

			Misregulated genes in <i>VP16:GPL2</i> plants						
Name	CATMA R factor	Name/Function	Description	Biological process	Molecular function	Cellular component			
AT1G02000	0.78	GAE2 (UDP-D-GLUCURONATE 4-EPIMERASE 2); NAD binding / catalytic	UDP-D-glucuronate 4-epimerase	(GO:0009225) nucleotide-sugar metabolic process [ISS]	(GO:0050378) UDP-glucuronate 4-epimerase activity [ISS]	(GO:0003824) catalytic activity [ISS]	(GO:0005575) cellular_component [ND]		
AT1G03850	0.97	electron transporter/ thiol-disulfide exchange intermediate	Identical to Monothiol glutaredoxin-S13 (GRXS13) [Arabidopsis thaliana] (GB:Q84TF4;GB:Q94CA3;GB:Q9ZWA7); similar to GRX480, thiol-disulfide exchange intermediate [Arabidopsis thaliana] (TAIR:AT1G28480.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO62683.1); contains InterPro domain Thioredoxin-like fold (InterPro:IPR012336); contains InterPro domain Thioredoxin fold (InterPro:IPR012335); contains InterPro domain Glutaredoxin; (InterPro:IPR002109); contains InterPro domain Glutaredoxin-like, plant II (InterPro:IPR011905)	(GO:0009735) response to cytokinin stimulus [IEP]	No annotation for molecular_function	No annotation for cellular_component			
AT1G03880	1.32	CRU2 (CRUCIFERIN 2); nutrient reservoir	Identical to 12S seed storage protein CRB precursor [Contains: 12S seed storage protein CRB alpha chain (CRB) [Arabidopsis thaliana] (GB:P15456;GB:Q9SAW0); similar to CRA1 (CRUCIFERINA), nutrient reservoir [Arabidopsis thaliana] (TAIR:AT5G44120.3); similar to cruciferin cru4 subunit [Brassica napus] (GB:CAA40980.1); similar to Cruciferin CRU4 precursor (11S globulin) (12S storage protein) [Contains: Cruciferin CRU4 alpha chain; Cruciferin CRU4 beta chain] (GB:P33522); contains InterPro domain RmlC-like jelly roll fold (InterPro:IPR014710); contains InterPro domain Cupin 1; (InterPro:IPR006045); contains InterPro domain Cupin, RmlC-type (InterPro:IPR011051); contains InterPro domain 11-S plant seed storage protein; (InterPro:IPR006044)	(GO:0009845) seed germination [TAS]	(GO:0045735) nutrient reservoir activity [ISS]	(GO:0012505) endomembrane system [IEA]			
AT1G05540	1.27	unknown protein	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G30160.2); contains InterPro domain Protein of unknown function DUF295 (InterPro:IPR006574)	(GO:0008150) biological_processes [ND]	(GO:0003674) molecular_function [ND]	(GO:0005739) mitochondrion [IEA]			
AT1G05710	1.08	transcription factor	[Arabidopsis thaliana] (TAIR:AT2G31730.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN65949.1); contains InterPro domain Basic helix-loop-helix dimerisation region bHLH; (InterPro:IPR001092); contains InterPro domain Helix-loop-helix DNA-binding; (InterPro:IPR011598)	(GO:0009723) response to ethylene stimulus [ISS]	(GO:0003700) transcription factor activity [ISS]	(GO:0005634) nucleus [IEA]			
AT1G07240	0.79	UDP-glycosyltransferase/ transferase, transferring glycosyl groups	similar to UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis thaliana] (TAIR:AT1G07250.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN76057.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO21482.1); contains InterPro domain UDP-glucuronosyl/UDP-glucosyltransferase; (InterPro:IPR002213)	(GO:0008152) metabolic process [IEA]	(GO:0008194) UDP-glycosyltransferase activity [ISS]	(GO:0016757) transferase activity, transferring glycosyl groups [ISS]	(GO:0005575) cellular_component [ND]		

AT1G07400	1.00	unknown protein	similar to 17.6 kDa class I heat shock protein (HSP17.6A-CI) [Arabidopsis thaliana] (TAIR:AT1G59860.1); similar to 17.5 kDa class I heat shock protein [Carica papaya] (GB:AAR25848.1); contains InterPro domain HSP20-like chaperone (InterPro:IPR008978); contains InterPro domain Heat shock protein Hsp20 (InterPro:IPR002068)	(GO:0006979) response to oxidative stress [IEP]	(GO:0009408) response to heat [ISS]	No annotation for molecular_function	No annotation for cellular_component		
AT1G08940	0.92	catalytic	similar to phosphoglycerate/bisphosphoglycerate mutase family protein [Arabidopsis thaliana] (TAIR:AT3G05170.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO68574.1); contains InterPro domain Phosphoglycerate mutase (InterPro:IPR013078)	(GO:0008152) metabolic process [ISS]	(GO:0003824) catalytic activity [ISS]	(GO:0005575) cellular_component [ND]			
AT1G09970	1.03	ATP binding / kinase/ protein serine/threonine kinase	protein kinase [Arabidopsis thaliana] (TAIR:AT3G19700.1); similar to leucine-rich repeat transmembrane protein kinase, putative [Arabidopsis thaliana] (TAIR:AT5G49660.1); similar to HSL1 (HAESA-LIKE 1), ATP binding / kinase/ protein serine/threonine kinase [Arabidopsis thaliana] (TAIR:AT1G28440.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO61543.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO49802.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN65551.1); contains InterPro domain Protein kinase, core; (InterPro:IPR000719); contains InterPro domain Protein kinase-like (InterPro:IPR011009); contains InterPro domain Serine/threonine protein kinase, active site; (InterPro:IPR008271); contains InterPro domain Leucine-rich repeat, N-terminal (InterPro:IPR013210); contains InterPro domain Leucine-rich repeat; (InterPro:IPR001611)	(GO:0007169) transmembrane receptor protein tyrosine kinase signaling pathway [ISS]	(GO:0006468) protein amino acid phosphorylation [ISS]	(GO:0004674) protein serine/threonine kinase activity [ISS]	(GO:0005524) ATP binding [ISS]	(GO:0016301) kinase activity [ISS]	(GO:0005886) plasma membrane [IDA]
AT1G10070	1.04	branched-chain-amino-acid transaminase/ catalytic unknown protein	Encodes a chloroplast branched-chain amino acid aminotransferase. Complements the yeast leu/iso-leu/val auxotrophy mutant.	(GO:0008152) metabolic process [IEA]	(GO:0009081) branched chain family amino acid metabolic process [IEA]	(GO:0004084) branched-chain-amino-acid transaminase activity [IGI]	(GO:0003824) catalytic activity [ISS]	(GO:0009507) chloroplast [IDA]	
AT1G12010	0.65	unknown protein	encodes a protein whose sequence is similar to 1-amino-cyclopropane-1-carboxylic acid oxidase	(GO:0008150) biological_processes [ND]	(GO:0009815) 1-aminocyclopropane-1-carboxylate oxidase activity [ISS]	(GO:0005575) cellular_component [ND]			
AT1G12800	-1.19	RNA binding	similar to S1 RNA-binding domain-containing protein [Arabidopsis thaliana] (TAIR:AT3G23700.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN68047.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO63706.1); contains InterPro domain S1, RNA binding; (InterPro:IPR003029); contains InterPro domain Nucleic acid-binding, OB-fold (InterPro:IPR012340); contains InterPro domain Nucleic acid-binding, OB-fold-like (InterPro:IPR016602)	No annotation for biological_processes	(GO:0003723) RNA binding [ISS]	(GO:0009507) chloroplast [IDA]			
AT1G13330	1.56	unknown protein unknown protein	(GB:CAO42122.1); contains InterPro domain Tat binding protein 1-interacting (InterPro:IPR010776)	(GO:0008150) biological_processes [ND]	(GO:0003674) molecular_function [ND]	(GO:0005575) cellular_component [ND]			

AT1G13650	-1,46	unknown protein	similar to 18S pre-ribosomal assembly protein gar2-related [Arabidopsis thaliana] (TAIR:AT2G03810.4); similar to 18S pre-ribosomal assembly protein gar2-related [Arabidopsis thaliana] (TAIR:AT2G03810.2); similar to 18S pre-ribosomal assembly protein gar2-related [Arabidopsis thaliana] (TAIR:AT2G03810.3); similar to hypothetical protein Tc00.1047053503999.40 [Trypanosoma cruzi strain CL Brener] (GB:XP_813437.1)	(GO:0008150) biological_processes [ND]	(GO:0003674) molecular_function [ND]	(GO:0005575) cellular_component [ND]			
AT1G14880	1,10	unknown protein	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G14870.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO42338.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO42335.1); contains InterPro domain Protein of unknown function Cys-rich (InterPro:IPR006461)	(GO:0008150) biological_processes [ND]	(GO:0003674) molecular_function [ND]	(GO:0005773) vacuole [IDA]			
AT1G15030	1,23	unknown protein unknown protein	Encodes a Cysteine-rich peptide (CRP) family protein	(GO:0008150) biological_processes [ND]	(GO:0003674) molecular_function [ND]	(GO:0005575) cellular_component [ND]			
AT1G15380	1,42	lactoylglutathione lyase	protein / glyoxalase I family protein [Arabidopsis thaliana] (TAIR:AT1G80160.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO62772.1); contains InterPro domain Glyoxalase/bleomycin resistance protein/dioxygenase (InterPro:IPR004360); contains InterPro domain Glyoxalase/extradiol ring-cleavage dioxygenase (InterPro:IPR011588)	(GO:0005975) carbohydrate_metabolic_process [ISS]	(GO:0004462) lactoylglutathione lyase activity [ISS]	(GO:0005575) cellular_component [ND]			
AT1G19530	1,11	unknown protein	similar to unnamed protein product [Vitis vinifera] (GB:CAO61141.1)	No annotation for biological_processes	(GO:0003674) molecular_function [ND]	(GO:0005575) cellular_component [ND]			
AT1G19610	1,54	LCR78/PDF1.4	rich protein LCR78 precursor (LCR78) [Arabidopsis Thaliana] (GB:P82787;GB:Q8VZQ7;GB:Q9FWR6); similar to LCR67/PDF1.1 (Low-molecular-weight cysteine-rich 67) [Arabidopsis thaliana] (TAIR:AT1G75830.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN64556.1); contains InterPro domain Gamma thionin; (InterPro:IPR008176); contains InterPro domain Knottin; (InterPro:IPR003614)	(GO:0006952) defense_response [ISS]	(GO:0003674) molecular_function [ND]	(GO:0012505) endomembrane_system [IEA]			
AT1G19640	0,73	JMT (JASMONIC ACID CARBOXYLMETHYLTRANSFERASE); jasmonate O-methyltransferase	Encodes a S-adenosyl-L-methionine:jasmonic acid carboxyl methyltransferase that catalyzes the formation of methyljasmonate from jasmonic acid. Its expression is induced in response to wounding or methyljasmonate treatment.	(GO:0009611) response_to_wounding [IEP]	(GO:0009867) jasmonic acid mediated signaling pathway [IMP]	(GO:0009695) jasmonic acid biosynthetic process [IDA]	(GO:0009694) jasmonic acid metabolic process [IDA]	(GO:0030795) jasmonate O-methyltransferase activity [IMP]	(GO:0005737) cytoplasm [NAS]
AT1G20800	-1,09	unknown protein	Pseudogene of F-box family protein	(GO:0008150) biological_processes [ND]	(GO:0003674) molecular_function [ND]	(GO:0005575) cellular_component [ND]			
AT1G20900	0,61	ESC (ESCAROLA)	ESCAROLA (ESC)	(GO:0010150) leaf senescence [IMP]	(GO:0006325) establishment or maintenance of chromatin architecture [IMP]	(GO:0009640) photomorphogenesis [IMP]	(GO:0003674) molecular_function [ISS]	(GO:0003690) double-stranded DNA binding [IDA]	(GO:0005634) nucleus [IDA]

AT1G21500	-0.67	unknown protein	similar to hypothetical protein OsI_030994 [Oryza sativa (indica cultivar-group)] (GB:EAZ09762.1); similar to Os09g0517000 [Oryza sativa (japonica cultivar-group)] (GB:NP_001063677.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:BAD33829.1)	No annotation for biological_processes	No annotation for molecular_function	(GO:0005943) 1-phosphatidylinositol-4-phosphate 3-kinase, class IA complex [ISS]			
AT1G21520	0.93	unknown protein	No description	(GO:0006979) response to oxidative stress [IMP]	(GO:0003674) molecular_function [ND]	(GO:0005783) endoplasmic reticulum [IMP]			
AT1G21540	1.65	catalytic	similar to AMP-binding protein, putative [Arabidopsis thaliana] (TAIR:AT1G21530.1); similar to AMP-binding protein, putative [Arabidopsis thaliana] (TAIR:AT1G21530.2); similar to AMP-binding protein, putative [Arabidopsis thaliana] (TAIR:AT1G77240.1); similar to amp-binding protein [Brassica napus] (GB:CAA64328.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO22162.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN64147.1); contains InterPro domain AMP-dependent synthetase and ligase; (InterPro:IPR000873)	(GO:0008152) metabolic process [IEA]	(GO:0003824) catalytic activity [IEA]	No annotation for cellular_component			
AT1G21670	0.92	unknown protein	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G21680.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN73514.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO61906.1); contains InterPro domain WD40-like Beta Propeller (InterPro:IPR011659); contains InterPro domain Six-bladed beta-propeller, TolB-like (InterPro:IPR011042)	No annotation for biological_processes	No annotation for molecular_function	(GO:0009505) plant-type cell wall [IDA]	(GO:0005618) cell wall [IDA]		
AT1G26560	-0.63	hydrolase, hydrolyzing O-glycosyl compounds	similar to glycosyl hydrolase family 1 protein [Arabidopsis thaliana] (TAIR:AT5G54570.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO41891.1); similar to hypothetical protein OsI_010256 [Oryza sativa (indica cultivar-group)] (GB:EAY89023.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO41892.1); contains InterPro domain Glycoside hydrolase, catalytic core; (InterPro:IPR013781); contains InterPro domain Glycoside hydrolase, family 1; (InterPro:IPR001360)	(GO:0005975) carbohydrate metabolic process [IEA]	(GO:0004553) hydrolase activity, hydrolyzing O-glycosyl compounds [ISS]	(GO:0048046) apoplast [IDA]	(GO:0009507) chloroplast [IDA]		
AT1G26760	-0.74	unknown protein	similar to ASHR2 (ASH1-RELATED PROTEIN 2) [Arabidopsis thaliana] (TAIR:AT2G19640.2); similar to ASHR2 (ASH1-RELATED PROTEIN 2) [Arabidopsis thaliana] (TAIR:AT2G19640.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO69710.1); contains InterPro domain Tetratricopeptide-like helical; (InterPro:IPR011990); contains InterPro domain Tetratricopeptide TPR-1 (InterPro:IPR001440); contains InterPro domain Tetratricopeptide region (InterPro:IPR013026); contains InterPro domain SET; (InterPro:IPR001214)	(GO:0008150) biological_processes [ND]	(GO:0005488) binding [IEA]	(GO:0005634) nucleus [IEA]			
AT1G27670	1.39	unknown protein	No description	(GO:0008150) biological_processes [ND]	(GO:0003674) molecular_function [ND]	(GO:0005575) cellular_component [ND]			

AT1G28580	1.19	carboxylic ester hydrolase/ hydrolase, acting on ester bonds / lipase	similar to GDSL-motif lipase, putative [Arabidopsis thaliana] (TAIR:AT1G28570.1); similar to lipase 1 [Brassica napus] (GB:AAx59709.1); contains InterPro domain Lipase_GDSL (InterPro:IPR001087)	(GO:0006629) lipid metabolic process [IEA]	(GO:0004091) carboxylesterase activity [ISS]	(GO:0016298) lipase activity [ISS]	(GO:0005773) vacuole [IDA]		
AT1G28590	0.87	carboxylic ester hydrolase/ hydrolase, acting on ester bonds	(TAIR:AT2G27360.1); similar to lipase 1 [Brassica napus] (GB:AAx59709.1); contains InterPro domain Lipase, GDSL; (InterPro:IPR001087)	(GO:0006629) lipid metabolic process [IEA]	(GO:0004091) carboxylesterase activity [ISS]	(GO:0012505) endomembrane system [IEA]			
AT1G28680	0.57	transferase	similar to transferase family protein [Arabidopsis thaliana] (TAIR:AT5G07080.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO66345.1); contains InterPro domain Transferase (InterPro:IPR003480)	(GO:0008150) biological_processes [ND]	(GO:0016740) transferase activity [ISS]	(GO:0005575) cellular_component [ND]			
AT1G29050	0.92	unknown protein	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G34070.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO48076.1); contains InterPro domain Protein of unknown function DUF231, plant (InterPro:IPR004253)	(GO:0008150) biological_processes [ND]	No annotation for molecular_function [IEA]	(GO:0012505) endomembrane system [IEA]			
AT1G29660	-0.71	carboxylic ester hydrolase/ hydrolase, acting on ester bonds	similar to GDSL-motif lipase/hydrolase family protein [Arabidopsis thaliana] (TAIR:AT1G29670.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO70243.1); contains InterPro domain Lipase, GDSL; (InterPro:IPR001087)	(GO:0006629) lipid metabolic process [IEA]	(GO:0004091) carboxylesterase activity [ISS]	(GO:0048046) apoplast [IDA]	(GO:0005634) nucleus [IDA]		
AT1G32790	0.61	CID11; RNA binding	RNA-binding protein, putative, similar to RNA-binding protein GB:CAB40027 G1:4539439 from (Arabidopsis thaliana). Member of a family of PAB2 binding domain proteins.	(GO:0008150) biological_processes [ND]	(GO:0003723) RNA binding [ISS]	(GO:0005515) protein binding [TAS]	No annotation for cellular_component		
AT1G33560	0.71	ADR1 (ACTIVATED DISEASE RESISTANCE 1)	Encodes a NBS-LRR disease resistance protein that possesses N-terminal kinase subdomains. Activation tagged mutant of ADR1 showed elevated levels of SA and reactive oxygen species in addition to number of defense gene transcripts. Exhibits resistance to number of microbial pathogens.	(GO:0009414) response to water deprivation [IMP]	(GO:0006952) defense response [ISS]	(GO:0051707) response to other organism [IEP]	(GO:0016301) kinase activity [TAS]	(GO:0012505) endomembrane system [IEA]	
AT1G33700	1.49	unknown protein	similar to catalytic [Arabidopsis thaliana] (TAIR:AT5G49900.1); similar to catalytic [Arabidopsis thaliana] (TAIR:AT4G10060.1); similar to catalytic [Arabidopsis thaliana] (TAIR:AT3G24180.2); similar to unnamed protein product [Vitis vinifera] (GB:CAO16273.1); similar to hypothetical protein OsI_034437 [Oryza sativa (indica cultivar-group)] (GB:EAY80478.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO46877.1); contains InterPro domain Six-hairpin glycosidase-like; (InterPro:IPR008928); contains InterPro domain Beta-glucosidase, GBA2 type (InterPro:IPR014551); contains InterPro domain Protein of unknown function DUF608 (InterPro:IPR006775)	(GO:0008150) biological_processes [ND]	(GO:0003824) catalytic activity [IEA]	(GO:0005773) vacuole [IDA]			
AT1G34080	2.40	unknown protein	transposable element gene; gypsy-like retrotransposon family, has a 4.0e-88 P-value blast match to GB:AAD19359 polyprotein (gypsy_Ty3-element) (Sorghum bicolor)						

AT1G34090	0,74	unknown protein	transposable element gene; copia-like retrotransposon family, has a 8.8e-131 P-value blast match to GB:BAA78423 polyprotein (Ty1_Copia-element) (Arabidopsis thaliana)GB:BAA78423 polyprotein (Ty1_Copia-element) (Arabidopsis thaliana)GB:BAA78423 polyprotein (Ty1_Copia-element) (Arabidopsis thaliana)gij4996361 dbjBAA78423.1 polyprotein (Arabidopsis thaliana) (Ty1_Copia-element)						
AT1G36060	0,74	DNA binding / transcription factor	encodes a member of the DREB subfamily A-6 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 8 members in this subfamily including RAP2.4.	(GO:0006355) regulation of transcription, DNA-dependent [ISS]	(GO:0003677) DNA binding [TAS]	(GO:0003700) transcription factor activity [ISS]	(GO:0005634) nucleus [IC]		
AT1G49900	0,62	nucleic acid binding / transcription factor/ zinc ion binding	similar to AZF2 (ARABIDOPSIS ZINC-FINGER PROTEIN 2) [Arabidopsis thaliana] (TAIR:AT3G19580.2); similar to AZF2 (ARABIDOPSIS ZINC-FINGER PROTEIN 2), nucleic acid binding / transcription factor/ zinc ion binding [Arabidopsis thaliana] (TAIR:AT3G19580.1); similar to C2H2 zinc finger protein 1 [Thellungiella halophila] (GB:ABI74621.1); contains InterPro domain Zinc finger, C2H2-like; (InterPro:IPR015880); contains InterPro domain Zinc finger, C2H2-type; (InterPro:IPR007087)	No annotation for biological_processes	(GO:0008270) zinc ion binding [ISS]	(GO:0003700) transcription factor activity [ISS]	(GO:0003676) nucleic acid binding [ISS]	(GO:0005622) intracellular [IEA]	
AT1G51500	-0,81	CER5 (ECERIFERUM 5); ATPase, coupled to transmembrane movement of substances	Encodes an ABC transporter involved in cuticular wax biosynthesis. Lines carrying recessive mutations in this locus have weakly glaucous stem surface, and relative elevated secondary alcohols and ketones.	(GO:0010025) wax biosynthetic process [IMP]	(GO:0042626) ATPase activity, coupled to transmembrane movement of substances [ISS]	No annotation for cellular_component			
AT1G52000	-0,89	unknown protein	similar to MBP1 (MYROSINASE-BINDING PROTEIN 1) [Arabidopsis thaliana] (TAIR:AT1G52040.1); similar to myrosinase binding protein [Brassica napus] (GB:CAA70587.1); contains InterPro domain Mannose-binding lectin (InterPro:IPR001229); contains InterPro domain Protein of unknown function GLTT (InterPro:IPR008165)	No annotation for biological_processes	(GO:0003674) molecular_function [ND]	(GO:0005575) cellular_component [ND]			
AT1G52340	-0,60	ABA2 (ABA DEFICIENT 2); oxidoreductase	Encodes a cytosolic short-chain dehydrogenase/reductase involved in the conversion of xanthoxin to ABA-aldehyde during ABA biosynthesis. Mutants are insensitive to sucrose and glucose.	(GO:0006561) proline biosynthetic process [IMP]	(GO:0009414) response to water deprivation [IMP]	(GO:0010115) regulation of abscisic acid biosynthetic process [IMP]	(GO:0009408) response to heat [IMP]	(GO:0009688) abscisic acid biosynthetic process [IMP]	(GO:0010182) sugar mediated signaling [TAS]
AT1G53645	0,68	unknown protein	hydroxyproline-rich glycoprotein family protein; similar to unnamed protein product [Vitis vinifera] (GB:CAO16819.1); contains InterPro domain HMG-I and HMG-Y, DNA-binding (InterPro:IPR000637)						
AT1G55120	0,68	ATFRUCT5 (BETA-FRUCTOFURANOSIDASE 5); hydrolase, hydrolyzing O-glycosyl compounds	Encodes a protein with fructan exohydrolase (FEH) activity acting on levan-type fructans (6-FEH, levanase). The enzyme does not have invertase activity.	(GO:0005975) carbohydrate metabolic process [IEA]	(GO:0004553) hydrolase activity, hydrolyzing O-glycosyl compounds [ISS]	(GO:0031219) levanase activity [IDA]	(GO:0005773) vacuole [IDA]		
AT1G56660	0,83	unknown protein	No description	(GO:0008150) biological_processes [ND]	(GO:0003674) molecular_function [ND]	(GO:0005575) cellular_component [ND]			

AT1G56680	0,79	chitin binding / chitinase	similar to glycoside hydrolase family 19 protein [Arabidopsis thaliana] (TAIR:AT2G43600.1); similar to chitinase [Brassica rapa subsp. pekinensis] (GB:BAF35569.1); contains InterPro domain Endochitinase (InterPro:IPR016283); contains InterPro domain Glycoside hydrolase, family 19, catalytic; (InterPro:IPR000726); contains InterPro domain Chitin-binding, type 1; (InterPro:IPR001002)	(GO:0016998) cell wall catabolic process [IEA]	(GO:0004568) chitinase activity [ISS]	(GO:0012505) endomembrane system [IEA]			
AT1G58270	-0,79	ZW9	ZW9 mRNA, complete cds	(GO:0008150) biological_processes [ND]	(GO:0003674) molecular_function [ND]	(GO:0012505) endomembrane system [IEA]			
AT1G58340	2,29	ZF14; antiporter/ drug transporter/ transporter	similar to MATE efflux protein-related [Arabidopsis thaliana] (TAIR:AT4G23030.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN77415.1); contains InterPro domain Multi antimicrobial extrusion protein MatE; (InterPro:IPR002528)	(GO:0009624) response to nematode [IEP]	(GO:0005215) transporter activity [ISS]	(GO:0016020) membrane [ISS]			
AT1G60950	-1,04	FED A; electron transporter/ iron ion binding IRT3; cation transporter/ metal ion transporter	encodes a ferredoxin gene	(GO:0009767) photosynthetic electron transport chain [TAS]	(GO:0009416) response to light stimulus [IEP]	(GO:0009055) electron carrier activity [IEA]	(GO:0051537) 2 iron, 2 sulfur cluster binding [IEA]	(GO:0051536) iron-sulfur cluster binding [IEA]	(GO:0009570) chloroplast stroma [TAS]
AT1G62420	1,74	unknown protein	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G12030.1); similar to Protein of unknown function DUF506, plant [Medicago truncatula] (GB:ABN05810.1); contains InterPro domain Protein of unknown function DUF506, plant (InterPro:IPR006502)	(GO:0008150) biological_processes [ND]	No annotation for molecular_function	(GO:0005575) cellular_component [ND]			
AT1G62810	0,77	copper ion binding	[Arabidopsis thaliana] (TAIR:AT3G43670.1); similar to copper amine oxidase, putative [Arabidopsis thaliana] (TAIR:AT4G12290.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO70301.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO16983.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO63652.1); contains InterPro domain Copper amine oxidase, N3-terminal; (InterPro:IPR015802); contains InterPro domain Copper amine oxidase, C-terminal; (InterPro:IPR015798); contains InterPro domain Copper amine oxidase, N2/N3-terminal; (InterPro:IPR015801); contains InterPro domain Copper amine oxidase, N-terminal region; (InterPro:IPR016182); contains InterPro domain Copper amine oxidase, N2-terminal; (InterPro:IPR015800); contains InterPro domain Copper amine oxidase; (InterPro:IPR000269)	(GO:0009308) cellular amine metabolic process [IEA]	(GO:0005507) copper ion binding [ISS]	(GO:0012505) endomembrane system [IEA]			
AT1G62870	-0,63	unknown protein	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G12380.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO49735.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN79336.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO16969.1)	No annotation for biological_processes	No annotation for molecular_function	(GO:0005575) cellular_component [ND]			

			similar to pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] (TAIR:AT1G63080.1); similar to pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] (TAIR:AT1G62670.1); similar to pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] (TAIR:AT1G63130.1); similar to hypothetical protein [Brassica rapa] (GB:ABQ50546.1); contains InterPro domain Pentatricopeptide repeat (InterPro:IPR002885)	(GO:0008150) biological_processes [ND]	No annotation for molecular_function	No annotation for cellular_component			
AT1G63070	-0.62	unknown protein							
AT1G64660	0.96	catalytic	Encodes a functional methionine gamma-lyase, a cytosolic enzyme catalyzes the degradation of methionine into methanethiol, alpha-ketobutyrate and ammonia. The catabolism of excess methionine is important to methionine homeostasis.	(GO:0006520) amino acid metabolic process [ISS]	(GO:0019458) methionine catabolic process via 2-oxobutanoate [TAS]	(GO:0018826) methionine gamma-lyase activity [IDA]	(GO:0003824) catalytic activity [ISS]	(GO:0005829) cytosol [IDA]	
AT1G64740	1.37	TUA1 (ALPHA-1 TUBULIN)	alpha-tubulin expressed primarily in stamens and mature pollen	(GO:0007017) microtubule-based process [ISS]	(GO:0005200) structural constituent of cytoskeleton [ISS]	(GO:0015630) microtubule cytoskeleton [ISS]	(GO:0005886) plasma membrane [IDA]		
AT1G64860	-0.90	SIGA (SIGMA FACTOR A); DNA binding / DNA-directed RNA polymerase/ transcription factor	Subunit of chloroplast RNA polymerase, confers the ability to recognize promoter sequences on the core enzyme	(GO:0006355) regulation of transcription, DNA-dependent [ISS]	(GO:0006352) transcription initiation [TAS]	(GO:0003899) DNA-directed RNA polymerase activity [ISS]	(GO:0003677) DNA binding [ISS]	(GO:0016987) sigma factor activity [ISS]	(GO:0003700) transcription factor activity [ISS]
AT1G64970	-0.76	G-TMT (GAMMA-TOCOPHEROL METHYLTRANSFERASE)	gamma-tocopherol methyltransferase (g-TMT) mRNA, nuclear; mutant has Deficient in alpha and beta tocopherol; Accumulates gamma tocopherol in leaves	(GO:0010189) vitamin E biosynthetic process [IMP]	(GO:0050342) tocopherol O-methyltransferase activity [IDA]	(GO:0009507) chloroplast [ISS]			
AT1G65060	0.78	4CL3; 4-coumarate-CoA ligase	encodes an isoform of 4-coumarate:CoA ligase (4CL), which is involved in the last step of the general phenylpropanoid pathway. mRNA levels are not induced in response to wounding or to fungal infection by P. parasitica. mRNA is expressed in flowers, to a lesser degree in mature leaves and siliques and marginally in seedling roots and bolting stems of mature plants. The catalytic efficiency was in the following (descending) order: p-coumaric acid, caffeic acid, ferulic acid, cinnamic acid and 5-OH-ferulic acid. At4CL3 was unable to use sinapic acid as substrate.	(GO:0050832) defense response to fungus [IEP]	(GO:0009611) response to wounding [IEP]	(GO:0009411) response to UV [IEP]	(GO:0009698) phenylpropanoid metabolic process [TAS]	(GO:0010584) pollen exine formation [IMP]	(GO:0016207) 4-coumarate-CoA ligase activity [IDA]
AT1G65820	0.54	glutathione transferase	similar to Os03g0709000 [Oryza sativa (japonica cultivar-group)] (GB:NP_001051042.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO22230.1); contains InterPro domain Membrane-associated proteins in eicosanoid and glutathione metabolism (MAPEG) (InterPro:IPR001129)	(GO:0008150) biological_processes [ND]	(GO:0004364) glutathione transferase activity [ISS]	(GO:0016020) membrane [IDA]	(GO:0005783) endoplasmic reticulum [IDA]	(GO:0005773) vacuole [IDA]	
AT1G66100	-2.42	toxin receptor binding	Identical to Probable thionin-2.4 precursor [Contains: Probable thionin-2.4; Acidic protein] [Arabidopsis Thaliana] (GB:Q9C8D6); similar to TH12.2 (THIONIN 2.2), toxin receptor binding [Arabidopsis thaliana] (TAIR:AT5G36910.1); similar to crambin precursor=thionin variant Th12Ca2 [Crambe abyssinica, seeds, Peptide Partial, 134 aa] (GB:AAB33004.1); contains InterPro domain Thionin; (InterPro:IPR001010)	(GO:0006952) defense response [ISS]	(GO:0003674) molecular_function [ISS]	(GO:0050827) toxin receptor binding [ISS]	(GO:0012505) endomembrane system [IEA]		

AT1G66880	0,71	ATP binding / protein kinase/ protein serine/threonine kinase/ protein-tyrosine kinase	(TAIR:AT5G38210.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO68095.1); contains InterPro domain Serine/threonine protein kinase; (InterPro:IPR002290); contains InterPro domain Protein kinase, core; (InterPro:IPR000719); contains InterPro domain Protein kinase-like (InterPro:IPR011009); contains InterPro domain Serine/threonine protein kinase, active site; (InterPro:IPR008271); contains InterPro domain Tyrosine protein kinase; (InterPro:IPR001245)	(GO:0006468) protein amino acid phosphorylation [IEA]	(GO:0004674) protein serine/threonine kinase activity [ISS]	(GO:0005886) plasma membrane [IDA]			
AT1G67330	1,76	unknown protein	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G27930.1); similar to unknown [Populus trichocarpa] (GB:ABK93495.1); contains InterPro domain Protein of unknown function DUF579, plant (InterPro:IPR006514)	(GO:0008150) biological processes [ND]	(GO:0003674) molecular_function [ND]	(GO:0012505) endomembrane system [IEA]			
AT1G69530	-0,84	ATEXPA1 (ARABIDOPSIS THALIANA EXPANSIN A1)	Member of Alpha-Expansin Gene Family. Naming convention from the Expansin Working Group (Kende et al, Plant Mol Bio). Involved in the formation of nematode-induced syncytia in roots of Arabidopsis thaliana.	(GO:0009826) unidimensional cell growth [NAS]	(GO:0009828) plant-type cell wall loosening [NAS]	(GO:0009739) response to gibberellin stimulus [TAS]	(GO:0010114) response to red light [IEP]	(GO:0006949) syncytium formation [IEP]	(GO:0003674) molecular_function [TAS]
AT1G69880	1,68	electron transporter/ thiol-disulfide exchange intermediate	similar to ATH7 (thioredoxin H-type 7), thiol-disulfide exchange intermediate [Arabidopsis thaliana] (TAIR:AT1G59730.1); similar to thioredoxin [Brassica juncea] (GB:ABM54166.1); contains InterPro domain Thioredoxin family (InterPro:IPR015467); contains InterPro domain Thioredoxin-like fold (InterPro:IPR012336); contains InterPro domain Thioredoxin fold (InterPro:IPR012335); contains InterPro domain Thioredoxin-related; (InterPro:IPR006662); contains InterPro domain Thioredoxin domain (InterPro:IPR003766)	(GO:0045454) cell redox homeostasis [IEA]	No annotation for molecular_function	(GO:0005575) cellular_component [ND]			
AT1G70700	-0,80	unknown protein	Thaliana] (GB:Q8W4J8;GB:Q0WLN3;GB:Q2V4D4;GB:Q9CAC0); similar to JAZ4/TIFY6A (JASMONATE-ZIM-DOMAIN PROTEIN 4) [Arabidopsis thaliana] (TAIR:AT1G48500.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO42344.1); contains InterPro domain ZIM (InterPro:IPR010399)	(GO:0009753) response to jasmonic acid stimulus [IEP]	(GO:0003674) molecular_function [ND]	(GO:0005575) cellular_component [ND]			
AT1G70850	-1,33	unknown protein	Identical to MLP-like protein 34 (MLP34) [Arabidopsis thaliana] (GB:Q9SSK7); similar to MLP28 (MLP-LIKE PROTEIN 28) [Arabidopsis thaliana] (TAIR:AT1G70830.1); similar to major latex-like protein [Prunus persica] (GB:AAK14060.1); contains InterPro domain Bet v I allergen; (InterPro:IPR000916)	(GO:0006952) defense response [IEA]	(GO:0009607) response to biotic stimulus [IEA]	(GO:0003674) molecular_function [ND]	(GO:0005575) cellular_component [ND]		
AT1G72060	0,96	serine-type endopeptidase inhibitor / heat shock protein binding / unfolded protein binding	similar to putative serine type endopeptidase inhibitor [Zea mays] (GB:NP_001105983.1); contains InterPro domain Proteinase inhibitor I20, Pin2; (InterPro:IPR003465)	(GO:0006979) response to oxidative stress [IMP]	(GO:0004867) serine-type endopeptidase inhibitor activity [IEA]	(GO:0012505) endomembrane system [IEA]			

AT1G73260	1.85	endopeptidase inhibitor	protein / Kunitz family protein [Arabidopsis thaliana] (TAIR:AT1G17860.1); similar to trypsin inhibitor propeptide [Brassica oleracea] (GB:AAB68964.1); contains InterPro domain Kunitz inhibitor ST1-like (InterPro:IPR011065); contains InterPro domain Proteinase inhibitor I3, Kunitz legume; (InterPro:IPR002160)	(GO:0009651) response to salt stress [IEP]	(GO:0004866) endopeptidase inhibitor activity [ISS]	(GO:0005739) mitochondrion [IDA]			
AT1G73330	-1.06	ATDR4	encodes a plant-specific protease inhibitor-like protein whose transcript level in root disappears in response to progressive drought stress. The decrease in transcript level is independent from abscisic acid level.	(GO:0009414) response to water deprivation [IEP]	(GO:0009737) response to abscisic acid stimulus [IEP]	(GO:0030414) protease inhibitor activity [ISS]	(GO:0012505) endomembrane system [IEA]		
AT1G73480	-0.62	catalytic/ hydrolase	similar to hydrolase, alpha/beta fold family protein [Arabidopsis thaliana] (TAIR:AT1G18360.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO68547.1); contains InterPro domain Alpha/beta hydrolase; (InterPro:IPR003089); contains InterPro domain Alpha/beta hydrolase fold-1 (InterPro:IPR000073)	No annotation for biological_processes	(GO:0016787) hydrolase activity [ISS]	No annotation for cellular_component			
AT1G73800	0.78	calmodulin binding	unknown						
AT1G73870	-1.01	transcription factor/ zinc ion binding	Identical to Zinc finger protein CONSTANS-LIKE 7 (COL7) [Arabidopsis Thaliana] (GB:Q9C9A9;GB:Q5XF76); similar to zinc finger (B-box type) family protein [Arabidopsis thaliana] (TAIR:AT1G25440.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO42139.1); contains InterPro domain Zinc finger, B-box; (InterPro:IPR000315); contains InterPro domain Zinc finger, CONSTANS-type; (InterPro:IPR002926); contains InterPro domain CCT (InterPro:IPR010402)	(GO:0045449) regulation of transcription [TAS]	(GO:0008270) zinc ion binding [ISS]	(GO:0003700) transcription factor activity [ISS]	(GO:0005622) intracellular [IEA]		
AT1G74000	1.183	SS3 (STRICTOSIDINE SYNTHASE)	encodes a protein similar to strictosidine synthase, which is involved in the production of monoterpene indole alkaloids. This gene belongs to a family of 13 members in Arabidopsis.	(GO:0009058) biosynthetic process [IEA]	(GO:0016844) strictosidine synthase activity [ISS]	(GO:0009505) plant-type cell wall [IDA]	(GO:0005618) cell wall [IDA]		
AT1G74020	1.202	SS2 (STRICTOSIDINE SYNTHASE)	Encodes AtSS-2 strictosidine synthase.	(GO:0009611) response to wounding [IEP]	(GO:0009753) response to jasmonic acid stimulus [IEP]	(GO:0016844) strictosidine synthase activity [IEA]	(GO:0005886) plasma membrane [IDA]	(GO:0005773) vacuole [IDA]	
AT1G74030	0.75	phosphopyruvate hydratase	similar to LOS2 (Low expression of osmotically responsive genes 1), phosphopyruvate hydratase [Arabidopsis thaliana] (TAIR:AT2G36530.1); similar to hypothetical protein OsI_030111 [Oryza sativa (indica cultivar-group)] (GB:EAZ08879.1); similar to predicted protein [Physcomitrella patens subsp. patens] (GB:EDQ69744.1); similar to plastid enolase [Helianthus annuus] (GB:ABO36543.1); contains InterPro domain Enolase (InterPro:IPR000944); contains InterPro domain Phosphopyruvate hydratase (InterPro:IPR000944)	(GO:0006096) glycolysis [IEA]	(GO:0004634) phosphopyruvate hydratase activity [ISS]	(GO:0000015) phosphopyruvate hydratase complex [IEA]	(GO:0009507) chloroplast [IEA]		
AT1G74070	-0.76	peptidyl-prolyl cis-trans isomerase	[Arabidopsis thaliana] (TAIR:AT5G35100.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO68001.1); contains InterPro domain Cyclophilin-like (InterPro:IPR015891); contains InterPro domain Peptidyl-prolyl cis-trans isomerase, cyclophilin-type; (InterPro:IPR002130)	(GO:0006457) protein folding [ISS]	(GO:0003755) peptidyl-prolyl cis-trans isomerase activity [ISS]	(GO:0009543) chloroplast thylakoid lumen [ISS]	(GO:0009507) chloroplast [IDA]		

		ICS1 (ISOCHORISMATE SYNTHASE); isochorismate synthase	Encodes a protein with isochorismate synthase activity. Mutants fail to accumulate salicylic acid. Its function may be redundant with that of ICS2 (AT1G18870).	(GO:0050832) defense response to fungus [IMP]	(GO:0010118) stomatal movement [IMP]	(GO:0042742) defense response to bacterium [IMP]	(GO:0009627) systemic acquired resistance [IEP]	(GO:0009697) salicylic acid biosynthetic process [TAS]	(GO:0009617) response to bacterium [IMP]
AT1G74710	0.97		Identical to HIPL1 protein precursor (HIPL1) [Arabidopsis thaliana] (GB:Q9SGG3); similar to catalytic [Arabidopsis thaliana] (TAIR:AT5G39970.1); similar to HIPL2 (HIPL2 PROTEIN PRECURSOR), catalytic [Arabidopsis thaliana] (TAIR:AT5G62630.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO62479.1); similar to hypothetical protein Osl_012701 [Oryza sativa (indica cultivar-group)] (GB:EAY91468.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO41002.1); contains InterPro domain Soluble quinoprotein glucose dehydrogenase; (InterPro:IPR011041); contains InterPro domain Six-bladed beta-propeller, TolB-like (InterPro:IPR011042)	(GO:0008150) biological processes [ND]	(GO:0003824) catalytic activity [IEA]	(GO:0031225) anchored to membrane [TAS]	(GO:0046658) anchored to plasma membrane [IDA]	(GO:0005886) plasma membrane [IDA]	
AT1G74790	0.73	unknown protein							
AT1G75040	1.86	PR5 (PATHOGENESIS-RELATED GENE 5)	Thaumatococcus protein involved in response to pathogens. mRNA level of the PR-5 gene (At1g75040) is significantly changed after cutting the inflorescence stem indicating the existence of a network of signal transducing pathways as other stress-regulated genes (At5g01410, At3g17800, At1g29930) do not response to the treatment.	(GO:0009627) systemic acquired resistance [IEP]	(GO:0010224) response to UV-B [IGI]	(GO:0051707) response to other organism [ISS]	(GO:0031540) regulation of anthocyanin biosynthetic process [IEP]	(GO:0003674) molecular_function [ND]	(GO:0048046) apoplast [IDA]
AT1G76070	0.79	unknown protein	Identical to Uncharacterized protein At1g76070 [Arabidopsis thaliana] (GB:Q9SGS5;GB:Q8LAC9;GB:Q9LQR1); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G20310.1); similar to hypothetical protein [Vitis vinifera] (GB:CAO62479.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO62479.1)	(GO:0008150) biological processes [ND]	(GO:0003674) molecular_function [ND]	(GO:0005886) plasma membrane [IDA]			
AT1G76110	-0.71	transcription factor	protein / ARID/BRIGHT DNA-binding domain-containing protein [Arabidopsis thaliana] (TAIR:AT1G04880.1); similar to unknown [Populus trichocarpa] (GB:ABK95398.1); contains InterPro domain High mobility group box, HMG1/HMG2; (InterPro:IPR000910); contains InterPro domain AT-rich interaction region; (InterPro:IPR01606); contains InterPro domain High mobility group box, HMG (InterPro:IPR009071)	(GO:0045449) regulation of transcription [TAS]	(GO:0003700) transcription factor activity [IEA]	(GO:0005622) intracellular [IEA]			
AT1G77380	1.07	AAP3; amino acid permease	Amino acid permease which transports basic amino acids.	(GO:0015802) basic amino acid transport [IDA]	amino acid transmembrane transporter activity [ISS]	(GO:0016020) membrane [ISS]			
AT1G79530	0.90	NAD binding / glyceraldehyde-3-phosphate dehydrogenase (phosphorylating)/ glyceraldehyde-3-phosphate dehydrogenase	similar to GAPCP-2, glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana] (TAIR:AT1G16300.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO64922.1); contains InterPro domain Glyceraldehyde-3-phosphate dehydrogenase, type I; (InterPro:IPR006424); contains InterPro domain NAD(P)-binding; (InterPro:IPR016040); contains InterPro domain Glyceraldehyde-3-phosphate dehydrogenase; (InterPro:IPR000173)	(GO:0006096) glycolysis [ISS]	(GO:0008943) glyceraldehyde-3-phosphate dehydrogenase activity [ISS]	(GO:0016020) membrane [IDA]	(GO:0009536) plastid [ISS]		

AT2G01490	-0,74	phytanoyl-CoA dioxygenase	similar to unknown [Populus trichocarpa] (GB:ABK94889.1); contains InterPro domain Phytanoyl-CoA dioxygenase (InterPro:IPR006679)	No annotation for biological_processes	(GO:0048244) phytanoyl-CoA dioxygenase activity [ISS]	(GO:0005886) plasma membrane [IDA]			
AT2G03520	-1,04	ATUPS4	[Arabidopsis thaliana] (GB:Q9ZQ88;GB:Q1PFA1;GB:Q6E273;GB:Q6E274;GB:Q6E275); similar to ATUPS1 (Arabidopsis thaliana ureide permease 1), allantoin uptake transmembrane transporter [Arabidopsis thaliana] (TAIR:AT2G03590.1); similar to allantoin permease [Phaseolus vulgaris] (GB:AAS19930.1); contains InterPro domain Fatty acid elongase 3-ketoacyl-CoA synthase 1 (InterPro:IPR009834)	No annotation for biological_processes	No annotation for molecular_function	(GO:0009507) chloroplast [IDA]			
AT2G04038	1,03	DNA binding / transcription factor	similar to ATBZIP58 (ARABIDOPSIS THALIANA BASIC LEUCINE-ZIPPER 58), DNA binding / protein heterodimerization/ protein homodimerization/ transcription factor [Arabidopsis thaliana] (TAIR:AT1G13600.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN76820.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO15359.1); contains InterPro domain Basic-leucine zipper (bZIP) transcription factor; (InterPro:IPR004827); contains InterPro domain Basic leucine zipper; (InterPro:IPR011700)	(GO:0006355) regulation of transcription, DNA-dependent [IEA]	(GO:0003677) DNA binding [ISS]	(GO:0003700) transcription factor activity [ISS]	(GO:0005634) nucleus [IEA]		
AT2G05620	-0,76	PGR5	Involved in electron flow in Photosystem I. Essential for photoprotection.	(GO:0009644) response to high light intensity [IMP]	(GO:0009773) photosynthetic electron transport in photosystem I [IMP]	(GO:0009414) response to water deprivation [IMP]	(GO:0009055) electron carrier activity [IMP]	(GO:0009534) chloroplast thylakoid [IDA]	(GO:0009507) chloroplast [IDA]
AT2G14796	0,77	unknown protein	transposable element gene; non-LTR retrotransposon family (LINE), has a 1.7e-05 P-value blast match to GB:NP_038605 L1 repeat, Tf1 subfamily, member 30 (LINE-element) (Mus musculus)						
AT2G14900	1,30	unknown protein	[Arabidopsis thaliana] (TAIR:AT5G59845.1); similar to unknown [Populus trichocarpa] (GB:ABK94917.1); contains InterPro domain Gibberellin regulated protein (InterPro:IPR003854)	(GO:0009739) response to gibberellin stimulus [ISS]	(GO:0003674) molecular_function [ND]	(GO:0012505) endomembrane system [IEA]			
AT2G15490	1,24	UDP-glycosyltransferase	TRANSFERASE 73B5), UDP-glycosyltransferase/ transferase, transferring glycosyl groups [Arabidopsis thaliana] (TAIR:AT2G15480.1); similar to immediate-early salicylate-induced glucosyltransferase (GB:AAB36653.1); contains InterPro domain UDP-glucuronosyl/UDP-glucosyltransferase; (InterPro:IPR002213)	(GO:0051707) response to other organism [IEP]	(GO:0035251) UDP-glycosyltransferase activity [IDA]	(GO:0008194) UDP-glycosyltransferase activity [ISS]	(GO:0016757) transferase activity, transferring glycosyl groups [ISS]	(GO:0012505) endomembrane system [IEA]	
AT2G16005	-0,74	unknown protein	similar to MD-2-related lipid recognition domain-containing protein / ML domain-containing protein [Arabidopsis thaliana] (TAIR:AT3G44100.1); similar to unknown [Populus trichocarpa] (GB:ABK93234.1); contains InterPro domain MD-2-related lipid-recognition (InterPro:IPR003172)	(GO:0008150) biological_process [ND]	(GO:0003674) molecular_function [ND]	(GO:0012505) endomembrane system [IEA]			
AT2G17420	0,63	NTRA	NADPH-dependent thioredoxin reductase, major cytosolic isoform	(GO:0046686) response to cadmium ion [IEP]	(GO:0004791) thioredoxin-disulfide reductase activity [IDA]	(GO:0005759) mitochondrial matrix [IDA]	(GO:0005829) cytosol [IDA]		

AT2G18193	0.96	ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding	similar to AAA-type ATPase family protein [Arabidopsis thaliana] (TAIR:AT2G18190.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO46634.1); contains InterPro domain AAA+ ATPase, core; (InterPro:IPR003593); contains InterPro domain AAA ATPase, core; (InterPro:IPR003959)	No annotation for biological_processes	(GO:0005524) ATP binding [ISS]	(GO:0016887) ATPase activity [ISS]	(GO:0012505) endomembrane system [IEA]		
AT2G18680	1.48	unknown protein	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G18690.1); similar to hypothetical protein Osl_029427 [Oryza sativa (indica cultivar-group)] (GB:EAZ08195.1)	(GO:0008150) biological_processes [ND]	(GO:0003674) molecular_function [ND]	(GO:0012505) endomembrane system [IEA]			
AT2G20290	0.75	XIG; motor/ protein binding	member of Myosin-like proteins	(GO:0030048) actin filament-based movement [TAS]	(GO:0003774) motor activity [ISS]	(GO:0005515) protein binding [ISS]	(GO:0016459) myosin complex [ISS]		
AT2G21640	1.38	unknown protein	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G05570.1); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G39235.1); similar to hypothetical protein Osl_027197 [Oryza sativa (indica cultivar-group)] (GB:EAZ05965.1)	(GO:0006979) response to oxidative stress [IDA]	(GO:0003674) molecular_function [ND]	(GO:0005739) mitochondrion [IDA]			
AT2G23900	1.06	polygalacturonase	similar to glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein [Arabidopsis thaliana] (TAIR:AT3G48950.1); similar to Glycoside hydrolase, family 28 [Medicago truncatula] (GB:ABD32865.1); contains InterPro domain Pectin lyase fold (InterPro:IPR012334); contains InterPro domain Parallel beta-helix repeat (InterPro:IPR006626); contains InterPro domain Glycoside hydrolase, family 28; (InterPro:IPR000743); contains InterPro domain Pectin lyase fold/virulence factor (InterPro:IPR011050)	(GO:0005975) carbohydrate metabolic process [ISS]	(GO:0004650) polygalacturonase activity [ISS]	(GO:0012505) endomembrane system [IEA]			
AT2G24270	-0.77	ALDH11A3; aldehyde dehydrogenase/ oxidoreductase	Encodes a protein with non-phosphorylating NADP-dependent glyceraldehyde-3-phosphate dehydrogenase activity. The activity of the enzyme was determined from leaf extracts; the enzyme has not been purified to confirm activity.	(GO:0008152) metabolic process [IEA]	(GO:0004028) 3-chloroallyl aldehyde dehydrogenase activity [ISS]	(GO:0008886) glyceraldehyde-3-phosphate dehydrogenase (NADP+) activity [IDA]	No annotation for cellular_component		
AT2G25510	1.37	unknown protein	No description	(GO:0008150) biological_processes [ND]	(GO:0003674) molecular_function [ND]	No annotation for cellular_component			
AT2G25520	0.64	organic anion transporter	similar to phosphate translocator-related [Arabidopsis thaliana] (TAIR:AT4G32390.1); similar to plastidic phosphate translocator-like protein1 [Mesembryanthemum crystallinum] (GB:BAD91176.1); contains InterPro domain Protein of unknown function DUF250 (InterPro:IPR044859); similar to DUF250 storekeeper protein-related [Arabidopsis thaliana] (TAIR:AT4G00270.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO39806.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO38810.1); contains InterPro domain Protein of unknown function DUF573 (InterPro:IPR007592)	No annotation for biological_processes	(GO:0008514) organic anion transmembrane transporter activity [ISS]	(GO:0012505) endomembrane system [IEA]			
AT2G25650	1.28	transcription regulator		(GO:0008150) biological_processes [ND]	(GO:0030528) transcription regulator activity [TAS]	(GO:0003674) molecular_function [ISS]	(GO:0005575) cellular_component [ND]		

			similar to protein kinase, putative [Arabidopsis thaliana] (TAIR:AT2G05940.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO65243.1); contains InterPro domain Protein kinase, core; (InterPro:IPR000719); contains InterPro domain Protein kinase-like (InterPro:IPR011009)	No annotation for biological_processes	(GO:0016301) kinase activity [ISS]	No annotation for cellular_component			
AT2G26290	0.92	ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein-tyrosine kinase							
AT2G26440	1.23	enzyme inhibitor/ pectinesterase	[Arabidopsis thaliana] (TAIR:AT4G02330.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO65169.1); contains InterPro domain Pectin lyase fold (InterPro:IPR012334); contains InterPro domain Pectinesterase, catalytic; (InterPro:IPR000070); contains InterPro domain Pectin lyase fold/virulence factor (InterPro:IPR011050); contains InterPro domain Pectinesterase inhibitor; (InterPro:IPR006501)	(GO:0042545) cell wall modification [IEA]	(GO:0030599) pectinesterase activity [ISS]	(GO:0009505) plant-type cell wall [ISS]			
AT2G26560	1.62	nutrient reservoir	substrate specificity that accumulates upon infection by fungal and bacterial pathogens. Protein is localized in the cytoplasm in healthy leaves, and in membranes in infected cells.	(GO:0046686) response to cadmium ion [IEP]	(GO:0009626) plant-type hypersensitive response [IMP]	(GO:0006629) lipid metabolic process [IDA]	(GO:0045735) nutrient reservoir activity [ISS]	(GO:0016298) lipase activity [IDA]	(GO:0016020) membrane [IDA]
AT2G27550	0.98	ATC (ARABIDOPSIS THALIANA CENTRORADIALIS); phosphatidylethanolamine binding	encodes a protein similar to TFL1. overexpression leads to similar phenotype as TFL1 overexpression. expressed specifically in the hypocotyl and null mutation does not result in phenotypes exhibited by TFL1 null mutations.	(GO:0008150) biological_processes [ND]	(GO:0008429) phosphatidylethanolamine binding [ISS]	(GO:0005575) cellular_component [ND]			
AT2G29720	0.93	monooxygenase/ oxidoreductase	Encodes CTF2B.	(GO:0008152) metabolic process [IEA]	(GO:0004497) monooxygenase activity [ISS]	(GO:0005739) mitochondrion [IEA]			
AT2G29750	1.61	UDP-glycosyltransferase/ transferase, transferring glycosyl groups	similar to UDP-glucuronosyl/UDP-glucosyl transferase family protein [Arabidopsis thaliana] (TAIR:AT1G07260.1); similar to UDP-glucuronosyl/UDP-glucosyl transferase family protein [Arabidopsis thaliana] (TAIR:AT2G29740.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN76057.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO21482.1); contains InterPro domain UDP-glucuronosyl/UDP-glucosyltransferase; (InterPro:IPR002213)	(GO:0008152) metabolic process [IEA]	(GO:0008194) UDP-glycosyltransferase activity [ISS]	(GO:0016757) transferase activity, transferring glycosyl groups [ISS]	(GO:0005575) cellular_component [ND]		
AT2G30490	0.68	ATC4H (CINNAMATE-4-HYDROXYLASE)	Encodes a cinnamate-4-hydroxylase.	(GO:0009611) response to wounding [IMP]	(GO:0009416) response to light stimulus [IEP]	(GO:0009699) phenylpropanoid biosynthetic process [TAS]	(GO:0016710) trans-cinnamate 4-monooxygenase activity [IDA]	(GO:0016020) membrane [IDA]	(GO:0005783) endoplasmic reticulum [TAS]
AT2G31460	-1.28	unknown protein	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G27410.1); contains InterPro domain Protein of unknown function DUF313 (InterPro:IPR005508)	(GO:0008150) biological_processes [ND]	(GO:0003674) molecular_function [ND]	(GO:0005575) cellular_component [ND]			
AT2G31560	0.78	unknown protein	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G05870.1); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G05870.2); similar to hypothetical protein [Vitis vinifera] (GB:CAN60580.1); contains InterPro domain Protein of unknown function DUF1685 (InterPro:IPR012881)	(GO:0008150) biological_processes [ND]	(GO:0003674) molecular_function [ND]	(GO:0005575) cellular_component [ND]			

AT2G34320	0.63	unknown protein	similar to reverse transcriptase, putative / RNA-dependent DNA polymerase, putative [Arabidopsis thaliana] (TAIR:AT4G29090.1); similar to 52O08_2 [Brassica rapa subsp. pekinensis] (GB:AAZ67547.1); contains InterPro domain Polynucleotidyl transferase, Ribonuclease H fold; (InterPro:IPR012337)	(GO:0008150) biological_processes [ND]	(GO:0003676) nucleic acid binding [IEA]	No annotation for cellular_component			
AT2G34500	1.17	CYP710A1; heme binding / iron ion binding / monooxygenase/ oxygen binding	Encodes a protein with C22-sterol desaturase activity. The enzyme was shown to catalyze in the presence of NADPH the conversion of _ - sitosterol to stigmasterol, but not that of 24-epi-campesterol to brassicasterol (unlike CYP710A2).	No annotation for biological_processes	(GO:0000249) C-22 sterol desaturase activity [IDA]	(GO:0019825) oxygen binding [ISS]	(GO:0012505) endomembrane system [IEA]		
AT2G35130	-0.66	unknown protein	similar to pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] (TAIR:AT5G02860.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO42005.1); similar to hypothetical protein OsI_005882 [Oryza sativa (indica cultivar-group)] (GB:EAY84649.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN70089.1); contains InterPro domain Pentatricopeptide repeat (InterPro:IPR002885)	(GO:0008150) biological_processes [ND]	No annotation for molecular_function	(GO:0012505) endomembrane system [IEA]			
AT2G35980	1.49	YLS9 (YELLOW-LEAF-SPECIFIC GENE 9)	Encodes a protein whose sequence is similar to tobacco hairpin-induced gene (HIN1) and Arabidopsis non-race specific disease resistance gene (NDR1). Expression of this gene is induced by cucumber mosaic virus, spermine and during senescence. The gene product is localized to the chloroplast.	(GO:0051607) defense response to virus [IEP]	(GO:0051707) response to other organism [TAS]	(GO:0003674) molecular_function [ND]	(GO:0009507) chloroplast [IDA]		
AT2G36120	0.92	unknown protein	pseudogene, glycine-rich protein	(GO:0010305) leaf vascular tissue pattern formation [IMP]	(GO:0010588) cotyledon vascular tissue pattern formation [IMP]	(GO:0048366) leaf development [IMP]	(GO:0010087) phloem or xylem histogenesis [IMP]	No annotation for molecular_function	No annotation for cellular_component
AT2G36470	0.75	unknown protein	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G27770.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO15960.1); contains InterPro domain Protein of unknown function DUF868, plant (InterPro:IPR008586)	(GO:0008150) biological_processes [ND]	(GO:0003674) molecular_function [ND]	(GO:0005575) cellular_component [ND]			
AT2G36490	-0.92	ROS1	A repressor of transcriptional gene silencing. Functions by demethylating the target promoter DNA. Interacts physically with RPA2/ROR1. In the ros1 mutants, an increase in methylation is observed in a number of gene promoters. Among the loci affected by ros1, a few (RD29A and At1g76930) are affected in cytosine methylation in all sequence contexts (CpG, CpNpG or CpNpN), although many others are affected primarily in non-CpG contexts.	(GO:0006342) chromatin silencing [IMP]	(GO:0006281) DNA repair [IMP]	(GO:0031936) negative regulation of chromatin silencing [IMP]	(GO:0006306) DNA methylation [IDA]	(GO:0003906) DNA-(apurinic or apyrimidinic site) lyase activity [IDA]	(GO:0005515) protein binding [IPI]

AT2G36870	-0.63	hydrolase, acting on glycosyl bonds / hydrolase, hydrolyzing O-glycosyl compounds	Identical to Probable xyloglucan endotransglucosylase/hydrolase protein 32 precursor (XTH32) [Arabidopsis thaliana] (GB:Q9SJL9); similar to XTR8 (xyloglucan:xyloglucosyl transferase 8), hydrolase, acting on glycosyl bonds [Arabidopsis thaliana] (TAIR:AT3G44990.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO63020.1); contains InterPro domain Concanavalin A-like lectin/glucanase, subgroup (InterPro:IPR013320); contains InterPro domain Xyloglucan endotransglucosylase/hydrolase (InterPro:IPR016455); contains InterPro domain Xyloglucan endo-transglycosylase, C-terminal; (InterPro:IPR010713); contains InterPro domain Glycoside hydrolase, family 16; (InterPro:IPR000757); contains InterPro domain Concanavalin A-like lectin/glucanase (InterPro:IPR008985)	(GO:0006073) glucan metabolic process [IEA]	(GO:0005975) carbohydrate metabolic process [IEA]	(GO:0016798) hydrolase activity, acting on glycosyl bonds [ISS]	(GO:0048046) apoplast [IEA]	(GO:0012505) endomembrane system [IEA]	(GO:0005618) cell wall [IEA]
AT2G37110	0.67	unknown protein	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G40935.1); similar to unknown [Populus trichocarpa] (GB:ABK96163.1); contains InterPro domain Protein of unknown function Cys-rich (InterPro:IPR006461)	(GO:0008150) biological_process [ND]	(GO:0003674) molecular_function [ND]	(GO:0005575) cellular_component [ND]			
AT2G37130	1.53	peroxidase	[Arabidopsis thaliana] (GB:Q42580;GB:Q43733;GB:Q93YM9); similar to PRXR1 (peroxidase 42), peroxidase [Arabidopsis thaliana] (TAIR:AT4G21960.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO18132.1); contains InterPro domain Plant peroxidase; (InterPro:IPR000823); contains InterPro domain Haem peroxidase; (InterPro:IPR010255); contains InterPro domain Haem peroxidase, plant/fungal/bacterial; (InterPro:IPR002016)	(GO:0050832) defense response to fungus [IMP]	(GO:0003674) molecular_function [TAS]	(GO:0004601) peroxidase activity [ISS]	(GO:0012505) endomembrane system [IEA]		
AT2G38110	0.68	ATGPAT6/GPAT6; 1-acylglycerol-3-phosphate O-acyltransferase/acyltransferase	Encodes a protein with glycerol-3-phosphate acyltransferase activity.	(GO:0008152) metabolic process [ISS]	(GO:0003841) 1-acylglycerol-3-phosphate O-acyltransferase activity [IGI]	(GO:0008415) acyltransferase activity [ISS]	No annotation for cellular_component		
AT2G38860	0.98	YLS5	Encodes protease I (ptpl)-like protein YLS5.	No annotation for biological_process	No annotation for molecular_function	(GO:0012505) endomembrane system [IEA]			
AT2G38870	1.08	serine-type endopeptidase inhibitor	similar to serine protease inhibitor, potato inhibitor I-type family protein [Arabidopsis thaliana] (TAIR:AT2G38900.1); similar to type I proteinase inhibitor-like protein [Citrus x paradisi] (GB:AA76363.1); contains InterPro domain Proteinase inhibitor I13, potato inhibitor I; (InterPro:IPR000864)	(GO:0050832) defense response to fungus [IMP]	(GO:0009611) response to wounding [ISS]	(GO:0004867) serine-type endopeptidase inhibitor activity [ISS]	(GO:0005618) cell wall [IDA]		

AT2G39530	0.71	unknown protein	Identical to UPF0497 membrane protein At2g39530 [Arabidopsis thaliana] (GB:Q8GWD5;GB:O80640); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G39518.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN64094.1); contains InterPro domain Conserved hypothetical protein CHP01569, trans-membrane plant (InterPro:IPR006459); contains InterPro domain Protein of unknown function DUF588 (InterPro:IPR006702)	(GO:0008150) biological_processes [ND]	(GO:0003674) molecular_function [ND]	(GO:0016020) membrane [ISS]			
AT2G40140	0.92	transcription factor	similar to zinc finger (CCCH-type) family protein [Arabidopsis thaliana] (TAIR:AT3G55980.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN68018.1); contains InterPro domain Zinc finger, CCCH-type; (InterPro:IPR000571); contains InterPro domain Ankyrin (InterPro:IPR002110)	(GO:0050832) defense response to fungus [IMP]	(GO:0009409) response to cold [IEP]	(GO:0010200) response to chitin [IEP]	(GO:0045449) regulation of transcription [TAS]	(GO:0003700) transcription factor activity [ISS]	(GO:0005575) cellular_component [ND]
AT2G41240	1.45	DNA binding / transcription factor	similar to BHLH039/ORG3 (OBP3-RESPONSIVE GENE 3), DNA binding / transcription factor [Arabidopsis thaliana] (TAIR:AT3G56980.1); similar to basic helix-loop-helix family protein [Thlaspi caerulescens] (GB:ABD37969.1); contains InterPro domain Achaete-scute transcription factor related (InterPro:IPR015660); contains InterPro domain Basic helix-loop-helix dimerisation region bHLH; (InterPro:IPR001092); contains InterPro domain Helix-loop-helix DNA-binding; (InterPro:IPR011598)	(GO:0009414) response to water deprivation [IEP]	(GO:0045449) regulation of transcription [TAS]	(GO:0003677) DNA binding [ISS]	(GO:0003700) transcription factor activity [ISS]	(GO:0005634) nucleus [IEA]	
AT2G41260	1.60	M17	Late-embryogenesis-abundant gene. Involved in the acquisition of desiccation tolerance during maturation of embryo. Contains a zinc finger domain-containing protein [Arabidopsis thaliana] (TAIR:AT3G08920.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO23371.1); contains InterPro domain Rhodanese-like (InterPro:IPR001763)	(GO:0009790) embryonic development [TAS]	(GO:0003674) molecular_function [ND]	(GO:0012505) endomembrane system [IEA]			
AT2G42220	-0.88	unknown protein	protein [Arabidopsis thaliana] (TAIR:AT3G08920.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO23371.1); contains InterPro domain Rhodanese-like (InterPro:IPR001763)	(GO:0008150) biological_processes [ND]	(GO:0003674) molecular_function [ND]	(GO:0009535) chloroplast thylakoid membrane [IDA]	(GO:0009507) chloroplast [IDA]		
AT2G42380	-0.97	DNA binding / transcription factor	similar to bZIP transcription factor family protein [Arabidopsis thaliana] (TAIR:AT3G58120.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO39360.1); contains InterPro domain Basic-leucine zipper (bZIP) transcription factor; (InterPro:IPR004827); contains InterPro domain Basic leucine zipper; (InterPro:IPR011700)	(GO:0006355) regulation of transcription, DNA-dependent [IEA]	(GO:0003677) DNA binding [IDA]	(GO:0016563) transcription activator activity [IDA]	(GO:0003700) transcription factor activity [ISS]	(GO:0005634) nucleus [IDA]	
AT2G43010	-0.95	PIF4 (PHYTOCHROME INTERACTING FACTOR 4); DNA binding / transcription factor	Isolated as a semidominant mutation defective in red -light responses. Encodes a nuclear localized bHLH protein that interacts with active PhyB protein. Negatively regulates phyB mediated red light responses. Encodes PIF4	(GO:0010161) red light signaling pathway [IGI]	(GO:0010017) red or far red light signaling pathway [IMP]	(GO:0009704) de-etiolation [IMP]	(GO:0003677) DNA binding [IDA]	(GO:0005515) protein binding [IPI]	(GO:0003700) transcription factor activity [ISS]
AT2G43510	1.43	ATT1	Member of the defensin-like (DEFL) family. Encodes putative trypsin inhibitor protein which may function in defense against herbivory.	(GO:0050832) defense response to fungus [IMP]	(GO:0006952) defense response [TAS]	(GO:0030304) trypsin inhibitor activity [TAS]	(GO:0012505) endomembrane system [IEA]	(GO:0005576) extracellular region [IEA]	

AT2G43590	0.88	chitin binding / chitinase	thaliana] (TAIR:AT2G43580.1); similar to Basic endochitinase CHB4 precursor (GB:Q06209); contains InterPro domain Endochitinase (InterPro:IPR016283); contains InterPro domain Glycoside hydrolase, family 19, catalytic; (InterPro:IPR000726); contains InterPro domain Chitin-binding, type 1; (InterPro:IPR001002)	(GO:0016998) cell wall catabolic process [IEA]	(GO:0004568) chitinase activity [ISS]	(GO:0012505) endomembrane system [IEA]			
AT2G43610	1.83	chitin binding / chitinase	similar to chitinase, putative [Arabidopsis thaliana] (TAIR:AT2G43620.1); similar to Basic endochitinase CHB4 precursor (GB:Q06209); contains InterPro domain Endochitinase (InterPro:IPR016283); contains InterPro domain Glycoside hydrolase, family 19, catalytic; (InterPro:IPR000726); contains InterPro domain Chitin-binding, type 1; (InterPro:IPR001002)	(GO:0016998) cell wall catabolic process [IEA]	(GO:0004568) chitinase activity [ISS]	(GO:0005886) plasma membrane [IDA]			
AT2G43620	2.31	chitin binding / chitinase	similar to glycoside hydrolase family 19 protein [Arabidopsis thaliana] (TAIR:AT2G43610.1); similar to chitinase [Chenopodium amaranticolor] (GB:BAA22968.1); similar to chitinase [Chenopodium amaranticolor] (GB:BAA22966.1); contains InterPro domain Endochitinase (InterPro:IPR016283); contains InterPro domain Glycoside hydrolase, family 19, catalytic; (InterPro:IPR000726); contains InterPro domain Chitin-binding, type 1; (InterPro:IPR001002)	No annotation for biological_process	(GO:0004568) chitinase activity [ISS]	(GO:0048046) apoplast [IDA]			
AT2G44230	-0.91	unknown protein	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G44260.1); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G44260.2); similar to Protein of unknown function DUF946, plant [Medicago truncatula] (GB:ABN08108.1); contains InterPro domain Protein of unknown function DUF946, plant (InterPro:IPR009291)	No annotation for biological_processes	(GO:0003674) molecular_function [ND]	(GO:0009507) chloroplast [IEA]			
AT2G44370	0.71	unknown protein	Response to plant pathogen DC3000 DC1 domain-containing protein ; similar to DC1 domain-containing protein [Arabidopsis thaliana] (TAIR:AT2G17740.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO67189.1); contains InterPro domain C1-like (InterPro:IPR011424); contains InterPro domain DC1 (InterPro:IPR004146)						
AT2G47630	0.90	catalytic/ hydrolase	similar to esterase/lipase/thioesterase family protein [Arabidopsis thaliana] (TAIR:AT3G62860.1); similar to hypothetical protein Osl_001580 [Oryza sativa (indica cultivar-group)] (GB:EAY73733.1); similar to Os05g0363100 [Oryza sativa (japonica cultivar-group)] (GB:NP_001055317.1); contains InterPro domain Alpha/beta hydrolase; (InterPro:IPR002098); similar to responsive NPH3 family protein [Arabidopsis thaliana] (TAIR:AT1G03010.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO22403.1); contains InterPro domain NPH3; (InterPro:IPR004249)	No annotation for biological_processes	(GO:0003824) catalytic activity [ISS]	(GO:0005886) plasma membrane [IDA]			
AT2G47860	1.00	signal transducer	protein [Arabidopsis thaliana] (TAIR:AT1G03010.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO22403.1); contains InterPro domain NPH3; (InterPro:IPR004249)	(GO:0009416) response to light stimulus [ISS]	(GO:0004871) signal transducer activity [ISS]	(GO:0005886) plasma membrane [IDA]			

AT3G01440	-0,74	calcium ion binding	similar to PSBQ/PSBQ-1/PSBQA, calcium ion binding [Arabidopsis thaliana] (TAIR:AT4G21280.2); similar to hypothetical protein [Vitis vinifera] (GB:CAN78127.1); contains InterPro domain Photosystem II oxygen evolving complex protein PsbQ; (InterPro:IPR008797)	(GO:0019684) photosynthesis, light reaction [TAS]	(GO:0005509) calcium ion binding [IEA]	(GO:0009535) chloroplast thylakoid membrane [IDA]	(GO:0030095) chloroplast photosystem II [ISS]	(GO:0009654) oxygen evolving complex [TAS]	(GO:0009543) chloroplast thylakoid lumen [IDA]
AT3G01720	0,91	unknown protein	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G13500.3); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G13500.2); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G13500.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO14632.1); similar to predicted protein [Physcomitrella patens subsp. patens] (GB:EDQ59308.1); similar to predicted protein [Physcomitrella patens subsp. patens] (GB:EDQ59308.1) [ADENOSINE	(GO:0008150) biological_process [ND]	(GO:0003674) molecular_function [ND]	(GO:0012505) endomembrane system [IEA]			
AT3G01820	1,02	ATP binding / nucleotide kinase	KINASE), adenylate kinase/ nucleotide kinase [Arabidopsis thaliana] (TAIR:AT2G37250.1); similar to adenylate kinase family-like protein [Solanum tuberosum] (GB:ABB16966.1); contains InterPro domain Adenylate kinase; (InterPro:IPR000850); contains InterPro domain Adenylate/cytidine kinase, N-terminal; (InterPro:IPR011769)	(GO:0006139) nucleobase, nucleoside, nucleotide and nucleic acid metabolic process [IEA]	(GO:0019201) nucleotide kinase activity [ISS]	(GO:0005739) mitochondrion [IEA]			
AT3G01830	1,20	calcium ion binding ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein-tyrosine kinase	similar to calmodulin-like protein [Datura metel] (GB:AAM95458.1); contains InterPro domain EF-Hand type; (InterPro:IPR011992); contains InterPro domain Calcium-binding EF-hand; (InterPro:IPR02048)	(GO:0008150) biological_process [ND]	(GO:0005509) calcium ion binding [ISS]	(GO:0005575) cellular_component [ND]			
AT3G01970	0,79	WRKY45; transcription factor	member of WRKY Transcription Factor; Group I	(GO:0006355) regulation of transcription, DNA-dependent [ISS]	(GO:0003700) transcription factor activity [ISS]	(GO:0005634) nucleus [IEA]			
AT3G02380	-0,90	COL2 (CONSTANS-LIKE 2); transcription factor/ zinc ion binding	homologous to the flowering-time gene CONSTANS (CO) encoding zinc-finger proteins	(GO:0009909) regulation of flower development [IMP]	(GO:0008270) zinc ion binding [ISS]	(GO:0003700) transcription factor activity [ISS]	(GO:0005622) intracellular [IEA]		
AT3G04070	0,94	ANAC047; transcription factor	similar to NAM (Arabidopsis NAC domain containing protein 18), transcription factor [Arabidopsis thaliana] (TAIR:AT1G52880.1); similar to NAC domain protein [Cymbidium hybrid cultivar] (GB:BAF36563.1); contains InterPro domain No apical meristem (NAM) protein; (InterPro:IPR003441)	(GO:0007275) multicellular organismal development [ISS]	(GO:0003700) transcription factor activity [ISS]	(GO:0005575) cellular_component [ND]			

AT3G04690	-0.77	ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein-tyrosine kinase	similar to protein kinase family protein [Arabidopsis thaliana] (TAIR:AT5G28680.1); similar to FER (FERONIA), kinase/ protein kinase [Arabidopsis thaliana] (TAIR:AT3G51550.1); similar to FERONIA receptor-like kinase [Arabidopsis lyrata] (GB:ABT18096.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO40132.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO44912.1); contains InterPro domain Protein kinase, core; (InterPro:IPR000719); contains InterPro domain Protein kinase-like (InterPro:IPR011009); contains InterPro domain Serine/threonine protein kinase, active site; (InterPro:IPR008271); contains InterPro domain Tyrosine protein kinase; (InterPro:IPR001245)	(GO:0006468) protein amino acid phosphorylation [IEA]	(GO:0016301) kinase activity [ISS]	(GO:0012505) endomembrane system [IEA]			
AT3G06145	-0.96	unknown protein	similar to unnamed protein product [Vitis vinifera] (GB:CAO71096.1)	(GO:0008150) biological_process [ND]	(GO:0003674) molecular_function [ND]	(GO:0005575) cellular_component [ND]			
AT3G07000	0.59	protein binding / zinc ion binding	similar to DC1 domain-containing protein [Arabidopsis thaliana] (TAIR:AT3G06990.1); similar to DC1 domain-containing protein [Arabidopsis thaliana] (TAIR:AT5G45730.1); similar to DC1 domain-containing protein [Brassica oleracea] (GB:ABD65623.1); contains InterPro domain Protein kinase C, phorbol ester/diacylglycerol binding; (InterPro:IPR002219); contains InterPro domain C1-like (InterPro:IPR011424); contains InterPro domain Zinc finger, PHD-type; (InterPro:IPR001965); contains InterPro domain DC1 (InterPro:IPR004146)	(GO:0007242) intracellular signaling cascade [IEA]	(GO:0005515) protein binding [IEA]	(GO:0008270) zinc ion binding [IEA]	(GO:0005575) cellular_component [ND]		
AT3G08940	-0.65	LHCB4.2	Lhcb4.2 protein (Lhcb4.2, protein involved in the light harvesting complex of photosystem II)	(GO:0009765) photosynthesis, light harvesting [IEA]	(GO:0016168) chlorophyll binding [ISS]	(GO:0016020) membrane [IDA]	(GO:0009535) chloroplast thylakoid membrane [IDA]	(GO:0009579) thylakoid [IDA]	(GO:0009941) chloroplast envelope [IDA]
AT3G09740	0.82	SYP71 (SYNTAXIN OF PLANTS 71)	syntaxin of plants 71 (SYP71)	(GO:0006612) protein targeting to membrane [IDA]	(GO:0006886) intracellular protein transport [TAS]	(GO:0008565) protein transporter activity [TAS]	(GO:0016021) integral to membrane [TAS]	(GO:0005886) plasma membrane [IDA]	
AT3G09922	-0.65	unknown protein	AF236376 Arabidopsis thaliana IPS1 mRNA, complete sequence	(GO:0016036) cellular response to phosphate starvation [IEP]	(GO:0003674) molecular_function [ND]	(GO:0005575) cellular_component [ND]			
AT3G10230	-0.77	LYC (LYCOPENE CYCLASE); lycopene beta cyclase	Encodes a protein with lycopene __cyclase activity. This enzyme uses the linear, symmetrical lycopene as substrate. However, unlike the __- cyclase which adds only one ring, the __-cyclase introduces a ring at both ends of lycopene to form the bicyclic __-carotene.	(GO:0016120) carotene biosynthetic process [IGI]	(GO:0045436) lycopene beta cyclase activity [IGI]	(GO:0009507) chloroplast [TAS]			

AT3G10400	0.92	RNA binding / nucleic acid binding	similar to ATSC35 (ARABIDOPSIS THALIANA ARGININE/SERINE-RICH SPLICING FACTOR 35, 35 KDA PROTEIN), RNA binding [Arabidopsis thaliana] (TAIR:AT5G64200.1); similar to ATSC35 (ARABIDOPSIS THALIANA ARGININE/SERINE-RICH SPLICING FACTOR 35, 35 KDA PROTEIN), RNA binding [Arabidopsis thaliana] (TAIR:AT5G64200.2); similar to unnamed protein product [Vitis vinifera] (GB:CAO68868.1); contains InterPro domain Zinc finger, CCHC-type; (InterPro:IPR01878); contains InterPro domain Ribonucleoprotein, BRUNO-like (InterPro:IPR015903); contains InterPro domain RNA recognition motif, RNP-1; (InterPro:IPR000504); contains InterPro domain Nucleotide-binding, alpha-beta plait; (InterPro:IPR012671); protein [Arabidopsis thaliana] (TAIR:AT1G05080.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO63564.1); contains InterPro domain Leucine-rich repeat 2 (InterPro:IPR013101); contains InterPro domain FBD (InterPro:IPR013596)	(GO:0008150) biological_process [ND]	(GO:0003723) RNA binding [ISS]	(GO:0005575) cellular_component [ND]			
AT3G10750	2.58	unknown protein	similar to ATPTPKIS1/DSP4/SEX4 (STARCH-EXCESS 4), polysaccharide binding / protein tyrosine/serine/threonine phosphatase [Arabidopsis thaliana] (TAIR:AT3G52180.1); similar to ATPTPKIS1/DSP4/SEX4 (STARCH-EXCESS 4), protein tyrosine/serine/threonine phosphatase [Arabidopsis thaliana] (TAIR:AT3G52180.2); similar to unnamed protein product [Vitis vinifera] (GB:CAO41479.1); contains InterPro domain Protein-tyrosine phosphatase, dual specificity; (InterPro:IPR000340); contains InterPro domain Protein-tyrosine phosphatase; (InterPro:IPR000387)	(GO:0008150) biological_process [ND]	(GO:0003674) molecular_function [ND]	(GO:0005575) cellular_component [ND]			
AT3G10940	-0.68	phosphoprotein phosphatase/ protein tyrosine/serine/threonine phosphatase	similar to ATPTPKIS1/DSP4/SEX4 (STARCH-EXCESS 4), polysaccharide binding / protein tyrosine/serine/threonine phosphatase [Arabidopsis thaliana] (TAIR:AT3G52180.1); similar to ATPTPKIS1/DSP4/SEX4 (STARCH-EXCESS 4), protein tyrosine/serine/threonine phosphatase [Arabidopsis thaliana] (TAIR:AT3G52180.2); similar to unnamed protein product [Vitis vinifera] (GB:CAO41479.1); contains InterPro domain Protein-tyrosine phosphatase, dual specificity; (InterPro:IPR000340); contains InterPro domain Protein-tyrosine phosphatase; (InterPro:IPR000387)	(GO:0006470) protein amino acid dephosphorylation [IEA]	(GO:0016311) dephosphorylation [IEA]	(GO:0016791) phosphatase activity [IEA]	(GO:0008138) protein tyrosine/serine/threonine phosphatase activity [IEA]	(GO:0009507) chloroplast [IDA]	
AT3G11340	1.16	UDP-glycosyltransferase/ transferase, transferring hexosyl groups	similar to UGT76C2 (UDP-glucosyl transferase 76C2), UDP-glycosyltransferase/ transferase, transferring glycosyl groups [Arabidopsis thaliana] (TAIR:AT5G05860.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO69089.1); contains InterPro domain UDP-glucuronosyl/UDP-glycosyltransferase; (InterPro:IPR002213)	(GO:0008152) metabolic process [IEA]	(GO:0008194) UDP-glycosyltransferase activity [ISS]	(GO:0012505) endomembrane system [IEA]			
AT3G12170	0.83	heat shock protein binding / unfolded protein binding	similar to ATJ6 (ARABIDOPSIS J-DOMAIN PROTEIN 6), heat shock protein binding / unfolded protein binding [Arabidopsis thaliana] (TAIR:AT5G06910.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO23538.1); contains InterPro domain Heat shock protein DnaJ; (InterPro:IPR003095); contains InterPro domain Heat shock protein DnaJ, N-terminal; (InterPro:IPR001623); contains InterPro domain Molecular chaperone, heat shock protein, Hsp40, DnaJ (InterPro:IPR015609)	(GO:0006457) protein folding [ISS]	(GO:0031072) heat shock protein binding [IEA]	(GO:0051082) unfolded protein binding [IEA]	(GO:0005575) cellular_component [ND]		
AT3G13950	0.73	unknown protein	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G13266.1); similar to Ankyrin [Medicago truncatula] (GB:ABN08906.1)	No annotation for biological_process	(GO:0003674) molecular_function [ND]	No annotation for cellular_component			

AT3G14990	0.80	catalytic	similar to DJ-1 family protein [Arabidopsis thaliana] (TAIR:AT1G53280.1); similar to ThiJ-like protein [Brassica rapa subsp. pekinensis] (GB:AAP96742.1); contains InterPro domain DJ-1 (InterPro:IPR006287); contains InterPro domain ThiJ/PtpI (InterPro:IPR002818)	(GO:0009228) thiamin biosynthetic process [ISS]	(GO:0046686) response to cadmium ion [IEP]	(GO:0003824) catalytic activity [ISS]	(GO:0005773) vacuole [IDA]	(GO:0005886) plasma membrane [IDA]	
AT3G15356	1.13	carbohydrate binding	[Arabidopsis thaliana] (TAIR:AT3G16530.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO69752.1); contains InterPro domain Legume lectin, alpha; (InterPro:IPR000985); contains InterPro domain Concanavalin A-like lectin/glucanase, subgroup (InterPro:IPR013320); contains InterPro domain L-type lectin, plant (InterPro:IPR016363); contains InterPro domain Legume lectin, beta domain; (InterPro:IPR001220); contains InterPro domain Concanavalin A-like lectin/glucanase (InterPro:IPR008985)	(GO:0008150) biological_processes [ND]	(GO:0030246) carbohydrate binding [ISS]	(GO:0048046) apoplast [IDA]	(GO:0005618) cell wall [IDA]		
AT3G15520	0.91	peptidyl-prolyl cis-trans isomerase	CYP37, chloroplast precursor (CYP37) [Arabidopsis Thaliana] (GB:P82869;GB:Q1JPN6;GB:Q9LDZ3); similar to CYP38 (CYCLOPHILIN 38), peptidyl-prolyl cis-trans isomerase [Arabidopsis thaliana] (TAIR:AT3G01480.1); similar to Os07g0565600 [Oryza sativa (japonica cultivar-group)] (GB:NP_001060013.1); similar to putative peptidyl-prolyl-cis-trans isomerase protein [Oryza sativa (japonica cultivar-group)] (GB:BAC79666.1); contains InterPro domain Cyclophilin-like (InterPro:IPR015891); contains InterPro domain Peptidyl-prolyl cis-trans isomerase, cyclophilin-type; (InterPro:IPR002190)	(GO:0006457) protein folding [IEA]	(GO:0003755) peptidyl-prolyl cis-trans isomerase activity [ISS]	(GO:0009535) chloroplast thylakoid membrane [IDA]	(GO:0009579) thylakoid [IDA]	(GO:0031977) thylakoid lumen [IDA]	(GO:0009543) chloroplast thylakoid lumen [IDA]
AT3G15570	-0.65	signal transducer	protein [Arabidopsis thaliana] (TAIR:AT1G52770.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO46021.1); contains InterPro domain NPH3; (InterPro:IPR006420)	(GO:0009416) response to light stimulus [ISS]	(GO:0004871) signal transducer activity [ISS]	(GO:0005575) cellular_component [ND]			
AT3G15660	0.60	electron transporter	(GRXS15) [Arabidopsis Thaliana] (GB:Q8LBK6;GB:Q9LW13); similar to thioredoxin family protein [Arabidopsis thaliana] (TAIR:AT4G04950.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO46047.1); contains InterPro domain Thioredoxin-like fold (InterPro:IPR012336); contains InterPro domain Glutaredoxin; (InterPro:IPR002109); contains InterPro domain Glutaredoxin-related protein (InterPro:IPR004480)	(GO:0045454) cell redox homeostasis [IEA]	(GO:0009055) electron carrier activity [IEA]	(GO:0015035) protein disulfide oxidoreductase activity [IEA]	(GO:0005739) mitochondrion [IDA]		
AT3G16440	0.88	ATMLP-300B (MYROSINASE-BINDING PROTEIN-LIKE PROTEIN-300B)	myrosinase-binding protein-like protein (AtMLP-300B) mRNA,	(GO:0009793) embryonic development ending in seed dormancy [IMP]	(GO:0003674) molecular_function [ND]	(GO:0005575) cellular_component [ND]			
AT3G18250	0.83	unknown protein	contains domain PROKAR_LIPOPROTEIN (PS51257)	(GO:0008150) biological_processes [ND]	(GO:0003674) molecular_function [ND]	(GO:0005575) cellular_component [ND]			

AT3G18280	1,11	lipid binding	similar to protease inhibitor/seed storage/lipid transfer protein (LTP) family protein [Arabidopsis thaliana] (TAIR:AT1G48750.1); similar to TED4 [Zinnia elegans] (GB:BAA06462.1); contains InterPro domain Plant lipid transfer protein/seed storage/trypsin-alpha amylase inhibitor (InterPro:IPR003612); contains InterPro domain Bifunctional inhibitor/plant lipid transfer protein/seed storage (InterPro:IPR016140); contains InterPro domain Plant lipid transfer protein and hydrophobic protein, helical; (InterPro:IPR013770)	(GO:0006869) lipid transport [ISS]	(GO:0008289) lipid binding [ISS]	(GO:0012505) endomembrane system [IEA]			
AT3G19390	0,85	cysteine-type endopeptidase/ cysteine-type peptidase	protease, putative [Arabidopsis thaliana] (TAIR:AT5G43060.1); similar to senescence-associated cysteine protease [Brassica oleracea] (GB:AAL60578.1); contains InterPro domain Peptidase C1A, papain; (InterPro:IPR013128); contains InterPro domain Peptidase C1A, papain C-terminal; (InterPro:IPR000668); contains InterPro domain Peptidase, cysteine peptidase active site; (InterPro:IPR000169); contains InterPro domain Proteinase inhibitor I29, cathepsin propeptide (InterPro:IPR013201); contains InterPro domain Granulin (InterPro:IPR000118)	(GO:0006508) proteolysis [IEA]	(GO:0008234) cysteine-type peptidase activity [ISS]	(GO:0012505) endomembrane system [IEA]			
AT3G20340	0,88	unknown protein	Expression of the gene is downregulated in the presence of paraquat, an inducer of photooxidative stress.	(GO:0006979) response to oxidative stress [IMP]	(GO:0003674) molecular_function [ND]	(GO:0005575) cellular_component [ND]			
AT3G20910	0,61	transcription factor	(GB:Q945M9;GB:Q9LIH3); similar to HAP2A (EMBRYO DEFECTIVE 2220), transcription factor [Arabidopsis thaliana] (TAIR:AT5G12840.4); similar to HAP2A (EMBRYO DEFECTIVE 2220), transcription factor [Arabidopsis thaliana] (TAIR:AT5G12840.3); similar to HAP2A (EMBRYO DEFECTIVE 2220), transcription factor [Arabidopsis thaliana] (TAIR:AT5G12840.2); similar to CCAAT-binding factor B subunit homolog (GB:AAC49266.1); similar to CCAAT-binding factor:SUBUNIT=B (GB:2204247A); contains InterPro domain CCAAT-binding transcription factor, subunit B; (InterPro:IPR001289)	(GO:0006355) regulation of transcription, DNA-dependent [ISS]	(GO:0003700) transcription factor activity [ISS]	(GO:0016602) CCAAT-binding factor complex [ISS]			
AT3G21080	2,76	unknown protein	similar to ABC transporter family protein [Arabidopsis thaliana] (TAIR:AT3G21090.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO16797.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN77224.1)	(GO:0008150) biological_process [ND]	(GO:0003674) molecular_function [ND]	(GO:0005575) cellular_component [ND]			

AT3G21720	1,12	catalytic/ isocitrate lyase	Identical to Isocitrate lyase (ICL) [Arabidopsis thaliana] (GB:P28297;GB:Q41948;GB:Q9LSZ2); similar to Isocitrate lyase (Isocitrase) (Isocitratase) (ICL) (GB:P17069); similar to Isocitrate lyase (Isocitrase) (Isocitratase) (ICL) (GB:P25248); similar to glyoxysomal isocitrate lyase [Brassica napus] (GB:CAA73792.1); contains InterPro domain Isocitrate lyase and phosphorylmutase; (InterPro:IPR000918); contains InterPro domain Isocitrate lyase; (InterPro:IPR006254); contains InterPro domain Isocitrate lyase and phosphorylmutase, core; (InterPro:IPR015809); contains InterPro domain Pyruvate/Phosphoenolpyruvate kinase, catalytic core; (InterPro:IPR015813)	(GO:0008152) metabolic process [ISS]	(GO:0004451) isocitrate lyase activity [ISS]	(GO:0005575) cellular_component [ND]		
AT3G22840	2,47	ELIP1 (EARLY LIGHT-INDUCIBLE PROTEIN); chlorophyll binding	Encodes an early light-inducible protein.	(GO:0009409) response to cold [IEP]	(GO:0016168) chlorophyll binding [ISS]	No annotation for cellular_component		
AT3G23120	0,93	kinase/ protein binding	LRR family protein [Arabidopsis thaliana] (TAIR:AT3G05360.1); similar to disease resistance family protein / LRR family protein [Arabidopsis thaliana] (TAIR:AT3G23010.1); similar to disease resistance family protein [Arabidopsis thaliana] (TAIR:AT3G23110.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO41175.1); contains InterPro domain Leucine-rich repeat, N-terminal (InterPro:IPR013210); contains InterPro domain Leucine-rich repeat; (InterPro:IPR001611)	(GO:0007165) signal transduction [IC]	(GO:0006952) defense response [ISS]	(GO:0016301) kinase activity [ISS]	(GO:0005515) protein binding [NAS]	(GO:0012505) endomembrane system [IEA]
AT3G23250	0,77	DNA binding	Member of the R2R3 factor gene family.	(GO:0009733) response to auxin stimulus [IEP]	regulation of transcription, DNA-dependent [ISS]	(GO:0009753) response to jasmonic acid stimulus [IEP]	(GO:0009723) response to ethylene stimulus [IEP]	(GO:0046686) response to cadmium ion [IEP]
AT3G23550	2,21	antiporter/ drug transporter/ transporter	similar to ALF5 (ABERRANT LATERAL ROOT FORMATION 5), antiporter/ transporter [Arabidopsis thaliana] (TAIR:AT3G23560.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO39304.1); contains InterPro domain Multi antimicrobial extrusion protein MatE; (InterPro:IPR002528)	(GO:0006855) multidrug transport [IEA]	(GO:0015297) antiporter activity [ISS]	(GO:0005215) transporter activity [ISS]	(GO:0016020) membrane [ISS]	
AT3G23560	1,33	ALF5 (ABERRANT LATERAL ROOT FORMATION 5); antiporter/ drug transporter/ transporter	Member of the multidrug and toxic compound extrusion (MATE) family, protects roots from inhibitory compounds.	(GO:0009636) response to toxin [ISS]	(GO:0015297) antiporter activity [ISS]	(GO:0005215) transporter activity [ISS]	(GO:0016020) membrane [ISS]	
AT3G28060	-0,93	unknown protein	similar to nodulin MtN21 family protein [Arabidopsis thaliana] (TAIR:AT5G40210.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN62735.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO14809.1); contains domain Multidrug resistance efflux transporter EmrE (SSF103481)	(GO:0008150) biological_processes [ND]	(GO:0003674) molecular_function [ND]	(GO:0016020) membrane [ISS]		
AT3G28210	1,22	PMZ	Encodes a putative zinc finger protein (PMZ).	(GO:0009737) response to abscisic acid stimulus [IEP]	(GO:0010200) response to chitin [IEP]	(GO:0008270) zinc ion binding [IEA]	(GO:0005575) cellular_component [ND]	

AT3G28270	-0.60	unknown protein	Identical to UPF0496 protein At3g28270 [Arabidopsis thaliana] (GB:Q9LHD9;GB:Q8H7D0;GB:Q8H7E9;GB:Q944H3); similar to AT14A [Arabidopsis thaliana] (TAIR:AT3G28290.1); similar to AT14A [Arabidopsis thaliana] (TAIR:AT3G28300.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO22906.1); contains InterPro domain Protein of unknown function DUF677 (InterPro:IPR007749)	(GO:0008150) biological_processes [ND]	(GO:0003674) molecular_function [ND]	(GO:0005575) cellular_component [ND]			
AT3G29030	-0.90	ATEXPA5 (ARABIDOPSIS THALIANA EXPANSIN A5)	Encodes an expansin. Naming convention from the Expansin Working Group (Kende et al, 2004. Plant Mol Bio)	(GO:0009826) unidimensional cell growth [NAS]	(GO:0009831) plant-type cell wall modification during multidimensional cell growth [ISS]	(GO:0009828) plant-type cell wall loosening [NAS]	(GO:0003674) molecular_function [TAS]	(GO:0012505) endomembrane system [IEA]	(GO:0005576) extracellular region [IEA]
AT3G30720	0.94	unknown protein	No description	(GO:0008150) biological_processes [ND]	(GO:0003674) molecular_function [ND]	(GO:0005575) cellular_component [ND]			
AT3G43835	0.99	unknown protein	transposable element gene; non-LTR retrotransposon family (LINE), has a 3.4e-26 P-value blast match to GB:NP_038604 L1 repeat, Tf1 subfamily, member 26 (LINE-element) (Mus musculus)						
AT3G46220	1.35	unknown protein ATHSP17.4	similar to unnamed protein product [Vitis vinifera] (GB:CAO21736.1)	(GO:0008150) biological_processes [ND]	No annotation for molecular_function	No annotation for cellular_component			
AT3G46300	0.92	unknown protein	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G46310.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN66779.1)	(GO:0008150) biological_processes [ND]	(GO:0003674) molecular_function [ND]	(GO:0005575) cellular_component [ND]			
AT3G46780	-0.76	unknown protein	similar to binding / catalytic/ coenzyme binding [Arabidopsis thaliana] (TAIR:AT3G18890.1); similar to unknown [Populus trichocarpa] (GB:ABK95703.1); contains InterPro domain NAD(P)-binding; (InterPro:IPR016040)	(GO:0008152) metabolic process [IEA]	(GO:0003824) catalytic activity [IEA]	(GO:0005488) binding [IEA]	(GO:0016020) membrane [IDA]	(GO:0009508) plastid chromosome [IDA]	(GO:0009535) chloroplast thylakoid membrane [IDA]
AT3G47620	-0.93	transcription factor	Encodes a transcription factor AtTCP14 that regulates seed germination. AtTCP14 shows elevated expression level just prior to germination. AtTCP14 is predominantly expressed in the vascular tissue of the embryo, and affects gene expression in radicles in a non-cell-autonomous manner.	(GO:0009739) response to gibberellin stimulus [IMP]	(GO:0010029) regulation of seed germination [IEP]	(GO:0009737) response to abscisic acid stimulus [IMP]	(GO:0045449) regulation of transcription [TAS]	(GO:0003700) transcription factor activity [ISS]	(GO:0005575) cellular_component [ND]
AT3G48140	0.57	unknown protein	similar to germination protein-related [Arabidopsis thaliana] (TAIR:AT3G29970.1); similar to HvB12D [Hordeum vulgare subsp. vulgare] (GB:CAA54065.1); contains InterPro domain B12D (InterPro:IPR010530)	(GO:0010150) leaf senescence [ISS]	(GO:0003674) molecular_function [ND]	(GO:0012505) endomembrane system [IEA]			
AT3G50260	2.37	DNA binding / transcription factor	encodes a member of the DREB subfamily A-5 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 16 members in this subfamily including RAP2.1, RAP2.9 and RAP2.10.	(GO:0006355) regulation of transcription, DNA-dependent [ISS]	(GO:0010200) response to chitin [IEP]	(GO:0003677) DNA binding [ISS]	(GO:0003700) transcription factor activity [ISS]	(GO:0005634) nucleus [ISS]	
AT3G50410	1.03	OBP1; DNA binding / transcription factor	Arabidopsis Dof protein containing a single 51-amino acid zinc finger DNA-binding domain, which may play an important roles in plant growth and development.	(GO:0009733) response to auxin stimulus [IEP]	(GO:0045941) positive regulation of transcription [TAS]	(GO:0009751) response to salicylic acid stimulus [IEP]	(GO:0045787) positive regulation of cell cycle [IMP]	(GO:0042545) cell wall modification [IMP]	(GO:0003677) DNA binding [IDA]

AT3G50930	1.40	ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding	similar to AAA-type ATPase family protein [Arabidopsis thaliana] (TAIR:AT3G50940.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN63838.1); contains InterPro domain AAA+ ATPase, core; (InterPro:IPR003593); contains InterPro domain AAA ATPase, core; (InterPro:IPR003959)	No annotation for biological process	(GO:0005524) ATP binding [ISS]	(GO:0016887) ATPase activity [ISS]	(GO:0009536) plastid [IDA]	(GO:0005739) mitochondrion [IDA]	
AT3G51240	0.87	F3H (TRANSPARENT TESTA 6); naringenin 3-dioxygenase	Encodes flavanone 3-hydroxylase that is coordinately expressed with chalcone synthase and chalcone isomerases. Regulates flavonoid biosynthesis.	(GO:0009813) flavonoid biosynthetic process [IMP]	(GO:0010224) response to UV-B [IMP]	(GO:0045486) naringenin 3-dioxygenase activity [IMP]	(GO:0005575) cellular_component [ND]		
AT3G51660	1.48	unknown protein	factor family protein / MIF family protein [Arabidopsis thaliana] (TAIR:AT5G01650.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO48792.1); contains InterPro domain Tautomerase (InterPro:IPR014347); contains InterPro domain Macrophage migration inhibitory factor (InterPro:IPR001398)	(GO:0006954) inflammatory response [ISS]	(GO:0051707) response to other organism [ISS]	(GO:0003674) molecular_function [ND]	(GO:0005777) peroxisome [IDA]		
AT3G52080	0.90	monovalent cation:proton antiporter	encodes a cation:proton exchanger expressed in pollen	(GO:0006812) cation transport [IC]	(GO:0005451) monovalent cation:proton antiporter activity [NAS]	(GO:0016020) membrane [IDA]			
AT3G54150	0.69	S-adenosylmethionine-dependent methyltransferase	similar to embryo-abundant protein-related [Arabidopsis thaliana] (TAIR:AT1G55450.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO67377.1); contains InterPro domain Methyltransferase type 11; (InterPro:IPR013216)	(GO:0008152) metabolic process [IEA]	(GO:0008168) methyltransferase activity [IEA]	(GO:0005575) cellular_component [ND]			
AT3G54420	0.83	ATEP3; chitinase	encodes an EP3 chitinase that is expressed during somatic embryogenesis in 'nursing' cells surrounding the embryos but not in embryos themselves. The gene is also expressed in mature pollen and growing pollen tubes until they enter the receptive synergid, but not in endosperm and integuments as in carrot. Post-embryonically, expression is found in hydathodes, stipules, root epidermis and emerging root hairs.	(GO:0010262) somatic embryogenesis [IEP]	(GO:0009626) plant-type hypersensitive response [TAS]	(GO:0004568) chitinase activity [ISS]	(GO:0005618) cell wall [IDA]		
AT3G54580	1.11	structural constituent of cell wall	contains InterPro domain Extensin-like region; (InterPro:IPR006706)	(GO:0009664) plant-type cell wall organization [IEA]	(GO:0005199) structural constituent of cell wall [IEA]	(GO:0012505) endomembrane system [IEA]			
AT3G55610	-1.03	catalytic/ glutamate 5-kinase/ glutamate-5-semialdehyde dehydrogenase	encodes delta 1-pyrroline-5-carboxylate synthetase B. Gene expression is induced by dehydration, high salt and ABA.	(GO:0006561) proline biosynthetic process [TAS]	(GO:0042538) hyperosmotic salinity response [IEP]	(GO:0009737) response to abscisic acid stimulus [IEP]	(GO:0009793) embryonic development ending in seed dormancy [IMP]	(GO:0004350) glutamate-5-semialdehyde dehydrogenase activity [IEA]	(GO:0003824) catalytic activity [IEA]
AT3G55980	-0.73	transcription factor	similar to CZF1/ZFAR1 [Arabidopsis thaliana] (TAIR:AT2G40140.2); similar to CZF1/ZFAR1, transcription factor [Arabidopsis thaliana] (TAIR:AT2G40140.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN68018.1); contains InterPro domain Zinc finger, CCCH-type; (InterPro:IPR000571); contains InterPro domain Ankyrin (InterPro:IPR002110)	(GO:0010200) response to chitin [IEP]	(GO:0045449) regulation of transcription [TAS]	(GO:0003700) transcription factor activity [ISS]	(GO:0005575) cellular_component [ND]		

AT3G56970	1,16	ORG2; DNA binding / transcription factor	GENE 3), DNA binding / transcription factor [Arabidopsis thaliana] (TAIR:AT3G56980.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO63053.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN64266.1); contains InterPro domain Achaete-scute transcription factor related (InterPro:IPR015660); contains InterPro domain Basic helix-loop-helix dimerisation region bHLH; (InterPro:IPR001092); contains InterPro domain Helix-loop-helix DNA-binding; (InterPro:IPR011598)	(GO:0045449) regulation of transcription [TAS]	(GO:0003677) DNA binding [ISS]	(GO:0003700) transcription factor activity [ISS]	(GO:0005634) nucleus [IEA]		
AT3G57010	1,65	strictosidine synthase	similar to strictosidine synthase family protein [Arabidopsis thaliana] (TAIR:AT3G57020.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO63060.1); contains InterPro domain Strictosidine synthase; (InterPro:IPR004141); contains InterPro domain Six-bladed beta-propeller, TolB-like (InterPro:IPR011042)	(GO:0009821) alkaloid biosynthetic process [ISS]	(GO:0016844) strictosidine synthase activity [ISS]	(GO:0005783) endoplasmic reticulum [IDA]			
AT3G57510	2,60	ADPG1; polygalacturonase	Arabidopsis thaliana ADPG1 gene	(GO:0005975) carbohydrate metabolic process [ISS]	(GO:0004650) polygalacturonase activity [ISS]	(GO:0012505) endomembrane system [IEA]			
AT3G59400	-0,92	GUN4	GUN, genomes uncoupled, is necessary for coupling the expression of some nuclear genes to the functional state of the chloroplast. Binds to the magnesium chelatase complex and promotes formation of the substrate, a tetrapyrrole signaling molecule. Porphyrin-binding protein that enhances the activity of Mg-chelatase. Although required for chlorophyll accumulation under normal growth conditions, GUN4 is not essential for chlorophyll synthesis.	(GO:0010019) chloroplast-nucleus signaling pathway [IMP]	(GO:0015995) chlorophyll biosynthetic process [TAS]	(GO:0043085) positive regulation of catalytic activity [TAS]	(GO:0046906) tetrapyrrole binding [IDA]	(GO:0019899) enzyme binding [IPI]	(GO:0009507) chloroplast [IDA]
AT3G59700	0,65	ATHLECRK (ARABIDOPSIS THALIANA LECTIN-RECEPTOR KINASE); kinase	member of Receptor kinase-like protein family	(GO:0006468) protein amino acid phosphorylation [IEA]	(GO:0016301) kinase activity [ISS]	(GO:0012505) endomembrane system [IEA]			
AT3G60140	1,48	DIN2 (DARK INDUCIBLE 2); hydrolase, hydrolyzing O-glycosyl compounds	Encodes a protein similar to beta-glucosidase and is a member of glycoside hydrolase family 1. Expression is induced after 24 hours of dark treatment, in senescing leaves and treatment with exogenous photosynthesis inhibitor. Induction of gene expression was suppressed in excised leaves supplied with sugar. The authors suggest that the gene's expression pattern is responding to the level of sugar in the cell.	(GO:0007568) aging [IEP]	(GO:0004553) hydrolase activity, hydrolyzing O-glycosyl compounds [ISS]	(GO:0012505) endomembrane system [IEA]			
AT3G62780	0,96	unknown protein	similar to C2 domain-containing protein [Arabidopsis thaliana] (TAIR:AT3G16510.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO70977.1); contains InterPro domain C2 calcium-dependent membrane targeting (InterPro:IPR000008); contains InterPro domain C2 calcium/lipid-binding region, CaLB (InterPro:IPR008973)	(GO:0008150) biological_process [ND]	(GO:0003674) molecular_function [ND]	(GO:0005575) cellular_component [ND]			

AT3G63010	0,74	catalytic	Encodes a gibberellin (GA) receptor ortholog of the rice GA receptor gene (OsGID1). Has GA-binding activity, showing higher affinity to GA4. Interacts with DELLA proteins in vivo in the presence of GA4.	(GO:0009939) positive regulation of gibberellic acid mediated signaling [IGI]	(GO:0010325) raffinose family oligosaccharide biosynthetic process [IGI]	(GO:0010476) gibberellin-mediated signaling [IGI]	(GO:0048444) floral organ morphogenesis [IGI]	(GO:0016787) hydrolase activity [IEA]	(GO:0005575) cellular_component [ND]
AT4G01830	1,10	ATPase, coupled to transmembrane movement of substances	5 (MDR5) [Arabidopsis thaliana] (GB:Q8SY13); similar to PGP11 (P-GLYCOPROTEIN 11), ATPase, coupled to transmembrane movement of substances [Arabidopsis thaliana] (TAIR:AT1G02520.1); similar to PGP12 (P-GLYCOPROTEIN 12), ATPase, coupled to transmembrane movement of substances [Arabidopsis thaliana] (TAIR:AT1G02530.1); similar to MDR3/PGP3 (P-GLYCOPROTEIN 3), ATPase, coupled to transmembrane movement of substances [Arabidopsis thaliana] (TAIR:AT4G01820.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN76787.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO70937.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO40233.1); contains InterPro domain ABC transporter, transmembrane region, type 1; (InterPro:IPR011527); contains InterPro domain ABC transporter, transmembrane region; (InterPro:IPR001140); contains InterPro domain ABC transporter related; (InterPro:IPR003439); contains InterPro domain AAA+ ATPase, core; (InterPro:IPR003593)	(GO:0006810) transport [IEA]	(GO:0042626) ATPase activity, coupled to transmembrane movement of substances [ISS]	(GO:0016021) integral to membrane [IEA]			
AT4G02380	1,00	SAG21 (SENESCENCE-ASSOCIATED GENE 21)	abundant like protein). Also known as SENESCENCE-ASSOCIATED GENE 21 (SAG21). Has a role on oxidative stress tolerance. mRNA levels are elevated in response to various stresses.	(GO:0009409) response to cold [IEP]	(GO:0000302) response to reactive oxygen species [IEP]	(GO:0006979) response to oxidative stress [IMP]	(GO:0009790) embryonic development [ISS]	(GO:0042631) cellular response to water deprivation [IEP]	(GO:0003674) molecular_function [ND]
AT4G02520	1,61	ATGSTF2; glutathione transferase	Encodes glutathione transferase belonging to the phi class of GSTs. Naming convention according to Wagner et al. (2002). The expression of this gene is upregulated by herbicide safeners such as benoxacor and fenclorim.	(GO:0009409) response to cold [IEP]	(GO:0042742) defense response to bacterium [IEP]	(GO:0046686) response to cadmium ion [IEP]	(GO:0009407) toxin catabolic process [TAS]	(GO:0009651) response to salt stress [IEP]	(GO:0004364) glutathione transferase activity [IDA]
AT4G02570	0,73	ATCUL1 (CULLIN 1)	Encodes a cullin that is a component of SCF ubiquitin ligase complexes involved in mediating responses to auxin and jasmonic acid. Homozygous auxin-resistant mutants arrest growth soon after germination, lacking a root and hypocotyl. Heterozygotes display a variety of phenotypes consistent with impaired auxin response.	(GO:0009733) response to auxin stimulus [IMP]	(GO:0010265) SCF complex assembly [IPI]	(GO:0009753) response to jasmonic acid stimulus [IMP]	(GO:0042752) regulation of circadian rhythm [IMP]	(GO:0009867) jasmonic acid mediated signaling pathway [TAS]	(GO:0007049) cell cycle [ISS]
AT4G05310	-1,16	unknown protein	similar to ubiquitin family protein [Arabidopsis thaliana] (TAIR:AT4G05270.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN76119.1); contains InterPro domain Ubiquitin; (InterPro:IPR000626)	No annotation for biological_processes	(GO:0003674) molecular_function [ND]	(GO:0005575) cellular_component [ND]			

AT4G09010	-0.79	peroxidase	Encodes a microsomal ascorbate peroxidase APX4. Ascorbate peroxidases are enzymes that scavenge hydrogen peroxide in plant cells. Eight types of APX have been described for Arabidopsis: three cytosolic (APX1, APX2, APX6), two chloroplastic types (stromal sAPX, thylakoid tAPX), and three microsomal (APX3, APX4, APX5) isoforms.	(GO:0006979) response to oxidative stress [IEA]	(GO:0004601) peroxidase activity [ISS]	(GO:0005634) nucleus [IDA]	(GO:0009535) chloroplast thylakoid membrane [IDA]	(GO:0005737) cytoplasm [IDA]	(GO:0031977) thylakoid lumen [IDA]
AT4G12300	0.91	CYP706A4; heme binding / iron ion binding / monooxygenase/ oxygen binding	similar to CYP706A dehydrogenase/reductase (SDR) family protein [Arabidopsis thaliana] (TAIR:AT3G03980.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO23493.1); contains InterPro domain Glucose/ribitol dehydrogenase; (InterPro:IPR002347); contains InterPro domain Short-chain dehydrogenase/reductase SDR; (InterPro:IPR002198); contains InterPro domain NAD(P)-binding; (InterPro:IPR016040)	No annotation for biological_processes	(GO:0019825) oxygen binding [ISS]	(GO:0005575) cellular_component [ND]			
AT4G13180	1.21	oxidoreductase		(GO:0046685) response to arsenic [IEP]	(GO:0016491) oxidoreductase activity [ISS]	No annotation for cellular_component			
AT4G13660	0.97	unknown protein	encodes a protein whose sequence is similar to pinorensinol-laricresinol reductase from pine.	(GO:0009807) lignan biosynthetic process [IDA]	(GO:0010283) pinorensinol reductase activity [IDA]	(GO:0005575) cellular_component [ND]			
AT4G14130	1.11	XTR7 (XYLOGLUCAN ENDOTRANSGLYCOSYLASE 7); hydrolase, acting on glycosyl bonds / hydrolase, hydrolyzing O-glycosyl compounds	xyloglucan endotransglycosylase-related protein (XTR7)	(GO:0006073) glucan metabolic process [IEA]	(GO:0005975) carbohydrate metabolic process [IEA]	(GO:0016798) hydrolase activity, acting on glycosyl bonds [ISS]	(GO:0048046) apoplast [IEA]	(GO:0012505) endomembrane system [IEA]	(GO:0005618) cell wall [IEA]
AT4G14365	1.00	protein binding / ubiquitin-protein ligase/ zinc ion binding	finger) family protein / ankyrin repeat family protein [Arabidopsis thaliana] (TAIR:AT3G23280.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO71418.1); contains InterPro domain Zinc finger, RING/FYVE/PHD-type (InterPro:IPR013083); contains InterPro domain Zinc finger, RING-type; (InterPro:IPR001841); contains InterPro domain Ankyrin (InterPro:IPR002110)	No annotation for biological_processes	(GO:0005515) protein binding [ISS]	(GO:0008270) zinc ion binding [ISS]	No annotation for cellular_component		
AT4G15610	1.46	unknown protein	Identical to UPF0497 membrane protein At4g15610 [Arabidopsis Thaliana] (GB:Q9FE29;GB:O23412); similar to integral membrane family protein [Arabidopsis thaliana] (TAIR:AT3G06390.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO71018.1); contains InterPro domain Conserved hypothetical protein CHP01569, trans-membrane plant (InterPro:IPR006459); contains InterPro domain Protein of unknown function DUF559 (InterPro:IPR006470)	(GO:0008150) biological_processes [ND]	(GO:0003674) molecular_function [ND]	(GO:0005575) cellular_component [ND]			
AT4G15910	1.06	ATDI21	and leaves increases to progressive drought stress. The transcript level is also affected by changes of endogenous or exogenous abscisic acid level. It appears to be a member of plant-specific gene family that includes late embryo-abundant and zinc- IAA-induced proteins in other plants.	(GO:0009414) response to water deprivation [IEP]	(GO:0009737) response to abscisic acid stimulus [IGI]	(GO:0009790) embryonic development [ISS]	(GO:0003674) molecular_function [ND]	No annotation for cellular_component	

AT4G16260	1.12	hydrolase, hydrolyzing O-glycosyl compounds	hydrolase, hydrolyzing O-glycosyl compounds [Arabidopsis thaliana] (TAIR:AT3G57270.1); similar to beta-1,3-glucanase [Hevea brasiliensis] (GB:ABG49448.1); contains InterPro domain Glycoside hydrolase, family 17; (InterPro:IPR000490); contains InterPro domain Glycoside hydrolase, catalytic core; (InterPro:IPR013781)	(GO:0009651) response to salt stress [IEP]	(GO:0004553) hydrolase activity, hydrolyzing O-glycosyl compounds [ISS]	(GO:0005618) cell wall [IDA]	(GO:0005886) plasma membrane [IDA]		
AT4G16515	-1.00	unknown protein	No description	(GO:0008150) biological_processes [ND]	(GO:0003674) molecular_function [ND]	(GO:0012505) endomembrane system [IEA]			
AT4G16563	0.88	pepsin A	similar to aspartyl protease family protein [Arabidopsis thaliana] (TAIR:AT5G45120.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO16479.1); contains InterPro domain Peptidase aspartic, catalytic; (InterPro:IPR009007); contains InterPro domain Peptidase A1; (InterPro:IPR001461)	(GO:0006508) proteolysis [ISS]	No annotation for molecular_function	(GO:0009505) plant-type cell wall [IDA]			
AT4G16745	1.17	unknown protein	similar to exostosin family protein [Arabidopsis thaliana] (TAIR:AT5G19670.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO16155.1); contains InterPro domain Cysteine dipeptidase (InterPro:IPR004266)	(GO:0008150) biological_processes [ND]	(GO:0003674) molecular_function [ND]	(GO:0016020) membrane [ISS]			
AT4G18930	0.60	cyclic-nucleotide phosphodiesterase	[Arabidopsis thaliana] (GB:O04147); similar to cyclic phosphodiesterase, putative [Arabidopsis thaliana] (TAIR:AT4G18940.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO47982.1); contains InterPro domain 2, 3 cyclic phosphodiesterase, plant; (InterPro:IPR012386); contains InterPro domain tRNA ligase/cyclic nucleotide phosphodiesterase; (InterPro:IPR009097)	(GO:0006388) tRNA splicing [TAS]	(GO:0004112) cyclic-nucleotide phosphodiesterase activity [IDA]	(GO:0005737) cytoplasm [IDA]			
AT4G19170	-1.23	NCED4 (NINE-CIS-EPOXYCAROTENOID DIOXYGENASE 4)	chloroplast-targeted member of a family of enzymes similar to nine-cis-epoxycarotenoid dioxygenase	No annotation for biological_processes	No annotation for molecular_function	(GO:0010287) plastoglobule [IDA]	(GO:0009507) chloroplast [IDA]		
AT4G21280	-0.94	calcium ion binding	Encodes the PsbQ subunit of the oxygen evolving complex of photosystem II.	(GO:0009626) plant-type hypersensitive response [IDA]	(GO:0005509) calcium ion binding [IEA]	(GO:0009535) chloroplast thylakoid membrane [IDA]	(GO:0030095) chloroplast photosystem II [ISS]	(GO:0009579) thylakoid [IDA]	(GO:0009654) oxygen evolving complex [ISS]
AT4G22470	1.94	lipid binding	thaliana] (TAIR:AT4G22485.1); similar to extensin like protein [Ipomoea nil] (GB:BAF46299.1); contains InterPro domain Plant lipid transfer protein/seed storage/trypsin-alpha amylase inhibitor (InterPro:IPR003612); contains InterPro domain Bifunctional inhibitor/plant lipid transfer protein/seed storage (InterPro:IPR016140); contains InterPro domain Plant lipid transfer protein and hydrophobic protein, helical; (InterPro:IPR013770)	(GO:0006869) lipid transport [ISS]	(GO:0008289) lipid binding [ISS]	(GO:0012505) endomembrane system [IEA]			

AT4G24690	0,75	zinc ion binding	similar to unknown [Populus trichocarpa] (GB:ABK95898.1); similar to Os02g0593700 [Oryza sativa (japonica cultivar-group)] (GB:NP_001047302.1); contains InterPro domain Zinc finger, ZZ-type; (InterPro:IPR000433); contains InterPro domain Octicosapeptide/Phox/Bem1p (InterPro:IPR000270); contains InterPro domain Ubiquitin-associated/translation elongation factor EF1B, N-terminal (InterPro:IPR000449)	(GO:0008150) biological_processes [ND]	(GO:0008270) zinc ion binding [IEA]	(GO:0005737) cytoplasm [IDA]			
AT4G25110	0,86	AT4G25110.3.6-MITO	cysteine-type endopeptidase [Arabidopsis thaliana] (TAIR:AT1G02170.1); similar to unknown [Populus trichocarpa] (GB:ABK95057.1); contains InterPro domain Peptidase C14, caspase catalytic; (InterPro:IPR011600); contains InterPro domain Zinc finger, LSD1-type (InterPro:IPR005735)	(GO:0006508) proteolysis [ISS]	No annotation for molecular_function	No annotation for cellular_component			
AT4G25200	0,95	(MITOCHONDRION-LOCALIZED SMALL HEAT SHOCK PROTEIN 23.6)	AtHSP23.6-mito mRNA, nuclear gene encoding mitochondrial	(GO:0009408) response to heat [ISS]	(GO:0046686) response to cadmium ion [IEP]	(GO:0003674) molecular_function [ND]	No annotation for cellular_component		
AT4G25580	0,76	unknown protein	similar to LTI65/RD29B (RESPONSIVE TO DESSICATION 29B) [Arabidopsis thaliana] (TAIR:AT5G52300.1); similar to LTI65/RD29B (RESPONSIVE TO DESSICATION 29B) [Arabidopsis thaliana] (TAIR:AT5G52300.2); similar to stress responsive protein [Brassica oleracea var. acephala] (GB:AAR21079.1); contains InterPro domain CAP160 (InterPro:IPR012418)	No annotation for biological_processes	No annotation for molecular_function	(GO:0005575) cellular_component [ND]			
AT4G26530	-1,44	fructose-bisphosphate aldolase	similar to fructose-bisphosphate aldolase, cytoplasmic [Arabidopsis thaliana] (TAIR:AT4G26520.1); similar to unknown [Populus trichocarpa] (GB:ABK94744.1); contains InterPro domain Aldolase-type TIM barrel; (InterPro:IPR013785); contains InterPro domain Fructose-bisphosphate aldolase, class-I; (InterPro:IPR000741)	(GO:0006096) glycolysis [ISS]	(GO:0004332) fructose-bisphosphate aldolase activity [ISS]	(GO:0009507) chloroplast [IDA]			
AT4G26920	0,84	unknown protein	similar to homeobox protein-related [Arabidopsis thaliana] (TAIR:AT5G07260.1); similar to baby boom interacting protein 2 [Brassica napus] (GB:ABA70760.1); contains InterPro domain Zinc-binding START domain [Arabidopsis thaliana] (TAIR:AT5G07260.1)	(GO:0008150) biological_processes [ND]	(GO:0003674) molecular_function [ND]	(GO:0005575) cellular_component [ND]			
AT4G27340	2,34	unknown protein	thaliana] (TAIR:AT3G56120.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO39182.1); contains InterPro domain Protein of unknown function Met10 (InterPro:IPR003402)	(GO:0008150) biological_processes [ND]	No annotation for molecular_function	No annotation for cellular_component			
AT4G27710	0,75	CYP709B3; heme binding / iron ion binding / monooxygenase/ oxygen binding	member of CYP709B	No annotation for biological_processes [ISS]	(GO:0019825) oxygen binding [IEA]	(GO:0012505) endomembrane system [IEA]			
AT4G27730	0,82	ATOPT6; oligopeptide transporter	oligopeptide transporter	(GO:0006857) oligopeptide transport [IGI]	(GO:0015198) oligopeptide transporter activity [IGI]	(GO:0016020) membrane [ISS]	(GO:0005886) plasma membrane [IDA]		

AT4G28088	1.25	unknown protein	similar to hydrophobic protein, putative / low temperature and salt responsive protein, putative [Arabidopsis thaliana] (TAIR:AT2G24040.1); similar to unknown [Populus trichocarpa] (GB:ABK93775.1); contains InterPro domain Protein of unknown function UPF0057; (InterPro:IPR000612)	(GO:0008150) biological_processes [ND]	No annotation for molecular_function [IEA]	(GO:0012505) endomembrane system [IEA]	(GO:0016021) integral to membrane [IEA]		
AT4G28190	1.63	ULT1 (ULTRAPETALA1); DNA binding	Encodes a novel Cys-rich protein with a B-box like domain that acts as a negative regulator of meristem cell accumulation in inflorescence and floral meristems as loss-of-function ult1 mutations cause inflorescence meristem enlargement, the production of extra flowers and floral organs, and a decrease in floral meristem determinacy.	(GO:0010022) meristem determinacy [IMP]	(GO:0010582) floral meristem determinacy [IGI]	(GO:0010081) regulation of inflorescence meristem growth [IMP]	(GO:0010080) regulation of floral meristem growth [IMP]	(GO:0003677) DNA binding [IEA]	(GO:0005488) binding [IEA]
AT4G28250	-1.41	ATEXPB3 (ARABIDOPSIS THALIANA EXPANSIN B3)	putative beta-expansin/allergen protein. Naming convention from the Expansin Working Group (Kende et al, 2004. Plant Mol Bio). Involved in the formation of nematode-induced syncytia in roots of Arabidopsis thaliana.	(GO:0009826) unidimensional cell growth [NAS]	(GO:0009664) plant-type cell wall organization [ISS]	(GO:0009828) plant-type cell wall loosening [NAS]	(GO:0006949) syncytium formation [IEP]	(GO:0003674) molecular_function [TAS]	(GO:0012505) endomembrane system [IEA]
AT4G28400	0.67	2C unknown protein	similar to protein phosphatase 2C, putative / PP2C, putative [Arabidopsis thaliana] (TAIR:AT2G20630.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN81770.1); contains InterPro domain Protein phosphatase 2C-related; (InterPro:IPR001932); contains InterPro domain Protein phosphatase 2C; (InterPro:IPR015655); contains InterPro domain Protein phosphatase 2C, N-terminal (InterPro:IPR014045)	No annotation for biological_processes [ND]	(GO:0004722) protein serine/threonine phosphatase activity [ISS]	(GO:0005575) cellular_component [ND]			
AT4G30290	0.93	ATXTH19; hydrolase, acting on glycosyl bonds / hydrolase, hydrolyzing O-glycosyl compounds	putative xyloglucan endotransglycosylase/hydrolase, expressed throughout both the main and the lateral root, with intensive expression at the dividing and elongating regions. Is expressed in lateral root primordia but expression ceases after lateral root begins to grow.	(GO:0006073) glucan metabolic process [IEA]	(GO:0005975) carbohydrate metabolic process [IEA]	(GO:0016798) hydrolase activity, acting on glycosyl bonds [ISS]	(GO:0048046) apoplast [IEA]	(GO:0012505) endomembrane system [IEA]	(GO:0005618) cell wall [IEA]
AT4G30910	2.13	aminopeptidase	chloroplast precursor [Arabidopsis Thaliana] (GB:Q8RX72;GB:O65558); similar to cytosol aminopeptidase [Arabidopsis thaliana] (TAIR:AT2G24200.1); similar to cytosol aminopeptidase family protein [Arabidopsis thaliana] (TAIR:AT4G30920.1); similar to cytosol aminopeptidase [Arabidopsis thaliana] (TAIR:AT2G24200.2); similar to neutral leucine aminopeptidase preprotein; preLAP-N; metallo-exopeptidase; leucyl aminopeptidase; LAP [Lycopersicon esculentum] (GB:AAO15916.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO66676.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN66364.1); contains InterPro domain Peptidase M17, leucyl aminopeptidase; (InterPro:IPR011356); contains InterPro domain Peptidase M17, leucyl aminopeptidase, N-terminal; (InterPro:IPR008283); contains InterPro domain Peptidase M17, leucyl aminopeptidase, C-terminal; (InterPro:IPR000819)	(GO:0006508) proteolysis [ISS]	(GO:0004177) aminopeptidase activity [ISS]	(GO:0009507) chloroplast [IDA]			
AT4G31500	0.91	CYP83B1 (CYTOCHROME P450 MONOOXYGENASE 83B1); oxygen binding	Encodes an oxime-metabolizing enzyme in the biosynthetic pathway of glucosinolates. Is required for phytochrome signal transduction in red light. Mutation confers auxin overproduction.	(GO:0048830) adventitious root development [TAS]	(GO:0000162) tryptophan biosynthetic process [IMP]	(GO:0009759) indole glucosinolate biosynthetic process [IDA]	(GO:0009641) shade avoidance [IMP]	(GO:0009684) indoleacetic acid biosynthetic process [IMP]	(GO:0010114) response to red light [IMP]

AT4G31800	1,10	WRKY18; transcription factor	Pathogen-induced transcription factor. Binds W-box sequences in vitro. Forms protein complexes with itself and with WRKY40 and WRKY60. Constitutive expression of WRKY18 enhanced resistance to <i>P. syringae</i> , but its coexpression with WRKY40 or WRKY60 made plants more susceptible to both <i>P. syringae</i> and <i>B. cinerea</i> . WRKY18, WRKY40, and WRKY60 have partially redundant roles in response to the hemibiotrophic bacterial pathogen <i>Pseudomonas syringae</i> and the necrotrophic fungal pathogen <i>Botrytis cinerea</i> , with WRKY18 playing a more important role than the other two.	(GO:0050832) defense response to fungus [IEP]	(GO:0006355) regulation of transcription, DNA-dependent [ISS]	(GO:0042742) defense response to bacterium [IEP]	(GO:0009751) response to salicylic acid stimulus [IEP]	(GO:0010200) response to chitin [IEP]	(GO:0031347) regulation of defense response [IMP]
AT4G32150	0,91	VAMP7C (VESICLE-ASSOCIATED MEMBRANE PROTEIN 7C)	AtVAMP711 is a member of Synaptobrevin-like AtVAMP7C, v-SNARE (soluble N-ethyl-maleimide sensitive factor attachment protein receptors) protein family. SNAREs have been divided into four subgroups: Qa-, Qb-, Qc- and R-SNAREs. R-SNAREs are classified into three groups, the Sec22-, YKT6- and VAMP7-like R-SNAREs. One R-SNARE and three Q-SNAREs (one of each subgroup) form the trans-SNARE complex, which governs specific membrane fusions. VAMP7 proteins consist of three distinct domain, the N-terminal longin-domain (LD), the SNARE motif (SNM) and a transmembrane domain. In spite of the high similarities among the VAMP7 proteins, they show different subcellular localizations. VAMP7C is vacuolar-localized and its LD is essential for the correct localization. Generally, it is suggested that the complete LD is the determinant of subcellular sorting in both animal and plant R-SNAREs.	(GO:0006944) membrane fusion [TAS]	(GO:0046909) intermembrane transport [TAS]	(GO:0009651) response to salt stress [IMP]	No annotation for molecular_function	(GO:0016020) membrane [ISS]	(GO:0005773) vacuole [IDA]
AT4G33070	0,90	pyruvate decarboxylase	similar to PDC3 (PYRUVATE DECARBOXYLASE-3), pyruvate decarboxylase [Arabidopsis thaliana] (TAIR:AT5G01330.1); similar to PDC2 (PYRUVATE DECARBOXYLASE-2), pyruvate decarboxylase [Arabidopsis thaliana] (TAIR:AT5G54960.1); similar to pyruvate decarboxylase, putative [Arabidopsis thaliana] (TAIR:AT5G01320.1); similar to pyruvate decarboxylase [Fragaria x ananassa] (GB:AAL37492.1); similar to pyruvate decarboxylase [Dianthus caryophyllus] (GB:AAP96920.1); similar to pyruvate decarboxylase 1 [Lotus corniculatus] (GB:AAO72533.1); contains InterPro domain Thiamine pyrophosphate enzyme, N-terminal TPP binding region; (InterPro:IPR012001); contains InterPro domain Pyruvate decarboxylase/indolepyruvate decarboxylase; (InterPro:IPR012110); contains InterPro domain Thiamine pyrophosphate enzyme, C-terminal TPP-binding; (InterPro:IPR011766); contains InterPro domain Thiamine pyrophosphate enzyme, central region; (InterPro:IPR012000)	No annotation for biological_process	(GO:0004737) pyruvate decarboxylase activity [ISS]	(GO:0016020) membrane [IDA]			

AT4G33355	0,83	lipid binding unknown protein	similar to LTP3 (LIPID TRANSFER PROTEIN 3), lipid binding [Arabidopsis thaliana] (TAIR:AT5G59320.1); similar to non-specific lipid transfer-like protein [Prosopis juliflora] (GB:ABF06565.1); contains InterPro domain Plant lipid transfer protein/seed storage/trypsin-alpha amylase inhibitor (InterPro:IPR003612); contains InterPro domain Plant lipid transfer protein/Par allergen; (InterPro:IPR000528); contains InterPro domain Bifunctional inhibitor/plant lipid transfer protein/seed storage (InterPro:IPR016140); contains InterPro domain Plant lipid transfer protein and hydrophobic protein, helical; (InterPro:IPR013770)	(GO:0006869) lipid transport [ISS]	(GO:0008289) lipid binding [ISS]	(GO:0012505) endomembrane system [IEA]			
AT4G34590	0,63	GBF6; DNA binding / transcription factor	Encodes a basic domain leucine zipper (bZip) transcription factor.	(GO:0006355) regulation of transcription, DNA-dependent [ISS]	(GO:0009744) response to sucrose stimulus [IEP]	(GO:0003677) DNA binding [ISS]	(GO:0046982) protein heterodimerization activity [IPI]	(GO:0003700) transcription factor activity [ISS]	(GO:0005634) nucleus [IEA]
AT4G34950	1,20	unknown protein	nodulin family protein; similar to nodulin family protein [Arabidopsis thaliana] (TAIR:AT2G16660.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO47362.1); similar to hypothetical protein OsJ_030248 [Oryza sativa (japonica cultivar-group)] (GB:EAZ16039.1); similar to hypothetical protein Osl_031123 [Oryza sativa (indica cultivar-group)] (GB:EAZ09891.1); contains InterPro domain Major facilitator superfamily MFS-1 (InterPro:IPR011701); contains InterPro domain MFS general substrate transporter (InterPro:IPR016196); contains InterPro domain Nodulin-like (InterPro:IPR010658)						
AT4G36010	1,07	unknown protein	similar to pathogenesis-related thaumatin family protein [Arabidopsis thaliana] (TAIR:AT2G17860.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN59783.1); contains InterPro domain Thaumatin, pathogenesis-related (InterPro:IPR001938)	(GO:0051707) response to other organism [ISS]	(GO:0003674) molecular_function [ND]	(GO:0031225) anchored to membrane [TAS]			
AT4G36670	1,02	carbohydrate transporter/ sugar porter	(PLT6) [Arabidopsis thaliana] (GB:Q8GXR2;GB:O23213); similar to mannitol transporter, putative [Arabidopsis thaliana] (TAIR:AT2G18480.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN68316.1); contains InterPro domain General substrate transporter; (InterPro:IPR005828); contains InterPro domain Major facilitator superfamily; (InterPro:IPR007114); contains InterPro domain Sugar transporter, conserved site; (InterPro:IPR005829); contains InterPro domain MFS general substrate transporter (InterPro:IPR016196); contains InterPro domain Sugar transporter; (InterPro:IPR003663)	(GO:0006810) transport [IEA]	(GO:0008643) carbohydrate transport [IEA]	(GO:0015144) carbohydrate transmembrane transporter activity [ISS]	(GO:0005351) sugar:hydrogen symporter activity [ISS]	(GO:0016020) membrane [ISS]	
AT4G37295	1,54	unknown protein	No description	(GO:0008150) biological_process [ND]	(GO:0003674) molecular_function [ND]	(GO:0012505) endomembrane system [IEA]			

AT4G37530	1.45	peroxidase	[Arabidopsis Thaliana] (GB:Q9SE7;GB:Q8VYK8); similar to peroxidase 50 (PER50) (P50) (PRXR2) [Arabidopsis thaliana] (TAIR:AT4G37520.1); similar to peroxidase 1 [Artemisia annua] (GB:AAO45182.1); contains InterPro domain Plant peroxidase; (InterPro:IPR000823); contains InterPro domain Haem peroxidase; (InterPro:IPR010255); contains InterPro domain Haem peroxidase, plant/fungal/bacterial; (InterPro:IPR002016)	(GO:0009651) response to salt stress [IEP]	(GO:0004601) peroxidase activity [ISS]	(GO:0012505) endomembrane system [IEA]			
AT4G38770	-0.85	PRP4 (PROLINE-RICH PROTEIN 4)	Encodes one of four proline-rich proteins in Arabidopsis which are predicted to localize to the cell wall. Transcripts are most abundant in aerial organs of the plant.	No annotation for biological_processes	No annotation for molecular_function	(GO:0005618) cell wall [ISS]			
AT4G39260	0.69	ATGRP8 (GLYCINE-RICH PROTEIN 8); RNA binding / nucleic acid binding	Encodes a glycine-rich protein with RNA binding domain at the N-terminus. Protein is structurally similar to proteins induced by stress in other plants. Gene expression is induced by cold. Transcript undergoes circadian oscillations that is depressed by overexpression of AGRP7.	(GO:0009409) response to cold [IEP]	(GO:0009651) response to salt stress [IEP]	(GO:0045087) innate immune response [IDA]	(GO:0003723) RNA binding [ISS]	(GO:0005777) peroxisome [IDA]	(GO:0005618) cell wall [IDA]
AT4G39270	1.26	ATP binding / protein kinase/ protein serine/threonine kinase/ protein-tyrosine kinase	protein kinase, putative [Arabidopsis thaliana] (TAIR:AT2G16250.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO47625.1); contains InterPro domain Protein kinase, core; (InterPro:IPR000719); contains InterPro domain Protein kinase-like (InterPro:IPR011009); contains InterPro domain Leucine-rich repeat, N-terminal (InterPro:IPR013210); contains InterPro domain Leucine-rich repeat; (InterPro:IPR001611)	(GO:0006468) protein amino acid phosphorylation [ISS]	(GO:0007169) transmembrane receptor protein tyrosine kinase signaling pathway [ISS]	(GO:0005524) ATP binding [ISS]	(GO:0004674) protein serine/threonine kinase activity [ISS]	(GO:0012505) endomembrane system [IEA]	
AT4G39675	0.91	unknown protein	No description	(GO:0008150) biological_processes [ND]	(GO:0003674) molecular_function [ND]	(GO:0005575) cellular_component [ND]			
AT5G01870	3.01	lipid binding	similar to LTP6 (Lipid transfer protein 6), lipid binding [Arabidopsis thaliana] (TAIR:AT3G08770.1); similar to unknown [Populus trichocarpa] (GB:ABK95728.1); contains InterPro domain Plant lipid transfer protein/seed storage/trypsin-alpha amylase inhibitor (InterPro:IPR003612); contains InterPro domain Plant lipid transfer protein/Par allergen; (InterPro:IPR000528); contains InterPro domain Bifunctional inhibitor/plant lipid transfer protein/seed storage (InterPro:IPR016140); contains InterPro domain Plant lipid transfer protein and hydrophobic protein, helical; (InterPro:IPR013770)	(GO:0006869) lipid transport [ISS]	(GO:0008289) lipid binding [ISS]	(GO:0012505) endomembrane system [IEA]			
AT5G03910	0.92	ATATH12; ATPase, coupled to transmembrane movement of substances	member of ATH subfamily	(GO:0006810) transport [IEA]	(GO:0042626) ATPase activity, coupled to transmembrane movement of substances [ISS]	(GO:0005215) transporter activity [ISS]	(GO:0009941) chloroplast envelope [IDA]	(GO:0009507) chloroplast [IDA]	

AT5G04330	0.65	heme binding / iron ion binding / monooxygenase/ oxygen binding	similar to FAH1 (FERULATE-5-HYDROXYLASE 1), ferulate 5-hydroxylase [Arabidopsis thaliana] (TAIR:AT4G36220.1); similar to cytochrome P450 [Isatis tinctoria] (GB:ABL07485.1); contains InterPro domain Cytochrome P450, E-class, group I; (InterPro:IPR002401); contains InterPro domain Cytochrome P450, E-class, group I; (InterPro:IPR002401); contains InterPro domain Cytochrome P450, E-class, group I; (InterPro:IPR002401)	No annotation for biological_processes	(GO:0019825) oxygen binding [ISS]	(GO:0012505) endomembrane system [IEA]			
AT5G06500	0.98	DNA binding / transcription factor	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G40210.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO39914.1); contains InterPro domain Transcription factor, MADS-box; (InterPro:IPR002100)	(GO:0006355) regulation of transcription, DNA-dependent [IEA]	(GO:0003677) DNA binding [ISS]	(GO:0003700) transcription factor activity [ISS]	(GO:0005634) nucleus [IEA]		
AT5G06610	0.67	unknown protein	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G27690.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO23452.1); contains InterPro domain Protein of unknown function DUF620 (InterPro:IPR006873)	(GO:0008150) biological_processes [ND]	(GO:0003674) molecular_function [ND]	(GO:0005575) cellular_component [ND]			
AT5G09420	1.32	amidase	similar to ATTOC64-III (ARABIDOPSIS THALIANA TRANSLOCON AT THE OUTER MEMBRANE OF CHLOROPLASTS 64-III), binding / carbon-nitrogen ligase, with glutamine as amido-N-donor [Arabidopsis thaliana] (TAIR:AT3G17970.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO62642.1); contains InterPro domain Amidase signature enzyme; (InterPro:IPR000120); contains InterPro domain Tetra(tri)copeptide-like helical; (InterPro:IPR011990); contains InterPro domain Tetra(tri)copeptide TPR-1 (InterPro:IPR001440); contains InterPro domain Tetra(tri)copeptide TPR2 (InterPro:IPR013105); contains InterPro domain Tetra(tri)copeptide region (InterPro:IPR013026)	(GO:0006626) protein targeting to mitochondrion [IMP]	(GO:0004040) amidase activity [ISS]	(GO:0005739) mitochondrion [IDA]			
AT5G09440	1.14	unknown protein	similar to phosphate-responsive protein, putative [Arabidopsis thaliana] (TAIR:AT5G64260.1); similar to unknown [Populus trichocarpa x Populus deltoides] (GB:ABK96539.1); contains InterPro domain Phosphate-induced protein 1 conserved region (InterPro:IPR006766)	(GO:0008150) biological_processes [ND]	(GO:0003674) molecular_function [ND]	(GO:0016020) membrane [IDA]			
AT5G11110	0.67	unknown protein	Encodes a protein with putative sucrose-phosphate synthase activity.	(GO:0005985) sucrose metabolic process [IEA]	(GO:0009058) biosynthetic process [IEA]	(GO:0046524) sucrose-phosphate synthase activity [RCA]	(GO:0005886) plasma membrane [IDA]		
AT5G11190	1.00	DNA binding / transcription factor	encodes a member of the ERF (ethylene response factor) subfamily B-6 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 12 members in this subfamily including RAP2.11.	(GO:0006355) regulation of transcription, DNA-dependent [ISS]	(GO:0003677) DNA binding [ISS]	(GO:0003700) transcription factor activity [ISS]	(GO:0005634) nucleus [ISS]		
AT5G11670	0.88	malic enzyme/ oxidoreductase, acting on NADH or NADPH, NAD or NADP as acceptor	The malic enzyme (EC 1.1.1.40) encoded by AtNADP-ME2 is presumably a cytosolic enzyme involved in malate metabolism and possibly assisting the oxidative pentose phosphate pathway. AtNADP-ME2 counts for the major part of NADP-ME activity in mature tissues of Arabidopsis.	(GO:0009051) pentose-phosphate shunt, oxidative branch [TAS]	(GO:0006108) malate metabolic process [TAS]	(GO:0046686) response to cadmium ion [IEP]	(GO:0016652) oxidoreductase activity, acting on NADH or NADPH, NAD or NADP as acceptor [ISS]	(GO:0004473) malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+) activity [IDA]	(GO:0004470) malic enzyme activity [ISS]

AT5G13080	0,96	WRKY75; transcription factor	WRKY75 is one of several transcription factors induced during Pi deprivation. It is nuclear localized and regulated differentially during Pi starvation. RNAi mediated suppression of WRKY75 made the plants more susceptible to Pi stress as indicated by the higher accumulation of anthocyanin during Pi starvation.	(GO:0006355) regulation of transcription, DNA-dependent [ISS]	(GO:0048527) lateral root development [IMP]	(GO:0043620) regulation of transcription in response to stress [IMP]	(GO:0032107) regulation of response to nutrient levels [IMP]	(GO:0003700) transcription factor activity [ISS]	(GO:0005634) nucleus [IDA]
AT5G13330	1,09	DNA binding / transcription factor	encodes a member of the ERF (ethylene response factor) subfamily B-4 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 7 members in this subfamily.	(GO:0006355) regulation of transcription, DNA-dependent [ISS]	(GO:0003677) DNA binding [ISS]	(GO:0003700) transcription factor activity [ISS]	(GO:0005634) nucleus [ISS]		
AT5G13420	1,73	transaldolase	similar to unnamed protein product [Vitis vinifera] (GB:CAO68704.1); contains InterPro domain Transaldolase, bacterial/plant type (InterPro:IPR014634); contains InterPro domain Transaldolase subfamily; (InterPro:IPR004732); contains InterPro domain Transaldolase; (InterPro:IPR001585); contains InterPro domain Aldolase-type TIM barrel; (InterPro:IPR013785)	(GO:0046686) response to cadmium ion [IEP]	(GO:0004801) transaldolase activity [ISS]	(GO:0005739) mitochondrion [IDA]	(GO:0009570) chloroplast stroma [IDA]	(GO:0009507) chloroplast [IDA]	
AT5G13710	0,58	SMT1 (STEROL METHYLTRANSFERASE 1)	SMT1 controls the level of cholesterol in plants	(GO:0016126) sterol biosynthetic process [TAS]	(GO:0009793) embryonic development ending in seed dormancy [IMP]	(GO:0003838) sterol 24-C-methyltransferase activity [IGI]	(GO:0005773) vacuole [IDA]		
AT5G13880	1,24	unknown protein	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G47920.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN74736.1)	(GO:0008150) biological_processes [ND]	(GO:0003674) molecular_function [ND]	(GO:0005575) cellular_component [ND]			
AT5G14180	1,02	carboxylic ester hydrolase/ catalytic	identical to Triacylglycerol lipase 2 precursor (LIP2) [Arabidopsis thaliana] (GB:Q67ZU1;GB:Q681B0;GB:Q6VY31;GB:Q94AE7;GB:Q9FMT2;GB:Q9FMT3); similar to ATLIP1 (ARABIDOPSIS THALIANA LIPASE 1), galactolipase/ hydrolase/ phospholipase/ triacylglycerol lipase [Arabidopsis thaliana] (TAIR:AT2G15230.1); similar to lipase [Ricinus communis] (GB:AA17358.1); contains InterPro domain Lipase, active site; (InterPro:IPR008262); contains InterPro domain AB-hydrolase associated lipase region; (InterPro:IPR006693)	(GO:0006629) lipid metabolic process [IEA]	(GO:0003824) catalytic activity [ISS]	(GO:0012505) endomembrane system [IEA]			
AT5G14280	5,19	transcription regulator	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G27270.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO14611.1); contains InterPro domain TRAM, LAG1 and CLN8 homology; (InterPro:IPR006634); contains InterPro domain Protein of unknown function DUF573 (InterPro:IPR007592)	(GO:0008150) biological_processes [ND]	(GO:0030528) transcription regulator activity [TAS]	(GO:0003674) molecular_function [ISS]	(GO:0016021) integral to membrane [IEA]		
AT5G15880	1,25	unknown protein unknown protein	similar to hypothetical protein [Cleome spinosa] (GB:ABD96950.1); contains InterPro domain Polyadenylate-binding protein/Hyperplastic disc protein; (InterPro:IPR002004)	(GO:0016071) mRNA metabolic process [IEA]	(GO:0003674) molecular_function [ND]	(GO:0005575) cellular_component [ND]			
AT5G16360	1,76	unknown protein	similar to NC domain-containing protein [Arabidopsis thaliana] (TAIR:AT3G02700.1); similar to unknown [Populus trichocarpa] (GB:ABK92854.1); contains InterPro domain NC (InterPro:IPR007053)	(GO:0008150) biological_processes [ND]	(GO:0003674) molecular_function [ND]	(GO:0005575) cellular_component [ND]			

AT5G17380	0.84	pyruvate decarboxylase	(CHLORSULFURON/IMIDAZOLINONE RESISTANT 1) [Arabidopsis thaliana] (TAIR:AT3G48560.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN69570.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO68769.1); similar to hypothetical protein OsI_002072 [Oryza sativa (indica cultivar-group)] (GB:EAY74225.1); contains InterPro domain Thiamine pyrophosphate enzyme, N-terminal TPP binding region; (InterPro:IPR012001); contains InterPro domain Thiamine pyrophosphate enzyme, C-terminal TPP-binding; (InterPro:IPR011766); contains InterPro domain Thiamine pyrophosphate enzyme, central region; (InterPro:IPR012000)	No annotation for biological_processes	(GO:0004737) pyruvate decarboxylase activity [ISS]	(GO:0005575) cellular_component [ND]			
AT5G18310	0.79	unknown protein	similar to unnamed protein product [Vitis vinifera] (GB:CAO38794.1)	(GO:0008150) biological_process [ND]	(GO:0003674) molecular_function [ND]	(GO:0005886) plasma membrane [IDA]			
AT5G19220	-0.95	ADG2 (ADPG PYROPHOSPHORYLASE 2); glucose-1-phosphate adenylyltransferase/nucleotidyltransferase	Encodes the large subunit of ADP-glucose pyrophosphorylase which catalyzes the first, rate limiting step in starch biosynthesis. The large subunit plays a regulatory role whereas the small subunit (ApS) is the catalytic isoform. Four isoforms (ApL1-4) have been identified. ApL1 is the major large subunit isoform present in leaves.	(GO:0009058) biosynthetic process [IEA]	(GO:0008878) glucose-1-phosphate adenylyltransferase activity [IDA]	(GO:0009941) chloroplast envelope [IDA]	(GO:0010319) stromule [IDA]	(GO:0009507) chloroplast [IDA]	(GO:0009570) chloroplast stroma [IDA]
AT5G19550	1.27	ASP2 (ASPARTATE AMINOTRANSFERASE 2)	Nitrogen metabolism. Major cytosolic isoenzyme controlling aspartate biosynthesis in the light.	(GO:0006807) nitrogen compound metabolic process [IMP]	(GO:0004069) aspartate transaminase activity [IDA]	(GO:0005618) cell wall [IDA]	(GO:0005829) cytosol [IDA]	(GO:0005886) plasma membrane [IDA]	
AT5G19970	0.78	unknown protein	similar to unnamed protein product [Vitis vinifera] (GB:CAO65601.1)	(GO:0008150) biological_processes [ND]	(GO:0003674) molecular_function [ND]	No annotation for cellular_component			
AT5G20230	0.83	ATBCB (ARABIDOPSIS BLUE-COPPER-BINDING PROTEIN); copper ion binding / electron transporter	Al-stress-induced gene	(GO:0009611) response to wounding [IEP]	(GO:0006979) response to oxidative stress [TAS]	(GO:0009646) response to absence of light [IEP]	(GO:0015690) aluminum ion transport [IMP]	(GO:0005507) copper ion binding [ISS]	(GO:0031225) anchored to membrane [TAS]
AT5G20240	2.16	PI (PISTILLATA); DNA binding / transcription factor	Floral homeotic gene encoding a MADS domain transcription factor. Required for the specification of petal and stamen identities.	(GO:0006355) regulation of transcription, DNA-dependent [IEA]	(GO:0003677) DNA binding [IDA]	(GO:0003700) transcription factor activity [ISS]	(GO:0005634) nucleus [IDA]	(GO:0005737) cytoplasm [IDA]	
AT5G20330	0.62	BETAG4; hydrolase, hydrolyzing O-glycosyl compounds	similar to BG5 (BETA-1,3-GLUCANASE 5), hydrolase, hydrolyzing O-glycosyl compounds [Arabidopsis thaliana] (TAIR:AT5G20340.1); similar to Glycoside hydrolase, family 17 [Medicago truncatula] (GB:ABN05913.1); contains InterPro domain Glycoside hydrolase, family 17; (InterPro:IPR000490); contains InterPro domain Glycoside hydrolase, catalytic similar to SP4HPR1 (HOMOLOGUE 2), transporter [Arabidopsis thaliana] (TAIR:AT4G27970.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO49547.1); contains InterPro domain C4-dicarboxylate transporter/malic acid transport protein; (InterPro:IPR004695)	(GO:0005975) carbohydrate metabolic process [IEA]	(GO:0004553) hydrolase activity, hydrolyzing O-glycosyl compounds [ISS]	(GO:0012505) endomembrane system [IEA]			
AT5G24030	1.38	transporter		(GO:0006873) cellular ion homeostasis [IMP]	(GO:0005215) transporter activity [ISS]	(GO:0016021) integral to membrane [ISS]	(GO:0005886) plasma membrane [IDA]		

AT5G24420	-1.12	6-phosphogluconolactonase	phosphogluconolactonase 3 [Arabidopsis thaliana] (GB:Q8LEV7;GB:Q9FIN0); similar to glucosamine/galactosamine-6-phosphate isomerase family protein [Arabidopsis thaliana] (TAIR:AT3G49360.1); similar to putative 6-phosphogluconolactonase [Brassica carinata] (GB:AAK50346.1); contains InterPro domain Glucosamine/galactosamine-6-phosphate isomerase; (InterPro:IPR006148); contains InterPro domain 6-phosphogluconolactonase; (InterPro:IPR005900)	(GO:0006098) pentose-phosphate shunt [IEA]	(GO:0005975) carbohydrate metabolic process [IEA]	(GO:0017057) 6-phosphogluconolactonase activity [IEA]	(GO:0005575) cellular_component [ND]		
AT5G24530	0.81	oxidoreductase, 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	similar to oxidoreductase, 2OG-Fe(II) oxygenase family protein [Arabidopsis thaliana] (TAIR:AT4G10490.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO46190.1); contains InterPro domain 2OG-Fe(II) oxygenase (InterPro:IPR005123)	(GO:0009620) response to fungus [IEP]	(GO:0009813) flavonoid biosynthetic process [ISS]	(GO:0009617) response to bacterium [IGI]	(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 [ISS]	(GO:0005575) cellular_component [ND]	
AT5G25450	0.75	ubiquinol-cytochrome-c reductase	similar to ubiquinol-cytochrome C reductase complex 14 kDa protein, putative [Arabidopsis thaliana] (TAIR:AT4G32470.1); similar to unknown [Populus trichocarpa] (GB:ABK92701.1); contains InterPro domain Cytochrome bd ubiquinol oxidase, 14 kDa subunit; (InterPro:IPR003197)	(GO:0006122) mitochondrial electron transport, ubiquinol to cytochrome c [ISS]	(GO:0008121) ubiquinol-cytochrome-c reductase activity [ISS]	(GO:0016020) membrane [IDA]	(GO:0005750) mitochondrial respiratory chain complex III [IDA]	(GO:0005739) mitochondrion [IDA]	
AT5G26340	1.06	MSS1; carbohydrate transporter/sugar porter	Encodes a protein with high affinity, hexose-specific/H+ symporter activity. The activity of the transporter appears to be negatively regulated by phosphorylation. Importantly, microarray analysis, as well as the study of the expression of this gene in mutants involved in programmed cell death (PCD) demonstrated a tight correlation between this gene's expression and PCD.	No annotation for biological_process	(GO:0015144) carbohydrate transmembrane transporter activity [ISS]	(GO:0005351) sugar:hydrogen symporter activity [ISS]	(GO:0009679) hexose:hydrogen symporter activity [IDA]	(GO:0005358) high-affinity hydrogen:glucose symporter activity [IDA]	(GO:0016020) membrane [ISS]
AT5G26690	0.87	metal ion binding	similar to heavy-metal-associated domain-containing protein [Arabidopsis thaliana] (TAIR:AT3G05920.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN78416.1); contains InterPro domain Heavy metal transport/detoxification protein; (InterPro:IPR006121)	(GO:0030001) metal ion transport [IEA]	(GO:0046872) metal ion binding [ISS]	(GO:0005575) cellular_component [ND]			
AT5G27760	0.86	unknown protein	similar to hypoxia-responsive family protein [Arabidopsis thaliana] (TAIR:AT3G05550.1); similar to hypoxia-responsive family protein [Citrus sinensis] (GB:AAZ05072.1); contains InterPro domain Hypoxia induced protein conserved region (InterPro:IPR007667)	(GO:0001666) response to hypoxia [ISS]	(GO:0003674) molecular_function [ND]	(GO:0005575) cellular_component [ND]			
AT5G27845	1.58	unknown protein	transposable element gene; non-LTR retrotransposon family (LINE), has a 6.6e-32 P-value blast match to GB:AAA39398 ORF2 (Mus musculus) (LINE-element)						

AT5G28830	0.67	calcium ion binding	similar to calcium-binding EF hand family protein [Arabidopsis thaliana] (TAIR:AT4G38810.2); similar to hypothetical protein [Vitis vinifera] (GB:CAN78056.1); contains InterPro domain Calcium-binding EF-hand; (InterPro:IPR002048)	(GO:0008150) biological_processes [ND]	(GO:0005509) calcium ion binding [ISS]	(GO:0005575) cellular_component [ND]			
AT5G35200	0.60	binding	Identical to Putative clathrin assembly protein At5g35200 [Arabidopsis thaliana] (GB:Q9LHS0); similar to epsin N-terminal homology (ENTH) domain-containing protein [Arabidopsis thaliana] (TAIR:AT2G01600.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO65729.1); similar to ANTH [Medicago truncatula] (GB:ABP03857.1); contains InterPro domain Epsin-like, N-terminal (InterPro:IPR013809); contains InterPro domain ENTH/VHS (InterPro:IPR008942); contains InterPro domain ANTH; (InterPro:IPR011417); contains InterPro domain Clathrin adaptor, phosphoinositide-binding, GAT-like; (InterPro:IPR014712)	(GO:0048268) clathrin coat assembly [IEA]	(GO:0005488) binding [ISS]	(GO:0005886) plasma membrane [IDA]			
AT5G36880	0.62	catalytic	similar to acyl-activating enzyme 17 (AAE17) [Arabidopsis thaliana] (TAIR:AT5G23050.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO49143.1); similar to acetyl-CoA synthetase [Solanum tuberosum] (GB:CAA67130.1); similar to H0502B1.1.5 [Oryza sativa (indica cultivar-group)] (GB:CAH66525.1); contains InterPro domain Acetate--CoA ligase; (InterPro:IPR011904); contains InterPro domain AMP-dependent synthetase and ligase; (InterPro:IPR000873)	(GO:0008152) metabolic process [ISS]	(GO:0003987) acetate-CoA ligase activity [IEA]	(GO:0016208) AMP binding [IEA]	(GO:0003824) catalytic activity [IEA]	(GO:0009570) chloroplast stroma [IDA]	(GO:0009507) chloroplast [IDA]
AT5G36910	-1.18	THI2.2.2 (THIONIN 2.2); toxin receptor binding	Encodes a thionin that is expressed at a low basal level in seedlings and shows circadian variation.	(GO:0006952) defense response [IEA]	(GO:0003674) molecular_function [TAS]	(GO:0050827) toxin receptor binding [TAS]	(GO:0012505) endomembrane system [IEA]		
AT5G37740	0.89	unknown protein	similar to C2 domain-containing protein [Arabidopsis thaliana] (TAIR:AT1G66360.1); similar to unknown [Populus trichocarpa] (GB:ABK92911.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN69475.1); contains InterPro domain C2 calcium-dependent membrane targeting (InterPro:IPR000008); contains InterPro domain C2 calcium/lipid-binding region, CaLB (InterPro:IPR008973)	(GO:0008150) biological_processes [ND]	(GO:0003674) molecular_function [ND]	No annotation for cellular_component			
AT5G38410	-0.77	ribulose-bisphosphate carboxylase	small chain 3B, chloroplast precursor (RBCS-3B) [Arabidopsis thaliana] (GB:P10798;GB:Q9FF21); similar to ribulose bisphosphate carboxylase small chain 2B / RuBisCO small subunit 2B (RBCS-2B) (ATS2B) [Arabidopsis thaliana] (TAIR:AT5G38420.1); similar to Ribulose bisphosphate carboxylase small chain, chloroplast precursor (RuBisCO small subunit) (GB:P08135); contains InterPro domain Ribulose bisphosphate carboxylase, small chain; (InterPro:IPR000894)	(GO:0015977) carbon utilization by fixation of carbon dioxide [ISS]	(GO:0016984) ribulose-bisphosphate carboxylase activity [ISS]	(GO:0016020) membrane [IDA]	(GO:0048046) apoplast [IDA]	(GO:0009573) chloroplast ribulose bisphosphate carboxylase complex [ISS]	(GO:0009579) thylakoid [IDA]

AT5G39670	0.76	calcium ion binding EMB2744	similar to calcium-binding EF hand family protein [Arabidopsis thaliana] (TAIR:AT3G29000.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO15001.1); contains InterPro domain EF-Hand type; (InterPro:IPR011992); contains InterPro domain Calcium-binding EF-hand; (InterPro:IPR002048)	(GO:0008150) biological_process [ND]	(GO:0005509) calcium ion binding [ISS]	(GO:0005575) cellular_component [ND]			
AT5G41040	0.78	transferase	similar to transferase family protein [Arabidopsis thaliana] (TAIR:AT5G63560.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO68331.1); contains InterPro domain Transferase (InterPro:IPR003480)	(GO:0008150) biological_process [ND]	(GO:0016740) transferase activity [ISS]	(GO:0005575) cellular_component [ND]			
AT5G41670	0.80	phosphogluconate dehydrogenase (decarboxylating)	(TAIR:AT3G02360.2); similar to 6-phosphogluconate dehydrogenase family protein [Arabidopsis thaliana] (TAIR:AT1G64190.1); similar to 6-phosphogluconate dehydrogenase family protein [Arabidopsis thaliana] (TAIR:AT3G02360.1); similar to predicted protein [Physcomitrella patens subsp. patens] (GB:EDQ64210.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN63456.1); similar to plastidic 6-phosphogluconate dehydrogenase [Spinacia oleracea] (GB:AAK49897.1); contains InterPro domain 6-phosphogluconate dehydrogenase, C-terminal; (InterPro:IPR006114); contains InterPro domain 6-phosphogluconate dehydrogenase, decarboxylating; (InterPro:IPR006113); contains InterPro domain NAD(P)-binding; (InterPro:IPR016040); contains InterPro domain Dehydrogenase, multihelical; (InterPro:IPR013328); contains InterPro domain 6-phosphogluconate dehydrogenase, C-terminal-like; (InterPro:IPR008927); contains InterPro domain 6-phosphogluconate dehydrogenase, NAD-binding; (InterPro:IPR006115); contains InterPro domain Fibrin/6-phosphogluconate dehydrogenase, C-terminal extension (InterPro:IPR012284); contains InterPro domain 6-phosphogluconate dehydrogenase; (InterPro:IPR006183)	(GO:0046686) response to cadmium ion [IEP]	(GO:0004616) phosphogluconate dehydrogenase (decarboxylating) activity [ISS]	(GO:0005739) mitochondrion [IDA]	(GO:0009507) chloroplast [IDA]		
AT5G42830	1.43	transferase	similar to transferase family protein [Arabidopsis thaliana] (TAIR:AT5G07850.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO61376.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN78155.1); contains InterPro domain Transferase (InterPro:IPR003480)	(GO:0008150) biological_process [ND]	(GO:0016740) transferase activity [ISS]	(GO:0005575) cellular_component [ND]			
AT5G44920	0.85	transmembrane receptor catalytic	similar to disease resistance protein (TIR class), putative [Arabidopsis thaliana] (TAIR:AT4G19920.1); similar to unknown [Arabidopsis lyrata] (GB:AAO42473.1); contains InterPro domain Toll-Interleukin receptor; (InterPro:IPR000157)	(GO:0006952) defense response [ISS]	(GO:0004888) transmembrane receptor activity [IEA]	(GO:0005783) endoplasmic reticulum [IDA]			

AT5G45220	0.59	transmembrane receptor	similar to disease resistance protein (TIR-NBS-LRR class), putative [Arabidopsis thaliana] (TAIR:AT5G45060.1); similar to unknown [Arabidopsis lyrata] (GB:AAO42473.1); contains InterPro domain Toll-Interleukin receptor; (InterPro:IPR000157)	(GO:0006952) defense response [ISS]	(GO:0004888) transmembrane receptor activity [ISS]	(GO:0031224) intrinsic to membrane [IEA]			
AT5G49730	-0.85	oxidoreductase	Encodes a putative ferric chelate reductase. Its mRNA is expressed in green aerial tissues (shoot, flower and cotyledon) in a light- and cell differentiation-specific manner. However, in vitro assays in yeast have not shown ferric chelate reductase activity for this protein. T	(GO:0009416) response to light stimulus [IEP]	(GO:0000293) ferric-chelate reductase activity [IDA]	(GO:0016491) oxidoreductase activity [ISS]	(GO:0016020) membrane [ISS]	(GO:0005886) plasma membrane [IDA]	
AT5G54490	-0.65	PBP1 (PINOID-BINDING PROTEIN 1); calcium ion binding	Encodes a PINOID (PID)-binding protein containing putative EF-hand calcium-binding motifs. The interaction is dependent on the presence of calcium. mRNA expression is up-regulated by auxin. Not a phosphorylation target of PID, likely acts upstream of PID to regulate the activity of this protein in response to changes in calcium levels.	(GO:0009733) response to auxin stimulus [IEP]	(GO:0005515) protein binding [IPI]	(GO:0005509) calcium ion binding [ISS]	(GO:0005575) cellular_component [ND]		
AT5G54960	1.02	PDC2 (PYRUVATE DECARBOXYLASE-2); pyruvate decarboxylase		(GO:0001666) response to hypoxia [IEP]	(GO:0004737) pyruvate decarboxylase activity [ISS]	(GO:0005575) cellular_component [ND]			
AT5G58330	-0.83	malate dehydrogenase/oxidoreductase	similar to malate dehydrogenase, cytosolic, putative [Arabidopsis thaliana] (TAIR:AT5G56720.1); similar to Malate dehydrogenase [NADP], chloroplast precursor (NADP-MDH) (GB:O48902); contains InterPro domain Lactate dehydrogenase/glycoside hydrolase, family 4, C-terminal; (InterPro:IPR015955); contains InterPro domain Lactate/malate dehydrogenase; (InterPro:IPR001236); contains InterPro domain Malate dehydrogenase; (InterPro:IPR008267); contains InterPro domain Malate dehydrogenase, NAD or NADP; (InterPro:IPR010945); contains InterPro domain NAD(P)-binding; (InterPro:IPR016040); contains InterPro domain Malate dehydrogenase, NADP-dependent, plants; (InterPro:IPR011273); contains InterPro domain L-lactate/malate dehydrogenase; (InterPro:IPR001557); contains InterPro domain Malate dehydrogenase, active site; (InterPro:IPR001252)	(GO:0008152) metabolic process [IEA]	(GO:0006096) glycolysis [IEA]	(GO:0044262) cellular carbohydrate metabolic process [IEA]	(GO:0006108) malate metabolic process [IEA]	(GO:0005975) carbohydrate metabolic process [IEA]	(GO:0016615) malate dehydrogenase activity [ISS]
AT5G58375	0.82	unknown protein	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G14602.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO21327.1); contains domain PTHR12133 (PTHR12133)	(GO:0008150) biological_processes [ND]	(GO:0003674) molecular_function [ND]	(GO:0012505) endomembrane system [IEA]			

AT5G58820	1.23	subtilase	similar to subtilase family protein [Arabidopsis thaliana] (TAIR:AT5G58830.1); similar to ATSBT4.12, subtilase [Arabidopsis thaliana] (TAIR:AT5G59090.1); similar to subtilase family protein [Arabidopsis thaliana] (TAIR:AT5G58840.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO67394.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN62173.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO21564.1); contains InterPro domain Peptidase S8 and S53, subtilisin, kexin, sedolisin; (InterPro:IPR000209); contains InterPro domain Proteinase inhibitor I9, subtilisin propeptide; (InterPro:IPR010259); contains InterPro domain Peptidase S8, subtilisin-related (InterPro:IPR015500)	(GO:0006508) proteolysis [ISS]	No annotation for molecular_function	(GO:0012505) endomembrane system [IEA]			
AT5G59090	1.11	peptidase/ subtilase	similar to ATSBT4.13, subtilase [Arabidopsis thaliana] (TAIR:AT5G59120.1); similar to subtilase family protein [Arabidopsis thaliana] (TAIR:AT5G58820.1); similar to subtilase family protein [Arabidopsis thaliana] (TAIR:AT5G58840.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO67394.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO67395.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO21564.1); contains InterPro domain Protease-associated PA (InterPro:IPR003137); contains InterPro domain Peptidase S8 and S53, subtilisin, kexin, sedolisin; (InterPro:IPR000209); contains InterPro domain Proteinase inhibitor I9, subtilisin propeptide; (InterPro:IPR010259); contains InterPro domain Peptidase S8, subtilisin-related (InterPro:IPR015500)	(GO:0006508) proteolysis [ISS]	No annotation for molecular_function	(GO:0005634) nucleus [IDA]	(GO:0048046) apoplast [IDA]	(GO:0005737) cytoplasm [IDA]	
AT5G60350	0.86	unknown protein	No description	(GO:0008150) biological_processes [ND]	(GO:0003674) molecular_function [ND]	(GO:0005575) cellular_component [ND]			
AT5G62790	1.03	DXR (1-DEOXY-D-XYLULOSE 5-PHOSPHATE REDUCTOISOMERASE)	1-Deoxy-d-xylulose 5-phosphate reductoisomerase (DXR) catalyzes the first committed step of the 2-C-methyl-d-erythritol 4-phosphate pathway for isoprenoid biosynthesis. In Arabidopsis, DXR is encoded by a single-copy gene. Arabidopsis DXR is targeted to plastids and localizes into chloroplasts of leaf cells. DXR knockout or strongly silenced lines have a seedling lethal, albino phenotype. Transgenic, partially silenced lines expressing 35S:DXR have a variegated phenotype.	(GO:0008299) isoprenoid biosynthetic process [TAS]	(GO:0019288) isopentenyl diphosphate biosynthetic process, mevalonate-independent pathway [TAS]	(GO:0046686) response to cadmium ion [IEP]	(GO:0030604) 1-deoxy-D-xylulose-5-phosphate reductoisomerase activity [IDA]	(GO:0010319) stromule [IDA]	(GO:0009507) chloroplast [IDA]
AT5G62920	0.63	ARR6 (RESPONSE REGULATOR 6); transcription regulator/ two-component response regulator	Encodes a Type-A response regulator that is responsive to cytokinin treatment. Its C-ter domain is very short in comparison to other Arabidopsis ARR6s (17 total). Arr6 protein is stabilized by cytokinin.	(GO:0009736) cytokinin mediated signaling [IMP]	(GO:0000160) two-component signal transduction system (phosphorelay) [TAS]	(GO:0009735) response to cytokinin stimulus [IEP]	(GO:0030528) transcription regulator activity [TAS]	(GO:0000156) two-component response regulator activity [TAS]	(GO:0005575) cellular_component [ND]
AT5G65020	0.96	ANNAT2: calcium ion binding / calcium-dependent phospholipid binding	Annexins are calcium binding proteins that are localized in the cytoplasm. When cytosolic Ca2+ increases, they relocate to the plasma membrane. They may be involved in the Golgi-mediated secretion of polysaccharides.	(GO:0015774) polysaccharide transport [TAS]	(GO:0005544) calcium-dependent phospholipid binding [ISS]	(GO:0005509) calcium ion binding [ISS]	(GO:0009986) cell surface [NAS]		

AT5G66280	0.84	GMD1 (GDP-D-MANNOSE 4,6-DEHYDRATASE 1); GDP-mannose 4,6-dehydratase/ NAD binding / catalytic	GDP-D-mannose 4,6-dehydratase	(GO:0009225) nucleotide-sugar metabolic process [ISS]	(GO:0008446) GDP-mannose 4,6-dehydratase activity [ISS]	(GO:0005622) intracellular [IEA]		
AT5G67530	1.02	peptidyl-prolyl cis-trans isomerase/ ubiquitin-protein ligase	similar to peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein [Arabidopsis thaliana] (TAIR:AT1G01940.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN75902.1); similar to hypothetical protein Osl_010162 [Oryza sativa (indica cultivar-group)] (GB:EAY88929.1); similar to peptidylprolyl isomerase, putative, expressed [Oryza sativa (japonica cultivar-group)] (GB:ABF94499.1); contains InterPro domain Zinc finger, RING/FYVE/PHD-type (InterPro:IPR013083); contains InterPro domain Cyclophilin-like (InterPro:IPR015891); contains InterPro domain Peptidyl-prolyl cis-trans isomerase, cyclophilin-type; (InterPro:IPR002130); contains InterPro domain U box; (InterPro:IPR003613)	(GO:0006457) protein folding [ISS]	(GO:0003755) peptidyl-prolyl cis-trans isomerase activity [ISS]	(GO:0000151) ubiquitin ligase complex [IEA]		
AT5G67550	-1.29	unknown protein	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G71110.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN65326.1)	(GO:0008150) biological_processes [ND]	(GO:0003674) molecular_function [ND]	(GO:0012505) endomembrane system [IEA]		
ATCG00160	-0.88	RPS2 (RIBOSOMAL PROTEIN S2)	Chloroplast ribosomal protein S2	(GO:0006412) translation [TAS]	(GO:0003735) structural constituent of ribosome [IEA]	(GO:0016020) membrane [IDA]	(GO:0000312) plastid small ribosomal subunit [TAS]	(GO:0010319) stromaule [IDA]
ATCG00280	-0.64	PSBC	chloroplast gene encoding a CP43 subunit of the photosystem II reaction center. promoter contains a blue-light responsive element.	(GO:0019684) photosynthesis, light reaction [TAS]	(GO:0016168) chlorophyll binding [TAS]	(GO:0016020) membrane [IDA]	(GO:0009539) photosystem II reaction center [TAS]	(GO:0010287) plastoglobule [IDA]
ATCG00430	-0.92	PSBG NDHC	Encodes a protein which was originally thought to be part of photosystem II but its wheat homolog was later shown to encode for subunit K of NADH dehydrogenase.	(GO:0006120) mitochondrial electron transport, NADH to ubiquinone [IEA]	(GO:0016651) oxidoreductase activity, acting on NADH or NADPH [IEA]	(GO:0051539) 4 iron, 4 sulfur cluster binding [IEA]	(GO:0008137) NADH dehydrogenase (ubiquinone) activity [IEA]	(GO:0030095) chloroplast photosystem II [TAS]
ATCG00570	-1.27	PSBF PSBE	PSII cytochrome b559	(GO:0019684) photosynthesis, light reaction [IEA]	(GO:0009767) photosynthetic electron transport chain [IEA]	(GO:0015979) photosynthesis [IEA]	(GO:0020037) heme binding [IEA]	(GO:0046872) metal ion binding [IEA]
ATCG00640	-0.98	RPL33	encodes a chloroplast ribosomal protein L33, a constituent of the large subunit of the ribosomal complex	(GO:0006412) translation [TAS]	(GO:0003735) structural constituent of ribosome [TAS]	(GO:0000311) plastid large ribosomal subunit [TAS]	(GO:0009507) chloroplast [IDA]	
ATCG00640	-0.81	RPL33 RPS18	encodes a chloroplast ribosomal protein L33, a constituent of the large subunit of the ribosomal complex	(GO:0006412) translation [TAS]	(GO:0003735) structural constituent of ribosome [TAS]	(GO:0000311) plastid large ribosomal subunit [TAS]	(GO:0009507) chloroplast [IDA]	
ATCG00720	-0.56	PETB PETD	Encodes the cytochrome b(6) subunit of the cytochrome b6f complex.	(GO:0019684) photosynthesis, light reaction [TAS]	(GO:0020037) heme binding [TAS]	(GO:0016020) membrane [IDA]	(GO:0009535) chloroplast thylakoid membrane [IDA]	(GO:0009512) cytochrome b6f complex [TAS]
ATCG00740	-1.13	RPOA RPS11	RNA polymerase alpha subunit	(GO:0006354) RNA elongation [TAS]	(GO:0003899) DNA-directed RNA polymerase activity [TAS]	(GO:0009295) nucleoid [IDA]	(GO:0009507) chloroplast [IDA]	

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

(GO:0004022) alcohol dehydrogenase activity [IDA]	(GO:0010301) xanthoxin dehydrogenase activity [IDA]	(GO:0016491) oxidoreductase activity [ISS]	(GO:0005829) cytosol [IDA]	

(GO:0009507) chloroplast [IDA]				

(GO:0009507) chloroplast [IDA]				
(GO:0005575) cellular_component [ND]				

(GO:0009505) plant-type cell wall (IDA)				

[illegible]

(GO:0042372) phyloquinone biosynthetic process [IMP]	(GO:0031348) negative regulation of defense response [IMP]	(GO:0008909) isochorismate synthase activity [IMP]	(GO:0009536) plastid [IDA]	
(GO:0005773) vacuole [IDA]	(GO:0005618) cell wall [IDA]			

[illegible]

[illegible]

(GO:0005737) cytoplasm [IDA]				
(GO:0009505) plant-type cell wall [IDA]	(GO:0005886) plasma membrane [IDA]			

(GO:0019104) DNA N-glycosylase activity [IDA]	(GO:0005634) nucleus [IDA]			

[illegible]

(GO:0005634) nucleus [IDA]				

[illegible]

(GO:0009507) chloroplast [IDA]				

[illegible]

(GO:0009507) chloroplast [IDA]				

(GO:0009651) response to salt stress [IEP]	(GO:0003677) DNA binding [ISS]	(GO:0003700) transcription factor activity [ISS]	No annotation for cellular_component	

(GO:0009295) nucleoid [IDA]	(GO:0009941) chloroplast envelope [IDA]	(GO:0009507) chloroplast [IDA]		
(GO:0005515) protein binding [IPI]	(GO:0003700) transcription factor activity [ISS]	No annotation for cellular_component		

(GO:0004349) glutamate 5-kinase activity [IEA]	(GO:0016491) oxidoreductase activity [IEA]	(GO:0005737) cytoplasm [IDA]	(GO:0009507) chloroplast [IDA]	

[illegible]

No annotation for cellular_component				
(GO:0016020) membrane [IDA]	(GO:0005792) microsome [IDA]	(GO:0048046) apoplast [IDA]	(GO:0005773) vacuole [IDA]	(GO:0010319) stromule [IDA]
(GO:0009793) embryonic development ending in seed dormancy [IMP]	(GO:0005515) protein binding [IPI]	(GO:0005634) nucleus [IDA]	(GO:0005737) cytoplasm [IDA]	(GO:0009524) phragmoplast [IDA]

[illegible]

(GO:0031977) thylakoid lumen [IDA]	(GO:0009543) chloroplast thylakoid lumen [IDA]	(GO:0010319) stromule [IDA]	(GO:0009570) chloroplast stroma [IDA]	(GO:0009507) chloroplast [IDA]

[illegible]

(GO:0005634) nucleus [IDA]	(GO:0005829) cytosol [IDA]			
(GO:0005576) extracellular region [IEA]				
(GO:0016709) oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, NADH or NADPH as one donor, and incorporation of one atom of oxygen [IDA]	(GO:0019825) oxygen binding [ISS]	(GO:0016020) membrane [IDA]	(GO:0005783) endoplasmic reticulum [IDA]	(GO:0005739) mitochondrion [IDA]

(GO:0050691) regulation of defense response to virus by host [IGI]	(GO:0003700) transcription factor activity [IMP]	(GO:0005634) nucleus [IDA]		
(GO:0005774) vacuolar membrane [IDA]	(GO:0005886) plasma membrane [IDA]			

(GO:0009507) chloroplast [IEA]				

(GO:0005730) nucleolus [IDA]	(GO:0005886) plasma membrane [IDA]	(GO:0009507) chloroplast [IDA]		

(GO:0016020) membrane [IDA]	(GO:0048046) apoplast [IDA]	(GO:0005618) cell wall [IDA]	(GO:0005886) plasma membrane [IDA]	(GO:0009507) chloroplast [IDA]

[illegible]

(GO:0005773) vacuole [IDA]	(GO:0046658) anchored to plasma membrane [IDA]	(GO:0005886) plasma membrane [IDA]		

(GO:0005886) plasma membrane [IDA]				

(GO:0005618) cell wall [IDA]	(GO:0010319) stromule [IDA]	(GO:0009570) chloroplast stroma [IDA]	(GO:0022626) cytosolic ribosome [IDA]	(GO:0009507) chloroplast [IDA]

[illegible]

(GO:0048046) apoplast [IDA]	(GO:0009579) thylakoid [IDA]	(GO:0005739) mitochondrion [IDA]	(GO:0009941) chloroplast envelope [IDA]	(GO:0010319) stromule [IDA]

[illegible]

(GO:0009579) thylakoid [IDA]	(GO:0009533) chloroplast stromal thylakoid [IDA]	(GO:0009507) chloroplast [IDA]		
(GO:0009507) chloroplast [IDA]				
(GO:0009507) chloroplast [IDA]				

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(GO:0005886) plasma membrane [IDA]	(GO:0009570) chloroplast stroma [IDA]	(GO:0009507) chloroplast [IDA]
(GO:0000794) condensed nuclear chromosome [IDA]	(GO:0000151) ubiquitin ligase complex [IP]	(GO:0005819) spindle [IDA]

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[illegible]

[illegible]

(GO:0009507) chloroplast [IDA]	(GO:0009570) chloroplast stroma [IDA]	

[illegible]

[illegible]
