:IPR013154 InterPro:IPR016040 Pfam:PF00107 Pfam:PF08240 PROSITE:PS00059 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0005886 GO:GO:0046686 GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 GO:GO:0008270 GO:GO:0001666 GO:GO:0009651 InterPro:IPR011032 PANTHER:PTHR11695 SUPFAM:SSF50129 eggNOG:COG1062 GO:GO:0004022 EMBL:M12196 EMBL:X77943 EMBL:D84240 EMBL:D84241 EMBL:D84242 EMBL:D84243 EMBL:D84244 EMBL:D84245 EMBL:D84246 EMBL:D84247 EMBL:D84248 EMBL:D84249 EMBL:D63460 EMBL:D63461 EMBL:D63462 EMBL:D63463 EMBL:D63464 EMBL:AF110456 EMBL:AB048394 EMBL:AB048395 EMBL:AY536888 EMBL:AC002291 EMBL:AY045612 EMBL:AY090330 EMBL:AY088010 IPI:IPI00539119 PIR:A23815 RefSeq:NP_177837.1 UniGene:At.22653 UniGene:At.64099 ProteinModelPortal:P06525 SMR:P06525 STRING:P06525 PRIDE:P06525 EnsemblPlants:AT1G77120.1 GeneID:844047 KEGG:ath:AT1G77120 TAIR:At1g77120 InParanoid:P06525 KO:K00001 OMA:ECTGSVQ PhylomeDB:P06525 ProtClustDB:CLSN2717044 ArrayExpress:P06525 Genevestigator:P06525 Uniprot:P06525
Leaf	Isotig06528	81	32	1.869	4.37E-11	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Leaf	Isotig06539	19	7	1.970	0.000947153	TAIR|locus:2126749 - symbol:SIP3 "AT4G30960" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0016301 "kinase activity" evidence=ISS] [GO:0005515 "protein binding" evidence=IPI] [GO:0007275 "multicellular organismal development" evidence=IMP] [GO:0009414 "response to water deprivation" evidence=IEP] [GO:0009628 "response to abiotic stimulus" evidence=IMP] [GO:0009651 "response to

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						salt stress" evidence=IEP] [GO:0010540 "basipetal auxin transport" evidence=IMP] [GO:0042538 "hyperosmotic salinity response" evidence=IDA] InterPro:IPR000719 InterPro:IPR002290 InterPro:IPR004041 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 InterPro:IPR018451 Pfam:PF00069 Pfam:PF03822 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 PROSITE:PS50816 SMART:SM00220 GO:GO:0007275 GO:GO:0005524 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0007165 GO:GO:0005515 eggNOG:COG0515 SUPFAM:SSF56112 GO:GO:0004674 HOGENOM:HBG755340 GO:GO:0010540 GO:GO:0009414 EMBL:AL022198 EMBL:AL161578 GO:GO:0042538 HSSP:P49137 EMBL:AF285106 EMBL:AF339145 EMBL:AF436831 EMBL:AY035046 EMBL:AY051051 IPI:IPI00518255 PIR:E85362 RefSeq:NP_194825.1 UniGene:At.2154 ProteinModelPortal:O65554 SMR:O65554 DIP:DIP-34749N IntAct:O65554 STRING:O65554 PRIDE:O65554 EnsemblPlants:AT4G30960.1 GeneID:829221 KEGG:ath:AT4G30960 TAIR:At4g30960 InParanoid:O65554 OMA:SEHLKQD PhylomeDB:O65554 ProtClustDB:CLSN2685825 Genevestigator:O65554 Uniprot:O65554
Leaf	Isotig06569	2	20	-2.793	0.00051744	TAIR|locus:2204858 - symbol:AT1G02260 "AT1G02260" species:3702 "Arabidopsis thaliana" [GO:0005215 "transporter activity" evidence=ISS] [GO:0015137 "citrate transmembrane transporter activity" evidence=IEA] [GO:0015746 "citrate transport" evidence=IEA] [GO:0016021 "integral to membrane" evidence=IEA;ISS] [GO:0055085 "transmembrane transport" evidence=IEA] InterPro:IPR004680 Pfam:PF03600 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR eggNOG:COG1055 OMA:SANVICA GO:GO:0015137 EMBL:U89959 HOGENOM:HBG727257 EMBL:BT023463 IPI:IPI00519219 RefSeq:NP_171728.2 UniGene:At.48101 STRING:O81915 PRIDE:O81915 EnsemblPlants:AT1G02260.1 GeneID:839344 KEGG:ath:AT1G02260 TAIR:At1g02260 InParanoid:O81915 PhylomeDB:O81915 ProtClustDB:CLSN2918462 Genevestigator:O81915 Uniprot:O81915
Leaf	Isotig06630	27	6	2.699	1.95E-06	TAIR|locus:2094167 - symbol:AFP3 "AT3G29575" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0005515 "protein binding" evidence=IPI] GO:GO:0005634 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005515 InterPro:IPR012463 Pfam:PF07897 EMBL:AP002457 EMBL:AF385741 EMBL:AY133676 EMBL:AK317411 IPI:IPI00517851 RefSeq:NP_001030794.1 RefSeq:NP_001078222.1 RefSeq:NP_189598.1 UniGene:At.6431 DIP:DIP-40552N IntAct:Q94F39 STRING:Q94F39 PRIDE:Q94F39 EnsemblPlants:AT3G29575.1 EnsemblPlants:AT3G29575.3 EnsemblPlants:AT3G29575.4 GeneID:822619 KEGG:ath:AT3G29575 TAIR:At3g29575 eggNOG:NOG284974 InParanoid:Q94F39 OMA:SIASICS PhylomeDB:Q94F39 ProtClustDB:CLSN2684487 Genevestigator:Q94F39 Uniprot:Q94F39
Leaf	Isotig06650	17	58	-1.242	0.000584441	UNIPROTKB|P10933 - symbol:PETH "Ferredoxin--NADP reductase, leaf isozyme, chloroplastic" species:3888 "Pisum sativum" [GO:0005515 "protein binding" evidence=IPI] InterPro:IPR001433 InterPro:IPR001709 InterPro:IPR012146 InterPro:IPR015701 InterPro:IPR017927 InterPro:IPR017938 Pfam:PF00175 PIRSF:PIRSF000361 PRINTS:PR00371 PROSITE:PS51384 InterPro:IPR008333 Pfam:PF00970 GO:GO:0009570 GO:GO:0005515 GO:GO:0050660 GO:GO:0006810 GO:GO:0050661 GO:GO:0022900 GO:GO:0004324 SUPFAM:SSF63380 GO:GO:0009535 GO:GO:0015979 EMBL:X12446 EMBL:L15565 EMBL:L15567 EMBL:L15569 PIR:S04030 PDB:1QFY PDB:1QFZ PDB:1QG0 PDB:1QGA PDB:2XNC PDB:3MHP PDBsum:1QFY PDBsum:1QFZ PDBsum:1QG0 PDBsum:1QGA PDBsum:2XNC PDBsum:3MHP ProteinModelPortal:P10933 SMR:P10933 IntAct:P10933 PANTHER:PTHR19384:SF1 Uniprot:P10933
Leaf	Isotig06654	23	2	4.053	1.83E-07	TAIR|locus:2081378 - symbol:J3 species:3702 "Arabidopsis thaliana" [GO:0005524 "ATP binding" evidence=IEA] [GO:0006457 "protein folding" evidence=ISS] [GO:0031072 "heat shock protein binding" evidence=IEA] [GO:0051082 "unfolded protein binding" evidence=IEA] [GO:0005730 "nucleolus" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IMP] [GO:0043462 "regulation of ATPase activity" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] [GO:0009911 "positive regulation of flower development" evidence=IMP] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR001305 InterPro:IPR001623 InterPro:IPR002939 InterPro:IPR003095 InterPro:IPR008971 InterPro:IPR012724 InterPro:IPR018253 Pfam:PF00226 Pfam:PF00684 Pfam:PF01556 PRINTS:PR00625 PROSITE:PS00636 PROSITE:PS50076 PROSITE:PS51188 SMART:SM00271 GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 GO:GO:0005524 GO:GO:0005618 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0006457 GO:GO:0005730 GO:GO:0046872 GO:GO:0051082 GO:GO:0009651 GO:GO:0009408 GO:GO:0009911 GO:GO:0043462 eggNOG:COG0484 HOGENOM:HBG635315 GO:GO:0031072 Gene3D:G3DSA:1.10.287.110 Gene3D:G3DSA:2.10.230.10 SUPFAM:SSF46565

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						SUPFAM:SSF49493 SUPFAM:SSF57938 ProtClustDB:CLSN2684452 EMBL:U22340 EMBL:AF032883 EMBL:AL353814 EMBL:AY035087 EMBL:AY045655 EMBL:AY113878 EMBL:AY088078 IPI:IPI00544081 PIR:S71199 PIR:T49127 RefSeq:NP_189997.1 UniGene:At.20860 UniGene:At.24417 ProteinModelPortal:Q94AW8 SMR:Q94AW8 IntAct:Q94AW8 STRING:Q94AW8 PRIDE:Q94AW8 ProMEX:Q94AW8 EnsemblPlants:AT3G44110.1 GeneID:823531 KEGG:ath:AT3G44110 GeneFarm:2846 TAIR:At3g44110 InParanoid:Q94AW8 OMA:QCKGDKV PhylomeDB:Q94AW8 ArrayExpress:O22663 Genevestigator:Q94AW8 Uniprot:Q94AW8
Leaf	Isotig06661	10	1	3.851	0.00071293	TAIR|locus:2124256 - symbol:MCCB "AT4G34030" species:3702 "Arabidopsis thaliana" [GO:0004075 "biotin carboxylase activity" evidence=ISS] [GO:0005759 "mitochondrial matrix" evidence=ISS] [GO:0005739 "mitochondrion" evidence=IDA;TAS] [GO:0006552 "leucine catabolic process" evidence=IDA] [GO:0008270 "zinc ion binding" evidence=IDA] [GO:0050897 "cobalt ion binding" evidence=IDA] InterPro:IPR000022 InterPro:IPR011762 InterPro:IPR011763 Pfam:PF01039 PROSITE:PS50980 PROSITE:PS50989 GO:GO:0005524 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005759 GO:GO:0008270 GO:GO:0050897 EMBL:AL021961 EMBL:AL031032 EMBL:AL161584 GO:GO:0006552 BRENDA:6.4.1.4 GO:GO:0004485 EMBL:AF059511 EMBL:AF059510 EMBL:AF386926 EMBL:BT000384 IPI:IPI00531611 RefSeq:NP_567950.1 UniGene:At.19955 ProteinModelPortal:Q9LDD8 SMR:Q9LDD8 IntAct:Q9LDD8 STRING:Q9LDD8 PRIDE:Q9LDD8 EnsemblPlants:AT4G34030.1 GeneID:829549 KEGG:ath:AT4G34030 TAIR:At4g34030 eggNOG:COG4799 HOGENOM:HBG461319 InParanoid:Q9LDD8 KO:K01969 OMA:YLWPNAR PhylomeDB:Q9LDD8 ProtClustDB:PLN02820 ArrayExpress:Q9LDD8 Genevestigator:Q9LDD8 GermOnline:AT4G34030 Uniprot:Q9LDD8
Leaf	Isotig06672	20	64	-1.149	0.000680614	TAIR|locus:2200231 - symbol:HPR "hydroxypyruvate reductase" species:3702 "Arabidopsis thaliana" [GO:0005777 "peroxisome" evidence=IDA] [GO:0008465 "glycerate dehydrogenase activity" evidence=NAS] [GO:0008266 "poly(U) RNA binding" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009853 "photorespiration" evidence=TAS] InterPro:IPR006139 InterPro:IPR006140 InterPro:IPR016040 Pfam:PF00389 Pfam:PF02826 PROSITE:PS00065 EMBL:CP002684 GO:GO:0048046 GO:GO:0009507 GO:GO:0008266 GO:GO:0005777 Gene3D:G3DSA:3.40.50.720 GO:GO:0051287 EMBL:AC012563 HSSP:P30901 GO:GO:0008465 EMBL:AF370221 EMBL:AY099552 EMBL:AY113871 EMBL:BT001237 EMBL:AK226564 IPI:IPI00523994 PIR:B96703 RefSeq:NP_176968.1 UniGene:At.339 ProteinModelPortal:Q9C9W5 SMR:Q9C9W5 IntAct:Q9C9W5 STRING:Q9C9W5 PRIDE:Q9C9W5 ProMEX:Q9C9W5 EnsemblPlants:AT1G68010.1 GeneID:843129 KEGG:ath:AT1G68010 TAIR:At1g68010 InParanoid:Q9C9W5 OMA:KTRREMA PhylomeDB:Q9C9W5 ProtClustDB:PLN02306 ArrayExpress:Q9C9W5 Genevestigator:Q9C9W5 Uniprot:Q9C9W5
Leaf	Isotig06679	36	121	-1.220	9.63E-07	TAIR|locus:2200231 - symbol:HPR "hydroxypyruvate reductase" species:3702 "Arabidopsis thaliana" [GO:0005777 "peroxisome" evidence=IDA] [GO:0008465 "glycerate dehydrogenase activity" evidence=NAS] [GO:0008266 "poly(U) RNA binding" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009853 "photorespiration" evidence=TAS] InterPro:IPR006139 InterPro:IPR006140 InterPro:IPR016040 Pfam:PF00389 Pfam:PF02826 PROSITE:PS00065 EMBL:CP002684 GO:GO:0048046 GO:GO:0009507 GO:GO:0008266 GO:GO:0005777 Gene3D:G3DSA:3.40.50.720 GO:GO:0051287 EMBL:AC012563 HSSP:P30901 GO:GO:0008465 EMBL:AF370221 EMBL:AY099552 EMBL:AY113871 EMBL:BT001237 EMBL:AK226564 IPI:IPI00523994 PIR:B96703 RefSeq:NP_176968.1 UniGene:At.339 ProteinModelPortal:Q9C9W5 SMR:Q9C9W5 IntAct:Q9C9W5 STRING:Q9C9W5 PRIDE:Q9C9W5 ProMEX:Q9C9W5 EnsemblPlants:AT1G68010.1 GeneID:843129 KEGG:ath:AT1G68010 TAIR:At1g68010 InParanoid:Q9C9W5 OMA:KTRREMA PhylomeDB:Q9C9W5 ProtClustDB:PLN02306 ArrayExpress:Q9C9W5 Genevestigator:Q9C9W5 Uniprot:Q9C9W5
Leaf	Isotig06691	11	0	4.988	0.000159591	TAIR|locus:2092160 - symbol:AT3G26010 "AT3G26010" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] InterPro:IPR001810 Pfam:PF00646 PROSITE:PS50181 SMART:SM00256 EMBL:CP002686 EMBL:AB023041 SUPFAM:SSF81383 EMBL:DQ446701 IPI:IPI00542440 RefSeq:NP_189230.1 UniGene:At.27941 ProteinModelPortal:Q9LU90 SMR:Q9LU90 PRIDE:Q9LU90 EnsemblPlants:AT3G26010.1 GeneID:822198 KEGG:ath:AT3G26010 TAIR:At3g26010 eggNOG:NOG298717 InParanoid:Q9LU90 OMA:STIESVY ProtClustDB:CLSN2684708 Genevestigator:Q9LU90 Uniprot:Q9LU90
Leaf	Isotig06712	15	1	4.436	1.60E-05	TAIR|locus:2168586 - symbol:AT5G53480 "AT5G53480" species:3702 "Arabidopsis thaliana" [GO:0000059 "protein import into nucleus, docking" evidence=ISS] [GO:0005634 "nucleus" evidence=ISS] [GO:0005643 "nuclear pore" evidence=ISS] [GO:0005737 "cytoplasm" evidence=ISS] [GO:0006886 "intracellular protein transport"

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						evidence=IEA] [GO:0008565 "protein transporter activity" evidence=IEA;ISS] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] InterPro:IPR001494 InterPro:IPR011989 InterPro:IPR016024 Pfam:PF03810 PROSITE:PS50166 SMART:SM00913 EMBL:CP002688 GO:GO:0009507 GO:GO:0006886 GO:GO:0005488 SUPFAM:SSF48371 Gene3D:G3DSA:1.25.10.10 GO:GO:0008565 EMBL:AB015476 KO:K14293 OMA:EPSNHVR HSSP:Q14974 IPI:IPI00538987 RefSeq:NP_200160.1 UniGene:At.21940 ProteinModelPortal:Q9FJD4 SMR:Q9FJD4 STRING:Q9FJD4 PRIDE:Q9FJD4 EnsemblPlants:AT5G53480.1 GeneID:835429 KEGG:ath:AT5G53480 TAIR:At5g53480 InParanoid:Q9FJD4 PhylomeDB:Q9FJD4 ProtClustDB:CLSN2686540 Genevestigator:Q9FJD4 Uniprot:Q9FJD4
Leaf	Isotig06722	22	2	3.988	3.84E-07	TAIR|locus:2058384 - symbol:LACS8 "long-chain acyl-CoA synthetase 8" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004467 "long-chain fatty acid-CoA ligase activity" evidence=ISS;IDA] [GO:0006633 "fatty acid biosynthetic process" evidence=ISS] [GO:0008152 "metabolic process" evidence=IEA] [GO:0006631 "fatty acid metabolic process" evidence=TAS] [GO:0005783 "endoplasmic reticulum" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR000873 Pfam:PF00501 Prosite:PS00455 GO:GO:0005783 GO:GO:0005524 EMBL:CP002685 GenomeReviews:CT485783_GR InterPro:IPR020845 HSSP:P08659 GO:GO:0004467 GO:GO:0006631 eggNOG:COG1022 KO:K01897 GO:GO:0009941 EMBL:AC007213 EMBL:AC006951 EMBL:AF503758 EMBL:AY052664 EMBL:BT002288 IPI:IPI00542638 PIR:E84456 RefSeq:NP_178516.1 RefSeq:NP_849934.1 UniGene:At.21686 ProteinModelPortal:Q9SJD4 PRIDE:Q9SJD4 EnsemblPlants:AT2G04350.1 EnsemblPlants:AT2G04350.2 GeneID:814974 KEGG:ath:AT2G04350 TAIR:At2g04350 InParanoid:Q9SJD4 OMA:GPLVCCE PhylomeDB:Q9SJD4 ProtClustDB:PLN02387 ArrayExpress:Q9SJD4 Genevestigator:Q9SJD4 Uniprot:Q9SJD4
Leaf	Isotig06734	13	156	-3.056	3.80E-24	TAIR|locus:2131513 - symbol:AT4G26530 "AT4G26530" species:3702 "Arabidopsis thaliana" [GO:0004332 "fructose-bisphosphate aldolase activity" evidence=ISS;NAS] [GO:0006096 "glycolysis" evidence=IEA;ISS] [GO:0008152 "metabolic process" evidence=IEA] [GO:0009507 "chloroplast" evidence=IDA] InterPro:IPR000741 InterPro:IPR013785 Pfam:PF00274 PROSITE:PS00158 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0009507 Gene3D:G3DSA:3.20.20.70 GO:GO:0006096 EMBL:AL161565 eggNOG:COG3588 HOGENOM:HBG559178 KO:K01623 GO:GO:0004332 PANTHER:PTHR11627 OMA:LHRSKAN EMBL:AL022223 ProtClustDB:PLN02455 EMBL:AY087376 EMBL:BT002006 EMBL:BT008844 IPI:IPI00548350 PIR:T05051 RefSeq:NP_001031721.1 RefSeq:NP_194383.1 UniGene:At.57980 HSSP:P00883 ProteinModelPortal:O65581 SMR:O65581 IntAct:O65581 STRING:O65581 PRIDE:O65581 ProMEX:O65581 EnsemblPlants:AT4G26530.1 EnsemblPlants:AT4G26530.2 GeneID:828759 KEGG:ath:AT4G26530 TAIR:At4g26530 InParanoid:O65581 PhylomeDB:O65581 Genevestigator:O65581 Uniprot:O65581
Leaf	Isotig06735	11	0	4.988	0.000159591	TAIR|locus:2088756 - symbol:AT3G20930 species:3702 "Arabidopsis thaliana" [GO:0000166 "nucleotide binding" evidence=IEA] [GO:0003676 "nucleic acid binding" evidence=IEA] [GO:0003723 "RNA binding" evidence=ISS] [GO:0008150 "biological_process" evidence=ND] InterPro:IPR000504 InterPro:IPR012677 Pfam:PF00076 PROSITE:PS50102 SMART:SM00360 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0000166 Gene3D:G3DSA:3.30.70.330 GO:GO:0003676 HSSP:Q9V535 eggNOG:COG0724 EMBL:AY099828 EMBL:AY084565 EMBL:BT002195 IPI:IPI00537313 RefSeq:NP_566672.1 UniGene:At.43817 ProteinModelPortal:Q8L440 SMR:Q8L440 PRIDE:Q8L440 EnsemblPlants:AT3G20930.1 GeneID:821642 KEGG:ath:AT3G20930 TAIR:At3g20930 HOGENOM:HBG172977 InParanoid:Q8L440 OMA:INGWMIV PhylomeDB:Q8L440 ProtClustDB:CLSN2688611 ArrayExpress:Q8L440 Genevestigator:Q8L440 Uniprot:Q8L440
Leaf	Isotig06749	11	1	3.988	0.000330755	TAIR|locus:2154334 - symbol:HCT "AT5G48930" species:3702 "Arabidopsis thaliana" [GO:0016740 "transferase activity" evidence=ISS] [GO:0047172 "shikimate O-hydroxycinnamoyltransferase activity" evidence=IMP] [GO:0047205 "quinate O-hydroxycinnamoyltransferase activity" evidence=IMP] [GO:0009809 "lignin biosynthetic process" evidence=IMP] [GO:0009963 "positive regulation of flavonoid biosynthetic process" evidence=IMP] [GO:0010252 "auxin homeostasis" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR003480 Pfam:PF02458 GO:GO:0005829 EMBL:CP002688 InterPro:IPR023213 Gene3D:G3DSA:3.30.559.10 GO:GO:0016787 EMBL:AB017061 GO:GO:0009809 GO:GO:0010252 EMBL:BT026488 EMBL:AK226213 EMBL:AY084652 IPI:IPI00532885 RefSeq:NP_199704.1 UniGene:At.24445 ProteinModelPortal:Q9FI78 SMR:Q9FI78 IntAct:Q9FI78 STRING:Q9FI78 PRIDE:Q9FI78 DNASU:834951 GeneID:834951 KEGG:ath:AT5G48930 TAIR:At5g48930 InParanoid:Q9FI78 KO:K13065 OMA:INTWSDM PhylomeDB:Q9FI78

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						ProtClustDB:PLN02663 Genevestigator:Q9FI78 GO:GO:0047205 GO:GO:0047172 GO:GO:0009963 Uniprot:Q9FI78
Leaf	Isotig06753	12	51	-1.559	0.000127438	UNIPROTKB|P10933 - symbol:PETH "Ferredoxin--NADP reductase, leaf isozyme, chloroplastic" species:3888 "Pisum sativum" [GO:0005515 "protein binding" evidence=IPI] InterPro:IPR001433 InterPro:IPR001709 InterPro:IPR012146 InterPro:IPR015701 InterPro:IPR017927 InterPro:IPR017938 Pfam:PF00175 PIRSF:PIRSF000361 PRINTS:PR00371 PROSITE:PS51384 InterPro:IPR008333 Pfam:PF00970 GO:GO:0009570 GO:GO:0005515 GO:GO:0050660 GO:GO:0006810 GO:GO:0050661 GO:GO:0022900 GO:GO:0004324 SUPFAM:SSF63380 GO:GO:0009535 GO:GO:0015979 EMBL:X12446 EMBL:L15565 EMBL:L15567 EMBL:L15569 PIR:S04030 PDB:1QFY PDB:1QFZ PDB:1QG0 PDB:1QGA PDB:2XNC PDB:3MHP PDBsum:1QFY PDBsum:1QFZ PDBsum:1QG0 PDBsum:1QGA PDBsum:2XNC PDBsum:3MHP ProteinModelPortal:P10933 SMR:P10933 IntAct:P10933 PANTHER:PTHR19384:SF1 Uniprot:P10933
Leaf	Isotig06765	0	13	-4.171	0.000994782	TAIR|locus:2129930 - symbol:CIPK4 "CBL-interacting protein kinase 4" species:3702 "Arabidopsis thaliana" [GO:0004672 "protein kinase activity" evidence=IEA] [GO:0004674 "protein serine/threonine kinase activity" evidence=IEA] [GO:0005524 "ATP binding" evidence=IEA] [GO:0006468 "protein phosphorylation" evidence=IEA] [GO:0007165 "signal transduction" evidence=IEA] [GO:0016301 "kinase activity" evidence=ISS] InterPro:IPR000719 InterPro:IPR002290 InterPro:IPR004041 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 InterPro:IPR018451 Pfam:PF00069 Pfam:PF03822 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 PROSITE:PS50816 SMART:SM00220 GO:GO:0005524 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0007165 eggNOG:COG0515 SUPFAM:SSF56112 GO:GO:0004674 HOGENOM:HBG755340 HSSP:P06782 EMBL:Z97336 EMBL:AL161539 EMBL:AY007221 IPI:IPI00548657 PIR:C71408 RefSeq:NP_193194.1 UniGene:At.64185 ProteinModelPortal:Q9SUL7 SMR:Q9SUL7 IntAct:Q9SUL7 STRING:Q9SUL7 PRIDE:Q9SUL7 EnsemblPlants:AT4G14580.1 GeneID:827106 KEGG:ath:AT4G14580 TAIR:At4g14580 InParanoid:Q9SUL7 OMA:IELHEVM PhylomeDB:Q9SUL7 ProtClustDB:CLSN2717554 ArrayExpress:Q9SUL7 Genevestigator:Q9SUL7 Uniprot:Q9SUL7
Leaf	Isotig06767	10	0	4.851	0.000336918	TAIR|locus:2023865 - symbol:AT1G13640 "AT1G13640" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0016773 "phosphotransferase activity, alcohol group as acceptor" evidence=IEA] InterPro:IPR000403 Pfam:PF00454 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0016773 GO:GO:0016301 eggNOG:NOG287949 HOGENOM:HBG603679 EMBL:AY060574 EMBL:AY149944 IPI:IPI00546784 RefSeq:NP_563930.1 UniGene:At.27453 UniGene:At.71901 ProteinModelPortal:Q8W4R8 SMR:Q8W4R8 PRIDE:Q8W4R8 EnsemblPlants:AT1G13640.1 GeneID:837925 KEGG:ath:AT1G13640 TAIR:At1g13640 InParanoid:Q8W4R8 OMA:QTANDIV PhylomeDB:Q8W4R8 ProtClustDB:CLSN2687794 Genevestigator:Q8W4R8 Uniprot:Q8W4R8
Leaf	Isotig06768	16	1	4.529	7.58E-06	TAIR|locus:2126634 - symbol:AT4G31080 "AT4G31080" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] GenomeReviews:CT486007_GR InterPro:IPR019273 Pfam:PF10058 EMBL:AK176449 IPI:IPI00525084 STRING:Q67YL9 PRIDE:Q67YL9 TAIR:At4g31080 PhylomeDB:Q67YL9 Genevestigator:Q67YL9 Uniprot:Q67YL9
Leaf	Isotig06776	24	0	6.114	1.86E-08	TAIR|locus:2019449 - symbol:MGL "AT1G64660" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=ISS] [GO:0006520 "cellular amino acid metabolic process" evidence=ISS] [GO:0005829 "cytosol" evidence=IDA] [GO:0018826 "methionine gamma-lyase activity" evidence=IDA] [GO:0019458 "methionine catabolic process via 2-oxobutanoate" evidence=TAS] InterPro:IPR000277 InterPro:IPR015421 InterPro:IPR015422 Pfam:PF01053 PIRSF:PIRSF001434 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0030170 InterPro:IPR015424 Gene3D:G3DSA:3.40.640.10 Gene3D:G3DSA:3.90.1150.10 SUPFAM:SSF53383 EMBL:AC009519 eggNOG:COG0626 HOGENOM:HBG754729 PANTHER:PTHR11808 HSSP:P13254 EMBL:AY054546 EMBL:AF428413 EMBL:BT006588 EMBL:AK226375 IPI:IPI00518615 PIR:G96669 RefSeq:NP_176647.1 UniGene:At.16566 UniGene:At.35974 ProteinModelPortal:Q9SGU9 SMR:Q9SGU9 STRING:Q9SGU9 PRIDE:Q9SGU9 EnsemblPlants:AT1G64660.1 GeneID:842774 KEGG:ath:AT1G64660 TAIR:At1g64660 InParanoid:Q9SGU9 KO:K01761 OMA:YETLMSC PhylomeDB:Q9SGU9 ProtClustDB:PLN02242 Genevestigator:Q9SGU9 GO:GO:0018826 GO:GO:0019458 Uniprot:Q9SGU9
Leaf	Isotig06822	31	9	2.313	2.97E-06	FB|FBgn0016977 - symbol:spen "split ends" species:7227 "Drosophila melanogaster" [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IMP] [GO:0007379 "segment specification" evidence=IMP] [GO:0005634 "nucleus" evidence=NAS;IDA] [GO:0007411 "axon guidance" evidence=IMP] [GO:0007400 "neuroblast fate determination" evidence=IMP] [GO:0008347 "glial cell migration" evidence=IMP] [GO:0007403 "glial cell fate

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						determination" evidence=IMP] [GO:0007173 "epidermal growth factor receptor signaling pathway" evidence=IMP] [GO:0016055 "Wnt receptor signaling pathway" evidence=IMP] [GO:0003676 "nucleic acid binding" evidence=IEA] [GO:0000166 "nucleotide binding" evidence=IEA] [GO:0007422 "peripheral nervous system development" evidence=IMP] [GO:0008586 "imaginal disc-derived wing vein morphogenesis" evidence=IMP] [GO:0035321 "maintenance of imaginal disc-derived wing hair orientation" evidence=IMP] [GO:0048106 "establishment of thoracic bristle planar orientation" evidence=IMP] InterPro:IPR000504 InterPro:IPR010912 InterPro:IPR012677 InterPro:IPR016194 Pfam:PF00076 PROSITE:PS50102 PROSITE:PS50917 SMART:SM00360 GO:GO:0005634 GO:GO:0007411 GO:GO:0007173 EMBL:AE014134 GO:GO:0006355 GO:GO:0016055 GO:GO:0000166 GO:GO:0035321 GO:GO:0008586 Gene3D:G3DSA:3.30.70.330 GO:GO:0007422 GO:GO:0006351 GO:GO:0003723 GO:GO:0007400 GO:GO:0007379 eggNOG:NOG12793 InterPro:IPR012921 Pfam:PF07744 GO:GO:0007403 GO:GO:0048106 Gene3D:G3DSA:2.40.290.10 SUPFAM:SSF100939 CTD:23013 GeneTree:ENSGT00530000063730 EMBL:AF188205 EMBL:AF184612 EMBL:AF221715 EMBL:AY094788 RefSeq:NP_524718.2 RefSeq:NP_722615.1 RefSeq:NP_722616.1 UniGene:Dm.3450 ProteinModelPortal:Q8SX83 SMR:Q8SX83 IntAct:Q8SX83 MINT:MINT-763765 STRING:Q8SX83 EnsemblMetazoa:FBtr0078122 GeneID:44205 KEGG:dme:Dmel_CG18497 FlyBase:FBgn0016977 InParanoid:Q8SX83 OMA:QIDTDTE OrthoDB:EOG4BCC2T PhylomeDB:Q8SX83 NextBio:836951 Bgee:Q8SX83 GermOnline:CG18497 Uniprot:Q8SX83
Leaf	Isotig06846	75	189	-0.804	1.43E-05	TAIR|locus:2040934 - symbol:LHB1B2 "AT2G34420" species:3702 "Arabidopsis thaliana" [GO:0009769 "photosynthesis, light harvesting in photosystem II" evidence=TAS] [GO:0016168 "chlorophyll binding" evidence=ISS;TAS] [GO:0030076 "light-harvesting complex" evidence=ISS] [GO:0042651 "thylakoid membrane" evidence=TAS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0015979 "photosynthesis" evidence=ISS] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR001344 Pfam:PF00504 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009535 GO:GO:0010287 EMBL:AC004077 EMBL:AC004481 HOGENOM:HBG618504 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 UniGene:At.10812 UniGene:At.24351 UniGene:At.32199 UniGene:At.66422 UniGene:At.71449 UniGene:At.71528 KO:K08912 ProtClustDB:PLN00025 UniGene:At.23647 UniGene:At.27457 UniGene:At.24888 EMBL:AF372886 EMBL:AY039561 EMBL:AY045806 EMBL:AF428397 EMBL:AF419548 EMBL:AF419587 EMBL:AY065125 EMBL:AY079101 EMBL:AY079110 EMBL:AY081587 EMBL:AY142513 EMBL:AK229627 EMBL:X64460 IPI:IPI00530785 PIR:S23546 RefSeq:NP_565786.1 UniGene:At.24064 UniGene:At.71003 UniGene:At.71384 ProteinModelPortal:Q39141 SMR:Q39141 IntAct:Q39141 STRING:Q39141 PRIDE:Q39141 EnsemblPlants:AT2G34420.1 GeneID:818005 KEGG:ath:AT2G34420 TAIR:At2g34420 InParanoid:Q39141 OMA:SILAIWG PhylomeDB:Q39141 ArrayExpress:Q39141 Genevestigator:Q39141 Uniprot:Q39141
Leaf	Isotig06864	11	60	-1.919	1.54E-06	TAIR|locus:2203028 - symbol:CRB "chloroplast RNA binding" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0050662 "coenzyme binding" evidence=IEA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0010319 "stromule" evidence=IDA] [GO:0042742 "defense response to bacterium" evidence=IEP] [GO:0016020 "membrane" evidence=IDA] [GO:0007623 "circadian rhythm" evidence=IEP;IMP] [GO:0009658 "chloroplast organization" evidence=IMP] [GO:0005777 "peroxisome" evidence=IDA] [GO:0005840 "ribosome" evidence=IDA] [GO:0006364 "rRNA processing" evidence=IGI] [GO:0048046 "apoplast" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR016040 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009506 GO:GO:0048046 GO:GO:0005773 GO:GO:0042742 GO:GO:0005777 GO:GO:0016020 eggNOG:COG0451 GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 GO:GO:0007623 GO:GO:0009941 GO:GO:0010319 GO:GO:0009409 GO:GO:0009658 GO:GO:0010287 GO:GO:0005840 GO:GO:0006364 EMBL:AC006416 UniGene:At.50307 EMBL:Y10557 EMBL:Y15382 EMBL:AY070022 EMBL:AF428282 EMBL:AY035050 EMBL:AF325043 EMBL:AY062570 EMBL:AY087609 IPI:IPI00548101 PIR:E86226 PIR:T51863 PIR:T52072 RefSeq:NP_172405.1 UniGene:At.21708 ProteinModelPortal:Q9SA52 SMR:Q9SA52 STRING:Q9SA52 PRIDE:Q9SA52 ProMEX:Q9SA52 EnsemblPlants:AT1G09340.1 GeneID:837455 KEGG:ath:AT1G09340 TAIR:At1g09340 HOGENOM:HBG620021 InParanoid:Q9SA52 OMA:PTYIYGP PhylomeDB:Q9SA52 ProtClustDB:PLN00016 ArrayExpress:Q9SA52 Genevestigator:Q9SA52 Uniprot:Q9SA52

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig06867	1	19	-3.719	0.000124272	TAIR|locus:2180054 - symbol:AT5G18630 species:3702 "Arabidopsis thaliana" [GO:0004806 "triglyceride lipase activity" evidence=IEA;ISS] [GO:0006629 "lipid metabolic process" evidence=IEA;ISS] InterPro:IPR002921 Pfam:PF01764 EMBL:CP002688 GO:GO:0004806 GO:GO:0006629 EMBL:BT015039 IPI:IPI00525192 RefSeq:NP_850848.2 UniGene:At.20654 ProteinModelPortal:Q6DBI3 SMR:Q6DBI3 STRING:Q6DBI3 PRIDE:Q6DBI3 EnsemblPlants:AT5G18630.1 GeneID:831981 KEGG:ath:AT5G18630 TAIR:At5g18630 eggNOG:NOG264838 InParanoid:Q6DBI3 OMA:ANINIIV PhylomeDB:Q6DBI3 ProtClustDB:CLSN2686575 Genevestigator:Q6DBI3 Uniprot:Q6DBI3
Leaf	Isotig06872	12	0	5.114	7.63E-05	TAIR|locus:2197379 - symbol:SNRK2.4 "AT1G10940" species:3702 "Arabidopsis thaliana" [GO:0016301 "kinase activity" evidence=ISS;IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0006970 "response to osmotic stress" evidence=IGI;IDA] [GO:0009651 "response to salt stress" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0009737 "response to abscisic acid stimulus" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR000719 InterPro:IPR002290 InterPro:IPR008271 InterPro:IPR011009 InterPro:IPR017441 Pfam:PF00069 PROSITE:PS00107 PROSITE:PS00108 PROSITE:PS50011 SMART:SM00220 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0005524 GO:GO:0009737 GO:GO:0005634 GO:GO:0005515 eggNOG:COG0515 SUPFAM:SSF56112 GO:GO:0004674 HOGENOM:HBG755340 BRENDA:2.7.11.1 GO:GO:0009651 EMBL:U95973 EMBL:M91548 EMBL:AY093130 EMBL:BT008850 EMBL:AY084221 IPI:IPI00522193 PIR:S36944 RefSeq:NP_172563.1 UniGene:At.23750 ProteinModelPortal:P43291 SMR:P43291 IntAct:P43291 STRING:P43291 PRIDE:P43291 ProMEX:P43291 EnsemblPlants:AT1G10940.1 GeneID:837637 KEGG:ath:AT1G10940 TAIR:At1g10940 InParanoid:P43291 KO:K14498 OMA:LAIAMEY PhylomeDB:P43291 ProtClustDB:CLSN2681826 ArrayExpress:P43291 Genevestigator:P43291 GermOnline:AT1G10940 Uniprot:P43291
Leaf	Isotig06876	11	1	3.988	0.000330755	TAIR|locus:2178378 - symbol:AT5G55960 "AT5G55960" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002688 eggNOG:NOG272528 InterPro:IPR002549 PANTHER:PTHR21716 Pfam:PF01594 EMBL:AY059863 EMBL:BT003364 IPI:IPI00543076 RefSeq:NP_568833.1 UniGene:At.26758 PRIDE:Q93XX1 EnsemblPlants:AT5G55960.1 GeneID:835694 KEGG:ath:AT5G55960 TAIR:At5g55960 InParanoid:Q93XX1 OMA:EIQEDIP PhylomeDB:Q93XX1 ProtClustDB:CLSN2690027 ArrayExpress:Q93XX1 Genevestigator:Q93XX1 Uniprot:Q93XX1
Leaf	Isotig06917	79	272	-1.255	5.91E-14	TAIR|locus:2042148 - symbol:LHCB2.1 "AT2G05100" species:3702 "Arabidopsis thaliana" [GO:0015979 "photosynthesis" evidence=ISS] [GO:0016168 "chlorophyll binding" evidence=ISS] [GO:0030076 "light-harvesting complex" evidence=ISS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009637 "response to blue light" evidence=IEP] [GO:0010114 "response to red light" evidence=IEP] [GO:0010218 "response to far red light" evidence=IEP] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR001344 Pfam:PF00504 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009941 GO:GO:0009637 GO:GO:0010218 GO:GO:0010114 GO:GO:0009535 GO:GO:0010287 HOGENOM:HBG618504 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 ProtClustDB:PLN00025 UniGene:At.48420 UniGene:At.63397 KO:K08913 EMBL:AC007443 EMBL:AY052275 EMBL:AY052348 EMBL:BT001933 IPI:IPI00535929 RefSeq:NP_178585.1 ProteinModelPortal:Q9SHR7 SMR:Q9SHR7 STRING:Q9SHR7 PRIDE:Q9SHR7 EnsemblPlants:AT2G05100.1 GeneID:815058 KEGG:ath:AT2G05100 TAIR:At2g05100 InParanoid:Q9SHR7 OMA:HQTTSFL PhylomeDB:Q9SHR7 ArrayExpress:Q9SHR7 Genevestigator:Q9SHR7 Uniprot:Q9SHR7
Leaf	Isotig06939	22	1	4.988	9.32E-08	TAIR|locus:2020522 - symbol:AT1G55760 "AT1G55760" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] InterPro:IPR000210 InterPro:IPR013069 Pfam:PF00651 PROSITE:PS50097 SMART:SM00225 EMBL:CP002684 GenomeReviews:CT485782_GR InterPro:IPR011333 Gene3D:G3DSA:3.30.710.10 SUPFAM:SSF54695 EMBL:AC002328 ProtClustDB:CLSN2679751 EMBL:AK175625 EMBL:AK175859 EMBL:BT022097 IPI:IPI00519325 RefSeq:NP_175972.1 UniGene:At.49979 ProteinModelPortal:Q680K8 SMR:Q680K8 PRIDE:Q680K8 EnsemblPlants:AT1G55760.1 GeneID:842025 KEGG:ath:AT1G55760 TAIR:At1g55760 eggNOG:NOG248759 HOGENOM:HBG320285 InParanoid:Q680K8 OMA:SIGAHRA PhylomeDB:Q680K8 ArrayExpress:Q680K8 Genevestigator:Q680K8 Uniprot:Q680K8

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig06968	8	36	-1.641	0.000834246	TAIR|locus:2193844 - symbol:ZKT "protein containing PDZ domain, a K-box domain, and a TPR region" species:3702 "Arabidopsis thaliana" [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009611 "response to wounding" evidence=IEP] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] InterPro:IPR001478 InterPro:IPR011990 InterPro:IPR013026 InterPro:IPR019734 PROSITE:PS50005 PROSITE:PS50106 PROSITE:PS50293 EMBL:CP002684 GO:GO:0009570 GO:GO:0009611 GO:GO:0005488 GO:GO:0009941 Gene3D:G3DSA:1.25.40.10 SUPFAM:SSF50156 GO:GO:0009535 EMBL:AY039926 EMBL:AY079359 EMBL:AY986818 EMBL:AB190499 IPI:IPI00548632 RefSeq:NP_564691.1 UniGene:At.19231 ProteinModelPortal:Q94BS2 SMR:Q94BS2 STRING:Q94BS2 PRIDE:Q94BS2 ProMEX:Q94BS2 EnsemblPlants:AT1G55480.1 GeneID:841995 KEGG:ath:AT1G55480 TAIR:At1g55480 InParanoid:Q94BS2 OMA:ASYNVAC PhylomeDB:Q94BS2 ProtClustDB:CLSN2688838 ArrayExpress:Q94BS2 Genevestigator:Q94BS2 Uniprot:Q94BS2
Leaf	Isotig06983	10	0	4.851	0.000336918	TAIR|locus:2169288 - symbol:AT5G43310 species:3702 "Arabidopsis thaliana" [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] GO:GO:0005886 GenomeReviews:BA000015_GR EMBL:AB025638 EMBL:AB017070 IPI:IPI00516817 PRIDE:Q9FHR5 TAIR:At5g43310 InParanoid:Q9FHR5 PhylomeDB:Q9FHR5 Genevestigator:Q9FHR5 Uniprot:Q9FHR5
Leaf	Isotig06989	24	1	5.114	2.21E-08	UNIPROTKB|P93332 - symbol:N3 "Bidirectional sugar transporter N3" species:3880 "Medicago truncatula" [GO:0005887 "integral to plasma membrane" evidence=ISS] [GO:0051119 "sugar transmembrane transporter activity" evidence=ISS] InterPro:IPR004316 Pfam:PF03083 GO:GO:0005887 GO:GO:0051119 PANTHER:PTHR10791 EMBL:Y08726 TCDB:9.A.58.1.1 Uniprot:P93332
Leaf	Isotig06999	31	9	2.313	2.97E-06	TAIR|locus:2087388 - symbol:EMB3126 "EMBRYO DEFECTIVE 3126" species:3702 "Arabidopsis thaliana" [GO:0003723 "RNA binding" evidence=IEA] [GO:0003735 "structural constituent of ribosome" evidence=IEA;ISS] [GO:0005840 "ribosome" evidence=ISS] [GO:0006396 "RNA processing" evidence=IEA] [GO:0006412 "translation" evidence=IEA;ISS] [GO:0005634 "nucleus" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] InterPro:IPR002143 InterPro:IPR005878 InterPro:IPR016094 InterPro:IPR016095 InterPro:IPR023674 Pfam:PF00687 Prosite:PS01199 GO:GO:0009570 GO:GO:0005634 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0006412 GO:GO:0009941 EMBL:AL163818 GO:GO:0003735 GO:GO:0009535 GO:GO:0019843 GO:GO:0015934 SUPFAM:SSF56808 UniGene:At.24203 UniGene:At.69654 eggNOG:COG0081 InterPro:IPR023673 Gene3D:G3DSA:3.30.190.20 Gene3D:G3DSA:3.40.50.790 EMBL:X90855 EMBL:BT001191 EMBL:AY133519 EMBL:AY059929 EMBL:AY053410 IPI:IPI00522851 PIR:T49190 PIR:T51934 RefSeq:NP_191908.1 HSSP:Q5SLP7 ProteinModelPortal:Q9LY66 SMR:Q9LY66 STRING:Q9LY66 PRIDE:Q9LY66 ProMEX:Q9LY66 EnsemblPlants:AT3G63490.1 GeneID:825524 KEGG:ath:AT3G63490 GeneFarm:61 TAIR:At3g63490 HOGENOM:HBG297400 InParanoid:Q9LY66 OMA:KAGTVTM PhylomeDB:Q9LY66 ProtClustDB:CLSN2914724 ArrayExpress:Q9LY66 Genevestigator:Q9LY66 TIGRFAMs:TIGR01169 Uniprot:Q9LY66
Leaf	Isotig07006	25	9	2.003	0.000126076	TAIR|locus:2200507 - symbol:AT1G16180 "AT1G16180" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0016020 "membrane" evidence=ISS] InterPro:IPR005016 Pfam:PF03348 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0016020 EMBL:AC010924 eggNOG:NOG308011 PANTHER:PTHR10383 OMA:DNDSRAC HOGENOM:HBG409729 ProtClustDB:CLSN2679769 IPI:IPI00542885 PIR:F86296 RefSeq:NP_001185008.1 RefSeq:NP_173069.1 UniGene:At.11862 STRING:Q9S9L9 PRIDE:Q9S9L9 EnsemblPlants:AT1G16180.1 EnsemblPlants:AT1G16180.2 GeneID:838187 KEGG:ath:AT1G16180 TAIR:At1g16180 InParanoid:Q9S9L9 PhylomeDB:Q9S9L9 Genevestigator:Q9S9L9 Uniprot:Q9S9L9
Leaf	Isotig07013	24	2	4.114	8.70E-08	TAIR|locus:2007372 - symbol:AT1G07040 "AT1G07040" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] EMBL:CP002684 GenomeReviews:CT485782_GR EMBL:AC067971 InterPro:IPR009770 Pfam:PF07063 HOGENOM:HBG298188 ProtClustDB:CLSN2682860 EMBL:AY087534 EMBL:BT002383 EMBL:BT008835 EMBL:AK226231 IPI:IPI00538607 PIR:B86205 RefSeq:NP_563777.1 UniGene:At.17142 ProteinModelPortal:Q9LMJ7 SMR:Q9LMJ7 STRING:Q9LMJ7 PRIDE:Q9LMJ7 EnsemblPlants:AT1G07040.1 GeneID:837215 KEGG:ath:AT1G07040 TAIR:At1g07040 eggNOG:NOG268275 InParanoid:Q9LMJ7 OMA:KLNSEGG PhylomeDB:Q9LMJ7 ArrayExpress:Q9LMJ7 Genevestigator:Q9LMJ7 Uniprot:Q9LMJ7

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig07015	10	0	4.851	0.000336918	TAIR|locus:2011030 - symbol:LOX1 "AT1G55020" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0010386 "lateral root primordium development" evidence=IMP] [GO:0048364 "root development" evidence=IMP] [GO:0016165 "lipoxygenase activity" evidence=ISS;IMP;IDA] [GO:0006952 "defense response" evidence=TAS] [GO:0009611 "response to wounding" evidence=TAS] [GO:0009695 "jasmonic acid biosynthetic process" evidence=TAS] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] [GO:0009753 "response to jasmonic acid stimulus" evidence=IEP] [GO:0009816 "defense response to bacterium, incompatible interaction" evidence=IEP] [GO:0030397 "membrane disassembly" evidence=TAS] [GO:0040007 "growth" evidence=TAS] InterPro:IPR000907 InterPro:IPR001024 InterPro:IPR001246 InterPro:IPR013819 InterPro:IPR020833 InterPro:IPR020834 Pfam:PF00305 Pfam:PF01477 PRINTS:PR00087 PRINTS:PR00468 PROSITE:PS00081 PROSITE:PS00711 PROSITE:PS50095 PROSITE:PS51393 SMART:SM00308 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009737 GO:GO:0005737 GO:GO:0009753 GO:GO:0005506 GO:GO:0031408 GO:GO:0010386 EMBL:AC064840 EMBL:AC069144 InterPro:IPR008976 Gene3D:G3DSA:2.60.60.20 SUPFAM:SSF49723 GO:GO:0016165 PANTHER:PTHR11771 SUPFAM:SSF48484 eggNOG:NOG69653 EMBL:L04637 EMBL:U01843 EMBL:AY093104 EMBL:BT010358 IPI:IPI00547307 PIR:JQ2267 RefSeq:NP_175900.1 UniGene:At.19984 UniGene:At.67309 ProteinModelPortal:Q06327 SMR:Q06327 STRING:Q06327 PRIDE:Q06327 EnsemblPlants:AT1G55020.1 GeneID:841944 KEGG:ath:AT1G55020 TAIR:At1g55020 HOGENOM:HBG749429 InParanoid:Q06327 KO:K15718 OMA:TPKEFDS PhylomeDB:Q06327 ProtClustDB:PLN02337 ArrayExpress:Q06327 Genevestigator:Q06327 GermOnline:AT1G55020 Uniprot:Q06327
Leaf	Isotig07030	23	3	3.468	7.83E-07	UNIPROTKB|Q9LEH3 - symbol:pod "Peroxidase 15" species:4120 "Ipomoea batatas" [GO:0004601 "peroxidase activity" evidence=IDA] [GO:0020037 "heme binding" evidence=IDA] InterPro:IPR000823 InterPro:IPR002016 InterPro:IPR010255 InterPro:IPR019793 InterPro:IPR019794 Pfam:PF00141 PRINTS:PR00458 PRINTS:PR00461 PROSITE:PS00435 PROSITE:PS00436 PROSITE:PS50873 GO:GO:0005576 GO:GO:0020037 GO:GO:0004601 GO:GO:0042744 SUPFAM:SSF48113 EMBL:AJ242742 HSSP:Q42578 ProteinModelPortal:Q9LEH3 SMR:Q9LEH3 PeroxiBase:296 Uniprot:Q9LEH3
Leaf	Isotig07069	29	0	6.387	7.28E-10	TAIR|locus:2121249 - symbol:AT4G38700 "AT4G38700" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0006952 "defense response" evidence=ISS] Pfam:PF03018 GenomeReviews:CT486007_GR EMBL:AL161593 EMBL:AL035540 InterPro:IPR004265 HOGENOM:HBG605442 IPI:IPI00527382 PIR:T05698 PRIDE:Q9SZP7 TAIR:At4g38700 eggNOG:NOG319111 InParanoid:Q9SZP7 PhylomeDB:Q9SZP7 ArrayExpress:Q9SZP7 Genevestigator:Q9SZP7 Uniprot:Q9SZP7
Leaf	Isotig07071	11	0	4.988	0.000159591	No hit
Leaf	Isotig07072	14	2	3.336	0.000148753	TAIR|locus:2134163 - symbol:AT4G33540 "AT4G33540" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=ISS] [GO:0008152 "metabolic process" evidence=ISS] [GO:0016787 "hydrolase activity" evidence=IEA] [GO:0046685 "response to arsenic-containing substance" evidence=IEP] InterPro:IPR001279 Pfam:PF00753 SMART:SM00849 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0046685 GO:GO:0016787 eggNOG:COG0491 EMBL:AY093148 EMBL:BT003391 EMBL:AK226283 IPI:IPI00537482 RefSeq:NP_195080.2 UniGene:At.44785 HSSP:P46797 ProteinModelPortal:Q8RWE1 PRIDE:Q8RWE1 EnsemblPlants:AT4G33540.1 GeneID:829493 KEGG:ath:AT4G33540 TAIR:At4g33540 HOGENOM:HBG285932 InParanoid:Q8RWE1 OMA:THRDDVA PhylomeDB:Q8RWE1 ProtClustDB:CLSN2690357 Genevestigator:Q8RWE1 Uniprot:Q8RWE1
Leaf	Isotig07083	11	0	4.988	0.000159591	TAIR|locus:2184123 - symbol:ANNAT7 "annexin 7" species:3702 "Arabidopsis thaliana" [GO:0005509 "calcium ion binding" evidence=IEA;ISS] [GO:0005544 "calcium-dependent phospholipid binding" evidence=IEA;ISS] [GO:0009408 "response to heat" evidence=IEP] [GO:0009409 "response to cold" evidence=IEP] [GO:0009414 "response to water deprivation" evidence=IEP] [GO:0009651 "response to salt stress" evidence=IEP] InterPro:IPR001464 InterPro:IPR018252 InterPro:IPR018502 Pfam:PF00191 PRINTS:PR00196 PROSITE:PS00223 SMART:SM00335 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005509 GO:GO:0009409 GO:GO:0009651 GO:GO:0009414 GO:GO:0009408 GO:GO:0005544 Gene3D:G3DSA:1.10.220.10 PANTHER:PTHR10502 SUPFAM:SSF47874 HOGENOM:HBG745057 eggNOG:NOG243599 ProtClustDB:CLSN2681929 InterPro:IPR009118 PANTHER:PTHR10502:SF10 PRINTS:PR01814 HSSP:P04083 EMBL:AL356332 EMBL:AY014799 EMBL:BT029226 IPI:IPI00531238 PIR:T50027 RefSeq:NP_196585.1 UniGene:At.1636 ProteinModelPortal:Q9LX07 SMR:Q9LX07 PRIDE:Q9LX07 EnsemblPlants:AT5G10230.1

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GeneID:830887 KEGG:ath:AT5G10230 GeneFarm:1478 TAIR:At5g10230 InParanoid:Q9LX07 OMA:KPKYYGT PhylomeDB:Q9LX07 Genevestigator:Q9LX07 Uniprot:Q9LX07
Leaf	Isotig07088	11	0	4.988	0.000159591	TAIR|locus:2121899 - symbol:NBR1 "AT4G24690" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0008270 "zinc ion binding" evidence=IEA] [GO:0005737 "cytoplasm" evidence=IDA] InterPro:IPR000270 InterPro:IPR000433 InterPro:IPR000449 InterPro:IPR009060 Pfam:PF00564 Pfam:PF00569 Pfam:PF00627 PROSITE:PS50135 SMART:SM00291 SMART:SM00666 EMBL:CP002687 GO:GO:0005737 GO:GO:0008270 EMBL:AL035356 EMBL:AL161562 SUPFAM:SSF46934 EMBL:AY062827 EMBL:AY128759 EMBL:AY140081 EMBL:BT008425 IPI:IPI00543691 PIR:T05565 RefSeq:NP_194200.1 UniGene:At.24692 UniGene:At.71380 ProteinModelPortal:Q9SB64 SMR:Q9SB64 IntAct:Q9SB64 PRIDE:Q9SB64 EnsemblPlants:AT4G24690.1 GeneID:828571 KEGG:ath:AT4G24690 TAIR:At4g24690 InParanoid:Q9SB64 OMA:CGVSEWD PhylomeDB:Q9SB64 ProtClustDB:CLSN2685439 Genevestigator:Q9SB64 Uniprot:Q9SB64
Leaf	Isotig07107	16	0	5.529	4.31E-06	TAIR|locus:2026884 - symbol:AT1G68570 "AT1G68570" species:3702 "Arabidopsis thaliana" [GO:0005215 "transporter activity" evidence=ISS] [GO:0006857 "oligopeptide transport" evidence=IEA;ISS] [GO:0016020 "membrane" evidence=IEA;ISS] InterPro:IPR000109 Pfam:PF00854 PROSITE:PS01022 PROSITE:PS01023 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005215 InterPro:IPR016196 SUPFAM:SSF103473 EMBL:AC008075 GO:GO:0042128 eggNOG:COG3104 GO:GO:0006857 HOGENOM:HBG605267 EMBL:AY091784 EMBL:BT002278 EMBL:AK226963 IPI:IPI00547183 PIR:A96710 RefSeq:NP_177024.1 UniGene:At.43526 ProteinModelPortal:Q9SX20 TCDB:2.A.17.3.6 PRIDE:Q9SX20 EnsemblPlants:AT1G68570.1 GeneID:843186 KEGG:ath:AT1G68570 TAIR:At1g68570 InParanoid:Q9SX20 OMA:FHANMIS PhylomeDB:Q9SX20 ProtClustDB:CLSN2682303 Genevestigator:Q9SX20 Uniprot:Q9SX20
Leaf	Isotig07111	10	1	3.851	0.00071293	TAIR|locus:2144781 - symbol:PMDH2 "peroxisomal NAD-malate dehydrogenase 2" species:3702 "Arabidopsis thaliana" [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005777 "peroxisome" evidence=IDA] [GO:0031998 "regulation of fatty acid beta-oxidation" evidence=IGI;IMP] [GO:0048046 "apoplast" evidence=IDA] [GO:0080093 "regulation of photorespiration" evidence=IMP] [GO:0016615 "malate dehydrogenase activity" evidence=ISS] [GO:0042579 "microbody" evidence=ISS] InterPro:IPR001236 InterPro:IPR001252 InterPro:IPR001557 InterPro:IPR010097 InterPro:IPR015955 InterPro:IPR016040 InterPro:IPR022383 Pfam:PF00056 Pfam:PF02866 PIRSF:PIRSF000102 PROSITE:PS00068 GO:GO:0048046 GO:GO:0005773 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 GO:GO:0009941 GO:GO:0009514 GO:GO:0006097 GO:GO:0006099 Gene3D:G3DSA:3.90.110.10 SUPFAM:SSF56327 EMBL:AB020752 EMBL:AL353994 GO:GO:0031998 GO:GO:0006108 eggNOG:COG0039 HOGENOM:HBG566126 GO:GO:0030060 KO:K00026 PANTHER:PTHR11540:SF1 TIGRFAMs:TIGR01772 EMBL:AJ131206 EMBL:AF428373 EMBL:AY037252 EMBL:AY077653 IPI:IPI00534849 PIR:T49932 RefSeq:NP_196528.1 UniGene:At.40751 UniGene:At.47611 ProteinModelPortal:Q9ZP05 SMR:Q9ZP05 STRING:Q9ZP05 PRIDE:Q9ZP05 ProMEX:Q9ZP05 EnsemblPlants:AT5G09660.1 GeneID:830825 KEGG:ath:AT5G09660 TAIR:At5g09660 InParanoid:Q9ZP05 OMA:AKFADAC PhylomeDB:Q9ZP05 ProtClustDB:PLN00106 ArrayExpress:Q9ZP05 Genevestigator:Q9ZP05 GO:GO:0080093 Uniprot:Q9ZP05
Leaf	Isotig07120	12	1	4.114	0.000154103	TAIR|locus:2116900 - symbol:XDH1 "AT4G34890" species:3702 "Arabidopsis thaliana" [GO:0004854 "xanthine dehydrogenase activity" evidence=ISS;IDA] [GO:0006145 "purine base catabolic process" evidence=IMP;TAS] [GO:0006950 "response to stress" evidence=TAS] [GO:0042554 "superoxide anion generation" evidence=IMP] [GO:0046110 "xanthine metabolic process" evidence=IMP] [GO:0000302 "response to reactive oxygen species" evidence=IMP] [GO:0009414 "response to water deprivation" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR001041 InterPro:IPR002346 InterPro:IPR002888 InterPro:IPR006058 InterPro:IPR008274 InterPro:IPR016166 InterPro:IPR016167 InterPro:IPR016169 InterPro:IPR016208 Pfam:PF00111 Pfam:PF00941 Pfam:PF01799 Pfam:PF02738 PIRSF:PIRSF000127 PROSITE:PS00197 PROSITE:PS51085 PROSITE:PS51387 InterPro:IPR000674 Pfam:PF01315 GO:GO:0005829 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005506 GO:GO:0009055 GO:GO:0050660 GO:GO:0009414 GO:GO:0000302 GO:GO:0008762 Gene3D:G3DSA:3.30.43.10 SUPFAM:SSF56176 eggNOG:COG4630 GO:GO:0051537 InterPro:IPR012675 InterPro:IPR005107 Gene3D:G3DSA:1.10.150.120 Gene3D:G3DSA:3.30.365.10 Gene3D:G3DSA:3.90.1170.50 Gene3D:G3DSA:3.30.390.50 Gene3D:G3DSA:3.30.465.10 Gene3D:G3DSA:3.10.20.30 Pfam:PF03450 SMART:SM01008 SMART:SM01092 SUPFAM:SSF47741 SUPFAM:SSF56003 SUPFAM:SSF54665 SUPFAM:SSF55447 SUPFAM:SSF54292 HOGENOM:HBG386245 GO:GO:0004854 GO:GO:0006145

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0042554 KO:K00106 HSSP:P80457 GO:GO:0046110 OMA:SGRAFNY EMBL:AY171562 IPI:IPI00529753 RefSeq:NP_195215.2 UniGene:At.27839 ProteinModelPortal:Q8GUQ8 STRING:Q8GUQ8 PRIDE:Q8GUQ8 ProMEX:Q8GUQ8 EnsemblPlants:AT4G34890.1 GeneID:829641 KEGG:ath:AT4G34890 TAIR:At4g34890 InParanoid:Q8GUQ8 PhylomeDB:Q8GUQ8 ProtClustDB:PLN02906 BRENDA:1.17.1.4 Genevestigator:Q8GUQ8 Uniprot:Q8GUQ8
Leaf	Isotig07128	11	65	-2.034	2.01E-07	TAIR|locus:2031103 - symbol:FBP "AT1G43670" species:3702 "Arabidopsis thaliana" [GO:0006000 "fructose metabolic process" evidence=ISS] [GO:0042132 "fructose 1,6-bisphosphate 1-phosphatase activity" evidence=ISS;IDA] [GO:0005986 "sucrose biosynthetic process" evidence=IMP] [GO:0005983 "starch catabolic process" evidence=IMP] [GO:0015979 "photosynthesis" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0009737 "response to abscisic acid stimulus" evidence=IMP] [GO:0009750 "response to fructose stimulus" evidence=IMP] [GO:0030388 "fructose 1,6-bisphosphate metabolic process" evidence=IDA] InterPro:IPR000146 InterPro:IPR020548 Pfam:PF00316 PIRSF:PIRSF000904 PRINTS:PR00115 PROSITE:PS00124 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0009737 GO:GO:0005634 GO:GO:0046872 GO:GO:0009750 GO:GO:0005983 GO:GO:0030388 GO:GO:0015979 UniGene:At.23691 GO:GO:0042132 eggNOG:COG0158 HOGENOM:HBG731261 KO:K03841 PANTHER:PTHR11556 OMA:YGSATMV EMBL:AC009526 EMBL:BT000470 EMBL:BT008732 IPI:IPI00520560 PIR:H96499 RefSeq:NP_175032.1 UniGene:At.12074 ProteinModelPortal:Q9MA79 SMR:Q9MA79 IntAct:Q9MA79 STRING:Q9MA79 PRIDE:Q9MA79 EnsemblPlants:AT1G43670.1 GeneID:840953 KEGG:ath:AT1G43670 TAIR:At1g43670 InParanoid:Q9MA79 PhylomeDB:Q9MA79 ProtClustDB:PLN02262 BioCyc:ARA:AT1G43670-MONOMER BioCyc:MetaCyc:AT1G43670-MONOMER ArrayExpress:Q9MA79 Genevestigator:Q9MA79 GermOnline:AT1G43670 GO:GO:0005986 Uniprot:Q9MA79
Leaf	Isotig07132	24	4	3.114	1.45E-06	TAIR|locus:2177881 - symbol:AT5G41350 species:3702 "Arabidopsis thaliana" [GO:0008270 "zinc ion binding" evidence=IEA;ISS] [GO:0005739 "mitochondrion" evidence=IDA] InterPro:IPR001841 PROSITE:PS50089 SMART:SM00184 GO:GO:0005739 EMBL:CP002688 GO:GO:0008270 InterPro:IPR013083 Gene3D:G3DSA:3.30.40.10 ProtClustDB:CLSN2697998 EMBL:AY048293 EMBL:AY143828 IPI:IPI00528415 RefSeq:NP_568590.1 UniGene:At.6481 ProteinModelPortal:Q94AB7 SMR:Q94AB7 IntAct:Q94AB7 EnsemblPlants:AT5G41350.1 GeneID:834137 KEGG:ath:AT5G41350 TAIR:At5g41350 eggNOG:NOG314203 InParanoid:Q94AB7 OMA:AYYYYPR PhylomeDB:Q94AB7 Genevestigator:Q94AB7 Uniprot:Q94AB7
Leaf	Isotig07135	15	1	4.436	1.60E-05	TAIR|locus:2012572 - symbol:MIOX1 "myo-inositol oxygenase 1" species:3702 "Arabidopsis thaliana" [GO:0005737 "cytoplasm" evidence=IEA] [GO:0016491 "oxidoreductase activity" evidence=ISS] [GO:0050113 "inositol oxygenase activity" evidence=IMP] [GO:0006949 "syncytium formation" evidence=IGI] InterPro:IPR007828 Pfam:PF05153 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005737 GO:GO:0005506 EMBL:AC010657 EMBL:AC012188 GO:GO:0006949 GO:GO:0019853 GO:GO:0019310 EMBL:AY136388 EMBL:BT000187 EMBL:AK118307 EMBL:AK175115 EMBL:AK175818 EMBL:AK175833 EMBL:AK176690 EMBL:AK221931 IPI:IPI00531494 RefSeq:NP_172904.2 UniGene:At.23143 ProteinModelPortal:Q8L799 SMR:Q8L799 PRIDE:Q8L799 EnsemblPlants:AT1G14520.1 GeneID:838014 KEGG:ath:AT1G14520 TAIR:At1g14520 eggNOG:NOG135479 HOGENOM:HBG332059 InParanoid:Q8L799 KO:K00469 OMA:CELLNEF PhylomeDB:Q8L799 ProtClustDB:CLSN2687348 BioCyc:MetaCyc:AT1G14520-MONOMER Genevestigator:Q8L799 GO:GO:0050113 PANTHER:PTHR12588 Uniprot:Q8L799
Leaf	Isotig07148	0	13	-4.171	0.000994782	TAIR|locus:2174683 - symbol:AT5G14120 species:3702 "Arabidopsis thaliana" [GO:0005773 "vacuole" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] GO:GO:0005774 EMBL:CP002688 EMBL:AB007650 InterPro:IPR016196 SUPFAM:SSF103473 UniGene:At.49020 UniGene:At.70997 InterPro:IPR010658 Pfam:PF06813 IPI:IPI00543793 RefSeq:NP_196916.1 ProteinModelPortal:Q9FMT8 SMR:Q9FMT8 PRIDE:Q9FMT8 ProMEX:Q9FMT8 EnsemblPlants:AT5G14120.1 GeneID:831262 KEGG:ath:AT5G14120 TAIR:At5g14120 InParanoid:Q9FMT8 OMA:VAVGPTM PhylomeDB:Q9FMT8 ProtClustDB:CLSN2687204 Genevestigator:Q9FMT8 Uniprot:Q9FMT8
Leaf	Isotig07176	14	3	2.751	0.000536578	TAIR|locus:2051749 - symbol:AT2G44060 "AT2G44060" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0009269 "response to desiccation" evidence=ISS] [GO:0009793 "embryo development ending in seed dormancy" evidence=ISS] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA]

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						InterPro:IPR013990 SMART:SM00769 InterPro:IPR004864 GO:GO:0005829 GO:GO:0005886 GO:GO:0009506 GO:GO:0046686 EMBL:CP002685 GenomeReviews:CT485783_GR InterPro:IPR013783 Gene3D:G3DSA:2.60.40.10 GO:GO:0009269 EMBL:AC004005 Pfam:PF03168 EMBL:BT024723 IPI:IPI00538194 PIR:T00686 RefSeq:NP_181934.1 RefSeq:NP_850408.1 UniGene:At.23563 ProteinModelPortal:O80576 SMR:O80576 STRING:O80576 PRIDE:O80576 ProMEX:O80576 DNASU:819011 EnsemblPlants:AT2G44060.1 EnsemblPlants:AT2G44060.2 GeneID:819011 KEGG:ath:AT2G44060 TAIR:At2g44060 eggNOG:NOG271585 HOGENOM:HBG595330 InParanoid:O80576 OMA:FIHDIGE PhylomeDB:O80576 ProtClustDB:CLSN2683184 ArrayExpress:O80576 Genevestigator:O80576 Uniprot:O80576
Leaf	Isotig07210	13	1	4.229	7.21E-05	TAIR|locus:505006599 - symbol:AT5G12310 species:3702 "Arabidopsis thaliana" [GO:0008270 "zinc ion binding" evidence=IEA;ISS] InterPro:IPR001841 PROSITE:PS50089 SMART:SM00184 Prosite:PS00518 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0008270 InterPro:IPR013083 Gene3D:G3DSA:3.30.40.10 EMBL:AL592312 InterPro:IPR017907 HSSP:P28990 eggNOG:NOG265787 EMBL:AY116954 EMBL:AK117718 IPI:IPI00535079 RefSeq:NP_568264.1 UniGene:At.28632 ProteinModelPortal:Q94CL1 SMR:Q94CL1 EnsemblPlants:AT5G12310.1 GeneID:831106 KEGG:ath:AT5G12310 TAIR:At5g12310 HOGENOM:HBG316377 InParanoid:Q94CL1 OMA:EKPTCPQ PhylomeDB:Q94CL1 ProtClustDB:CLSN2689629 ArrayExpress:Q94CL1 Genevestigator:Q94CL1 Uniprot:Q94CL1
Leaf	Isotig07213	11	0	4.988	0.000159591	UNIPROTKB|Q5ALT5 - symbol:MSB2 "Potential cell surface flocculin" species:237561 "Candida albicans SC5314" [GO:0003674 "molecular_function" evidence=ND] [GO:0005576 "extracellular region" evidence=IDA] [GO:0031505 "fungal-type cell wall organization" evidence=IMP] [GO:0090033 "positive regulation of filamentous growth" evidence=IMP] CGD:CAL0004775 GO:GO:0005576 GO:GO:0031505 eggNOG:NOG12793 EMBL:AACQ01000008 EMBL:AACQ01000007 GO:GO:0090033 RefSeq:XP_722401.1 RefSeq:XP_722538.1 STRING:Q5ALT5 GeneID:3635830 GeneID:3635923 KEGG:cal:CaO19.1490 KEGG:cal:CaO19.9067 PhylomeDB:Q5ALT5 Uniprot:Q5ALT5
Leaf	Isotig07250	60	350	-2.015	3.84E-33	TAIR|locus:2127393 - symbol:PSBQA "photosystem II subunit QA" species:3702 "Arabidopsis thaliana" [GO:0005509 "calcium ion binding" evidence=IEA] [GO:0009654 "oxygen evolving complex" evidence=ISS] [GO:0030095 "chloroplast photosystem II" evidence=ISS] [GO:0009543 "chloroplast thylakoid lumen" evidence=IDA] [GO:0031977 "thylakoid lumen" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] InterPro:IPR008797 Pfam:PF05757 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0009570 GO:GO:0005509 EMBL:AL161554 GO:GO:0019898 EMBL:AL021960 GO:GO:0009535 GO:GO:0031977 GO:GO:0015979 EMBL:AL031187 InterPro:IPR023222 SUPFAM:SSF101112 GO:GO:0009654 EMBL:Y16847 EMBL:AY050328 EMBL:AY094048 EMBL:AY088330 IPI:IPI00532582 IPI:IPI00657124 PIR:T04959 RefSeq:NP_001031687.1 RefSeq:NP_193860.1 UniGene:At.24610 ProteinModelPortal:Q9XFT3 SMR:Q9XFT3 STRING:Q9XFT3 SWISS-2DPAGE:Q9XFT3 PRIDE:Q9XFT3 ProMEX:Q9XFT3 EnsemblPlants:AT4G21280.2 GeneID:827877 KEGG:ath:AT4G21280 TAIR:At4g21280 eggNOG:NOG313473 HOGENOM:HBG318859 InParanoid:Q9XFT3 KO:K08901 OMA:DRFYLQP PhylomeDB:Q9XFT3 ProtClustDB:CLSN2685363 BioCyc:MetaCyc:MONOMER-1076 ArrayExpress:Q9XFT3 Genevestigator:Q9XFT3 Uniprot:Q9XFT3
Leaf	Isotig07251	12	1	4.114	0.000154103	TAIR|locus:2062912 - symbol:AT2G46220 "AT2G46220" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002685 GenomeReviews:CT485783_GR EMBL:AC005397 InterPro:IPR018790 Pfam:PF10184 EMBL:AF361857 EMBL:AY050447 EMBL:AF428419 EMBL:AY093803 IPI:IPI00543967 PIR:B84900 RefSeq:NP_566066.1 UniGene:At.23006 UniGene:At.67245 ProteinModelPortal:O82347 STRING:O82347 PRIDE:O82347 EnsemblPlants:AT2G46220.1 GeneID:819229 KEGG:ath:AT2G46220 TAIR:At2g46220 eggNOG:NOG254618 HOGENOM:HBG176591 InParanoid:O82347 OMA:TVHGIPR PhylomeDB:O82347 ProtClustDB:CLSN2688963 ArrayExpress:O82347 Genevestigator:O82347 Uniprot:O82347
Leaf	Isotig07353	19	2	3.777	3.57E-06	TAIR|locus:2136383 - symbol:AT4G39230 "AT4G39230" species:3702 "Arabidopsis thaliana" [GO:0032442 "phenylcoumaran benzylic ether reductase activity" evidence=ISS] [GO:0046686 "response to cadmium ion" evidence=IEP] InterPro:IPR016040 InterPro:IPR008030 EMBL:CP002687 GO:GO:0046686 GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 EMBL:AL161594 EMBL:AL050351 Pfam:PF05368 EMBL:AY150409 IPI:IPI00541617 PIR:T08571 RefSeq:NP_195634.1 UniGene:At.31110 ProteinModelPortal:Q9T030 SMR:Q9T030 PRIDE:Q9T030

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EnsemblPlants:AT4G39230.1 GeneID:830078 KEGG:ath:AT4G39230 TAIR:At4g39230 InParanoid:Q9T030 OMA:VISTVGH PhylomeDB:Q9T030 ProtClustDB:CLSN2915976 Genevestigator:Q9T030 Uniprot:Q9T030
Leaf	Isotig07356	12	1	4.114	0.000154103	TAIR|locus:2130329 - symbol:AT4G16260 species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004553 "hydrolase activity, hydrolyzing O-glycosyl compounds" evidence=IEA;ISS] [GO:0043169 "cation binding" evidence=IEA] [GO:0005618 "cell wall" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0009817 "defense response to fungus, incompatible interaction" evidence=IDA] InterPro:IPR000490 InterPro:IPR013781 Pfam:PF00332 PROSITE:PS00587 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005774 GO:GO:0005618 GO:GO:0043169 InterPro:IPR017853 Gene3D:G3DSA:3.20.20.80 SUPFAM:SSF51445 GO:GO:0005975 GO:GO:0004553 GO:GO:0009651 GO:GO:0009817 CAZy:GH17 HSSP:P15737 EMBL:AY064130 EMBL:AY143867 IPI:IPI00944240 RefSeq:NP_193361.4 UniGene:At.22570 ProteinModelPortal:Q8VZJ2 SMR:Q8VZJ2 PRIDE:Q8VZJ2 EnsemblPlants:AT4G16260.1 GeneID:827320 KEGG:ath:AT4G16260 TAIR:At4g16260 PhylomeDB:Q8VZJ2 ProtClustDB:CLSN2927419 Genevestigator:Q8VZJ2 Uniprot:Q8VZJ2
Leaf	Isotig07361	10	1	3.851	0.00071293	TAIR|locus:2035211 - symbol:PLDALPHA2 "AT1G52570" species:3702 "Arabidopsis thaliana" [GO:0004630 "phospholipase D activity" evidence=ISS] [GO:0008152 "metabolic process" evidence=IEA] [GO:0046470 "phosphatidylcholine metabolic process" evidence=IEA] [GO:0009941 "chloroplast envelope" evidence=IDA] InterPro:IPR000008 InterPro:IPR001736 InterPro:IPR008973 InterPro:IPR011402 Pfam:PF00168 Pfam:PF00614 PIRSF:PIRSF036470 PROSITE:PS50035 SMART:SM00155 SMART:SM00239 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005773 GO:GO:0005509 GO:GO:0009738 GO:GO:0009873 GO:GO:0016020 GO:GO:0046470 GO:GO:0016042 GO:GO:0009941 GO:GO:0030136 SUPFAM:SSF49562 PROSITE:PS50004 eggNOG:COG1502 InterPro:IPR015679 PANTHER:PTHR18896 EMBL:AC008016 GO:GO:0070290 GO:GO:0004630 KO:K01115 HOGENOM:HBG748198 ProtClustDB:PLN02270 InterPro:IPR024632 Pfam:PF12357 IPI:IPI00542684 PIR:D96566 RefSeq:NP_175666.1 UniGene:At.52162 ProteinModelPortal:Q9SSQ9 SMR:Q9SSQ9 PRIDE:Q9SSQ9 EnsemblPlants:AT1G52570.1 GeneID:841689 KEGG:ath:AT1G52570 TAIR:At1g52570 InParanoid:Q9SSQ9 OMA:GIASEGN PhylomeDB:Q9SSQ9 ArrayExpress:Q9SSQ9 Genevestigator:Q9SSQ9 GermOnline:AT1G52570 Uniprot:Q9SSQ9
Leaf	Isotig07368	12	1	4.114	0.000154103	TAIR|locus:2199767 - symbol:ECH2 "AT1G76150" species:3702 "Arabidopsis thaliana" [GO:0008152 "metabolic process" evidence=ISS] [GO:0016491 "oxidoreductase activity" evidence=ISS] [GO:0005777 "peroxisome" evidence=IDA] [GO:0033542 "fatty acid beta-oxidation, unsaturated, even number" evidence=IMP] [GO:0080023 "3R-hydroxyacyl-CoA dehydratase activity" evidence=IGI;IDA] InterPro:IPR002539 Pfam:PF01575 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005777 GO:GO:0016491 EMBL:AC009978 eggNOG:COG2030 EMBL:AY070763 EMBL:AY093712 IPI:IPI00530293 RefSeq:NP_177742.2 UniGene:At.16593 ProteinModelPortal:Q8VYI3 SMR:Q8VYI3 IntAct:Q8VYI3 STRING:Q8VYI3 PRIDE:Q8VYI3 EnsemblPlants:AT1G76150.1 GeneID:843947 KEGG:ath:AT1G76150 TAIR:At1g76150 HOGENOM:HBG658242 InParanoid:Q8VYI3 OMA:NEYTARD PhylomeDB:Q8VYI3 ProtClustDB:PLN02864 Genevestigator:Q8VYI3 GO:GO:0080023 GO:GO:0033542 Uniprot:Q8VYI3
Leaf	Isotig07385	18	3	3.114	3.02E-05	TAIR|locus:2025625 - symbol:ACHT4 "atypical CYS HIS rich thioredoxin 4" species:3702 "Arabidopsis thaliana" [GO:0045454 "cell redox homeostasis" evidence=IEA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0016671 "oxidoreductase activity, acting on a sulfur group of donors, disulfide as acceptor" evidence=IDA] [GO:0031969 "chloroplast membrane" evidence=IDA] InterPro:IPR005746 InterPro:IPR013766 Pfam:PF00085 PROSITE:PS00194 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009570 GO:GO:0009055 GO:GO:0006810 GO:GO:0031969 GO:GO:0022900 InterPro:IPR012336 Gene3D:G3DSA:3.40.30.10 SUPFAM:SSF52833 EMBL:AC003981 GO:GO:0045454 PROSITE:PS51352 GO:GO:0015035 GO:GO:0006662 PANTHER:PTHR10438 eggNOG:COG0526 GO:GO:0016671 EMBL:AF144387 EMBL:AY034938 EMBL:AY063115 EMBL:AK318661 IPI:IPI00525220 IPI:IPI00892256 PIR:T00710 RefSeq:NP_001117248.1 RefSeq:NP_001117249.1 RefSeq:NP_172333.1 UniGene:At.24182 ProteinModelPortal:O64654 SMR:O64654 PRIDE:O64654 EnsemblPlants:AT1G08570.1 GeneID:837379 KEGG:ath:AT1G08570 GeneFarm:2500 TAIR:At1g08570 HOGENOM:HBG750015 InParanoid:O64654 OMA:ANKELNF PhylomeDB:O64654 ProtClustDB:CLSN2708430 ArrayExpress:O64654 Genevestigator:O64654 GermOnline:AT1G08570 Uniprot:O64654
Leaf	Isotig07408	22	327	-3.365	5.82E-53	TAIR|locus:2040934 - symbol:LHB1B2 "AT2G34420" species:3702 "Arabidopsis thaliana" [GO:0009769 "photosynthesis, light harvesting in photosystem II" evidence=TAS] [GO:0016168 "chlorophyll binding"

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						evidence=ISS;TAS] [GO:0030076 "light-harvesting complex" evidence=ISS] [GO:0042651 "thylakoid membrane" evidence=TAS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0015979 "photosynthesis" evidence=ISS] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR001344 Pfam:PF00504 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009535 GO:GO:0010287 EMBL:AC004077 EMBL:AC004481 HOGENOM:HBG618504 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 UniGene:At.10812 UniGene:At.24351 UniGene:At.32199 UniGene:At.66422 UniGene:At.71449 UniGene:At.71528 KO:K08912 ProtClustDB:PLN00025 UniGene:At.23647 UniGene:At.27457 UniGene:At.24888 EMBL:AF372886 EMBL:AY039561 EMBL:AY045806 EMBL:AF428397 EMBL:AF419548 EMBL:AF419587 EMBL:AY065125 EMBL:AY079101 EMBL:AY079110 EMBL:AY081587 EMBL:AY142513 EMBL:AK229627 EMBL:X64460 IPI:IPI00530785 PIR:S23546 RefSeq:NP_565786.1 UniGene:At.24064 UniGene:At.71003 UniGene:At.71384 ProteinModelPortal:Q39141 SMR:Q39141 IntAct:Q39141 STRING:Q39141 PRIDE:Q39141 EnsemblPlants:AT2G34420.1 GeneID:818005 KEGG:ath:AT2G34420 TAIR:At2g34420 InParanoid:Q39141 OMA:SILAIWG PhylomeDB:Q39141 ArrayExpress:Q39141 Genevestigator:Q39141 Uniprot:Q39141
Leaf	Isotig07426	29	11	1.928	5.67E-05	TAIR|locus:2060529 - symbol:ERD15 "AT2G41430" species:3702 "Arabidopsis thaliana" [GO:0009617 "response to bacterium" evidence=IEP] [GO:0005737 "cytoplasm" evidence=ISS] [GO:0009644 "response to high light intensity" evidence=IEP] [GO:0005515 "protein binding" evidence=IPI] [GO:0009414 "response to water deprivation" evidence=NAS] EMBL:CP002685 GO:GO:0009617 GO:GO:0005515 GO:GO:0009414 GO:GO:0009644 EMBL:AC004625 EMBL:AC005662 UniGene:At.24137 EMBL:AF372909 EMBL:AY056399 EMBL:AY065120 EMBL:AY081636 EMBL:BT002663 EMBL:D30719 EMBL:AK317136 IPI:IPI00543434 PIR:T02438 RefSeq:NP_001189727.1 RefSeq:NP_181674.1 RefSeq:NP_850350.1 RefSeq:NP_973658.1 UniGene:At.23985 UniGene:At.24253 UniGene:At.69477 UniGene:At.73065 IntAct:Q39096 STRING:Q39096 PRIDE:Q39096 EnsemblPlants:AT2G41430.1 EnsemblPlants:AT2G41430.2 EnsemblPlants:AT2G41430.4 EnsemblPlants:AT2G41430.5 GeneID:818741 KEGG:ath:AT2G41430 TAIR:At2g41430 eggNOG:NOG300714 InParanoid:Q39096 OMA:ENENGGG PhylomeDB:Q39096 ProtClustDB:CLSN2683774 ArrayExpress:Q39096 Genevestigator:Q39096 Uniprot:Q39096
Leaf	Isotig07444	26	6	2.644	3.85E-06	TAIR|locus:2128238 - symbol:BTI2 "AT4G11220" species:3702 "Arabidopsis thaliana" [GO:0005783 "endoplasmic reticulum" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005789 "endoplasmic reticulum membrane" evidence=IDA] [GO:0071458 "integral to cytosolic side of endoplasmic reticulum membrane" evidence=IDA] [GO:0071782 "endoplasmic reticulum tubular network" evidence=IDA] [GO:0071786 "endoplasmic reticulum tubular network organization" evidence=IMP] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR003388 Pfam:PF02453 PROSITE:PS50845 GO:GO:0005886 EMBL:CP002687 GenomeReviews:CT486007_GR EMBL:AL096882 EMBL:AL161531 GO:GO:0071458 PANTHER:PTHR10994 GO:GO:0071786 GO:GO:0071782 eggNOG:NOG303514 ProtClustDB:CLSN2685988 EMBL:AY034901 EMBL:AY048273 EMBL:AY057606 EMBL:BT002368 EMBL:AY086294 IPI:IPI00525362 PIR:T13013 RefSeq:NP_192861.1 UniGene:At.3649 ProteinModelPortal:Q9SUT9 SMR:Q9SUT9 IntAct:Q9SUT9 STRING:Q9SUT9 PRIDE:Q9SUT9 EnsemblPlants:AT4G11220.1 GeneID:826724 KEGG:ath:AT4G11220 TAIR:At4g11220 HOGENOM:HBG596795 InParanoid:Q9SUT9 OMA:HEESSPN PhylomeDB:Q9SUT9 Genevestigator:Q9SUT9 Uniprot:Q9SUT9
Leaf	Isotig07462	1	21	-3.863	4.36E-05	TAIR|locus:2015581 - symbol:UBC36 "AT1G16890" species:3702 "Arabidopsis thaliana" [GO:0004842 "ubiquitin-protein ligase activity" evidence=ISS;IDA] [GO:0006511 "ubiquitin-dependent protein catabolic process" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0031372 "UBC13-MMS2 complex" evidence=IPI] [GO:0010039 "response to iron ion" evidence=IMP] [GO:0010053 "root epidermal cell differentiation" evidence=IGI] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR000608 Pfam:PF00179 PROSITE:PS50127 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0005886 GO:GO:0005524 GO:GO:0005515 GO:GO:0010039 GO:GO:0006511 GO:GO:0004842 InterPro:IPR016135 Gene3D:G3DSA:3.10.110.10 SUPFAM:SSF54495 EMBL:AC051629 eggNOG:COG5078 PROSITE:PS00183 HOGENOM:HBG756483 GO:GO:0010053 HSSP:P61088 InterPro:IPR023313 GO:GO:0031372 KO:K10580 OMA:LGAPNPD ProtClustDB:CLSN2687835 EMBL:DQ027049 EMBL:AY052307 EMBL:AY061926 EMBL:AY086780 IPI:IPI00520285 IPI:IPI00542106 PIR:C86304

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						RefSeq:NP_564011.1 RefSeq:NP_849678.1 UniGene:At.16052 UniGene:At.24697 ProteinModelPortal:Q9FZ48 SMR:Q9FZ48 IntAct:Q9FZ48 STRING:Q9FZ48 PRIDE:Q9FZ48 EnsemblPlants:AT1G16890.2 GeneID:838260 KEGG:ath:AT1G16890 TAIR:At1g16890 InParanoid:Q9FZ48 PhylomeDB:Q9FZ48 Genevestigator:Q9FZ48 Uniprot:Q9FZ48
Leaf	Isotig07472	8	119	-3.366	2.44E-20	TAIR|locus:2036209 - symbol:LHCB6 "AT1G15820" species:3702 "Arabidopsis thaliana" [GO:0016168 "chlorophyll binding" evidence=ISS] [GO:0015979 "photosynthesis" evidence=IMP;NAS] [GO:0009783 "photosystem II antenna complex" evidence=NAS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0010196 "nonphotochemical quenching" evidence=IMP] [GO:0009534 "chloroplast thylakoid" evidence=IDA] InterPro:IPR001344 Pfam:PF00504 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009941 GO:GO:0009535 GO:GO:0010287 EMBL:AC034256 HOGENOM:HBG618504 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 GO:GO:0009783 GO:GO:0010196 UniGene:At.25300 EMBL:AF332425 EMBL:AY065113 EMBL:AY081644 IPI:IPI00524194 PIR:F86292 RefSeq:NP_173034.1 UniGene:At.15569 UniGene:At.72611 UniGene:At.74824 UniGene:At.74983 ProteinModelPortal:Q9LMQ2 SMR:Q9LMQ2 STRING:Q9LMQ2 PRIDE:Q9LMQ2 DNASU:838151 EnsemblPlants:AT1G15820.1 GeneID:838151 KEGG:ath:AT1G15820 TAIR:At1g15820 eggNOG:NOG277110 InParanoid:Q9LMQ2 KO:K08917 OMA:RLAMLAM PhylomeDB:Q9LMQ2 ProtClustDB:PLN00170 ArrayExpress:Q9LMQ2 Genevestigator:Q9LMQ2 Uniprot:Q9LMQ2
Leaf	Isotig07506	175	0	8.980	5.65E-42	UNIPROTKB|G4MN25 - symbol:MGG_05575 "Putative uncharacterized protein" species:242507 "Magnaporthe oryzae 70-15" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CM001231 RefSeq:XP_360201.1 GeneID:2676055 InterPro:IPR021054 Pfam:PF12296 Uniprot:G4MN25
Leaf	Isotig07507	32	165	-1.837	9.80E-15	TAIR|locus:2122794 - symbol:LHCB5 "AT4G10340" species:3702 "Arabidopsis thaliana" [GO:0009533 "chloroplast stromal thylakoid" evidence=IDA] [GO:0015979 "photosynthesis" evidence=ISS;IMP] [GO:0016168 "chlorophyll binding" evidence=ISS] [GO:0030076 "light-harvesting complex" evidence=ISS] [GO:0009783 "photosystem II antenna complex" evidence=IMP] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0010196 "nonphotochemical quenching" evidence=IMP] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009637 "response to blue light" evidence=IEP] [GO:0010114 "response to red light" evidence=IEP] [GO:0010218 "response to far red light" evidence=IEP] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0009517 "PSII associated light-harvesting complex II" evidence=IDA] InterPro:IPR001344 Pfam:PF00504 GO:GO:0016021 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0046872 GO:GO:0009637 GO:GO:0010218 GO:GO:0010114 GO:GO:0018298 GO:GO:0010287 EMBL:AL049488 EMBL:AL161517 HOGENOM:HBG618504 GO:GO:0009522 GO:GO:0016168 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 EMBL:AF134129 EMBL:AF326900 EMBL:AF339718 EMBL:AF424597 EMBL:AF380631 EMBL:AY054126 EMBL:AY087939 IPI:IPI00535216 PIR:T04049 RefSeq:NP_192772.1 UniGene:At.23060 ProteinModelPortal:Q9XF89 SMR:Q9XF89 DIP:DIP-59004N STRING:Q9XF89 PRIDE:Q9XF89 EnsemblPlants:AT4G10340.1 GeneID:826626 KEGG:ath:AT4G10340 TAIR:At4g10340 eggNOG:NOG321165 InParanoid:Q9XF89 KO:K08916 OMA:EGPVENL PhylomeDB:Q9XF89 ProtClustDB:CLSN2685679 ArrayExpress:Q9XF89 Genevestigator:Q9XF89 GermOnline:AT4G10340 GO:GO:0009783 GO:GO:0009517 GO:GO:0010196 Uniprot:Q9XF89
Leaf	Isotig07517	89	21	2.612	2.07E-17	TAIR|locus:2034369 - symbol:ERD10 "AT1G20450" species:3702 "Arabidopsis thaliana" [GO:0006950 "response to stress" evidence=ISS] [GO:0009409 "response to cold" evidence=IEP;IDA;IMP] [GO:0009415 "response to water" evidence=ISS] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0009631 "cold acclimation" evidence=IGI] [GO:0016020 "membrane" evidence=IDA] [GO:0005634 "nucleus" evidence=ISS] [GO:0003779 "actin binding" evidence=IDA] [GO:0009414 "response to water deprivation" evidence=IEP;IMP] [GO:0010029 "regulation of seed germination" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] InterPro:IPR000167 Pfam:PF00257 PROSITE:PS00315 PROSITE:PS00823 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0009506 GO:GO:0009737 GO:GO:0003779 GO:GO:0016020 EMBL:AC027665 GO:GO:0009414 GO:GO:0010029 GO:GO:0009631 HOGENOM:HBG593091 ProtClustDB:CLSN2679400 EMBL:D17714

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EMBL:X90958 EMBL:AF360351 EMBL:AY136407 EMBL:AY142491 EMBL:BT002131 EMBL:AY048208 EMBL:X77614 EMBL:AF083731 IPI:IPI00548649 PIR:S60480 RefSeq:NP_850947.1 UniGene:At.24491 UniGene:At.67298 IntAct:P42759 STRING:P42759 PRIDE:P42759 EnsemblPlants:AT1G20450.1 GeneID:838633 KEGG:ath:AT1G20450 TAIR:At1g20450 eggNOG:NOG281319 InParanoid:P42759 OMA:TLASEFE PhylomeDB:P42759 ArrayExpress:P42759 Genevestigator:P42759 Uniprot:P42759
Leaf	Isotig07562	10	0	4.851	0.000336918	TAIR|locus:2167225 - symbol:PSY "AT5G17230" species:3702 "Arabidopsis thaliana" [GO:0016117 "carotenoid biosynthetic process" evidence=IMP] [GO:0016767 "geranylgeranyl-diphosphate geranylgeranyltransferase activity" evidence=ISS;TAS] [GO:0046905 "phytoene synthase activity" evidence=TAS] [GO:0009507 "chloroplast" evidence=IDA] InterPro:IPR002060 InterPro:IPR019845 Pfam:PF00494 PROSITE:PS01044 PROSITE:PS01045 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009507 InterPro:IPR008949 Gene3D:G3DSA:1.10.600.10 SUPFAM:SSF48576 EMBL:AB005238 eggNOG:COG1562 GO:GO:0016767 GO:GO:0046905 EMBL:L25812 EMBL:AF009954 EMBL:BT000450 EMBL:BT002084 EMBL:AY085565 IPI:IPI00527204 RefSeq:NP_001031895.1 RefSeq:NP_197225.1 UniGene:At.23726 ProteinModelPortal:P37271 SMR:P37271 STRING:P37271 PRIDE:P37271 EnsemblPlants:AT5G17230.1 EnsemblPlants:AT5G17230.2 GeneID:831587 KEGG:ath:AT5G17230 TAIR:At5g17230 HOGENOM:HBG693191 InParanoid:P37271 KO:K02291 OMA:ELKLYCY PhylomeDB:P37271 ProtClustDB:PLN02632 BioCyc:ARA:AT5G17230-MONOMER BioCyc:MetaCyc:AT5G17230-MONOMER ArrayExpress:P37271 Genevestigator:P37271 GermOnline:AT5G17230 Uniprot:P37271
Leaf	Isotig07569	85	256	-1.062	1.84E-10	TAIR|locus:2042148 - symbol:LHCB2.1 "AT2G05100" species:3702 "Arabidopsis thaliana" [GO:0015979 "photosynthesis" evidence=ISS] [GO:0016168 "chlorophyll binding" evidence=ISS] [GO:0030076 "light-harvesting complex" evidence=ISS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009637 "response to blue light" evidence=IEP] [GO:0010114 "response to red light" evidence=IEP] [GO:0010218 "response to far red light" evidence=IEP] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR001344 Pfam:PF00504 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009941 GO:GO:0009637 GO:GO:0010218 GO:GO:0010114 GO:GO:0009535 GO:GO:0010287 HOGENOM:HBG618504 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 ProtClustDB:PLN00025 UniGene:At.48420 UniGene:At.63397 KO:K08913 EMBL:AC007443 EMBL:AY052275 EMBL:AY052348 EMBL:BT001933 IPI:IPI00535929 RefSeq:NP_178585.1 ProteinModelPortal:Q9SHR7 SMR:Q9SHR7 STRING:Q9SHR7 PRIDE:Q9SHR7 EnsemblPlants:AT2G05100.1 GeneID:815058 KEGG:ath:AT2G05100 TAIR:At2g05100 InParanoid:Q9SHR7 OMA:HQTTSFL PhylomeDB:Q9SHR7 ArrayExpress:Q9SHR7 Genevestigator:Q9SHR7 Uniprot:Q9SHR7
Leaf	Isotig07573	37	2	4.738	6.47E-12	TAIR|locus:2128238 - symbol:BTI2 "AT4G11220" species:3702 "Arabidopsis thaliana" [GO:0005783 "endoplasmic reticulum" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005789 "endoplasmic reticulum membrane" evidence=IDA] [GO:0071458 "integral to cytosolic side of endoplasmic reticulum membrane" evidence=IDA] [GO:0071782 "endoplasmic reticulum tubular network" evidence=IDA] [GO:0071786 "endoplasmic reticulum tubular network organization" evidence=IMP] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR003388 Pfam:PF02453 PROSITE:PS50845 GO:GO:0005886 EMBL:CP002687 GenomeReviews:CT486007_GR EMBL:AL096882 EMBL:AL161531 GO:GO:0071458 PANTHER:PTHR10994 GO:GO:0071786 GO:GO:0071782 eggNOG:NOG303514 ProtClustDB:CLSN2685988 EMBL:AY034901 EMBL:AY048273 EMBL:AY057606 EMBL:BT002368 EMBL:AY086294 IPI:IPI00525362 PIR:T13013 RefSeq:NP_192861.1 UniGene:At.3649 ProteinModelPortal:Q9SUT9 SMR:Q9SUT9 IntAct:Q9SUT9 STRING:Q9SUT9 PRIDE:Q9SUT9 EnsemblPlants:AT4G11220.1 GeneID:826724 KEGG:ath:AT4G11220 TAIR:At4g11220 HOGENOM:HBG596795 InParanoid:Q9SUT9 OMA:HEESSPN PhylomeDB:Q9SUT9 Genevestigator:Q9SUT9 Uniprot:Q9SUT9
Leaf	Isotig07578	0	13	-4.171	0.000994782	UNIPROTKB|A8QW53 - symbol:OMT3 "5-pentadecatrienyl resorcinol O-methyltransferase" species:4558 "Sorghum bicolor" [GO:0008171 "O-methyltransferase activity" evidence=IDA] [GO:0008757 "S-adenosylmethionine-dependent methyltransferase activity" evidence=IDA] [GO:0032259 "methylation" evidence=IDA] InterPro:IPR001077 InterPro:IPR012967 InterPro:IPR016461 Pfam:PF00891 Pfam:PF08100 PIRSF:PIRSF005739 InterPro:IPR011991 Gene3D:G3DSA:1.10.10.10 GO:GO:0046983 GO:GO:0008171 GO:GO:0008757 EMBL:EF189708 EMBL:CM000765 RefSeq:XP_002447425.1 UniGene:Sbi.19698 ProteinModelPortal:A8QW53

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EnsemblPlants:Sb06g000820.1 GeneID:8080259 KEGG:sbi:SORBI_06g000820 eggNOG:NOG272168 PhylomeDB:A8QW53 ProtClustDB:CLSN2725062 Uniprot:A8QW53
Leaf	Isotig07598	11	1	3.988	0.000330755	TAIR|locus:2056103 - symbol:AT2G39210 "AT2G39210" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0050832 "defense response to fungus" evidence=IEP] InterPro:IPR011701 Pfam:PF07690 GO:GO:0016021 GO:GO:0009506 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0050832 GO:GO:0055085 EMBL:AC004697 InterPro:IPR016196 SUPFAM:SSF103473 InterPro:IPR010658 Pfam:PF06813 HOGENOM:HBG317009 EMBL:AF419593 IPI:IPI00544383 PIR:T02581 RefSeq:NP_181454.1 UniGene:At.27387 ProteinModelPortal:O80960 STRING:O80960 PRIDE:O80960 EnsemblPlants:AT2G39210.1 GeneID:818506 KEGG:ath:AT2G39210 TAIR:At2g39210 eggNOG:NOG311390 InParanoid:O80960 OMA:TIWETLM PhylomeDB:O80960 ProtClustDB:CLSN2912996 ArrayExpress:O80960 Genevestigator:O80960 Uniprot:O80960
Leaf	Isotig07610	12	52	-1.587	8.88E-05	TAIR|locus:2122009 - symbol:RBP31 "AT4G24770" species:3702 "Arabidopsis thaliana" [GO:0003723 "RNA binding" evidence=ISS;TAS] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0045087 "innate immune response" evidence=IDA] [GO:0008266 "poly(U) RNA binding" evidence=IDA] [GO:0009451 "RNA modification" evidence=IMP] [GO:0006396 "RNA processing" evidence=TAS] InterPro:IPR000504 InterPro:IPR012677 Pfam:PF00076 PROSITE:PS50102 SMART:SM00360 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0009570 GO:GO:0008266 GO:GO:0000166 GO:GO:0006397 Gene3D:G3DSA:3.30.70.330 GO:GO:0045087 GO:GO:0009941 GO:GO:0030529 EMBL:AL035356 EMBL:AL161562 GO:GO:0009535 eggNOG:COG0724 GO:GO:0009451 HOGENOM:HBG756718 EMBL:M94554 EMBL:X65255 EMBL:U08467 EMBL:D31712 EMBL:D31713 IPI:IPI00523699 IPI:IPI00542634 IPI:IPI00760320 PIR:S28057 PIR:S53492 RefSeq:NP_194208.1 UniGene:At.38112 UniGene:At.70990 ProteinModelPortal:Q04836 SMR:Q04836 STRING:Q04836 PRIDE:Q04836 ProMEX:Q04836 EnsemblPlants:AT4G24770.1 GeneID:828579 KEGG:ath:AT4G24770 GeneFarm:4009 TAIR:At4g24770 InParanoid:Q04836 OMA:PERAPRV PhylomeDB:Q04836 ProtClustDB:CLSN2915857 ArrayExpress:Q04836 Genevestigator:Q04836 GermOnline:AT4G24770 Uniprot:Q04836
Leaf	Isotig07611	190	0	9.099	8.89E-45	TIGR_CMR|BA_1222 - symbol:BA_1222 "conserved hypothetical protein" species:198094 "Bacillus anthracis str. Ames" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:AE016879 EMBL:AE017334 GenomeReviews:AE016879_GR GenomeReviews:AE017334_GR InterPro:IPR008160 Pfam:PF01391 EMBL:AB281483 EMBL:AJ516936 RefSeq:NP_843695.1 RefSeq:YP_017836.1 PDB:2R6Q PDBsum:2R6Q ProteinModelPortal:Q81JD7 SMR:Q81JD7 IntAct:Q81JD7 EnsemblBacteria:EBBACT00000011819 EnsemblBacteria:EBBACT00000016984 GeneID:1084744 GeneID:2814858 KEGG:ban:BA_1222 KEGG:bar:GBAA_1222 PATRIC:18780046 TIGR:BA_1222 TIGR:GBAA1222 HOGENOM:HBG342646 OMA:SDGLNPD ProtClustDB:CLSK824721 Uniprot:Q81JD7
Leaf	Isotig07633	1	16	-3.471	0.000601166	TAIR|locus:2032748 - symbol:PS2 "phosphate starvation-induced gene 2" species:3702 "Arabidopsis thaliana" [GO:0008152 "metabolic process" evidence=IEA] [GO:0004427 "inorganic diphosphatase activity" evidence=IDA] [GO:0016036 "cellular response to phosphate starvation" evidence=IEP] [GO:0016462 "pyrophosphatase activity" evidence=IDA] [GO:0051262 "protein tetramerization" evidence=IDA] InterPro:IPR006383 InterPro:IPR006384 InterPro:IPR016965 Pfam:PF06888 PIRSF:PIRSF031051 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0051262 GO:GO:0046872 InterPro:IPR023214 Gene3D:G3DSA:3.40.50.1000 SUPFAM:SSF56784 GO:GO:0016036 GO:GO:0016791 GO:GO:0004427 EMBL:AC008017 TIGRFAMs:TIGR01489 TIGRFAMs:TIGR01488 eggNOG:NOG331523 HOGENOM:HBG319786 EMBL:AK176548 EMBL:BT030334 EMBL:AY085944 IPI:IPI00545079 PIR:E96755 RefSeq:NP_565052.1 UniGene:At.11680 ProteinModelPortal:Q67YC0 SMR:Q67YC0 DNASU:843632 EnsemblPlants:AT1G73010.1 GeneID:843632 KEGG:ath:AT1G73010 TAIR:At1g73010 InParanoid:Q67YC0 OMA:ASVVPWE PhylomeDB:Q67YC0 ProtClustDB:CLSN2685367 ArrayExpress:Q67YC0 Genevestigator:Q67YC0 Uniprot:Q67YC0
Leaf	Isotig07746	31	8	2.483	1.11E-06	TAIR|locus:2128238 - symbol:BTI2 "AT4G11220" species:3702 "Arabidopsis thaliana" [GO:0005783 "endoplasmic reticulum" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005789 "endoplasmic reticulum membrane" evidence=IDA] [GO:0071458 "integral to cytosolic side of endoplasmic reticulum membrane" evidence=IDA] [GO:0071782 "endoplasmic reticulum tubular network" evidence=IDA] [GO:0071786 "endoplasmic

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						reticulum tubular network organization" evidence=IMP] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR003388 Pfam:PF02453 PROSITE:PS50845 GO:GO:0005886 EMBL:CP002687 GenomeReviews:CT486007_GR EMBL:AL096882 EMBL:AL161531 GO:GO:0071458 PANTHER:PTHR10994 GO:GO:0071786 GO:GO:0071782 eggNOG:NOG303514 ProtClustDB:CLSN2685988 EMBL:AY034901 EMBL:AY048273 EMBL:AY057606 EMBL:BT002368 EMBL:AY086294 IPI:IPI00525362 PIR:T13013 RefSeq:NP_192861.1 UniGene:At.3649 ProteinModelPortal:Q9SUT9 SMR:Q9SUT9 IntAct:Q9SUT9 STRING:Q9SUT9 PRIDE:Q9SUT9 EnsemblPlants:AT4G11220.1 GeneID:826724 KEGG:ath:AT4G11220 TAIR:At4g11220 HOGENOM:HBG596795 InParanoid:Q9SUT9 OMA:HEESSPN PhylomeDB:Q9SUT9 Genevestigator:Q9SUT9 Uniprot:Q9SUT9
Leaf	Isotig07778	12	1	4.114	0.000154103	TAIR|locus:504955645 - symbol:PIMT1 "protein-l-isoaspartate methyltransferase 1" species:3702 "Arabidopsis thaliana" [GO:0004719 "protein-L-isoaspartate (D-aspartate) O-methyltransferase activity" evidence=IEA;ISS] [GO:0006464 "protein modification process" evidence=ISS] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0007568 "aging" evidence=IMP] [GO:0009651 "response to salt stress" evidence=IMP] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] [GO:0009845 "seed germination" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR000682 Pfam:PF01135 PROSITE:PS01279 GO:GO:0005829 GO:GO:0009737 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0007568 GO:GO:0009651 GO:GO:0009845 EMBL:AL049659 UniGene:At.3161 UniGene:At.70492 eggNOG:COG2518 GO:GO:0004719 PANTHER:PTHR11579 EMBL:U31288 EMBL:BT029372 IPI:IPI00518020 PIR:T06709 RefSeq:NP_680112.2 RefSeq:NP_851013.2 ProteinModelPortal:Q42539 SMR:Q42539 STRING:Q42539 PRIDE:Q42539 EnsemblPlants:AT3G48330.1 EnsemblPlants:AT3G48330.2 GeneID:823991 KEGG:ath:AT3G48330 TAIR:At3g48330 HOGENOM:HBG699907 InParanoid:Q42539 PhylomeDB:Q42539 ProtClustDB:CLSN2708507 Genevestigator:Q42539 TIGRFAMs:TIGR00080 Uniprot:Q42539
Leaf	Isotig07779	48	18	1.944	1.90E-07	No hit
Leaf	Isotig07783	14	2	3.336	0.000148753	TAIR|locus:2134638 - symbol:LIF2 "LHP1-Interacting Factor 2" species:3702 "Arabidopsis thaliana" [GO:0000166 "nucleotide binding" evidence=IEA] [GO:0003676 "nucleic acid binding" evidence=IEA] [GO:0003723 "RNA binding" evidence=ISS] [GO:0008150 "biological_process" evidence=ND] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR000504 InterPro:IPR012677 Pfam:PF00076 PROSITE:PS50102 SMART:SM00360 GO:GO:0005829 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0000166 Gene3D:G3DSA:3.30.70.330 GO:GO:0003676 UniGene:At.24279 HSSP:Q9Y5S9 EMBL:AF367357 EMBL:AY113171 EMBL:AK227578 IPI:IPI00532730 RefSeq:NP_001031566.1 RefSeq:NP_567192.1 ProteinModelPortal:Q9ASP6 SMR:Q9ASP6 PRIDE:Q9ASP6 EnsemblPlants:AT4G00830.1 EnsemblPlants:AT4G00830.2 GeneID:827998 KEGG:ath:AT4G00830 TAIR:At4g00830 HOGENOM:HBG587494 InParanoid:Q9ASP6 OMA:IRCSLSE PhylomeDB:Q9ASP6 ProtClustDB:CLSN2698006 Genevestigator:Q9ASP6 Uniprot:Q9ASP6
Leaf	Isotig07787	16	4	2.529	0.000407249	TAIR|locus:2075601 - symbol:AT3G47160 species:3702 "Arabidopsis thaliana" [GO:0008270 "zinc ion binding" evidence=IEA] InterPro:IPR001841 PROSITE:PS50089 SMART:SM00184 Prosite:PS00518 EMBL:CP002686 GO:GO:0008270 InterPro:IPR013083 Gene3D:G3DSA:3.30.40.10 EMBL:AL133292 InterPro:IPR017907 ProtClustDB:CLSN2685154 EMBL:AY099618 EMBL:BT002136 EMBL:DQ086845 IPI:IPI00525617 PIR:T45652 RefSeq:NP_190300.1 UniGene:At.43855 ProteinModelPortal:Q9SD57 SMR:Q9SD57 STRING:Q9SD57 PRIDE:Q9SD57 EnsemblPlants:AT3G47160.1 GeneID:823869 KEGG:ath:AT3G47160 TAIR:At3g47160 InParanoid:Q9SD57 OMA:TIERENK PhylomeDB:Q9SD57 ArrayExpress:Q9SD57 Genevestigator:Q9SD57 Uniprot:Q9SD57
Leaf	Isotig07806	26	6	2.644	3.85E-06	TAIR|locus:2151326 - symbol:GSTL3 "Glutathione transferase L3" species:3702 "Arabidopsis thaliana" [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR004045 PROSITE:PS50404 GO:GO:0005829 GO:GO:0046686 EMBL:CP002688 GO:GO:0009636 InterPro:IPR012336 Gene3D:G3DSA:3.40.30.10 SUPFAM:SSF52833 InterPro:IPR010987 Gene3D:G3DSA:1.20.1050.10 SUPFAM:SSF47616 PROSITE:PS50405 EMBL:AL162973 InterPro:IPR017933 GO:GO:0004364 eggNOG:COG0625 HSSP:O65032 ProtClustDB:CLSN2687366 EMBL:AY140069 EMBL:BT002166 EMBL:AK227162 EMBL:AY085126 IPI:IPI00535440 PIR:T48300 RefSeq:NP_195899.1 UniGene:At.33363 ProteinModelPortal:Q9LZ06 SMR:Q9LZ06 STRING:Q9LZ06 PRIDE:Q9LZ06 EnsemblPlants:AT5G02790.1 GeneID:831798 KEGG:ath:AT5G02790 TAIR:At5g02790 InParanoid:Q9LZ06 OMA:IPFVERF PhylomeDB:Q9LZ06 Genevestigator:Q9LZ06 Uniprot:Q9LZ06

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig07823	14	0	5.336	1.79E-05	UNIPROTKB|F1N3D4 - symbol:BT.12647 "Uncharacterized protein" species:9913 "Bos taurus" [GO:0046965 "retinoid X receptor binding" evidence=IEA] InterPro:IPR021394 InterPro:IPR021397 InterPro:IPR021419 Pfam:PF11232 Pfam:PF11235 Pfam:PF11265 GeneTree:ENSGT00520000055653 OMA:PGQMLLS EMBL:DAAA02047485 EMBL:DAAA02047486 IPI:IPI00907370 Ensembl:ENSBTAT00000043183 Uniprot:F1N3D4
Leaf	Isotig07824	24	109	-1.654	4.98E-09	TAIR|locus:2082767 - symbol:LHCA2 "AT3G61470" species:3702 "Arabidopsis thaliana" [GO:0009768 "photosynthesis, light harvesting in photosystem I" evidence=TAS] [GO:0009782 "photosystem I antenna complex" evidence=TAS] [GO:0015979 "photosynthesis" evidence=ISS] [GO:0016168 "chlorophyll binding" evidence=ISS] [GO:0030076 "light-harvesting complex" evidence=ISS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] InterPro:IPR001344 Pfam:PF00504 EMBL:CP002686 GO:GO:0009535 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 TCDB:5.B.4.1.1 KO:K08908 EMBL:AF134120 EMBL:AY054670 EMBL:AY065429 EMBL:AY072483 EMBL:BT002070 IPI:IPI00543126 PIR:T50550 RefSeq:NP_191706.2 UniGene:At.46743 UniGene:At.55066 ProteinModelPortal:Q9SYW8 SMR:Q9SYW8 STRING:Q9SYW8 PRIDE:Q9SYW8 EnsemblPlants:AT3G61470.1 GeneID:825320 KEGG:ath:AT3G61470 TAIR:At3g61470 InParanoid:Q9SYW8 PhylomeDB:Q9SYW8 ProtClustDB:CLSN2696878 ArrayExpress:Q9SYW8 Genevestigator:Q9SYW8 Uniprot:Q9SYW8
Leaf	Isotig07871	57	194	-1.238	3.48E-10	TAIR|locus:2040934 - symbol:LHB1B2 "AT2G34420" species:3702 "Arabidopsis thaliana" [GO:0009769 "photosynthesis, light harvesting in photosystem II" evidence=TAS] [GO:0016168 "chlorophyll binding" evidence=ISS;TAS] [GO:0030076 "light-harvesting complex" evidence=ISS] [GO:0042651 "thylakoid membrane" evidence=TAS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0015979 "photosynthesis" evidence=ISS] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR001344 Pfam:PF00504 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009535 GO:GO:0010287 EMBL:AC004077 EMBL:AC004481 HOGENOM:HBG618504 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 UniGene:At.10812 UniGene:At.24351 UniGene:At.32199 UniGene:At.66422 UniGene:At.71449 UniGene:At.71528 KO:K08912 ProtClustDB:PLN00025 UniGene:At.23647 UniGene:At.27457 UniGene:At.24888 EMBL:AF372886 EMBL:AY039561 EMBL:AY045806 EMBL:AF428397 EMBL:AF419548 EMBL:AF419587 EMBL:AY065125 EMBL:AY079101 EMBL:AY079110 EMBL:AY081587 EMBL:AY142513 EMBL:AK229627 EMBL:X64460 IPI:IPI00530785 PIR:S23546 RefSeq:NP_565786.1 UniGene:At.24064 UniGene:At.71003 UniGene:At.71384 ProteinModelPortal:Q39141 SMR:Q39141 IntAct:Q39141 STRING:Q39141 PRIDE:Q39141 EnsemblPlants:AT2G34420.1 GeneID:818005 KEGG:ath:AT2G34420 TAIR:At2g34420 InParanoid:Q39141 OMA:SILAIWG PhylomeDB:Q39141 ArrayExpress:Q39141 Genevestigator:Q39141 Uniprot:Q39141
Leaf	Isotig07874	16	2	3.529	3.35E-05	TAIR|locus:2062754 - symbol:HB-7 "homeobox 7" species:3702 "Arabidopsis thaliana" [GO:0005634 "nucleus" evidence=IEA;ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=ISS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0045893 "positive regulation of transcription, DNA-dependent" evidence=IDA] [GO:0009414 "response to water deprivation" evidence=IEP] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] [GO:0009738 "abscisic acid mediated signaling pathway" evidence=IGI] InterPro:IPR000047 InterPro:IPR001356 InterPro:IPR003106 InterPro:IPR009057 InterPro:IPR017970 Pfam:PF00046 Pfam:PF02183 PRINTS:PR00031 PROSITE:PS00027 PROSITE:PS50071 SMART:SM00389 GO:GO:0005634 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0045893 GO:GO:0009738 GO:GO:0003700 GO:GO:0006351 GO:GO:0009414 Gene3D:G3DSA:1.10.10.60 SUPFAM:SSF46689 GO:GO:0000976 eggNOG:NOG252905 HOGENOM:HBG593038 ProtClustDB:CLSN2683559 EMBL:X67032 EMBL:AC005819 EMBL:AY045826 EMBL:AY091364 IPI:IPI00544746 PIR:H84905 PIR:S47137 RefSeq:NP_182191.1 UniGene:At.136 ProteinModelPortal:P46897 SMR:P46897 STRING:P46897 EnsemblPlants:AT2G46680.1 GeneID:819280 KEGG:ath:AT2G46680 GeneFarm:3966 TAIR:At2g46680 InParanoid:P46897 OMA:ALVIQLQ PhylomeDB:P46897 ArrayExpress:P46897 Genevestigator:P46897 Uniprot:P46897
Leaf	Isotig07890	9	0	4.699	0.000718283	TAIR|locus:2025197 - symbol:AT1G75290 "AT1G75290" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0008152 "metabolic process" evidence=IEA] [GO:0016651

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						"oxidoreductase activity, acting on NADH or NADPH" evidence=ISS] InterPro:IPR016040 InterPro:IPR008030 EMBL:CP002684 GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 eggNOG:COG0702 ProtClustDB:CLSN2682501 Pfam:PF05368 EMBL:BT033106 IPI:IPI00521965 RefSeq:NP_177664.4 UniGene:At.52521 ProteinModelPortal:B3LFB7 SMR:B3LFB7 PRIDE:B3LFB7 EnsemblPlants:AT1G75290.1 GeneID:843866 KEGG:ath:AT1G75290 TAIR:At1g75290 PhylomeDB:B3LFB7 Genevestigator:B3LFB7 Uniprot:B3LFB7
Leaf	Isotig07892	0	14	-4.278	0.000582768	TAIR|locus:2136718 - symbol:PFA-DSP4 "AT4G03960" species:3702 "Arabidopsis thaliana" [GO:0004721 "phosphoprotein phosphatase activity" evidence=ISS] [GO:0004725 "protein tyrosine phosphatase activity" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0016311 "dephosphorylation" evidence=IEA] [GO:0016791 "phosphatase activity" evidence=IEA] InterPro:IPR000387 InterPro:IPR016130 InterPro:IPR020428 PRINTS:PR01911 PROSITE:PS00383 PROSITE:PS50056 Pfam:PF03162 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0004725 eggNOG:COG2365 HOGENOM:HBG527347 InterPro:IPR004861 EMBL:AY054279 EMBL:AF458342 EMBL:AY086713 EMBL:AK118704 IPI:IPI00543891 RefSeq:NP_567261.1 UniGene:At.26383 ProteinModelPortal:Q940L5 SMR:Q940L5 PRIDE:Q940L5 EnsemblPlants:AT4G03960.1 GeneID:825706 KEGG:ath:AT4G03960 TAIR:At4g03960 InParanoid:Q940L5 OMA:CKEPFVN PhylomeDB:Q940L5 ProtClustDB:CLSN2917496 Genevestigator:Q940L5 Uniprot:Q940L5
Leaf	Isotig07930	18	101	-1.959	2.55E-10	TAIR|locus:2036209 - symbol:LHCB6 "AT1G15820" species:3702 "Arabidopsis thaliana" [GO:0016168 "chlorophyll binding" evidence=ISS] [GO:0015979 "photosynthesis" evidence=IMP;NAS] [GO:0009783 "photosystem II antenna complex" evidence=NAS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0010196 "nonphotochemical quenching" evidence=IMP] [GO:0009534 "chloroplast thylakoid" evidence=IDA] InterPro:IPR001344 Pfam:PF00504 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009941 GO:GO:0009535 GO:GO:0010287 EMBL:AC034256 HOGENOM:HBG618504 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 GO:GO:0009783 GO:GO:0010196 UniGene:At.25300 EMBL:AF332425 EMBL:AY065113 EMBL:AY081644 IPI:IPI00524194 PIR:F86292 RefSeq:NP_173034.1 UniGene:At.15569 UniGene:At.72611 UniGene:At.74824 UniGene:At.74983 ProteinModelPortal:Q9LMQ2 SMR:Q9LMQ2 STRING:Q9LMQ2 PRIDE:Q9LMQ2 DNASU:838151 EnsemblPlants:AT1G15820.1 GeneID:838151 KEGG:ath:AT1G15820 TAIR:At1g15820 eggNOG:NOG277110 InParanoid:Q9LMQ2 KO:K08917 OMA:RLAMLAM PhylomeDB:Q9LMQ2 ProtClustDB:PLN00170 ArrayExpress:Q9LMQ2 Genevestigator:Q9LMQ2 Uniprot:Q9LMQ2
Leaf	Isotig07966	44	180	-1.503	2.37E-12	TAIR|locus:2040934 - symbol:LHB1B2 "AT2G34420" species:3702 "Arabidopsis thaliana" [GO:0009769 "photosynthesis, light harvesting in photosystem II" evidence=TAS] [GO:0016168 "chlorophyll binding" evidence=ISS;TAS] [GO:0030076 "light-harvesting complex" evidence=ISS] [GO:0042651 "thylakoid membrane" evidence=TAS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0015979 "photosynthesis" evidence=ISS] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR001344 Pfam:PF00504 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009535 GO:GO:0010287 EMBL:AC004077 EMBL:AC004481 HOGENOM:HBG618504 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 UniGene:At.10812 UniGene:At.24351 UniGene:At.32199 UniGene:At.66422 UniGene:At.71449 UniGene:At.71528 KO:K08912 ProtClustDB:PLN00025 UniGene:At.23647 UniGene:At.27457 UniGene:At.24888 EMBL:AF372886 EMBL:AY039561 EMBL:AY045806 EMBL:AF428397 EMBL:AF419548 EMBL:AF419587 EMBL:AY065125 EMBL:AY079101 EMBL:AY079110 EMBL:AY081587 EMBL:AY142513 EMBL:AK229627 EMBL:X64460 IPI:IPI00530785 PIR:S23546 RefSeq:NP_565786.1 UniGene:At.24064 UniGene:At.71003 UniGene:At.71384 ProteinModelPortal:Q39141 SMR:Q39141 IntAct:Q39141 STRING:Q39141 PRIDE:Q39141 EnsemblPlants:AT2G34420.1 GeneID:818005 KEGG:ath:AT2G34420 TAIR:At2g34420 InParanoid:Q39141 OMA:SILAIWG PhylomeDB:Q39141 ArrayExpress:Q39141 Genevestigator:Q39141 Uniprot:Q39141
Leaf	Isotig07981	9	0	4.699	0.000718283	TAIR|locus:2155720 - symbol:AT5G65550 species:3702 "Arabidopsis thaliana" [GO:0008152 "metabolic process" evidence=IEA] [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS] InterPro:IPR002213 Pfam:PF00201 PROSITE:PS00375 EMBL:CP002688 GO:GO:0016758 EMBL:AB026639 CAZy:GT1 eggNOG:COG1819 PANTHER:PTHR11926 EMBL:AK118506 EMBL:BT026361 IPI:IPI00524593

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						RefSeq:NP_201358.1 UniGene:At.44104 UniGene:At.66710 ProteinModelPortal:Q9LSM0 SMR:Q9LSM0 PRIDE:Q9LSM0 EnsemblPlants:AT5G65550.1 GeneID:836681 KEGG:ath:AT5G65550 TAIR:At5g65550 InParanoid:Q9LSM0 OMA:PSKVAFR PhylomeDB:Q9LSM0 Genevestigator:Q9LSM0 Uniprot:Q9LSM0
Leaf	Isotig07989	15	2	3.436	7.06E-05	TAIR|locus:2146178 - symbol:AT5G18400 "AT5G18400" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0005515 "protein binding" evidence=IPI] GO:GO:0005737 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0006915 InterPro:IPR007785 PANTHER:PTHR13273 Pfam:PF05093 HOGENOM:HBG316506 eggNOG:COG5636 EMBL:AC051626 EMBL:AY080855 EMBL:AY123986 EMBL:BT000943 EMBL:BT001035 EMBL:AY088356 IPI:IPI00544195 RefSeq:NP_001078602.1 RefSeq:NP_568363.1 RefSeq:NP_850844.1 UniGene:At.31429 ProteinModelPortal:Q8L7Z3 SMR:Q8L7Z3 IntAct:Q8L7Z3 STRING:Q8L7Z3 PRIDE:Q8L7Z3 EnsemblPlants:AT5G18400.2 EnsemblPlants:AT5G18400.3 GeneID:831958 KEGG:ath:AT5G18400 TAIR:At5g18400 InParanoid:Q8L7Z3 OMA:CGTCPYK PhylomeDB:Q8L7Z3 ProtClustDB:CLSN2689770 Genevestigator:Q8L7Z3 Uniprot:Q8L7Z3
Leaf	Isotig08031	12	0	5.114	7.63E-05	TAIR|locus:2064712 - symbol:RIPK "AT2G05940" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0016301 "kinase activity" evidence=ISS] [GO:0004674 "protein serine/threonine kinase activity" evidence=IDA] [GO:0042742 "defense response to bacterium" evidence=IMP] InterPro:IPR000719 InterPro:IPR001245 InterPro:IPR008271 InterPro:IPR011009 Pfam:PF07714 PROSITE:PS00108 PROSITE:PS50011 GO:GO:0005524 GO:GO:0042742 EMBL:CP002685 GenomeReviews:CT485783_GR eggNOG:COG0515 SUPFAM:SSF56112 GO:GO:0004674 HOGENOM:HBG755340 EMBL:AC005970 EMBL:AY056245 EMBL:AY113963 IPI:IPI00547996 PIR:C84473 RefSeq:NP_178651.1 UniGene:At.23011 ProteinModelPortal:Q9ZUF4 SMR:Q9ZUF4 STRING:Q9ZUF4 PRIDE:Q9ZUF4 EnsemblPlants:AT2G05940.1 GeneID:815147 KEGG:ath:AT2G05940 TAIR:At2g05940 InParanoid:Q9ZUF4 OMA:MLNDPRK PhylomeDB:Q9ZUF4 ProtClustDB:CLSN2912989 ArrayExpress:Q9ZUF4 Genevestigator:Q9ZUF4 Uniprot:Q9ZUF4
Leaf	Isotig08038	11	0	4.988	0.000159591	TAIR|locus:2061136 - symbol:COI1 "AT2G39940" species:3702 "Arabidopsis thaliana" [GO:0006511 "ubiquitin-dependent protein catabolic process" evidence=TAS] [GO:0009861 "jasmonic acid and ethylene-dependent systemic resistance" evidence=TAS] [GO:0005515 "protein binding" evidence=IPI] [GO:0009867 "jasmonic acid mediated signaling pathway" evidence=IGI;TAS] [GO:0009625 "response to insect" evidence=IMP] [GO:0009611 "response to wounding" evidence=IMP] [GO:0009753 "response to jasmonic acid stimulus" evidence=IMP] [GO:0019005 "SCF ubiquitin ligase complex" evidence=IPI] [GO:0031348 "negative regulation of defense response" evidence=IMP] [GO:0010118 "stomatal movement" evidence=IMP] [GO:0042742 "defense response to bacterium" evidence=IMP] [GO:0050832 "defense response to fungus" evidence=IMP] [GO:0031146 "SCF-dependent proteasomal ubiquitin-dependent protein catabolic process" evidence=IMP] [GO:0009641 "shade avoidance" evidence=IMP] [GO:0009909 "regulation of flower development" evidence=IMP] [GO:0010218 "response to far red light" evidence=IMP] [GO:0004842 "ubiquitin-protein ligase activity" evidence=ISS] [GO:0006952 "defense response" evidence=TAS] PROSITE:PS50181 GO:GO:0042742 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0005515 GO:GO:0031348 GO:GO:0050832 GO:GO:0010218 GO:GO:0010118 GO:GO:0019005 GO:GO:0031146 HOGENOM:HBG319412 GO:GO:0009625 GO:GO:0009909 GO:GO:0009641 GO:GO:0009867 EMBL:AF002109 EMBL:AF036340 EMBL:EF470606 EMBL:EF470607 EMBL:EF470608 EMBL:EF470609 EMBL:EF470610 EMBL:EF470611 EMBL:EF470612 EMBL:EF470613 EMBL:EF470614 EMBL:EF470615 EMBL:EF470616 EMBL:EF470617 EMBL:EF470619 EMBL:EF470620 EMBL:EF470621 EMBL:EF470622 EMBL:EF470623 EMBL:EF470624 EMBL:AY045625 EMBL:AY133556 IPI:IPI00516922 PIR:T52139 RefSeq:NP_565919.1 UniGene:At.20831 UniGene:At.71018 PDB:3OGK PDB:3OGL PDB:3OGM PDBsum:3OGK PDBsum:3OGL PDBsum:3OGM ProteinModelPortal:O04197 SMR:O04197 DIP:DIP-31324N IntAct:O04197 STRING:O04197 PRIDE:O04197 EnsemblPlants:AT2G39940.1 GeneID:818581 KEGG:ath:AT2G39940 GeneFarm:4758 TAIR:At2g39940 eggNOG:NOG262527 InParanoid:O04197 KO:K13463 OMA:ARNCRSL PhylomeDB:O04197 ProtClustDB:CLSN2688817 ArrayExpress:O04197 Genevestigator:O04197 GermOnline:AT2G39940 GO:GO:0009861 Uniprot:O04197
Leaf	Isotig08041	15	0	5.436	8.75E-06	TAIR|locus:2010419 - symbol:AT1G27990 "AT1G27990" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002684 GenomeReviews:CT485782_GR EMBL:AC069471 UniGene:At.66881 EMBL:AK317213 IPI:IPI00523350 PIR:D86405 RefSeq:NP_174120.1 PRIDE:Q9C7F4 EnsemblPlants:AT1G27990.1 GeneID:839692 KEGG:ath:AT1G27990 TAIR:At1g27990 HOGENOM:HBG319949

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						InParanoid:Q9C7F4 OMA:IPRFLPR PhylomeDB:Q9C7F4 ProtClustDB:CLSN2679353 Genevestigator:Q9C7F4 Uniprot:Q9C7F4
Leaf	Isotig08042	14	0	5.336	1.79E-05	TAIR|locus:2120993 - symbol:CGL1 "AT4G38240" species:3702 "Arabidopsis thaliana" [GO:0016757 "transferase activity, transferring glycosyl groups" evidence=ISS;IMP] [GO:0005794 "Golgi apparatus" evidence=IC;IDA;TAS] [GO:0003827 "alpha-1,3-mannosylglycoprotein 2-beta-N-acetylglucosaminyltransferase activity" evidence=IDA] [GO:0006972 "hyperosmotic response" evidence=IMP] [GO:0006491 "N-glycan processing" evidence=IMP] [GO:0006486 "protein glycosylation" evidence=IMP] [GO:0016262 "protein N-acetylglucosaminyltransferase activity" evidence=IMP] InterPro:IPR004139 Pfam:PF03071 GO:GO:0016021 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0000139 GO:GO:0046872 GO:GO:0006972 EMBL:AL035538 EMBL:AL161593 GO:GO:0016262 EMBL:AL035539 GO:GO:0006491 EMBL:AJ243198 EMBL:AJ249881 EMBL:AY099838 EMBL:BT000334 IPI:IPI00545584 PIR:JC7084 PIR:T05651 RefSeq:NP_195537.2 RefSeq:NP_849517.1 UniGene:At.22245 HSSP:P27115 ProteinModelPortal:Q9XGM8 SMR:Q9XGM8 STRING:Q9XGM8 CAZy:GT13 PRIDE:Q9XGM8 EnsemblPlants:AT4G38240.1 EnsemblPlants:AT4G38240.2 GeneID:829981 KEGG:ath:AT4G38240 TAIR:At4g38240 eggNOG:NOG148227 HOGENOM:HBG717617 InParanoid:Q9XGM8 KO:K00726 OMA:PPDHRKF PhylomeDB:Q9XGM8 ProtClustDB:CLSN2680320 Genevestigator:Q9XGM8 GO:GO:0003827 PANTHER:PTHR10468 Uniprot:Q9XGM8
Leaf	Isotig08073	64	8	3.529	1.07E-16	TAIR|locus:2168459 - symbol:LTP4 "lipid transfer protein 4" species:3702 "Arabidopsis thaliana" [GO:0008289 "lipid binding" evidence=IEA] [GO:0006869 "lipid transport" evidence=TAS] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] [GO:0009414 "response to water deprivation" evidence=IEP] [GO:0009651 "response to salt stress" evidence=IEP] InterPro:IPR000528 InterPro:IPR013770 PRINTS:PR00382 PROSITE:PS00597 Pfam:PF00234 GO:GO:0009737 EMBL:CP002688 GenomeReviews:BA000015_GR InterPro:IPR016140 SMART:SM00499 SUPFAM:SSF47699 GO:GO:0006869 GO:GO:0009651 GO:GO:0009414 GO:GO:0008289 Gene3D:G3DSA:1.10.110.10 EMBL:AB016890 HOGENOM:HBG744832 ProtClustDB:CLSN2690050 EMBL:AF159801 EMBL:AY058233 EMBL:AY035015 EMBL:AY045644 EMBL:AY059081 EMBL:BT002397 EMBL:BT006514 EMBL:AY088209 IPI:IPI00517749 RefSeq:NP_568904.1 UniGene:At.25116 ProteinModelPortal:Q9LLR6 SMR:Q9LLR6 PRIDE:Q9LLR6 EnsemblPlants:AT5G59310.1 GeneID:836050 KEGG:ath:AT5G59310 TAIR:At5g59310 eggNOG:NOG246791 InParanoid:Q9LLR6 OMA:TSTNCAT PhylomeDB:Q9LLR6 ArrayExpress:Q9LLR6 Genevestigator:Q9LLR6 GermOnline:AT5G59310 Uniprot:Q9LLR6
Leaf	Isotig08080	18	2	3.699	7.53E-06	UNIPROTKB|P51614 - symbol:CHIT3 "Acidic endochitinase" species:29760 "Vitis vinifera" [GO:0006032 "chitin catabolic process" evidence=NAS] [GO:0016798 "hydrolase activity, acting on glycosyl bonds" evidence=NAS] InterPro:IPR001223 InterPro:IPR001579 InterPro:IPR013781 Pfam:PF00704 PROSITE:PS01095 GO:GO:0043169 InterPro:IPR017853 Gene3D:G3DSA:3.20.20.80 SUPFAM:SSF51445 eggNOG:NOG12793 GO:GO:0004568 GO:GO:0006032 CAZy:GH18 EMBL:Z68123 UniGene:Vvi.18 ProteinModelPortal:P51614 SMR:P51614 Uniprot:P51614
Leaf	Isotig08083	19	5	2.455	0.000151807	TAIR|locus:2046595 - symbol:SAR1 "AT2G33120" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0016020 "membrane" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA;TAS] [GO:0005768 "endosome" evidence=TAS] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0009504 "cell plate" evidence=IDA] [GO:0009920 "cell plate formation involved in plant-type cell wall biogenesis" evidence=IGI] [GO:0072661 "protein targeting to plasma membrane" evidence=IGI] InterPro:IPR001388 InterPro:IPR011012 Pfam:PF00957 PRINTS:PR00219 PROSITE:PS00417 PROSITE:PS50892 InterPro:IPR010908 GO:GO:0016021 GO:GO:0005886 GO:GO:0009506 GO:GO:0005774 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0005768 GO:GO:0016192 SUPFAM:SSF64356 EMBL:AC002334 GO:GO:0009504 GO:GO:0009920 GO:GO:0072661 eggNOG:COG5143 Gene3D:G3DSA:3.30.450.50 PROSITE:PS50859 HOGENOM:HBG736701 UniGene:At.20250 ProtClustDB:CLSN2682136 EMBL:M90418 EMBL:AF419564 EMBL:AY072422 EMBL:AY079037 EMBL:AY114706 EMBL:AY128288 EMBL:AY086363 IPI:IPI00517346 PIR:D44088 PIR:F84741 RefSeq:NP_180871.1 UniGene:At.20806 ProteinModelPortal:P47192 SMR:P47192 IntAct:P47192 STRING:P47192 PRIDE:P47192 EnsemblPlants:AT2G33120.1 GeneID:817874 KEGG:ath:AT2G33120 GeneFarm:4145 TAIR:At2g33120 InParanoid:P47192 PhylomeDB:P47192 ArrayExpress:P47192 Genevestigator:P47192 Uniprot:P47192
Leaf	Isotig08096	20	7	2.044	0.00051229	TAIR|locus:2175458 - symbol:ACR12 "ACT domain repeats 12" species:3702 "Arabidopsis thaliana" [GO:0008152 "metabolic process" evidence=IEA] [GO:0016597 "amino acid binding" evidence=IEA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma"

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						evidence=IDA] InterPro:IPR002912 Pfam:PF01842 GO:GO:0009570 EMBL:CP002688 GO:GO:0016597 GO:GO:0009535 GO:GO:0008152 EMBL:AL162972 EMBL:AB008271 EMBL:AY072401 EMBL:AY114702 EMBL:JF797177 IPI:IPI00527532 PIR:T48470 RefSeq:NP_196094.1 UniGene:At.22197 ProteinModelPortal:Q9LZ23 IntAct:Q9LZ23 PRIDE:Q9LZ23 EnsemblPlants:AT5G04740.1 GeneID:830352 KEGG:ath:AT5G04740 TAIR:At5g04740 InParanoid:Q9LZ23 OMA:HVSYRGA PhylomeDB:Q9LZ23 ProtClustDB:CLSN2916259 ArrayExpress:Q9LZ23 Genevestigator:Q9LZ23 Uniprot:Q9LZ23
Leaf	Isotig08121	25	5	2.851	2.46E-06	TAIR|locus:2030230 - symbol:HAB1 "AT1G72770" species:3702 "Arabidopsis thaliana" [GO:0004722 "protein serine/threonine phosphatase activity" evidence=ISS;IDA] [GO:0006470 "protein dephosphorylation" evidence=IEA] [GO:0008287 "protein serine/threonine phosphatase complex" evidence=IEA] [GO:0005515 "protein binding" evidence=IPI] InterPro:IPR000222 InterPro:IPR001932 Pfam:PF00481 PROSITE:PS01032 SMART:SM00331 SMART:SM00332 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005634 GO:GO:0005737 GO:GO:0005515 GO:GO:0006470 GO:GO:0009738 GO:GO:0004722 GO:GO:0046872 EMBL:AC010926 eggNOG:COG0631 Gene3D:G3DSA:3.60.40.10 SUPFAM:SSF81606 GO:GO:0008287 InterPro:IPR015655 PANTHER:PTHR13832 HOGENOM:HBG747569 ProtClustDB:CLSN2679602 EMBL:AJ003119 EMBL:BT015409 EMBL:AK230171 EMBL:AK318665 IPI:IPI00538917 IPI:IPI00846864 PIR:F96752 RefSeq:NP_001077815.1 RefSeq:NP_001185385.1 RefSeq:NP_177421.1 UniGene:At.46635 UniGene:At.67356 PDB:3KB3 PDB:3NMT PDB:3QN1 PDB:3RT0 PDBsum:3KB3 PDBsum:3NMT PDBsum:3QN1 PDBsum:3RT0 ProteinModelPortal:Q9CAJ0 SMR:Q9CAJ0 DIP:DIP-48988N IntAct:Q9CAJ0 STRING:Q9CAJ0 PRIDE:Q9CAJ0 EnsemblPlants:AT1G72770.1 EnsemblPlants:AT1G72770.3 GeneID:843609 KEGG:ath:AT1G72770 TAIR:At1g72770 InParanoid:Q9CAJ0 OMA:YARIENA PhylomeDB:Q9CAJ0 Genevestigator:Q9CAJ0 Uniprot:Q9CAJ0
Leaf	Isotig08122	97	63	1.152	4.83E-07	ZFIN|ZDB-GENE-070410-9 - symbol:zgc:158463 "zgc:158463" species:7955 "Danio rerio" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] ZFIN:ZDB-GENE-070410-9 EMBL:BX296557 EMBL:BX537263 EMBL:BC129240 IPI:IPI00837201 RefSeq:NP_001091866.1 RefSeq:XP_003200836.1 UniGene:Dr.155369 Ensembl:ENSDART00000102863 Ensembl:ENSDART00000126982 GeneID:100037361 GeneID:100151188 KEGG:dre:100037361 KEGG:dre:100151188 eggNOG:NOG298153 GeneTree:ENSGT00390000016898 InParanoid:A2VD29 OMA:ACHQHAL OrthoDB:EOG4FJ8BF Bgee:A2VD29 Uniprot:A2VD29
Leaf	Isotig08134	5	43	-2.575	1.09E-06	TAIR|locus:2040934 - symbol:LHB1B2 "AT2G34420" species:3702 "Arabidopsis thaliana" [GO:0009769 "photosynthesis, light harvesting in photosystem II" evidence=TAS] [GO:0016168 "chlorophyll binding" evidence=ISS;TAS] [GO:0030076 "light-harvesting complex" evidence=ISS] [GO:0042651 "thylakoid membrane" evidence=TAS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0015979 "photosynthesis" evidence=ISS] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR001344 Pfam:PF00504 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009535 GO:GO:0010287 EMBL:AC004077 EMBL:AC004481 HOGENOM:HBG618504 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 UniGene:At.10812 UniGene:At.24351 UniGene:At.32199 UniGene:At.66422 UniGene:At.71449 UniGene:At.71528 KO:K08912 ProtClustDB:PLN00025 UniGene:At.23647 UniGene:At.27457 UniGene:At.24888 EMBL:AF372886 EMBL:AY039561 EMBL:AY045806 EMBL:AF428397 EMBL:AF419548 EMBL:AF419587 EMBL:AY065125 EMBL:AY079101 EMBL:AY079110 EMBL:AY081587 EMBL:AY142513 EMBL:AK229627 EMBL:X64460 IPI:IPI00530785 PIR:S23546 RefSeq:NP_565786.1 UniGene:At.24064 UniGene:At.71003 UniGene:At.71384 ProteinModelPortal:Q39141 SMR:Q39141 IntAct:Q39141 STRING:Q39141 PRIDE:Q39141 EnsemblPlants:AT2G34420.1 GeneID:818005 KEGG:ath:AT2G34420 TAIR:At2g34420 InParanoid:Q39141 OMA:SILAIWG PhylomeDB:Q39141 ArrayExpress:Q39141 Genevestigator:Q39141 Uniprot:Q39141
Leaf	Isotig08136	4	44	-2.930	1.32E-07	DICTYBASE|DDB_G0293168 - symbol:ddx17 "putative RNA helicase,DEAD/DEAH box helicase" species:44689 "Dictyostelium discoideum" [GO:0003723 "RNA binding" evidence=ISS] [GO:0003724 "RNA helicase activity" evidence=ISS] [GO:0005524 "ATP binding" evidence=ISS] [GO:0005634 "nucleus" evidence=ISS] [GO:0006396 "RNA processing" evidence=ISS] [GO:0008186 "RNA-dependent ATPase activity" evidence=ISS] InterPro:IPR000629 InterPro:IPR001650 InterPro:IPR011545 Pfam:PF00270 Pfam:PF00271 PROSITE:PS00039 PROSITE:PS51194 SMART:SM00490 dictyBase:DDB_G0293168 InterPro:IPR014001 GO:GO:0005524 GO:GO:0005634 GO:GO:0005737 GenomeReviews:CM000155_GR GO:GO:0000184 GO:GO:0003723

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						SMART:SM00487 PROSITE:PS51192 GO:GO:0006364 GO:GO:0008026 eggNOG:COG0513 HOGENOM:HBG737336 InterPro:IPR014014 PROSITE:PS51195 EMBL:AAFI02000199 KO:K12823 GO:GO:0003724 GO:GO:0008186 RefSeq:XP_629279.1 HSSP:P09052 ProteinModelPortal:Q54CE0 PRIDE:Q54CE0 EnsemblProtists:DDB0233431 GeneID:8629001 KEGG:ddi:DDB_G0293168 PhylomeDB:Q54CE0 Uniprot:Q54CE0
Leaf	Isotig08164	3	97	-4.486	5.31E-20	TAIR|locus:2036209 - symbol:LHCB6 "AT1G15820" species:3702 "Arabidopsis thaliana" [GO:0016168 "chlorophyll binding" evidence=ISS] [GO:0015979 "photosynthesis" evidence=IMP;NAS] [GO:0009783 "photosystem II antenna complex" evidence=NAS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0010196 "nonphotochemical quenching" evidence=IMP] [GO:0009534 "chloroplast thylakoid" evidence=IDA] InterPro:IPR001344 Pfam:PF00504 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009941 GO:GO:0009535 GO:GO:0010287 EMBL:AC034256 HOGENOM:HBG618504 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 GO:GO:0009783 GO:GO:0010196 UniGene:At.25300 EMBL:AF332425 EMBL:AY065113 EMBL:AY081644 IPI:IPI00524194 PIR:F86292 RefSeq:NP_173034.1 UniGene:At.15569 UniGene:At.72611 UniGene:At.74824 UniGene:At.74983 ProteinModelPortal:Q9LMQ2 SMR:Q9LMQ2 STRING:Q9LMQ2 PRIDE:Q9LMQ2 DNASU:838151 EnsemblPlants:AT1G15820.1 GeneID:838151 KEGG:ath:AT1G15820 TAIR:At1g15820 eggNOG:NOG277110 InParanoid:Q9LMQ2 KO:K08917 OMA:RLAMLAM PhylomeDB:Q9LMQ2 ProtClustDB:PLN00170 ArrayExpress:Q9LMQ2 Genevestigator:Q9LMQ2 Uniprot:Q9LMQ2
Leaf	Isotig08183	13	2	3.229	0.00031313	UNIPROTKB|Q8GTQ9 - symbol:SCOA "Succinyl-CoA ligase [ADP-forming] subunit alpha-1, mitochondrial" species:4081 "Solanum lycopersicum" [GO:0004775 "succinate-CoA ligase (ADP-forming) activity" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0006099 "tricarboxylic acid cycle" evidence=IDA] [GO:0006104 "succinyl-CoA metabolic process" evidence=IDA] [GO:0006105 "succinate metabolic process" evidence=IDA] InterPro:IPR003781 InterPro:IPR005810 InterPro:IPR005811 InterPro:IPR016040 InterPro:IPR017440 Pfam:PF00549 Pfam:PF02629 PIRSF:PIRSF001553 PRINTS:PR01798 PROSITE:PS00399 PROSITE:PS01216 SMART:SM00881 Prosite:PS01217 GO:GO:0005739 GO:GO:0005524 Gene3D:G3DSA:3.40.50.720 GO:GO:0006099 GO:GO:0003878 InterPro:IPR016102 Gene3D:G3DSA:3.40.50.261 SUPFAM:SSF52210 HSSP:P07459 GO:GO:0004775 GO:GO:0006104 GO:GO:0006105 TIGRFAMs:TIGR01019 EMBL:AY167586 RefSeq:NP_001234277.1 UniGene:Les.4025 ProteinModelPortal:Q8GTQ9 SMR:Q8GTQ9 GeneID:543860 Uniprot:Q8GTQ9
Leaf	Isotig08213	14	1	4.336	3.39E-05	TAIR|locus:2043142 - symbol:HAI3 "highly ABA-induced PP2C gene 3" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004722 "protein serine/threonine phosphatase activity" evidence=IEA;ISS] [GO:0006470 "protein dephosphorylation" evidence=IEA] [GO:0008287 "protein serine/threonine phosphatase complex" evidence=IEA] InterPro:IPR000222 InterPro:IPR001932 Pfam:PF00481 PROSITE:PS01032 SMART:SM00331 SMART:SM00332 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0006470 GO:GO:0004722 GO:GO:0046872 eggNOG:COG0631 Gene3D:G3DSA:3.60.40.10 SUPFAM:SSF81606 EMBL:AC004561 GO:GO:0008287 InterPro:IPR015655 PANTHER:PTHR13832 HSSP:P35813 HOGENOM:HBG747569 KO:K14497 ProtClustDB:CLSN2682567 EMBL:DQ056553 EMBL:BT022047 EMBL:BT023483 IPI:IPI00536276 PIR:F84695 RefSeq:NP_180499.1 UniGene:At.50109 ProteinModelPortal:Q9ZW21 SMR:Q9ZW21 DIP:DIP-48991N IntAct:Q9ZW21 PRIDE:Q9ZW21 EnsemblPlants:AT2G29380.1 GeneID:817487 KEGG:ath:AT2G29380 TAIR:At2g29380 InParanoid:Q9ZW21 OMA:CRNGKPV PhylomeDB:Q9ZW21 ArrayExpress:Q9ZW21 Genevestigator:Q9ZW21 Uniprot:Q9ZW21
Leaf	Isotig08231	2	24	-3.056	7.02E-05	TAIR|locus:2040934 - symbol:LHB1B2 "AT2G34420" species:3702 "Arabidopsis thaliana" [GO:0009769 "photosynthesis, light harvesting in photosystem II" evidence=TAS] [GO:0016168 "chlorophyll binding" evidence=ISS;TAS] [GO:0030076 "light-harvesting complex" evidence=ISS] [GO:0042651 "thylakoid membrane" evidence=TAS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0015979 "photosynthesis" evidence=ISS] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR001344 Pfam:PF00504 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009535 GO:GO:0010287 EMBL:AC004077 EMBL:AC004481 HOGENOM:HBG618504 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 UniGene:At.10812 UniGene:At.24351 UniGene:At.32199 UniGene:At.66422 UniGene:At.71449 UniGene:At.71528 KO:K08912 ProtClustDB:PLN00025 UniGene:At.23647 UniGene:At.27457 UniGene:At.24888 EMBL:AF372886 EMBL:AY039561 EMBL:AY045806 EMBL:AF428397 EMBL:AF419548 EMBL:AF419587 EMBL:AY065125 EMBL:AY079101 EMBL:AY079110 EMBL:AY081587 EMBL:AY142513 EMBL:AK229627 EMBL:X64460 IPI:IPI00530785 PIR:S23546 RefSeq:NP_565786.1 UniGene:At.24064 UniGene:At.71003 UniGene:At.71384 ProteinModelPortal:Q39141 SMR:Q39141 IntAct:Q39141 STRING:Q39141 PRIDE:Q39141 EnsemblPlants:AT2G34420.1 GeneID:818005 KEGG:ath:AT2G34420 TAIR:At2g34420 InParanoid:Q39141 OMA:SILAIWG PhylomeDB:Q39141 ArrayExpress:Q39141 Genevestigator:Q39141 Uniprot:Q39141
Leaf	Isotig08254	12	0	5.114	7.63E-05	TAIR|locus:2184707 - symbol:AAP2 "AT5G09220" species:3702 "Arabidopsis thaliana" [GO:0006865 "amino acid transport" evidence=ISS] [GO:0015171 "amino acid transmembrane transporter activity" evidence=IGI;ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0015800 "acidic amino acid transport" evidence=IDA] [GO:0015804 "neutral amino acid transport" evidence=IDA] [GO:0005887 "integral to plasma membrane" evidence=TAS] EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005887 eggNOG:NOG126188 GO:GO:0015293 InterPro:IPR013057 Pfam:PF01490 GO:GO:0015171 EMBL:X71787 EMBL:AL391712 EMBL:AY090341 EMBL:AY084665 IPI:IPI00534416 PIR:S52421 RefSeq:NP_196484.1 UniGene:At.23992 UniGene:At.72977 ProteinModelPortal:Q38967 STRING:Q38967 PRIDE:Q38967 EnsemblPlants:AT5G09220.1 GeneID:830781 KEGG:ath:AT5G09220 TAIR:At5g09220 HOGENOM:HBG319901 InParanoid:Q38967 OMA:CNISSTP PhylomeDB:Q38967 ProtClustDB:CLSN2686208 GO:GO:0015800 GO:GO:0015804 Uniprot:Q38967
Leaf	Isotig08268	9	0	4.699	0.000718283	UNIPROTKB|Q8I4R4 - symbol:PFL2510w "Chitinase" species:36329 "Plasmodium falciparum 3D7" [GO:0008061 "chitin binding" evidence=TAS] InterPro:IPR001223 InterPro:IPR013781 Pfam:PF00704 GO:GO:0043169 InterPro:IPR017853 Gene3D:G3DSA:3.20.20.80 SUPFAM:SSF51445 GO:GO:0005975 EMBL:AE014188 GO:GO:0008061 GO:GO:0004568 CAZy:GH18 KO:K01183 RefSeq:XP_001350904.1 ProteinModelPortal:Q8I4R4 EnsemblProtists:PFL2510w:mRNA GeneID:811552 KEGG:pfa:PFL2510w EuPathDB:EupathDB:PFL2510w ProtClustDB:CLSZ2501012 Uniprot:Q8I4R4
Leaf	Isotig08280	25	3	3.588	1.80E-07	TAIR|locus:2171198 - symbol:AT5G58420 "AT5G58420" species:3702 "Arabidopsis thaliana" [GO:0003735 "structural constituent of ribosome" evidence=ISS] [GO:0006412 "translation" evidence=ISS] [GO:0022627 "cytosolic small ribosomal subunit" evidence=ISS;IDA] [GO:0005730 "nucleolus" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR000876 InterPro:IPR002942 Pfam:PF01479 PIRSF:PIRSF002116 PROSITE:PS50889 SMART:SM00363 Pfam:PF00467 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005730 GO:GO:0016020 GO:GO:0006412 GO:GO:0003735 GO:GO:0019843 EMBL:AB025632 GO:GO:0022627 InterPro:IPR005824 SMART:SM00739 UniGene:At.25091 HOGENOM:HBG392118 KO:K02987 ProtClustDB:PLN00036 InterPro:IPR013845 InterPro:IPR013843 InterPro:IPR018199 PANTHER:PTHR11581 Pfam:PF00900 Pfam:PF08071 ProDom:PD002667 PROSITE:PS00528 EMBL:AF428285 EMBL:AY070467 EMBL:AY143834 EMBL:AY086206 IPI:IPI00545444 RefSeq:NP_200650.1 UniGene:At.9748 ProteinModelPortal:Q8VYK6 SMR:Q8VYK6 STRING:Q8VYK6 PRIDE:Q8VYK6 EnsemblPlants:AT5G58420.1 GeneID:835955 KEGG:ath:AT5G58420 TAIR:At5g58420 InParanoid:Q8VYK6 OMA:QLNLHDG PhylomeDB:Q8VYK6 Genevestigator:Q8VYK6 GermOnline:AT5G58420 Uniprot:Q8VYK6
Leaf	Isotig08300	12	58	-1.744	9.53E-06	TAIR|locus:2084066 - symbol:PPa4 "AT3G53620" species:3702 "Arabidopsis thaliana" [GO:0004427 "inorganic diphosphatase activity" evidence=IDA] [GO:0008152 "metabolic process" evidence=ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA] HAMAP:MF_00209 InterPro:IPR008162 Pfam:PF00719 PROSITE:PS00387 GO:GO:0005829 GO:GO:0046686 EMBL:CP002686 GO:GO:0000287 EMBL:AL132966 GO:GO:0006796 KO:K01507 GO:GO:0004427 Gene3D:G3DSA:3.90.80.10 PANTHER:PTHR10286 SUPFAM:SSF50324 ProtClustDB:PLN02373 OMA:PNDFNVI HSSP:O59570 EMBL:AK226578 IPI:IPI00524492 PIR:T45902 RefSeq:NP_190930.1 UniGene:At.19820 ProteinModelPortal:Q9LFF9 SMR:Q9LFF9 STRING:Q9LFF9 PRIDE:Q9LFF9 EnsemblPlants:AT3G53620.1 GeneID:824530 KEGG:ath:AT3G53620 TAIR:At3g53620 InParanoid:Q9LFF9 PhylomeDB:Q9LFF9 Genevestigator:Q9LFF9 Uniprot:Q9LFF9
Leaf	Isotig08322	10	1	3.851	0.00071293	TAIR|locus:2119931 - symbol:HXK1 "AT4G29130" species:3702 "Arabidopsis thaliana" [GO:0004396 "hexokinase activity" evidence=ISS;IDA] [GO:0005524 "ATP binding" evidence=ISS] [GO:0004340 "glucokinase activity" evidence=IDA] [GO:0008865 "fructokinase activity" evidence=IDA] [GO:0019320 "hexose catabolic process"

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						evidence=IDA] [GO:0010182 "sugar mediated signaling pathway" evidence=TAS] [GO:0010255 "glucose mediated signaling pathway" evidence=IMP] [GO:0005739 "mitochondrion" evidence=IDA;TAS] [GO:0005773 "vacuole" evidence=IDA] [GO:0009536 "plastid" evidence=IDA] [GO:0012501 "programmed cell death" evidence=IMP] [GO:0005634 "nucleus" evidence=IDA] [GO:0005774 "vacuolar membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] [GO:0008270 "zinc ion binding" evidence=IDA] [GO:0009750 "response to fructose stimulus" evidence=IMP] InterPro:IPR001312 InterPro:IPR019807 InterPro:IPR022672 InterPro:IPR022673 Pfam:PF00349 Pfam:PF03727 PRINTS:PR00475 PROSITE:PS00378 GO:GO:0016021 GO:GO:0005524 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005634 GO:GO:0005774 GO:GO:0005515 GO:GO:0005741 GO:GO:0008270 GO:GO:0006096 GO:GO:0010255 EMBL:AL078470 EMBL:AL161574 GO:GO:0004340 GO:GO:0012501 GO:GO:0009536 eggNOG:COG5026 HOGENOM:HBG522186 PANTHER:PTHR19443 KO:K00844 EMBL:U18754 EMBL:U28214 EMBL:AY075658 EMBL:AY124809 IPI:IPI00542953 PIR:S71205 RefSeq:NP_194642.1 UniGene:At.24726 UniGene:At.70249 ProteinModelPortal:Q42525 SMR:Q42525 IntAct:Q42525 STRING:Q42525 PRIDE:Q42525 EnsemblPlants:AT4G29130.1 GeneID:829034 KEGG:ath:AT4G29130 GeneFarm:4274 TAIR:At4g29130 InParanoid:Q42525 OMA:GIQMFEK PhylomeDB:Q42525 ProtClustDB:PLN02405 BioCyc:ARA:AT4G29130-MONOMER BioCyc:MetaCyc:AT4G29130-MONOMER BRENDA:2.7.1.1 ArrayExpress:Q42525 Genevestigator:Q42525 GermOnline:AT4G29130 GO:GO:0008865 Uniprot:Q42525
Leaf	Isotig08361	3	24	-2.471	0.000374243	TAIR|locus:2059999 - symbol:AT2G42220 "AT2G42220" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] Pfam:PF00581 EMBL:CP002685 GenomeReviews:CT485783_GR EMBL:AC002561 GO:GO:0009535 InterPro:IPR001763 Gene3D:G3DSA:3.40.250.10 SMART:SM00450 SUPFAM:SSF52821 PROSITE:PS50206 IPI:IPI00520188 PIR:T00931 RefSeq:NP_565969.1 UniGene:At.12443 UniGene:At.48581 ProteinModelPortal:O48529 SMR:O48529 STRING:O48529 PRIDE:O48529 EnsemblPlants:AT2G42220.1 GeneID:818822 KEGG:ath:AT2G42220 TAIR:At2g42220 eggNOG:NOG261813 HOGENOM:HBG602337 InParanoid:O48529 OMA:VCAYLFI PhylomeDB:O48529 ProtClustDB:CLSN2688883 ArrayExpress:O48529 Genevestigator:O48529 Uniprot:O48529
Leaf	Isotig08394	9	0	4.699	0.000718283	TAIR|locus:2025797 - symbol:AT1G80930 "AT1G80930" species:3702 "Arabidopsis thaliana" [GO:0003723 "RNA binding" evidence=ISS] [GO:0006412 "translation" evidence=ISS] [GO:0016070 "RNA metabolic process" evidence=IEA] [GO:0005634 "nucleus" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR003890 InterPro:IPR016021 InterPro:IPR016024 Pfam:PF02854 SMART:SM00543 EMBL:CP002684 GO:GO:0005829 GO:GO:0005634 GO:GO:0005488 SUPFAM:SSF48371 GO:GO:0016070 Gene3D:G3DSA:1.25.40.180 EMBL:AC011713 KO:K13100 InterPro:IPR003891 Pfam:PF02847 SMART:SM00544 PROSITE:PS51366 EMBL:AY139757 EMBL:BT004547 IPI:IPI00532679 PIR:C96842 RefSeq:NP_178208.1 UniGene:At.43915 ProteinModelPortal:Q9SAG7 STRING:Q9SAG7 PRIDE:Q9SAG7 EnsemblPlants:AT1G80930.1 GeneID:844433 KEGG:ath:AT1G80930 TAIR:At1g80930 InParanoid:Q9SAG7 OMA:VGFLKEC PhylomeDB:Q9SAG7 ProtClustDB:CLSN2682123 Genevestigator:Q9SAG7 Uniprot:Q9SAG7
Leaf	Isotig08428	3	36	-3.056	1.12E-06	TAIR|locus:2040934 - symbol:LHB1B2 "AT2G34420" species:3702 "Arabidopsis thaliana" [GO:0009769 "photosynthesis, light harvesting in photosystem II" evidence=TAS] [GO:0016168 "chlorophyll binding" evidence=ISS;TAS] [GO:0030076 "light-harvesting complex" evidence=ISS] [GO:0042651 "thylakoid membrane" evidence=TAS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0015979 "photosynthesis" evidence=ISS] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR001344 Pfam:PF00504 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009535 GO:GO:0010287 EMBL:AC004077 EMBL:AC004481 HOGENOM:HBG618504 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 UniGene:At.10812 UniGene:At.24351 UniGene:At.32199 UniGene:At.66422 UniGene:At.71449 UniGene:At.71528 KO:K08912 ProtClustDB:PLN00025 UniGene:At.23647 UniGene:At.27457 UniGene:At.24888 EMBL:AF372886 EMBL:AY039561 EMBL:AY045806 EMBL:AF428397 EMBL:AF419548 EMBL:AF419587 EMBL:AY065125 EMBL:AY079101 EMBL:AY079110 EMBL:AY081587 EMBL:AY142513 EMBL:AK229627 EMBL:X64460 IPI:IPI00530785 PIR:S23546 RefSeq:NP_565786.1 UniGene:At.24064 UniGene:At.71003 UniGene:At.71384 ProteinModelPortal:Q39141

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						SMR:Q39141 IntAct:Q39141 STRING:Q39141 PRIDE:Q39141 EnsemblPlants:AT2G34420.1 GeneID:818005 KEGG:ath:AT2G34420 TAIR:At2g34420 InParanoid:Q39141 OMA:SILAIWG PhylomeDB:Q39141 ArrayExpress:Q39141 Genevestigator:Q39141 Uniprot:Q39141
Leaf	Isotig08457	7	61	-2.594	5.57E-09	TAIR|locus:2040934 - symbol:LHB1B2 "AT2G34420" species:3702 "Arabidopsis thaliana" [GO:0009769 "photosynthesis, light harvesting in photosystem II" evidence=TAS] [GO:0016168 "chlorophyll binding" evidence=ISS;TAS] [GO:0030076 "light-harvesting complex" evidence=ISS] [GO:0042651 "thylakoid membrane" evidence=TAS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0015979 "photosynthesis" evidence=ISS] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR001344 Pfam:PF00504 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009535 GO:GO:0010287 EMBL:AC004077 EMBL:AC004481 HOGENOM:HBG618504 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 UniGene:At.10812 UniGene:At.24351 UniGene:At.32199 UniGene:At.66422 UniGene:At.71449 UniGene:At.71528 KO:K08912 ProtClustDB:PLN00025 UniGene:At.23647 UniGene:At.27457 UniGene:At.24888 EMBL:AF372886 EMBL:AY039561 EMBL:AY045806 EMBL:AF428397 EMBL:AF419548 EMBL:AF419587 EMBL:AY065125 EMBL:AY079101 EMBL:AY079110 EMBL:AY081587 EMBL:AY142513 EMBL:AK229627 EMBL:X64460 IPI:IPI00530785 PIR:S23546 RefSeq:NP_565786.1 UniGene:At.24064 UniGene:At.71003 UniGene:At.71384 ProteinModelPortal:Q39141 SMR:Q39141 IntAct:Q39141 STRING:Q39141 PRIDE:Q39141 EnsemblPlants:AT2G34420.1 GeneID:818005 KEGG:ath:AT2G34420 TAIR:At2g34420 InParanoid:Q39141 OMA:SILAIWG PhylomeDB:Q39141 ArrayExpress:Q39141 Genevestigator:Q39141 Uniprot:Q39141
Leaf	Isotig08459	13	119	-2.665	1.43E-16	TAIR|locus:2162540 - symbol:LHCB3 "AT5G54270" species:3702 "Arabidopsis thaliana" [GO:0015979 "photosynthesis" evidence=ISS;IMP] [GO:0030076 "light-harvesting complex" evidence=ISS] [GO:0005198 "structural molecule activity" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] InterPro:IPR001344 Pfam:PF00504 EMBL:CP002688 GO:GO:0005198 EMBL:AB010695 GO:GO:0009535 UniGene:At.49175 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 UniGene:At.10812 UniGene:At.32199 UniGene:At.66422 ProtClustDB:PLN00025 UniGene:At.21173 EMBL:AF134126 EMBL:AF143691 EMBL:AF361858 EMBL:AF372917 EMBL:AY057735 IPI:IPI00532626 PIR:T52318 RefSeq:NP_200238.1 UniGene:At.70236 ProteinModelPortal:Q9S7M0 SMR:Q9S7M0 STRING:Q9S7M0 PRIDE:Q9S7M0 EnsemblPlants:AT5G54270.1 GeneID:835515 KEGG:ath:AT5G54270 TAIR:At5g54270 InParanoid:Q9S7M0 KO:K08914 OMA:ADDPVTF PhylomeDB:Q9S7M0 Genevestigator:Q9S7M0 Uniprot:Q9S7M0
Leaf	Isotig08520	65	201	-1.100	6.17E-09	TAIR|locus:2040944 - symbol:LHB1B1 "AT2G34430" species:3702 "Arabidopsis thaliana" [GO:0009769 "photosynthesis, light harvesting in photosystem II" evidence=TAS] [GO:0016168 "chlorophyll binding" evidence=ISS;TAS] [GO:0030076 "light-harvesting complex" evidence=ISS] [GO:0042651 "thylakoid membrane" evidence=TAS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0015979 "photosynthesis" evidence=ISS] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR001344 Pfam:PF00504 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009941 GO:GO:0009535 GO:GO:0010287 EMBL:AC004077 EMBL:AC004481 HOGENOM:HBG618504 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 UniGene:At.10812 UniGene:At.24351 UniGene:At.66422 UniGene:At.71449 UniGene:At.71528 KO:K08912 ProtClustDB:PLN00025 UniGene:At.22980 UniGene:At.71384 EMBL:AF326864 EMBL:AF339687 EMBL:AY120776 EMBL:BT002103 EMBL:X64459 IPI:IPI00535697 PIR:S25677 RefSeq:NP_565787.1 UniGene:At.67299 UniGene:At.71696 ProteinModelPortal:Q39142 SMR:Q39142 STRING:Q39142 PRIDE:Q39142 EnsemblPlants:AT2G34430.1 GeneID:818006 KEGG:ath:AT2G34430 TAIR:At2g34430 InParanoid:Q39142 OMA:MRKASKP PhylomeDB:Q39142 ArrayExpress:Q39142 Genevestigator:Q39142 Uniprot:Q39142
Leaf	Isotig08530	12	0	5.114	7.63E-05	TAIR|locus:2183329 - symbol:AT5G07330 "AT5G07330" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002688

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GenomeReviews:BA000015_GR EMBL:AL163912 HOGENOM:HBG746117 ProtClustDB:CLSN2687068 EMBL:BT010400 EMBL:AK118558 IPI:IPI00533921 PIR:T49872 RefSeq:NP_196350.1 UniGene:At.32734 PRIDE:Q9LY27 EnsemblPlants:AT5G07330.1 GeneID:830624 KEGG:ath:AT5G07330 TAIR:At5g07330 eggNOG:NOG262444 InParanoid:Q9LY27 OMA:HIHEFES PhylomeDB:Q9LY27 Genevestigator:Q9LY27 Uniprot:Q9LY27
Leaf	Isotig08537	1	34	-4.559	5.31E-08	TAIR|locus:2040934 - symbol:LHB1B2 "AT2G34420" species:3702 "Arabidopsis thaliana" [GO:0009769 "photosynthesis, light harvesting in photosystem II" evidence=TAS] [GO:0016168 "chlorophyll binding" evidence=ISS;TAS] [GO:0030076 "light-harvesting complex" evidence=ISS] [GO:0042651 "thylakoid membrane" evidence=TAS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0015979 "photosynthesis" evidence=ISS] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR001344 Pfam:PF00504 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009535 GO:GO:0010287 EMBL:AC004077 EMBL:AC004481 HOGENOM:HBG618504 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 UniGene:At.10812 UniGene:At.24351 UniGene:At.32199 UniGene:At.66422 UniGene:At.71449 UniGene:At.71528 KO:K08912 ProtClustDB:PLN00025 UniGene:At.23647 UniGene:At.27457 UniGene:At.24888 EMBL:AF372886 EMBL:AY039561 EMBL:AY045806 EMBL:AF428397 EMBL:AF419548 EMBL:AF419587 EMBL:AY065125 EMBL:AY079101 EMBL:AY079110 EMBL:AY081587 EMBL:AY142513 EMBL:AK229627 EMBL:X64460 IPI:IPI00530785 PIR:S23546 RefSeq:NP_565786.1 UniGene:At.24064 UniGene:At.71003 UniGene:At.71384 ProteinModelPortal:Q39141 SMR:Q39141 IntAct:Q39141 STRING:Q39141 PRIDE:Q39141 EnsemblPlants:AT2G34420.1 GeneID:818005 KEGG:ath:AT2G34420 TAIR:At2g34420 InParanoid:Q39141 OMA:SILAIWG PhylomeDB:Q39141 ArrayExpress:Q39141 Genevestigator:Q39141 Uniprot:Q39141
Leaf	Isotig08544	4	59	-3.354	8.20E-11	TAIR|locus:2040934 - symbol:LHB1B2 "AT2G34420" species:3702 "Arabidopsis thaliana" [GO:0009769 "photosynthesis, light harvesting in photosystem II" evidence=TAS] [GO:0016168 "chlorophyll binding" evidence=ISS;TAS] [GO:0030076 "light-harvesting complex" evidence=ISS] [GO:0042651 "thylakoid membrane" evidence=TAS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0015979 "photosynthesis" evidence=ISS] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR001344 Pfam:PF00504 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009535 GO:GO:0010287 EMBL:AC004077 EMBL:AC004481 HOGENOM:HBG618504 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 UniGene:At.10812 UniGene:At.24351 UniGene:At.32199 UniGene:At.66422 UniGene:At.71449 UniGene:At.71528 KO:K08912 ProtClustDB:PLN00025 UniGene:At.23647 UniGene:At.27457 UniGene:At.24888 EMBL:AF372886 EMBL:AY039561 EMBL:AY045806 EMBL:AF428397 EMBL:AF419548 EMBL:AF419587 EMBL:AY065125 EMBL:AY079101 EMBL:AY079110 EMBL:AY081587 EMBL:AY142513 EMBL:AK229627 EMBL:X64460 IPI:IPI00530785 PIR:S23546 RefSeq:NP_565786.1 UniGene:At.24064 UniGene:At.71003 UniGene:At.71384 ProteinModelPortal:Q39141 SMR:Q39141 IntAct:Q39141 STRING:Q39141 PRIDE:Q39141 EnsemblPlants:AT2G34420.1 GeneID:818005 KEGG:ath:AT2G34420 TAIR:At2g34420 InParanoid:Q39141 OMA:SILAIWG PhylomeDB:Q39141 ArrayExpress:Q39141 Genevestigator:Q39141 Uniprot:Q39141
Leaf	Isotig08575	7	49	-2.278	1.26E-06	TAIR|locus:2040934 - symbol:LHB1B2 "AT2G34420" species:3702 "Arabidopsis thaliana" [GO:0009769 "photosynthesis, light harvesting in photosystem II" evidence=TAS] [GO:0016168 "chlorophyll binding" evidence=ISS;TAS] [GO:0030076 "light-harvesting complex" evidence=ISS] [GO:0042651 "thylakoid membrane" evidence=TAS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0015979 "photosynthesis" evidence=ISS] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR001344 Pfam:PF00504 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009535 GO:GO:0010287 EMBL:AC004077 EMBL:AC004481 HOGENOM:HBG618504 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 UniGene:At.10812 UniGene:At.24351 UniGene:At.32199 UniGene:At.66422 UniGene:At.71449 UniGene:At.71528 KO:K08912 ProtClustDB:PLN00025

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						UniGene:At.23647 UniGene:At.27457 UniGene:At.24888 EMBL:AF372886 EMBL:AY039561 EMBL:AY045806 EMBL:AF428397 EMBL:AF419548 EMBL:AF419587 EMBL:AY065125 EMBL:AY079101 EMBL:AY079110 EMBL:AY081587 EMBL:AY142513 EMBL:AK229627 EMBL:X64460 IPI:IPI00530785 PIR:S23546 RefSeq:NP_565786.1 UniGene:At.24064 UniGene:At.71003 UniGene:At.71384 ProteinModelPortal:Q39141 SMR:Q39141 IntAct:Q39141 STRING:Q39141 PRIDE:Q39141 EnsemblPlants:AT2G34420.1 GeneID:818005 KEGG:ath:AT2G34420 TAIR:At2g34420 InParanoid:Q39141 OMA:SILAIWG PhylomeDB:Q39141 ArrayExpress:Q39141 Genevestigator:Q39141 Uniprot:Q39141
Leaf	Isotig08606	31	143	-1.677	1.35E-11	TAIR|locus:2040944 - symbol:LHB1B1 "AT2G34430" species:3702 "Arabidopsis thaliana" [GO:0009769 "photosynthesis, light harvesting in photosystem II" evidence=TAS] [GO:0016168 "chlorophyll binding" evidence=ISS;TAS] [GO:0030076 "light-harvesting complex" evidence=ISS] [GO:0042651 "thylakoid membrane" evidence=TAS] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0015979 "photosynthesis" evidence=ISS] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR001344 Pfam:PF00504 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009941 GO:GO:0009535 GO:GO:0010287 EMBL:AC004077 EMBL:AC004481 HOGENOM:HBG618504 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 UniGene:At.10812 UniGene:At.24351 UniGene:At.66422 UniGene:At.71449 UniGene:At.71528 KO:K08912 ProtClustDB:PLN00025 UniGene:At.22980 UniGene:At.71384 EMBL:AF326864 EMBL:AF339687 EMBL:AY120776 EMBL:BT002103 EMBL:X64459 IPI:IPI00535697 PIR:S25677 RefSeq:NP_565787.1 UniGene:At.67299 UniGene:At.71696 ProteinModelPortal:Q39142 SMR:Q39142 STRING:Q39142 PRIDE:Q39142 EnsemblPlants:AT2G34430.1 GeneID:818006 KEGG:ath:AT2G34430 TAIR:At2g34430 InParanoid:Q39142 OMA:MRKASKP PhylomeDB:Q39142 ArrayExpress:Q39142 Genevestigator:Q39142 Uniprot:Q39142
Leaf	Isotig08642	0	50	-6.115	1.40E-11	TAIR|locus:2040934 - symbol:LHB1B2 "AT2G34420" species:3702 "Arabidopsis thaliana" [GO:0009769 "photosynthesis, light harvesting in photosystem II" evidence=TAS] [GO:0016168 "chlorophyll binding" evidence=ISS;TAS] [GO:0030076 "light-harvesting complex" evidence=ISS] [GO:0042651 "thylakoid membrane" evidence=TAS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0015979 "photosynthesis" evidence=ISS] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR001344 Pfam:PF00504 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009535 GO:GO:0010287 EMBL:AC004077 EMBL:AC004481 HOGENOM:HBG618504 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 UniGene:At.10812 UniGene:At.24351 UniGene:At.32199 UniGene:At.66422 UniGene:At.71449 UniGene:At.71528 KO:K08912 ProtClustDB:PLN00025 UniGene:At.23647 UniGene:At.27457 UniGene:At.24888 EMBL:AF372886 EMBL:AY039561 EMBL:AY045806 EMBL:AF428397 EMBL:AF419548 EMBL:AF419587 EMBL:AY065125 EMBL:AY079101 EMBL:AY079110 EMBL:AY081587 EMBL:AY142513 EMBL:AK229627 EMBL:X64460 IPI:IPI00530785 PIR:S23546 RefSeq:NP_565786.1 UniGene:At.24064 UniGene:At.71003 UniGene:At.71384 ProteinModelPortal:Q39141 SMR:Q39141 IntAct:Q39141 STRING:Q39141 PRIDE:Q39141 EnsemblPlants:AT2G34420.1 GeneID:818005 KEGG:ath:AT2G34420 TAIR:At2g34420 InParanoid:Q39141 OMA:SILAIWG PhylomeDB:Q39141 ArrayExpress:Q39141 Genevestigator:Q39141 Uniprot:Q39141
Leaf	Isotig08686	9	0	4.699	0.000718283	TAIR|locus:2098565 - symbol:GSL10 "AT3G07160" species:3702 "Arabidopsis thaliana" [GO:0000148 "1,3-beta-D-glucan synthase complex" evidence=ISS] [GO:0003843 "1,3-beta-D-glucan synthase activity" evidence=ISS] [GO:0006075 "(1->3)-beta-D-glucan biosynthetic process" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009555 "pollen development" evidence=IMP] [GO:0009556 "microsporogenesis" evidence=IMP] [GO:0048589 "developmental growth" evidence=IMP] [GO:0052543 "callose deposition in cell wall" evidence=IMP] [GO:0009846 "pollen germination" evidence=IMP] [GO:0055047 "generative cell mitosis" evidence=IMP] [GO:0080092 "regulation of pollen tube growth" evidence=IMP] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR003440 Pfam:PF02364 GO:GO:0016021 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0008360 GO:GO:0048589 GO:GO:0007047 GO:GO:0009846 CAZy:GT48 eggNOG:NOG307043 GO:GO:0000148 GO:GO:0003843 HOGENOM:HBG316390 KO:K11000 GO:GO:0006075

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0009556 GO:GO:0080092 EMBL:AC012395 EMBL:AY085106 IPI:IPI01020150 RefSeq:NP_187372.5 ProteinModelPortal:Q9SFU6 STRING:Q9SFU6 PRIDE:Q9SFU6 GeneID:819903 KEGG:ath:AT3G07160 TAIR:At3g07160 InParanoid:Q9SFU6 OMA:DPNSEGR PhylomeDB:Q9SFU6 Genevestigator:Q9SFU6 GO:GO:0052543 GO:GO:0055047 Uniprot:Q9SFU6
Leaf	Isotig08691	19	5	2.455	0.000151807	TAIR|locus:2161600 - symbol:RAN3 "AT5G55190" species:3702 "Arabidopsis thaliana" [GO:0005525 "GTP binding" evidence=ISS] [GO:0005829 "cytosol" evidence=RCA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] [GO:0003924 "GTPase activity" evidence=ISS] [GO:0005515 "protein binding" evidence=IPI] [GO:0006606 "protein import into nucleus" evidence=TAS] InterPro:IPR001806 InterPro:IPR002041 InterPro:IPR005225 Pfam:PF00071 PRINTS:PR00627 PROSITE:PS51418 SMART:SM00176 GO:GO:0005525 TIGRFAMs:TIGR00231 GO:GO:0009506 GO:GO:0005634 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005515 GO:GO:0003924 GO:GO:0007264 GO:GO:0006606 eggNOG:COG1100 HOGENOM:HBG745225 EMBL:AB010071 KO:K07936 OMA:EYFEISA ProtClustDB:PLN03071 EMBL:X97381 EMBL:U73810 EMBL:U75601 EMBL:AF017991 EMBL:AY042796 EMBL:AY050317 EMBL:AY116939 EMBL:BT000723 IPI:IPI00547198 RefSeq:NP_200330.1 UniGene:At.20354 ProteinModelPortal:Q8H156 SMR:Q8H156 IntAct:Q8H156 STRING:Q8H156 PRIDE:Q8H156 EnsemblPlants:AT5G55190.1 GeneID:835612 KEGG:ath:AT5G55190 GeneFarm:5098 TAIR:At5g55190 InParanoid:Q8H156 PhylomeDB:Q8H156 ArrayExpress:Q8H156 Genevestigator:Q8H156 GermOnline:AT5G55190 Uniprot:Q8H156
Leaf	Isotig08708	17	1	4.616	3.60E-06	TAIR|locus:2827800 - symbol:ERD7 "AT2G17840" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0009409 "response to cold" evidence=IEP] [GO:0009644 "response to high light intensity" evidence=IEP] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0009414 "response to water deprivation" evidence=IEP] GO:GO:0005886 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009409 GO:GO:0009651 GO:GO:0009414 GO:GO:0009644 UniGene:At.19461 UniGene:At.40094 InterPro:IPR009686 Pfam:PF06911 EMBL:AF325067 EMBL:AF428331 EMBL:AY081319 EMBL:BT001230 IPI:IPI00548818 PIR:T00840 RefSeq:NP_179374.1 STRING:O48832 PRIDE:O48832 EnsemblPlants:AT2G17840.1 GeneID:816293 KEGG:ath:AT2G17840 TAIR:At2g17840 eggNOG:NOG243611 HOGENOM:HBG318774 InParanoid:O48832 OMA:MTESVAN PhylomeDB:O48832 ProtClustDB:CLSN2683911 ArrayExpress:O48832 Genevestigator:O48832 Uniprot:O48832
Leaf	Isotig08728	10	0	4.851	0.000336918	ZFIN|ZDB-GENE-060503-506 - symbol:si:ch211-250g4.3 "si:ch211-250g4.3" species:7955 "Danio rerio" [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] ZFIN:ZDB-GENE-060503-506 InterPro:IPR011029 SUPFAM:SSF47986 GeneTree:ENSGT00650000093064 OrthoDB:EOG41JZBB eggNOG:NOG255112 EMBL:CR385063 IPI:IPI01005290 UniGene:Dr.156482 Ensembl:ENSDART00000139999 OMA:LERTITH Bgee:Q1L949 Uniprot:Q1L949
Leaf	Isotig08729	12	0	5.114	7.63E-05	TAIR|locus:2160897 - symbol:PFK2 "AT5G47810" species:3702 "Arabidopsis thaliana" [GO:0003872 "6-phosphofructokinase activity" evidence=ISS] [GO:0005945 "6-phosphofructokinase complex" evidence=ISS] [GO:0006096 "glycolysis" evidence=ISS] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR000023 InterPro:IPR012004 Pfam:PF00365 PIRSF:PIRSF000534 GO:GO:0005524 EMBL:CP002688 GenomeReviews:BA000015_GR EMBL:AB016886 GO:GO:0006096 eggNOG:COG0205 HOGENOM:HBG316947 KO:K00850 GO:GO:0005945 GO:GO:0003872 InterPro:IPR022953 PRINTS:PR00476 SUPFAM:SSF53784 EMBL:AY056779 EMBL:AY090379 IPI:IPI00532264 RefSeq:NP_199592.1 UniGene:At.9400 ProteinModelPortal:Q9FIK0 SMR:Q9FIK0 IntAct:Q9FIK0 STRING:Q9FIK0 PRIDE:Q9FIK0 EnsemblPlants:AT5G47810.1 GeneID:834832 KEGG:ath:AT5G47810 TAIR:At5g47810 InParanoid:Q9FIK0 OMA:AYHRAGP PhylomeDB:Q9FIK0 Genevestigator:Q9FIK0 Uniprot:Q9FIK0
Leaf	Isotig08760	4	36	-2.641	6.13E-06	TAIR|locus:2040934 - symbol:LHB1B2 "AT2G34420" species:3702 "Arabidopsis thaliana" [GO:0009769 "photosynthesis, light harvesting in photosystem II" evidence=TAS] [GO:0016168 "chlorophyll binding" evidence=ISS;TAS] [GO:0030076 "light-harvesting complex" evidence=ISS] [GO:0042651 "thylakoid membrane" evidence=TAS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0015979 "photosynthesis" evidence=ISS] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR001344 Pfam:PF00504 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009535 GO:GO:0010287 EMBL:AC004077 EMBL:AC004481 HOGENOM:HBG618504 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 UniGene:At.10812 UniGene:At.24351 UniGene:At.32199 UniGene:At.66422 UniGene:At.71449 UniGene:At.71528 KO:K08912 ProtClustDB:PLN00025 UniGene:At.23647 UniGene:At.27457 UniGene:At.24888 EMBL:AF372886 EMBL:AY039561 EMBL:AY045806 EMBL:AF428397 EMBL:AF419548 EMBL:AF419587 EMBL:AY065125 EMBL:AY079101 EMBL:AY079110 EMBL:AY081587 EMBL:AY142513 EMBL:AK229627 EMBL:X64460 IPI:IPI00530785 PIR:S23546 RefSeq:NP_565786.1 UniGene:At.24064 UniGene:At.71003 UniGene:At.71384 ProteinModelPortal:Q39141 SMR:Q39141 IntAct:Q39141 STRING:Q39141 PRIDE:Q39141 EnsemblPlants:AT2G34420.1 GeneID:818005 KEGG:ath:AT2G34420 TAIR:At2g34420 InParanoid:Q39141 OMA:SILAIWG PhylomeDB:Q39141 ArrayExpress:Q39141 Genevestigator:Q39141 Uniprot:Q39141
Leaf	Isotig08764	68	4	4.616	1.93E-20	TAIR|locus:2044641 - symbol:COR413-PM1 "AT2G15970" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005886 "plasma membrane" evidence=ISS] [GO:0009631 "cold acclimation" evidence=IEP] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] [GO:0042631 "cellular response to water deprivation" evidence=IEP] [GO:0005773 "vacuole" evidence=IDA] GO:GO:0009737 GO:GO:0005773 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0042631 GO:GO:0009631 EMBL:AC006438 UniGene:At.22305 HOGENOM:HBG595418 ProtClustDB:CLSN2717102 InterPro:IPR008892 Pfam:PF05562 eggNOG:NOG267474 EMBL:AF283004 EMBL:AY093767 EMBL:AY088558 EMBL:AY143813 EMBL:AB044404 IPI:IPI00547690 PIR:C84535 RefSeq:NP_179196.1 UniGene:At.24347 STRING:Q9XIM7 PRIDE:Q9XIM7 EnsemblPlants:AT2G15970.1 GeneID:816092 KEGG:ath:AT2G15970 TAIR:At2g15970 InParanoid:Q9XIM7 OMA:GTTFLEW PhylomeDB:Q9XIM7 ArrayExpress:Q9XIM7 Genevestigator:Q9XIM7 Uniprot:Q9XIM7
Leaf	Isotig08773	9	0	4.699	0.000718283	No hit
Leaf	Isotig08791	5	42	-2.541	1.74E-06	TAIR|locus:2040934 - symbol:LHB1B2 "AT2G34420" species:3702 "Arabidopsis thaliana" [GO:0009769 "photosynthesis, light harvesting in photosystem II" evidence=TAS] [GO:0016168 "chlorophyll binding" evidence=ISS;TAS] [GO:0030076 "light-harvesting complex" evidence=ISS] [GO:0042651 "thylakoid membrane" evidence=TAS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0015979 "photosynthesis" evidence=ISS] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR001344 Pfam:PF00504 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009535 GO:GO:0010287 EMBL:AC004077 EMBL:AC004481 HOGENOM:HBG618504 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 UniGene:At.10812 UniGene:At.24351 UniGene:At.32199 UniGene:At.66422 UniGene:At.71449 UniGene:At.71528 KO:K08912 ProtClustDB:PLN00025 UniGene:At.23647 UniGene:At.27457 UniGene:At.24888 EMBL:AF372886 EMBL:AY039561 EMBL:AY045806 EMBL:AF428397 EMBL:AF419548 EMBL:AF419587 EMBL:AY065125 EMBL:AY079101 EMBL:AY079110 EMBL:AY081587 EMBL:AY142513 EMBL:AK229627 EMBL:X64460 IPI:IPI00530785 PIR:S23546 RefSeq:NP_565786.1 UniGene:At.24064 UniGene:At.71003 UniGene:At.71384 ProteinModelPortal:Q39141 SMR:Q39141 IntAct:Q39141 STRING:Q39141 PRIDE:Q39141 EnsemblPlants:AT2G34420.1 GeneID:818005 KEGG:ath:AT2G34420 TAIR:At2g34420 InParanoid:Q39141 OMA:SILAIWG PhylomeDB:Q39141 ArrayExpress:Q39141 Genevestigator:Q39141 Uniprot:Q39141
Leaf	Isotig08820	1	19	-3.719	0.000124272	TAIR|locus:2040934 - symbol:LHB1B2 "AT2G34420" species:3702 "Arabidopsis thaliana" [GO:0009769 "photosynthesis, light harvesting in photosystem II" evidence=TAS] [GO:0016168 "chlorophyll binding" evidence=ISS;TAS] [GO:0030076 "light-harvesting complex" evidence=ISS] [GO:0042651 "thylakoid membrane" evidence=TAS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0015979 "photosynthesis" evidence=ISS] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR001344 Pfam:PF00504 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009535 GO:GO:0010287 EMBL:AC004077 EMBL:AC004481 HOGENOM:HBG618504 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 UniGene:At.10812 UniGene:At.24351 UniGene:At.32199 UniGene:At.66422 UniGene:At.71449 UniGene:At.71528 KO:K08912 ProtClustDB:PLN00025 UniGene:At.23647 UniGene:At.27457 UniGene:At.24888 EMBL:AF372886 EMBL:AY039561 EMBL:AY045806 EMBL:AF428397 EMBL:AF419548 EMBL:AF419587 EMBL:AY065125 EMBL:AY079101 EMBL:AY079110

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EMBL:AY081587 EMBL:AY142513 EMBL:AK229627 EMBL:X64460 IPI:IPI00530785 PIR:S23546 RefSeq:NP_565786.1 UniGene:At.24064 UniGene:At.71003 UniGene:At.71384 ProteinModelPortal:Q39141 SMR:Q39141 IntAct:Q39141 STRING:Q39141 PRIDE:Q39141 EnsemblPlants:AT2G34420.1 GeneID:818005 KEGG:ath:AT2G34420 TAIR:At2g34420 InParanoid:Q39141 OMA:SILAIWG PhylomeDB:Q39141 ArrayExpress:Q39141 Genevestigator:Q39141 Uniprot:Q39141
Leaf	Isotig08869	18	0	5.699	1.07E-06	TAIR|locus:2062754 - symbol:HB-7 "homeobox 7" species:3702 "Arabidopsis thaliana" [GO:0005634 "nucleus" evidence=IEA;ISS] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=ISS] [GO:0003700 "sequence-specific DNA binding transcription factor activity" evidence=ISS] [GO:0045893 "positive regulation of transcription, DNA-dependent" evidence=IDA] [GO:0009414 "response to water deprivation" evidence=IEP] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] [GO:0009738 "abscisic acid mediated signaling pathway" evidence=IGI] InterPro:IPR000047 InterPro:IPR001356 InterPro:IPR003106 InterPro:IPR009057 InterPro:IPR017970 Pfam:PF00046 Pfam:PF02183 PRINTS:PR00031 PROSITE:PS00027 PROSITE:PS50071 SMART:SM00389 GO:GO:0005634 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0045893 GO:GO:0009738 GO:GO:0003700 GO:GO:0006351 GO:GO:0009414 Gene3D:G3DSA:1.10.10.60 SUPFAM:SSF46689 GO:GO:0000976 eggNOG:NOG252905 HOGENOM:HBG593038 ProtClustDB:CLSN2683559 EMBL:X67032 EMBL:AC005819 EMBL:AY045826 EMBL:AY091364 IPI:IPI00544746 PIR:H84905 PIR:S47137 RefSeq:NP_182191.1 UniGene:At.136 ProteinModelPortal:P46897 SMR:P46897 STRING:P46897 EnsemblPlants:AT2G46680.1 GeneID:819280 KEGG:ath:AT2G46680 GeneFarm:3966 TAIR:At2g46680 InParanoid:P46897 OMA:ALVIQLQ PhylomeDB:P46897 ArrayExpress:P46897 Genevestigator:P46897 Uniprot:P46897
Leaf	Isotig08879	3	49	-3.501	1.69E-09	TAIR|locus:2040934 - symbol:LHB1B2 "AT2G34420" species:3702 "Arabidopsis thaliana" [GO:0009769 "photosynthesis, light harvesting in photosystem II" evidence=TAS] [GO:0016168 "chlorophyll binding" evidence=ISS;TAS] [GO:0030076 "light-harvesting complex" evidence=ISS] [GO:0042651 "thylakoid membrane" evidence=TAS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0015979 "photosynthesis" evidence=ISS] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR001344 Pfam:PF00504 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009535 GO:GO:0010287 EMBL:AC004077 EMBL:AC004481 HOGENOM:HBG618504 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 UniGene:At.10812 UniGene:At.24351 UniGene:At.32199 UniGene:At.66422 UniGene:At.71449 UniGene:At.71528 KO:K08912 ProtClustDB:PLN00025 UniGene:At.23647 UniGene:At.27457 UniGene:At.24888 EMBL:AF372886 EMBL:AY039561 EMBL:AY045806 EMBL:AF428397 EMBL:AF419548 EMBL:AF419587 EMBL:AY065125 EMBL:AY079101 EMBL:AY079110 EMBL:AY081587 EMBL:AY142513 EMBL:AK229627 EMBL:X64460 IPI:IPI00530785 PIR:S23546 RefSeq:NP_565786.1 UniGene:At.24064 UniGene:At.71003 UniGene:At.71384 ProteinModelPortal:Q39141 SMR:Q39141 IntAct:Q39141 STRING:Q39141 PRIDE:Q39141 EnsemblPlants:AT2G34420.1 GeneID:818005 KEGG:ath:AT2G34420 TAIR:At2g34420 InParanoid:Q39141 OMA:SILAIWG PhylomeDB:Q39141 ArrayExpress:Q39141 Genevestigator:Q39141 Uniprot:Q39141
Leaf	Isotig08900	69	17	2.550	1.63E-13	UNIPROTKB|P16033 - symbol:psbA2 "Photosystem Q(B) protein 2" species:1111708 "Synechocystis sp. PCC 6803 substr. Kazusa" [GO:0030096 "plasma membrane-derived thylakoid photosystem II" evidence=IDA] HAMAP:MF_01379 InterPro:IPR000484 InterPro:IPR005867 Pfam:PF00124 PRINTS:PR00256 PROSITE:PS00244 GO:GO:0016021 GO:GO:0009635 GO:GO:0046872 GO:GO:0006810 GO:GO:0016491 EMBL:BA000022 GenomeReviews:BA000022_GR GO:GO:0042651 GO:GO:0009772 GO:GO:0030096 TCDB:3.E.2.2.2 GO:GO:0045156 EMBL:X56000 EMBL:X13547 PIR:S13112 RefSeq:NP_439906.1 RefSeq:NP_441550.1 ProteinModelPortal:P16033 SMR:P16033 IntAct:P16033 STRING:P16033 GeneID:951890 GeneID:953105 KEGG:syn:sll1867 KEGG:syn:slr1311 PATRIC:23836870 eggNOG:NOG04871 HOGENOM:HBG284766 KO:K02703 OMA:GIWFTSM PhylomeDB:P16033 ProtClustDB:CLSK892431 BioCyc:SSP1148:SLL1867-MONOMER BioCyc:SSP1148:SLR1311-MONOMER GO:GO:0030076 Gene3D:G3DSA:1.20.85.10 SUPFAM:SSF81483 TIGRFAMs:TIGR01151 Uniprot:P16033
Leaf	Isotig08903	611	671	0.394	8.21E-07	No hit
Leaf	Isotig08912	0	37	-5.680	5.79E-09	TAIR|locus:2040934 - symbol:LHB1B2 "AT2G34420" species:3702 "Arabidopsis thaliana" [GO:0009769 "photosynthesis, light harvesting in photosystem II" evidence=TAS] [GO:0016168 "chlorophyll binding"

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						evidence=ISS;TAS] [GO:0030076 "light-harvesting complex" evidence=ISS] [GO:0042651 "thylakoid membrane" evidence=TAS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0015979 "photosynthesis" evidence=ISS] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR001344 Pfam:PF00504 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009535 GO:GO:0010287 EMBL:AC004077 EMBL:AC004481 HOGENOM:HBG618504 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 UniGene:At.10812 UniGene:At.24351 UniGene:At.32199 UniGene:At.66422 UniGene:At.71449 UniGene:At.71528 KO:K08912 ProtClustDB:PLN00025 UniGene:At.23647 UniGene:At.27457 UniGene:At.24888 EMBL:AF372886 EMBL:AY039561 EMBL:AY045806 EMBL:AF428397 EMBL:AF419548 EMBL:AF419587 EMBL:AY065125 EMBL:AY079101 EMBL:AY079110 EMBL:AY081587 EMBL:AY142513 EMBL:AK229627 EMBL:X64460 IPI:IPI00530785 PIR:S23546 RefSeq:NP_565786.1 UniGene:At.24064 UniGene:At.71003 UniGene:At.71384 ProteinModelPortal:Q39141 SMR:Q39141 IntAct:Q39141 STRING:Q39141 PRIDE:Q39141 EnsemblPlants:AT2G34420.1 GeneID:818005 KEGG:ath:AT2G34420 TAIR:At2g34420 InParanoid:Q39141 OMA:SILAIWG PhylomeDB:Q39141 ArrayExpress:Q39141 Genevestigator:Q39141 Uniprot:Q39141
Leaf	Isotig08931	44	0	6.988	7.41E-14	No hit
Leaf	Isotig08941	15	3	2.851	0.000262808	TAIR|locus:2145101 - symbol:MSBP1 "AT5G52240" species:3702 "Arabidopsis thaliana" [GO:0005496 "steroid binding" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0030308 "negative regulation of cell growth" evidence=IMP] [GO:0005783 "endoplasmic reticulum" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=IDA] InterPro:IPR001199 Pfam:PF00173 PROSITE:PS00191 PROSITE:PS50255 GO:GO:0005783 GO:GO:0016021 GO:GO:0005886 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0030308 GO:GO:0005496 GO:GO:0020037 GO:GO:0010008 Gene3D:G3DSA:3.10.120.10 SUPFAM:SSF55856 eggNOG:NOG291734 HOGENOM:HBG715794 EMBL:AB025603 EMBL:AF153284 EMBL:BT000922 EMBL:AY086811 IPI:IPI00522918 RefSeq:NP_200037.1 UniGene:At.21163 ProteinModelPortal:Q9XFM6 SMR:Q9XFM6 IntAct:Q9XFM6 STRING:Q9XFM6 PRIDE:Q9XFM6 EnsemblPlants:AT5G52240.1 GeneID:835300 KEGG:ath:AT5G52240 GeneFarm:4753 TAIR:At5g52240 InParanoid:Q9XFM6 OMA:NTVEADA PhylomeDB:Q9XFM6 ProtClustDB:CLSN2719635 ArrayExpress:Q9XFM6 Genevestigator:Q9XFM6 GermOnline:AT5G52240 Uniprot:Q9XFM6
Leaf	Isotig08980	2	53	-4.199	2.76E-11	TAIR|locus:2040934 - symbol:LHB1B2 "AT2G34420" species:3702 "Arabidopsis thaliana" [GO:0009769 "photosynthesis, light harvesting in photosystem II" evidence=TAS] [GO:0016168 "chlorophyll binding" evidence=ISS;TAS] [GO:0030076 "light-harvesting complex" evidence=ISS] [GO:0042651 "thylakoid membrane" evidence=TAS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0015979 "photosynthesis" evidence=ISS] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR001344 Pfam:PF00504 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009535 GO:GO:0010287 EMBL:AC004077 EMBL:AC004481 HOGENOM:HBG618504 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 UniGene:At.10812 UniGene:At.24351 UniGene:At.32199 UniGene:At.66422 UniGene:At.71449 UniGene:At.71528 KO:K08912 ProtClustDB:PLN00025 UniGene:At.23647 UniGene:At.27457 UniGene:At.24888 EMBL:AF372886 EMBL:AY039561 EMBL:AY045806 EMBL:AF428397 EMBL:AF419548 EMBL:AF419587 EMBL:AY065125 EMBL:AY079101 EMBL:AY079110 EMBL:AY081587 EMBL:AY142513 EMBL:AK229627 EMBL:X64460 IPI:IPI00530785 PIR:S23546 RefSeq:NP_565786.1 UniGene:At.24064 UniGene:At.71003 UniGene:At.71384 ProteinModelPortal:Q39141 SMR:Q39141 IntAct:Q39141 STRING:Q39141 PRIDE:Q39141 EnsemblPlants:AT2G34420.1 GeneID:818005 KEGG:ath:AT2G34420 TAIR:At2g34420 InParanoid:Q39141 OMA:SILAIWG PhylomeDB:Q39141 ArrayExpress:Q39141 Genevestigator:Q39141 Uniprot:Q39141
Leaf	Isotig09025	13	0	5.229	3.68E-05	TAIR|locus:2085181 - symbol:AT3G52960 "AT3G52960" species:3702 "Arabidopsis thaliana" [GO:0016209 "antioxidant activity" evidence=ISS] [GO:0016491 "oxidoreductase activity" evidence=IEA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0042742 "defense response to bacterium" evidence=IEP] [GO:0009505 "plant-type cell wall" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] InterPro:IPR013740 Pfam:PF08534 GO:GO:0009570

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0042742 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0009941 GO:GO:0009505 GO:GO:0009579 InterPro:IPR012336 Gene3D:G3DSA:3.40.30.10 SUPFAM:SSF52833 eggNOG:COG0678 HOGENOM:HBG493509 PROSITE:PS51352 GO:GO:0004601 GO:GO:0051920 EMBL:AL132969 HSSP:P30044 EMBL:AY050880 EMBL:AY054638 EMBL:AY072493 EMBL:AY150397 IPI:IPI00533612 PIR:PA0047 PIR:T47553 RefSeq:NP_190864.1 UniGene:At.9858 ProteinModelPortal:Q949U7 SMR:Q949U7 IntAct:Q949U7 STRING:Q949U7 PeroxiBase:4353 PRIDE:Q949U7 ProMEX:Q949U7 EnsemblPlants:AT3G52960.1 GeneID:824462 KEGG:ath:AT3G52960 TAIR:At3g52960 InParanoid:Q949U7 OMA:VIHLEES PhylomeDB:Q949U7 ProtClustDB:CLSN2720528 Genevestigator:Q949U7 Uniprot:Q949U7
Leaf	Isotig09049	9	0	4.699	0.000718283	No hit
Leaf	Isotig09087	623	433	1.054	1.50E-32	No hit
Leaf	Isotig09097	9	0	4.699	0.000718283	TAIR|locus:2141070 - symbol:AT4G17900 "AT4G17900" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] EMBL:CP002687 GenomeReviews:CT486007_GR HOGENOM:HBG747962 InterPro:IPR006734 Pfam:PF04640 EMBL:BT029385 EMBL:AK227244 IPI:IPI00529939 RefSeq:NP_193524.2 UniGene:At.2047 STRING:Q0WUB8 PRIDE:Q0WUB8 EnsemblPlants:AT4G17900.1 GeneID:827514 KEGG:ath:AT4G17900 TAIR:At4g17900 InParanoid:Q0WUB8 OMA:NRWPPWL PhylomeDB:Q0WUB8 ProtClustDB:CLSN2918589 Genevestigator:Q0WUB8 Uniprot:Q0WUB8
Leaf	Isotig09103	3	39	-3.171	2.53E-07	TAIR|locus:2040934 - symbol:LHB1B2 "AT2G34420" species:3702 "Arabidopsis thaliana" [GO:0009769 "photosynthesis, light harvesting in photosystem II" evidence=TAS] [GO:0016168 "chlorophyll binding" evidence=ISS;TAS] [GO:0030076 "light-harvesting complex" evidence=ISS] [GO:0042651 "thylakoid membrane" evidence=TAS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0015979 "photosynthesis" evidence=ISS] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR001344 Pfam:PF00504 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009535 GO:GO:0010287 EMBL:AC004077 EMBL:AC004481 HOGENOM:HBG618504 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 UniGene:At.10812 UniGene:At.24351 UniGene:At.32199 UniGene:At.66422 UniGene:At.71449 UniGene:At.71528 KO:K08912 ProtClustDB:PLN00025 UniGene:At.23647 UniGene:At.27457 UniGene:At.24888 EMBL:AF372886 EMBL:AY039561 EMBL:AY045806 EMBL:AF428397 EMBL:AF419548 EMBL:AF419587 EMBL:AY065125 EMBL:AY079101 EMBL:AY079110 EMBL:AY081587 EMBL:AY142513 EMBL:AK229627 EMBL:X64460 IPI:IPI00530785 PIR:S23546 RefSeq:NP_565786.1 UniGene:At.24064 UniGene:At.71003 UniGene:At.71384 ProteinModelPortal:Q39141 SMR:Q39141 IntAct:Q39141 STRING:Q39141 PRIDE:Q39141 EnsemblPlants:AT2G34420.1 GeneID:818005 KEGG:ath:AT2G34420 TAIR:At2g34420 InParanoid:Q39141 OMA:SILAIWG PhylomeDB:Q39141 ArrayExpress:Q39141 Genevestigator:Q39141 Uniprot:Q39141
Leaf	Isotig09149	1	23	-3.995	1.53E-05	TAIR|locus:2040934 - symbol:LHB1B2 "AT2G34420" species:3702 "Arabidopsis thaliana" [GO:0009769 "photosynthesis, light harvesting in photosystem II" evidence=TAS] [GO:0016168 "chlorophyll binding" evidence=ISS;TAS] [GO:0030076 "light-harvesting complex" evidence=ISS] [GO:0042651 "thylakoid membrane" evidence=TAS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0015979 "photosynthesis" evidence=ISS] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR001344 Pfam:PF00504 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009535 GO:GO:0010287 EMBL:AC004077 EMBL:AC004481 HOGENOM:HBG618504 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 UniGene:At.10812 UniGene:At.24351 UniGene:At.32199 UniGene:At.66422 UniGene:At.71449 UniGene:At.71528 KO:K08912 ProtClustDB:PLN00025 UniGene:At.23647 UniGene:At.27457 UniGene:At.24888 EMBL:AF372886 EMBL:AY039561 EMBL:AY045806 EMBL:AF428397 EMBL:AF419548 EMBL:AF419587 EMBL:AY065125 EMBL:AY079101 EMBL:AY079110 EMBL:AY081587 EMBL:AY142513 EMBL:AK229627 EMBL:X64460 IPI:IPI00530785 PIR:S23546 RefSeq:NP_565786.1 UniGene:At.24064 UniGene:At.71003 UniGene:At.71384 ProteinModelPortal:Q39141 SMR:Q39141 IntAct:Q39141 STRING:Q39141 PRIDE:Q39141 EnsemblPlants:AT2G34420.1 GeneID:818005 KEGG:ath:AT2G34420 TAIR:At2g34420 InParanoid:Q39141 OMA:SILAIWG PhylomeDB:Q39141 ArrayExpress:Q39141 Genevestigator:Q39141 Uniprot:Q39141

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig09169	0	16	-4.471	0.000202082	TAIR|locus:2040934 - symbol:LHB1B2 "AT2G34420" species:3702 "Arabidopsis thaliana" [GO:0009769 "photosynthesis, light harvesting in photosystem II" evidence=TAS] [GO:0016168 "chlorophyll binding" evidence=ISS;TAS] [GO:0030076 "light-harvesting complex" evidence=ISS] [GO:0042651 "thylakoid membrane" evidence=TAS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0015979 "photosynthesis" evidence=ISS] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR001344 Pfam:PF00504 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009535 GO:GO:0010287 EMBL:AC004077 EMBL:AC004481 HOGENOM:HBG618504 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 UniGene:At.10812 UniGene:At.24351 UniGene:At.32199 UniGene:At.66422 UniGene:At.71449 UniGene:At.71528 KO:K08912 ProtClustDB:PLN00025 UniGene:At.23647 UniGene:At.27457 UniGene:At.24888 EMBL:AF372886 EMBL:AY039561 EMBL:AY045806 EMBL:AF428397 EMBL:AF419548 EMBL:AF419587 EMBL:AY065125 EMBL:AY079101 EMBL:AY079110 EMBL:AY081587 EMBL:AY142513 EMBL:AK229627 EMBL:X64460 IPI:IPI00530785 PIR:S23546 RefSeq:NP_565786.1 UniGene:At.24064 UniGene:At.71003 UniGene:At.71384 ProteinModelPortal:Q39141 SMR:Q39141 IntAct:Q39141 STRING:Q39141 PRIDE:Q39141 EnsemblPlants:AT2G34420.1 GeneID:818005 KEGG:ath:AT2G34420 TAIR:At2g34420 InParanoid:Q39141 OMA:SILAIWG PhylomeDB:Q39141 ArrayExpress:Q39141 Genevestigator:Q39141 Uniprot:Q39141
Leaf	Isotig09239	0	16	-4.471	0.000202082	TAIR|locus:2180444 - symbol:GER3 "AT5G20630" species:3702 "Arabidopsis thaliana" [GO:0031012 "extracellular matrix" evidence=IDA] [GO:0050162 "oxalate oxidase activity" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0005618 "cell wall" evidence=IDA] [GO:0009505 "plant-type cell wall" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] InterPro:IPR001929 InterPro:IPR006045 InterPro:IPR019780 Pfam:PF00190 PRINTS:PR00325 PROSITE:PS00725 SMART:SM00835 GO:GO:0045735 InterPro:IPR011051 InterPro:IPR014710 Gene3D:G3DSA:2.60.120.10 SUPFAM:SSF51182 GO:GO:0048046 GO:GO:0005634 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0009409 GO:GO:0030145 GO:GO:0009505 GO:GO:0031012 EMBL:AF296832 HOGENOM:HBG744545 eggNOG:NOG117282 EMBL:Y12673 EMBL:D89374 EMBL:U75188 EMBL:U75193 EMBL:U75195 EMBL:U75203 EMBL:U75205 EMBL:AJ132237 EMBL:AY039516 EMBL:AY055786 IPI:IPI00524759 RefSeq:NP_197563.1 UniGene:At.22582 UniGene:At.72030 ProteinModelPortal:P94072 SMR:P94072 STRING:P94072 Allergome:779 PRIDE:P94072 EnsemblPlants:AT5G20630.1 GeneID:832185 KEGG:ath:AT5G20630 TAIR:At5g20630 InParanoid:P94072 OMA:FISSANK PhylomeDB:P94072 ProtClustDB:CLSN2916803 ArrayExpress:P94072 Genevestigator:P94072 GermOnline:AT5G20630 Uniprot:P94072
Leaf	Isotig09253	1	25	-4.115	5.42E-06	TAIR|locus:2040934 - symbol:LHB1B2 "AT2G34420" species:3702 "Arabidopsis thaliana" [GO:0009769 "photosynthesis, light harvesting in photosystem II" evidence=TAS] [GO:0016168 "chlorophyll binding" evidence=ISS;TAS] [GO:0030076 "light-harvesting complex" evidence=ISS] [GO:0042651 "thylakoid membrane" evidence=TAS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0015979 "photosynthesis" evidence=ISS] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR001344 Pfam:PF00504 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009535 GO:GO:0010287 EMBL:AC004077 EMBL:AC004481 HOGENOM:HBG618504 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 UniGene:At.10812 UniGene:At.24351 UniGene:At.32199 UniGene:At.66422 UniGene:At.71449 UniGene:At.71528 KO:K08912 ProtClustDB:PLN00025 UniGene:At.23647 UniGene:At.27457 UniGene:At.24888 EMBL:AF372886 EMBL:AY039561 EMBL:AY045806 EMBL:AF428397 EMBL:AF419548 EMBL:AF419587 EMBL:AY065125 EMBL:AY079101 EMBL:AY079110 EMBL:AY081587 EMBL:AY142513 EMBL:AK229627 EMBL:X64460 IPI:IPI00530785 PIR:S23546 RefSeq:NP_565786.1 UniGene:At.24064 UniGene:At.71003 UniGene:At.71384 ProteinModelPortal:Q39141 SMR:Q39141 IntAct:Q39141 STRING:Q39141 PRIDE:Q39141 EnsemblPlants:AT2G34420.1 GeneID:818005 KEGG:ath:AT2G34420 TAIR:At2g34420 InParanoid:Q39141 OMA:SILAIWG PhylomeDB:Q39141 ArrayExpress:Q39141 Genevestigator:Q39141 Uniprot:Q39141
Leaf	Isotig09255	9	0	4.699	0.000718283	TAIR|locus:2025317 - symbol:ACR3 "ACT domain repeat 3" species:3702 "Arabidopsis thaliana" [GO:0006807 "nitrogen compound metabolic process" evidence=IEA] [GO:0008152 "metabolic process" evidence=IEA]

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						[GO:0005829 "cytosol" evidence=TAS] [GO:0016597 "amino acid binding" evidence=ISS] InterPro:IPR002912 Pfam:PF01842 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0016597 EMBL:AC002291 GO:GO:0008152 eggNOG:COG2844 EMBL:AF360322 EMBL:AY113891 EMBL:AF528059 EMBL:AK317369 IPI:IPI00527978 PIR:H96798 RefSeq:NP_001031289.1 RefSeq:NP_001117608.1 RefSeq:NP_565146.1 RefSeq:NP_849896.1 RefSeq:NP_849897.1 UniGene:At.22030 ProteinModelPortal:O49285 SMR:O49285 STRING:O49285 PRIDE:O49285 EnsemblPlants:AT1G76990.1 EnsemblPlants:AT1G76990.2 EnsemblPlants:AT1G76990.3 EnsemblPlants:AT1G76990.4 EnsemblPlants:AT1G76990.5 GeneID:844035 KEGG:ath:AT1G76990 TAIR:At1g76990 HOGENOM:HBG316632 InParanoid:O49285 OMA:HNRRIAC PhylomeDB:O49285 ProtClustDB:CLSN2689253 ArrayExpress:O49285 Genevestigator:O49285 Uniprot:O49285
Leaf	Isotig09259	62	9	3.313	1.73E-15	TIGR_CMR|BA_4858 - symbol:BA_4858 "thioesterase family protein" species:198094 "Bacillus anthracis str. Ames" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] InterPro:IPR000524 InterPro:IPR000644 Pfam:PF00392 Pfam:PF00571 PROSITE:PS51371 SMART:SM00116 InterPro:IPR006683 Pfam:PF03061 EMBL:AE016879 EMBL:AE017334 EMBL:AE017225 GenomeReviews:AE016879_GR GenomeReviews:AE017225_GR GenomeReviews:AE017334_GR GO:GO:0003700 InterPro:IPR011991 Gene3D:G3DSA:1.10.10.10 GO:GO:0005622 InterPro:IPR010766 Pfam:PF07085 HOGENOM:HBG314023 OMA:PIISTSY ProtClustDB:CLSK873528 RefSeq:NP_847059.1 RefSeq:YP_021501.1 RefSeq:YP_030753.1 ProteinModelPortal:Q81KX8 DNASU:1084014 EnsemblBacteria:EBBACT00000012784 EnsemblBacteria:EBBACT00000018567 EnsemblBacteria:EBBACT00000019988 GeneID:1084014 GeneID:2818548 GeneID:2850363 KEGG:ban:BA_4858 KEGG:bar:GBAA_4858 KEGG:bat:BAS4505 TIGR:BA_4858 TIGR:GBAA4858 Uniprot:Q81KX8
Leaf	Isotig09267	0	23	-4.995	5.47E-06	TAIR|locus:2084841 - symbol:AT3G43110 "AT3G43110" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002686 GenomeReviews:BA000014_GR HOGENOM:HBG180338 EMBL:AL138643 EMBL:BT012527 EMBL:BT014820 IPI:IPI00523579 PIR:T47369 RefSeq:NP_189897.1 UniGene:At.36321 PRIDE:Q9M250 EnsemblPlants:AT3G43110.1 GeneID:823370 KEGG:ath:AT3G43110 TAIR:At3g43110 eggNOG:NOG288036 InParanoid:Q9M250 OMA:SFWRIRA PhylomeDB:Q9M250 ProtClustDB:CLSN2684262 Genevestigator:Q9M250 Uniprot:Q9M250
Leaf	Isotig09285	223	201	0.679	1.04E-06	No hit
Leaf	Isotig09297	123	0	8.471	9.46E-32	No hit
Leaf	Isotig09303	30	141	-1.704	1.11E-11	UNIPROTKB|P16048 - symbol:GDCSH "Glycine cleavage system H protein, mitochondrial" species:3888 "Pisum sativum" [GO:0005960 "glycine cleavage complex" evidence=IDA] InterPro:IPR002930 InterPro:IPR017453 Pfam:PF01597 GO:GO:0005739 InterPro:IPR011053 SUPFAM:SSF51230 GO:GO:0005960 GO:GO:0019464 InterPro:IPR003016 PANTHER:PTHR11715 TIGRFAMs:TIGR00527 PROSITE:PS00189 EMBL:J05164 EMBL:X53656 EMBL:X64726 PIR:S29122 PDB:1DXM PDB:1HPC PDB:1HTP PDBsum:1DXM PDBsum:1HPC PDBsum:1HTP ProteinModelPortal:P16048 SMR:P16048 IntAct:P16048 Uniprot:P16048
Leaf	Isotig09304	1	18	-3.641	0.000210051	TAIR|locus:4010713767 - symbol:AT3G22142 "AT3G22142" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0006869 "lipid transport" evidence=IEA] InterPro:IPR013770 Pfam:PF00234 EMBL:CP002686 GenomeReviews:BA000014_GR InterPro:IPR016140 SUPFAM:SSF47699 GO:GO:0006869 Gene3D:G3DSA:1.10.110.10 EMBL:AP001306 HSSP:P24337 IPI:IPI00531290 RefSeq:NP_001078199.1 UniGene:At.71418 ProteinModelPortal:Q9LIE8 SMR:Q9LIE8 EnsemblPlants:AT3G22142.1 GeneID:5008021 KEGG:ath:AT3G22142 TAIR:At3g22142 eggNOG:NOG252850 PhylomeDB:Q9LIE8 ProtClustDB:CLSN2920168 Genevestigator:Q9LIE8 Uniprot:Q9LIE8
Leaf	Isotig09384	203	22	3.735	1.83E-51	No hit
Leaf	Isotig09497	19	4	2.777	5.07E-05	TAIR|locus:2124286 - symbol:CCoAOMT1 "caffeoyl coenzyme A O-methyltransferase 1" species:3702 "Arabidopsis thaliana" [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0009805 "coumarin biosynthetic process" evidence=IMP] [GO:0042409 "caffeoyl-CoA O-methyltransferase activity" evidence=IDA] [GO:0005829 "cytosol" evidence=TAS] InterPro:IPR002935 Pfam:PF01596 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0046686 GO:GO:0046872 EMBL:AL021961 EMBL:AL161584 GO:GO:0009809 GO:GO:0009805 eggNOG:COG4122 HOGENOM:HBG496808 GO:GO:0042409 PANTHER:PTHR10509 OMA:REKTGHH EMBL:AY057554 EMBL:AY062630 EMBL:AY081457 EMBL:AY143979 EMBL:AY088577 IPI:IPI00521545 PIR:T05431 RefSeq:NP_195131.1 UniGene:At.23175 ProteinModelPortal:O49499 SMR:O49499 STRING:O49499 PRIDE:O49499 EnsemblPlants:AT4G34050.1 GeneID:829551 KEGG:ath:AT4G34050 TAIR:At4g34050

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						InParanoid:O49499 KO:K00588 PhylomeDB:O49499 ProtClustDB:PLN02589 ArrayExpress:O49499 Genevestigator:O49499 Uniprot:O49499
Leaf	Isotig09503	0	13	-4.171	0.000994782	TAIR|locus:2040934 - symbol:LHB1B2 "AT2G34420" species:3702 "Arabidopsis thaliana" [GO:0009769 "photosynthesis, light harvesting in photosystem II" evidence=TAS] [GO:0016168 "chlorophyll binding" evidence=ISS;TAS] [GO:0030076 "light-harvesting complex" evidence=ISS] [GO:0042651 "thylakoid membrane" evidence=TAS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0015979 "photosynthesis" evidence=ISS] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR001344 Pfam:PF00504 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009535 GO:GO:0010287 EMBL:AC004077 EMBL:AC004481 HOGENOM:HBG618504 GO:GO:0009765 InterPro:IPR022796 InterPro:IPR023329 Gene3D:G3DSA:1.10.3460.10 PANTHER:PTHR21649 SUPFAM:SSF103511 UniGene:At.10812 UniGene:At.24351 UniGene:At.32199 UniGene:At.66422 UniGene:At.71449 UniGene:At.71528 KO:K08912 ProtClustDB:PLN00025 UniGene:At.23647 UniGene:At.27457 UniGene:At.24888 EMBL:AF372886 EMBL:AY039561 EMBL:AY045806 EMBL:AF428397 EMBL:AF419548 EMBL:AF419587 EMBL:AY065125 EMBL:AY079101 EMBL:AY079110 EMBL:AY081587 EMBL:AY142513 EMBL:AK229627 EMBL:X64460 IPI:IPI00530785 PIR:S23546 RefSeq:NP_565786.1 UniGene:At.24064 UniGene:At.71003 UniGene:At.71384 ProteinModelPortal:Q39141 SMR:Q39141 IntAct:Q39141 STRING:Q39141 PRIDE:Q39141 EnsemblPlants:AT2G34420.1 GeneID:818005 KEGG:ath:AT2G34420 TAIR:At2g34420 InParanoid:Q39141 OMA:SILAIWG PhylomeDB:Q39141 ArrayExpress:Q39141 Genevestigator:Q39141 Uniprot:Q39141
Leaf	Isotig09531	1	19	-3.719	0.000124272	TAIR|locus:2084898 - symbol:EMB3119 "EMBRYO DEFECTIVE 3119" species:3702 "Arabidopsis thaliana" [GO:0004751 "ribose-5-phosphate isomerase activity" evidence=IEA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0042742 "defense response to bacterium" evidence=IEP] [GO:0019253 "reductive pentose-phosphate cycle" evidence=NAS] HAMAP:MF_00170 InterPro:IPR004788 InterPro:IPR020672 Pfam:PF06026 GO:GO:0009570 GO:GO:0042742 EMBL:CP002686 GO:GO:0009941 EMBL:AC009465 GO:GO:0009535 EMBL:AC011437 GO:GO:0019253 GO:GO:0009052 KO:K01807 GO:GO:0004751 PANTHER:PTHR11934 TIGRFAMs:TIGR00021 HSSP:O50083 EMBL:AY045785 EMBL:AY142600 IPI:IPI00539339 RefSeq:NP_187130.1 UniGene:At.24856 UniGene:At.75161 UniGene:At.75369 ProteinModelPortal:Q9S726 SMR:Q9S726 STRING:Q9S726 PRIDE:Q9S726 ProMEX:Q9S726 EnsemblPlants:AT3G04790.1 GeneID:819639 KEGG:ath:AT3G04790 TAIR:At3g04790 InParanoid:Q9S726 OMA:NLSLYVD PhylomeDB:Q9S726 ProtClustDB:CLSN2719924 ArrayExpress:Q9S726 Genevestigator:Q9S726 Uniprot:Q9S726
Leaf	Isotig09554	2	23	-2.995	0.000115946	TAIR|locus:2827471 - symbol:AT2G04039 "AT2G04039" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0009507 "chloroplast" evidence=IDA] GO:GO:0009507 EMBL:CP002685 EMBL:AC007178 UniGene:At.26662 UniGene:At.41354 UniGene:At.1794 IPI:IPI00846848 RefSeq:NP_001077877.1 STRING:A8MR59 PRIDE:A8MR59 EnsemblPlants:AT2G04039.3 GeneID:814937 KEGG:ath:AT2G04039 TAIR:At2g04039 eggNOG:NOG42516 ProtClustDB:CLSN2687951 Genevestigator:A8MR59 InterPro:IPR021374 Pfam:PF11210 Uniprot:A8MR59
Leaf	Isotig09564	20	7	2.044	0.00051229	TAIR|locus:2139574 - symbol:AT4G34670 "AT4G34670" species:3702 "Arabidopsis thaliana" [GO:0003735 "structural constituent of ribosome" evidence=ISS] [GO:0006412 "translation" evidence=ISS] [GO:0022627 "cytosolic small ribosomal subunit" evidence=ISS;IDA] [GO:0005730 "nucleolus" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0005618 "cell wall" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR001593 InterPro:IPR018281 Pfam:PF01015 PROSITE:PS01191 GO:GO:0005886 GO:GO:0009506 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005618 GO:GO:0005730 GO:GO:0006412 GO:GO:0003735 EMBL:AL161585 EMBL:AL023094 PANTHER:PTHR11830 GO:GO:0022627 eggNOG:COG1890 HOGENOM:HBG402643 KO:K02984 ProtClustDB:CLSN2684298 EMBL:AJ001342 EMBL:AY062500 EMBL:Z33754 EMBL:Z35368 IPI:IPI00543912 PIR:T05287 RefSeq:NP_195193.1 UniGene:At.24 ProteinModelPortal:Q42262 SMR:Q42262 IntAct:Q42262 STRING:Q42262 PRIDE:Q42262 DNASU:829619 EnsemblPlants:AT4G34670.1

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GeneID:829619 KEGG:ath:AT4G34670 TAIR:At4g34670 InParanoid:Q42262 OMA:GHDTTRE PhylomeDB:Q42262 Genevestigator:Q42262 GermOnline:AT4G34670 Uniprot:Q42262
Leaf	Isotig09570	10	0	4.851	0.000336918	TAIR|locus:2175118 - symbol:AT5G60390 "AT5G60390" species:3702 "Arabidopsis thaliana" [GO:0003746 "translation elongation factor activity" evidence=ISS] [GO:0006414 "translational elongation" evidence=IEA] [GO:0005516 "calmodulin binding" evidence=ISS] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0005773 "vacuole" evidence=IDA] [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0005829 "cytosol" evidence=RCA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] PROSITE:PS00301 EMBL:CP002684 EMBL:U63815 EMBL:AC026875 EMBL:X16430 EMBL:AY039583 EMBL:BT000595 IPI:IPI00548618 PIR:S06724 UniGene:At.69737 UniGene:At.74830 EnsemblPlants:AT1G07940.1 EnsemblPlants:AT1G07940.2 TAIR:At1g07940 OMA:FLKAGDA GermOnline:AT1G07940 Uniprot:P0DH99
Leaf	Isotig09613	10	0	4.851	0.000336918	TAIR|locus:2091176 - symbol:MGT4 "AT3G19640" species:3702 "Arabidopsis thaliana" [GO:0016020 "membrane" evidence=ISS] [GO:0030001 "metal ion transport" evidence=IEA;ISS] [GO:0046873 "metal ion transmembrane transporter activity" evidence=ISS] [GO:0055085 "transmembrane transport" evidence=IEA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0015095 "magnesium ion transmembrane transporter activity" evidence=IDA] InterPro:IPR002523 Pfam:PF01544 GO:GO:0016021 GO:GO:0005886 EMBL:CP002686 GenomeReviews:BA000014_GR EMBL:AP000417 GO:GO:0015095 HOGENOM:HBG316327 EMBL:AY150288 EMBL:BT000458 EMBL:BT006622 IPI:IPI00542696 PIR:T52392 RefSeq:NP_188598.2 UniGene:At.20611 ProteinModelPortal:Q9LJN2 IntAct:Q9LJN2 STRING:Q9LJN2 PRIDE:Q9LJN2 EnsemblPlants:AT3G19640.1 GeneID:821501 KEGG:ath:AT3G19640 TAIR:At3g19640 eggNOG:NOG282642 InParanoid:Q9LJN2 OMA:MNITIEL PhylomeDB:Q9LJN2 ProtClustDB:CLSN2721568 ArrayExpress:Q9LJN2 Genevestigator:Q9LJN2 Uniprot:Q9LJN2
Leaf	Isotig09631	29	0	6.387	7.28E-10	TAIR|locus:2025346 - symbol:LEA14 "AT1G01470" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0009269 "response to desiccation" evidence=ISS] [GO:0009793 "embryo development ending in seed dormancy" evidence=ISS] [GO:0009644 "response to high light intensity" evidence=IEP] [GO:0009611 "response to wounding" evidence=IEP] [GO:0050832 "defense response to fungus" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR013990 SMART:SM00769 InterPro:IPR004864 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 InterPro:IPR013783 Gene3D:G3DSA:2.60.40.10 EMBL:Y12776 EMBL:AC061957 GO:GO:0009611 GO:GO:0050832 GO:GO:0009644 GO:GO:0009269 EMBL:Y10085 EMBL:AY074855 EMBL:BT015111 EMBL:Z37258 IPI:IPI00525938 PIR:D86145 RefSeq:NP_171654.1 UniGene:At.25113 PDB:1XO8 PDBsum:1XO8 ProteinModelPortal:O03983 SMR:O03983 IntAct:O03983 STRING:O03983 PRIDE:O03983 DNASU:837071 EnsemblPlants:AT1G01470.1 GeneID:837071 KEGG:ath:AT1G01470 TAIR:At1g01470 eggNOG:NOG271766 HOGENOM:HBG320411 InParanoid:O03983 OMA:YSHSIPI PhylomeDB:O03983 ProtClustDB:CLSN2682861 Genevestigator:O03983 GermOnline:AT1G01470 Pfam:PF03168 Uniprot:O03983
Leaf	Isotig09649	15	1	4.436	1.60E-05	TAIR|locus:2138753 - symbol:EXO "AT4G08950" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005618 "cell wall" evidence=IDA] [GO:0009505 "plant-type cell wall" evidence=IDA] [GO:0009741 "response to brassinosteroid stimulus" evidence=IMP] [GO:0005829 "cytosol" evidence=RCA] [GO:0005794 "Golgi apparatus" evidence=IDA] EMBL:AL161513 EMBL:CP002687 GO:GO:0009505 EMBL:AF128396 GO:GO:0009741 InterPro:IPR006766 Pfam:PF04674 EMBL:AY054486 EMBL:AY093295 EMBL:AF496655 IPI:IPI00538314 PIR:C85090 RefSeq:NP_192634.1 UniGene:At.22399 STRING:Q9ZPE7 PRIDE:Q9ZPE7 EnsemblPlants:AT4G08950.1 GeneID:826473 KEGG:ath:AT4G08950 TAIR:At4g08950 InParanoid:Q9ZPE7 OMA:TWWKTTE PhylomeDB:Q9ZPE7 ProtClustDB:CLSN2916156 Genevestigator:Q9ZPE7 Uniprot:Q9ZPE7
Leaf	Isotig09687	24	4	3.114	1.45E-06	TAIR|locus:2120237 - symbol:VHA-C3 "vacuolar-type H(+)-ATPase C3" species:3702 "Arabidopsis thaliana" [GO:0015986 "ATP synthesis coupled proton transport" evidence=IEA] [GO:0016887 "ATPase activity" evidence=ISS] [GO:0005773 "vacuole" evidence=IDA] InterPro:IPR000245 InterPro:IPR002379 InterPro:IPR011555 Pfam:PF00137 PRINTS:PR00122 EMBL:CP002687 GenomeReviews:CT486007_GR EMBL:AL161586 EMBL:AL023094 Gene3D:G3DSA:1.20.20.10 SUPFAM:SSF81333 EMBL:L44581 EMBL:AF372872 EMBL:AY127950 EMBL:AY086410 IPI:IPI00530428 PIR:S60130 RefSeq:NP_179244.1 RefSeq:NP_195198.1 RefSeq:NP_195603.1 GeneID:816150 GeneID:829624 GeneID:830047 TAIR:At4g34720 GermOnline:AT4G34720 TIGRFAMs:TIGR01100 Uniprot:P0DH92

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig09707	12	0	5.114	7.63E-05	TAIR|locus:2158544 - symbol:AT5G63350 "AT5G63350" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0005515 "protein binding" evidence=IPI] EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005515 EMBL:AB023035 EMBL:BT002821 EMBL:BT004383 IPI:IPI00523793 RefSeq:NP_201140.1 UniGene:At.29001 IntAct:Q9FGW7 PRIDE:Q9FGW7 EnsemblPlants:AT5G63350.1 GeneID:836455 KEGG:ath:AT5G63350 TAIR:At5g63350 eggNOG:NOG314236 HOGENOM:HBG745108 InParanoid:Q9FGW7 OMA:DINIPME PhylomeDB:Q9FGW7 ProtClustDB:CLSN2687559 Genevestigator:Q9FGW7 Uniprot:Q9FGW7
Leaf	Isotig09711	9	0	4.699	0.000718283	No hit
Leaf	Isotig09718	10	0	4.851	0.000336918	TAIR|locus:2019409 - symbol:ABCF3 "AT1G64550" species:3702 "Arabidopsis thaliana" [GO:0005215 "transporter activity" evidence=ISS] [GO:0046686 "response to cadmium ion" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA] [GO:0042742 "defense response to bacterium" evidence=IMP] InterPro:IPR003439 InterPro:IPR003593 InterPro:IPR017871 Pfam:PF00005 PROSITE:PS00211 PROSITE:PS50893 SMART:SM00382 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0005524 GO:GO:0046686 GO:GO:0042742 GO:GO:0006810 GO:GO:0016887 HOGENOM:HBG758042 eggNOG:COG0488 EMBL:AC009519 EMBL:BT002015 EMBL:BT010544 IPI:IPI00524684 PIR:A96669 RefSeq:NP_176636.1 UniGene:At.42980 ProteinModelPortal:Q8H0V6 SMR:Q8H0V6 PRIDE:Q8H0V6 EnsemblPlants:AT1G64550.1 GeneID:842763 KEGG:ath:AT1G64550 TAIR:At1g64550 InParanoid:Q8H0V6 KO:K06158 OMA:LVCKELW PhylomeDB:Q8H0V6 ProtClustDB:PLN03073 ArrayExpress:Q8H0V6 Genevestigator:Q8H0V6 Uniprot:Q8H0V6
Leaf	Isotig09752	17	91	-1.891	4.55E-09	TAIR|locus:2127393 - symbol:PSBQA "photosystem II subunit QA" species:3702 "Arabidopsis thaliana" [GO:0005509 "calcium ion binding" evidence=IEA] [GO:0009654 "oxygen evolving complex" evidence=ISS] [GO:0030095 "chloroplast photosystem II" evidence=ISS] [GO:0009543 "chloroplast thylakoid lumen" evidence=IDA] [GO:0031977 "thylakoid lumen" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] InterPro:IPR008797 Pfam:PF05757 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0009570 GO:GO:0005509 EMBL:AL161554 GO:GO:0019898 EMBL:AL021960 GO:GO:0009535 GO:GO:0031977 GO:GO:0015979 EMBL:AL031187 InterPro:IPR023222 SUPFAM:SSF101112 GO:GO:0009654 EMBL:Y16847 EMBL:AY050328 EMBL:AY094048 EMBL:AY088330 IPI:IPI00532582 IPI:IPI00657124 PIR:T04959 RefSeq:NP_001031687.1 RefSeq:NP_193860.1 UniGene:At.24610 ProteinModelPortal:Q9XFT3 SMR:Q9XFT3 STRING:Q9XFT3 SWISS-2DPAGE:Q9XFT3 PRIDE:Q9XFT3 ProMEX:Q9XFT3 EnsemblPlants:AT4G21280.2 GeneID:827877 KEGG:ath:AT4G21280 TAIR:At4g21280 eggNOG:NOG313473 HOGENOM:HBG318859 InParanoid:Q9XFT3 KO:K08901 OMA:DRFYLQP PhylomeDB:Q9XFT3 ProtClustDB:CLSN2685363 BioCyc:MetaCyc:MONOMER-1076 ArrayExpress:Q9XFT3 Genevestigator:Q9XFT3 Uniprot:Q9XFT3
Leaf	Isotig09771	0	18	-4.641	7.10E-05	TAIR|locus:2131859 - symbol:ACYB-2 "AT4G25570" species:3702 "Arabidopsis thaliana" [GO:0008805 "carbon-monoxide oxygenase activity" evidence=ISS] [GO:0016021 "integral to membrane" evidence=ISS] [GO:0005773 "vacuole" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005515 "protein binding" evidence=IPI] InterPro:IPR004877 Pfam:PF03188 GO:GO:0016021 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005774 GO:GO:0009507 GO:GO:0005515 GO:GO:0046872 GO:GO:0006810 GO:GO:0016491 EMBL:AL022197 EMBL:AL161563 EMBL:AB049628 EMBL:AY120730 EMBL:BT002176 EMBL:AY085603 IPI:IPI00543014 PIR:E85295 PIR:T05790 RefSeq:NP_567723.1 UniGene:At.25580 IntAct:Q8L856 PRIDE:Q9M0K3 EnsemblPlants:AT4G25570.1 GeneID:828662 KEGG:ath:AT4G25570 TAIR:At4g25570 eggNOG:NOG262597 HOGENOM:HBG606716 InParanoid:Q8L856 PhylomeDB:Q8L856 ProtClustDB:PLN02810 Genevestigator:Q8L856 GO:GO:0022900 InterPro:IPR006593 SMART:SM00665 PROSITE:PS50939 Uniprot:Q8L856
Leaf	Isotig09845	12	2	3.114	0.000658121	TAIR|locus:2075306 - symbol:HRS1 "AT3G46100" species:3702 "Arabidopsis thaliana" [GO:0004821 "histidine-tRNA ligase activity" evidence=ISS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0006427 "histidyl-tRNA aminoacylation" evidence=ISS] HAMAP:MF_00127 InterPro:IPR002314 InterPro:IPR004516 InterPro:IPR006195 InterPro:IPR015807 Pfam:PF00587 PIRSF:PIRSF001549 PROSITE:PS50862 InterPro:IPR004154 GO:GO:0005739 GO:GO:0005524 GO:GO:0009507 EMBL:CP002686 GenomeReviews:BA000014_GR SUPFAM:SSF52954 Gene3D:G3DSA:3.40.50.800 Pfam:PF03129 EMBL:AL355775 HOGENOM:HBG616575 GO:GO:0004821 GO:GO:0006427 PANTHER:PTHR11476 eggNOG:COG0124 KO:K01892 TIGRFAMs:TIGR00442 BRENDA:6.1.1.21 EMBL:AF020715 EMBL:AY056233 EMBL:AY117252 IPI:IPI00521949 PIR:T49251 RefSeq:NP_190196.1 UniGene:At.22106 HSSP:P60906

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						ProteinModelPortal:O82413 SMR:O82413 STRING:O82413 PRIDE:O82413 EnsemblPlants:AT3G46100.1 GeneID:823753 KEGG:ath:AT3G46100 TAIR:At3g46100 InParanoid:O82413 OMA:QVENIVC PhylomeDB:O82413 ProtClustDB:PLN02530 ArrayExpress:O82413 Genevestigator:O82413 Uniprot:O82413
Leaf	Isotig09882	10	1	3.851	0.00071293	TAIR|locus:2135912 - symbol:AT4G24290 "AT4G24290" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0005886 "plasma membrane" evidence=IDA] GO:GO:0005886 EMBL:CP002687 GenomeReviews:CT486007_GR EMBL:AL078637 EMBL:AL161561 InterPro:IPR020864 SMART:SM00457 Pfam:PF01823 PROSITE:PS00279 PROSITE:PS51412 EMBL:BX826919 EMBL:BT032874 IPI:IPI00519372 IPI:IPI00541232 PIR:T09892 RefSeq:NP_567698.1 RefSeq:NP_849433.1 UniGene:At.3459 UniGene:At.67135 ProteinModelPortal:Q9STW5 STRING:Q9STW5 PRIDE:Q9STW5 EnsemblPlants:AT4G24290.2 GeneID:828532 KEGG:ath:AT4G24290 TAIR:At4g24290 eggNOG:NOG305050 HOGENOM:HBG319976 InParanoid:Q9STW5 OMA:DRRYYEK PhylomeDB:Q9STW5 ProtClustDB:CLSN2680054 ArrayExpress:Q9STW5 Genevestigator:Q9STW5 Uniprot:Q9STW5
Leaf	Isotig09885	11	1	3.988	0.000330755	TAIR|locus:2180642 - symbol:FC1 "AT5G26030" species:3702 "Arabidopsis thaliana" [GO:0004325 "ferrochelatase activity" evidence=IGI;ISS] [GO:0006783 "heme biosynthetic process" evidence=ISS;IMP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009536 "plastid" evidence=IDA] [GO:0006979 "response to oxidative stress" evidence=IEP] [GO:0033014 "tetrapyrrole biosynthetic process" evidence=IMP] InterPro:IPR001015 InterPro:IPR019772 Pfam:PF00762 PROSITE:PS00534 GO:GO:0005739 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0006979 GO:GO:0031969 GO:GO:0009535 EMBL:AF149413 GO:GO:0006783 UniGene:At.58 UniGene:At.70191 EMBL:X73417 EMBL:Y13382 IPI:IPI00539854 PIR:A54125 RefSeq:NP_001031941.1 RefSeq:NP_197975.3 ProteinModelPortal:P42043 SMR:P42043 STRING:P42043 PRIDE:P42043 EnsemblPlants:AT5G26030.1 EnsemblPlants:AT5G26030.2 GeneID:832672 KEGG:ath:AT5G26030 TAIR:At5g26030 eggNOG:COG0276 HOGENOM:HBG697135 InParanoid:P42043 KO:K01772 OMA:LLQMGGP PhylomeDB:P42043 ProtClustDB:PLN02449 BioCyc:ARA:AT5G26030-MONOMER ArrayExpress:P42043 Genevestigator:P42043 GermOnline:AT5G26030 GO:GO:0004325 PANTHER:PTHR11108 TIGRFAMs:TIGR00109 Uniprot:P42043
Leaf	Isotig09894	10	140	-3.278	3.69E-23	TAIR|locus:2033686 - symbol:RBCS1A "AT1G67090" species:3702 "Arabidopsis thaliana" [GO:0009573 "chloroplast ribulose bisphosphate carboxylase complex" evidence=ISS] [GO:0015977 "carbon fixation" evidence=ISS] [GO:0016984 "ribulose-bisphosphate carboxylase activity" evidence=ISS] [GO:0031977 "thylakoid lumen" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009637 "response to blue light" evidence=IEP] [GO:0010114 "response to red light" evidence=IEP] [GO:0010218 "response to far red light" evidence=IEP] [GO:0015979 "photosynthesis" evidence=IMP] [GO:0080158 "chloroplast ribulose bisphosphate carboxylase complex biogenesis" evidence=IMP] InterPro:IPR000894 Pfam:PF00101 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0048046 GO:GO:0009570 GO:GO:0004497 GO:GO:0005507 GO:GO:0009409 GO:GO:0009637 GO:GO:0010218 GO:GO:0010114 GO:GO:0031969 EMBL:AC007152 GO:GO:0009853 GO:GO:0009535 GO:GO:0022626 GO:GO:0031977 EMBL:AC004146 GO:GO:0019253 UniGene:At.46639 GO:GO:0016984 UniGene:At.37531 Gene3D:G3DSA:3.30.190.10 EMBL:X13611 EMBL:AF325011 EMBL:AF325004 EMBL:AF372874 EMBL:AF410291 EMBL:AY054188 EMBL:AY054581 EMBL:AY058831 EMBL:AY059940 EMBL:AY062612 EMBL:AY062711 EMBL:AY065101 EMBL:AY093380 EMBL:AY093388 EMBL:AY097366 EMBL:BT000362 EMBL:BT002076 EMBL:X68342 IPI:IPI00539020 PIR:G96694 PIR:S03720 RefSeq:NP_176880.1 UniGene:At.12721 UniGene:At.30194 UniGene:At.49098 UniGene:At.67454 UniGene:At.68122 UniGene:At.70053 UniGene:At.75196 ProteinModelPortal:P10795 SMR:P10795 IntAct:P10795 MINT:MINT-2584041 STRING:P10795 World-2DPAGE:0003:P10795 PRIDE:P10795 ProMEX:P10795 EnsemblPlants:AT1G67090.1 GeneID:843029 KEGG:ath:AT1G67090 TAIR:At1g67090 eggNOG:COG4451 HOGENOM:HBG608223 InParanoid:P10795 KO:K01602 OMA:AFPATRK PhylomeDB:P10795 ProtClustDB:PLN02289 ArrayExpress:P10795 Genevestigator:P10795 InterPro:IPR024681 InterPro:IPR024680 Pfam:PF12338 PRINTS:PR00152 SMART:SM00961 SUPFAM:SSF55239 Uniprot:P10795
Leaf	Isotig09900	0	16	-4.471	0.000202082	TAIR|locus:2081207 - symbol:GUN4 "AT3G59400" species:3702 "Arabidopsis thaliana" [GO:0009507 "chloroplast" evidence=IDA] [GO:0010019 "chloroplast-nucleus signaling pathway" evidence=IMP] [GO:0019899 "enzyme

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						binding" evidence=IPI] [GO:0043085 "positive regulation of catalytic activity" evidence=TAS] [GO:0046906 "tetrapyrrole binding" evidence=IDA] [GO:0015995 "chlorophyll biosynthetic process" evidence=TAS] EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0019899 GO:GO:0031969 GO:GO:0015995 EMBL:AL356014 GO:GO:0043085 GO:GO:0046906 EMBL:AY063918 EMBL:AY150510 IPI:IPI00516475 PIR:T49008 RefSeq:NP_191499.1 UniGene:At.1522 ProteinModelPortal:Q9LX31 SMR:Q9LX31 STRING:Q9LX31 PRIDE:Q9LX31 EnsemblPlants:AT3G59400.1 GeneID:825109 KEGG:ath:AT3G59400 TAIR:At3g59400 eggNOG:NOG08265 HOGENOM:HBG610809 InParanoid:Q9LX31 OMA:QNFRQAD PhylomeDB:Q9LX31 ProtClustDB:CLSN2684879 ArrayExpress:Q9LX31 Genevestigator:Q9LX31 GermOnline:AT3G59400 GO:GO:0010019 InterPro:IPR008629 Pfam:PF05419 Uniprot:Q9LX31
Leaf	Isotig09920	12	1	4.114	0.000154103	TAIR|locus:2169503 - symbol:AT5G35430 "AT5G35430" species:3702 "Arabidopsis thaliana" [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] InterPro:IPR011990 InterPro:IPR013026 InterPro:IPR019734 PROSITE:PS50293 SMART:SM00028 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005488 Gene3D:G3DSA:1.25.40.10 eggNOG:NOG256461 KO:K12607 OMA:VVRYNLA EMBL:AY057505 EMBL:AY103308 EMBL:AK175967 IPI:IPI00544788 RefSeq:NP_198393.2 UniGene:At.6875 ProteinModelPortal:Q93ZI7 SMR:Q93ZI7 IntAct:Q93ZI7 STRING:Q93ZI7 PRIDE:Q93ZI7 EnsemblPlants:AT5G35430.1 GeneID:833507 KEGG:ath:AT5G35430 TAIR:At5g35430 HOGENOM:HBG602642 InParanoid:Q93ZI7 PhylomeDB:Q93ZI7 ProtClustDB:CLSN2680349 ArrayExpress:Q93ZI7 Genevestigator:Q93ZI7 Uniprot:Q93ZI7
Leaf	Isotig09924	11	0	4.988	0.000159591	No hit
Leaf	Isotig09946	19	0	5.777	5.37E-07	No hit
Leaf	Isotig09950	9	147	-3.501	1.70E-25	TAIR|locus:2033686 - symbol:RBCS1A "AT1G67090" species:3702 "Arabidopsis thaliana" [GO:0009573 "chloroplast ribulose bisphosphate carboxylase complex" evidence=ISS] [GO:0015977 "carbon fixation" evidence=ISS] [GO:0016984 "ribulose-bisphosphate carboxylase activity" evidence=ISS] [GO:0031977 "thylakoid lumen" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009637 "response to blue light" evidence=IEP] [GO:0010114 "response to red light" evidence=IEP] [GO:0010218 "response to far red light" evidence=IEP] [GO:0015979 "photosynthesis" evidence=IMP] [GO:0080158 "chloroplast ribulose bisphosphate carboxylase complex biogenesis" evidence=IMP] InterPro:IPR000894 Pfam:PF00101 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0048046 GO:GO:0009570 GO:GO:0004497 GO:GO:0005507 GO:GO:0009409 GO:GO:0009637 GO:GO:0010218 GO:GO:0010114 GO:GO:0031969 EMBL:AC007152 GO:GO:0009853 GO:GO:0009535 GO:GO:0022626 GO:GO:0031977 EMBL:AC004146 GO:GO:0019253 UniGene:At.46639 GO:GO:0016984 UniGene:At.37531 Gene3D:G3DSA:3.30.190.10 EMBL:X13611 EMBL:AF325011 EMBL:AF325004 EMBL:AF372874 EMBL:AF410291 EMBL:AY054188 EMBL:AY054581 EMBL:AY058831 EMBL:AY059940 EMBL:AY062612 EMBL:AY062711 EMBL:AY065101 EMBL:AY093380 EMBL:AY093388 EMBL:AY097366 EMBL:BT000362 EMBL:BT002076 EMBL:X68342 IPI:IPI00539020 PIR:G96694 PIR:S03720 RefSeq:NP_176880.1 UniGene:At.12721 UniGene:At.30194 UniGene:At.49098 UniGene:At.67454 UniGene:At.68122 UniGene:At.70053 UniGene:At.75196 ProteinModelPortal:P10795 SMR:P10795 IntAct:P10795 MINT:MINT-2584041 STRING:P10795 World-2DPAGE:0003:P10795 PRIDE:P10795 ProMEX:P10795 EnsemblPlants:AT1G67090.1 GeneID:843029 KEGG:ath:AT1G67090 TAIR:At1g67090 eggNOG:COG4451 HOGENOM:HBG608223 InParanoid:P10795 KO:K01602 OMA:AFPATRK PhylomeDB:P10795 ProtClustDB:PLN02289 ArrayExpress:P10795 Genevestigator:P10795 InterPro:IPR024681 InterPro:IPR024680 Pfam:PF12338 PRINTS:PR00152 SMART:SM00961 SUPFAM:SSF55239 Uniprot:P10795
Leaf	Isotig09982	15	3	2.851	0.000262808	TAIR|locus:2047329 - symbol:TIC55-II "translocon at the inner envelope membrane of chloroplasts 55-II" species:3702 "Arabidopsis thaliana" [GO:0010277 "chlorophyllide a oxygenase [overall] activity" evidence=IEA] [GO:0016491 "oxidoreductase activity" evidence=IEA] [GO:0051537 "2 iron, 2 sulfur cluster binding" evidence=IEA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0045036 "protein targeting to chloroplast" evidence=IMP] InterPro:IPR013626 InterPro:IPR017941 Pfam:PF00355 Pfam:PF08417 PROSITE:PS51296 GO:GO:0016021 EMBL:CP002685 GO:GO:0046872 GO:GO:0009706 GO:GO:0051537 EMBL:AC006585 Gene3D:G3DSA:2.102.10.10 SUPFAM:SSF50022 GO:GO:0045036

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						UniGene:At.22189 UniGene:At.69630 eggNOG:COG4638 GO:GO:0010277 EMBL:AK221423 IPI:IPI00540398 PIR:H84640 RefSeq:NP_180055.1 ProteinModelPortal:Q9SK50 SMR:Q9SK50 STRING:Q9SK50 PRIDE:Q9SK50 EnsemblPlants:AT2G24820.1 GeneID:817019 KEGG:ath:AT2G24820 TAIR:At2g24820 InParanoid:Q9SK50 OMA:KVFEQDM PhylomeDB:Q9SK50 ProtClustDB:CLSN2683134 ArrayExpress:Q9SK50 Genevestigator:Q9SK50 Uniprot:Q9SK50
Leaf	Isotig09987	13	0	5.229	3.68E-05	TAIR|locus:2063208 - symbol:AT2G41050 "AT2G41050" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0016020 "membrane" evidence=ISS] EMBL:CP002685 GenomeReviews:CT485783_GR InterPro:IPR006603 SMART:SM00679 eggNOG:NOG326634 HOGENOM:HBG736343 UniGene:At.12544 UniGene:At.42876 OMA:EEDANCT EMBL:AY080611 EMBL:AY133749 IPI:IPI00524039 RefSeq:NP_850340.1 PRIDE:Q8RXY4 EnsemblPlants:AT2G41050.1 GeneID:818704 KEGG:ath:AT2G41050 TAIR:At2g41050 InParanoid:Q8RXY4 PhylomeDB:Q8RXY4 ProtClustDB:CLSN2918226 Genevestigator:Q8RXY4 Uniprot:Q8RXY4
Leaf	Isotig10022	7	146	-3.854	4.81E-27	TAIR|locus:2033686 - symbol:RBCS1A "AT1G67090" species:3702 "Arabidopsis thaliana" [GO:0009573 "chloroplast ribulose bisphosphate carboxylase complex" evidence=ISS] [GO:0015977 "carbon fixation" evidence=ISS] [GO:0016984 "ribulose-bisphosphate carboxylase activity" evidence=ISS] [GO:0031977 "thylakoid lumen" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009637 "response to blue light" evidence=IEP] [GO:0010114 "response to red light" evidence=IEP] [GO:0010218 "response to far red light" evidence=IEP] [GO:0015979 "photosynthesis" evidence=IMP] [GO:0080158 "chloroplast ribulose bisphosphate carboxylase complex biogenesis" evidence=IMP] InterPro:IPR000894 Pfam:PF00101 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0048046 GO:GO:0009570 GO:GO:0004497 GO:GO:0005507 GO:GO:0009409 GO:GO:0009637 GO:GO:0010218 GO:GO:0010114 GO:GO:0031969 EMBL:AC007152 GO:GO:0009853 GO:GO:0009535 GO:GO:0022626 GO:GO:0031977 EMBL:AC004146 GO:GO:0019253 UniGene:At.46639 GO:GO:0016984 UniGene:At.37531 Gene3D:G3DSA:3.30.190.10 EMBL:X13611 EMBL:AF325011 EMBL:AF325004 EMBL:AF372874 EMBL:AF410291 EMBL:AY054188 EMBL:AY054581 EMBL:AY058831 EMBL:AY059940 EMBL:AY062612 EMBL:AY062711 EMBL:AY065101 EMBL:AY093380 EMBL:AY093388 EMBL:AY097366 EMBL:BT000362 EMBL:BT002076 EMBL:X68342 IPI:IPI00539020 PIR:G96694 PIR:S03720 RefSeq:NP_176880.1 UniGene:At.12721 UniGene:At.30194 UniGene:At.49098 UniGene:At.67454 UniGene:At.68122 UniGene:At.70053 UniGene:At.75196 ProteinModelPortal:P10795 SMR:P10795 IntAct:P10795 MINT:MINT-2584041 STRING:P10795 World-2DPAGE:0003:P10795 PRIDE:P10795 ProMEX:P10795 EnsemblPlants:AT1G67090.1 GeneID:843029 KEGG:ath:AT1G67090 TAIR:At1g67090 eggNOG:COG4451 HOGENOM:HBG608223 InParanoid:P10795 KO:K01602 OMA:AFPATRK PhylomeDB:P10795 ProtClustDB:PLN02289 ArrayExpress:P10795 Genevestigator:P10795 InterPro:IPR024681 InterPro:IPR024680 Pfam:PF12338 PRINTS:PR00152 SMART:SM00961 SUPFAM:SSF55239 Uniprot:P10795
Leaf	Isotig10027	72	9	3.529	1.36E-18	TAIR|locus:2044641 - symbol:COR413-PM1 "AT2G15970" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005886 "plasma membrane" evidence=ISS] [GO:0009631 "cold acclimation" evidence=IEP] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] [GO:0042631 "cellular response to water deprivation" evidence=IEP] [GO:0005773 "vacuole" evidence=IDA] GO:GO:0009737 GO:GO:0005773 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0042631 GO:GO:0009631 EMBL:AC006438 UniGene:At.22305 HOGENOM:HBG595418 ProtClustDB:CLSN2717102 InterPro:IPR008892 Pfam:PF05562 eggNOG:NOG267474 EMBL:AF283004 EMBL:AY093767 EMBL:AY088558 EMBL:AY143813 EMBL:AB044404 IPI:IPI00547690 PIR:C84535 RefSeq:NP_179196.1 UniGene:At.24347 STRING:Q9XIM7 PRIDE:Q9XIM7 EnsemblPlants:AT2G15970.1 GeneID:816092 KEGG:ath:AT2G15970 TAIR:At2g15970 InParanoid:Q9XIM7 OMA:GTTFLEW PhylomeDB:Q9XIM7 ArrayExpress:Q9XIM7 Genevestigator:Q9XIM7 Uniprot:Q9XIM7
Leaf	Isotig10087	4	78	-3.756	6.04E-15	TAIR|locus:2033686 - symbol:RBCS1A "AT1G67090" species:3702 "Arabidopsis thaliana" [GO:0009573 "chloroplast ribulose bisphosphate carboxylase complex" evidence=ISS] [GO:0015977 "carbon fixation" evidence=ISS] [GO:0016984 "ribulose-bisphosphate carboxylase activity" evidence=ISS] [GO:0031977 "thylakoid lumen" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA]

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						[GO:0009409 "response to cold" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009637 "response to blue light" evidence=IEP] [GO:0010114 "response to red light" evidence=IEP] [GO:0010218 "response to far red light" evidence=IEP] [GO:0015979 "photosynthesis" evidence=IMP] [GO:0080158 "chloroplast ribulose bisphosphate carboxylase complex biogenesis" evidence=IMP] InterPro:IPR000894 Pfam:PF00101 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0048046 GO:GO:0009570 GO:GO:0004497 GO:GO:0005507 GO:GO:0009409 GO:GO:0009637 GO:GO:0010218 GO:GO:0010114 GO:GO:0031969 EMBL:AC007152 GO:GO:0009853 GO:GO:0009535 GO:GO:0022626 GO:GO:0031977 EMBL:AC004146 GO:GO:0019253 UniGene:At.46639 GO:GO:0016984 UniGene:At.37531 Gene3D:G3DSA:3.30.190.10 EMBL:X13611 EMBL:AF325011 EMBL:AF325004 EMBL:AF372874 EMBL:AF410291 EMBL:AY054188 EMBL:AY054581 EMBL:AY058831 EMBL:AY059940 EMBL:AY062612 EMBL:AY062711 EMBL:AY065101 EMBL:AY093380 EMBL:AY093388 EMBL:AY097366 EMBL:BT000362 EMBL:BT002076 EMBL:X68342 IPI:IPI00539020 PIR:G96694 PIR:S03720 RefSeq:NP_176880.1 UniGene:At.12721 UniGene:At.30194 UniGene:At.49098 UniGene:At.67454 UniGene:At.68122 UniGene:At.70053 UniGene:At.75196 ProteinModelPortal:P10795 SMR:P10795 IntAct:P10795 MINT:MINT-2584041 STRING:P10795 World-2DPAGE:0003:P10795 PRIDE:P10795 ProMEX:P10795 EnsemblPlants:AT1G67090.1 GeneID:843029 KEGG:ath:AT1G67090 TAIR:At1g67090 eggNOG:COG4451 HOGENOM:HBG608223 InParanoid:P10795 KO:K01602 OMA:AFPATRK PhylomeDB:P10795 ProtClustDB:PLN02289 ArrayExpress:P10795 Genevestigator:P10795 InterPro:IPR024681 InterPro:IPR024680 Pfam:PF12338 PRINTS:PR00152 SMART:SM00961 SUPFAM:SSF55239 Uniprot:P10795
Leaf	Isotig10182	15	3	2.851	0.000262808	No hit
Leaf	Isotig10185	420	370	0.712	2.76E-12	No hit
Leaf	Isotig10232	13	58	-1.629	2.46E-05	TAIR|locus:2033802 - symbol:AT1G32470 "AT1G32470" species:3702 "Arabidopsis thaliana" [GO:0004375 "glycine dehydrogenase (decarboxylating) activity" evidence=ISS] [GO:0005960 "glycine cleavage complex" evidence=ISS] [GO:0006546 "glycine catabolic process" evidence=IEA;ISS] [GO:0019464 "glycine decarboxylation via glycine cleavage system" evidence=IEA] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] InterPro:IPR002930 InterPro:IPR017453 Pfam:PF01597 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005739 GO:GO:0009507 EMBL:AC007767 InterPro:IPR011053 SUPFAM:SSF51230 GO:GO:0005960 GO:GO:0019464 eggNOG:COG0509 HOGENOM:HBG693789 KO:K02437 ProtClustDB:CLSN2682803 InterPro:IPR003016 PANTHER:PTHR11715 TIGRFAMs:TIGR00527 PROSITE:PS00189 EMBL:AF332465 EMBL:AF385740 EMBL:AY078028 IPI:IPI00520638 PIR:A86450 RefSeq:NP_174525.1 UniGene:At.15531 UniGene:At.22333 UniGene:At.69604 ProteinModelPortal:Q9LQL0 SMR:Q9LQL0 STRING:Q9LQL0 PRIDE:Q9LQL0 ProMEX:Q9LQL0 EnsemblPlants:AT1G32470.1 GeneID:840141 KEGG:ath:AT1G32470 TAIR:At1g32470 InParanoid:Q9LQL0 OMA:TPKELRY PhylomeDB:Q9LQL0 ArrayExpress:Q9LQL0 Genevestigator:Q9LQL0 GermOnline:AT1G32470 Uniprot:Q9LQL0
Leaf	Isotig10326	11	198	-3.641	9.72E-35	TAIR|locus:2033686 - symbol:RBCS1A "AT1G67090" species:3702 "Arabidopsis thaliana" [GO:0009573 "chloroplast ribulose bisphosphate carboxylase complex" evidence=ISS] [GO:0015977 "carbon fixation" evidence=ISS] [GO:0016984 "ribulose-bisphosphate carboxylase activity" evidence=ISS] [GO:0031977 "thylakoid lumen" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009637 "response to blue light" evidence=IEP] [GO:0010114 "response to red light" evidence=IEP] [GO:0010218 "response to far red light" evidence=IEP] [GO:0015979 "photosynthesis" evidence=IMP] [GO:0080158 "chloroplast ribulose bisphosphate carboxylase complex biogenesis" evidence=IMP] InterPro:IPR000894 Pfam:PF00101 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0048046 GO:GO:0009570 GO:GO:0004497 GO:GO:0005507 GO:GO:0009409 GO:GO:0009637 GO:GO:0010218 GO:GO:0010114 GO:GO:0031969 EMBL:AC007152 GO:GO:0009853 GO:GO:0009535 GO:GO:0022626 GO:GO:0031977 EMBL:AC004146 GO:GO:0019253 UniGene:At.46639 GO:GO:0016984 UniGene:At.37531 Gene3D:G3DSA:3.30.190.10 EMBL:X13611 EMBL:AF325011 EMBL:AF325004 EMBL:AF372874 EMBL:AF410291 EMBL:AY054188 EMBL:AY054581

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EMBL:AY058831 EMBL:AY059940 EMBL:AY062612 EMBL:AY062711 EMBL:AY065101 EMBL:AY093380 EMBL:AY093388 EMBL:AY097366 EMBL:BT000362 EMBL:BT002076 EMBL:X68342 IPI:IPI00539020 PIR:G96694 PIR:S03720 RefSeq:NP_176880.1 UniGene:At.12721 UniGene:At.30194 UniGene:At.49098 UniGene:At.67454 UniGene:At.68122 UniGene:At.70053 UniGene:At.75196 ProteinModelPortal:P10795 SMR:P10795 IntAct:P10795 MINT:MINT-2584041 STRING:P10795 World-2DPAGE:0003:P10795 PRIDE:P10795 ProMEX:P10795 EnsemblPlants:AT1G67090.1 GeneID:843029 KEGG:ath:AT1G67090 TAIR:At1g67090 eggNOG:COG4451 HOGENOM:HBG608223 InParanoid:P10795 KO:K01602 OMA:AFPATRK PhylomeDB:P10795 ProtClustDB:PLN02289 ArrayExpress:P10795 Genevestigator:P10795 InterPro:IPR024681 InterPro:IPR024680 Pfam:PF12338 PRINTS:PR00152 SMART:SM00961 SUPFAM:SSF55239 Uniprot:P10795
Leaf	Isotig10343	24	6	2.529	1.49E-05	No hit
Leaf	Isotig10434	79	0	7.833	2.86E-22	TIGR_CMR|BA_1222 - symbol:BA_1222 "conserved hypothetical protein" species:198094 "Bacillus anthracis str. Ames" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:AE016879 EMBL:AE017334 GenomeReviews:AE016879_GR GenomeReviews:AE017334_GR InterPro:IPR008160 Pfam:PF01391 EMBL:AB281483 EMBL:AJ516936 RefSeq:NP_843695.1 RefSeq:YP_017836.1 PDB:2R6Q PDBsum:2R6Q ProteinModelPortal:Q81JD7 SMR:Q81JD7 IntAct:Q81JD7 EnsemblBacteria:EBBACT00000011819 EnsemblBacteria:EBBACT00000016984 GeneID:1084744 GeneID:2814858 KEGG:ban:BA_1222 KEGG:bar:GBAA_1222 PATRIC:18780046 TIGR:BA_1222 TIGR:GBAA1222 HOGENOM:HBG342646 OMA:SDGLNPD ProtClustDB:CLSK824721 Uniprot:Q81JD7
Leaf	Isotig10484	18	75	-1.530	4.57E-06	UNIPROTKB|P07591 - symbol:P07591 "Thioredoxin M-type, chloroplastic" species:3562 "Spinacia oleracea" [GO:0005515 "protein binding" evidence=IPI] InterPro:IPR005746 InterPro:IPR013766 InterPro:IPR017937 Pfam:PF00085 PRINTS:PR00421 PROSITE:PS00194 GO:GO:0009507 GO:GO:0005515 GO:GO:0009055 GO:GO:0006810 GO:GO:0022900 InterPro:IPR012336 Gene3D:G3DSA:3.40.30.10 SUPFAM:SSF52833 GO:GO:0045454 PROSITE:PS51352 GO:GO:0015035 GO:GO:0006662 PANTHER:PTHR10438 TIGRFAMs:TIGR01068 EMBL:X51462 EMBL:X51463 PIR:S20496 PDB:1FB0 PDB:1FB6 PDB:1GL8 PDB:2PUK PDBsum:1FB0 PDBsum:1FB6 PDBsum:1GL8 PDBsum:2PUK ProteinModelPortal:P07591 SMR:P07591 IntAct:P07591 Uniprot:P07591
Leaf	Isotig10485	13	74	-1.980	5.02E-08	TAIR|locus:2038942 - symbol:PSAE-2 "photosystem I subunit E-2" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0009538 "photosystem I reaction center" evidence=ISS] [GO:0015979 "photosynthesis" evidence=IEA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] InterPro:IPR003375 Pfam:PF02427 ProDom:PD004772 INTERPRO:IPR008990 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009941 GO:GO:0009535 EMBL:AC006569 GO:GO:0010287 GO:GO:0015979 UniGene:At.23286 UniGene:At.39720 SUPFAM:SSF50090 GO:GO:0009538 TCDB:5.B.4.1.1 HOGENOM:HBG599647 KO:K02693 ProtClustDB:PLN00045 EMBL:AJ245909 EMBL:AY042823 EMBL:BT002540 IPI:IPI00532807 PIR:A84587 RefSeq:NP_179616.1 ProteinModelPortal:Q9S714 SMR:Q9S714 STRING:Q9S714 PRIDE:Q9S714 ProMEX:Q9S714 EnsemblPlants:AT2G20260.1 GeneID:816545 KEGG:ath:AT2G20260 TAIR:At2g20260 eggNOG:NOG316512 InParanoid:Q9S714 OMA:FLPMRSF PhylomeDB:Q9S714 BioCyc:MetaCyc:MONOMER-1096 ArrayExpress:Q9S714 Genevestigator:Q9S714 GermOnline:AT2G20260 Uniprot:Q9S714
Leaf	Isotig10488	13	0	5.229	3.68E-05	TAIR|locus:2174984 - symbol:AT5G66780 "AT5G66780" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002688 GenomeReviews:BA000015_GR EMBL:AB010700 EMBL:AY048239 EMBL:AY072623 IPI:IPI00539273 RefSeq:NP_201479.1 UniGene:At.6618 PRIDE:Q9FL02 EnsemblPlants:AT5G66780.1 GeneID:836811 KEGG:ath:AT5G66780 TAIR:At5g66780 eggNOG:NOG276454 HOGENOM:HBG748513 OMA:NEIHENH PhylomeDB:Q9FL02 ProtClustDB:CLSN2686878 Genevestigator:Q9FL02 Uniprot:Q9FL02
Leaf	Isotig10503	9	0	4.699	0.000718283	TAIR|locus:2165765 - symbol:AT5G42050 "AT5G42050" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] EMBL:CP002688 GenomeReviews:BA000015_GR InterPro:IPR013989 Pfam:PF10539 SMART:SM00767 PROSITE:PS51222 EMBL:AY080773 EMBL:AY114057 EMBL:AY088465 IPI:IPI00517664 RefSeq:NP_568600.1 UniGene:At.21438 STRING:Q8RXN8 PRIDE:Q8RXN8 EnsemblPlants:AT5G42050.1 GeneID:834210 KEGG:ath:AT5G42050 TAIR:At5g42050 eggNOG:NOG301088

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						HOGENOM:HBG185259 InParanoid:Q8RXN8 OMA:SLNDSIW PhylomeDB:Q8RXN8 ProtClustDB:CLSN2917728 ArrayExpress:Q8RXN8 Genevestigator:Q8RXN8 Uniprot:Q8RXN8
Leaf	Isotig10506	26	6	2.644	3.85E-06	TAIR|locus:2040555 - symbol:RPL24A "ribosomal protein L24" species:3702 "Arabidopsis thaliana" [GO:0003735 "structural constituent of ribosome" evidence=IEA;ISS] [GO:0005840 "ribosome" evidence=ISS] [GO:0006412 "translation" evidence=IEA;ISS] [GO:0042254 "ribosome biogenesis" evidence=ISS] [GO:0009507 "chloroplast" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0022625 "cytosolic large ribosomal subunit" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR023442 PROSITE:PS01073 InterPro:IPR000988 Pfam:PF01246 GO:GO:0005886 GO:GO:0009507 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0006412 EMBL:AC006919 GO:GO:0003735 EMBL:AC006282 GO:GO:0022625 EMBL:AJ293729 EMBL:AY058086 EMBL:AY072350 EMBL:AY114728 EMBL:AY085323 EMBL:F20030 IPI:IPI00522443 PIR:F84782 RefSeq:NP_565851.1 UniGene:At.45956 ProteinModelPortal:Q42347 SMR:Q42347 STRING:Q42347 PRIDE:Q42347 ProMEX:Q42347 EnsemblPlants:AT2G36620.1 GeneID:818234 KEGG:ath:AT2G36620 GeneFarm:256 TAIR:At2g36620 eggNOG:COG2075 HOGENOM:HBG600564 InParanoid:Q42347 KO:K02896 OMA:CERSYLM PhylomeDB:Q42347 ProtClustDB:CLSN2684901 ArrayExpress:Q9SKP1 Genevestigator:Q42347 GermOnline:AT2G36620 InterPro:IPR023441 Gene3D:G3DSA:2.30.170.20 PANTHER:PTHR10792 Uniprot:Q42347
Leaf	Isotig10507	1	104	-6.171	2.02E-22	TAIR|locus:2033686 - symbol:RBCS1A "AT1G67090" species:3702 "Arabidopsis thaliana" [GO:0009573 "chloroplast ribulose bisphosphate carboxylase complex" evidence=ISS] [GO:0015977 "carbon fixation" evidence=ISS] [GO:0016984 "ribulose-bisphosphate carboxylase activity" evidence=ISS] [GO:0031977 "thylakoid lumen" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009637 "response to blue light" evidence=IEP] [GO:0010114 "response to red light" evidence=IEP] [GO:0010218 "response to far red light" evidence=IEP] [GO:0015979 "photosynthesis" evidence=IMP] [GO:0080158 "chloroplast ribulose bisphosphate carboxylase complex biogenesis" evidence=IMP] InterPro:IPR000894 Pfam:PF00101 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0048046 GO:GO:0009570 GO:GO:0004497 GO:GO:0005507 GO:GO:0009409 GO:GO:0009637 GO:GO:0010218 GO:GO:0010114 GO:GO:0031969 EMBL:AC007152 GO:GO:0009853 GO:GO:0009535 GO:GO:0022626 GO:GO:0031977 EMBL:AC004146 GO:GO:0019253 UniGene:At.46639 GO:GO:0016984 UniGene:At.37531 Gene3D:G3DSA:3.30.190.10 EMBL:X13611 EMBL:AF325011 EMBL:AF325004 EMBL:AF372874 EMBL:AF410291 EMBL:AY054188 EMBL:AY054581 EMBL:AY058831 EMBL:AY059940 EMBL:AY062612 EMBL:AY062711 EMBL:AY065101 EMBL:AY093380 EMBL:AY093388 EMBL:AY097366 EMBL:BT000362 EMBL:BT002076 EMBL:X68342 IPI:IPI00539020 PIR:G96694 PIR:S03720 RefSeq:NP_176880.1 UniGene:At.12721 UniGene:At.30194 UniGene:At.49098 UniGene:At.67454 UniGene:At.68122 UniGene:At.70053 UniGene:At.75196 ProteinModelPortal:P10795 SMR:P10795 IntAct:P10795 MINT:MINT-2584041 STRING:P10795 World-2DPAGE:0003:P10795 PRIDE:P10795 ProMEX:P10795 EnsemblPlants:AT1G67090.1 GeneID:843029 KEGG:ath:AT1G67090 TAIR:At1g67090 eggNOG:COG4451 HOGENOM:HBG608223 InParanoid:P10795 KO:K01602 OMA:AFPATRK PhylomeDB:P10795 ProtClustDB:PLN02289 ArrayExpress:P10795 Genevestigator:P10795 InterPro:IPR024681 InterPro:IPR024680 Pfam:PF12338 PRINTS:PR00152 SMART:SM00961 SUPFAM:SSF55239 Uniprot:P10795
Leaf	Isotig10517	4	66	-3.515	2.49E-12	TAIR|locus:2033686 - symbol:RBCS1A "AT1G67090" species:3702 "Arabidopsis thaliana" [GO:0009573 "chloroplast ribulose bisphosphate carboxylase complex" evidence=ISS] [GO:0015977 "carbon fixation" evidence=ISS] [GO:0016984 "ribulose-bisphosphate carboxylase activity" evidence=ISS] [GO:0031977 "thylakoid lumen" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009637 "response to blue light" evidence=IEP] [GO:0010114 "response to red light" evidence=IEP] [GO:0010218 "response to far red light" evidence=IEP] [GO:0015979 "photosynthesis" evidence=IMP] [GO:0080158 "chloroplast ribulose bisphosphate carboxylase complex biogenesis" evidence=IMP] InterPro:IPR000894 Pfam:PF00101 EMBL:CP002684

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GenomeReviews:CT485782_GR GO:GO:0048046 GO:GO:0009570 GO:GO:0004497 GO:GO:0005507 GO:GO:0009409 GO:GO:0009637 GO:GO:0010218 GO:GO:0010114 GO:GO:0031969 EMBL:AC007152 GO:GO:0009853 GO:GO:0009535 GO:GO:0022626 GO:GO:0031977 EMBL:AC004146 GO:GO:0019253 UniGene:At.46639 GO:GO:0016984 UniGene:At.37531 Gene3D:G3DSA:3.30.190.10 EMBL:X13611 EMBL:AF325011 EMBL:AF325004 EMBL:AF372874 EMBL:AF410291 EMBL:AY054188 EMBL:AY054581 EMBL:AY058831 EMBL:AY059940 EMBL:AY062612 EMBL:AY062711 EMBL:AY065101 EMBL:AY093380 EMBL:AY093388 EMBL:AY097366 EMBL:BT000362 EMBL:BT002076 EMBL:X68342 IPI:IPI00539020 PIR:G96694 PIR:S03720 RefSeq:NP_176880.1 UniGene:At.12721 UniGene:At.30194 UniGene:At.49098 UniGene:At.67454 UniGene:At.68122 UniGene:At.70053 UniGene:At.75196 ProteinModelPortal:P10795 SMR:P10795 IntAct:P10795 MINT:MINT-2584041 STRING:P10795 World-2DPAGE:0003:P10795 PRIDE:P10795 ProMEX:P10795 EnsemblPlants:AT1G67090.1 GeneID:843029 KEGG:ath:AT1G67090 TAIR:At1g67090 eggNOG:COG4451 HOGENOM:HBG608223 InParanoid:P10795 KO:K01602 OMA:AFPATRK PhylomeDB:P10795 ProtClustDB:PLN02289 ArrayExpress:P10795 Genevestigator:P10795 InterPro:IPR024681 InterPro:IPR024680 Pfam:PF12338 PRINTS:PR00152 SMART:SM00961 SUPFAM:SSF55239 Uniprot:P10795
Leaf	Isotig10522	114	0	8.362	6.95E-30	No hit
Leaf	Isotig10531	22	0	5.988	7.04E-08	UNIPROTKB|G4MW14 - symbol:MGG_08940 "Putative uncharacterized protein" species:242507 "Magnaporthe oryzae 70-15" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CM001232 RefSeq:XP_364095.2 GeneID:2679926 Uniprot:G4MW14
Leaf	Isotig10580	0	20	-4.793	2.52E-05	TAIR|locus:1009023311 - symbol:NdhM "NADH dehydrogenase-like complex M" species:3702 "Arabidopsis thaliana" [GO:0016655 "oxidoreductase activity, acting on NADH or NADPH, quinone or similar compound as acceptor" evidence=IEA] [GO:0009535 "chloroplast thylakoid membrane" evidence=TAS] [GO:0010258 "NADH dehydrogenase complex (plastoquinone) assembly" evidence=IMP] [GO:0010598 "NAD(P)H dehydrogenase complex (plastoquinone)" evidence=TAS] [GO:0009507 "chloroplast" evidence=IDA] InterPro:IPR018922 Pfam:PF10664 EMBL:CP002687 GenomeReviews:CT486007_GR EMBL:AL161592 GO:GO:0048038 EMBL:AL035538 GO:GO:0016655 GO:GO:0009535 GO:GO:0010598 EMBL:BX829112 EMBL:AK227138 IPI:IPI00656913 PIR:T05619 RefSeq:NP_001031804.1 UniGene:At.49770 STRING:Q2V2S7 PRIDE:Q2V2S7 EnsemblPlants:AT4G37925.1 GeneID:3770591 KEGG:ath:AT4G37925 TAIR:At4g37925 eggNOG:NOG08035 HOGENOM:HBG318808 OMA:PVEPQVN PhylomeDB:Q2V2S7 ProtClustDB:CLSN2681467 Genevestigator:Q2V2S7 GO:GO:0010258 Uniprot:Q2V2S7
Leaf	Isotig10647	16	87	-1.914	7.54E-09	TAIR|locus:2033686 - symbol:RBCS1A "AT1G67090" species:3702 "Arabidopsis thaliana" [GO:0009573 "chloroplast ribulose bisphosphate carboxylase complex" evidence=ISS] [GO:0015977 "carbon fixation" evidence=ISS] [GO:0016984 "ribulose-bisphosphate carboxylase activity" evidence=ISS] [GO:0031977 "thylakoid lumen" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009637 "response to blue light" evidence=IEP] [GO:0010114 "response to red light" evidence=IEP] [GO:0010218 "response to far red light" evidence=IEP] [GO:0015979 "photosynthesis" evidence=IMP] [GO:0080158 "chloroplast ribulose bisphosphate carboxylase complex biogenesis" evidence=IMP] InterPro:IPR000894 Pfam:PF00101 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0048046 GO:GO:0009570 GO:GO:0004497 GO:GO:0005507 GO:GO:0009409 GO:GO:0009637 GO:GO:0010218 GO:GO:0010114 GO:GO:0031969 EMBL:AC007152 GO:GO:0009853 GO:GO:0009535 GO:GO:0022626 GO:GO:0031977 EMBL:AC004146 GO:GO:0019253 UniGene:At.46639 GO:GO:0016984 UniGene:At.37531 Gene3D:G3DSA:3.30.190.10 EMBL:X13611 EMBL:AF325011 EMBL:AF325004 EMBL:AF372874 EMBL:AF410291 EMBL:AY054188 EMBL:AY054581 EMBL:AY058831 EMBL:AY059940 EMBL:AY062612 EMBL:AY062711 EMBL:AY065101 EMBL:AY093380 EMBL:AY093388 EMBL:AY097366 EMBL:BT000362 EMBL:BT002076 EMBL:X68342 IPI:IPI00539020 PIR:G96694 PIR:S03720 RefSeq:NP_176880.1 UniGene:At.12721 UniGene:At.30194 UniGene:At.49098 UniGene:At.67454 UniGene:At.68122 UniGene:At.70053 UniGene:At.75196 ProteinModelPortal:P10795 SMR:P10795 IntAct:P10795 MINT:MINT-2584041 STRING:P10795 World-2DPAGE:0003:P10795 PRIDE:P10795 ProMEX:P10795 EnsemblPlants:AT1G67090.1 GeneID:843029 KEGG:ath:AT1G67090 TAIR:At1g67090 eggNOG:COG4451

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						HOGENOM:HBG608223 InParanoid:P10795 KO:K01602 OMA:AFPATRK PhylomeDB:P10795 ProtClustDB:PLN02289 ArrayExpress:P10795 Genevestigator:P10795 InterPro:IPR024681 InterPro:IPR024680 Pfam:PF12338 PRINTS:PR00152 SMART:SM00961 SUPFAM:SSF55239 Uniprot:P10795
Leaf	Isotig10706	0	16	-4.471	0.000202082	UNIPROTKB|Q9XHE8 - symbol:CYP71D18 "Cytochrome P450 71D18" species:29719 "Mentha spicata" [GO:0005792 "microsome" evidence=IDA] [GO:0018675 "(S)-limonene 6-monooxygenase activity" evidence=IDA] [GO:0055114 "oxidation-reduction process" evidence=IDA] InterPro:IPR001128 InterPro:IPR002401 InterPro:IPR017972 Pfam:PF00067 PRINTS:PR00385 PRINTS:PR00463 PROSITE:PS00086 GO:GO:0005792 GO:GO:0016021 GO:GO:0005789 GO:GO:0009055 GO:GO:0020037 Gene3D:G3DSA:1.10.630.10 SUPFAM:SSF48264 HSSP:P14779 EMBL:AF124815 ProteinModelPortal:Q9XHE8 BioCyc:MetaCyc:MONOMER-15424 GO:GO:0018675 Uniprot:Q9XHE8
Leaf	Isotig10731	43	3	4.370	3.35E-13	TAIR|locus:2139777 - symbol:OSM34 "AT4G11650" species:3702 "Arabidopsis thaliana" [GO:0051707 "response to other organism" evidence=ISS] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0009817 "defense response to fungus, incompatible interaction" evidence=IDA] [GO:0009816 "defense response to bacterium, incompatible interaction" evidence=ISS] Pfam:PF00314 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0009651 GO:GO:0009817 EMBL:AL161532 EMBL:AL049500 EMBL:X89008 IPI:IPI00528920 PIR:T04212 RefSeq:NP_192902.1 UniGene:At.25216 ProteinModelPortal:P50700 SMR:P50700 STRING:P50700 PRIDE:P50700 EnsemblPlants:AT4G11650.1 GeneID:826770 KEGG:ath:AT4G11650 TAIR:At4g11650 eggNOG:NOG304630 HOGENOM:HBG748210 InParanoid:P50700 OMA:RVVFCPR PhylomeDB:P50700 ProtClustDB:CLSN2915891 ArrayExpress:P50700 Genevestigator:P50700 GermOnline:AT4G11650 InterPro:IPR001938 InterPro:IPR017949 Gene3D:G3DSA:2.60.110.10 PIRSF:PIRSF002703 PRINTS:PR00347 SMART:SM00205 SUPFAM:SSF49870 PROSITE:PS00316 PROSITE:PS51367 Uniprot:P50700
Leaf	Isotig10820	6	34	-1.974	0.000227442	TAIR|locus:2139900 - symbol:PSB28 "AT4G28660" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0009539 "photosystem II reaction center" evidence=ISS] [GO:0015979 "photosynthesis" evidence=IEA;ISS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] InterPro:IPR005610 Pfam:PF03912 ProDom:PD012692 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0009570 EMBL:AL161573 GO:GO:0009535 GO:GO:0015979 UniGene:At.23067 GO:GO:0009654 EMBL:AF462867 EMBL:AY113018 EMBL:AY086344 IPI:IPI00541411 PIR:T10660 RefSeq:NP_567814.1 UniGene:At.28252 ProteinModelPortal:Q8W0Y8 SMR:Q8W0Y8 STRING:Q8W0Y8 PRIDE:Q8W0Y8 ProMEX:Q8W0Y8 EnsemblPlants:AT4G28660.1 GeneID:828984 KEGG:ath:AT4G28660 TAIR:At4g28660 eggNOG:NOG08123 HOGENOM:HBG493836 InParanoid:Q8W0Y8 KO:K08903 OMA:PREWDRF PhylomeDB:Q8W0Y8 ProtClustDB:PLN00039 ArrayExpress:Q9M0G6 Genevestigator:Q8W0Y8 TIGRFAMs:TIGR03047 Uniprot:Q8W0Y8
Leaf	Isotig10823	9	0	4.699	0.000718283	TAIR|locus:2093307 - symbol:AT3G15670 "AT3G15670" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0009793 "embryo development ending in seed dormancy" evidence=ISS] [GO:0005634 "nucleus" evidence=IDA] GO:GO:0005634 EMBL:CP002686 EMBL:AB017071 ProtClustDB:CLSN2679745 EMBL:AY040026 EMBL:AY054162 EMBL:AY079410 IPI:IPI00542660 RefSeq:NP_188188.1 UniGene:At.5382 STRING:Q9LW12 PRIDE:Q9LW12 ProMEX:Q9LW12 EnsemblPlants:AT3G15670.1 GeneID:820810 KEGG:ath:AT3G15670 TAIR:At3g15670 InParanoid:Q9LW12 OMA:QYTKETA PhylomeDB:Q9LW12 ArrayExpress:Q9LW12 Genevestigator:Q9LW12 Uniprot:Q9LW12
Leaf	Isotig10892	20	195	-2.756	4.92E-27	TAIR|locus:2033686 - symbol:RBCS1A "AT1G67090" species:3702 "Arabidopsis thaliana" [GO:0009573 "chloroplast ribulose bisphosphate carboxylase complex" evidence=ISS] [GO:0015977 "carbon fixation" evidence=ISS] [GO:0016984 "ribulose-bisphosphate carboxylase activity" evidence=ISS] [GO:0031977 "thylakoid lumen" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009637 "response to blue light" evidence=IEP] [GO:0010114 "response to red light" evidence=IEP] [GO:0010218 "response to far red light" evidence=IEP] [GO:0015979 "photosynthesis" evidence=IMP] [GO:0080158 "chloroplast ribulose bisphosphate carboxylase complex biogenesis" evidence=IMP] InterPro:IPR000894 Pfam:PF00101 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0048046 GO:GO:0009570 GO:GO:0004497 GO:GO:0005507

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0009409 GO:GO:0009637 GO:GO:0010218 GO:GO:0010114 GO:GO:0031969 EMBL:AC007152 GO:GO:0009853 GO:GO:0009535 GO:GO:0022626 GO:GO:0031977 EMBL:AC004146 GO:GO:0019253 UniGene:At.46639 GO:GO:0016984 UniGene:At.37531 Gene3D:G3DSA:3.30.190.10 EMBL:X13611 EMBL:AF325011 EMBL:AF325004 EMBL:AF372874 EMBL:AF410291 EMBL:AY054188 EMBL:AY054581 EMBL:AY058831 EMBL:AY059940 EMBL:AY062612 EMBL:AY062711 EMBL:AY065101 EMBL:AY093380 EMBL:AY093388 EMBL:AY097366 EMBL:BT000362 EMBL:BT002076 EMBL:X68342 IPI:IPI00539020 PIR:G96694 PIR:S03720 RefSeq:NP_176880.1 UniGene:At.12721 UniGene:At.30194 UniGene:At.49098 UniGene:At.67454 UniGene:At.68122 UniGene:At.70053 UniGene:At.75196 ProteinModelPortal:P10795 SMR:P10795 IntAct:P10795 MINT:MINT-2584041 STRING:P10795 World-2DPAGE:0003:P10795 PRIDE:P10795 ProMEX:P10795 EnsemblPlants:AT1G67090.1 GeneID:843029 KEGG:ath:AT1G67090 TAIR:At1g67090 eggNOG:COG4451 HOGENOM:HBG608223 InParanoid:P10795 KO:K01602 OMA:AFPATRK PhylomeDB:P10795 ProtClustDB:PLN02289 ArrayExpress:P10795 Genevestigator:P10795 InterPro:IPR024681 InterPro:IPR024680 Pfam:PF12338 PRINTS:PR00152 SMART:SM00961 SUPFAM:SSF55239 Uniprot:P10795
Leaf	Isotig10901	11	0	4.988	0.000159591	TAIR|locus:2026884 - symbol:AT1G68570 "AT1G68570" species:3702 "Arabidopsis thaliana" [GO:0005215 "transporter activity" evidence=ISS] [GO:0006857 "oligopeptide transport" evidence=IEA;ISS] [GO:0016020 "membrane" evidence=IEA;ISS] InterPro:IPR000109 Pfam:PF00854 PROSITE:PS01022 PROSITE:PS01023 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005215 InterPro:IPR016196 SUPFAM:SSF103473 EMBL:AC008075 GO:GO:0042128 eggNOG:COG3104 GO:GO:0006857 HOGENOM:HBG605267 EMBL:AY091784 EMBL:BT002278 EMBL:AK226963 IPI:IPI00547183 PIR:A96710 RefSeq:NP_177024.1 UniGene:At.43526 ProteinModelPortal:Q9SX20 TCDB:2.A.17.3.6 PRIDE:Q9SX20 EnsemblPlants:AT1G68570.1 GeneID:843186 KEGG:ath:AT1G68570 TAIR:At1g68570 InParanoid:Q9SX20 OMA:FHANMIS PhylomeDB:Q9SX20 ProtClustDB:CLSN2682303 Genevestigator:Q9SX20 Uniprot:Q9SX20
Leaf	Isotig10905	12	183	-3.402	1.17E-30	TAIR|locus:2033686 - symbol:RBCS1A "AT1G67090" species:3702 "Arabidopsis thaliana" [GO:0009573 "chloroplast ribulose bisphosphate carboxylase complex" evidence=ISS] [GO:0015977 "carbon fixation" evidence=ISS] [GO:0016984 "ribulose-bisphosphate carboxylase activity" evidence=ISS] [GO:0031977 "thylakoid lumen" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009637 "response to blue light" evidence=IEP] [GO:0010114 "response to red light" evidence=IEP] [GO:0010218 "response to far red light" evidence=IEP] [GO:0015979 "photosynthesis" evidence=IMP] [GO:0080158 "chloroplast ribulose bisphosphate carboxylase complex biogenesis" evidence=IMP] InterPro:IPR000894 Pfam:PF00101 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0048046 GO:GO:0009570 GO:GO:0004497 GO:GO:0005507 GO:GO:0009409 GO:GO:0009637 GO:GO:0010218 GO:GO:0010114 GO:GO:0031969 EMBL:AC007152 GO:GO:0009853 GO:GO:0009535 GO:GO:0022626 GO:GO:0031977 EMBL:AC004146 GO:GO:0019253 UniGene:At.46639 GO:GO:0016984 UniGene:At.37531 Gene3D:G3DSA:3.30.190.10 EMBL:X13611 EMBL:AF325011 EMBL:AF325004 EMBL:AF372874 EMBL:AF410291 EMBL:AY054188 EMBL:AY054581 EMBL:AY058831 EMBL:AY059940 EMBL:AY062612 EMBL:AY062711 EMBL:AY065101 EMBL:AY093380 EMBL:AY093388 EMBL:AY097366 EMBL:BT000362 EMBL:BT002076 EMBL:X68342 IPI:IPI00539020 PIR:G96694 PIR:S03720 RefSeq:NP_176880.1 UniGene:At.12721 UniGene:At.30194 UniGene:At.49098 UniGene:At.67454 UniGene:At.68122 UniGene:At.70053 UniGene:At.75196 ProteinModelPortal:P10795 SMR:P10795 IntAct:P10795 MINT:MINT-2584041 STRING:P10795 World-2DPAGE:0003:P10795 PRIDE:P10795 ProMEX:P10795 EnsemblPlants:AT1G67090.1 GeneID:843029 KEGG:ath:AT1G67090 TAIR:At1g67090 eggNOG:COG4451 HOGENOM:HBG608223 InParanoid:P10795 KO:K01602 OMA:AFPATRK PhylomeDB:P10795 ProtClustDB:PLN02289 ArrayExpress:P10795 Genevestigator:P10795 InterPro:IPR024681 InterPro:IPR024680 Pfam:PF12338 PRINTS:PR00152 SMART:SM00961 SUPFAM:SSF55239 Uniprot:P10795
Leaf	Isotig10926	20	0	5.851	2.71E-07	No hit
Leaf	Isotig10937	22	92	-1.535	3.59E-07	TAIR|locus:2012928 - symbol:DRT112 "DNA-DAMAGE-REPAIR/TOLERATION PROTEIN 112" species:3702 "Arabidopsis thaliana" [GO:0005507 "copper ion binding" evidence=IEA] [GO:0009055 "electron carrier activity" evidence=IEA] [GO:0009543 "chloroplast thylakoid lumen" evidence=IDA] [GO:0031977 "thylakoid lumen" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						"chloroplast stroma" evidence=IDA] [GO:0046688 "response to copper ion" evidence=IEP] [GO:0055070 "copper ion homeostasis" evidence=IMP] [GO:0017148 "negative regulation of translation" evidence=IMP] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0009411 "response to UV" evidence=IGI] [GO:0042221 "response to chemical stimulus" evidence=IGI] InterPro:IPR000923 InterPro:IPR001235 InterPro:IPR002387 Pfam:PF00127 PRINTS:PR00156 PRINTS:PR00157 PROSITE:PS00196 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009570 GO:GO:0009411 GO:GO:0017148 GO:GO:0009055 GO:GO:0006810 GO:GO:0005507 GO:GO:0046688 GO:GO:0022900 HOGENOM:HBG653810 InterPro:IPR008972 Gene3D:G3DSA:2.60.40.420 SUPFAM:SSF49503 GO:GO:0055070 GO:GO:0009543 EMBL:AC026234 eggNOG:COG3794 KO:K02638 ProtClustDB:CLSN2679397 TIGRFAMs:TIGR02656 EMBL:M98456 EMBL:AJ271355 EMBL:AF324702 EMBL:AF326879 EMBL:AF334383 EMBL:AF361853 EMBL:BT001030 EMBL:AY086284 EMBL:AY374308 IPI:IPI00520177 PIR:B86337 PIR:PA0004 PIR:S33707 RefSeq:NP_173459.1 UniGene:At.24399 UniGene:At.71481 UniGene:At.71708 UniGene:At.72031 ProteinModelPortal:P42699 SMR:P42699 STRING:P42699 PRIDE:P42699 ProMEX:P42699 EnsemblPlants:AT1G20340.1 GeneID:838622 KEGG:ath:AT1G20340 TAIR:At1g20340 InParanoid:P42699 OMA:WEETFSE PhylomeDB:P42699 ArrayExpress:P42699 Genevestigator:P42699 GermOnline:AT1G20340 Uniprot:P42699
Leaf	Isotig10956	16	0	5.529	4.31E-06	TAIR|locus:2093307 - symbol:AT3G15670 "AT3G15670" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0009793 "embryo development ending in seed dormancy" evidence=ISS] [GO:0005634 "nucleus" evidence=IDA] GO:GO:0005634 EMBL:CP002686 EMBL:AB017071 ProtClustDB:CLSN2679745 EMBL:AY040026 EMBL:AY054162 EMBL:AY079410 IPI:IPI00542660 RefSeq:NP_188188.1 UniGene:At.5382 STRING:Q9LW12 PRIDE:Q9LW12 ProMEX:Q9LW12 EnsemblPlants:AT3G15670.1 GeneID:820810 KEGG:ath:AT3G15670 TAIR:At3g15670 InParanoid:Q9LW12 OMA:QYTKETA PhylomeDB:Q9LW12 ArrayExpress:Q9LW12 Genevestigator:Q9LW12 Uniprot:Q9LW12
Leaf	Isotig10979	11	1	3.988	0.000330755	TAIR|locus:2196292 - symbol:BCA6 "beta carbonic anhydrase 6" species:3702 "Arabidopsis thaliana" [GO:0004089 "carbonate dehydratase activity" evidence=IEA;ISS] [GO:0008270 "zinc ion binding" evidence=IEA;ISS] [GO:0015976 "carbon utilization" evidence=IEA;ISS] [GO:0005739 "mitochondrion" evidence=IDA] InterPro:IPR001765 InterPro:IPR015892 Pfam:PF00484 PROSITE:PS00704 PROSITE:PS00705 SMART:SM00947 EMBL:CP002684 GO:GO:0005739 GO:GO:0008270 GO:GO:0015976 GO:GO:0004089 Gene3D:G3DSA:3.40.1050.10 PANTHER:PTHR11002 SUPFAM:SSF53056 KO:K01673 EMBL:AC079604 HSSP:P17067 IPI:IPI00539588 RefSeq:NP_001185259.1 RefSeq:NP_176114.2 UniGene:At.25362 ProteinModelPortal:Q9C6F5 SMR:Q9C6F5 STRING:Q9C6F5 EnsemblPlants:AT1G58180.2 EnsemblPlants:AT1G58180.4 GeneID:842185 KEGG:ath:AT1G58180 TAIR:At1g58180 InParanoid:Q9C6F5 OMA:EHIIVLG PhylomeDB:Q9C6F5 ProtClustDB:PLN02154 Genevestigator:Q9C6F5 Uniprot:Q9C6F5
Leaf	Isotig10981	71	0	7.679	1.97E-20	No hit
Leaf	Isotig10993	11	0	4.988	0.000159591	No hit
Leaf	Isotig11000	12	2	3.114	0.000658121	TAIR|locus:2045663 - symbol:CYP5 "AT2G29960" species:3702 "Arabidopsis thaliana" [GO:0003755 "peptidyl-prolyl cis-trans isomerase activity" evidence=ISS;IDA] [GO:0006457 "protein folding" evidence=IEA;ISS] [GO:0005624 "membrane fraction" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] [GO:0005783 "endoplasmic reticulum" evidence=IDA] [GO:0005771 "multivesicular body" evidence=IDA] [GO:0005795 "Golgi stack" evidence=IDA] [GO:0005794 "Golgi apparatus" evidence=RCA] InterPro:IPR002130 InterPro:IPR020892 InterPro:IPR024936 Pfam:PF00160 PIRSF:PIRSF001467 PRINTS:PR00153 PROSITE:PS00170 PROSITE:PS50072 GO:GO:0005783 GO:GO:0005829 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0006457 GO:GO:0005624 GO:GO:0016020 GO:GO:0005795 EMBL:AC004680 GO:GO:0042277 GO:GO:0005771 eggNOG:COG0652 HOGENOM:HBG610621 GO:GO:0003755 Gene3D:G3DSA:2.40.100.10 SUPFAM:SSF50891 EMBL:AF020433 EMBL:AY054593 EMBL:BT000068 EMBL:AY085875 IPI:IPI00544481 PIR:T02489 PIR:T50837 RefSeq:NP_180557.1 UniGene:At.26460 ProteinModelPortal:Q8LDP4 SMR:Q8LDP4 STRING:Q8LDP4 PRIDE:Q8LDP4 EnsemblPlants:AT2G29960.1 GeneID:817546 KEGG:ath:AT2G29960 TAIR:At2g29960 InParanoid:Q8LDP4 OMA:SMANSGE PhylomeDB:Q8LDP4 ProtClustDB:CLSN2683841 ArrayExpress:O80876 Genevestigator:Q8LDP4 GermOnline:AT2G29960 Uniprot:Q8LDP4
Leaf	Isotig11015	5	32	-2.149	0.000158227	UNIPROTKB|P07591 - symbol:P07591 "Thioredoxin M-type, chloroplastic" species:3562 "Spinacia oleracea" [GO:0005515 "protein binding" evidence=IPI] InterPro:IPR005746 InterPro:IPR013766 InterPro:IPR017937 Pfam:PF00085 PRINTS:PR00421 PROSITE:PS00194 GO:GO:0009507 GO:GO:0005515 GO:GO:0009055 GO:GO:0006810 GO:GO:0022900 InterPro:IPR012336 Gene3D:G3DSA:3.40.30.10 SUPFAM:SSF52833

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0045454 PROSITE:PS51352 GO:GO:0015035 GO:GO:0006662 PANTHER:PTHR10438 TIGRFAMs:TIGR01068 EMBL:X51462 EMBL:X51463 PIR:S20496 PDB:1FB0 PDB:1FB6 PDB:1GL8 PDB:2PUK PDBsum:1FB0 PDBsum:1FB6 PDBsum:1GL8 PDBsum:2PUK ProteinModelPortal:P07591 SMR:P07591 IntAct:P07591 Uniprot:P07591
Leaf	Isotig11027	18	0	5.699	1.07E-06	MGI|MGI:3781672 - symbol:Gm3495 "predicted gene 3495" species:10090 "Mus musculus" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] MGI:MGI:3781672 InterPro:IPR006907 Pfam:PF04822 EMBL:AC084416 IPI:IPI00989117 Ensembl:ENSMUST00000166086 GeneTree:ENSGT00520000055655 Uniprot:E9Q366
Leaf	Isotig11039	17	1	4.616	3.60E-06	TAIR|locus:2117547 - symbol:AT4G25790 "AT4G25790" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005576 "extracellular region" evidence=IEA;ISS] [GO:0008150 "biological_process" evidence=ND] InterPro:IPR018244 PROSITE:PS01009 PROSITE:PS01010 Pfam:PF00188 INTERPRO:IPR001283 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005576 EMBL:AL161564 EMBL:AL049480 InterPro:IPR014044 Gene3D:G3DSA:3.40.33.10 PANTHER:PTHR10334 PRINTS:PR00837 SMART:SM00198 SUPFAM:SSF55797 HSSP:P04284 InterPro:IPR002413 PRINTS:PR00838 eggNOG:COG2340 HOGENOM:HBG689653 ProtClustDB:CLSN2685865 EMBL:BT010823 EMBL:BT011300 IPI:IPI00533611 PIR:T04233 RefSeq:NP_194309.1 UniGene:At.32231 ProteinModelPortal:Q9SW04 SMR:Q9SW04 STRING:Q9SW04 EnsemblPlants:AT4G25790.1 GeneID:828684 KEGG:ath:AT4G25790 TAIR:At4g25790 InParanoid:Q9SW04 OMA:FAVESWT PhylomeDB:Q9SW04 ArrayExpress:Q9SW04 Genevestigator:Q9SW04 Uniprot:Q9SW04
Leaf	Isotig11058	61	0	7.460	4.54E-18	TAIR|locus:2050095 - symbol:LEA "AT2G21490" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0006950 "response to stress" evidence=IEA;ISS] [GO:0009415 "response to water" evidence=IEA;ISS] InterPro:IPR000167 Pfam:PF00257 PROSITE:PS00315 PROSITE:PS00823 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0006950 EMBL:AC006841 EMBL:X91920 EMBL:AY052342 EMBL:AY061911 EMBL:BT000900 EMBL:AY088292 EMBL:Z32586 IPI:IPI00532525 PIR:H84601 RefSeq:NP_179744.1 UniGene:At.34 UniGene:At.75010 STRING:Q96261 PRIDE:Q96261 ProMEX:Q96261 EnsemblPlants:AT2G21490.1 GeneID:816688 KEGG:ath:AT2G21490 GeneFarm:5053 TAIR:At2g21490 eggNOG:NOG272869 HOGENOM:HBG319086 InParanoid:Q96261 OMA:DQPHEKK PhylomeDB:Q96261 ProtClustDB:CLSN2683593 ArrayExpress:Q96261 Genevestigator:Q96261 GermOnline:AT2G21490 GO:GO:0009415 Uniprot:Q96261
Leaf	Isotig11111	9	0	4.699	0.000718283	TAIR|locus:2052511 - symbol:AT2G21820 "AT2G21820" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002685 GenomeReviews:CT485783_GR EMBL:AC007019 EMBL:AF324676 EMBL:AF339727 IPI:IPI00548056 PIR:E84605 RefSeq:NP_565518.1 UniGene:At.14263 PRIDE:Q9SJ17 DNASU:816718 EnsemblPlants:AT2G21820.1 GeneID:816718 KEGG:ath:AT2G21820 TAIR:At2g21820 eggNOG:NOG284848 HOGENOM:HBG600959 InParanoid:Q9SJ17 OMA:YESVEGG PhylomeDB:Q9SJ17 ProtClustDB:CLSN2688322 ArrayExpress:Q9SJ17 Genevestigator:Q9SJ17 Uniprot:Q9SJ17
Leaf	Isotig11131	16	215	-3.219	3.68E-34	TAIR|locus:2033686 - symbol:RBCS1A "AT1G67090" species:3702 "Arabidopsis thaliana" [GO:0009573 "chloroplast ribulose bisphosphate carboxylase complex" evidence=ISS] [GO:0015977 "carbon fixation" evidence=ISS] [GO:0016984 "ribulose-bisphosphate carboxylase activity" evidence=ISS] [GO:0031977 "thylakoid lumen" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009409 "response to cold" evidence=IEP] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0022626 "cytosolic ribosome" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0005507 "copper ion binding" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0048046 "apoplast" evidence=IDA] [GO:0009637 "response to blue light" evidence=IEP] [GO:0010114 "response to red light" evidence=IEP] [GO:0010218 "response to far red light" evidence=IEP] [GO:0015979 "photosynthesis" evidence=IMP] [GO:0080158 "chloroplast ribulose bisphosphate carboxylase complex biogenesis" evidence=IMP] InterPro:IPR000894 Pfam:PF00101 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0048046 GO:GO:0009570 GO:GO:0004497 GO:GO:0005507 GO:GO:0009409 GO:GO:0009637 GO:GO:0010218 GO:GO:0010114 GO:GO:0031969 EMBL:AC007152 GO:GO:0009853 GO:GO:0009535 GO:GO:0022626 GO:GO:0031977 EMBL:AC004146 GO:GO:0019253 UniGene:At.46639 GO:GO:0016984 UniGene:At.37531 Gene3D:G3DSA:3.30.190.10 EMBL:X13611 EMBL:AF325011 EMBL:AF325004 EMBL:AF372874 EMBL:AF410291 EMBL:AY054188 EMBL:AY054581

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						EMBL:AY058831 EMBL:AY059940 EMBL:AY062612 EMBL:AY062711 EMBL:AY065101 EMBL:AY093380 EMBL:AY093388 EMBL:AY097366 EMBL:BT000362 EMBL:BT002076 EMBL:X68342 IPI:IPI00539020 PIR:G96694 PIR:S03720 RefSeq:NP_176880.1 UniGene:At.12721 UniGene:At.30194 UniGene:At.49098 UniGene:At.67454 UniGene:At.68122 UniGene:At.70053 UniGene:At.75196 ProteinModelPortal:P10795 SMR:P10795 IntAct:P10795 MINT:MINT-2584041 STRING:P10795 World-2DPAGE:0003:P10795 PRIDE:P10795 ProMEX:P10795 EnsemblPlants:AT1G67090.1 GeneID:843029 KEGG:ath:AT1G67090 TAIR:At1g67090 eggNOG:COG4451 HOGENOM:HBG608223 InParanoid:P10795 KO:K01602 OMA:AFPATRK PhylomeDB:P10795 ProtClustDB:PLN02289 ArrayExpress:P10795 Genevestigator:P10795 InterPro:IPR024681 InterPro:IPR024680 Pfam:PF12338 PRINTS:PR00152 SMART:SM00961 SUPFAM:SSF55239 Uniprot:P10795
Leaf	Isotig11144	21	2	3.921	8.06E-07	TAIR|locus:2025346 - symbol:LEA14 "AT1G01470" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0009269 "response to desiccation" evidence=ISS] [GO:0009793 "embryo development ending in seed dormancy" evidence=ISS] [GO:0009644 "response to high light intensity" evidence=IEP] [GO:0009611 "response to wounding" evidence=IEP] [GO:0050832 "defense response to fungus" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR013990 SMART:SM00769 InterPro:IPR004864 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 InterPro:IPR013783 Gene3D:G3DSA:2.60.40.10 EMBL:Y12776 EMBL:AC061957 GO:GO:0009611 GO:GO:0050832 GO:GO:0009644 GO:GO:0009269 EMBL:Y10085 EMBL:AY074855 EMBL:BT015111 EMBL:Z37258 IPI:IPI00525938 PIR:D86145 RefSeq:NP_171654.1 UniGene:At.25113 PDB:1XO8 PDBsum:1XO8 ProteinModelPortal:O03983 SMR:O03983 IntAct:O03983 STRING:O03983 PRIDE:O03983 DNASU:837071 EnsemblPlants:AT1G01470.1 GeneID:837071 KEGG:ath:AT1G01470 TAIR:At1g01470 eggNOG:NOG271766 HOGENOM:HBG320411 InParanoid:O03983 OMA:YSHSIPI PhylomeDB:O03983 ProtClustDB:CLSN2682861 Genevestigator:O03983 GermOnline:AT1G01470 Pfam:PF03168 Uniprot:O03983
Leaf	Isotig11194	26	0	6.229	5.03E-09	No hit
Leaf	Isotig11195	75	35	1.628	8.33E-09	TAIR|locus:2093307 - symbol:AT3G15670 "AT3G15670" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0009793 "embryo development ending in seed dormancy" evidence=ISS] [GO:0005634 "nucleus" evidence=IDA] GO:GO:0005634 EMBL:CP002686 EMBL:AB017071 ProtClustDB:CLSN2679745 EMBL:AY040026 EMBL:AY054162 EMBL:AY079410 IPI:IPI00542660 RefSeq:NP_188188.1 UniGene:At.5382 STRING:Q9LW12 PRIDE:Q9LW12 ProMEX:Q9LW12 EnsemblPlants:AT3G15670.1 GeneID:820810 KEGG:ath:AT3G15670 TAIR:At3g15670 InParanoid:Q9LW12 OMA:QYTKETA PhylomeDB:Q9LW12 ArrayExpress:Q9LW12 Genevestigator:Q9LW12 Uniprot:Q9LW12
Leaf	Isotig11251	15	0	5.436	8.75E-06	TAIR|locus:2174774 - symbol:C/VIF2 "AT5G64620" species:3702 "Arabidopsis thaliana" [GO:0046910 "pectinesterase inhibitor activity" evidence=ISS] [GO:0004857 "enzyme inhibitor activity" evidence=IDA] [GO:0043086 "negative regulation of catalytic activity" evidence=IDA] [GO:0080167 "response to karrikin" evidence=IEP] InterPro:IPR006501 Pfam:PF04043 SMART:SM00856 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0004857 GO:GO:0080167 EMBL:AB010076 GO:GO:0030599 Gene3D:G3DSA:1.20.140.40 SUPFAM:SSF101148 TIGRFAMs:TIGR01614 EMBL:AY086575 EMBL:BT003882 EMBL:BT004919 EMBL:Y12807 IPI:IPI00521854 RefSeq:NP_201267.1 UniGene:At.25570 ProteinModelPortal:O49603 SMR:O49603 EnsemblPlants:AT5G64620.1 GeneID:836583 KEGG:ath:AT5G64620 TAIR:At5g64620 eggNOG:NOG281989 HOGENOM:HBG596372 InParanoid:O49603 OMA:TIIESTC PhylomeDB:O49603 ProtClustDB:CLSN2686283 ArrayExpress:O49603 Genevestigator:O49603 Uniprot:O49603
Leaf	Isotig11300	10	1	3.851	0.00071293	UNIPROTKB|F1NUG6 - symbol:RPGR "Uncharacterized protein" species:9031 "Gallus gallus" [GO:0005737 "cytoplasm" evidence=IEA] [GO:0005929 "cilium" evidence=IEA] [GO:0007601 "visual perception" evidence=IEA] [GO:0042462 "eye photoreceptor cell development" evidence=IEA] InterPro:IPR000408 Pfam:PF00415 InterPro:IPR009091 Gene3D:G3DSA:2.130.10.30 SUPFAM:SSF50985 PRINTS:PR00633 PROSITE:PS00626 PROSITE:PS50012 GeneTree:ENSGT00650000092861 EMBL:AADN02011054 IPI:IPI00586770 Ensembl:ENSGALT00000026211 OMA:ENGLMFT Uniprot:F1NUG6
Leaf	Isotig11372	8	37	-1.680	0.000570683	TAIR|locus:2125018 - symbol:AT4G01150 "AT4G01150" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] GO:GO:0016021 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0009941 GO:GO:0009535 GO:GO:0010287 EMBL:AL161491 EMBL:AF007269 HOGENOM:HBG593250

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						InterPro:IPR025564 Pfam:PF14159 EMBL:U19925 EMBL:AY091679 EMBL:AF389292 IPI:IPI00529234 PIR:T01726 RefSeq:NP_567210.1 UniGene:At.48817 IntAct:O04616 STRING:O04616 PRIDE:O04616 EnsemblPlants:AT4G01150.1 GeneID:828181 KEGG:ath:AT4G01150 TAIR:At4g01150 eggNOG:NOG85035 InParanoid:O04616 OMA:NELITDL PhylomeDB:O04616 ProtClustDB:CLSN2917477 ArrayExpress:O04616 Genevestigator:O04616 Uniprot:O04616
Leaf	Isotig11403	21	0	5.921	1.38E-07	No hit
Leaf	Isotig11458	505	490	0.572	2.69E-10	ZFIN|ZDB-GENE-070410-9 - symbol:zgc:158463 "zgc:158463" species:7955 "Danio rerio" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] ZFIN:ZDB-GENE-070410-9 EMBL:BX296557 EMBL:BX537263 EMBL:BC129240 IPI:IPI00837201 RefSeq:NP_001091866.1 RefSeq:XP_003200836.1 UniGene:Dr.155369 Ensembl:ENSDART00000102863 Ensembl:ENSDART00000126982 GeneID:100037361 GeneID:100151188 KEGG:dre:100037361 KEGG:dre:100151188 eggNOG:NOG298153 GeneTree:ENSGT00390000016898 InParanoid:A2VD29 OMA:ACHQHAL OrthoDB:EOG4FJ8BF Bgee:A2VD29 Uniprot:A2VD29
Leaf	Isotig11518	16	3	2.944	0.000128177	TAIR|locus:2058389 - symbol:AT2G04520 species:3702 "Arabidopsis thaliana" [GO:0003723 "RNA binding" evidence=IEA] [GO:0003743 "translation initiation factor activity" evidence=IEA;ISS] [GO:0006413 "translational initiation" evidence=IEA;ISS] [GO:0005829 "cytosol" evidence=IDA] HAMAP:MF_00216 InterPro:IPR001253 InterPro:IPR006196 InterPro:IPR018104 Pfam:PF01176 ProDom:PD005579 PROSITE:PS01262 PROSITE:PS50832 SMART:SM00652 GO:GO:0005829 EMBL:CP002685 GO:GO:0003743 InterPro:IPR012340 Gene3D:G3DSA:2.40.50.140 InterPro:IPR016027 SUPFAM:SSF50249 EMBL:AC006951 KO:K03236 PANTHER:PTHR21668 TIGRFAMs:TIGR00523 OMA:QGDIILI HSSP:P47813 ProtClustDB:PLN00208 EMBL:AY088924 IPI:IPI00520938 PIR:D84458 RefSeq:NP_178531.1 UniGene:At.14182 ProteinModelPortal:Q9SJB9 SMR:Q9SJB9 STRING:Q9SJB9 PRIDE:Q9SJB9 ProMEX:Q9SJB9 EnsemblPlants:AT2G04520.1 GeneID:814994 KEGG:ath:AT2G04520 TAIR:At2g04520 InParanoid:Q9SJB9 PhylomeDB:Q9SJB9 ArrayExpress:Q9SJB9 Genevestigator:Q9SJB9 Uniprot:Q9SJB9
Leaf	Isotig11523	15	78	-1.850	8.96E-08	UNIPROTKB|P83522 - symbol:P83522 "Ferredoxin" species:4513 "Hordeum vulgare" [GO:0006124 "ferredoxin metabolic process" evidence=TAS] [GO:0009055 "electron carrier activity" evidence=TAS] InterPro:IPR001041 InterPro:IPR006058 InterPro:IPR010241 Pfam:PF00111 PROSITE:PS00197 PROSITE:PS51085 GO:GO:0009507 GO:GO:0009055 GO:GO:0046872 GO:GO:0006810 GO:GO:0022900 GO:GO:0051537 InterPro:IPR012675 Gene3D:G3DSA:3.10.20.30 SUPFAM:SSF54292 TIGRFAMs:TIGR02008 GO:GO:0006124 ProteinModelPortal:P83522 SMR:P83522 Gramene:P83522 Genevestigator:P83522 Uniprot:P83522
Leaf	Isotig11544	10	1	3.851	0.00071293	TAIR|locus:2020317 - symbol:AT1G17080 "AT1G17080" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0005515 "protein binding" evidence=IPI] InterPro:IPR021138 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005515 GO:GO:0006412 GO:GO:0003735 GO:GO:0005840 EMBL:AC007651 HOGENOM:HBG598539 PANTHER:PTHR10052 UniGene:At.20092 UniGene:At.69774 EMBL:AY045595 EMBL:AY097384 IPI:IPI00534834 PIR:F86306 RefSeq:NP_564013.1 IntAct:Q9SHG7 STRING:Q9SHG7 EnsemblPlants:AT1G17080.1 GeneID:838278 KEGG:ath:AT1G17080 TAIR:At1g17080 eggNOG:NOG276765 InParanoid:Q9SHG7 OMA:YIPVVEG PhylomeDB:Q9SHG7 Genevestigator:Q9SHG7 Uniprot:Q9SHG7
Leaf	Isotig11547	107	25	2.627	9.93E-21	No hit
Leaf	Isotig11549	1	20	-3.793	7.36E-05	No hit
Leaf	Isotig11551	9	0	4.699	0.000718283	TAIR|locus:2057727 - symbol:AT2G26230 species:3702 "Arabidopsis thaliana" [GO:0004846 "urate oxidase activity" evidence=IEA;ISS] [GO:0006144 "purine base metabolic process" evidence=IEA;ISS] [GO:0016491 "oxidoreductase activity" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0005777 "peroxisome" evidence=IDA] InterPro:IPR019842 PROSITE:PS00366 InterPro:IPR002042 Pfam:PF01014 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0005777 GO:GO:0006144 EMBL:AC004484 Gene3D:G3DSA:3.10.270.10 EMBL:Y11120 EMBL:AY050318 EMBL:AY101530 EMBL:AY087805 IPI:IPI00518603 PIR:H84657 RefSeq:NP_180191.1 UniGene:At.5406 ProteinModelPortal:O04420 SMR:O04420 STRING:O04420 PRIDE:O04420 ProMEX:O04420 EnsemblPlants:AT2G26230.1 GeneID:817163 KEGG:ath:AT2G26230 TAIR:At2g26230 eggNOG:COG3648 HOGENOM:HBG558657 InParanoid:O04420 KO:K00365 OMA:NSDIVAT PhylomeDB:O04420 ProtClustDB:PLN02415 ArrayExpress:O04420 Genevestigator:O04420 GO:GO:0004846 PANTHER:PTHR10395:SF1 PIRSF:PIRSF000241 PRINTS:PR00093 TIGRFAMs:TIGR03383 Uniprot:O04420

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig11553	31	11	2.024	1.72E-05	TAIR|locus:2093307 - symbol:AT3G15670 "AT3G15670" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0009793 "embryo development ending in seed dormancy" evidence=ISS] [GO:0005634 "nucleus" evidence=IDA] GO:GO:0005634 EMBL:CP002686 EMBL:AB017071 ProtClustDB:CLSN2679745 EMBL:AY040026 EMBL:AY054162 EMBL:AY079410 IPI:IPI00542660 RefSeq:NP_188188.1 UniGene:At.5382 STRING:Q9LW12 PRIDE:Q9LW12 ProMEX:Q9LW12 EnsemblPlants:AT3G15670.1 GeneID:820810 KEGG:ath:AT3G15670 TAIR:At3g15670 InParanoid:Q9LW12 OMA:QYTKETA PhylomeDB:Q9LW12 ArrayExpress:Q9LW12 Genevestigator:Q9LW12 Uniprot:Q9LW12
Leaf	Isotig11555	1	16	-3.471	0.000601166	TAIR|locus:2100063 - symbol:AT3G10060 "AT3G10060" species:3702 "Arabidopsis thaliana" [GO:0000413 "protein peptidyl-prolyl isomerization" evidence=IBA] [GO:0003755 "peptidyl-prolyl cis-trans isomerase activity" evidence=ISS;IBA] [GO:0005528 "FK506 binding" evidence=ISS;IBA] [GO:0018208 "peptidyl-proline modification" evidence=IBA] [GO:0009543 "chloroplast thylakoid lumen" evidence=ISS;IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] InterPro:IPR001179 Pfam:PF00254 PROSITE:PS50059 PANTHER:PTHR10516 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0006457 GO:GO:0009535 GO:GO:0003755 EMBL:AC010927 eggNOG:COG0545 HOGENOM:HBG731200 InterPro:IPR023566 EMBL:AY094442 EMBL:AY122895 IPI:IPI00546942 RefSeq:NP_187617.1 UniGene:At.23399 UniGene:At.39997 HSSP:Q02790 ProteinModelPortal:Q9SR70 SMR:Q9SR70 STRING:Q9SR70 PRIDE:Q9SR70 ProMEX:Q9SR70 EnsemblPlants:AT3G10060.1 GeneID:820167 KEGG:ath:AT3G10060 TAIR:At3g10060 GeneTree:EPGT00070000031103 InParanoid:Q9SR70 OMA:KYYDIKV PhylomeDB:Q9SR70 ProtClustDB:CLSN2915705 Genevestigator:Q9SR70 Uniprot:Q9SR70
Leaf	Isotig11573	31	0	6.483	2.05E-10	No hit
Leaf	Isotig11608	23	0	6.053	3.61E-08	TAIR|locus:2025346 - symbol:LEA14 "AT1G01470" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0009269 "response to desiccation" evidence=ISS] [GO:0009793 "embryo development ending in seed dormancy" evidence=ISS] [GO:0009644 "response to high light intensity" evidence=IEP] [GO:0009611 "response to wounding" evidence=IEP] [GO:0050832 "defense response to fungus" evidence=IEP] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR013990 SMART:SM00769 InterPro:IPR004864 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 InterPro:IPR013783 Gene3D:G3DSA:2.60.40.10 EMBL:Y12776 EMBL:AC061957 GO:GO:0009611 GO:GO:0050832 GO:GO:0009644 GO:GO:0009269 EMBL:Y10085 EMBL:AY074855 EMBL:BT015111 EMBL:Z37258 IPI:IPI00525938 PIR:D86145 RefSeq:NP_171654.1 UniGene:At.25113 PDB:1XO8 PDBsum:1XO8 ProteinModelPortal:O03983 SMR:O03983 IntAct:O03983 STRING:O03983 PRIDE:O03983 DNASU:837071 EnsemblPlants:AT1G01470.1 GeneID:837071 KEGG:ath:AT1G01470 TAIR:At1g01470 eggNOG:NOG271766 HOGENOM:HBG320411 InParanoid:O03983 OMA:YSHSIPI PhylomeDB:O03983 ProtClustDB:CLSN2682861 Genevestigator:O03983 GermOnline:AT1G01470 Pfam:PF03168 Uniprot:O03983
Leaf	Isotig11711	29	6	2.802	4.91E-07	SGD|S000028567 - symbol:RRT15 "Putative protein of unknown function" species:4932 "Saccharomyces cerevisiae" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0006355 "regulation of transcription, DNA-dependent" evidence=IEA] [GO:0003674 "molecular_function" evidence=ND] SGD:S000028567 GO:GO:0006355 GO:GO:0006351 EMBL:BK006945 EMBL:U51921 RefSeq:NP_878128.1 ProteinModelPortal:Q3E811 STRING:Q3E811 EnsemblFungi:YLR162W-A GeneID:1466416 KEGG:sce:YLR162W-A CYGD:YLR162w-a GeneTree:ENSGT00530000064745 OMA:FYINCIM OrthoDB:EOG45TGXP NextBio:983475 ArrayExpress:Q3E811 Genevestigator:Q3E811 Uniprot:Q3E811
Leaf	Isotig11736	7	47	-2.218	3.02E-06	TAIR|locus:2164371 - symbol:PSAN "AT5G64040" species:3702 "Arabidopsis thaliana" [GO:0009522 "photosystem I" evidence=TAS] [GO:0009773 "photosynthetic electron transport in photosystem I" evidence=TAS] [GO:0030093 "chloroplast photosystem I" evidence=IPI] [GO:0009543 "chloroplast thylakoid lumen" evidence=IDA] [GO:0005516 "calmodulin binding" evidence=TAS;IPI] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] InterPro:IPR008796 Pfam:PF05479 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0005516 GO:GO:0009535 GO:GO:0015979 GO:GO:0009522 EMBL:AB008266 EMBL:U32176 EMBL:AY062835 EMBL:AY081594 IPI:IPI00547610 IPI:IPI00895629 RefSeq:NP_201209.1 UniGene:At.21476 ProteinModelPortal:P49107 SMR:P49107 IntAct:P49107 STRING:P49107 PRIDE:P49107 EnsemblPlants:AT5G64040.1 GeneID:836525 KEGG:ath:AT5G64040 GeneFarm:2295 TAIR:At5g64040

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						eggNOG:NOG284850 HOGENOM:HBG589689 InParanoid:P49107 KO:K02701 OMA:SCKFPEN PhylomeDB:P49107 ProtClustDB:PLN00054 BioCyc:MetaCyc:MONOMER-1095 ArrayExpress:P49107 Genevestigator:P49107 Uniprot:P49107
Leaf	Isotig11740	16	1	4.529	7.58E-06	TAIR|locus:2132090 - symbol:ISU1 "AT4G22220" species:3702 "Arabidopsis thaliana" [GO:0016226 "iron-sulfur cluster assembly" evidence=IGI;ISS] [GO:0005198 "structural molecule activity" evidence=ISS] [GO:0005739 "mitochondrion" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] InterPro:IPR002871 InterPro:IPR011339 Pfam:PF01592 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005506 GO:GO:0005759 GO:GO:0016226 EMBL:AL161556 GO:GO:0051537 EMBL:AL021712 eggNOG:COG0822 HOGENOM:HBG584215 OMA:SSMVTEM TIGRFAMs:TIGR01999 EMBL:AJ866966 EMBL:AF361579 EMBL:AY081721 EMBL:AY088584 IPI:IPI00516740 PIR:T04903 RefSeq:NP_193953.1 UniGene:At.43669 HSSP:Q57074 ProteinModelPortal:O49627 SMR:O49627 IntAct:O49627 STRING:O49627 PRIDE:O49627 EnsemblPlants:AT4G22220.1 GeneID:828316 KEGG:ath:AT4G22220 TAIR:At4g22220 InParanoid:O49627 PhylomeDB:O49627 ProtClustDB:CLSN2684974 ArrayExpress:O49627 Genevestigator:O49627 Uniprot:O49627
Leaf	Isotig11752	22	108	-1.766	1.09E-09	TAIR|locus:2012928 - symbol:DRT112 "DNA-DAMAGE-REPAIR/TOLERATION PROTEIN 112" species:3702 "Arabidopsis thaliana" [GO:0005507 "copper ion binding" evidence=IEA] [GO:0009055 "electron carrier activity" evidence=IEA] [GO:0009543 "chloroplast thylakoid lumen" evidence=IDA] [GO:0031977 "thylakoid lumen" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0046688 "response to copper ion" evidence=IEP] [GO:0055070 "copper ion homeostasis" evidence=IMP] [GO:0017148 "negative regulation of translation" evidence=IMP] [GO:0009534 "chloroplast thylakoid" evidence=IDA] [GO:0009411 "response to UV" evidence=IGI] [GO:0042221 "response to chemical stimulus" evidence=IGI] InterPro:IPR000923 InterPro:IPR001235 InterPro:IPR002387 Pfam:PF00127 PRINTS:PR00156 PRINTS:PR00157 PROSITE:PS00196 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009570 GO:GO:0009411 GO:GO:0017148 GO:GO:0009055 GO:GO:0006810 GO:GO:0005507 GO:GO:0046688 GO:GO:0022900 HOGENOM:HBG653810 InterPro:IPR008972 Gene3D:G3DSA:2.60.40.420 SUPFAM:SSF49503 GO:GO:0055070 GO:GO:0009543 EMBL:AC026234 eggNOG:COG3794 KO:K02638 ProtClustDB:CLSN2679397 TIGRFAMs:TIGR02656 EMBL:M98456 EMBL:AJ271355 EMBL:AF324702 EMBL:AF326879 EMBL:AF334383 EMBL:AF361853 EMBL:BT001030 EMBL:AY086284 EMBL:AY374308 IPI:IPI00520177 PIR:B86337 PIR:PA0004 PIR:S33707 RefSeq:NP_173459.1 UniGene:At.24399 UniGene:At.71481 UniGene:At.71708 UniGene:At.72031 ProteinModelPortal:P42699 SMR:P42699 STRING:P42699 PRIDE:P42699 ProMEX:P42699 EnsemblPlants:AT1G20340.1 GeneID:838622 KEGG:ath:AT1G20340 TAIR:At1g20340 InParanoid:P42699 OMA:WEETFSE PhylomeDB:P42699 ArrayExpress:P42699 Genevestigator:P42699 GermOnline:AT1G20340 Uniprot:P42699
Leaf	Isotig11784	9	0	4.699	0.000718283	No hit
Leaf	Isotig11850	13	0	5.229	3.68E-05	No hit
Leaf	Isotig11923	15	2	3.436	7.06E-05	TAIR|locus:2183795 - symbol:AT5G10980 species:3702 "Arabidopsis thaliana" [GO:0003677 "DNA binding" evidence=IEA;ISS] [GO:0006334 "nucleosome assembly" evidence=IEA] InterPro:IPR000164 InterPro:IPR007125 InterPro:IPR009072 Pfam:PF00125 PRINTS:PR00622 PROSITE:PS00322 PROSITE:PS00959 SMART:SM00428 EMBL:CP002687 GenomeReviews:CT486007_GR GO:GO:0005634 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0003677 EMBL:AL035708 EMBL:AL161596 Gene3D:G3DSA:1.10.20.10 SUPFAM:SSF47113 EMBL:AL391222 GO:GO:0006334 GO:GO:0000786 EMBL:AL365234 eggNOG:COG2036 PANTHER:PTHR11426 HOGENOM:HBG715487 UniGene:At.10968 KO:K11253 ProtClustDB:PLN00121 OMA:FAMARTK EMBL:X60429 EMBL:AF385735 EMBL:AY078027 EMBL:AY070749 EMBL:AY097375 EMBL:BT002391 EMBL:BT003326 EMBL:AY086668 EMBL:BT025499 IPI:IPI00539437 PIR:S24346 RefSeq:NP_001031816.1 RefSeq:NP_001078517.1 RefSeq:NP_195713.1 RefSeq:NP_196659.1 RefSeq:NP_849529.1 UniGene:At.24091 UniGene:At.25092 UniGene:At.6019 UniGene:At.67362 ProteinModelPortal:P59169 SMR:P59169 STRING:P59169 PRIDE:P59169 EnsemblPlants:AT4G40030.1 EnsemblPlants:AT4G40030.3 EnsemblPlants:AT4G40040.1 EnsemblPlants:AT4G40040.2 EnsemblPlants:AT5G10980.1 GeneID:830164 GeneID:830165 GeneID:830965 KEGG:ath:AT4G40030 KEGG:ath:AT4G40040 KEGG:ath:AT5G10980 TAIR:At4g40030 TAIR:At4g40040 TAIR:At5g10980 InParanoid:P59169 PhylomeDB:P59169 ArrayExpress:P59169 Genevestigator:P59169 GermOnline:AT4G40030 Uniprot:P59169

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig11969	10	1	3.851	0.00071293	TAIR|locus:2010637 - symbol:AT1G04850 "AT1G04850" species:3702 "Arabidopsis thaliana" [GO:0008150 "biological_process" evidence=ND] [GO:0008270 "zinc ion binding" evidence=IEA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR000449 InterPro:IPR006567 InterPro:IPR007087 InterPro:IPR009060 InterPro:IPR015880 Pfam:PF00627 PROSITE:PS00028 SMART:SM00355 SMART:SM00580 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0005829 GO:GO:0008270 InterPro:IPR015940 SMART:SM00165 PROSITE:PS50030 EMBL:AC004809 SUPFAM:SSF46934 InterPro:IPR018997 Pfam:PF09409 eggNOG:NOG126397 EMBL:AY062609 EMBL:AY088435 EMBL:BT000147 IPI:IPI00534720 PIR:G86181 RefSeq:NP_563718.1 UniGene:At.21872 ProteinModelPortal:Q9MAT3 SMR:Q9MAT3 IntAct:Q9MAT3 PRIDE:Q9MAT3 EnsemblPlants:AT1G04850.1 GeneID:839399 KEGG:ath:AT1G04850 TAIR:At1g04850 HOGENOM:HBG316965 InParanoid:Q9MAT3 OMA:KNPDEEK PhylomeDB:Q9MAT3 ProtClustDB:CLSN2687675 ArrayExpress:Q9MAT3 Genevestigator:Q9MAT3 Uniprot:Q9MAT3
Leaf	Isotig11977	83	38	1.656	8.55E-10	TAIR|locus:2168459 - symbol:LTP4 "lipid transfer protein 4" species:3702 "Arabidopsis thaliana" [GO:0008289 "lipid binding" evidence=IEA] [GO:0006869 "lipid transport" evidence=TAS] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] [GO:0009414 "response to water deprivation" evidence=IEP] [GO:0009651 "response to salt stress" evidence=IEP] InterPro:IPR000528 InterPro:IPR013770 PRINTS:PR00382 PROSITE:PS00597 Pfam:PF00234 GO:GO:0009737 EMBL:CP002688 GenomeReviews:BA000015_GR InterPro:IPR016140 SMART:SM00499 SUPFAM:SSF47699 GO:GO:0006869 GO:GO:0009651 GO:GO:0009414 GO:GO:0008289 Gene3D:G3DSA:1.10.110.10 EMBL:AB016890 HOGENOM:HBG744832 ProtClustDB:CLSN2690050 EMBL:AF159801 EMBL:AY058233 EMBL:AY035015 EMBL:AY045644 EMBL:AY059081 EMBL:BT002397 EMBL:BT006514 EMBL:AY088209 IPI:IPI00517749 RefSeq:NP_568904.1 UniGene:At.25116 ProteinModelPortal:Q9LLR6 SMR:Q9LLR6 PRIDE:Q9LLR6 EnsemblPlants:AT5G59310.1 GeneID:836050 KEGG:ath:AT5G59310 TAIR:At5g59310 eggNOG:NOG246791 InParanoid:Q9LLR6 OMA:TSTNCAT PhylomeDB:Q9LLR6 ArrayExpress:Q9LLR6 Genevestigator:Q9LLR6 GermOnline:AT5G59310 Uniprot:Q9LLR6
Leaf	Isotig11996	5	38	-2.397	1.09E-05	TAIR|locus:2037440 - symbol:PSAH2 "AT1G52230" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0009538 "photosystem I reaction center" evidence=ISS] [GO:0015979 "photosynthesis" evidence=IEA;ISS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] InterPro:IPR004928 Pfam:PF03244 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009535 GO:GO:0010287 GO:GO:0015979 EMBL:AC022354 GO:GO:0009538 TCDB:5.B.4.1.1 UniGene:At.25110 eggNOG:NOG314087 HOGENOM:HBG560928 KO:K02695 ProtClustDB:PLN00017 EMBL:AJ245632 EMBL:AF385712 EMBL:AY133667 EMBL:AY085302 IPI:IPI00536453 PIR:C96562 RefSeq:NP_175633.1 ProteinModelPortal:Q9SUI6 SMR:Q9SUI6 STRING:Q9SUI6 PRIDE:Q9SUI6 EnsemblPlants:AT1G52230.1 GeneID:841653 KEGG:ath:AT1G52230 TAIR:At1g52230 InParanoid:Q9SUI6 OMA:KKGPQLP PhylomeDB:Q9SUI6 ArrayExpress:Q9SUI6 Genevestigator:Q9SUI6 GermOnline:AT1G52230 Uniprot:Q9SUI6
Leaf	Isotig12023	21	92	-1.602	1.52E-07	TAIR|locus:2020502 - symbol:PSAG "AT1G55670" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0009522 "photosystem I" evidence=ISS] [GO:0015979 "photosynthesis" evidence=ISS;IMP] [GO:0016020 "membrane" evidence=ISS] [GO:0009773 "photosynthetic electron transport in photosystem I" evidence=IMP] [GO:0050821 "protein stabilization" evidence=IMP] [GO:0009941 "chloroplast envelope" evidence=IDA] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009780 "photosynthetic NADP+ reduction" evidence=IMP] [GO:0042550 "photosystem I stabilization" evidence=IMP] [GO:0030093 "chloroplast photosystem I" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] InterPro:IPR000549 InterPro:IPR023618 Pfam:PF01241 PROSITE:PS01026 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0050821 GO:GO:0009941 EMBL:AC002328 GO:GO:0016168 UniGene:At.71449 UniGene:At.21811 GO:GO:0042550 GO:GO:0009773 TCDB:5.B.4.1.1 EMBL:AJ245630 EMBL:AF326870 EMBL:AF324710 EMBL:AF339692 EMBL:AF378859 EMBL:AY050463 EMBL:Z37244 IPI:IPI00546886 RefSeq:NP_175963.1 UniGene:At.16919 UniGene:At.25349 ProteinModelPortal:Q9S7N7 SMR:Q9S7N7 STRING:Q9S7N7 PRIDE:Q9S7N7 EnsemblPlants:AT1G55670.1 GeneID:842016 KEGG:ath:AT1G55670 TAIR:At1g55670 eggNOG:NOG236059 HOGENOM:HBG609679 InParanoid:Q9S7N7 KO:K08905 OMA:QNGKTHF PhylomeDB:Q9S7N7 ProtClustDB:PLN00091 BioCyc:MetaCyc:MONOMER-1090 ArrayExpress:Q9S7N7

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						Genevestigator:Q9S7N7 GermOnline:AT1G55670 GO:GO:0030093 GO:GO:0009780 InterPro:IPR016370 InterPro:IPR017494 Gene3D:G3DSA:1.10.286.40 PIRSF:PIRSF002912 TIGRFAMs:TIGR03051 Uniprot:Q9S7N7
Leaf	Isotig12043	6	33	-1.930	0.00034472	TAIR|locus:2201836 - symbol:PSAO "AT1G08380" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0009522 "photosystem I" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009768 "photosynthesis, light harvesting in photosystem I" evidence=IC] [GO:0009507 "chloroplast" evidence=IDA] EMBL:CP002684 GO:GO:0009507 GO:GO:0009522 GO:GO:0009768 UniGene:At.23691 EMBL:AY050960 EMBL:AY091345 EMBL:AY087368 EMBL:AJ493060 IPI:IPI00545431 RefSeq:NP_563815.1 STRING:Q949Q5 PRIDE:Q949Q5 EnsemblPlants:AT1G08380.1 GeneID:837358 KEGG:ath:AT1G08380 TAIR:At1g08380 InParanoid:Q949Q5 KO:K14332 OMA:WLRRDLN PhylomeDB:Q949Q5 ProtClustDB:PLN00046 Genevestigator:Q949Q5 InterPro:IPR017498 TIGRFAMs:TIGR03059 Uniprot:Q949Q5
Leaf	Isotig12047	16	0	5.529	4.31E-06	UNIPROTKB|A8CVF3 - symbol:DHN1 "Dehydrin DHN1" species:82927 "Avicennia marina" [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0010555 "response to mannitol stimulus" evidence=IEP] [GO:0042631 "cellular response to water deprivation" evidence=IEP] [GO:0071472 "cellular response to salt stress" evidence=IEP] [GO:0071482 "cellular response to light stimulus" evidence=IEP] InterPro:IPR000167 Pfam:PF00257 PROSITE:PS00315 PROSITE:PS00823 GO:GO:0005634 GO:GO:0005737 GO:GO:0071472 GO:GO:0042631 GO:GO:0010555 EMBL:EU121850 EMBL:EU121851 GO:GO:0071482 Uniprot:A8CVF3
Leaf	Isotig12056	18	0	5.699	1.07E-06	MGI|MGI:3781672 - symbol:Gm3495 "predicted gene 3495" species:10090 "Mus musculus" [GO:0003674 "molecular_function" evidence=ND] [GO:0008150 "biological_process" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] MGI:MGI:3781672 InterPro:IPR006907 Pfam:PF04822 EMBL:AC084416 IPI:IPI00989117 Ensembl:ENSMUST00000166086 GeneTree:ENSGT00520000055655 Uniprot:E9Q366
Leaf	Isotig12149	53	35	1.128	0.000254482	TAIR|locus:2133144 - symbol:AT4G21020 "AT4G21020" species:3702 "Arabidopsis thaliana" [GO:0009793 "embryo development ending in seed dormancy" evidence=ISS] EMBL:CP002687 GenomeReviews:CT486007_GR EMBL:AL080282 EMBL:AL161554 ProtClustDB:CLSN2687244 EMBL:AY072166 EMBL:AY117321 IPI:IPI00539152 PIR:T10644 RefSeq:NP_193834.1 UniGene:At.32674 PRIDE:Q9SUB2 EnsemblPlants:AT4G21020.1 GeneID:827849 KEGG:ath:AT4G21020 TAIR:At4g21020 eggNOG:NOG268376 HOGENOM:HBG744068 InParanoid:Q9SUB2 OMA:EDTKERA PhylomeDB:Q9SUB2 Genevestigator:Q9SUB2 Uniprot:Q9SUB2
Leaf	Isotig12211	8	68	-2.559	1.01E-09	No hit
Leaf	Isotig12230	14	0	5.336	1.79E-05	TAIR|locus:2198175 - symbol:ADF11 "actin depolymerizing factor 11" species:3702 "Arabidopsis thaliana" [GO:0003779 "actin binding" evidence=IEA] [GO:0005622 "intracellular" evidence=IEA;ISS] [GO:0008150 "biological_process" evidence=ND] InterPro:IPR002108 Pfam:PF00241 PROSITE:PS51263 SMART:SM00102 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0003779 GO:GO:0005622 EMBL:AC009273 EMBL:AY072410 EMBL:BT001250 EMBL:AY088305 IPI:IPI00533839 PIR:A86149 RefSeq:NP_171680.1 UniGene:At.43294 ProteinModelPortal:Q9LQ81 SMR:Q9LQ81 STRING:Q9LQ81 PRIDE:Q9LQ81 EnsemblPlants:AT1G01750.1 GeneID:839281 KEGG:ath:AT1G01750 TAIR:At1g01750 eggNOG:NOG303866 HOGENOM:HBG628477 InParanoid:Q9LQ81 OMA:IVFKINE PhylomeDB:Q9LQ81 ProtClustDB:CLSN2682878 ArrayExpress:Q9LQ81 Genevestigator:Q9LQ81 GermOnline:AT1G01750 Uniprot:Q9LQ81
Leaf	Isotig12253	20	3	3.266	7.04E-06	TAIR|locus:2084918 - symbol:PR4 "AT3G04720" species:3702 "Arabidopsis thaliana" [GO:0009627 "systemic acquired resistance" evidence=IEP] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0080027 "response to herbivore" evidence=IEP] [GO:0009817 "defense response to fungus, incompatible interaction" evidence=IDA] [GO:0008061 "chitin binding" evidence=ISS] [GO:0009615 "response to virus" evidence=IEP] [GO:0009723 "response to ethylene stimulus" evidence=IEP] InterPro:IPR001002 InterPro:IPR001153 InterPro:IPR018226 InterPro:IPR018371 Pfam:PF00187 Pfam:PF00967 PRINTS:PR00451 PRINTS:PR00602 ProDom:PD000609 ProDom:PD004535 PROSITE:PS00026 PROSITE:PS00771 PROSITE:PS00772 PROSITE:PS50941 PROSITE:PS51174 SMART:SM00270 GO:GO:0042742 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0009651 GO:GO:0009817 GO:GO:0009627 GO:GO:0009723 GO:GO:0009615 GO:GO:0080027 CAZy:CBM18 GO:GO:0008061 Gene3D:G3DSA:3.30.60.10 SUPFAM:SSF57016 EMBL:AC011437 InterPro:IPR014733 InterPro:IPR009009 Gene3D:G3DSA:2.40.40.10 SUPFAM:SSF50685 EMBL:U01880 EMBL:AF370536 EMBL:BT000046 EMBL:AY088644 IPI:IPI00529373 RefSeq:NP_187123.1 UniGene:At.252 ProteinModelPortal:P43082 SMR:P43082 IntAct:P43082 STRING:P43082 PRIDE:P43082 EnsemblPlants:AT3G04720.1 GeneID:819632 KEGG:ath:AT3G04720 TAIR:At3g04720 eggNOG:NOG306084 HOGENOM:HBG588395 InParanoid:P43082 OMA:QQGHLIV PhylomeDB:P43082 ProtClustDB:CLSN2914702 ArrayExpress:P43082 Genevestigator:P43082 GermOnline:AT3G04720 Uniprot:P43082

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig12322	12	1	4.114	0.000154103	TAIR|locus:2103237 - symbol:AT3G10770 species:3702 "Arabidopsis thaliana" [GO:0003676 "nucleic acid binding" evidence=IEA] [GO:0008150 "biological_process" evidence=ND] InterPro:IPR001374 PROSITE:PS51061 EMBL:CP002686 GO:GO:0003676 EMBL:AC011708 InterPro:IPR024771 Pfam:PF12752 ProtClustDB:CLSN2684204 InterPro:IPR024773 PANTHER:PTHR15672:SF1 EMBL:AK226352 IPI:IPI00543158 RefSeq:NP_566381.1 UniGene:At.21804 ProteinModelPortal:Q9SG83 SMR:Q9SG83 STRING:Q9SG83 PRIDE:Q9SG83 EnsemblPlants:AT3G10770.1 GeneID:820246 KEGG:ath:AT3G10770 TAIR:At3g10770 InParanoid:Q9SG83 OMA:CINRNET PhylomeDB:Q9SG83 Genevestigator:Q9SG83 Uniprot:Q9SG83
Leaf	Isotig12344	62	0	7.483	2.61E-18	UNIPROTKB|A8CVF3 - symbol:DHN1 "Dehydrin DHN1" species:82927 "Avicennia marina" [GO:0005634 "nucleus" evidence=IDA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0010555 "response to mannitol stimulus" evidence=IEP] [GO:0042631 "cellular response to water deprivation" evidence=IEP] [GO:0071472 "cellular response to salt stress" evidence=IEP] [GO:0071482 "cellular response to light stimulus" evidence=IEP] InterPro:IPR000167 Pfam:PF00257 PROSITE:PS00315 PROSITE:PS00823 GO:GO:0005634 GO:GO:0005737 GO:GO:0071472 GO:GO:0042631 GO:GO:0010555 EMBL:EU121850 EMBL:EU121851 GO:GO:0071482 Uniprot:A8CVF3
Leaf	Isotig12455	14	0	5.336	1.79E-05	No hit
Leaf	Isotig12487	42	2	4.921	1.79E-13	UNIPROTKB|Q84N29 - symbol:LTP3 "Probable non-specific lipid-transfer protein 3" species:4565 "Triticum aestivum" [GO:0009611 "response to wounding" evidence=IDA] [GO:0009723 "response to ethylene stimulus" evidence=IDA] [GO:0009751 "response to salicylic acid stimulus" evidence=IDA] [GO:0042542 "response to hydrogen peroxide" evidence=IDA] InterPro:IPR000528 InterPro:IPR013770 PRINTS:PR00382 PROSITE:PS00597 Pfam:PF00234 GO:GO:0009611 InterPro:IPR016140 SMART:SM00499 SUPFAM:SSF47699 GO:GO:0006869 GO:GO:0009723 GO:GO:0009751 GO:GO:0042542 GO:GO:0008289 Gene3D:G3DSA:1.10.110.10 EMBL:AY226580 UniGene:Ta.50482 HSSP:P19656 ProteinModelPortal:Q84N29 SMR:Q84N29 Gramene:Q84N29 Uniprot:Q84N29
Leaf	Isotig12669	10	0	4.851	0.000336918	No hit
Leaf	Isotig12672	5	50	-2.793	4.04E-08	TAIR|locus:2037440 - symbol:PSAH2 "AT1G52230" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0009538 "photosystem I reaction center" evidence=ISS] [GO:0015979 "photosynthesis" evidence=IEA;ISS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] InterPro:IPR004928 Pfam:PF03244 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009535 GO:GO:0010287 GO:GO:0015979 EMBL:AC022354 GO:GO:0009538 TCDB:5.B.4.1.1 UniGene:At.25110 eggNOG:NOG314087 HOGENOM:HBG560928 KO:K02695 ProtClustDB:PLN00017 EMBL:AJ245632 EMBL:AF385712 EMBL:AY133667 EMBL:AY085302 IPI:IPI00536453 PIR:C96562 RefSeq:NP_175633.1 ProteinModelPortal:Q9SUI6 SMR:Q9SUI6 STRING:Q9SUI6 PRIDE:Q9SUI6 EnsemblPlants:AT1G52230.1 GeneID:841653 KEGG:ath:AT1G52230 TAIR:At1g52230 InParanoid:Q9SUI6 OMA:KKGPQLP PhylomeDB:Q9SUI6 ArrayExpress:Q9SUI6 Genevestigator:Q9SUI6 GermOnline:AT1G52230 Uniprot:Q9SUI6
Leaf	Isotig12739	23	123	-1.890	9.55E-12	TAIR|locus:2201836 - symbol:PSAO "AT1G08380" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0009522 "photosystem I" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009768 "photosynthesis, light harvesting in photosystem I" evidence=IC] [GO:0009507 "chloroplast" evidence=IDA] EMBL:CP002684 GO:GO:0009507 GO:GO:0009522 GO:GO:0009768 UniGene:At.23691 EMBL:AY050960 EMBL:AY091345 EMBL:AY087368 EMBL:AJ493060 IPI:IPI00545431 RefSeq:NP_563815.1 STRING:Q949Q5 PRIDE:Q949Q5 EnsemblPlants:AT1G08380.1 GeneID:837358 KEGG:ath:AT1G08380 TAIR:At1g08380 InParanoid:Q949Q5 KO:K14332 OMA:WLRRDLN PhylomeDB:Q949Q5 ProtClustDB:PLN00046 Genevestigator:Q949Q5 InterPro:IPR017498 TIGRFAMs:TIGR03059 Uniprot:Q949Q5
Leaf	Isotig12755	20	5	2.529	7.73E-05	TAIR|locus:2168459 - symbol:LTP4 "lipid transfer protein 4" species:3702 "Arabidopsis thaliana" [GO:0008289 "lipid binding" evidence=IEA] [GO:0006869 "lipid transport" evidence=TAS] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] [GO:0009414 "response to water deprivation" evidence=IEP] [GO:0009651 "response to salt stress" evidence=IEP] InterPro:IPR000528 InterPro:IPR013770 PRINTS:PR00382 PROSITE:PS00597 Pfam:PF00234 GO:GO:0009737 EMBL:CP002688 GenomeReviews:BA000015_GR InterPro:IPR016140 SMART:SM00499 SUPFAM:SSF47699 GO:GO:0006869 GO:GO:0009651 GO:GO:0009414 GO:GO:0008289 Gene3D:G3DSA:1.10.110.10 EMBL:AB016890 HOGENOM:HBG744832 ProtClustDB:CLSN2690050 EMBL:AF159801 EMBL:AY058233 EMBL:AY035015 EMBL:AY045644 EMBL:AY059081 EMBL:BT002397 EMBL:BT006514 EMBL:AY088209 IPI:IPI00517749 RefSeq:NP_568904.1 UniGene:At.25116

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						ProteinModelPortal:Q9LLR6 SMR:Q9LLR6 PRIDE:Q9LLR6 EnsemblPlants:AT5G59310.1 GeneID:836050 KEGG:ath:AT5G59310 TAIR:At5g59310 eggNOG:NOG246791 InParanoid:Q9LLR6 OMA:TSTNCAT PhylomeDB:Q9LLR6 ArrayExpress:Q9LLR6 Genevestigator:Q9LLR6 GermOnline:AT5G59310 Uniprot:Q9LLR6
Leaf	Isotig12845	40	7	3.044	7.58E-10	ZFIN|ZDB-GENE-070410-9 - symbol:zgc:158463 "zgc:158463" species:7955 "Danio rerio" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] ZFIN:ZDB-GENE-070410-9 EMBL:BX296557 EMBL:BX537263 EMBL:BC129240 IPI:IPI00837201 RefSeq:NP_001091866.1 RefSeq:XP_003200836.1 UniGene:Dr.155369 Ensembl:ENSDART00000102863 Ensembl:ENSDART00000126982 GeneID:100037361 GeneID:100151188 KEGG:dre:100037361 KEGG:dre:100151188 eggNOG:NOG298153 GeneTree:ENSGT00390000016898 InParanoid:A2VD29 OMA:ACHQHAL OrthoDB:EOG4FJ8BF Bgee:A2VD29 Uniprot:A2VD29
Leaf	Isotig12884	53	2	5.257	7.63E-17	TAIR|locus:2084918 - symbol:PR4 "AT3G04720" species:3702 "Arabidopsis thaliana" [GO:0009627 "systemic acquired resistance" evidence=IEP] [GO:0009651 "response to salt stress" evidence=IEP] [GO:0080027 "response to herbivore" evidence=IEP] [GO:0009817 "defense response to fungus, incompatible interaction" evidence=IDA] [GO:0008061 "chitin binding" evidence=ISS] [GO:0009615 "response to virus" evidence=IEP] [GO:0009723 "response to ethylene stimulus" evidence=IEP] InterPro:IPR001002 InterPro:IPR001153 InterPro:IPR018226 InterPro:IPR018371 Pfam:PF00187 Pfam:PF00967 PRINTS:PR00451 PRINTS:PR00602 ProDom:PD000609 ProDom:PD004535 PROSITE:PS00026 PROSITE:PS00771 PROSITE:PS00772 PROSITE:PS50941 PROSITE:PS51174 SMART:SM00270 GO:GO:0042742 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0009651 GO:GO:0009817 GO:GO:0009627 GO:GO:0009723 GO:GO:0009615 GO:GO:0080027 CAZy:CBM18 GO:GO:0008061 Gene3D:G3DSA:3.30.60.10 SUPFAM:SSF57016 EMBL:AC011437 InterPro:IPR014733 InterPro:IPR009009 Gene3D:G3DSA:2.40.40.10 SUPFAM:SSF50685 EMBL:U01880 EMBL:AF370536 EMBL:BT000046 EMBL:AY088644 IPI:IPI00529373 RefSeq:NP_187123.1 UniGene:At.252 ProteinModelPortal:P43082 SMR:P43082 IntAct:P43082 STRING:P43082 PRIDE:P43082 EnsemblPlants:AT3G04720.1 GeneID:819632 KEGG:ath:AT3G04720 TAIR:At3g04720 eggNOG:NOG306084 HOGENOM:HBG588395 InParanoid:P43082 OMA:QQGHLIV PhylomeDB:P43082 ProtClustDB:CLSN2914702 ArrayExpress:P43082 Genevestigator:P43082 GermOnline:AT3G04720 Uniprot:P43082
Leaf	Isotig12908	5	63	-3.126	7.52E-11	TAIR|locus:2066291 - symbol:AT2G26500 "AT2G26500" species:3702 "Arabidopsis thaliana" [GO:0009496 "plastoquinol--plastocyanin reductase activity" evidence=ISS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] HAMAP:MF_00396 InterPro:IPR012595 Pfam:PF08041 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009535 EMBL:AC002505 GO:GO:0009512 EMBL:AF375459 EMBL:AY060541 EMBL:AY088737 IPI:IPI00530642 PIR:T00983 RefSeq:NP_565623.1 RefSeq:NP_850079.1 UniGene:At.22912 ProteinModelPortal:O48717 SMR:O48717 STRING:O48717 PRIDE:O48717 EnsemblPlants:AT2G26500.1 EnsemblPlants:AT2G26500.2 GeneID:817191 KEGG:ath:AT2G26500 TAIR:At2g26500 HOGENOM:HBG746644 InParanoid:O48717 OMA:TEQCFAN PhylomeDB:O48717 ProtClustDB:CLSN2688447 ArrayExpress:O48717 Genevestigator:O48717 Uniprot:O48717
Leaf	Isotig13087	11	1	3.988	0.000330755	UNIPROTKB|Q84N29 - symbol:LTP3 "Probable non-specific lipid-transfer protein 3" species:4565 "Triticum aestivum" [GO:0009611 "response to wounding" evidence=IDA] [GO:0009723 "response to ethylene stimulus" evidence=IDA] [GO:0009751 "response to salicylic acid stimulus" evidence=IDA] [GO:0042542 "response to hydrogen peroxide" evidence=IDA] InterPro:IPR000528 InterPro:IPR013770 PRINTS:PR00382 PROSITE:PS00597 Pfam:PF00234 GO:GO:0009611 InterPro:IPR016140 SMART:SM00499 SUPFAM:SSF47699 GO:GO:0006869 GO:GO:0009723 GO:GO:0009751 GO:GO:0042542 GO:GO:0008289 Gene3D:G3DSA:1.10.110.10 EMBL:AY226580 UniGene:Ta.50482 HSSP:P19656 ProteinModelPortal:Q84N29 SMR:Q84N29 Gramene:Q84N29 Uniprot:Q84N29
Leaf	Isotig13162	80	3	5.266	1.26E-24	TAIR|locus:2083519 - symbol:MT2A "AT3G09390" species:3702 "Arabidopsis thaliana" [GO:0006878 "cellular copper ion homeostasis" evidence=ISS] [GO:0005507 "copper ion binding" evidence=IDA] InterPro:IPR000347 Pfam:PF01439 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005507 EMBL:AC011436 EMBL:D11394 EMBL:X62818 EMBL:U15108 EMBL:AY037263 EMBL:AY077669 EMBL:Z26416 IPI:IPI00529178 PIR:S18069 PIR:S57861 RefSeq:NP_187550.1 UniGene:At.24444 UniGene:At.42166 UniGene:At.67557 STRING:P25860 PRIDE:P25860 EnsemblPlants:AT3G09390.1 GeneID:820098 KEGG:ath:AT3G09390 TAIR:At3g09390 eggNOG:NOG259977 HOGENOM:HBG749344 InParanoid:P25860 OMA:CKMYPDL PhylomeDB:P25860 ProtClustDB:CLSN2685132 ArrayExpress:P25860 Genevestigator:P25860 GermOnline:AT3G09390 Uniprot:P25860

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig13254	9	48	-1.886	2.14E-05	TAIR|locus:2037440 - symbol:PSAH2 "AT1G52230" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0009538 "photosystem I reaction center" evidence=ISS] [GO:0015979 "photosynthesis" evidence=IEA;ISS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0010287 "plastoglobule" evidence=IDA] [GO:0016020 "membrane" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] InterPro:IPR004928 Pfam:PF03244 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR GO:GO:0009535 GO:GO:0010287 GO:GO:0015979 EMBL:AC022354 GO:GO:0009538 TCDB:5.B.4.1.1 UniGene:At.25110 eggNOG:NOG314087 HOGENOM:HBG560928 KO:K02695 ProtClustDB:PLN00017 EMBL:AJ245632 EMBL:AF385712 EMBL:AY133667 EMBL:AY085302 IPI:IPI00536453 PIR:C96562 RefSeq:NP_175633.1 ProteinModelPortal:Q9SUI6 SMR:Q9SUI6 STRING:Q9SUI6 PRIDE:Q9SUI6 EnsemblPlants:AT1G52230.1 GeneID:841653 KEGG:ath:AT1G52230 TAIR:At1g52230 InParanoid:Q9SUI6 OMA:KKGPQLP PhylomeDB:Q9SUI6 ArrayExpress:Q9SUI6 Genevestigator:Q9SUI6 GermOnline:AT1G52230 Uniprot:Q9SUI6
Leaf	Isotig13395	3	35	-3.015	1.84E-06	TAIR|locus:2066291 - symbol:AT2G26500 "AT2G26500" species:3702 "Arabidopsis thaliana" [GO:0009496 "plastoquinol--plastocyanin reductase activity" evidence=ISS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] HAMAP:MF_00396 InterPro:IPR012595 Pfam:PF08041 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009535 EMBL:AC002505 GO:GO:0009512 EMBL:AF375459 EMBL:AY060541 EMBL:AY088737 IPI:IPI00530642 PIR:T00983 RefSeq:NP_565623.1 RefSeq:NP_850079.1 UniGene:At.22912 ProteinModelPortal:O48717 SMR:O48717 STRING:O48717 PRIDE:O48717 EnsemblPlants:AT2G26500.1 EnsemblPlants:AT2G26500.2 GeneID:817191 KEGG:ath:AT2G26500 TAIR:At2g26500 HOGENOM:HBG746644 InParanoid:O48717 OMA:TEQCFAN PhylomeDB:O48717 ProtClustDB:CLSN2688447 ArrayExpress:O48717 Genevestigator:O48717 Uniprot:O48717
Leaf	Isotig13490	9	0	4.699	0.000718283	TAIR|locus:2056700 - symbol:ARPN "plantacyanin" species:3702 "Arabidopsis thaliana" [GO:0005507 "copper ion binding" evidence=IEA;ISS] [GO:0009055 "electron carrier activity" evidence=IEA] [GO:0009856 "pollination" evidence=IMP] [GO:0048196 "plant extracellular matrix" evidence=TAS] [GO:0048653 "anther development" evidence=IMP] [GO:0048046 "apoplast" evidence=IDA] InterPro:IPR003245 Pfam:PF02298 ProDom:PD003122 PROSITE:PS00196 PROSITE:PS51485 EMBL:AC004138 GO:GO:0048046 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0009055 GO:GO:0006810 GO:GO:0005507 GO:GO:0022900 GO:GO:0048653 EMBL:AC002521 InterPro:IPR008972 Gene3D:G3DSA:2.60.40.420 SUPFAM:SSF49503 EMBL:U76297 EMBL:AF325063 EMBL:AY064141 EMBL:AY097407 EMBL:AY084407 IPI:IPI00540939 PIR:F84441 PIR:T00843 RefSeq:NP_178388.1 UniGene:At.23668 ProteinModelPortal:Q8LG89 SMR:Q8LG89 PRIDE:Q8LG89 ProMEX:Q8LG89 EnsemblPlants:AT2G02850.1 GeneID:814816 KEGG:ath:AT2G02850 TAIR:At2g02850 eggNOG:NOG271220 HOGENOM:HBG748847 InParanoid:Q8LG89 OMA:SWSARAI PhylomeDB:Q8LG89 ProtClustDB:CLSN2913208 ArrayExpress:Q8LG89 Genevestigator:Q8LG89 GermOnline:AT2G02850 GO:GO:0048196 GO:GO:0009856 Uniprot:Q8LG89
Leaf	Isotig13692	9	0	4.699	0.000718283	TAIR|locus:2116762 - symbol:AT4G31830 "AT4G31830" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002687 GenomeReviews:CT486007_GR EMBL:AL161579 EMBL:AL049607 EMBL:BT010813 EMBL:BT011290 IPI:IPI00539008 PIR:T06305 RefSeq:NP_194911.1 UniGene:At.31710 IntAct:Q9SZ50 PRIDE:Q9SZ50 EnsemblPlants:AT4G31830.1 GeneID:829312 KEGG:ath:AT4G31830 TAIR:At4g31830 eggNOG:NOG287408 HOGENOM:HBG748438 InParanoid:Q9SZ50 OMA:THKMSPE PhylomeDB:Q9SZ50 ProtClustDB:CLSN2685982 ArrayExpress:Q9SZ50 Genevestigator:Q9SZ50 Uniprot:Q9SZ50
Leaf	Isotig13697	21	1	4.921	1.92E-07	TAIR|locus:2170239 - symbol:LEA4-5 "AT5G06760" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0009793 "embryo development ending in seed dormancy" evidence=ISS] [GO:0009409 "response to cold" evidence=IDA] [GO:0006970 "response to osmotic stress" evidence=IMP] [GO:0009414 "response to water deprivation" evidence=IMP] [GO:0048316 "seed development" evidence=IMP] InterPro:IPR005513 Pfam:PF03760 ProDom:PD005538 EMBL:CP002688 GO:GO:0009790 GO:GO:0009409 GO:GO:0009414 GO:GO:0006970 GO:GO:0048316 EMBL:AP002032 EMBL:AY050936 EMBL:AY091171 IPI:IPI00545605 RefSeq:NP_196294.1 UniGene:At.48991 STRING:Q9FG31 PRIDE:Q9FG31 ProMEX:Q9FG31 EnsemblPlants:AT5G06760.1 GeneID:830565 KEGG:ath:AT5G06760 TAIR:At5g06760 InParanoid:Q9FG31 OMA:GTHQMSA PhylomeDB:Q9FG31 ProtClustDB:CLSN2686892 ArrayExpress:Q9FG31 Genevestigator:Q9FG31 Uniprot:Q9FG31

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
Leaf	Isotig13716	208	193	0.637	8.29E-06	No hit
Leaf	Isotig13752	12	0	5.114	7.63E-05	TAIR|locus:2176712 - symbol:AT5G38170 species:3702 "Arabidopsis thaliana" [GO:0006869 "lipid transport" evidence=IEA;ISS] [GO:0008289 "lipid binding" evidence=ISS] InterPro:IPR013770 EMBL:CP002688 GenomeReviews:BA000015_GR InterPro:IPR016140 SMART:SM00499 SUPFAM:SSF47699 EMBL:AB005247 GO:GO:0006869 Gene3D:G3DSA:1.10.110.10 Pfam:PF14368 HOGENOM:HBG587265 HSSP:Q9FEK9 EMBL:BT003991 EMBL:BT005091 IPI:IPI00516861 RefSeq:NP_198633.1 UniGene:At.30430 ProteinModelPortal:Q9FF39 SMR:Q9FF39 IntAct:Q9FF39 PRIDE:Q9FF39 EnsemblPlants:AT5G38170.1 GeneID:833797 KEGG:ath:AT5G38170 TAIR:At5g38170 eggNOG:NOG330162 InParanoid:Q9FF39 OMA:KTLATCG PhylomeDB:Q9FF39 ProtClustDB:CLSN2687085 ArrayExpress:Q9FF39 Genevestigator:Q9FF39 Uniprot:Q9FF39
Leaf	Isotig13945	9	0	4.699	0.000718283	No hit
Leaf	Isotig14007	9	0	4.699	0.000718283	TAIR|locus:2007958 - symbol:PEPC1 "AT1G17710" species:3702 "Arabidopsis thaliana" [GO:0052731 "phosphocholine phosphatase activity" evidence=IDA] [GO:0052732 "phosphoethanolamine phosphatase activity" evidence=IDA] InterPro:IPR006383 InterPro:IPR006384 InterPro:IPR016965 Pfam:PF06888 PIRSF:PIRSF031051 EMBL:CP002684 GenomeReviews:CT485782_GR EMBL:AC034257 GO:GO:0051262 GO:GO:0046872 InterPro:IPR023214 Gene3D:G3DSA:3.40.50.1000 SUPFAM:SSF56784 GO:GO:0004427 TIGRFAMs:TIGR01489 TIGRFAMs:TIGR01488 eggNOG:NOG331523 HOGENOM:HBG319786 GO:GO:0052731 GO:GO:0052732 OMA:DWVLEAT ProtClustDB:CLSN2685367 EMBL:BT015372 EMBL:BT015670 IPI:IPI00531491 IPI:IPI00846125 PIR:A86312 RefSeq:NP_001077556.1 RefSeq:NP_173213.2 UniGene:At.49892 ProteinModelPortal:Q9FZ62 SMR:Q9FZ62 PRIDE:Q9FZ62 EnsemblPlants:AT1G17710.1 GeneID:838347 KEGG:ath:AT1G17710 TAIR:At1g17710 InParanoid:Q9FZ62 PhylomeDB:Q9FZ62 Genevestigator:Q9FZ62 Uniprot:Q9FZ62
Leaf	Isotig14022	17	4	2.616	0.000204438	No hit
Leaf	Isotig14090	11	0	4.988	0.000159591	TAIR|locus:2045482 - symbol:AT2G32090 "AT2G32090" species:3702 "Arabidopsis thaliana" [GO:0004462 "lactoylglutathione lyase activity" evidence=ISS] [GO:0005975 "carbohydrate metabolic process" evidence=ISS] EMBL:CP002685 GO:GO:0016829 EMBL:AC006223 EMBL:AY058893 EMBL:AY079042 IPI:IPI00533148 PIR:H84728 RefSeq:NP_565737.1 UniGene:At.20803 ProteinModelPortal:Q9SKZ0 SMR:Q9SKZ0 PRIDE:Q9SKZ0 EnsemblPlants:AT2G32090.1 GeneID:817769 KEGG:ath:AT2G32090 TAIR:At2g32090 InParanoid:Q9SKZ0 OMA:PDGRTRQ PhylomeDB:Q9SKZ0 ProtClustDB:CLSN2688622 ArrayExpress:Q9SKZ0 Genevestigator:Q9SKZ0 Uniprot:Q9SKZ0
Leaf	Isotig14186	9	0	4.699	0.000718283	TAIR|locus:2078911 - symbol:P5CS2 "delta 1-pyrroline-5-carboxylate synthase 2" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=IEA] [GO:0004349 "glutamate 5-kinase activity" evidence=IEA] [GO:0004350 "glutamate-5-semialdehyde dehydrogenase activity" evidence=IEA] [GO:0016491 "oxidoreductase activity" evidence=IEA] [GO:0005737 "cytoplasm" evidence=IDA] [GO:0006561 "proline biosynthetic process" evidence=IMP;TAS] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009793 "embryo development ending in seed dormancy" evidence=IMP] [GO:0005829 "cytosol" evidence=IDA] [GO:0009506 "plasmodesma" evidence=IDA] [GO:0009737 "response to abscisic acid stimulus" evidence=IEP] [GO:0042538 "hyperosmotic salinity response" evidence=IEP] InterPro:IPR000965 InterPro:IPR001048 InterPro:IPR001057 InterPro:IPR005715 InterPro:IPR005766 InterPro:IPR016161 InterPro:IPR016162 InterPro:IPR016163 InterPro:IPR019797 InterPro:IPR020593 Pfam:PF00696 PIRSF:PIRSF036429 PRINTS:PR00474 PROSITE:PS00902 PROSITE:PS01223 GO:GO:0005829 GO:GO:0009506 GO:GO:0005524 GO:GO:0009507 EMBL:CP002686 GenomeReviews:BA000014_GR Gene3D:G3DSA:3.40.309.10 Gene3D:G3DSA:3.40.605.10 SUPFAM:SSF53720 GO:GO:0009793 GO:GO:0006561 Gene3D:G3DSA:3.40.1160.10 SUPFAM:SSF53633 GO:GO:0004349 EMBL:AL161667 eggNOG:COG0014 HOGENOM:HBG318080 KO:K12657 ProtClustDB:PLN02418 GO:GO:0004350 TIGRFAMs:TIGR01092 TIGRFAMs:TIGR00407 TIGRFAMs:TIGR01027 EMBL:X86778 EMBL:Y09355 EMBL:AY091766 IPI:IPI00542239 PIR:T47700 PIR:T50682 RefSeq:NP_191120.2 UniGene:At.25196 ProteinModelPortal:P54888 SMR:P54888 IntAct:P54888 STRING:P54888 PRIDE:P54888 EnsemblPlants:AT3G55610.1 GeneID:824727 KEGG:ath:AT3G55610 TAIR:At3g55610 InParanoid:P54888 OMA:HVDSACV PhylomeDB:P54888 ArrayExpress:P54888 Genevestigator:P54888 GermOnline:AT3G55610 Uniprot:P54888
Leaf	Isotig14402	10	0	4.851	0.000336918	No hit
Leaf	Isotig14609	10	0	4.851	0.000336918	SGD|S000028422 - symbol:TAR1 "Mitochondrial protein potentially involved in respiratory metabolism" species:4932 "Saccharomyces cerevisiae" [GO:0003674 "molecular_function" evidence=ND] [GO:0043457

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						"regulation of cellular respiration" evidence=IGI] [GO:0005739 "mitochondrion" evidence=IEA;IMP] SGD:S000028422 GO:GO:0005739 EMBL:BK006945 EMBL:U53879 GO:GO:0043457 EMBL:Z73326 EMBL:AF479964 RefSeq:NP_690845.1 ProteinModelPortal:Q8TGM6 STRING:Q8TGM6 EnsemblFungi:YLR154W-C GeneID:1466405 KEGG:sce:YLR154W-C CYGD:YLR154w-c eggNOG:NOG79861 OMA:SCSKEHR OrthoDB:EOG466ZX8 NextBio:967146 Genevestigator:Q8TGM6 GermOnline:YLR154W-C Uniprot:Q8TGM6
Leaf	Isotig14726	147	104	1.028	1.59E-08	UNIPROTKB|P16033 - symbol:psbA2 "Photosystem Q(B) protein 2" species:1111708 "Synechocystis sp. PCC 6803 substr. Kazusa" [GO:0030096 "plasma membrane-derived thylakoid photosystem II" evidence=IDA] HAMAP:MF_01379 InterPro:IPR000484 InterPro:IPR005867 Pfam:PF00124 PRINTS:PR00256 PROSITE:PS00244 GO:GO:0016021 GO:GO:0009635 GO:GO:0046872 GO:GO:0006810 GO:GO:0016491 EMBL:BA000022 GenomeReviews:BA000022_GR GO:GO:0042651 GO:GO:0009772 GO:GO:0030096 TCDB:3.E.2.2.2 GO:GO:0045156 EMBL:X56000 EMBL:X13547 PIR:S13112 RefSeq:NP_439906.1 RefSeq:NP_441550.1 ProteinModelPortal:P16033 SMR:P16033 IntAct:P16033 STRING:P16033 GeneID:951890 GeneID:953105 KEGG:syn:sll1867 KEGG:syn:slr1311 PATRIC:23836870 eggNOG:NOG04871 HOGENOM:HBG284766 KO:K02703 OMA:GIWFTSM PhylomeDB:P16033 ProtClustDB:CLSK892431 BioCyc:SSP1148:SLL1867-MONOMER BioCyc:SSP1148:SLR1311-MONOMER GO:GO:0030076 Gene3D:G3DSA:1.20.85.10 SUPFAM:SSF81483 TIGRFAMs:TIGR01151 Uniprot:P16033
Leaf	Isotig14809	11	1	3.988	0.000330755	TAIR|locus:2060604 - symbol:THIC "AT2G29630" species:3702 "Arabidopsis thaliana" [GO:0003824 "catalytic activity" evidence=ISS] [GO:0009228 "thiamine biosynthetic process" evidence=ISS;IMP] [GO:0016045 "detection of bacterium" evidence=IMP] [GO:0009570 "chloroplast stroma" evidence=IDA] [GO:0010266 "response to vitamin B1" evidence=IEP] [GO:0051536 "iron-sulfur cluster binding" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009536 "plastid" evidence=IDA] [GO:0080041 "ADP-ribose pyrophosphohydrolase activity" evidence=IGI] InterPro:IPR002817 Pfam:PF01964 GO:GO:0009570 EMBL:CP002685 GenomeReviews:CT485783_GR GO:GO:0051536 EMBL:AC005496 GO:GO:0009228 GO:GO:0010266 GO:GO:0080041 eggNOG:COG0422 HOGENOM:HBG285234 KO:K03147 TIGRFAMs:TIGR00190 EMBL:AY092989 EMBL:AY128756 IPI:IPI00519515 PIR:F84698 RefSeq:NP_001189634.1 RefSeq:NP_180524.1 RefSeq:NP_850135.1 UniGene:At.24797 ProteinModelPortal:O82392 SMR:O82392 STRING:O82392 PRIDE:O82392 EnsemblPlants:AT2G29630.1 EnsemblPlants:AT2G29630.2 EnsemblPlants:AT2G29630.3 GeneID:817513 KEGG:ath:AT2G29630 TAIR:At2g29630 InParanoid:O82392 OMA:DFLHIIE PhylomeDB:O82392 ProtClustDB:PLN02444 ArrayExpress:O82392 Genevestigator:O82392 Uniprot:O82392
Leaf	Isotig15034	10	1	3.851	0.00071293	TAIR|locus:2097983 - symbol:AT3G62070 "AT3G62070" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0005575 "cellular_component" evidence=ND] [GO:0008150 "biological_process" evidence=ND] EMBL:CP002686 GenomeReviews:BA000014_GR EMBL:AL138651 HOGENOM:HBG318198 EMBL:BT012529 EMBL:BT014831 EMBL:AK228777 IPI:IPI00535692 PIR:T47999 RefSeq:NP_191766.1 UniGene:At.34187 PRIDE:Q9M1R7 EnsemblPlants:AT3G62070.1 GeneID:825380 KEGG:ath:AT3G62070 TAIR:At3g62070 eggNOG:NOG243467 InParanoid:Q9M1R7 OMA:IATWRIS PhylomeDB:Q9M1R7 ProtClustDB:CLSN2684113 Genevestigator:Q9M1R7 Uniprot:Q9M1R7
Leaf	Isotig15127	10	0	4.851	0.000336918	No hit
Leaf	Isotig15363	22	3	3.403	1.63E-06	No hit
Leaf	Isotig15364	9	0	4.699	0.000718283	No hit
Leaf	Isotig15381	84	0	7.921	2.13E-23	ZFIN|ZDB-GENE-090313-207 - symbol:si:dkey-188i13.1 "si:dkey-188i13.1" species:7955 "Danio rerio" [GO:0006351 "transcription, DNA-dependent" evidence=IEA] [GO:0005634 "nucleus" evidence=IEA] [GO:0008270 "zinc ion binding" evidence=IEA] [GO:0046872 "metal ion binding" evidence=IEA] InterPro:IPR001965 InterPro:IPR003618 InterPro:IPR017890 InterPro:IPR019787 Pfam:PF00628 Pfam:PF07500 PROSITE:PS50016 PROSITE:PS51321 SMART:SM00249 SMART:SM00510 InterPro:IPR011011 ZFIN:ZDB-GENE-090313-207 GO:GO:0005634 GO:GO:0008270 GO:GO:0006351 InterPro:IPR013083 Gene3D:G3DSA:3.30.40.10 SUPFAM:SSF57903 InterPro:IPR019786 PROSITE:PS01359 InterPro:IPR012921 Gene3D:G3DSA:1.10.472.30 Pfam:PF07744 SUPFAM:SSF46942 GeneTree:ENSGT00530000063844 EMBL:BX005106 IPI:IPI00486005 UniGene:Dr.75445 Ensembl:ENSDART00000043440 Ensembl:ENSDART00000100352 OMA:HRKDSRD Bgee:B8A483 Uniprot:B8A483
Leaf	Isotig15433	13	2	3.229	0.00031313	TAIR|locus:2092492 - symbol:CYSB "AT3G12490" species:3702 "Arabidopsis thaliana" [GO:0004869 "cysteine-type endopeptidase inhibitor activity" evidence=ISS;IDA] [GO:0009628 "response to abiotic stimulus" evidence=IMP] [GO:0050897 "cobalt ion binding" evidence=IDA] [GO:0005829 "cytosol" evidence=IDA] InterPro:IPR000010

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						Pfam:PF00031 SMART:SM00043 GO:GO:0005829 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005576 GO:GO:0006952 GO:GO:0004869 GO:GO:0050897 EMBL:AP002047 EMBL:AC069474 GO:GO:0009628 InterPro:IPR018073 PROSITE:PS00287 InterPro:IPR020381 ProDom:PD001231 HSSP:P09229 EMBL:AY085950 EMBL:AY065127 EMBL:BT001195 EMBL:AF315737 IPI:IPI00521110 IPI:IPI00657156 RefSeq:NP_566425.1 RefSeq:NP_850570.2 UniGene:At.16910 UniGene:At.48650 ProteinModelPortal:Q8H0X6 SMR:Q8H0X6 STRING:Q8H0X6 PRIDE:Q8H0X6 ProMEX:Q8H0X6 EnsemblPlants:AT3G12490.2 GeneID:820428 KEGG:ath:AT3G12490 TAIR:At3g12490 eggNOG:NOG312503 HOGENOM:HBG317433 InParanoid:Q8H0X6 OMA:FPYELLE PhylomeDB:Q8H0X6 ProtClustDB:CLSN2914970 ArrayExpress:Q8H0X6 Genevestigator:Q8H0X6 Uniprot:Q8H0X6
Leaf	Isotig15555	0	13	-4.171	0.000994782	TAIR|locus:2097228 - symbol:TT5 "AT3G55120" species:3702 "Arabidopsis thaliana" [GO:0005515 "protein binding" evidence=IPI] [GO:0005783 "endoplasmic reticulum" evidence=IDA] [GO:0009705 "plant-type vacuole membrane" evidence=IDA] [GO:0042406 "extrinsic to endoplasmic reticulum membrane" evidence=IDA] [GO:0010224 "response to UV-B" evidence=IMP] [GO:0009813 "flavonoid biosynthetic process" evidence=IMP] [GO:0045430 "chalcone isomerase activity" evidence=IMP] [GO:0005634 "nucleus" evidence=IDA] [GO:0080167 "response to karrikin" evidence=IEP] [GO:0009733 "response to auxin stimulus" evidence=IEP] [GO:0009411 "response to UV" evidence=IMP] InterPro:IPR003466 InterPro:IPR016088 Pfam:PF02431 GO:GO:0005634 EMBL:CP002686 GenomeReviews:BA000014_GR GO:GO:0005515 GO:GO:0009733 GO:GO:0080167 EMBL:AL132970 GO:GO:0009705 GO:GO:0042398 InterPro:IPR016087 SUPFAM:SSF54626 GO:GO:0042406 GO:GO:0009813 GO:GO:0010224 EMBL:M86358 EMBL:AJ287299 EMBL:AJ287300 EMBL:AJ287301 EMBL:AJ287302 EMBL:AJ287303 EMBL:AJ287304 EMBL:AJ287305 EMBL:AJ287306 EMBL:AJ287307 EMBL:AJ287308 EMBL:AJ287309 EMBL:AJ287310 EMBL:AJ287311 EMBL:AJ287312 EMBL:AJ287313 EMBL:AJ287314 EMBL:AJ287315 EMBL:AJ287316 EMBL:AJ287317 EMBL:AJ287318 EMBL:AJ287319 EMBL:AJ287320 EMBL:AJ287321 EMBL:AJ492461 EMBL:AJ492462 EMBL:AJ492463 EMBL:AJ492464 EMBL:AJ492465 EMBL:AJ492466 EMBL:AJ492467 EMBL:AJ492468 EMBL:AJ492469 EMBL:AJ492470 EMBL:AJ492471 EMBL:AJ492472 EMBL:AJ492473 EMBL:AJ492474 EMBL:AJ492475 EMBL:AJ492476 EMBL:AJ492477 EMBL:AJ492478 EMBL:AJ492479 EMBL:AJ492480 EMBL:AJ492481 EMBL:AJ492482 EMBL:AJ492483 EMBL:AJ492484 EMBL:AJ492485 EMBL:AJ492486 EMBL:AJ492487 EMBL:AJ492488 EMBL:AJ492489 EMBL:AJ492490 EMBL:AJ492491 EMBL:AJ492492 EMBL:AJ492493 EMBL:AJ492494 EMBL:AJ492495 EMBL:AJ492496 EMBL:AJ492497 EMBL:AJ492498 EMBL:AJ492499 EMBL:AJ492500 EMBL:AJ492501 EMBL:AJ492502 EMBL:AJ492503 EMBL:AJ418046 EMBL:AF439537 EMBL:BT004265 EMBL:BT005528 EMBL:AY086088 IPI:IPI00534732 PIR:JQ1687 PIR:T47651 RefSeq:NP_191072.1 UniGene:At.27425 ProteinModelPortal:P41088 SMR:P41088 IntAct:P41088 STRING:P41088 PRIDE:P41088 EnsemblPlants:AT3G55120.1 GeneID:824678 KEGG:ath:AT3G55120 TAIR:At3g55120 eggNOG:NOG286273 HOGENOM:HBG318072 InParanoid:P41088 KO:K01859 OMA:KEETFPP PhylomeDB:P41088 ProtClustDB:PLN02559 ArrayExpress:P41088 Genevestigator:P41088 GermOnline:AT3G55120 GO:GO:0045430 Gene3D:G3DSA:3.50.70.10 Uniprot:P41088
Leaf	Isotig15735	478	505	0.450	8.21E-07	No hit
Leaf	Isotig15842	10	69	-2.258	1.07E-08	TAIR|locus:2033915 - symbol:AT1G51400 "AT1G51400" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0030095 "chloroplast photosystem II" evidence=ISS] [GO:0009543 "chloroplast thylakoid lumen" evidence=ISS] [GO:0009611 "response to wounding" evidence=IEP] [GO:0010193 "response to ozone" evidence=IEP] [GO:0010224 "response to UV-B" evidence=IEP] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] EMBL:CP002684 GO:GO:0009611 EMBL:AC024261 GO:GO:0010193 GO:GO:0009535 GO:GO:0010224 EMBL:AC006085 UniGene:At.11631 UniGene:At.66913 UniGene:At.68288 ProtClustDB:PLN00058 EMBL:AF385721 EMBL:AY050320 EMBL:AY133673 IPI:IPI00524381 PIR:B96552 RefSeq:NP_564589.1 STRING:Q9SYE2 PRIDE:Q9SYE2 EnsemblPlants:AT1G51400.1 GeneID:841564 KEGG:ath:AT1G51400 TAIR:At1g51400 InParanoid:Q9SYE2 OMA:MASVTMT PhylomeDB:Q9SYE2 Genevestigator:Q9SYE2 Uniprot:Q9SYE2
Leaf	Isotig15951	17	1	4.616	3.60E-06	No hit
Leaf	Isotig15966	11	1	3.988	0.000330755	TAIR|locus:2153904 - symbol:AT5G24510 species:3702 "Arabidopsis thaliana" [GO:0003735 "structural constituent of ribosome" evidence=IEA;ISS] [GO:0005840 "ribosome" evidence=ISS] [GO:0006414 "translational elongation" evidence=IEA;ISS] [GO:0022626 "cytosolic ribosome" evidence=IDA] InterPro:IPR001813 Pfam:PF00428 EMBL:CP002688 GenomeReviews:BA000015_GR GO:GO:0003735 GO:GO:0022626 EMBL:AB010068

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						GO:GO:0006414 eggNOG:COG2058 HOGENOM:HBG631105 KO:K02942 EMBL:DQ056686 IPI:IPI00530664 RefSeq:NP_197839.1 UniGene:At.54977 ProteinModelPortal:Q9FLV1 SMR:Q9FLV1 STRING:Q9FLV1 EnsemblPlants:AT5G24510.1 GeneID:832522 KEGG:ath:AT5G24510 TAIR:At5g24510 InParanoid:Q9FLV1 OMA:ELACISA PhylomeDB:Q9FLV1 Genevestigator:Q9FLV1 Uniprot:Q9FLV1
Leaf	Isotig15977	13	0	5.229	3.68E-05	TAIR|locus:2089673 - symbol:AT3G18280 species:3702 "Arabidopsis thaliana" [GO:0006869 "lipid transport" evidence=IEA;ISS] [GO:0008289 "lipid binding" evidence=ISS] InterPro:IPR013770 EMBL:CP002686 GenomeReviews:BA000014_GR InterPro:IPR016140 SMART:SM00499 SUPFAM:SSF47699 GO:GO:0006508 GO:GO:0006869 Gene3D:G3DSA:1.10.110.10 GO:GO:0008233 Pfam:PF14368 EMBL:AP000414 HOGENOM:HBG587265 HSSP:Q9FEK9 ProtClustDB:CLSN2684370 EMBL:AY039903 EMBL:AY077680 IPI:IPI00536914 RefSeq:NP_188456.1 UniGene:At.6715 ProteinModelPortal:Q9LJQ3 SMR:Q9LJQ3 IntAct:Q9LJQ3 PRIDE:Q9LJQ3 EnsemblPlants:AT3G18280.1 GeneID:821356 KEGG:ath:AT3G18280 TAIR:At3g18280 eggNOG:NOG292249 InParanoid:Q9LJQ3 OMA:STACCAG PhylomeDB:Q9LJQ3 Genevestigator:Q9LJQ3 Uniprot:Q9LJQ3
Leaf	Isotig16240	0	15	-4.378	0.000342594	No hit
Leaf	Isotig16508	32	16	1.529	0.000324709	No hit
Leaf	Isotig17134	3	26	-2.587	0.000145202	No hit
Leaf	Isotig17176	9	0	4.699	0.000718283	No hit
Leaf	Isotig17522	102	63	1.224	6.04E-08	UNIPROTKB|P16033 - symbol:psbA2 "Photosystem Q(B) protein 2" species:1111708 "Synechocystis sp. PCC 6803 substr. Kazusa" [GO:0030096 "plasma membrane-derived thylakoid photosystem II" evidence=IDA] HAMAP:MF_01379 InterPro:IPR000484 InterPro:IPR005867 Pfam:PF00124 PRINTS:PR00256 PROSITE:PS00244 GO:GO:0016021 GO:GO:0009635 GO:GO:0046872 GO:GO:0006810 GO:GO:0016491 EMBL:BA000022 GenomeReviews:BA000022_GR GO:GO:0042651 GO:GO:0009772 GO:GO:0030096 TCDB:3.E.2.2.2 GO:GO:0045156 EMBL:X56000 EMBL:X13547 PIR:S13112 RefSeq:NP_439906.1 RefSeq:NP_441550.1 ProteinModelPortal:P16033 SMR:P16033 IntAct:P16033 STRING:P16033 GeneID:951890 GeneID:953105 KEGG:syn:sll1867 KEGG:syn:slr1311 PATRIC:23836870 eggNOG:NOG04871 HOGENOM:HBG284766 KO:K02703 OMA:GIWFTSM PhylomeDB:P16033 ProtClustDB:CLSK892431 BioCyc:SSP1148:SLL1867-MONOMER BioCyc:SSP1148:SLR1311-MONOMER GO:GO:0030076 Gene3D:G3DSA:1.20.85.10 SUPFAM:SSF81483 TIGRFAMs:TIGR01151 Uniprot:P16033
Leaf	Isotig17582	242	106	1.720	5.28E-27	ECOCYC|G7323-MONOMER - symbol:YfhM "alpha-macroglobulin" species:511145 "Escherichia coli str. K-12 substr. MG1655" [GO:0010951 "negative regulation of endopeptidase activity" evidence=IEA] [GO:0006952 "defense response" evidence=ISS] [GO:0071575 "integral to external side of plasma membrane" evidence=IDA] [GO:0004866 "endopeptidase inhibitor activity" evidence=IEA;IDA] InterPro:IPR001599 InterPro:IPR002890 Pfam:PF00207 Pfam:PF01835 GO:GO:0005886 EMBL:U00096 EMBL:AP009048 GenomeReviews:AP009048_GR GenomeReviews:U00096_GR PROSITE:PS51257 eggNOG:COG2373 InterPro:IPR011625 InterPro:IPR008930 Pfam:PF07703 SUPFAM:SSF48239 GO:GO:0004866 PIR:G65028 RefSeq:NP_417015.1 ProteinModelPortal:P76578 SMR:P76578 DIP:DIP-28064N IntAct:P76578 MEROPS:I39.008 PRIDE:P76578 EnsemblBacteria:EBESCT00000003837 EnsemblBacteria:EBESCT00000015142 GeneID:947302 KEGG:ecj:JW2504 KEGG:eco:b2520 PATRIC:32120433 EchoBASE:EB3175 EcoGene:EG13394 HOGENOM:HBG536988 KO:K06894 OMA:ALPGFQF PhylomeDB:P76578 ProtClustDB:CLSK880420 BioCyc:EcoCyc:G7323-MONOMER Genevestigator:P76578 InterPro:IPR021868 Pfam:PF11974 Uniprot:P76578
Leaf	Isotig17897	88	72	0.818	0.000306767	No hit
Leaf	Isotig18099	458	404	0.710	3.28E-13	No hit
Leaf	Isotig18275	12	0	5.114	7.63E-05	TAIR|locus:2204207 - symbol:PSAK "AT1G30380" species:3702 "Arabidopsis thaliana" [GO:0003674 "molecular_function" evidence=ND] [GO:0009522 "photosystem I" evidence=ISS] [GO:0015979 "photosynthesis" evidence=IEA;ISS] [GO:0016020 "membrane" evidence=ISS] [GO:0009535 "chloroplast thylakoid membrane" evidence=IDA] [GO:0009507 "chloroplast" evidence=IDA] [GO:0009579 "thylakoid" evidence=IDA] [GO:0009534 "chloroplast thylakoid" evidence=IDA] InterPro:IPR000549 Pfam:PF01241 PROSITE:PS01026 GO:GO:0016021 EMBL:CP002684 GenomeReviews:CT485782_GR EMBL:AC025295 GO:GO:0009535 GO:GO:0015979 GO:GO:0009522 UniGene:At.24759 TCDB:5.B.4.1.1 InterPro:IPR016370 PIRSF:PIRSF002912 EMBL:AJ245866 EMBL:AY039848 EMBL:AY074826 IPI:IPI00525222 PIR:B86428 RefSeq:NP_174327.1 UniGene:At.24377 UniGene:At.67254 ProteinModelPortal:Q9SUI5 SMR:Q9SUI5 STRING:Q9SUI5 PRIDE:Q9SUI5 EnsemblPlants:AT1G30380.1 GeneID:839918 KEGG:ath:AT1G30380 TAIR:At1g30380 eggNOG:NOG238582

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						HOGENOM:HBG600339 InParanoid:Q9SUI5 KO:K02698 OMA:DTLACGA PhylomeDB:Q9SUI5 ProtClustDB:PLN03070 BioCyc:MetaCyc:MONOMER-1091 ArrayExpress:Q9SUI5 Genevestigator:Q9SUI5 GermOnline:AT1G30380 InterPro:IPR017493 TIGRFAMs:TIGR03050 Uniprot:Q9SUI5
Leaf	Isotig18428	229	236	0.486	0.000252082	FB|FBgn0051163 - symbol:SKIP "Shal K[+] channel interacting protein" species:7227 "Drosophila melanogaster" [GO:0005070 "SH3/SH2 adaptor activity" evidence=ISS] InterPro:IPR001452 InterPro:IPR001660 InterPro:IPR011510 Pfam:PF07647 PROSITE:PS50105 SMART:SM00326 SMART:SM00454 EMBL:AE014297 SUPFAM:SSF50044 InterPro:IPR013761 Gene3D:G3DSA:1.10.150.50 SUPFAM:SSF47769 InterPro:IPR011511 Pfam:PF07653 eggNOG:NOG319536 RefSeq:NP_001036742.2 UniGene:Dm.13728 ProteinModelPortal:Q0KI30 SMR:Q0KI30 STRING:Q0KI30 EnsemblMetazoa:FBtr0301028 EnsemblMetazoa:FBtr0305036 GeneID:42601 KEGG:dme:Dmel_CG31163 UCSC:CG31163-RD CTD:42601 FlyBase:FBgn0051163 GeneTree:ENSGT00510000048701 OrthoDB:EOG4GF1W8 PhylomeDB:Q0KI30 Bgee:Q0KI30 Uniprot:Q0KI30
Leaf	Isotig18431	355	372	0.461	1.36E-05	No hit
Leaf	Isotig18542	19	0	5.777	5.37E-07	ECOCYC|EG11815-MONOMER - symbol:TorC "TorC trimethylamine N-oxide reductase, cytochrome c-type subunit" species:511145 "Escherichia coli str. K-12 substr. MG1655" [GO:0022900 "electron transport chain" evidence=IEA] [GO:0046872 "metal ion binding" evidence=IEA] [GO:0005886 "plasma membrane" evidence=IEA] [GO:0009060 "aerobic respiration" evidence=IEP] [GO:0020037 "heme binding" evidence=IEA] [GO:0016021 "integral to membrane" evidence=IEA;IDA] [GO:0009276 "Gram-negative-bacterium-type cell wall" evidence=IEA] [GO:0009055 "electron carrier activity" evidence=IEA;IDA] [GO:0006810 "transport" evidence=IEA] [GO:0005506 "iron ion binding" evidence=IEA;ISS] [GO:0009061 "anaerobic respiration" evidence=IEP] InterPro:IPR009154 PIRSF:PIRSF000014 Pfam:PF03264 GO:GO:0016021 GO:GO:0005886 GO:GO:0009055 EMBL:U00096 EMBL:AP009048 GenomeReviews:AP009048_GR GenomeReviews:U00096_GR GO:GO:0006810 GO:GO:0020037 GO:GO:0022900 GO:GO:0009061 GO:GO:0009060 GO:GO:0009276 InterPro:IPR011031 PROSITE:PS51008 eggNOG:COG3005 InterPro:IPR005126 EMBL:X73888 TCDB:5.A.3.4.1 PIR:B64841 RefSeq:NP_415516.1 ProteinModelPortal:P33226 SMR:P33226 DIP:DIP-11014N IntAct:P33226 MINT:MINT-1285841 EnsemblBacteria:EBESCT00000004387 EnsemblBacteria:EBESCT00000017845 GeneID:946252 KEGG:ecj:JW0981 KEGG:eco:b0996 PATRIC:32117217 EchoBASE:EB1762 EcoGene:EG11815 HOGENOM:HBG303867 KO:K03532 OMA:DAMDHAR PhylomeDB:P33226 ProtClustDB:PRK15032 BioCyc:EcoCyc:EG11815-MONOMER Genevestigator:P33226 TIGRFAMs:TIGR02162 Uniprot:P33226
Leaf	Isotig18554	407	399	0.558	3.10E-08	ECOCYC|G6700-MONOMER - symbol:OmpN "outer membrane pore protein N, non-specific" species:511145 "Escherichia coli str. K-12 substr. MG1655" [GO:0034219 "carbohydrate transmembrane transport" evidence=IDA] [GO:0046930 "pore complex" evidence=IEA] [GO:0005886 "plasma membrane" evidence=IEA] [GO:0016021 "integral to membrane" evidence=IEA] [GO:0016020 "membrane" evidence=IEA;IDA] [GO:0006811 "ion transport" evidence=IEA] [GO:0009279 "cell outer membrane" evidence=IEA] [GO:0015288 "porin activity" evidence=IEA;IDA] InterPro:IPR001702 InterPro:IPR001897 Pfam:PF00267 PRINTS:PR00182 PRINTS:PR00183 GO:GO:0005886 EMBL:U00096 EMBL:AP009048 GenomeReviews:AP009048_GR GenomeReviews:U00096_GR GO:GO:0009279 GO:GO:0006811 GO:GO:0015288 GO:GO:0046930 InterPro:IPR023614 Gene3D:G3DSA:2.40.160.10 eggNOG:COG3203 HOGENOM:HBG673855 PIR:D64888 RefSeq:NP_415895.1 ProteinModelPortal:P77747 SMR:P77747 DIP:DIP-10400N PRIDE:P77747 EnsemblBacteria:EBESCT00000004018 EnsemblBacteria:EBESCT00000014891 GeneID:946313 KEGG:ecj:JW1371 KEGG:eco:b1377 PATRIC:32118038 EchoBASE:EB3157 EcoGene:EG13375 KO:K14062 OMA:SDSTIAN PhylomeDB:P77747 ProtClustDB:CLSK891744 BioCyc:EcoCyc:G6700-MONOMER Genevestigator:P77747 Uniprot:P77747
Leaf	Isotig18773	9	0	4.699	0.000718283	No hit
Leaf	Isotig18825	10	0	4.851	0.000336918	ECOCYC|G6868-MONOMER - symbol:YdgJ "YdgJ" species:511145 "Escherichia coli str. K-12 substr. MG1655" [GO:0000166 "nucleotide binding" evidence=IEA] [GO:0008152 "metabolic process" evidence=IEA] [GO:0055114 "oxidation-reduction process" evidence=IEA] [GO:0016491 "oxidoreductase activity" evidence=IEA] InterPro:IPR000683 InterPro:IPR004104 InterPro:IPR016040 Pfam:PF01408 Pfam:PF02894 GO:GO:0000166 Gene3D:G3DSA:3.40.50.720 EMBL:U00096 EMBL:AP009048 GenomeReviews:AP009048_GR GenomeReviews:U00096_GR GO:GO:0016491 eggNOG:COG0673 HOGENOM:HBG322267 PIR:B64919 RefSeq:NP_416141.4 ProteinModelPortal:P77376 SMR:P77376 DIP:DIP-11718N IntAct:P77376 EnsemblBacteria:EBESCT00000002387 EnsemblBacteria:EBESCT00000018126 GeneID:947164 KEGG:ecj:JW5265 KEGG:eco:b1624 PATRIC:32118550 EchoBASE:EB3690 EcoGene:EG13931 OMA:ATDYFHA

Tissue	Identification	# of reads (stress)	# of reads (control)	Fold Change	p-value	Description
						PhylomeDB:P77376 ProtClustDB:PRK11579 BioCyc:EcoCyc:G6868-MONOMER Genevestigator:P77376 Uniprot:P77376
Leaf	Isotig18848	9	0	4.699	0.000718283	ECOCYC|L-GLN-FRUCT-6-P-AMINOTRANS-MONOMER - symbol:GlmS "GlmS" species:511145 "Escherichia coli str. K-12 substr. MG1655" [GO:0005829 "cytosol" evidence=IDA] [GO:0006541 "glutamine metabolic process" evidence=IEA] [GO:0004360 "glutamine-fructose-6-phosphate transaminase (isomerizing) activity" evidence=IEA;IDA] [GO:0006048 "UDP-N-acetylglucosamine biosynthetic process" evidence=IMP] InterPro:IPR000583 InterPro:IPR001347 InterPro:IPR005855 Pfam:PF00310 Pfam:PF01380 PROSITE:PS51464 GO:GO:0005829 EMBL:U00096 EMBL:AP009048 GenomeReviews:AP009048_GR GenomeReviews:U00096_GR GO:GO:0005529 EMBL:L10328 GO:GO:0006048 GO:GO:0006541 InterPro:IPR017932 PROSITE:PS51278 EMBL:X01631 eggNOG:COG0449 KO:K00820 GO:GO:0004360 HOGENOM:HBG645312 OMA:YWFEALA TIGRFAMs:TIGR01135 ProtClustDB:PRK00331 HAMAP:MF_00164 EMBL:V00620 EMBL:M18980 PIR:B65176 RefSeq:NP_418185.1 PDB:1JXA PDB:1MOQ PDB:1MOR PDB:1MOS PDB:1XFF PDB:1XFG PDB:2BPL PDB:2J6H PDB:2VF4 PDB:2VF5 PDB:3OOJ PDBsum:1JXA PDBsum:1MOQ PDBsum:1MOR PDBsum:1MOS PDBsum:1XFF PDBsum:1XFG PDBsum:2BPL PDBsum:2J6H PDBsum:2VF4 PDBsum:2VF5 PDBsum:3OOJ ProteinModelPortal:P17169 SMR:P17169 DIP:DIP-9775N IntAct:P17169 MINT:MINT-1238536 PRIDE:P17169 EnsemblBacteria:EBESCT00000001451 EnsemblBacteria:EBESCT00000001452 EnsemblBacteria:EBESCT00000015274 GeneID:948241 KEGG:ecj:JW3707 KEGG:eco:b3729 PATRIC:32122955 EchoBASE:EB0377 EcoGene:EG10382 PhylomeDB:P17169 BioCyc:EcoCyc:L-GLN-FRUCT-6-P-AMINOTRANS-MONOMER BioCyc:MetaCyc:L-GLN-FRUCT-6-P-AMINOTRANS-MONOMER Genevestigator:P17169 Uniprot:P17169
Leaf	Isotig18877	77	302	-1.443	1.28E-18	ECOCYC|G7345-MONOMER - symbol:GlrK "GlrK sensory histidine kinase" species:511145 "Escherichia coli str. K-12 substr. MG1655" [GO:0005887 "integral to plasma membrane" evidence=RCA] [GO:0000166 "nucleotide binding" evidence=IEA] [GO:0046777 "protein autophosphorylation" evidence=IDA] [GO:0005886 "plasma membrane" evidence=IEA] [GO:0018106 "peptidyl-histidine phosphorylation" evidence=IEA] [GO:0016021 "integral to membrane" evidence=IEA] [GO:0016020 "membrane" evidence=IEA] [GO:0005524 "ATP binding" evidence=IEA] [GO:0000160 "two-component signal transduction system (phosphorelay)" evidence=IEA;IMP;IDA] [GO:0000155 "two-component sensor activity" evidence=IEA;IDA] InterPro:IPR003594 InterPro:IPR003660 InterPro:IPR003661 InterPro:IPR004358 InterPro:IPR005467 InterPro:IPR009082 Pfam:PF00512 Pfam:PF00672 Pfam:PF02518 PRINTS:PR00344 PROSITE:PS50109 SMART:SM00387 SMART:SM00388 GO:GO:0016021 GO:GO:0005886 GO:GO:0005524 EMBL:U00096 EMBL:AP009048 GenomeReviews:AP009048_GR GenomeReviews:U00096_GR EMBL:U36841 GO:GO:0000155 GO:GO:0018106 Gene3D:G3DSA:3.30.565.10 SUPFAM:SSF55874 SUPFAM:SSF47384 eggNOG:COG0642 PIR:C65033 RefSeq:NP_417051.2 ProteinModelPortal:P52101 SMR:P52101 DIP:DIP-12052N EnsemblBacteria:EBESCT00000003452 EnsemblBacteria:EBESCT00000017530 GeneID:947013 KEGG:ecj:JW5407 KEGG:eco:b2556 PATRIC:32120511 EchoBASE:EB3234 EcoGene:EG13461 HOGENOM:HBG544172 KO:K07711 OMA:INFSHET PhylomeDB:P52101 ProtClustDB:CLSK880434 BioCyc:EcoCyc:G7345-MONOMER Genevestigator:P52101 Uniprot:P52101
Leaf	Isotig19185	0	16	-4.471	0.000202082	No hit
Leaf	Isotig19280	10	0	4.851	0.000336918	No hit
Leaf	Isotig19351	39	0	6.814	1.47E-12	No hit