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Table S1. Gene ratios and functional annotation of spots passing filtering criteria in the initial hybridization experiment

Roots and leaves were collected separately from greenhouse-grown *Centaurea maculosa* plants. Root and leaf cDNAs were used to probe the *Arabidopsis* OAR27K microarray chip. Average median ratios of root/leaf were calculated. Accession numbers for each gene identified in the microarray analysis were used to query the *Arabidopsis* gene database to determine function, and genes were then grouped into functional categories based on the Kyoto Encyclopedia of Genes and Genomics (KEGG) Ontology System. Functional (KEGG) categories in table are as follows: CPS, Cell processing and signaling; GIP, Genetic information processing; EIP, Environmental information processing; M, Metabolism; U, Unknown. Transcripts related to photosynthesis are highlighted in green. Genes categorised as transposons fall into the unknown category

Name	Accession	ID	Median of Ratios (635/532) = Cy5/Cy3 = root/leaf	Function	Functional Category		
					KEGG	**KEGG2**	**KEGG3**
At2g46620 Arabidopsis thaliana chromosome II section 247 of 255 of the complete sequence. Sequence from clones F13A10	At2g46620	AC006418	0.027	AAA-type ATPase family protein, contains Pfam profile: ATPase family PF00004 , ATP binding, ATPase activity, endomembrane system (potentially part of class of chaperone-like ATPases, may help in ribosome biogenesis or protein degredation)	Genetic Information Processing; Folding, Sorting and Degradation; Protein folding and associated processing		
At5g67250 Arabidopsis thaliana SKP1 interacting partner 2 (SKIP2) mRNA, complete cds	At5g67250	AF263378	0.029	F-box SKP1 interacting partner 2 (SKIP2) , also many entries of F-box family protein, contains similarity to F-box protein FBX3 GI:6103643 from (Homo sapiens) ; similar to SKP1 interacting partner 2 (SKIP2)–HITS 63 LOCI	Genetic Information Processing; Folding, Sorting and Degradation	Environmental Information Processing; Signal Transduction	Cellular Processes; Cell Growth and Death; Cell cycle
At3g61470 Arabidopsis thaliana Lhca2 protein (Lhca2) mRNA, complete cds	At3g61470	AF134120	0.029	chlorophyll A-B binding protein (LHCA2), PF00504	Metabolism; energy; photosynthesis		
At5g10980 Arabidopsis thaliana DNA chromosome 5, BAC clone T30N20 (ESSA project)	At5g10980	AL365234	0.03	histone H3, identical to HISTONE H3.2, MINOR, Medicago sativa, SWISSPROT:P11105, histone H3 variant H3.3 Lycopersicon esculentum GI:1435157; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4	Genetic Information Processing; Transcription		
At5g14570 Arabidopsis thaliana putative high affinity nitrate transporter protein (T15N1_60/AT5g14570) mRNA, complete cds	At5g14570	AY035065	0.031	NRT7, member of High affinity nitrate transporter family, PF00083: Sugar (and other) transporter	Environmental Information Processing; Membrane Transport;	Cellular Processes and Signaling; Transporters	
At5g02490 Arabidopsis thaliana mRNA for Hsc70-G8 protein, partial	At5g02490	AL162971	0.031	heat shock cognate 70 kDa protein 2 (HSC70-2)	Genetic Information Processing; Folding, Sorting and Degradation	Environmental Information Processing; Signal Transduction	
At3g59540 Arabidopsis thaliana DNA chromosome 3, BAC clone T16L24	At3g59540	AL138659	0.031	60S ribosomal protein L38 (RPL38B),	Genetic Information Processing; Translation		
Arabidopsis thaliana DNA chromosome 4, BAC clone F28M20 (ESSAII project)		AL031004	0.032		unknown		
At1g66410 A.thaliana mRNA (clone ACaM4) for calmodulin	At1g66410	Z12022	0.033	calmodulin-1/4 (CAM4),	Environmental Information Processing; Signal Transduction		

At4g08400 Arabidopsis thaliana DNA chromosome 4, BAC clone T28D5, partial sequence (ESSA project)	At4g08400	AL109819	0.033	proline-rich extensin-like family protein	Metabolism; other
Arabidopsis thaliana DNA chromosome 3, BAC clone F17J16		AL163527	0.033		unknown
Arabidopsis thaliana DNA chromosome 3, BAC clone T20E23		AL133363	0.033		unknown
Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MJB24		AB019233	0.034		unknown
At3g17050 A.thaliana gene encoding a glycine-rich protein	At3g17050	AB026636	0.034	pseudogene, glycine-rich protein, similar to glycine-rich protein TIGR:At1g53620.1 (Arabidopsis thaliana)	unknown
At5g44060 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MRH10	At5g44060	AB006703	0.034	exp	unknown
At4g00810 Arabidopsis thaliana AT4g00810/A_TM018A10_9 gene, complete cds	At4g00810	AF361624	0.035	60S acidic ribosomal protein P1 (RPP1B),	Genetic Information Processing; Translation
At3g17020 Arabidopsis thaliana AT3g17020/K14A17_14 mRNA, complete cds	At3g17020	AF378888	0.035	universal stress protein (USP) family protein, PF00582	unknown
At5g28520 Arabidopsis thaliana BAC T26D3	At5g28520	AF262043	0.036	jacalin lectin family protein, similar to myrosinase-binding protein homolog (Arabidopsis thaliana) GI:2997767; contains Pfam profile PF01419	Cellular Processes and Signaling; CAM ligands
At2g41110 A.thaliana mRNA (clone ACaM5) for calmodulin (partial)	At2g41110	AC004261	0.036	calmodulin-2/3/5 (CAM2) (CAL1), also hits CAL4, Encodes a touch-inducible calmodulin-related protein.	Environmental Information Processing; Signal Transduction
At4g38680 Glycine-rich protein {clone atGRP-2} [Arabidopsis thaliana, C24, mRNA, 965 nt]	At4g38680	AF385696	0.036	GRP2, encodes a glycine-rich protein that is present as several copies in the genome. It is expressed equally abundantly in all tissues examined. cold-shock DNA-binding family protein, contains Pfam domains PF00313: 'Cold-shock' DNA-binding domain and PF00098: Zinc knuckle	Genetic Information Processing; Transcription
At1g26910 Arabidopsis thaliana chromosome I BAC T2P11 genomic sequence	At1g26910	AC005508	0.036	60S ribosomal protein L10 (RPL10B), Nearly identical to ribosomal protein L10.e, Wilm's tumor suppressor homologue, gi|17682 (Z15157), however differences in sequence indicate this is a different member of the L10 family , ribosome, structural constituent of ribosome, protein biosynthesis	Genetic Information Processing; Translation; Ribosome

At3g56800 Arabidopsis thaliana putative calmodulin-3 protein (T8M16_130/AT3g56800) mRNA, complete cds	At3g56800	AY046048	0.037	calmodulin-2/3/5 (CAM3),	Environmental Information Processing; signal transduction
At2g23320 Arabidopsis thaliana WRKY DNA-binding protein 15 (WRKY15) mRNA, complete cds	At2g23320	AC002391	0.037	WRKY family transcription factor, identical to WRKY DNA-binding protein 15	Genetic Information Processing; transcription
At3g03980 Arabidopsis thaliana AT3g03980/T11I18_9 mRNA, complete cds	At3g03980	AF385727	0.037	short-chain dehydrogenase/reductase (SDR) family protein	Metabolism; Other energy metabolism
Arabidopsis thaliana DNA chromosome 3, BAC clone F14D17		AL353992	0.037		unknown
Arabidopsis thaliana chromosome II section 19 of 255 of the complete sequence. Sequence from clones T16B23, T23O15		AC007293	0.037	unk	unknown
At3g24050 Arabidopsis thaliana mRNA for GATA transcription factor 1	At3g24050	Y13648	0.038	GATA transcription factor 1 (GATA-1),	Genetic Information Processing; transcription
At5g60390 Arabidopsis thaliana putative elongation factor 1-alpha protein (MUF9.4/AT5g60390) mRNA, complete cds	At5g60390	AF360167	0.038	elongation factor 1-alpha / EF-1-alpha, identical to SWISS-PROT:P13905 elongation factor 1-alpha (EF-1-alpha) (Arabidopsis thaliana) , cytoplasm, mitochondrion, nucleus, calmodulin binding, translation elongation factor activity, protein biosynthesis, translational elongation	Genetic Information Processing; Translation factors
At5g52310 Arabidopsis thaliana cor78 protein mRNA, complete cds	At5g52310	L22568	0.038	COR78, cold regulated gene, the 5' region of cor78 has cis-acting regulatory elements that can impart cold-regulated gene expression, low-temperature-responsive protein 78 (LTI78) / desiccation-responsive protein 29A (RD29A)	unknown
Arabidopsis thaliana chromosome II section 204 of 255 of the complete sequence. Sequence from clones F3G5, F13M22		AC004684	0.038	unk	unknown
At4g21140 Arabidopsis thaliana DNA chromosome 4, BAC clone F7J7 (ESSA project)	At4g21140	AL021960	0.039	expressed protein, Wnt receptor signaling pathway, developmental pathway	Environmental Information Processing; Signal Transduction
At5g02570 Arabidopsis thaliana DNA chromosome 5, BAC clone T22P11 (ESSA project)	At5g02570	AL162971	0.039	histone H2B, putative	Genetic Information Processing; Transcription
At3g53020 Arabidopsis thaliana DNA chromosome 3, BAC clone F8J2	At3g53020	AL132969	0.039	60S ribosomal protein L24 (RPL24B),	Genetic Information Processing; Translation
At2g27760 Arabidopsis thaliana tRNA isopentenyl transferase mRNA, complete cds	At2g27760	AF109376	0.039	tRNA isopentenyltransferase 2 / IPP transferase 2 (IPT2),	Genetic Information Processing; Translation; Other translation

A.thaliana hsc70 mRNA for heat shock cognate protein	A.thaliana	X74604	0.04	encodes a member of heat shock protein 70 family. response to heat, response to virus HSP70-1, The protective chaperone activities of hsp70 help to confer tolerance to heat, glucose deprivation, and drought., Extensive efforts to achieve underexpression of Hsc70-1 mRNA using a full-length antisense cDNA resulted in no viable transgenic plants, suggesting that reduced expression is lethal	Genetic Information Processing; Folding, Sorting and Degradation; Protein folding and associated processing	Environmental Information Processing; Signal Transduction
A.thaliana mRNA for glycine-rich RNA-binding protein	A.thaliana	X69377	0.04		Genetic Information Processing; Translation	
At1g48920 Arabidopsis thaliana At1g48920/F27K7_6 mRNA sequence	At1g48920	AC084414	0.04	nucleolin, putative, RNA binding, nucleic acid metabolism	Metabolism; nucleic acid	Genetic Information Processing; Translation
At4g05050 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 14	At4g05050	AL161502	0.04	polyubiquitin (UBQ11), identical to GI:304117 , polyubiquitin gene, belongs to a subtype group with UBQ10 and UBQ14. Various ecotypes of Arabidopsis have different numbers of ubiquitin repeats within this gene. intracellular, protein binding, ubiquitin-dependent protein catabolism , protein modification	Metabolism; Peptidases	
At5g37640 Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K12B20	At5g37640	AB018107	0.04	polyubiquitin (UBQ9), polyubiquitin gene with 4 ubiquitin repeats. The first ubiquitin repeat has 16 amino acid replacements	Metabolism; Peptidases	
Arabidopsis thaliana chromosome 3 BAC T8E24 genomic sequence	Arabidopsis	AC023912	0.04		unknown	
Arabidopsis thaliana mRNA for glycine-rich RNA-binding protein (AtGRP2)	At2g21060	AJ002892	0.041	cold-shock DNA-binding family protein / glycine-rich protein (GRP2), identical to Glycine-rich protein 2b (AtGRP2b) (Arabidopsis thaliana) SWISS-PROT:Q38896; contains Pfam domains PF00313: 'Cold-shock' DNA-binding domain and PF00098: Zinc knuckle , cellular component unknown, nucleic acid binding, regulation of transcription, DNA-dependent	Genetic Information Processing; Transcription	

EST	At5g04740	AA651471	0.041	ACT domain-containing protein, contains Pfam profile PF01842: ACT domain , thylakoid membrane (sensu Viridiplantae), amino acid binding, metabolism	Metabolims; amino acid	
EST	EST	F19940	0.041		unknown	
At5g39650 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MIJ24	At5g39650	AB012243	0.041	expressed	unknown	
Arabidopsis thaliana actin-2 mRNA, complete cds	actin	U37281	0.042	actin	Cellular Processes; Cell Motility; Regulation of actin cytoskeleton	
At2g17230 Arabidopsis thaliana chromosome II section 99 of 255 of the complete sequence. Sequence from clones F6P23, T23A1	At2g17230	AC007127	0.042	phosphate-responsive 1 family protein, PF04674	Environmental Information Processing; Membrane Transport	
Arabidopsis thaliana putative adenylate translocator (F17O14.5/AT3g08580) mRNA, complete cds		X65549	0.042	ADP, ATP carrier protein 1, mitochondrial / ADP/ATP translocase 1 / adenine nucleotide translocator 1 (ANT1), mitochondrial inner membrane, mitochondrion, ATP:ADP antiporter activity, binding, transport	Environmental Information Processing; Signal Transduction; Calcium signaling pathway	Environmental Information Processing; Membrane Transport
At2g24060 Arabidopsis thaliana chromosome II section 135 of 255 of the complete sequence. Sequence from clones F27L4, T29E15	At2g24060	AC005170	0.042	translation initiation factor 3 (IF-3) family protein	Genetic Information Processing; translation	
At3g28550 Arabidopsis thaliana partial mRNA for extensin-like protein (DiDi 4T-2 gene)	At3g28550	AJ286344	0.042	proline-rich extensin-like family protein	Metabolism; other	
At5g56260 Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K24C1	At5g56260	AB023029	0.042	dimethylmenaquinone methyltransferase family protein, Pfam profile PF03737 (convert dimethylmenaquinone (DMK) to menaquinone (MK) in the final step of menaquinone biosynthesis)	Metabolism; other biosynthesis; Menaquinone biosynthesis	
At4g02890 Arabidopsis thaliana Unknown protein mRNA, complete cds	At4g02890	AY042884	0.042	polyubiquitin (UBQ14),	Metabolism; Peptidases	
At3g07560 Arabidopsis thaliana chromosome III BAC F21O3 genomic sequence	At3g07560	AC009853	0.043	peroxisomal membrane, protein binding, protein import into peroxisome matrix , Encodes peroxin 13 (PEX13) involved in protein transport into peroxisomes.	Cellular Processes and Signaling; Transporters	
At3g22310 Arabidopsis thaliana mRNA for DEAD box RNA helicase, RH9	At3g22310	AB022215	0.043	DEAD box RNA helicase, putative (RH9), PF00270: DEAD/DEAH box helicase, PF00271: Helicase conserved C-terminal domain	Genetic Information Processing; Replication and Repair;	
At4g00270 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 1	At4g00270	AL161471	0.043	DNA-binding storekeeper protein-related, PF04504: Protein of unknown function, DUF573	Genetic Information Processing; transcription	

At5g40040 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MUD12	At5g40040	AB022222	0.043	60S acidic ribosomal protein P2 (RPP2E), acidic ribosomal protein P2, Parthenium argentatum	Genetic Information processing; translation	
At5g40490 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MNF13	At5g40490	AB009052	0.043	RNA recognition motif (RRM)-containing protein, ribonucleoprotein, Xenopus laevis, PIR:S40778; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)	Genetic Information Processing; Translation	
At1g61520 Arabidopsis thaliana PSI type III chlorophyll a/b-binding protein (Lhca3*1) mRNA, complete cds	At1g61520	U01103	0.043	chlorophyll A-B binding protein / LHCI type III (LHCA3.1), PSI type III chlorophyll a/b-binding protein (Lhca3*1)	Metabolism; energy	
At5g61550 Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K11J9	At5g61550	AB012239	0.043	protein kinase family protein	Metabolism; kinase	
At1g76930 Arabidopsis thaliana chromosome I BAC F22K20 genomic sequence	At1g76930	AC002291	0.043	proline-rich extensin-like family protein	Metabolism; other	
At2g16340 Arabidopsis thaliana chromosome II section 94 of 255 of the complete sequence. Sequence from clones F7H1, F16F14, F1P15	At2g16340	AC007047	0.043	expressed	unknown	
Genomic sequence for Arabidopsis thaliana BAC T25K16 from chromosome I	Genomic	AC007323	0.043	unk	unknown	
At4g34910 Arabidopsis thaliana mRNA for DEAD box RNA helicase, RH16	At4g34910	AL079347	0.044	DEAD/DEAH box helicase, putative (RH16), identical to cDNA DEAD box RNA helicase, RH16 GI:3776006	Genetic Information Processing; Replication and Repair;	
At1g75710 Genomic sequence for Arabidopsis thaliana BAC F10A5	At1g75710	AC006434	0.044	zinc finger (C2H2 type) family protein,	Genetic Information Processing; Transcription	
At1g20620 Arabidopsis thaliana catalase 1 (CAT1) mRNA, complete cds	At1g20620	U43147	0.044	catalase 3 (SEN2), (CAT3, Catalase, catalyzes the breakdown of hydrogen peroxide (H2O2) into water and oxygen.)	Metabolism; Amino Acid Metabolism; Tryptophan metabolism	Metabolism; Energy Metabolism;
At4g05320 Arabidopsis thaliana polyubiquitin (ubq10) mRNA, complete cds	At4g05320	L05361	0.044	polyubiquitin (UBQ10) (SEN3), senescence-associated protein; identical to GI:870791 , Induced by salicylic acid. Independent of NPR1 for their induction by salicylic acid, protein binding, protein modification, response to salicylic acid stimulus	Metabolism; Peptidases	
At5g03240 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MOK16	At5g03240	AB005240	0.044	polyubiquitin	Metabolism; Peptidases	
polyubiquitin (ubq3)	polyubiquitin	L05363	0.044	polyubiquitin	Metabolism; Peptidases	
ESTs	ESTs	AV566828	0.044		unknown	
At3g44140 Arabidopsis thaliana DNA chromosome 3, BAC clone F26G5	At3g44140	AL353814	0.044	expressed	unknown	

At3g56770 Arabidopsis thaliana DNA chromosome 3, BAC clone T8M16	At3g56770	AL390921	0.045	basic helix-loop-helix (bHLH) family protein	Genetic Information Processing; transcription	
At1g56075 Arabidopsis thaliana putative elongation factor (T6H22.13) mRNA, complete cds	At1g56075	AC009894	0.045	elongation factor 2, putative / EF-2, putative, (LOS1, encodes a translation elongation factor 2-like protein that is involved in cold-induced translation.)	Genetic information processing; translation	
Arabidopsis thaliana light-harvesting chlorophyll a/b-binding protein (Cab4) mRNA, complete cds	light-harvesting chlorophyll a/b-binding protein (Cab4)	M63931	0.045	light-harvesting chlorophyll a/b-binding protein (Cab4)	Metabolism; Energy Metabolism; Photosynthesis	
At4g22480 Arabidopsis thaliana DNA chromosome 4, BAC clone F7K2 (ESSA project)	At4g22480	AL033545	0.045	pseudogene, glycine-rich protein, 29% ID to secreted acid phosphatase 2 (SAP2)	Metabolism; other	
At1g19960 Arabidopsis thaliana unknown protein (T20H2.25) mRNA, complete cds	At1g19960	AC022472	0.045	expressed	unknown	
Arabidopsis thaliana mRNA for inositol-1,4,5-trisphosphate 5-phosphatase	At1g05630 (?)	AJ002295	0.046	Encodes an inositol polyphosphate 5-phosphatase with phosphatase activity toward only Ins(1,4,5)P3. Induced in response to ABA and wounding treatments. Expressed in young seedlings and flowers, while no transcripts were detectable in maturated roots, stems, and rosette leaves Modulates the development of cotyledon veins through its regulation of auxin homeostasis , inositol or phosphatidylinositol phosphatase activity, response to wounding, response to abscisic acid stimulus, vascular tissue development (sensu Tracheophyta), cotyledon, root, flower, stem, rosette leaf, auxin homeostasis, seedling growth	Environmental Information Processing; Signal Transduction	Metabolism; Carbohydrate Metabolism; Inositol phosphate metabolism
At5g17490 Arabidopsis thaliana DNA chromosome 5, BAC clone K3M16 (ESSA project)	At5g17490	AL391150	0.046	RGL3, DELLA subfamily member involved in GA signal transduction, gibberellin response modulator, putative / gibberellin-responsive modulator, putative, putative member of the VHIID domain transcription factor family RGAL - Arabidopsis thaliana, EMBL:AJ224957	Genetic Information and Processing; folding, sorting, regualtion	

At1g11100 Arabidopsis thaliana chromosome 1 BAC T19D16 genomic sequence	At1g11100	U95973	0.046	SNF2 domain-containing protein / helicase domain-containing protein / zinc finger protein-related, similar to RUSH-1alpha (Oryctolagus cuniculus) GI:1655930; contains Pfam profiles PF00271: Helicase conserved C-terminal domain, PF00176: SNF2 family N-terminal domain , ATP binding, DNA binding, helicase activity	Genetic Information Processing; Replication and Repair	
At3g05860 Arabidopsis thaliana chromosome III BAC F10A16 genomic sequence	At3g05860	AC012393	0.046	MADS-box protein (AGL45), similar to MADS-box protein; PMID: 12837945; contains Pfam profile PF00319: SRF-type transcription factor (DNA-binding and dimerisation domain)	Genetic Information Processing; transcription	
At3g28920 Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MYI13	At3g28920	AP002049	0.046	zinc finger homeobox family protein / ZF-HD homeobox family protein, PF04770: ZF-HD protein dimerisation region; contains Pfam TIGR01566: ZF-HD homeobox protein Cys/His-rich domain; contains TIGRFAM TIGR01565: homeobox domain, ZF-HD class; similar to ZF-HD homeobox protein	Genetic Information Processing; transcription	
At5g47220 Arabidopsis thaliana AtERF-2 mRNA for ethylene responsive element binding factor 2, complete cds	At5g47220	AB008104	0.046	ERF (ethylene response factor) subfamily B-3 of ERF/AP2 transcription factor family	Genetic Information Processing; transcription	
At3g16830 Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:K20I9	At3g16830	AB028608	0.046	WD-40 repeat family protein, contains 10 WD-40 repeats (PF00400) (1 weak)	Metabolism; Peptidases	
At5g07510 Glycine-rich protein {clone atGRP-4} [Arabidopsis thaliana, C24, mRNA Partial, 498 nt]	At5g07510	AL163912	0.046	glycine-rich protein (GRP14), oleosin; glycine-rich protein 14 (GRP14) PMID:11431566; PIR:JQ1063, encodes a glycine-rich protein that is expressed in low abundance in stems and leaves, and very low abundance in flowers.	unknown	
Arabidopsis thaliana actin depolymerizing factor 5 (ADF5) mRNA, complete cds	(ADF5)	AF102823	0.047	actin	Cellular Processes; Cell Motility; Regulation of actin cytoskeleton	
At4g28300 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68	At4g28300	AL161572	0.047	hydroxyproline-rich glycoprotein family protein, Encodes a protein with 13.6% proline amino acids that is predicted to localize to the cell wall.	Environmental Information Processing; Signaling Molecules	Cellular Processes and Signaling; CD molecules

At3g52760 Arabidopsis thaliana DNA chromosome 3, BAC clone F3C22	At3g52760	AL353912	0.047	integral membrane Yip1 family protein, contains Pfam domain, PF04893, vesicle mediated transport	Genetic Information Processing; Folding, Sorting and Degradation	
At1g69030 Arabidopsis thaliana chromosome 1 BAC T6L1 genomic sequence	At1g69030	AC011665	0.047	BSD domain-containing protein, contains Pfam profile PF03909	Genetic Information Processing; Transcription	
At2g21660 A.thaliana mRNA for glycine rich protein	At2g21660	AY042826	0.047	glycine-rich RNA-binding protein (GRP7), small glycine-rich protein (GRPs) that is part of a negative-feedback loop through which AtGRP7 regulates the circadian oscillations of its own transcript	Genetic Information Processing; translation	
At2g36880 Arabidopsis thaliana chromosome II section 201 of 255 of the complete sequence. Sequence from clones T1J8	At2g36880	AC006922	0.047	S-adenosylmethionine synthetase, putative	Metabolism; amino acid	
At5g64620 Arabidopsis thaliana mRNA for invertase inhibitor homolog	At5g64620	Y12807	0.047	C/VIF2, Plant cell wall (CWI) and vacuolar invertases (VI) play important roles in carbohydrate metabolism, stress responses and sugar signaling. invertase/pectin methylesterase inhibitor family protein, PF04043	Metabolism; carbohydrate	
At2g39730 Arabidopsis thaliana mRNA for rubisco activase	At2g39730	AC003000	0.047	ribulose bisphosphate carboxylase/oxygenase activase / RuBisCO activase	Metabolism; energy	Metabolism; carbohydrate
At3g28200 Arabidopsis thaliana putative peroxidase (T19D11.1/AT3g28200) mRNA, complete cds	At3g28200	AY034973	0.047	peroxidase, putative	Metabolism; Energy Metabolism;	Metabolism; Biosynthesis of Secondary Metabolites; Stilbene
At3g24480 Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MXP5	At3g24480	AP002048	0.047	leucine-rich repeat family protein / extensin family protein, PF00560; contains proline rich extensin domains	Metabolism; other	
Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:MSD24		AP000740	0.047		unknown	
At3g07030 Arabidopsis thaliana chromosome III BAC F17A9 genomic sequence	At3g07030	AC016827	0.047	expressed	unknown	
At5g62400 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MMI9	At5g62400	AB019235	0.047	expressed	unknown	
At4g02700 Arabidopsis thaliana mRNA for sulfate transporter, complete cds	At4g02700	AB004060	0.048	SULTR3;2, sulfate transporter, membrane protein	Cellular Processes and Signaling; Transporters	Environmental Information Processing; Membrane Transport;
At1g70210 A.thaliana mRNA for cyclin delta-1	At1g70210	X83369	0.048	cyclin delta-1 (CYCD1	Cellular Processes; Cell Growth and Death; Cell cycle	Environmental Information Processing; Signal Transduction

At5g57070 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MUL3	At5g57070	AB023042	0.048	hydroxyproline-rich glycoprotein family protein, Common family members: At5g26070, At5g19800, At1g72790 (Arabidopsis thaliana), hits At5g26070, Encodes a protein with 23.5% proline residues and proline-rich extensin domains, INTERPRO:IPR002965; similar to root nodule extensin (Pisum sativum)	Environmental Information Processing; Signaling Molecules	Cellular Processes and Signaling; CD molecules
At5g16400 Arabidopsis thaliana thioredoxin f2 mRNA, complete cds	At5g16400	AF144386	0.048	thioredoxin, putative, similar to SP|P29450 Thioredoxin F-type, chloroplast precursor (TRX-F) {Pisum sativum}; contains Pfam profile: PF00085 Thioredoxin	Genetic Information Processing; Folding, Sorting and Degradation	
At5g53300 A.thaliana UBC10 mRNA for ubiquitin conjugating enzyme homolog	At5g53300	Z14991	0.048	ubiquitin-conjugating enzyme 10 (UBC10), E2	Genetic Information Processing; Folding, Sorting and Degradation; proteolysis?	
At2g24940 Arabidopsis thaliana chromosome II section 140 of 255 of the complete sequence. Sequence from clones F27A10, F27C12, F13D4	At2g24940	AC006585	0.048	cytochrome b5 domain-containing protein, PF00173: Heme/Steroid binding domain	Metabolism; energy	
Arabidopsis thaliana chromosome 1 BAC T8F5 sequence	Arabidopsis	AC004512	0.048		unknown	
Genomic sequence for Arabidopsis thaliana BAC F10A5	Genomic	AC006434	0.048		unknown	
Arabidopsis thaliana DNA chromosome 3, BAC clone T5P19		AL163972	0.048		unknown	
Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K1F13		AB013389	0.048		unknown	
At5g67210 Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K21H1	At5g67210	AB020742	0.048	expressed	unknown	
At5g67620 Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K9I9	At5g67620	AB013390	0.048	expressed	unknown	
EST, Weakly similar to T48411 Terminal flower1 (TFL1) - Arabidopsis thaliana [A.thaliana]		AA394483	0.048	terminal flower 1 protein (TFL1), identical go SP|P93003 TERMINAL FLOWER 1 protein {Arabidopsis thaliana}; contains Pfam profile PF01161: Phosphatidylethanolamine-binding protein	unknown	
At2g46870 Arabidopsis thaliana chromosome II section 250 of 255 of the complete sequence. Sequence from clones F19D11, F14M4, T3D7	At2g46870	AC004411	0.049	DNA-binding protein, putative	Genetic Information Processing; transcription	
At2g19740 Arabidopsis thaliana chromosome II section 114 of 255 of the complete sequence. Sequence from clones F3P11, F6F22	At2g19740	AC005169	0.049	60S ribosomal protein L31 (RPL31A)	Genetic Information Processing; Translation; Ribosome	

Arabidopsis thaliana ribosomal protein L29, putative; 3222-3503 (T8E24.8) mRNA, complete cds		AF386978	0.049	ribosomal protein L29, putative	Genetic Information Processing; Translation; Ribosome	
At3g46100 Arabidopsis thaliana histidyl-tRNA synthetase mRNA, complete cds	At3g46100	AF020715	0.049	HRS1. histidyl-tRNA synthetase / histidine–tRNA ligase,	Metabolism; Amino Acid Metabolism; Histidine metabolism	Genetic Information Processing; Translation; Aminoacyl-tRNA
Arabidopsis thaliana putative fructose bisphosphate aldolase (F3K23.9/At2g21330) mRNA, complete cds	At2g21330	AC006841	0.049		Metabolism; Carbohydrate Metabolism; Glycolysis ; pentose phosphate pathway	Metabolism; Energy Metabolism; Carbon fixation
At4g13340 Arabidopsis thaliana DNA chromosome 4, BAC clone T9E8, partial sequence (ESSA project)	At4g13340	AL049608	0.049	leucine-rich repeat family protein / extensin family protein	Metabolism; other	
At4g07850 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20	At4g07850	AL161508	0.049	gypsy-like retrotransposon family	unknown	TRANSPOSON
Arabidopsis thaliana DNA chromosome 3, BAC clone T14K23		AL132909	0.049		unknown	
At1g29930 Arabidopsis thaliana At1g29930/F1N18_23 mRNA, complete cds	At1g29930	X03908	0.049	expressed	unknown	
At1g32570 Arabidopsis thaliana chromosome 1 BAC T9G5 genomic sequence	At1g32570	AC055769	0.049	expressed	unknown	
At4g36230 Arabidopsis thaliana DNA chromosome 4, BAC clone F23E13 (ESSAII project)	At4g36230	AL022141	0.049	pseudogene, glycine-rich protein, glycine-rich protein GRP22, rape, PIR2:S31415	unknown	
At3g25790 Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:K13N2	At3g25790	AB028607	0.05	myb family transcription factor, contains Pfam domain, PF00249	Genetic Information Processing; transcription	
At3g46090 A.thaliana mRNA for ZAT7 protein	At3g46090	X98676	0.05	zinc finger (C2H2 type) family protein (ZAT7),	Genetic Information Processing; transcription	
At4g30370 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 72	At4g30370	AL161576	0.05	zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097	Genetic Information Processing; transcription	
At2g24990 Arabidopsis thaliana chromosome II section 140 of 255 of the complete sequence. Sequence from clones F27A10, F27C12, F13D4	At2g24990	AC006585	0.05	RIO1 family protein, PF01163, processing of ribosomal RNA, as well as for proper cell cycle progression and chromosome maintenance	Genetic Information Processing; Translation;	Cellular Processes; Cell Growth and Death; Cell cycle
Arabidopsis thaliana chromosome I BAC T6J4 genomic sequence	Arabidopsis	AC011810	0.05		unknown	
At2g10020 Arabidopsis thaliana chromosome II section 50 of 255 of the complete sequence. Sequence from clones F7B19, T15D9	At2g10020	AC006586	0.05	expressed	unknown	
At2g37830 Arabidopsis thaliana chromosome II section 205 of 255 of the complete sequence. Sequence from clones F13M22, T8P21, F16M14	At2g37830	AC007661	0.05	pseudogene, glycine-rich protein	unknown	
At3g22070 Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:MZN24	At3g22070	AB028622	0.051	proline-rich family protein, contains proline-rich extensin domains,	Metabolism; other	

Sequence of BAC F16N3 from Arabidopsis thaliana chromosome 1	Sequence	AC007519	0.051		unknown
Arabidopsis thaliana DNA chromosome 4, BAC clone T30A10 (ESSA project)		AL161514	0.051		unknown
At4g16515 Arabidopsis thaliana AT4g16511 mRNA, complete cds	At4g16515	AF380632	0.051	expressed	unknown
At5g60530 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MUF9	At5g60530	AB011483	0.051	late embryogenesis abundant protein-related / LEA protein-related, endomembrane, auxin responsive protein	unknown
Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MCO15		AB010071	0.051	unk	unknown
A.thaliana mRNA (clone ACaM6) for calmodulin	A.thaliana	Z12024	0.052	calmodulin	Environmental Information Processing; signal transduction
At1g17950 Arabidopsis thaliana putative transcription factor (MYB52) mRNA, complete cds	At1g17950	AF062888	0.052	myb family transcription factor (MYB52), similar to myb-like protein GI:6979341 from (Oryza sativa) , nucleus, DNA binding, transcription factor activity, regulation of transcription, DNA-dependent, response to abscisic acid stimulus	Genetic Information Processing; Transcription
At2g47810 Arabidopsis thaliana chromosome II section 254 of 255 of the complete sequence. Sequence from clones T30B22, F17A22, T9J23	At2g47810	AC005309	0.052	histone-like transcription factor (CBF/NF-Y) family protein, contains Pfam PF00808	Genetic Information Processing; transcription
At3g06250 Arabidopsis thaliana unknown protein (F28L1.19) mRNA, complete cds	At3g06250	AF360270	0.052	far-red impaired responsive protein, putative, similar to far-red impaired response protein FAR1, cellular component unknown, zinc ion binding, response to red or far red light	Genetic Information Processing; transcription
At4g27330 Arabidopsis thaliana sporocyteless (SPL) mRNA, complete cds	At4g27330	AF159255	0.052	sporocyteless (SPL), identical to sporocyteless SPL (MADS-box related protein)	Genetic Information Processing; transcription
At4g36710 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 85	At4g36710	AL161589	0.052	scarecrow transcription factor family protein	Genetic Information Processing; transcription

EST, Moderately similar to T00448 hypothetical protein T14N5.5 - Arabidopsis thaliana [A.thaliana]	At1g77180	AV557234	0.052	chromatin protein family, contains Pfam domain, PF02731: SKIP/SNW domain found in chromatin proteins. similar to RNA recognition motif (RRM)-containing protein [Arabidopsis thaliana] (TAIR:At2g16940.1); similar to WD-40 repeat family protein [Arabidopsis thaliana] (TAIR:At5g67320.1); similar to GAMYB-binding protein [Hordeum vulgare subsp. vulgare] (GB:AAO25542.1); contains InterPro domain SKIP/SNW domain (InterPro:IPR004015)	Genetic Information Processing; Translation
At5g52650 Arabidopsis thaliana genomic DNA, chromosome 5, BAC clone:F6N7	At5g52650	AB025606	0.052	40S ribosomal protein S10 (RPS10C),	Genetic Information processing; translation
Arabidopsis thaliana putative ribosomal protein (F1O17.6) mRNA, complete cds		AF370320	0.052	ribosomal	Genetic Information Processing; Translation; Ribosome
At5g02890 Arabidopsis thaliana DNA chromosome 5, BAC clone F9G14 (ESSA project)	At5g02890	AL162973	0.052	transferase family protein, contains Pfam profile PF02458	Metabolism; other; transferase
At1g54410 Arabidopsis thaliana At1g54410 (At1g54410/F20D21_23) mRNA, complete cds	At1g54410	AF325000	0.052	dehydrin family protein	unknown
At4g25890 Arabidopsis thaliana DNA chromosome 4, BAC clone F14M19 (ESSA project)	At4g25890	AL049480	0.053	60S acidic ribosomal protein P3 (RPP3A),	Genetic Information Processing; Translation; Ribosome
Arabidopsis thaliana AT4g27090/T24A18_40 mRNA, complete cds	AT4g27090	AF378869	0.053	60S ribosomal protein L14 (RPL14B), ribosomal protein L14 - Human,PIR3:JC5954 , cytosolic ribosome (sensu Eukaryota), ribosome, structural constituent of ribosome, protein biosynthesis, ribosome biogenesis	Genetic Information Processing; Translation; Ribosome
At4g37230 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 87	At4g37230	AL161591	0.053	oxygen-evolving enhancer protein, chloroplast, putative / 33 kDa subunit of oxygen evolving system of photosystem II, putative,	Metabolism; energy; photosynthesis
At3g54590 Arabidopsis thaliana DNA chromosome 3, BAC clone T14E10	At3g54590	AL138656	0.053	proline-rich extensin-like family protein, contains proline-rich extensin domains, INTERPRO:IPR002965 (hits ATHRGP1, AB022782 Arabidopsis thaliana mRNA for hydroxyproline-rich glycoprotein)	Metabolism; other

At2g44290 Arabidopsis thaliana YLS3 mRNA for non-specific lipid transfer protein (nLTP) like protein, partial cds	At2g44290	AC004521	0.053	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	Metabolism; Peptidases	Metabolism; lipid	Genetic Information Processing; Folding, Sorting and Degradation
At5g20620 Arabidopsis thaliana UBQ4 gene for polyubiquitin	At5g20620	X12853	0.053	polyubiquitin (UBQ4), encodes a ubiquitin polyprotein.	Metabolism; Peptidases		
At2g17310 Arabidopsis thaliana chromosome II section 100 of 255 of the complete sequence. Sequence from clones T23A1, F5J6, MJB20	At2g17310	AC002329	0.053	F-box family protein	unknown		
At3g22160 Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:MKA23	At3g22160	AP001306	0.053	VQ motif-containing protein, contains PF05678:	unknown		
At3g28420 Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MFJ20	At3g28420	AB026644	0.053	expressed	unknown		
At5g15120 Arabidopsis thaliana DNA chromosome 5, BAC clone F8M21 (ESSA project)	At5g15120	AL353993	0.053	expressed	unknown		
At5g49610 Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K6M13	At5g49610	AB023033	0.053	F-box family protein, contains Pfam PF00646: F-box domain; contains TIGRFAM TIGR01640: F-box protein interaction domain; similar to unknown protein (gb|AAF30317.1)	unknown		
Arabidopsis thaliana mRNA for AtRAD17, complete cds	At5g66130	AB030250	0.054	cell cycle checkpoint protein-related, weak similarity to cell cycle checkpoint protein RAD17, mRNA for AtRAD17, complete cds; mutant has Increased sensitivity to MMS; Increased telomere lengths; Yeast RAD 17 Homolog.	Cellular Processes; Cell Growth and Death; Cell cycle		
Arabidopsis thaliana AT3g53750/F5K20_50 mRNA, complete cds	ACT3	U39480	0.054	actin 3 (ACT3), cytoskeleton, structural constituent of cytoskeleton, cytoskeleton organization and biogenesis, M germinated pollen stage	Cellular Processes; Cell Motility; Regulation of actin cytoskeleton		
EST	EST	AA394613	0.054	Arabidopsis thaliana expressed protein (At1g28240); gi|16973032|emb|AL513315.15| Human DNA sequence from clone RP11-262N9 on chromosome 1 Contains the IL10 gene for interleukin 10 and the IL19 gene for interleukin 19, complete sequence, 44.1 0.41; next best, gi|22651520|gb|AY082612.1| Ocimum basilicum p-coumaroyl shikimate 3'-hydroxylase isoform 2, 42.1 1.6	Environmental Information Processing; Signaling Molecules	Cellular Processes and Signaling; Cytokines	

At5g10570 Arabidopsis thaliana DNA chromosome 5, BAC clone F12B17 (ESSA project)	At5g10570	AL353995	0.054	basic helix-loop-helix (bHLH) family protein, bHLH transcription factor, Arabidopsis thaliana, EMBL:AC005167	Genetic Information and Processing; folding, sorting, regualtion		
At3g50080 Arabidopsis thaliana DNA chromosome 3, BAC clone F3A4	At3g50080	AL132978	0.054	F-box family protein (FBL16), contains similarity to SKP1 interacting partner 2, PF00646	Genetic Information Processing; Folding, Sorting and Degradation	Environmental Information Processing; Signal Transduction	Cellular Processes; Cell Growth and Death; Cell cycle
At5g26300 Arabidopsis thaliana BAC F9D12	At5g26300	AF077407	0.054	ubiquitin meprin and TRAF homology domain-containing protein / MATH domain-containing protein, low similarity to ubiquitin-specific protease 12 (Arabidopsis thaliana) GI:11993471; contains Pfam profile PF00917: MATH domain	Genetic Information Processing; Folding, Sorting and Degradation; proteolysis?		
At2g17870 Arabidopsis thaliana putative glycine-rich zinc-finger DNA-binding protein (T13L16.11/At2g17870) mRNA, complete cds	At2g17870	AY035133	0.054	cold-shock DNA-binding family protein, contains Pfam domains, PF00313: 'Cold-shock' DNA-binding domain and PF00098: Zinc knuckle	Genetic Information Processing; Transcription		
At4g21550 Arabidopsis thaliana DNA chromosome 4, BAC clone F18E5 (ESSAII project)	At4g21550	AL022603	0.054	transcriptional factor B3 family protein, Pfam profile PF02362	Genetic Information Processing; transcription		
At1g17640 Genomic sequence for Arabidopsis thaliana BAC F1L3 from chromosome I	At1g17640	AC022492	0.054	RNA recognition motif (RRM)-containing protein, similar to GB:L02953 from (Xenopus laevis), RNA binding	Genetic Information Processing; Translation		
At3g02190 Arabidopsis thaliana chromosome III BAC F14P3 genomic sequence	At3g02190	AC009755	0.054	60S ribosomal protein L39 (RPL39B), similar to ribosomal protein L39 GB:P51424 (Arabidopsis thaliana) , ribosome, structural constituent of ribosome, protein biosynthesis	Genetic Information Processing; Translation; Ribosome		
At3g11180 Arabidopsis thaliana chromosome 3 BAC F11B9 genomic sequence	At3g11180	AC073395	0.054	oxidoreductase, 2OG-Fe(II) oxygenase family protein, PF03171	Metabolism; Energy Metabolism; Reductive carboxylate cycle		
At4g15550 Arabidopsis thaliana UDP-glucose:indole-3-acetate beta-D-glucosyltransferase (iaglu) mRNA, complete cds	At4g15550	U81293	0.054	UDP-glucose:indole-3-acetate beta-D-glucosyltransferase (iaglu),	Metabolism; Glycan Biosynthesis and Metabolism; Lipopolysaccharide		
At1g68725 Arabidopsis thaliana chromosome 1 BAC F24J5 sequence	At1g68725	AC008075	0.054	arabinogalactan-protein, putative (AGP19), non-consensus splice site at the intron:exon boundary (AT:exon), extracellular proteoglycans implicated in plant growth and development	Metabolism; other		

At2g44300 Arabidopsis thaliana chromosome II section 238 of 255 of the complete sequence. Sequence from clones F4I1	At2g44300	AC004521	0.054	lipid transfer protein-related, PF00234: Protease inhibitor/seed storage/LTP family	Metabolism; Peptidases	Metabolism; lipid
At2g13330 Arabidopsis thaliana chromosome II section 73 of 255 of the complete sequence. Sequence from clones T17A11, F15O11	At2g13330	AC006446	0.054	gypsy-like retrotransposon family	unknown	TRANSPOSON
Arabidopsis thaliana chromosome I BAC T28P6 genomic sequence	Arabidopsis	AC007259	0.054		unknown	
EST	EST	F15183	0.054		unknown	
Genomic sequence for Arabidopsis thaliana BAC F1N19 from chromosome I	Genomic	AC009519	0.054		unknown	
Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MQB2		AB009053	0.054		unknown	
At1g11850 Arabidopsis thaliana chromosome 1 BAC F12F1 sequence, complete sequence	At1g11850	AC002131	0.054	expressed, endomembrane	unknown	
At4g08910 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 25	At4g08910	AL161513	0.054	expressed	unknown	
At4g30450 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 73	At4g30450	AL161577	0.054	glycine-rich protein	unknown	
At4g35610 Arabidopsis thaliana DNA chromosome 4, BAC clone F8D20 (ESSAII project)	At4g35610	AL031135	0.055	zinc finger (C2H2 type) family protein, contains Pfam domain PF00096: Zinc finger, C2H2 type - TF activity	Genetic Information Processing; transcription	
At3g17390 Arabidopsis thaliana AT3g17390/MGD8_20 mRNA, complete cds	At3g17390	AY037214	0.055	S-adenosylmethionine synthetase	Metabolism; amino acid	
At2g04850 Arabidopsis thaliana chromosome II section 23 of 255 of the complete sequence. Sequence from clones F28I8	At2g04850	AC006955	0.055	auxin-responsive protein-related, membrane, dopamine beta-monooxygenase activity	Metabolism; Amino Acid Metabolism; Tyrosine metabolism	
A.thaliana Cab mRNA for photossystem I chlorophyll A/B-binding protein	A.thaliana	AF326866	0.055		Metabolism; Energy Metabolism; Photosynthesis	
Arabidopsis thaliana genomic DNA, chromosome 5, BAC clone:F6B6		AP000368	0.055		unknown	
At5g12460 Arabidopsis thaliana DNA chromosome 5, BAC clone T2L20 (ESSA project)	At5g12460	AL592312	0.056	fringe-related protein	Environmental Information Processing; Signal Transduction;	
At5g22260 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MWD9	At5g22260	AB007651	0.056	male sterility 1 protein, putative (MS1), Sporophytic factor controlling anther and pollen development. Mutants fail to make functional pollen;pollen degeneration occurs after microspore release and the tapetum also appears abnormally vacuolated. Similar to PHD-finger motif transcription factors, PF00628: PHD-finger; identical to cDNA male sterility 1 protein (ms1 gene)	Genetic Information and Processing; folding, sorting, regualtion	

At5g60200 Arabidopsis thaliana genomic DNA, chromosome 5, BAC clone:F15L12	At5g60200	AB026632	0.056	Dof-type zinc finger domain-containing protein	Genetic Information and Processing; transcription	
At3g23100 Arabidopsis thaliana putative double strand break repair protein (XRCC4) mRNA, complete cds	At3g23100	AF233528	0.056	double strand break repair protein, putative (XRCC4),	Genetic Information Processing; Replication and Repair;	
At1g44030 Genomic sequence for Arabidopsis thaliana BAC F9C16 from chromosome I	At1g44030	AC022314	0.056	DC1 domain-containing protein, contains Pfam profile PF03107	Genetic Information Processing; Transcription	
At3g25900 Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MPE11	At3g25900	AB023041	0.056	homocysteine S-methyltransferase 1 (HMT-1),	Metabolism; Amino Acid Metabolism; Methionine metabolism	
At1g67090 Arabidopsis thaliana F1O19.10/F1O19.10 mRNA, complete cds	At1g67090	X13611	0.056	ribulose bisphosphate carboxylase small chain 1A / RuBisCO small subunit 1A (RBCS-1A) (ATS1A	Metabolism; Carbohydrate Metabolism; Glyoxylate and	Metabolism; Energy Metabolism; Carbon fixation
At4g08380 Arabidopsis thaliana DNA chromosome 4, BAC clone T28D5, partial sequence (ESSA project)	At4g08380	AL109819	0.056	proline-rich extensin-like family protein, contains proline-rich extensin domains, INTERPRO:IPR002965	Metabolism; other	
At4g16500 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 44	At4g16500	AL161544	0.056	cysteine protease inhibitor family protein / cystatin family protein, Pfam profile PF00031	Metabolism; Peptidases	
Arabidopsis thaliana DNA chromosome 3, BAC clone T27I15		AL358732	0.056		unknown	
At1g49150 Genomic sequence for Arabidopsis thaliana BAC F27J15 from chromosome I	At1g49150	AC016041	0.056	expressed	unknown	
At2g26120 Arabidopsis thaliana chromosome II section 146 of 255 of the complete sequence. Sequence from clones T19L18	At2g26120	AC004747	0.056	glycine-rich protein	unknown	
At5g39570 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MIJ24	At5g39570	AB012243	0.056	expressed	unknown	
At5g35630 Light-regulated glutamine synthetase isoenzyme [Arabidopsis thaliana, mRNA, 1548 nt]	At5g35630	S69727	0.057	glutamine synthetase (GS2)	Metabolism; amino acid	
At5g63650 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MBK5	At5g63650	AB005234	0.057	serine/threonine protein kinase, putative, similar to serine/threonine-protein kinase ASK2	Metabolism; kinase	Environmental Information Processing; Signal Transduction;
Glycine-rich protein {clone atGRP-1} [Arabidopsis thaliana, C24, mRNA Partial, 740 nt]		S47405	0.057		unknown	
At2g03360 Arabidopsis thaliana chromosome II section 14 of 255 of the complete sequence. Sequence from clones T18E12, T4M8, F19B11	At2g03360	AC006284	0.057	hypothetical protein	unknown	
ESTs, Weakly similar to T10681 hypothetical protein F3L17.80 - Arabidopsis thaliana [A.thaliana]	At4g31510	AV560371	0.057	expressed protein, low similarity to MTD1 (Medicago truncatula) GI:9294810 , chloroplast	unknown	

At4g38740 Arabidopsis thaliana cytosolic cyclophilin (ROC1) mRNA, complete cds	At4g38740	L14844	0.058	cytosolic cyclophilin (ROC1), peptidyl-prolyl cis-trans isomerase / cyclophilin / rotamase / cyclosporin A-binding protein (ROC1), identical to SP|P34790 Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8) (PPIase) (Rotamase) (Cyclophilin) (Cyclosporin A-binding protein) {Arabidopsis thaliana}	Environmental Information Processing; Signal Transduction
At5g09750 Arabidopsis thaliana DNA chromosome 5, BAC clone F17I14 (ESSA project)	At5g09750	AL353994	0.058	basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	Genetic Information and Processing; folding, sorting, regualtion
At1g47655 Sequence of BAC F16N3 from Arabidopsis thaliana chromosome 1	At1g47655	AC007519	0.058	Dof-type zinc finger domain-containing protein	Genetic Information Processing; Transcription
At3g47620 Arabidopsis thaliana DNA chromosome 3, BAC clone F1P2	At3g47620	AL132955	0.058	TCP family transcription factor, putative, auxin-induced basic helix-loop-helix transcription factor	Genetic Information Processing; transcription
At5g01880 Arabidopsis thaliana DNA chromosome 5, BAC clone T20L15 (ESSA project)	At5g01880	AL162351	0.058	zinc finger (C3HC4-type RING finger) family protein, contains Pfam domain, PF00097	Genetic Information Processing; transcription
At1g72180 Arabidopsis thaliana chromosome 1 BAC T9N14 genomic sequence	At1g72180	AC067754	0.058	leucine-rich repeat transmembrane protein kinase, putative	Metabolism; kinase
Arabidopsis thaliana DNA chromosome 3, BAC clone T10D17		AL353865	0.058		unknown
Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MCO15		AB010071	0.058		unknown
At1g09340 Arabidopsis thaliana g5bf mRNA	At1g09340	AY035050	0.058	expressed	unknown
At1g76180 Arabidopsis thaliana mRNA for ERD14 protein, complete cds	At1g76180	AF326904	0.058	dehydrin (ERD14), induced by dehydration and auxin, ERD14 protein is capable of binding Ca2+, especially when the protein is phosphorylated	unknown
At4g22020 Arabidopsis thaliana DNA chromosome 4, BAC clone F1N20 (ESSA project)	At4g22020	AL022140	0.058	pseudogene, hypothetical protein, similar to uncharacterized glycine-rich protein	unknown
At5g62440 Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K19B1	At5g62440	AB015469	0.058	expressed	unknown
At4g37930 Arabidopsis thaliana mRNA for serine hydroxymethyl transferase (shm1 gene)	At4g37930	AJ271726	0.059	serine hydroxymethyltransferase	Metabolism; amino acid
At3g42850 Arabidopsis thaliana DNA chromosome 3, BAC clone F18P9	At3g42850	AL138654	0.059	galactokinase, putative	Metabolism; Carbohydrate Metabolism; Galactose metabolism
At4g08410 Arabidopsis thaliana DNA chromosome 4, BAC clone T28D5, partial sequence (ESSA project)	At4g08410	AL109819	0.059	proline-rich extensin-like family protein	Metabolism; other

At3g23840 Arabidopsis thaliana genomic DNA, chromosome 3, BAC clone:F14O13	At3g23840	AP001297	0.059	transferase family protein	Metabolism; other; transferase	
ESTs	ESTs	AV555032	0.059		unknown	
At2g40080 Arabidopsis thaliana unknown protein (T28M21.24/At2g40080) mRNA, complete cds	At2g40080	AF002109	0.059	expressed protein (also hits ELF4 involved in photoperiod perception and circadian regulation	unknown	
At4g09840 Arabidopsis thaliana DNA chromosome 4, BAC clone F17A8 (ESSA project)	At4g09840	AL049482	0.059	expressed	unknown	
At3g51930 Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15	At3g51930	AL049711	0.06	transducin family protein / WD-40 repeat family protein, contains 7 WD-40 repeats (PF00400); myosin heavy chain kinase B	Environmental Information Processing; Signal Transduction	
At1g48470 Genomic sequence for Arabidopsis thaliana BAC T1N15 from chromosome I	At1g48470	AC020889	0.06	glutamine synthetase, putative (GLN1;5, Encodes cytosolic glutamine synthase isozyme. Expression of mRNA is not detectible in roots.)	Metabolism; amino acid	
At1g73670 Arabidopsis thaliana putative MAP kinase (F25P22.9) mRNA, complete cds	At1g73670	AF387019	0.06	mitogen-activated protein kinase, putative / MAPK, putative (MPK15), Pfam profile: PF00069 Eukaryotic protein kinase domain	Metabolism; kinase	Environmental Information Processing; Signal Transduction
At2g15880 Arabidopsis thaliana chromosome II section 92 of 255 of the complete sequence. Sequence from clones F19G14, F7H1	At2g15880	AC006438	0.06	leucine-rich repeat family protein / extensin family protein	Metabolism; other	
Arabidopsis thaliana AT4g17010/dl4535w mRNA, complete cds	AT4g17010	AY045651	0.06	expressed, mito	unknown	
At4g24370 Arabidopsis thaliana DNA chromosome 4, BAC clone T22A6 (ESSA project)	At4g24370	AL078637	0.06	expressed	unknown	
Arabidopsis thaliana DNA chromosome 4, BAC clone T5J17 (ESSA project)		AL035708	0.06	unk	unknown	
At5g12120 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MXC9	At5g12120	AB007727	0.061	ubiquitin-associated (UBA)/TS-N domain-containing protein, contains Pfam profile PF00627	Genetic Information Processing; Folding, Sorting and Degradation; proteolysis?	
At1g07620 Arabidopsis thaliana chromosome 1 BAC F24B9 sequence	At1g07620	AC007583	0.061	GTP1/OBG family protein, similar to SP|P20964 Spo0B-associated GTP-binding protein {Bacillus subtilis}; contains Pfam profile PF01018: GTP1/OBG family	Genetic Information Processing; Non-enzyme	
At1g42990 Arabidopsis thaliana putative bZIP transcription factor (F13A11.5) mRNA, complete cds	At1g42990	AY045964	0.061	bZIP transcription factor family protein, contains Pfam profile: PF00170	Genetic Information Processing; Transcription	
At5g09510 Arabidopsis thaliana DNA chromosome 5, BAC clone T5E8 (ESSA project)	At5g09510	AL391712	0.061	40S ribosomal protein S15 (RPS15D),	Genetic Information processing; translation	

At2g43050 Arabidopsis thaliana chromosome II section 233 of 255 of the complete sequence. Sequence from clones MFL8	At2g43050	AC006224	0.061	pectinesterase family protein, contains Pfam profile: PF01095	Metabolism; Carbohydrate Metabolism; Starch and sucrose metabolism		
At2g20530 Arabidopsis thaliana chromosome II section 117 of 255 of the complete sequence. Sequence from clones F11A3, T13C7, F23N11	At2g20530	AC007109	0.061	prohibitin, putative, PF01145: SPFH domain / Band 7 family	unknown		
At3g52460 Arabidopsis thaliana DNA chromosome 3, BAC clone F22O6	At3g52460	AL050300	0.062	hydroxyproline-rich glycoprotein family protein	Environmental Information Processing; Signaling Molecules	Cellular Processes and Signaling; CD molecules	
At5g60120 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MGO3	At5g60120	AB019231	0.062	AP2 domain-containing transcription factor, putative	Genetic Information and Processing; transcription		
At3g02000 Arabidopsis thaliana chromosome III BAC F28J7 genomic sequence	At3g02000	AC010797	0.062	glutaredoxin family protein	Genetic Information Processing; Folding, Sorting and Degradation		
At4g26230 Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA project)	At4g26230	AL049171	0.062	60S ribosomal protein L31 (RPL31B), ribosomal protein L31, Nicotiana glutinosa, U23784 , ribosome, structural constituent of ribosome, protein biosynthesis, ribosome biogenesis	Genetic Information Processing; Translation; Ribosome		
At4g15500 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 41	At4g15500	AL161541	0.062	UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201	Metabolism; Glycan Biosynthesis and Metabolism; Lipopolysaccharide		
At2g27380 Arabidopsis thaliana chromosome II section 154 of 255 of the complete sequence. Sequence from clones T22O13, F12K2	At2g27380	AC006233	0.062	ERP1, Encodes an extensin like gene involved in seed germination. proline-rich family protein, cell wall component	Metabolism; other		
At1g62790 Genomic sequence for Arabidopsis thaliana BAC F23N19 from chromosome I	At1g62790	AC007190	0.062	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein, contains Pfam protease inhibitor/seed storage/LTP family domain PF00234	Metabolism; Peptidases	Metabolism; lipid	Genetic Information Processing; Folding, Sorting and Degradation
Arabidopsis thaliana DNA chromosome 3, BAC clone F27K19		AL163832	0.062		unknown		
Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:K7P8		AB028609	0.062		unknown		
Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MAE1		AB015472	0.062		unknown		
Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MJB21		AB007647	0.062		unknown		
At1g05130 Arabidopsis thaliana chromosome 1 YAC yUP8H12 complete sequence	At1g05130	AC000098	0.062	obsolete, unknown	unknown		
At2g13320 Arabidopsis thaliana chromosome II section 73 of 255 of the complete sequence. Sequence from clones T17A11, F15O11	At2g13320	AC006446	0.062	expressed	unknown		
At2g18440 Arabidopsis thaliana GUT15 mRNA, complete cds	At2g18440	U84973	0.062	expressed	unknown		

At5g05100 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MUG13	At5g05100	AB005245	0.062	expressed protein	unknown		
Arabidopsis thaliana putative protein kinase (F2P16.21) mRNA, complete cds	At5g26751	AY046024	0.063	shaggy-related protein kinase alpha / ASK-alpha (ASK1), identical to shaggy-related protein kinase alpha SP:P43288 GI:460832 from (Arabidopsis thaliana) , cellular component unknown, protein serine/threonine kinase activity, meristem organization, inflorescence meristem	Cellular Processes; Cell Growth and Death; Cell cycle		
At4g38940 Arabidopsis thaliana DNA chromosome 4, BAC clone F19H22 (ESSA project)	At4g38940	AL035679	0.063	kelch repeat-containing F-box family protein, SKP1 interacting partner 6	Genetic Information Processing; Folding, Sorting and Degradation	Environmental Information Processing; Signal Transduction	Cellular Processes; Cell Growth and Death; Cell cycle
At1g68360 Arabidopsis thaliana chromosome 1 BAC T22E19 genomic sequence	At1g68360	AC016447	0.063	zinc finger protein-related,	Genetic Information Processing; Transcription		
At1g69780 Arabidopsis thaliana homeodomain leucine-zipper protein ATHB13 mRNA, complete cds	At1g69780	AF208044	0.063	homeobox-leucine zipper prot, nucleus, DNA binding, transcription factor activity, regulation of transcription, DNA-dependent	Genetic Information Processing; transcription		
At3g56400 Arabidopsis thaliana putative DNA-binding protein (T5P19_50/AT3g56400) mRNA, complete cds	At3g56400	AY039933	0.063	WRKY family transcription factor, TF group III	Genetic Information Processing; transcription		
At5g52190 Arabidopsis thaliana genomic DNA, chromosome 5, BAC clone:F17P19	At5g52190	AB025603	0.063	sugar isomerase (SIS) domain-containing protein, similar to 6-phospho-3-hexuloisomerase (Mycobacterium gastri) GI:6899860; contains Pfam profile PF01380: SIS domain	Metabolism; carbohydrate		
A.thaliana mRNA for SMT3 protein	A.thaliana	X99609	0.063	Encodes S-adenosyl-methionine-sterol-C-methyltransferase, an enzyme in the sterol biosynthetic pathway. S-adenosylmethionine-dependent methyltransferase activity	Metabolism; other; sterol methyltransferase		
At2g23200 Arabidopsis thaliana chromosome II section 132 of 255 of the complete sequence. Sequence from clones F21P24, T20D16, F26B6	At2g23200	AC002391	0.063	protein kinase family protein, contains protein kinase domain, Pfam:PF00069	Metabolism; Protein kinases	Cellular Processes and Signaling; Signal transduction	
Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:K17E7		AP000736	0.063		unknown		
Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MTG13		AB008270	0.063		unknown		
At1g76800 Arabidopsis thaliana chromosome 1 BAC F28O16 genomic sequence	At1g76800	AC010718	0.063	nodulin, putative	unknown		
At4g31830 Arabidopsis thaliana DNA chromosome 4, BAC clone F11C18 (ESSA project)	At4g31830	AL049607	0.063	expressed	unknown		

At5g48290 Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K23F3	At5g48290	AP000372	0.063	expressed	unknown	
At4g24060 Arabidopsis thaliana AT4g24060/T19F6_50 mRNA, complete cds	At4g24060	AY037220	0.064	Dof-type zinc finger domain-containing protein,	Genetic Information Processing; transcription	
Arabidopsis thaliana 14-3-3 protein isoform GF14 nu mRNA, complete cds	14-3-3 protein isoform GF14 nu	U60445	0.065	Arabidopsis thaliana 14-3-3 protein isoform GF14 nu mRNA, complete cds, multiple functions, Ca and receptor binding, may interact with PKC, binds DNA regulatory element	Cellular Processes and Signaling; signal transduction	
At3g05220 Arabidopsis thaliana chromosome III BAC T12H1 genomic sequence	At3g05220	AC009177	0.065	heavy-metal-associated domain-containing protein, similar to farnesylated protein 1, metal ion transport, endomembrane system, metal ion binding	Environmental Information Processing; Membrane Transport;	
At3g11940 Arabidopsis thaliana putative 40S ribosomal protein S5 (F26K24.23/AT3g11940) mRNA, complete cds	At3g11940	AY045846	0.065	signal recognition particle 14 kDa family protein / SRP14 family protein, similar to SP|P16254 Signal recognition particle 14 kDa protein (SRP14), signal recognition particle (sensu Eukaryota), RNA binding, protein targeting	Genetic Information Processing; Folding, Sorting and Degradation; protein export	
At2g15180 Arabidopsis thaliana chromosome II section 88 of 255 of the complete sequence. Sequence from clones F15A23	At2g15180	AC006298	0.065	zinc knuckle (CCHC-type) family protein, contains Pfam domain PF00098: Zinc knuckle	Genetic Information Processing; Transcription	
At5g44520 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MFC16	At5g44520	AB017065	0.065	ribose 5-phosphate isomerase-related, low similarity to SP|P47968 Ribose 5-phosphate isomerase (EC 5.3.1.6) (Phosphoriboisomerase) {Mus musculus}	Metabolism; Carbohydrate Metabolism; Pentose phosphate pathway	Metabolism; Energy Metabolism; Carbon fixation
At4g25000 Arabidopsis thaliana DNA chromosome 4, BAC clone F13M23 (ESSAII project)	At4g25000	AL035523	0.065	alpha-amylase, putative / 1,4-alpha-D-glucan glucanohydrolase, putative, Predicted to be secreted protein based on signalP prediction. Involved in starch mobilization	Metabolism; Carbohydrate Metabolism; Starch and sucrose metabolism	
At2g15300 Arabidopsis thaliana chromosome II section 89 of 255 of the complete sequence. Sequence from clones F15A23, F27O10, F26H6	At2g15300	AC007267	0.065	leucine-rich repeat transmembrane protein kinase, putative,	Metabolism; kinase	Environmental Information Processing; Signal Transduction
Arabidopsis thaliana chromosome 1 BAC T8L23 genomic sequence	Arabidopsis	AC079730	0.065		unknown	
Arabidopsis thaliana chromosome 1 BAC F9K20 sequence, complete sequence		AC005679	0.065		unknown	
At2g29950 Arabidopsis thaliana chromosome II section 169 of 255 of the complete sequence. Sequence from clones F23F1, T27E13	At2g29950	AC004680	0.065	expressed	unknown	

At5g13100 Arabidopsis thaliana DNA chromosome 5, BAC clone T19L5 (ESSA project)	At5g13100	AL391711	0.065	expressed	unknown	
At5g23920 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MRO11	At5g23920	AB005244	0.065	expressed	unknown	
At5g48470 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MJE7	At5g48470	AB020745	0.065	expressed	unknown	
At5g56420 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MCD7	At5g56420	AB009049	0.065	F-box family protein,	unknown	
At2g35960 Arabidopsis thaliana chromosome II section 196 of 255 of the complete sequence. Sequence from clones T20F21, F11F19	At2g35960	AC007017	0.066	harpin-induced family protein / HIN1 family protein / harpin-responsive family protein (NLH12)	unknown	
At3g22550 Arabidopsis thaliana genomic DNA, chromosome 3, BAC clone:F16J14	At3g22550	AP000731	0.066	senescence-associated protein-related, similar to senescence-associated protein SAG102 - mito	unknown	
EST	At5g47540	AA728481	0.066	Mo25 family protein, similar to MO25 protein (early mouse development protein family) (Mouse) SWISS-PROT:Q06138	unknown	
At2g37620 Arabidopsis thaliana actin (ACT1) gene, complete cds	At2g37620	U39449	0.067	ACT1, Member of the actin gene family. Expressed in mature pollen.	Cellular Processes; Cell Motility; Regulation of actin cytoskeleton	
At2g21140 Arabidopsis thaliana chromosome II section 120 of 255 of the complete sequence. Sequence from clones F26H11, F7O24	At2g21140	AC006264	0.067	hydroxyproline-rich glycoprotein family protein, identical to proline-rich protein 2 (PRP2)	Environmental Information Processing; Signaling Molecules	Cellular Processes and Signaling; CD molecules
At1g14170 Arabidopsis thaliana chromosome I BAC F7A19 genomic sequence	At1g14170	AC007576	0.067	KH domain-containing protein, location of EST 219C14T7 , gb|N38506 , cellular component unknown, nucleic acid binding, biological process unknown	Genetic Information Processing; transcription	
At3g54270 Arabidopsis thaliana DNA chromosome 3, BAC clone F24B22	At3g54270	AL132957	0.067	sucrose-phosphatase 3 (SPP3), nearly identical to sucrose-phosphatase (SPP3) (Arabidopsis thaliana) GI:16904077	Metabolism; Carbohydrate Metabolism; sugars	
At4g10340 Arabidopsis thaliana Lhcb5 protein (Lhcb5) mRNA, complete cds	At4g10340	AF134129	0.067	chlorophyll A-B binding protein CP26, chloroplast / light-harvesting complex II protein 5 / LHCIIc (LHCB5),	Metabolism; energy; photosynthesis	
ESTs	ESTs	AV565888	0.067		unknown	
Genomic sequence for Arabidopsis thaliana BAC F16A14 from chromosome I	Genomic	AC068197	0.067		unknown	
At5g09420 Arabidopsis thaliana DNA chromosome 5, BAC clone T5E8 (ESSA project)	At5g09420	AL391712	0.068	chloroplast outer membrane translocon subunit, putative	Cellular Processes and Signaling; Transporters	
At4g04890 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 14	At4g04890	AB056455	0.068	homeobox-leucine zipper protein protodermal factor 2 (PDF2),	Genetic Information Processing; transcription	

At5g02460 Arabidopsis thaliana DNA chromosome 5, BAC clone T22P11 (ESSA project)	At5g02460	AL162971	0.068	Dof-type zinc finger domain-containing protein, zinc finger protein OBP3, Arabidopsis thaliana, EMBL:AF155818	Genetic Information Processing; transcription	
Arabidopsis thaliana glutathione S-transferase (GST31) mRNA, complete cds	At1g02950	AF320055	0.068	glutathione S-transferase phi class, putative, similar to glutathione-S-transferase GI:169887 from (Silene vulgaris) cytoplasm, toxin catabolism, glutathione transferase activity	Metabolism; Metabolism of Other Amino Acids; Glutathione metabolism	Metabolism; Xenobiotics Biodegradation and Metabolism
Arabidopsis thaliana DNA chromosome 5, BAC clone T28J14 (ESSA project)		AB010697	0.068		unknown	
At4g13150 Arabidopsis thaliana DNA chromosome 4, BAC clone F17N18 (ESSA project)	At4g13150	AL049751	0.068	expressed	unknown	
Arabidopsis thaliana copper/zinc superoxide dismutase (CSD2) mRNA, nuclear gene encoding plastid protein, complete cds	At2g28190	AC006202	0.069	Encodes a chloroplastic copper/zinc superoxide dismutase CSD2 that can detoxify superoxide radicals. response to oxidative stress, response to stress, response to copper ion, response to iron ion, inflorescence, flower, rosette leaf	Cellular Processes and Signaling; Inorganic ion transport	
Arabidopsis thaliana putative metal-binding protein (MLE2.16/AT5g63530) mRNA, complete cds	AT5g63530	AF360327	0.069	copper chaperone (CCH)-related, low similarity to copper homeostasis factor (GI:3168840); nearly identical to farnesylated protein ATFP3 (GI:4097547); contains Pfam profile PF00403: Heavy-metal-associated domain , transition metal ion binding, transition metal ion homeostasis ATFP3 (Farnesylated protein that binds metals.)	Cellular Processes and Signaling; Inorganic ion transport and metabolism	
At4g31985 Arabidopsis thaliana AT4g31981/F13D4.162 mRNA, complete cds	At4g31985	AF372908	0.069	60S ribosomal protein L39 (RPL39C) , ribosome, structural constituent of ribosome, protein biosynthesis	Genetic Information Processing; Translation; Ribosome	
At3g62400 Arabidopsis thaliana DNA chromosome 3, BAC clone T12C14	At3g62400	AL162507	0.069	expressed protein, cytochrome c oxidase subunit 5c - Oryza sativa, EMBL:AB027123	Metabolism; Energy Metabolism; Oxidative phosphorylation	
At3g44650 Arabidopsis thaliana DNA chromosome 3, BAC clone T18B22	At3g44650	AL138652	0.069	non-LTR retrotransposon family (LINE),	unknown	TRANSPOSON
Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MXF12		AB016892	0.069		unknown	
At2g11890 Arabidopsis thaliana At2g11890/F23M2.5 mRNA, complete cds	At2g11890	AY045689	0.069	expressed	unknown	

ESTs, Weakly similar to T45948 hypothetical protein F7J8.60 - Arabidopsis thaliana [A.thaliana]	At5g01080	AV532622	0.069	expressed	unknown	
At1g09200 A.thaliana histone H3 gene, complete cds	At1g09200	M17131	0.07	histone H3, identical to histone H3 from Zea mays SP|P05203, Medicago sativa, chloroplast, nucleus, DNA binding, chromosome organization and biogenesis (sensu Eukaryota), nucleosome assembly, nucleosome, root, inflorescence, flower, leaf, seedling growth	Genetic Information Processing; Transcription	
At5g06550 Arabidopsis thaliana genomic DNA, chromosome 5, BAC clone:F15M7	At5g06550	AP002543	0.07	transcription factor jumonji (jmjC) domain-containing protein, contains Pfam PF00646: F-box domain; contains Pfam PF02373: jmjC domain; similar to apoptotic cell clearance receptor PtdSerR (GI:11037740) (Mus musculus)	Genetic Information Processing; Transcription	
At4g15590 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 42	At4g15590	AL161542	0.07	non-LTR retrotransposon family (LINE), also hits (At4g15580) ubiquitin family, low similarity to SP|Q15459 Splicing factor 3 subunit 1 (Spliceosome associated protein 114) {Homo sapiens}; contains Pfam profiles PF01805: Surp module (SWAP/Surp domain), PF00240: Ubiquitin family	unknown	TRANSPOSON
At1g41750 Arabidopsis thaliana chromosome 1 BAC F9M8 genomic sequence	At1g41750	AC083859	0.07	expressed	unknown	
At2g40300 Arabidopsis thaliana chromosome II section 218 of 255 of the complete sequence. Sequence from clones T3G21	At2g40300	AC007020	0.071	ferritin, putative, PF00210	Cellular Processes and Signaling; Inorganic ion transport	
Arabidopsis thaliana DNA chromosome 4, BAC clone F28M20 (ESSAII project)		AL031004	0.071		unknown	
At1g32290 Sequence of BAC F5D14 from Arabidopsis thaliana chromosome 1	At1g32290	AC007767	0.071	expressed	unknown	
At2g36210 Arabidopsis thaliana chromosome II section 198 of 255 of the complete sequence. Sequence from clones F9C22, F2H17	At2g36210	AC006921	0.071	auxin-responsive family protein, similar to auxin-induced protein SAUR-AC1	unknown	
At3g50250 Arabidopsis thaliana DNA chromosome 3, BAC clone F11C1	At3g50250	AL132976	0.071	expressed	unknown	
At3g52550 Arabidopsis thaliana DNA chromosome 3, BAC clone F22O6	At3g52550	AL050300	0.071	expressed	unknown	
At5g59770 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MTH12	At5g59770	AB006705	0.071	expressed	unknown	
At5g04260 Arabidopsis thaliana DNA chromosome 5, BAC clone F21E1 (ESSA project)	At5g04260	AL391716	0.072	thioredoxin family protein, PF00085	Genetic Information Processing; Folding, Sorting and Degradation	

Arabidopsis thaliana AT5g65360/MNA5_9 mRNA, complete cds	AT5g65360	AY039904	0.072	histone H3, chloroplast, nucleus, DNA binding, chromosome organization and biogenesis (sensu Eukaryota), nucleosome assembly, nucleosome, root, inflorescence, flower, leaf, seedling growth	Genetic Information Processing; Transcription		
At3g13740 Arabidopsis thaliana Unknown protein (MMM17.15) mRNA, complete cds	At3g13740	AF386979	0.072	URF 4-related, similar to URF 4 (GI:49224) - chloro, untranslated reading frame, chloroplast, RNA binding, ribonuclease III activity, RNA processing	Genetic Information Processing; Translation; Other translation		
At1g22480 Arabidopsis thaliana chromosome I BAC F12K8 genomic sequence	At1g22480	AC006551	0.072	plastocyanin-like domain-containing protein	Metabolism; Energy Metabolism; Photosynthesis		
At2g01340 Arabidopsis thaliana chromosome II section 2 of 255 of the complete sequence. Sequence from clones F23H14, F10A8	At2g01340	AC006200	0.072	expressed	unknown		
At5g35090 Arabidopsis thaliana genomic DNA, chromosome 5, BAC clone:T13C12	At5g35090	AP000421	0.072	expressed	unknown		
At3g49870 Arabidopsis thaliana DNA chromosome 3, BAC clone T16K5	At3g49870	AL132965	0.073	ADP-ribosylation factor, putative	Cellular Processes and Signaling; GTP-binding		
At5g59740 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MTH12	At5g59740	AB006705	0.073	UDP-sugar transport	Cellular Processes and Signaling; Transporters		
At5g43580 Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K9D7	At5g43580	AB016875	0.073	protease inhibitor, putative, similar to SP|P19873 Inhibitor of trypsin and hageman factor (CMTI-V) {Cucurbita maxima}; contains Pfam profile PF00280: Potato inhibitor I family	Genetic Information Processing; Folding, Sorting and Degradation	Metabolism; Peptidases	Metabolism; lipid
At5g57480 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MUA2	At5g57480	AB011482	0.073	AAA-type ATPase family protein	Genetic Information Processing; Folding, Sorting and Degradation		
At5g10360 Arabidopsis thaliana AT5g10360/F12B17_290 mRNA, complete cds	At5g10360	AY045594	0.073	40S ribosomal protein S6	Genetic Information processing; translation		
At4g14690 Arabidopsis thaliana putative light-induced protein (AT4g14690) mRNA, complete cds	At4g14690	AL161539	0.073	ELIP2, chlorophyll A-B binding family protein / early light-induced protein, PF00504 chlorophyll A-B binding protein	Metabolism; energy; photosynthesis		
At3g22420 Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MCB17	At3g22420	AB022215	0.073	protein kinase family protein, contains protein kinase domain, Pfam:PF00069 -related to WNK2	Metabolism; kinase		
Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K8A10		AB026640	0.073		unknown		
At1g07500 Genomic sequence for Arabidopsis thaliana BAC F22G5 from chromosome I	At1g07500	AC022464	0.073	expressed	unknown		
At1g49000 Genomic sequence for Arabidopsis thaliana BAC F27J15 from chromosome I	At1g49000	AC016041	0.073	expressed	unknown		

At4g08300 Arabidopsis thaliana DNA chromosome 4, BAC clone T12G13, partial sequence (ESSA project)	At4g08300	AL080252	0.073	nodulin MtN21 family protein	unknown	
At5g17980 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MCM23	At5g17980	AB015473	0.074	C2 domain-containing protein, contains INTERPRO:IPR000008 C2 domain	Environmental information processing; signal transduction	
At1g32760 Genomic sequence for Arabidopsis thaliana BAC F6N18 from chromosome I	At1g32760	AC017118	0.074	glutaredoxin family protein	Genetic Information Processing; Folding, Sorting and Degradation	
At1g55310 Arabidopsis thaliana Serine/arginine-rich protein mRNA, complete cds	At1g55310	AJ293799	0.074	SC35-like splicing factor, 33 kD (SCL33),	Genetic information processing; translation	
At1g01725 Arabidopsis thaliana unknown protein (T1N6.13) mRNA, complete cds	At1g01725	AC009273	0.074	expressed	unknown	
At1g75590 Genomic sequence for Arabidopsis thaliana BAC F10A5	At1g75590	AC006434	0.074	auxin-responsive family protein, similar to auxin-induced protein TGSAUR22	unknown	
At3g49270 Arabidopsis thaliana DNA chromosome 3, BAC clone F2K15	At3g49270	AL132956	0.074	exp	unknown	
At5g04470 Arabidopsis thaliana DNA chromosome 5, BAC clone T32M21 (ESSA project)	At5g04470	AL162875	0.074	expressed	unknown	
Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MCA23		AB016886	0.074	unk	unknown	
At1g56410 Arabidopsis thaliana chromosome 1 BAC F13N6 genomic sequence	At1g56410	AC058785	0.075	heat shock cognate 70 kDa protein, putative / HSC70, putative / HSP70, putative	Genetic Information Processing; Folding, Sorting and Degradation	Environmental Information Processing; Signal Transduction
At5g42980 A.thaliana (GIF1) mRNA for thioredoxin	At5g42980	Z35474	0.075	thioredoxin H-type 3 (TRX-H-3) (GIF1), encodes a cytosolic thioredoxin that reduces disulfide bridges of target proteins by the reversible formation of a disulfide bridge between two neighboring Cys residues present in the active site. Thioredoxins have been found to regulate a variety of biological reactions in prokaryotic and eukaryotic cells.	Genetic Information Processing; Folding, Sorting and Degradation	
At5g42300 Arabidopsis thaliana ubiquitin-like protein (K5J14.10) mRNA, complete cds	At5g42300	AF370527	0.075	ubiquitin family protein, contains INTERPRO:IPR000626 ubiquitin domain	Genetic Information Processing; Folding, Sorting and Degradation; proteolysis?	
At1g56340 Arabidopsis thaliana calreticulin (Crt1) mRNA, complete cds	At1g56340	U66343	0.075	calreticulin 1 (CRT1), Ca binding chaperone in ER	Genetic Information Processing; Folding, sorting, deg	

At5g49010 Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K19E20	At5g49010	AB017061	0.075	DNA replication protein-related, similar to Sld5 (Xenopus laevis) GI:29365477; contains Pfam profile PF05916: Eukaryotic protein of unknown function (DUF873)	Genetic information processing; replication	
AT1G48410, Arabidopsis thaliana Argonaute protein (AGO1) mRNA, complete cds	At1g48410	U91995	0.075	Encodes an RNA Slicer that selectively recruits microRNAs and siRNAs. Through its action on the regulation of ARF17 expression, the protein regulates genes involved at the cross talk between auxin and light signaling during adventitious root development. cytoplasm, endoribonuclease activity, posttranscriptional gene silencing, auxin metabolism, response to auxin stimulus, embryonic development (sensu Magnoliophyta), leaf morphogenesis, response to far red light, miRNA binding, siRNA binding, miRNA-mediated gene silencing, whole plant, adventitious root development	Genetic Information Processing; translation	
At5g66190 Arabidopsis thaliana mRNA for ferredoxin-NADP+ reductase precursor (petH gene)	At5g66190	AJ243705	0.075	ferredoxin–NADP(+) reductase, putative / adrenodoxin reductase, putative, chloroplast	Metabolism; Energy Metabolism;	
Genomic sequence for Arabidopsis thaliana BAC F14J16 from chromosome I	Genomic	AC002304	0.075		unknown	
At1g31175 Arabidopsis thaliana chromosome 1 BAC F28K20 sequence	At1g31175	AC004793	0.075	expressed	unknown	
At4g21620 Arabidopsis thaliana unknown protein (AT4g21620) mRNA, complete cds	At4g21620	AF360336	0.075	glycine-rich protein	unknown	
Arabidopsis thaliana actin (ACT1) gene, complete cds	actin	U39449	0.076	actin	Cellular Processes; Cell Motility; Regulation of actin cytoskeleton	
Arabidopsis thaliana putative ubiquitin/ribosomal protein (F9C22.10/At2g36170) mRNA, complete cds	At2g36170	AF360311	0.076	ubiquitin extension protein 2 (UBQ2) / 60S ribosomal protein L40 (RPL40A), identical to GI:166930, GI:166931 , intracellular, ribosome, protein binding, protein biosynthesis, protein modification	Genetic Information Processing; Folding, Sorting and Degradation; proteolysis?	Genetic Information Processing; Translation; Ribosome
At3g50060 A.thaliana mRNA for MYB-related protein (1107 bp)	At3g50060	Z54137	0.076	myb family transcription factor	Genetic Information Processing; transcription	

At1g72730 Arabidopsis thaliana mRNA for DEAD box RNA helicase, RH23	At1g72730	AJ010472	0.076	eukaryotic translation initiation factor 4A, putative / eIF-4A, putative	Genetic Information Processing; Translation	
At1g62520 Genomic sequence for Arabidopsis thaliana BAC T3P18 from Chromosome 1	At1g62520	AC005698	0.076	expressed	unknown	
At3g53530 Arabidopsis thaliana DNA chromosome 3, BAC clone F4P12	At3g53530	AL132966	0.077	myosin heavy chain-related	Cellular Processes; Cell Motility; Regulation of actin cytoskeleton	
At4g23470 Arabidopsis thaliana DNA chromosome 4, BAC clone F16G20 (ESSAII project)	At4g23470	AL031326	0.077	hydroxyproline-rich glycoprotein family protein, contains proline-rich extensin domains, INTERPRO:IPR002965	Environmental Information Processing; Signaling Molecules	Cellular Processes and Signaling; CD molecules
At3g17820 Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MEB5	At3g17820	AB019230	0.077	glutamine synthetase (GS1),	Metabolism; amino acid	
At2g45960 A.thaliana mRNA for transmembrane protein A	At2g45960	AY049238	0.078	plasma membrane intrinsic protein 1B (PIP1B) / aquaporin PIP1.2 (PIP1.2) / transmembrane protein A (TMPA),	Environmental Information Processing; Membrane Transport; Pores	
At5g54190 Arabidopsis thaliana light-dependent NADPH:protochlorophyllide oxidoreductase A (PorA) mRNA, nuclear gene encoding chloroplast protein, complete cds	At5g54190	U29699	0.078	protochlorophyllide reductase A, chloroplast / PCR A / NADPH-protochlorophyllide oxidoreductase A (PORA), light-dependent NADPH:protochlorophyllide oxidoreductase A	Metabolism; energy	
At2g47130 Arabidopsis thaliana chromosome II section 250 of 255 of the complete sequence. Sequence from clones F19D11, F14M4, T3D7	At2g47130	AC004411	0.078	short-chain dehydrogenase/reductase (SDR) family protein	Metabolism; Other energy metabolism	
At5g60630 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MUP24	At5g60630	AB005246	0.078	expressed	unknown	
At3g51380 Arabidopsis thaliana DNA chromosome 3, BAC clone F26O13	At3g51380	AL133452	0.079	calmodulin-binding family protein	Environmental Information Processing; signal transduction	
At3g04610 Arabidopsis thaliana chromosome III BAC F7O18 genomic sequence	At3g04610	AC011437	0.079	KH domain-containing protein, similar putative nucleic acid binding protein	Genetic Information Processing; transcription	
At5g44190 Arabidopsis thaliana golden2-like transcription factor (GLK2) mRNA, complete cds	At5g44190	AB005239	0.079	myb family transcription factor (GLK2, golden-like2), contains Pfam profile: PF00249, Encodes a protein containing a GARP DNA-binding domain which interacts with the Pro-rich regions of GBF1. Transactivates transcription in yeast, similar to the yeast Golden2 transcription factor that is required for photosynthetid differentiation.	Genetic Information Processing; transcription	
At2g19750 Arabidopsis thaliana chromosome II section 114 of 255 of the complete sequence. Sequence from clones F3P11, F6F22	At2g19750	AC005169	0.079	40S ribosomal protein S30 (RPS30A)	Genetic Information Processing; Translation; Ribosome	

At2g46850 Arabidopsis thaliana chromosome II section 250 of 255 of the complete sequence. Sequence from clones F19D11, F14M4, T3D7	At2g46850	AC004411	0.079	expressed protein - endomembrane, ATP binding, protein kinase activity, protein serine/threonine kinase activity, protein-tyrosine kinase activity, protein amino acid phosphorylation, endomembrane system	Metabolism; Protein kinases	
At2g33520 Arabidopsis thaliana chromosome II section 186 of 255 of the complete sequence. Sequence from clones F25I18, F4P9	At2g33520	AC002332	0.079	expressed	unknown	
At2g01570 Arabidopsis thaliana mRNA for GRS protein	At2g01570	Y11336	0.08	gibberellin response modulator (RGA1) / gibberellin-responsive modulator, identical to GB:Y11336, member of SCARECROW family	Genetic Information Processing; transcription	
At3g03550 Arabidopsis thaliana chromosome III BAC T12J13 genomic sequence	At3g03550	AC009327	0.08	zinc finger (C3HC4-type RING finger) family protein	Genetic Information Processing; transcription	
At5g15520 Arabidopsis thaliana DNA chromosome 5, BAC clone T20K14 (ESSA project)	At5g15520	AL391143	0.08	40S ribosomal protein S19 (RPS19B),	Genetic Information processing; translation	
At1g23310 Arabidopsis thaliana putative alanine aminotransferase (F26F24.16) mRNA, complete cds	At1g23310	AF360195	0.08	glutamate:glyoxylate aminotransferase 1 (GGT1), Localized to the peroxisome and thought to be involved in photorespiration/ metabolic salvage pathway.	Metabolism; Amino Acid Metabolism	
Arabidopsis thaliana DNA chromosome 4, contig fragment No. 73		AL161577	0.08		unknown	
At1g61920 Arabidopsis thaliana chromosome 1 BAC F8K4 sequence	At1g61920	AC004392	0.08	expressed	unknown	
At5g58500 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MQJ2	At5g58500	AB025632	0.08	expressed	unknown	
At1g16030 Arabidopsis thaliana chromosome 1 BAC T24D18 sequence	At1g16030	AC010924	0.081	heat shock protein 70, putative / HSP70, putative, similar to heat shock protein hsp70 GI:1771478 from (Pisum sativum) , cytosol, ATP binding, response to heat, protein folding	Genetic Information Processing; Folding, Sorting and Degradation	Environmental Information Processing; Signal Transduction
At1g07820 Arabidopsis thaliana putative histone H4 protein (F24B9.25) mRNA, complete cds	At1g07820	AC007583	0.081	histone H4, identical to histone H4 from Lycopersicon esculentum, nucleus, DNA binding, chromosome organization and biogenesis (sensu Eukaryota), nucleosome assembly, nucleosome	Genetic Information Processing; Transcription	
At1g35420 Arabidopsis thaliana chromosome 1 BAC F12A4 genomic sequence	At1g35420	AC023064	0.081	dienelactone hydrolase family protein	Metabolism; other	
Arabidopsis thaliana chromosome I BAC F2J6 genomic sequence	Arabidopsis	AC009526	0.081		unknown	

Genomic sequence for Arabidopsis thaliana BAC F27F5 from chromosome I	Genomic	AC007915	0.081		unknown	
At3g53750 Arabidopsis thaliana AT3g53750/F5K20_50 mRNA, complete cds	At3g53750	U39480	0.082	actin 3 (ACT3), Member of the Actin gene family. Expressed in mature pollen.	Cellular Processes; Cell Motility; Regulation of actin cytoskeleton	
At3g08580 Arabidopsis thaliana putative adenylate translocator (F17O14.5/AT3g08580) mRNA, complete cds	At3g08580	AY042814	0.082	mitochondrial ADP/ATP carrier	Environmental Information Processing; Membrane Transport; Other	
At1g69310 Arabidopsis thaliana chromosome 1 BAC F23O10 genomic sequence	At1g69310	AC018364	0.082	WRKY family transcription factor, contains Pfam profile: PF03106 WRKY DNA -binding domain	Genetic Information Processing; Transcription	
At2g33860 Arabidopsis thaliana auxin response transcription factor 3 (ARF3) mRNA, complete cds	At2g33860	AF007788	0.082	auxin-responsive factor (ARF3) / ETTIN protein (ETT), The ETTIN gene encodes a protein with homology to DNA binding proteins which bind to auxin response elements, involved in floral development	Genetic Information Processing; transcription	
At2g22350 Arabidopsis thaliana chromosome II section 127 of 255 of the complete sequence. Sequence from clones F14M13	At2g22350	AC006592	0.082	RNase H domain-containing protein	Genetic Information Processing; translation	
At4g17587 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46	At4g17587	AL161546	0.082	expressed	unknown	
At5g01790 Arabidopsis thaliana DNA chromosome 5, BAC clone T20L15 (ESSA project)	At5g01790	AL162351	0.082	expressed	unknown	
At5g15600 Arabidopsis thaliana DNA chromosome 5, BAC clone T20K14 (ESSA project)	At5g15600	AL391143	0.082	expressed	unknown	
At5g60790 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MAE1	At5g60790	AB015472	0.083	ABC transporter family protein	Cellular Processes and Signaling; Transporters	Environmental Information Processing; Membrane Transport; ABC
Arabidopsis thaliana chromosome II section 95 of 255 of the complete sequence. Sequence from clones F1P15, T24I21		AC007195	0.083		unknown	
Arabidopsis thaliana DNA chromosome 3, BAC clone F22O6		AL050300	0.083		unknown	
At4g33160 Arabidopsis thaliana DNA chromosome 4, BAC clone F4I10 (ESSA project)	At4g33160	AL035525	0.083	F-box family protein (FBX13), contains similarity to fimbriata GI:547307 from (Antirrhinum majus)	unknown	
At5g38870 Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K15E6	At5g38870	AB009048	0.083	expressed	unknown	
At1g50600 Arabidopsis thaliana putative scarecrow-like protein (F17J6.12) mRNA, complete cds	At1g50600	AY034929	0.084	scarecrow-like transcription factor 5 (SCL5),	Genetic Information Processing; Transcription	
At3g07070 Arabidopsis thaliana chromosome III BAC T1B9 genomic sequence	At3g07070	AC012395	0.084	protein kinase family protein, contains protein kinase domain, Pfam:PF00069	Metabolism; kinase	

Arabidopsis thaliana chromosome II section 202 of 255 of the complete sequence. Sequence from clones T1J8, T2N18, F3G5		AC006260	0.084		unknown	
At1g22850 Arabidopsis thaliana BAC F19G10, complete sequence	At1g22850	AF000657	0.084	expressed	unknown	
At4g27720 Arabidopsis thaliana putative protein (T29A15.210) mRNA, complete cds	At4g27720	AF325107	0.084	expressed	unknown	
At3g03230 Arabidopsis thaliana chromosome III BAC T17B22 genomic sequence	At3g03230	AC012328	0.085	esterase/lipase/thioesterase family protein	Metabolism; lipid	
At3g25110 A.thaliana mRNA for acyl-(acyl carrier protein) thioesterase	At3g25110	Z36912	0.085	acyl-(acyl carrier protein) thioesterase / acyl-ACP thioesterase / oleoyl-(acyl-carrier protein) hydrolase / S-acyl fatty acid synthase thioesterase	Metabolism; lipid	
Arabidopsis thaliana chromosome 3 BAC T21B14 genomic sequence	Arabidopsis	AC069473	0.085		unknown	
At4g07970 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20	At4g07970	AL161508	0.085	expressed	unknown	
At1g61250 Arabidopsis thaliana putative secretory carrier membrane protein (F11P17.4) mRNA, complete cds	At1g61250	AY045788	0.086	secretory carrier membrane protein (SCAMP) family protein (SC3), contains Pfam domain, PF04144	Environmental information processing; signal transduction	
At5g10400 Arabidopsis thaliana DNA chromosome 5, BAC clone F12B17 (ESSA project)	At5g10400	AL353995	0.086	histone H3	Genetic Information Processing; Transcription	
Arabidopsis thaliana 60S ribosomal protein L17 (T27C4.4) mRNA, complete cds	60S ribosomal protein L17 (T27C4.4)	AY042843	0.086	60S ribosomal protein L17	Genetic Information Processing; Translation; Ribosome	
At3g10920 Arabidopsis thaliana manganese superoxide dismutase (MSD1) mRNA, complete cds	At3g10920	AC009991	0.086	superoxide dismutase (Mn), mitochondrial (SODA) / manganese superoxide dismutase (MSD1),	Metabolism; energy	Cellular Processes and Signaling; Inorganic ion transport
Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6		AL161494	0.086		unknown	
At5g16930 Arabidopsis thaliana DNA chromosome 5, BAC clone F2K13 (ESSA project)	At5g16930	AL391141	0.087	AAA-type ATPase family protein, contains Pfam domain, PF00004: ATPase, AAA family	Genetic Information Processing; Folding, Sorting and Degradation	
At1g74670 Arabidopsis thaliana chromosome 1 BAC F1M20 genomic sequence	At1g74670	AC011765	0.087	gibberellin-responsive protein, putative, Pfam profile PF02704	Genetic Information Processing; transcription	
At2g47560 Arabidopsis thaliana chromosome II section 253 of 255 of the complete sequence. Sequence from clones T8I13, T30B22	At2g47560	AC002535	0.087	zinc finger (C3HC4-type RING finger) family protein, contains Pfam domain, PF00097	Genetic Information Processing; transcription	
At3g03450 Arabidopsis thaliana chromosome III BAC T21P5 genomic sequence	At3g03450	AC009895	0.087	gibberellin response modulator, putative / gibberellin-responsive modulator, putative, RGL2 (Encodes member of GRAS family of putative transcription factors, a family unique to plants.)	Genetic Information Processing; transcription	

At3g54210 Arabidopsis thaliana DNA chromosome 3, BAC clone F24B22	At3g54210	AL132957	0.087	ribosomal protein L17 family protein, contains Pfam profile: PF01196	Genetic Information Processing; Translation
At5g06630 Arabidopsis thaliana genomic DNA, chromosome 5, BAC clone:F15M7	At5g06630	AP002543	0.087	proline-rich extensin-like family protein	Metabolism; other
Arabidopsis thaliana BAC T15F16	Arabidopsis	AF076275	0.087		unknown
Arabidopsis thaliana DNA chromosome 3, BAC clone F4M19		AL356013	0.087		unknown
Arabidopsis thaliana DNA chromosome 4, BAC clone F19H22 (ESSA project)		AL035679	0.087		unknown
At5g64090 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MHJ24	At5g64090	AB008266	0.087	expressed	unknown
At5g03940 Arabidopsis thaliana mRNA for 54CP protein	At5g03940	Z21970	0.088	signal recognition particle 54 kDa protein, chloroplast / 54 chloroplast protein / SRP54 (FFC),	Genetic Information Processing; Folding, Sorting and Degradation
EST	At1g25230	AA394491	0.088	Arabidopsis thaliana purple acid phosphatase family protein (At1g25230)- PAP4	Metabolism; Metabolism of Cofactors and Vitamins;
At3g12510 Arabidopsis thaliana chromosome 3 BAC T2E22 genomic sequence	At3g12510	AC069474	0.088	expressed	unknown
At5g48860 Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K24G6	At5g48860	AB012242	0.088	expressed	unknown
At2g30740 Arabidopsis thaliana mRNA for putative PTI1-like protein tyrosine kinase (t11J7.13 gene)	At2g30740	AC002340	0.089	transcriptional factor B3 family protein	Genetic Information Processing; Transcription
At5g24510 Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K18P6	At5g24510	AB010068	0.089	60s acidic ribosomal protein P1, putative	Genetic Information processing; translation
At3g23820 Arabidopsis thaliana putative nucleotide sugar epimerase (F14O13.1/AT3g23820) mRNA, complete cds	At3g23820	AF370210	0.089	NAD-dependent epimerase/dehydratase family protein, PF01370	Metabolism; Carbohydrate Metabolism
At5g54270 Arabidopsis thaliana chromosome V Lhcb3 protein (Lhcb3) mRNA, complete cds	At5g54270	AF143691	0.089	chlorophyll A-B binding protein / LHCII type III (LHCB3)	Metabolism; energy
At5g45890 Arabidopsis thaliana putative senescence-specific cysteine protease (K15I22.9/AT5g45890) mRNA, complete cds	At5g45890	U37336	0.089	senescence-specific SAG12 protein (SAG12) / cysteine proteinase, putative, influenced by cytokinin, auxin, and sugars	Metabolism; Peptidases
Arabidopsis thaliana DNA chromosome 3, BAC clone F18L15		AL133298	0.089		unknown
Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MFJ20		AB026644	0.089		unknown
At4g37240 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 87	At4g37240	AL161591	0.089	expressed	unknown
At5g14300 Arabidopsis thaliana DNA chromosome 5, BAC clone F18O22 (ESSA project)	At5g14300	AL163817	0.089	prohibitin, putative, Pfam profile PF01145: SPFH domain / Band 7 family	unknown
At3g04590 Arabidopsis thaliana chromosome III BAC F7O18 genomic sequence	At3g04590	AC011437	0.09	DNA-binding family protein, contains a AT hook motif (DNA binding motifs with a preference for A/T rich regions), Pfam:PF02178	Genetic Information Processing; transcription

At1g61520 Arabidopsis thaliana PSI type III chlorophyll a/b-binding protein (Lhca3*1) mRNA, complete cds	At1g61520	U01103	0.09	chlorophyll A-B binding protein / LHCI type III (LHCA3.1), PSI type III chlorophyll a/b-binding protein (Lhca3*1)	Metabolism; energy	
EST	EST	BE038813	0.09		unknown	
Arabidopsis thaliana chromosome II section 119 of 255 of the complete sequence. Sequence from clones F5H14, F26H11		AC006234	0.09		unknown	
Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MNJ8		AB017069	0.09		unknown	
At3g18800 Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MVE11	At3g18800	AB026654	0.09	expressed	unknown	
Arabidopsis thaliana heat shock protein 70 (Hsc70-7) mRNA, complete cds; nuclear gene for chloroplas	At5g49910	AF217459	0.091	heat shock protein 70 / HSP70 (HSC70-7), identical to heat shock protein 70 (Arabidopsis thaliana) GI:6746592 , plastid stroma, ATP binding, protein folding CPHSC70-2	Genetic Information Processing; Folding, Sorting and Degradation	Environmental Information Processing; Signal Transduction
At4g19590 Arabidopsis thaliana DNA chromosome 4, BAC clone F24J7 (ESSA project)	At4g19590	AL021768	0.091	DNAJ heat shock N-terminal domain-containing protein	Genetic Information Processing; Folding, Sorting and Degradation	
At4g34050 Arabidopsis thaliana DNA chromosome 4, BAC clone F28A23 (ESSA project)	At4g34050	AL021961	0.091	caffeoyl-CoA 3-O-methyltransferase, putative	Metabolism; Biosynthesis of Secondary Metabolites; Stilbene,	
At1g76540 Arabidopsis thaliana mRNA for cyclin dependent kinase (CDKB2;1 gene)	At1g76540	AF389283	0.091	cell division control protein, putative (CDKB2;1, cyclin-dependent protein kinase involved in regulation of the G2/M transition of the mitotic cell cycle. Specifically binds to the cyclin CYCD4;1, expressed in shoot meristem, young leaves and vascular tissue during the G2/M phase.)	Metabolism; kinase	Cellular Processes; Cell Growth and Death; Cell cycle
At5g15460 Arabidopsis thaliana DNA chromosome 5, BAC clone T20K14 (ESSA project)	At5g15460	AL391143	0.091	expressed	unknown	
At5g37880 Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K18L3	At5g37880	AB012241	0.091	expressed	unknown	
At2g21600 Arabidopsis thaliana mRNA for AtRer1B, complete cds	At2g21600	AC007119	0.092	RER1B protein, Involved in the retrieval of endoplasmic reticulum membrane proteins from the early Golgi compartment	Cellular Processes and Signaling	

Arabidopsis thaliana mRNA for cyclin-dependent kinase inhibitor 6 (krp6 gene)	At3g19150	AP000419	0.092	Putative cyclin dependent kinase inhibitor.Binds to D type cyclins and may inhibit cell cycle. cyclin-dependent protein kinase inhibitor activity, cyclin binding, DNA endoreduplication, negative regulation of cyclin-dependent protein kinase activity	Cellular processes and signaling; cell cycle		
At2g24540 Arabidopsis thaliana chromosome II section 138 of 255 of the complete sequence. Sequence from clones F25P17	At2g24540	AC006954	0.092	kelch repeat-containing F-box family protein, kelch repeat-containing F-box family protein, similar to SKP1 interacting partner 4	Genetic Information Processing; Folding, Sorting and Degradation	Environmental Information Processing; Signal Transduction	Cellular Processes; Cell Growth and Death; Cell cycle
At5g26780 Arabidopsis thaliana putative glycine hydroxymethyltransferase (F2P16_40/AT5g26780) mRNA, complete cds	At5g26780	AY035117	0.092	glycine hydroxymethyltransferase, putative / serine hydroxymethyltransferase, putative / serine/threonine aldolase, putative	Metabolism; Amino Acid Metabolism; Glycine, serine and threonine		
At1g04610 Sequence of BAC T1G11 from Arabidopsis thaliana chromosome 1	At1g04610	AC002376	0.092	flavin-containing monooxygenase / FMO (YUCCA3), identical to gi:16555356, disulfide oxidoreductase activity, oxidoreductase activity, auxin biosynthesis	Metabolism; energy metabolism		
Arabidopsis thaliana chromosome 1 BAC F1O3 genomic sequence	Arabidopsis	AC068901	0.092		unknown		
ESTs	ESTs	AV518995	0.092		unknown		
Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K15I22		AB016870	0.092		unknown		
At5g13310 Arabidopsis thaliana DNA chromosome 5, BAC clone T31B5 (ESSA project)	At5g13310	AL163491	0.092	expressed	unknown		
At5g51200 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MWD22	At5g51200	AB023044	0.092	unk	unknown		
At5g57625 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MUA2	At5g57625	AB011482	0.092	allergen V5/Tpx-1-related family protein, low similarity to SP|Q40374 Pathogenesis-related protein PR-1 precursor {Medicago truncatula}; contains Pfam profile PF00188: SCP-like extracellular protein	unknown		
At4g35390 Arabidopsis thaliana DNA chromosome 4, BAC clone F23E12 (ESSA project)	At4g35390	AL022604	0.093	DNA-binding protein-related	Genetic Information Processing; transcription		
At3g58690 Arabidopsis thaliana DNA chromosome 3, BAC clone T20N10	At3g58690	AL353032	0.093	protein kinase family protein, contains protein kinase domain, Pfam:PF00069	Metabolism; kinase		
Arabidopsis thaliana DNA chromosome 4, BAC clone F1N20 (ESSA project)		AL022140	0.093	unk	unknown		

At2g37970 Arabidopsis thaliana Unknown protein (At2g37970; T8P21.12) mRNA, complete cds	At2g37970	AC007661	0.094	SOUL heme-binding family protein	Environmental Information Processing; Membrane Transport; ABC		
At5g17600 Arabidopsis thaliana DNA chromosome 5, BAC clone K10A8 (ESSA project)	At5g17600	AL391151	0.094	zinc finger (C3HC4-type RING finger) family protein	Genetic Information Processing; transcription		
At3g21380 Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:MHC9	At3g21380	AP001305	0.095	jacalin lectin family protein, PF01419	Cellular Processes and Signaling; CAM ligands		
At2g41420 Arabidopsis thaliana chromosome II section 224 of 255 of the complete sequence. Sequence from clones F13H10, T26J13, T32G6	At2g41420	AC004625	0.095	proline-rich family protein, integral to membrane, G-protein coupled receptor protein signaling pathway, rhodopsin-like receptor activity	Cellular Processes and Signaling; Receptors	Environmental Information Processing; Signaling Molecules	Metabolism; other
At3g12360 Arabidopsis thaliana chromosome 3 BAC T2E22 genomic sequence	At3g12360	AC069474	0.095	ankyrin repeat family protein, contains ankyrin repeat domains, Pfam:PF00023	Genetic Information Processing; Transcription		
At1g06430 Arabidopsis thaliana putative cell division protein (F12K11.22) mRNA, complete cds	At1g06430	AY045951	0.095	encodes a FtsH protease that is localized to the chloroplast , chloroplast, thylakoid membrane (sensu Viridiplantae), ATP-dependent peptidase activity, ATPase activity, metallopeptidase activity, zinc ion binding	Metabolim; peptide		
At1g62500 Arabidopsis thaliana putative proline-rich cell wall protein (T3P18.6) mRNA, complete cds	At1g62500	AY045962	0.095	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein, similar to auxin down regulated GB:X69640 GI:296442 from (Glycine max); contains Pfam profile PF00234	Metabolism; Peptidases	Metabolism; lipid	Genetic Information Processing; Folding, Sorting and Degradation
At1g33330 Arabidopsis thaliana chromosome 1 BAC F10C21 genomic sequence	At1g33330	AC027035	0.095	peptide chain release factor, putative, Pfam profile PF00472: Peptidyl-tRNA hydrolase domain	Metabolism; Peptidases		
Genomic sequence for Arabidopsis thaliana BAC T19E23 from chromosome I	Genomic	AC007654	0.095		unknown		

At1g10630 Genomic sequence for Arabidopsis thaliana BAC F20B24 from chromosome I	At1g10630	AC009398	0.096	A member of ARF GTPase family. A thaliana has 21 members of this family, known to be essential for vesicle coating and uncoating and functions in GTP-binding. Gene encoding ADP-ribosylation factor and similar to other ARFs and ARF-like proteins. The gene is shown to play a role in cell division, cell expansion and cellulose production using antisense construct. intracellular, mitochondrion, GTP binding, phospholipase activator activity, protein binding, N-terminal protein myristoylation	Cellular Processes and Signaling; GTP-binding	
At4g32210 Arabidopsis thaliana heat shock protein 70 (Hsc70-5) mRNA, complete cds; nuclear gene for mitochondrial product	At4g32210	AF217458	0.096	heat shock SDH3-2, Encodes one of the membrane anchor subunits of the mitochondrial respiratory complex II. The protein is encoded by the nuclear genome but is imported into the mitochondrion. There are two genes that encode this protein, the other is SDH3-1. retrotransposon family, weak similarity to heat shock protein 70, PF01127: Succinate dehydrogenase cytochrome b subunit, PF03732: Retrotransposon gag protein	Genetic Information Processing; Folding, Sorting and Degradation	Environmental Information Processing; Signal Transduction
At1g69960 Arabidopsis thaliana type 2A serine/threonine protein phosphatase (PP2A) mRNA, complete cds	At1g69960	AC010675	0.096	serine/threonine protein phosphatase PP2A-5 catalytic subunit (PP2A5),	Metabolism; kinase	Environmental Information Processing; Signal Transduction
At1g66920 Arabidopsis thaliana chromosome 1 BAC T4O24 genomic sequence	At1g66920	AC083891	0.096	serine/threonine protein kinase, putative	Metabolism; kinase	
At5g16340 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MQK4	At5g16340	AB005242	0.096	AMP-binding protein, putative, Pfam AMP-binding domain PF00501; identical to adenosine monophosphate binding protein 6 AMPBP6, isoprenoid biosynthesis, menaquinone biosynthesis, metabolism, teichoic acid biosynthesis	Metabolism; Metabolism of Cofactors and Vitamins	

At1g01900 Sequence of BAC F22M8 from Arabidopsis thaliana chromosome 1	At1g01900	AC020622	0.096	subtilase family protein, contains similarity to cucumisin-like serine protease GB:AAC18851 GI:3176874 from (Arabidopsis thaliana) , subtilase activity, proteolysis, endomembrane system	Metabolism; Peptidases
Arabidopsis thaliana DNA chromosome 3, BAC clone F14D17		AL353992	0.096	unk	unknown
Arabidopsis thaliana putative carrier protein (AT4g01100) mRNA, complete cds	AT4g01100	AF360168	0.097	mitochondrial substrate carrier family protein, contains Pfam profile: PF00153 mitochondrial carrier protein, mitochondrial inner membrane, mitochondrion, binding, mitochondrial transport, transport	Environmental Information Processing; Membrane Transport
At4g19130 Arabidopsis thaliana DNA chromosome 4, BAC clone T18B16 (ESSA project)	At4g19130	AL021687	0.097	replication protein-related	Genetic information processing; replication
At3g03920 Arabidopsis thaliana chromosome III BAC F20H23 genomic sequence	At3g03920	AC009540	0.097	Gar1 RNA-binding region family protein, contains Pfam profile PF04410:	Genetic Information Processing; translation
At5g26330 Arabidopsis thaliana BAC F9D12	At5g26330	AF077407	0.097	plastocyanin-like domain-containing protein / mavicyanin, putative	Metabolism; energy; photosynthesis
At4g13430 Arabidopsis thaliana unknown protein (AT4g13430) mRNA, complete cds	At4g13430	AY045842	0.097	aconitase family protein / aconitate hydratase family protein, contains Pfam profile PF00330, redox	Metabolism; other
At1g05010 A.thaliana EAT1 mRNA for ethylene forming enzyme	At1g05010	X66719	0.097	1-aminocyclopropane-1-carboxylate oxidase / ACC oxidase / ethylene-forming enzyme (ACO) (EAT1), Identical to 1-aminocyclopropane-1-carboxylate oxidase (ACC oxidase), 1 aminocyclopropane-1-carboxylate oxidase activity, ethylene biosynthesis	Metabolism; Other enzymes; ethylene biosynth
At1g56020 Arabidopsis thaliana chromosome I BAC T6H22 genomic sequence	At1g56020	AC009894	0.097	expressed	unknown
At3g10525 Arabidopsis thaliana chromosome III BAC F18K10 genomic sequence	At3g10525	AC013428	0.097	expressed	unknown
At5g67180 Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K21H1	At5g67180	AB020742	0.098	AP2 domain-containing transcription factor, putative, similar to (SP:P47927) Floral homeotic protein APETALA2.	Genetic Information Processing; Transcription
At1g27370 Arabidopsis thaliana (ecotype Columbia) mRNA for squamosa promoter binding protein-like 10	At1g27370	AJ011636	0.098	squamosa promoter-binding protein-like 10 (SPL10), Pfam profile PF03110: SBP domain	Cellular Processes; Signal transduction

At2g40220 Arabidopsis thaliana AP2 domain family transcription factor homolog (ABI4) gene, complete cds	At2g40220	AF040959	0.098	member of the DREB subfamily A-3 of ERF/AP2 transcription factor family (ABI4). The protein contains one AP2 domain. There is only one member in this family. Involved in abscisic acid (ABA) signal transduction, ABA-mediated glucose response, and hexokinase-dependent sugar responses.	Genetic Information Processing; transcription	
At5g56670 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MIK19	At5g56670	AB013392	0.098	40S ribosomal protein S30 (RPS30C) , ribosome, structural constituent of ribosome, protein biosynthesis	Genetic Information Processing; Translation; Ribosome	
At3g06620 Arabidopsis thaliana chromosome 3 BAC F5E6 genomic sequence	At3g06620	AC020580	0.098	protein kinase family protein, contains Pfam domain, PF00069	Metabolism; Protein kinases	Cellular Processes and Signaling; Signal transduction
Arabidopsis thaliana chromosome II section 228 of 255 of the complete sequence. Sequence from clones T6D20, T24P15		AC002561	0.098		unknown	
At4g28460 Arabidopsis thaliana DNA chromosome 4, BAC clone F20O9 (ESSA project)	At4g28460	AL021749	0.098	expressed	unknown	
Arabidopsis thaliana DNA chromosome 3, BAC clone F18P9		AL138654	0.098	unk	unknown	
At5g67300 A.thaliana mRNA for MYB-related protein (1195 bp)	At5g67300	Z54136	0.099	myb family transcription factor, contains PFAM profile	Genetic Information Processing; transcription	
At1g70600 Arabidopsis thaliana At1g70600/F5A18_22 mRNA, complete cds	At1g70600	AY048228	0.099	60S ribosomal protein L27A (RPL27aC)	Genetic Information Processing; Translation	
At4g13290 Arabidopsis thaliana DNA chromosome 4, BAC clone T9E8, partial sequence (ESSA project)	At4g13290	AL049608	0.099	cytochrome P450 71A19, putative (CYP71A19),	Metabolism; Cytochrome P450	
At5g39220 Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K3K3	At5g39220	AB010694	0.099	hydrolase, alpha/beta fold family protein, contains Pfam profile: PF00561 alpha/beta hydrolase fold	Metabolism; other	
Genomic sequence for Arabidopsis thaliana BAC F21B7 from chromosome I	Genomic	AC002560	0.099		unknown	
At3g60480 Arabidopsis thaliana DNA chromosome 3, BAC clone T8B10	At3g60480	AL138646	0.099	expressed	unknown	
At5g60880 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MAE1	At5g60880	AB015472	0.099	expressed	unknown	
At2g02080 Arabidopsis thaliana chromosome II section 8 of 255 of the complete sequence. Sequence from clones F14H20, F5O4	At2g02080	AC005936	0.1	zinc finger (C2H2 type) family protein, contains Pfam domain PF00096: Zinc finger, C2H2 type - TF activity, chloro	Genetic Information Processing; transcription	
At5g10390 Arabidopsis thaliana DNA chromosome 5, BAC clone F12B17 (ESSA project)	At5g10390	AL353995	0.1	histone H3, contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4	Genetic Information Processing; Transcription	

At5g26210 Arabidopsis thaliana BAC F9D12	At5g26210	AF077407	0.1	PHD finger family protein, contains Pfam domain, PF00628, zinc finger, is found in many regulatory proteins from plants or animals which are frequently associated with chromatin-mediated transcriptional regulation	Genetic Information Processing; transcription		
At4g04830 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13	At4g04830	AL161501	0.1	methionine sulfoxide reductase domain-containing protein / SeIR domain-containing protein, PF01641	Metabolism; amino acid		
At3g52300 Arabidopsis thaliana DNA chromosome 3, BAC clone T25B15	At3g52300	AL132972	0.1	ATP synthase D chain-related	Metabolism; Energy Metabolism; Oxidative phosphorylation		
At2g05100 Arabidopsis thaliana Lhcb2 protein (Lhcb2.2) mRNA, complete cds	At2g05100	AY045787	0.1	chlorophyll A-B binding protein / LHCII type II (LHCB2.1)	Metabolism; energy; photosynthesis		
Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence, complete sequence		AC002986	0.1		unknown		
EST	At1g63120	AA651363	0.101	Arabidopsis thaliana rhomboid family protein (At1g63120), putative membrane protein, 303 3e-79 , possible function as serine protease	Metabolism; peptidase		
At3g10510 Arabidopsis thaliana chromosome 3 BAC F13M14 genomic sequence	At3g10510	AC011560	0.102	kelch repeat-containing F-box family protein, Pfam profiles PF01344: Kelch motif, PF00646: F-box domain , kelch repeat-containing F-box family protein, similar to SKP1 interacting partner 6	Genetic Information Processing; Folding, Sorting and Degradation	Environmental Information Processing; Signal Transduction	Cellular Processes; Cell Growth and Death; Cell cycle
ESTs, Highly similar to T05255 RNA-binding protein homolog F18A5.250 - Arabidopsis thaliana [A.thaliana]		N37162	0.102		Genetic Information Processing; Translation		
At5g40760 Arabidopsis thaliana mRNA for cytosolic glucose-6-phosphate 1-dehydrogenase ACG12	At5g40760	AJ010971	0.102	Encodes a cytosolic glucose-6-phosphate dehydrogenase that is insensitive to reduction by DTT and whose mRNA is expressed ubiquitously.	Metabolism; carbohydrate		
Arabidopsis thaliana chromosome I BAC F20D21 genomic sequence	Arabidopsis	AC005287	0.102		unknown		
Arabidopsis thaliana chromosome III BAC F9F8 genomic sequence	Arabidopsis	AC009991	0.102		unknown		
At1g12790 Sequence of BAC F13K23 from Arabidopsis thaliana chromosome 1	At1g12790	AC012187	0.102	expressed	unknown		
At4g24110 Arabidopsis thaliana DNA chromosome 4, BAC clone T19F6, partial sequence (ESSA project)	At4g24110	AL109619	0.102	expressed	unknown		

At1g12040 Arabidopsis thaliana leucine-rich repeat/extensin 1 (LRX1) mRNA, complete cds	At1g12040	AY026364	0.103	leucine-rich repeat family protein / extensin family protein (LRX1), similar to extensin-like protein (Lycopersicon esculentum), encodes a a chimeric leucine-rich repeat/extensin protein that regulates root hair morphogenesis and elongation. Null mutants develop root hairs that frequently abort, swell, or branch. Gene is expressed in root hair cells and protein is specifically localized in the wall of the hair proper. cell wall (sensu Magnoliophyta), unidimensional cell growth, histidine phosphotransfer kinase activity, cellular morphogenesis during differentiation, trichoblast differentiation, root hair, trichoblast, root	Cellular processes and signaling; signal transduction	Metabolism; kinase; other
Arabidopsis thaliana heat shock protein 70 (Hsc70-7) mRNA, complete cds; nuclear gene for chloroplas	At5g49910	AF217459	0.103	heat shock protein 70 / HSP70 (HSC70-7), identical to heat shock protein 70 (Arabidopsis thaliana) GI:6746592 , plastid stroma, ATP binding, protein folding CPHSC70-2	Genetic Information Processing; Folding, Sorting and Degradation	Environmental Information Processing; Signal Transduction
At3g16770 Arabidopsis thaliana AP2 domain containing protein RAP2.3 mRNA, complete cds	At3g16770	AF003096	0.103	Encodes a member of the ERF (ethylene response factor) subfamily B-2 of ERF/AP2 transcription factor family (RAP2.3). The protein contains one AP2 domain. There are 5 members in this subfamily including RAP2.2 AND RAP2.12	Genetic Information Processing; Transcription	
At3g60800 Arabidopsis thaliana DNA chromosome 3, BAC clone T4C21	At3g60800	AL162295	0.103	zinc finger (DHHC type) family protein, contains DHHC zinc finger domain PF01529	Genetic Information Processing; transcription	
At4g24660 Arabidopsis thaliana DNA chromosome 4, BAC clone F22K18 (ESSAII project)	At4g24660	AL035356	0.103	zinc finger homeobox family protein	Genetic Information Processing; transcription	
At5g02330 Arabidopsis thaliana DNA chromosome 5, BAC clone T1E22 (ESSA project)	At5g02330	AL162874	0.103	DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	Genetic Information Processing; Transcription	
Arabidopsis thaliana putative ribulose-5-phosphate-3-epimerase (MFB13.19) mRNA, complete cds		AY045855	0.103		Metabolism; Carbohydrate Metabolism; Ascorbate and aldarate	

At3g24450 Arabidopsis thaliana unknown protein (MXP5.2/AT3g24450) mRNA, complete cds	At3g24450	AF370237	0.103	copper-binding family protein	unknown	
Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K11J9		AB012239	0.103		unknown	
At1g13930 Arabidopsis thaliana At1g13930/F16A14.27 mRNA, complete cds	At1g13930	AY045640	0.103	expressed protein, weakly similar to drought-induced protein SDi-6 (PIR:S71562) common sunflower (fragment)	unknown	
At1g52720 Arabidopsis thaliana chromosome 1 BAC F6D8 sequence	At1g52720	AC008016	0.103	expressed	unknown	
At2g17840 Arabidopsis thaliana putative senescence-related protein (At2g17840) mRNA, complete cds	At2g17840	AC003952	0.103	senescence/dehydration-associated protein-related (ERD7), Identified as drought-inducible gene by differential hybridization. Upregulated by high light, drought, cold and salt stress	unknown	
At5g65610 Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K21L13	At5g65610	AB026639	0.103	expressed	unknown	
At5g49665 Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K2I5	At5g49665	AB025613	0.104	zinc finger (C3HC4-type RING finger) family protein, contains Pfam profiles PF00097: Zinc finger, C3HC4 type (RING finger), PF00092: von Willebrand factor type A domain	Genetic Information Processing; transcription	
At5g01560 Arabidopsis thaliana DNA chromosome 5, BAC clone F7A7 (ESSA project)	At5g01560	AL161946	0.104	lectin protein kinase, putative, similar to receptor lectin kinase 3 (Arabidopsis thaliana) gi|4100060|gb|AAD00733; contains protein kinase domain, Pfam:PF00069; contains legume lectins alpha and beta domains, Pfam:PF00138 and Pfam:PF00139	Metabolism; kinase	Cellular Processes and Signaling; CAM ligands
At2g39710 Arabidopsis thaliana unknown protein (T5I7.1/At2g39710) mRNA, complete cds	At2g39710	AF370142	0.104	aspartyl protease family protein, contains profile Pfam PF00026: Eukaryotic aspartyl protease; contains Prosite PS00141: Eukaryotic and viral aspartyl proteases active site	Metabolism; Peptidases	
Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MXO21		AB026657	0.104		unknown	
Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MRB17		AB016879	0.104		unknown	
At2g05540 Arabidopsis thaliana chromosome II section 28 of 255 of the complete sequence. Sequence from clones F16J10, T20G20, T3P4	At2g05540	AC006220	0.104	glycine-rich protein	unknown	
At1g18830 Arabidopsis thaliana chromosome I BAC F6A14 genomic sequence	At1g18830	AC011809	0.105	transducin family protein / WD-40 repeat family protein	Environmental Information Processing; Signal Transduction	

ESTs, Weakly similar to T48060 beta-D-glucan exohydrolase-like protein - Arabidopsis thaliana [A.thaliana]		AV543737	0.105		Metabolism; carbohydrate; glycosyl hydrolase		
At1g49390 Arabidopsis thaliana chromosome I BAC F13F21 genomic sequence	At1g49390	AC007504	0.105	oxidoreductase, 2OG-Fe(II) oxygenase family protein, PF03171 2OG-Fe(II) oxygenase superfamily domain	Metabolism; Energy Metabolism; Reductive carboxylate cycle		
At5g10930 Arabidopsis thaliana CBL-interacting protein kinase 5 (CIPK5) mRNA, complete cds	At5g10930	AF285105	0.105	CBL-interacting protein kinase 5 (CIPK5),	Metabolism; kinase		
At2g42990 Arabidopsis thaliana chromosome II section 231 of 255 of the complete sequence. Sequence from clones F14N22, F7D19	At2g42990	AC006931	0.105	GDSL-motif lipase/hydrolase family protein,	Metabolism; lipid		
Arabidopsis thaliana actin-12 (ACT12) gene, complete cds	actin	U27982	0.106	actin	Cellular Processes; Cell Motility; Regulation of actin cytoskeleton		
At4g07400 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 17	At4g07400	AL161505	0.106	F-box family protein (FBL8) (FBL24), contains similarity to SKP1 interacting partner, PF00646	Genetic Information Processing; Folding, Sorting and Degradation	Environmental Information Processing; Signal Transduction	Cellular Processes; Cell Growth and Death; Cell cycle
At4g29410 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 70	At4g29410	AL161574	0.106	60S ribosomal protein L28 (RPL28C),	Genetic Information Processing; Translation; Ribosome		
At1g33055 Arabidopsis thaliana Unknown protein mRNA, complete cds	At1g33055	AF370464	0.106	expressed	unknown		
At2g13070 Arabidopsis thaliana chromosome II section 72 of 255 of the complete sequence. Sequence from clones T19K21, T17A11	At2g13070	AC006194	0.106	expressed	unknown		
At3g62270 Arabidopsis thaliana DNA chromosome 3, BAC clone T17J13	At3g62270	AL138651	0.107	anion exchange family protein	Cellular Processes and Signaling; CD molecules	Environmental Information Processing; Membrane Transport;	
At3g43810 Arabidopsis thaliana calmodulin 7 (CAM7) mRNA, complete cds	At3g43810	AF178073	0.107	calmodulin-7 (CAM7), EF hand domain protein encodes a calmodulin. Can functionally complement a yeast CaM mutant. Signal transduction	Environmental Information Processing; Signal Transduction; Calcium		
At2g36400 Arabidopsis thaliana chromosome II section 199 of 255 of the complete sequence. Sequence from clones F2H17, F1O11, F13K3	At2g36400	AC006919	0.107	expressed protein, nearly identical to transcription activator GRL3	Genetic Information Processing; transcription		
At5g17800 Arabidopsis thaliana putative transcription factor (MYB56) mRNA, partial cds	At5g17800	AF062891	0.107	myb family transcription factor (MYB56), identical to putative transcription factor (MYB56) GI:3941473 from (Arabidopsis thaliana)	Genetic Information Processing; transcription		
At3g44870 Arabidopsis thaliana DNA chromosome 3, BAC clone F28D10	At3g44870	AL391254	0.107	S-adenosyl-L-methionine:carboxyl methyltransferase family protein	Metabolism; amino acid		

At5g56170 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MDA7	At5g56170	AB011476	0.107	expressed protein, contains similarity to GPI-anchored protein (glycosylphosphatidylinositol (GPI))- gamete fusion, extracellular communication?	Metabolism; Glycan Biosynthesis and Metabolism;	
Arabidopsis thaliana chromosome I BAC F28N24 genomic sequence	Arabidopsis	AC021043	0.107		unknown	
At4g05640 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16	At4g05640	AL161504	0.107	expressed	unknown	
Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MBG8		AB005232	0.107	F-box family protein, contains Pfam:PF00646 F-box domain	unknown	
At3g24860 Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:K7P8	At3g24860	AB028609	0.108	hydroxyproline-rich glycoprotein family protein	Environmental Information Processing; Signaling Molecules	Cellular Processes and Signaling; CD molecules
At2g04390 Arabidopsis thaliana chromosome II section 21 of 255 of the complete sequence. Sequence from clones T1O3, F7D11	At2g04390	AC006951	0.108	40S ribosomal protein S17 (RPS17A)	Genetic Information Processing; translation	
Arabidopsis thaliana chromosome 1 BAC T18F15 genomic sequence	Arabidopsis	AC084807	0.108		unknown	
Arabidopsis thaliana chromosome II section 2 of 255 of the complete sequence. Sequence from clones F23H14, F10A8		AC006200	0.108		unknown	
At2g32960 Arabidopsis thaliana chromosome II section 184 of 255 of the complete sequence. Sequence from clones F24L7, T21L14, F25I18	At2g32960	AC003033	0.109	tyrosine specific protein phosphatase family protein	Cellular Processes and Signaling; cell communication	
At2g22590 Arabidopsis thaliana chromosome II section 128 of 255 of the complete sequence. Sequence from clones F14M13, T9I22, T30L20	At2g22590	AC006340	0.109	glycosyltransferase family protein, sugar synthesis	Metabolism; Glycan Biosynthesis and Metabolism; N-Glycan	
Arabidopsis thaliana DNA chromosome 4, BAC clone T6K21 (ESSA project)		AL021889	0.109		unknown	
At1g31814 Arabidopsis thaliana chromosome 1 BAC F5M6 genomic sequence	At1g31814	AC079041	0.109	expressed protein , hits FRL2, family member of FRI-related genes that is required for the winter-annual habit.	unknown	
At3g45460 Arabidopsis thaliana DNA chromosome 3, BAC clone F9K21	At3g45460	AL138657	0.109	expressed	unknown	
At5g22440 Arabidopsis thaliana AT5g22440/MWD9_24 mRNA, complete cds	At5g22440	AY037253	0.109	ovate family protein	unknown	
At5g28540 Arabidopsis thaliana mRNA for luminal binding protein (BiP), complete cds	At5g28540	D84414	0.109	luminal binding protein 1 (BiP-1) (BP1),	unknown	
At4g14550 Arabidopsis thaliana IAA14 (d13315c/AT4g14550) mRNA, complete cds	At4g14550	U18416	0.11	IAA14 is a member of the Aux/IAA protein family. Involved in lateral root development. Gain of function mutation decreases auxin-ducible gene expreesion. Protein is localized to the nucleus. auxin-responsive AUX/IAA family protein, transcription factor activity	Genetic Information Processing; transcription	
At5g14950 Arabidopsis thaliana DNA chromosome 5, BAC clone F2G14 (ESSA project)	At5g14950	AL391146	0.11	glycosyl hydrolase family 38 protein	Metabolism; Glycan Biosynthesis and Metabolism; N-Glycan	

At5g21950 Arabidopsis thaliana DNA chromosome 5, BAC clone T6G21 (ESSA project)	At5g21950	AL589883	0.11	hydrolase, alpha/beta fold family protein	Metabolism; other	
Arabidopsis thaliana DNA chromosome 3, BAC clone T20O10		AL163816	0.11		unknown	
Arabidopsis thaliana genomic DNA, chromosome 5, BAC clone:T30G6		AB026661	0.11		unknown	
At1g77400 Arabidopsis thaliana chromosome 1 BAC F2P24 genomic sequence	At1g77400	AC078898	0.11	expressed	unknown	
At2g42800 Arabidopsis thaliana chromosome II section 231 of 255 of the complete sequence. Sequence from clones F14N22, F7D19	At2g42800	AC006931	0.11	leucine-rich repeat family protein, PF00560	unknown	
At1g31630 Arabidopsis thaliana chromosome 1 BAC F27M3 genomic sequence	At1g31630	AC074360	0.111	MADS-box family protein, TF controlling many cellular and developmental processes	Genetic Information Processing; transcription	
At3g50650 Arabidopsis thaliana scarecrow-like 7 (SCL7) mRNA, partial cds	At3g50650	AL132979	0.111	scarecrow-like transcription factor 7 (SCL7),	Genetic Information Processing; transcription	
At1g70580 Arabidopsis thaliana putative alanine aminotransferase (F5A18.24) mRNA, complete cds	At1g70580	AY035130	0.111	Similar to glutamate-glyoxylate transaminase enzyme encoded by AOAT1, contains Pfam profile PF00155: aminotransferase, classes I and II	Metabolism; amino acid	
Arabidopsis thaliana unknown protein (F1P2.200/AT3g47650) mRNA, complete cds	AT3g47650	AF370246	0.111	bundle-sheath defective protein 2 family / bsd2 family, similar to bundle sheath defective protein 2 (Zea mays) GI:4732091 , chloro	unknown	
Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MVP7		AB025637	0.112		unknown	
At1g10800 Genomic sequence for Arabidopsis thaliana BAC F20B24 from chromosome I	At1g10800	AC009398	0.112	expressed, endomembrane	unknown	
Arabidopsis thaliana heat shock protein 70 (Hsc70-7) mRNA, complete cds; nuclear gene for chloroplas	At5g49910	AF217459	0.113	heat shock protein 70 / HSP70 (HSC70-7), identical to heat shock protein 70 (Arabidopsis thaliana) GI:6746592 , plastid stroma, ATP binding, protein folding CPHSC70-2	Genetic Information Processing; Folding, Sorting and Degradation	Environmental Information Processing; Signal Transduction
At5g41680 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MBK23	At5g41680	AB005233	0.113	protein kinase family protein, contains protein kinase domain, Pfam:PF00069	Metabolism; kinase	
Arabidopsis thaliana chromosome 1 BAC T9N14 genomic sequence	Arabidopsis	AC067754	0.113		unknown	
At2g28660 Arabidopsis thaliana chromosome II section 162 of 255 of the complete sequence. Sequence from clones T8O18, T11P11	At2g28660	AC007171	0.113	copper-binding family protein	unknown	
At1g44190 Arabidopsis thaliana chromosome 1 BAC T7O23 genomic sequence	At1g44190	AC074228	0.113	expressed	unknown	
At5g15820 Arabidopsis thaliana DNA chromosome 5, BAC clone F14F8 (ESSA project)	At5g15820	AL391144	0.114	zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097	Genetic Information Processing; transcription	

At5g50850 Arabidopsis thaliana pyruvate dehydrogenase E1 beta subunit mRNA, complete cds	At5g50850	U09137	0.114	pyruvate dehydrogenase E1 component beta subunit, mitochondrial / PDHE1-B (PDH2),	Metabolism; carbohydrate	Metabolism; energy
At1g72460 Arabidopsis thaliana chromosome 1 BAC T10D10 genomic sequence	At1g72460	AC016529	0.114	leucine-rich repeat transmembrane protein kinase, putative	Metabolism; kinase	
At1g75000 Arabidopsis thaliana chromosome 1 BAC F25A4 sequence	At1g75000	AC008263	0.114	GNS1/SUR4 membrane family protein, contains Pfam profile PF01151, elongation of fatty acids	Metabolism; lipid	
At5g55320 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MTE17	At5g55320	AB015479	0.114	membrane bound O-acyl transferase (MBOAT) family protein / wax synthase-related	Metabolism; Lipid metabolism	
At4g09320 Arabidopsis thaliana Unknown protein mRNA, complete cds	At4g09320	X69373	0.114	nucleoside diphosphate kinase 1 (NDK1),	Metabolism; Nucleotide Metabolism; Purine metabolism	
At2g38910 Arabidopsis thaliana chromosome II section 210 of 255 of the complete sequence. Sequence from clones F13I13, T7F6, T16B24	At2g38910	AC005770	0.114	calcium-dependent protein kinase, putative / CDPK, putative, protein kinase domain, Pfam:PF00069; contains EF hand domain (calcium-binding EF-hand), Pfam:PF00036,	Metabolism; Protein kinases	Environmental Information Processing; Signal Transduction
Arabidopsis thaliana DNA chromosome 3, BAC clone F24G16		AL138647	0.114		unknown	
Arabidopsis thaliana DNA chromosome 3, BAC clone T21C14		AL138639	0.114		unknown	
At3g60780 Arabidopsis thaliana DNA chromosome 3, BAC clone T4C21	At3g60780	AL162295	0.114	expressed	unknown	
At5g17670 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MVA3	At5g17670	AB006706	0.114	expressed	unknown	
ESTs, Weakly similar to T04261 hypothetical protein F20B18.170 - Arabidopsis thaliana [A.thaliana]		AV536337	0.114	expressed	unknown	
At3g06130 Arabidopsis thaliana unknown protein (F28L1.7) mRNA, complete cds	At3g06130	AF326899	0.115	heavy-metal-associated domain-containing protein, PF00403	Environmental Information Processing; Membrane Transport;	
At1g73840 Arabidopsis thaliana chromosome 1 BAC F25P22 genomic sequence	At1g73840	AC012679	0.115	hydroxyproline-rich glycoprotein family protein	Environmental Information Processing; Signaling Molecules	Cellular Processes and Signaling; CD molecules
At5g16590 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MTG13	At5g16590	AB008270	0.115	leucine-rich repeat transmembrane protein kinase, putative,	Metabolism; kinase	
At1g45232 Arabidopsis thaliana clone 2 abscisic acid responsive elements-binding factor (ABRE) mRNA, complete cds	At1g45232	AF093545	0.115	expressed	unknown	
At1g67540 Arabidopsis thaliana chromosome 1 BAC F12B7 genomic sequence	At1g67540	AC011020	0.115	expressed, mito	unknown	
At2g35830 Arabidopsis thaliana chromosome II section 196 of 255 of the complete sequence. Sequence from clones T20F21, F11F19	At2g35830	AC007017	0.115	expressed	unknown	

At5g66580 Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K1F13	At5g66580	AB013389	0.115	expressed	unknown	
At3g59060 Arabidopsis thaliana DNA chromosome 3, BAC clone F17J16	At3g59060	AL163527	0.116	PIL6, encodes a novel Myc-related bHLH transcription factor, which physically associated with APRR1/TOC1 and is a member of PIF3 transcription factor family. basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010	Genetic Information Processing; transcription	
At5g66055 Arabidopsis thaliana ankyrin repeat-containing protein (akr) gene, complete cds	At5g66055	M82883	0.116	ankyrin repeat protein / AKRP (AKR), EMBRYO DEFECTIVE 2036	Genetic Information Processing; Transcription	
At1g18140 Genomic sequence for Arabidopsis thaliana BAC T10O22 from chromosome I	At1g18140	AC034107	0.116	laccase family protein / diphenol oxidase family protein	Metabolism; other	
Arabidopsis thaliana chromosome III BAC T21P5 genomic sequence	Arabidopsis	AC009895	0.116		unknown	
Arabidopsis thaliana chromosome II section 202 of 255 of the complete sequence. Sequence from clones T1J8, T2N18, F3G5		AC006260	0.116		unknown	
At3g48120 Arabidopsis thaliana DNA chromosome 3, BAC clone T17F15	At3g48120	AL049658	0.116	expressed	unknown	
At5g05860 Arabidopsis thaliana AT5g05860/MJJ3_28 mRNA, complete cds	At5g05860	AY045617	0.117	UDP-glucoronosyl/UDP-glucosyl transferase family protein	Metabolism; other	
At1g19190 Sequence of BAC T29M8 from Arabidopsis thaliana chromosome 1	At1g19190	AC069143	0.117	expressed protein similarity to anther-specific and pathogenesis response protein	unknown	
At4g28630 Arabidopsis thaliana half-molecule ABC transporter ATM1 mRNA, complete cds	At4g28630	AF287697	0.118	ABC transporter family protein, identical to half-molecule ABC transporter ATM1 GI:9964117	Cellular Processes and Signaling; Transporters	Environmental Information Processing; Membrane Transport
At2g30950 Arabidopsis thaliana zinc dependent protease (VAR2) mRNA, complete cds; nuclear gene for chloroplast product	At2g30950	AF135189	0.118	FtsH protease (VAR2), metalloprotease that functions in thylakoid membrane biogenesis. This protein forms a complex with VAR1.	Metabolism; Peptidases	
Arabidopsis thaliana Unknown protein mRNA, complete cds		AF370469	0.118		unknown	
At4g28330 Arabidopsis thaliana DNA chromosome 4, BAC clone F20O9 (ESSA project)	At4g28330	AL021749	0.118	expressed	unknown	
At1g08170 Genomic sequence for Arabidopsis thaliana BAC T6D22 from chromosome I	At1g08170	AC026875	0.119	histone H2B family protein, similar to histone H2B from Chlamydomonas reinhardtii, nucleus, DNA binding, chromosome organization and biogenesis (sensu Eukaryota), nucleosome assembly, nucleosome	Genetic Information Processing; Transcription	

At3g09480 Arabidopsis thaliana chromosome 3 BAC F11F8 genomic sequence	At3g09480	AC016661	0.119	histone H2B, putative, PF00125 Core histone H2A/H2B/H3/H4	Genetic Information Processing; transcription	
At3g54340 A.thaliana homeotic flower (APETELA3) mRNA, complete cds	At3g54340	M86357	0.119	Floral homeotic gene encoding a MADS domain protein homologous to SRF transcription factors. Specifies petal and stamen identities. Associates with PISTILLATA. Floral homeotic protein APETALA3 (AP3) - nucleus	Genetic Information Processing; transcription	
Arabidopsis thaliana AT3g42050/F4M19_10 mRNA, complete cds	AT3g42050	AY037176	0.119	vacuolar ATP synthase subunit H family protein, identical to probable vacuolar ATP synthase subunit H, hydrogen-transporting ATPase V1 domain, ATP binding, ATP synthesis coupled proton transport, peripheral to membrane of membrane fraction, hydrogen-transporting ATP synthase activity, rotational mechanism, hydrogen-transporting ATPase activity, rotational mechanism	Metabolism; energy	
At1g25280 Arabidopsis thaliana chromosome 1 BAC F4F7 genomic sequence	At1g25280	AC079374	0.119	F-box family protein / tubby family protein	unknown	
ESTs, Weakly similar to T49123 hypothetical protein F26G5.20 - Arabidopsis thaliana [A.thaliana]		AV441101	0.119	expressed	unknown	
At5g47670 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MNJ7	At5g47670	AB025628	0.12	CCAAT-box binding transcription factor family protein / leafy cotyledon 1-related (L1L), PF00808 : Histone-like transcription factor (CBF/NF-Y) and archaeal histone; contains similarity to CCAAT-binding transcription factor subunit A (CBF-A) (NF-Y protein chain B) (NF-YB) (CAAT-box DNA binding protein subunit B) (Swiss-Prot:P25209) (Zea mays)	Genetic Information and Processing; transcription	
At2g36460 Arabidopsis thaliana putative fructose bisphosphate aldolase (F1O11.9/At2g36460) mRNA, complete cds	At2g36460	AC006919	0.12	fructose-bisphosphate aldolase, putative, PF00274	Metabolism; Carbohydrate Metabolism; Glycolysis	Metabolism; Energy Metabolism; Carbon fixation
At2g18530 Arabidopsis thaliana chromosome II section 108 of 255 of the complete sequence. Sequence from clones F24H14, MSF3	At2g18530	AC006135	0.12	protein kinase family protein	Metabolism; kinase	
Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MHM17		AB024035	0.12		unknown	

At1g13160 Arabidopsis thaliana chromosome 1 BAC F3F19 sequence	At1g13160	AC007357	0.12	SDA1 family protein, contains Pfam PF05285: SDA1 domain; similar to mystery 45A	unknown	
At3g46300 Arabidopsis thaliana DNA chromosome 3, BAC clone F18L15	At3g46300	AL133298	0.12	expressed	unknown	
Arabidopsis thaliana DNA chromosome 4, BAC clone F22K18 (ESSAII project)		AF120494	0.121		unknown	
At1g54540 Arabidopsis thaliana chromosome I BAC F20D21 genomic sequence	At1g54540	AC005287	0.121	expressed	unknown	
At2g39170 Arabidopsis thaliana chromosome II section 211 of 255 of the complete sequence. Sequence from clones T16B24, F12L6	At2g39170	AC004697	0.121	expressed	unknown	
Arabidopsis thaliana heat shock protein 70 (Hsc70-7) mRNA, complete cds; nuclear gene for chloroplas	At5g49910	AF217459	0.122	heat shock protein 70 / HSP70 (HSC70-7), identical to heat shock protein 70 (Arabidopsis thaliana) GI:6746592 , plastid stroma, ATP binding, protein folding CPHSC70-2	Genetic Information Processing; Folding, Sorting and Degradation	Environmental Information Processing; Signal Transduction
Arabidopsis thaliana heat shock protein 70 (Hsc70-7) mRNA, complete cds; nuclear gene for chloroplas	At5g49910	AF217459	0.122	heat shock protein 70 / HSP70 (HSC70-7), identical to heat shock protein 70 (Arabidopsis thaliana) GI:6746592 , plastid stroma, ATP binding, protein folding CPHSC70-2	Genetic Information Processing; Folding, Sorting and Degradation	Environmental Information Processing; Signal Transduction
At4g09130 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 26	At4g09130	AL161514	0.122	zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097	Genetic Information Processing; transcription	
At5g63160 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MDC12	At5g63160	AB008265	0.122	speckle-type POZ protein-related, contains Pfam PF00651 : BTB/POZ domain; contains Pfam PF02135 : TAZ zinc finger; similar to Speckle-type POZ protein (SP:O43791) (Homo sapiens) , nucleus, protein binding, regulation of transcription, DNA-dependent, transcription regulator activity	Genetic Information Processing; Transcription; RNA polymerase	
At2g33510 Arabidopsis thaliana chromosome II section 186 of 255 of the complete sequence. Sequence from clones F25I18, F4P9	At2g33510	AC002332	0.122	expressed	unknown	
At5g10850 Arabidopsis thaliana DNA chromosome 5, BAC clone T30N20 (ESSA project)	At5g10850	AL365234	0.122	expressed	unknown	
Arabidopsis thaliana heat shock protein 70 (Hsc70-7) mRNA, complete cds; nuclear gene for chloroplas	At5g49910	AF217459	0.123	heat shock protein 70 / HSP70 (HSC70-7), identical to heat shock protein 70 (Arabidopsis thaliana) GI:6746592 , plastid stroma, ATP binding, protein folding CPHSC70-2	Genetic Information Processing; Folding, Sorting and Degradation	Environmental Information Processing; Signal Transduction
At1g28480 Arabidopsis thaliana At1g28480 (At1g28480/F3M18_8) mRNA, complete cds	At1g28480	AF325030	0.123	glutaredoxin family protein	Genetic Information Processing; Folding, Sorting and Degradation	

At1g23410 Genomic sequence for Arabidopsis thaliana BAC F28C11 from chromosome I	At1g23410	AC007945	0.123	ubiquitin extension protein, putative / 40S ribosomal protein S27A	Genetic Information Processing; Folding, sorting, deg	Genetic Information Processing; translation
At1g55460 Arabidopsis thaliana putative Kin17 protein (T5A14.13) mRNA, complete cds	At1g55460	AF360132	0.123	Kin17 DNA-binding protein-related	Genetic Information Processing; Transcription	
At5g51570 Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K17N15	At5g51570	AB018109	0.123	band 7 family protein, similar to hypersensitive-induced response protein (Zea mays) GI:7716468; contains Pfam profile PF01145: SPFH domain / Band 7 family, N-terminal protein myristoylation	unknown	
At2g32670 Arabidopsis thaliana chromosome II section 183 of 255 of the complete sequence. Sequence from clones T26B15, F24L7	At2g32670	AC003974	0.124	VAMP725, member of Synaptobrevin -like protein family (vessicle associated)	Genetic Information Processing; Folding, Sorting and Degradation	
Arabidopsis thaliana Columbia cytosolic triose phosphate isomerase (Atctimc) mRNA, complete cds	AT3G55440	U02949	0.124	triosephosphate isomerase, cytosolic, putative, cytosol, mitochondrion, triose-phosphate isomerase activity, metabolism	Metabolism; Carbohydrate Metabolism; Glycolysis /	Metabolism; Energy metab
At3g55430 Arabidopsis thaliana putative beta-1,3-glucanase (T22E16.90/AT3g55430) mRNA, complete cds	At3g55430	AY045992	0.124	glycosyl hydrolase family 17 protein / beta-1,3-glucanase, putative	Metabolism; Glycan Biosynthesis and Metabolism; N-Glycan	
Sequence of BAC F7H2 from Arabidopsis thaliana chromosome 1	Sequence	AC034256	0.124		unknown	
At3g12390 Arabidopsis thaliana AT3g12390/T2E22_130 mRNA, complete cds	At3g12390	AY048232	0.125	nascent polypeptide associated complex alpha chain protein, putative / alpha-NAC, putative, similar to alpha-NAC, non-muscle form (Mus musculus) GI:1666690; contains Pfam profiles PF01849: NAC domain, PF00627: UBA/TS-N domain	Genetic Information Processing; Folding, Sorting and Degradation; Protein folding and associated processing	
At1g07980 Genomic sequence for Arabidopsis thaliana BAC T6D22 from chromosome I	At1g07980	AC026875	0.125	histone-like transcription factor (CBF/NF-Y) family protein, contains Pfam profile PF00808: Histone-like transcription factor (CBF/NF-Y) and archaeal histone; similar to Chromatin accessibility complex protein 1 (CHRAC-1) (CHRAC-15) (HuCHRAC15) (DNA polymerase epsilon subunit p15) (SP:Q9NRG0) {Homo sapiens} , chloroplast, intracellular, transcription factor activity, regulation of transcription	Genetic Information Processing; Transcription	

Arabidopsis thaliana putative DNA binding protein (AT4g27000) mRNA, complete cds	AT4g27000	AF370339	0.125	RNA-binding protein 45 (RBP45), putative, DNA binding protein ACBF - Nicotiana tabacum, PID:g1899188 , RNA binding, flower, leaf, stem, seedling growth	Genetic Information Processing; Translation	
Arabidopsis thaliana unknown protein (YUP8H12.20) mRNA, complete cds	At1g05190	AF360265	0.125	ribosomal protein L6 family protein, Similar to Mycobacterium RlpF (gb|Z84395). ESTs gb|T75785,gb|R30580,gb|T04698 come from this gene	Genetic Information Processing; Translation; Ribosome	
At4g03060 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 7	At4g03060	AL161495	0.125	AOP2, a 2-oxoglutarate-dependent dioxygenase that catalyzes the conversion of methylsulfinylalkyl glucosinolates to alkenyl glucosinolates. involved in glucosinolate biosynthesis and secondary metabolism	Metabolism; secondary metabolism	
At3g54700 Arabidopsis thaliana DNA chromosome 3, BAC clone T5N23	At3g54700	AL138650	0.126	phosphate transporter, putative	Cellular Processes and Signaling; Transporters	Environmental Information Processing; Membrane Transport
At4g15650 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 42	At4g15650	AL161542	0.126	protein kinase-related	Metabolism; kinase	
Arabidopsis thaliana BAC T15F16	Arabidopsis	AF076275	0.126		unknown	
At4g16110 Arabidopsis thaliana mRNA for receiver-like protein 5	At4g16110	AB016472	0.127	ARR2, two-component responsive regulator family protein / response regulator family protein, Encodes a pollen-specific transcription factor involved in the expression of nuclear genes for components of mitochondrial complex I in Arabidopsis	Genetic Information Processing; transcription	
Arabidopsis thaliana chromosome I BAC F28N24 genomic sequence	Arabidopsis	AC021043	0.127		unknown	
At4g26080 A.thaliana mRNA for ABI1 protein	At4g26080	U12856	0.128	protein phosphatase 2C ABI1 / PP2C ABI1 / abscisic acid-insensitive 1 (ABI1), ABA signal transduction. Facilitates the activation of slow anion channels and stomatal closure mediated by abscisic acid (ABA).	Environmental Information Processing; Signal Transduction	Cellular Processes; Cell Communication
At5g13980 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MAC12	At5g13980	AB005230	0.128	zinc finger (C2H2 type) family protein, contains Pfam profile: PF00096	Genetic Information and Processing; transcription	

Arabidopsis thaliana heat shock protein 70 (Hsc70-7) mRNA, complete cds; nuclear gene for chloroplas	At5g49910	AF217459	0.128	heat shock protein 70 / HSP70 (HSC70-7), identical to heat shock protein 70 (Arabidopsis thaliana) GI:6746592 , plastid stroma, ATP binding, protein folding CPHSC70-2	Genetic Information Processing; Folding, Sorting and Degradation	Environmental Information Processing; Signal Transduction
At2g19570 Arabidopsis thaliana cytidine deaminase 1 (cda1) mRNA, complete cds	At2g19570	AF134487	0.128	cytidine deaminase (CDD) / cytidine aminohydrolase	Metabolism; Nucleotide Metabolism; Pyrimidine metabolism	
At2g32150 Arabidopsis thaliana putative hydrolase (At2g32150; F22D22.10) mRNA, complete cds	At2g32150	AC006223	0.128	haloacid dehalogenase-like hydrolase family protein	Metabolism; Xenobiotics Biodegradation and Metabolism;	
Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:MWL2		AB025639	0.128		unknown	
At1g67740 Arabidopsis thaliana PsbY precursor (psbY) mRNA, nuclear gene encoding chloroplast protein, complete cds	At1g67740	AF079800	0.128	expressed	unknown	
At5g64840 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MXK3	At5g64840	AB019236	0.129	ABC transporter family protein, member of GCN subfamily	Cellular Processes and Signaling; Transporters	Environmental Information Processing; Membrane Transport
Arabidopsis thaliana heat shock protein 70 (Hsc70-7) mRNA, complete cds; nuclear gene for chloroplas	At5g49910	AF217459	0.129	heat shock protein 70 / HSP70 (HSC70-7), identical to heat shock protein 70 (Arabidopsis thaliana) GI:6746592 , plastid stroma, ATP binding, protein folding CPHSC70-2	Genetic Information Processing; Folding, Sorting and Degradation	Environmental Information Processing; Signal Transduction
Arabidopsis thaliana ubiquitin-like protein (K5J14.10) mRNA, complete cds	At5g42300	AF370527	0.129	ubiquitin family protein, contains INTERPRO:IPR000626 ubiquitin domain	Genetic Information Processing; Folding, Sorting and Degradation; proteolysis?	
At5g16050 Arabidopsis thaliana putative 14-3-3 protein (F1N13_190/AT5g16050) mRNA, complete cds	At5g16050	AY035170	0.129	14-3-3 protein GF14 upsilon (grf5), DNA regulatory binding element?	Genetic Information Processing; Transcription	
At3g44010 Arabidopsis thaliana DNA chromosome 3, BAC clone T15B3	At3g44010	AL163975	0.129	40S ribosomal protein S29 (RPS29B),	Genetic Information Processing; Translation	
At5g60670 Arabidopsis thaliana AT5g60670/mup24_80 mRNA, complete cds	At5g60670	AY039614	0.129	60S ribosomal protein L12 (RPL12C),	Genetic Information Processing; Translation; Ribosome	
At3g27820 Arabidopsis thaliana putative cytosolic monodehydroascorbate reductase (K16N12.2/AT3g27820) mRNA, complete cds	At3g27820	AY039980	0.129	monodehydroascorbate reductase, putative	Metabolism; Carbohydrate Metabolism; Ascorbate and aldarate	
Sequence of BAC F14O10 from Arabidopsis thaliana chromosome 1	Sequence	AC026234	0.129		unknown	
Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:MOA2		AB028617	0.129		unknown	
At2g22660 Arabidopsis thaliana chromosome II section 128 of 255 of the complete sequence. Sequence from clones F14M13, T9I22, T30L20	At2g22660	AC006340	0.129	glycine-rich protein,	unknown	

Arabidopsis thaliana origin recognition complex 1 mRNA, complete cds		AL161539	0.13		Cellular Processes; Cell Growth and Death; Cell cycle	
At5g44180 Arabidopsis thaliana Unknown protein (MLN1.10) mRNA, complete cds	At5g44180	AB005239	0.13	homeobox transcription factor, putative	Genetic Information and Processing; transcription	
Arabidopsis thaliana heat shock protein 70 (Hsc70-7) mRNA, complete cds; nuclear gene for chloroplas	At5g49910	AF217459	0.13	heat shock protein 70 / HSP70 (HSC70-7), identical to heat shock protein 70 (Arabidopsis thaliana) GI:6746592 , plastid stroma, ATP binding, protein folding CPHSC70-2	Genetic Information Processing; Folding, Sorting and Degradation	Environmental Information Processing; Signal Transduction
At2g18190 Arabidopsis thaliana chromosome II section 106 of 255 of the complete sequence. Sequence from clones F8D23, T30D6	At2g18190	AC007212	0.13	AAA-type ATPase family protein, contains Pfam profile: ATPase family PF00004	Genetic Information Processing; Folding, Sorting and Degradation	
At5g10920 Arabidopsis thaliana putative lyase (T30N20_190/AT5g10920) mRNA, complete cds	At5g10920	AY045898	0.13	argininosuccinate lyase, putative / arginosuccinase, putative, similar to argininosuccinate lyase (Nostoc punctiforme) GI:7672743; contains Pfam profile PF00206	Metabolism; Amino Acid Metabolism; Alanine and aspartate metabolism	
A.thaliana 2A6 mRNA	A.thaliana	AC002560	0.13	(?) 2-oxoglutarate-dependent dioxygenase, putative, identical to 2A6 (GI:599622), a homolog of the tomato ethylene synthesis regulatory protein E8; contains Pfam profile PF03171: oxidoreductase, 2OG-Fe(II) oxygenase family	Metabolism; Energy Metabolism; Reductive carboxylate cycle	
At2g36350 Arabidopsis thaliana chromosome II section 198 of 255 of the complete sequence. Sequence from clones F9C22, F2H17	At2g36350	AC006921	0.13	protein kinase, putative	Metabolism; kinase	
At4g08850 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 25	At4g08850	AL161513	0.13	leucine-rich repeat family protein / protein kinase family protein, contains Pfam domains PF00560:PF00069	Metabolism; kinase	
A.thaliana mRNA for ubiquitin-conjugating enzyme	A.thaliana	X68306	0.131	ubq conjugating	Genetic Information Processing; Folding, Sorting and Degradation; proteolysis?	
At5g41300 Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K1O13	At5g41300	AB019225	0.131	receptor-like protein kinase-related, Pfam profile: PF01657 Domain of unknown function DUF26	Metabolism, kinase	
At1g01300 Arabidopsis thaliana chromosome I BAC F6F3 genomic sequence	At1g01300	AC023628	0.131	aspartyl protease family protein, contains Pfam domain, PF00026: eukaryotic aspartyl protease , cell wall (sensu Magnoliophyta), pepsin A activity, proteolysis	Metabolism; Peptidases	

A.thaliana mRNA for chloroplast FtsH protease	A.thaliana	X99808	0.131		Metabolism; peptide; protein	
ESTs	ESTs	N65439	0.131		unknown	
At3g55070 Arabidopsis thaliana DNA chromosome 3, BAC clone T15C9	At3g55070	AL132970	0.131	expressed	unknown	
A.thaliana iron superoxide dismutase (FeSOD) mRNA, 3' end	iron superoxide dismutase (FeSOD)	AF326862	0.132	A.thaliana iron superoxide dismutase (FeSOD) mRNA, 3' end	Cellular Processes and Signaling; transport	
At2g33070 Arabidopsis thaliana chromosome II section 185 of 255 of the complete sequence. Sequence from clones F25I18	At2g33070	AC002334	0.132	jacalin lectin family protein, PF01419 jacalin-like lectin family, PF01344 Kelch motif	Cellular Processes and Signaling; CAM ligands	
At2g15550 Arabidopsis thaliana chromosome II section 91 of 255 of the complete sequence. Sequence from clones F26H6, F9O13, F19G14	At2g15550	AC006248	0.132	hypothetical protein, similar to zinc finger protein	Genetic Information Processing; Transcription	
Arabidopsis thaliana homogentisate 1,2-dioxygenase mRNA, complete cds	At5g54080	U80668	0.132	homogentisate 1,2-dioxygenase / homogentisicase/homogentisate oxygenase / homogentisic acid oxidase (HGO), cellular component unknown, homogentisate 1,2-dioxygenase activity, L-phenylalanine catabolism, tyrosine catabolism	Metabolism; Amino Acid Metabolism; Tyrosine metabolism	Metabolism; Xenobiotics Biodegradation and Metabolism;
At3g01700 Arabidopsis thaliana arabinogalactan protein (AGP11) mRNA, partial cds	At3g01700	AF195892	0.132	arabinogalactan-protein (AGP11), extracellular proteoglycans implicated in plant growth and development	Metabolism; other	
Arabidopsis thaliana chromosome II section 200 of 255 of the complete sequence. Sequence from clones F13K3, T1J8		AC006282	0.132		unknown	
Arabidopsis thaliana mRNA for AGP6 protein	At2g36680	AJ012459	0.132	expressed protein	unknown	
At3g54530 Arabidopsis thaliana DNA chromosome 3, BAC clone T14E10	At3g54530	AL138656	0.132	expressed	unknown	
At3g01490 Arabidopsis thaliana chromosome III BAC F4P13 genomic sequence	At3g01490	AC009325	0.133	protein kinase, putative, similar to ATMRK1 (Arabidopsis thaliana) gi|2351097|dbj|BAA22079, thre/tyr kinase	Metabolism; kinases	
At4g00740 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2	At4g00740	AL161472	0.133	dehydration-responsive protein-related, similar to early-responsive to dehydration stress ERD3. PF03141: Putative methyltransferase	Metabolism; other; methyltransferase	
At4g38080 Arabidopsis thaliana DNA chromosome 4, BAC clone F20D10 (ESSA project)	At4g38080	AL035538	0.134	hydroxyproline-rich glycoprotein family protein, contains proline-rich extensin domains, INTERPRO:IPR002965; Common family member: At2g22510	Environmental Information Processing; Signaling Molecules	Cellular Processes and Signaling; CD molecules

Arabidopsis thaliana heat shock protein 70 (Hsc70-7) mRNA, complete cds; nuclear gene for chloroplas	At5g49910	AF217459	0.134	heat shock protein 70 / HSP70 (HSC70-7), identical to heat shock protein 70 (Arabidopsis thaliana) GI:6746592 , plastid stroma, ATP binding, protein folding CPHSC70-2	Genetic Information Processing; Folding, Sorting and Degradation	Environmental Information Processing; Signal Transduction
At1g21670 Arabidopsis thaliana unknown protein (F8K7.9) mRNA, complete cds	At1g21670	AY035079	0.134	expressed protein, similar to TolB protein precursor (SP:P50601) {Pseudomonas aeruginosa} , endomembrane	Genetic Information Processing; Non-enzyme	
At4g14540 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 39	At4g14540	AL161539	0.134	CCAAT-box binding transcription factor subunit B (NF-YB) (HAP3) (AHAP3) family, contains Pfam PF00808 : Histone-like transcription factor (CBF/NF-Y) and archaeal histone; similar to LEC1-like protein (GI:22536010) (Phaseolus coccineus	Genetic Information Processing; transcription	
At3g11070 Arabidopsis thaliana chromosome 3 BAC F11B9 genomic sequence	At3g11070	AC009991	0.135	outer membrane OMP85 family protein, contains Pfam profile PF01103: outer membrane protein, OMP85 family	Cellular Processes and Signaling	
Arabidopsis thaliana 26S proteasome AAA-ATPase subunit RPT1a (RPT1a) mRNA, complete cds	26S proteasome AAA-ATPase subunit RPT1a (RPT1a)	AF123390	0.135		Metabolism; peptide; protein	Genetic Information Processing; Folding, Sorting and Degradation
Arabidopsis thaliana chromosome 1 BAC T12M4 sequence, complete sequence		AC003114	0.135		unknown	
Arabidopsis thaliana unknown protein (F2D10.18) mRNA, complete cds	At1g20690	AC069251	0.135	expressed	unknown	
At1g63360 Genomic sequence for Arabidopsis thaliana BAC F2K11 from chromosome I	At1g63360	AC008047	0.135	disease resistance protein (CC-NBS-LRR class), putative	unknown	
Arabidopsis thaliana chromosome 1 BAC F12F1 sequence, complete sequence		AC002131	0.135	expressed protein, hypothetical protein F12F1.4 - Arabidopsis thaliana, EMBL:AC002131	unknown	
At5g17560 Arabidopsis thaliana DNA chromosome 5, BAC clone K10A8 (ESSA project)	At5g17560	AL391151	0.136	BolA-like family protein, contains Pfam profile: PF01722, cell division	Cellular processes; cell cycle	
At5g62540 Arabidopsis thaliana AT5g62540/K19B1_15 mRNA, complete cds	At5g62540	AY048267	0.136	ubiquitin-conjugating enzyme 3 (UBC3), E2	Genetic Information Processing; Folding, Sorting and Degradation; proteolysis?	

At3g54340 A.thaliana homeotic flower (APETELA3) mRNA, complete cds	At3g54340	AF115800	0.136	Floral homeotic gene encoding a MADS domain protein homologous to SRF transcription factors. Specifies petal and stamen identities. Associates with PISTILLATA. Floral homeotic protein APETALA3 (AP3) - nucleus	Genetic Information Processing; transcription	
At2g26750 Arabidopsis thaliana chromosome II section 149 of 255 of the complete sequence. Sequence from clones T9J22, F18A8	At2g26750	AC003105	0.136	epoxide hydrolase, putative	Metabolism; Lipid Metabolism;	Metabolism; Xenobiotics Biodegradation and Metabolism
At3g46890 Arabidopsis thaliana DNA chromosome 3, BAC clone T6H20	At3g46890	AL096859	0.136	expressed	unknown	
At5g46800 Arabidopsis thaliana mRNA for carnitine acyl carrier-like protein (bou gene)	At5g46800	AJ277732	0.136	mitochondrial carrier BOU, Seedling lethal mutation; Mitochondrial Carnitine Acyl Carrier-Like Protein , mitochondrial carnitine/acyl carrier, putative / a bout de souffle (BOU) / CAC-like protein, transport	unknown	
At5g59990 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MMN10	At5g59990	AB015475	0.136	expressed	unknown	
At3g21660 Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MIL23	At3g21660	AB019232	0.137	UBX domain-containing protein, contains Pfam profile: PF00789	Genetic Information Processing; Folding, Sorting and Degradation	
At5g03870 Arabidopsis thaliana DNA chromosome 5, BAC clone F8F6 (ESSA project)	At5g03870	AL162873	0.137	glutaredoxin family protein, contains Pfam profile PF00462	Genetic Information Processing; Folding, Sorting and Degradation	
Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46		AL161546	0.137		unknown	
At3g25010 Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone: K3G3	At3g25010	AP000412	0.137	disease resistance family protein, contains leucine rich-repeat (LRR) domains (23 copies) Pfam:PF00560	unknown	
At1g62180 Arabidopsis thaliana putative adenosine-5'-phosphosulfate reductase (F19K23.11) mRNA, complete cds	At1g62180	AF360192	0.138	5'-adenylylsulfate reductase 2, chloroplast (APR2) (APSR) / adenosine 5'-phosphosulfate 5'-adenylylsulfate (APS) sulfotransferase 2 / 3'-phosphoadenosine-5'-phosphosulfate (PAPS) reductase homolog 43 (PRH-43), Encodes a protein disulfide isomerase-like (PDIL) protein, a member of a multigene family within the thioredoxin (TRX) superfamily. This protein also belongs to the adenosine 5'-phosphosulfate reductase-like (APRL) group	Genetic Information Processing; Folding, Sorting and Degradation	Metabolism; Energy Metabolism; Sulfur metabolism

At5g60600 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MUP24	At5g60600	AB005246	0.138	CBL4, encodes for hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate synthase (HDS), 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate synthase, PF04551: GcpE protein	Metabolism; other	
At3g58220 Arabidopsis thaliana DNA chromosome 3, BAC clone F9D24	At3g58220	AL137081	0.138	meprin and TRAF homology domain-containing protein, Meprins are mammalian tissue-specific metalloendopeptidases, TRAF promote cell survival by the activation of downstream protein kinases and, finally, transcription factors of the NF-kB and AP-1 family	Metabolism; Peptidases	
Genomic sequence for Arabidopsis thaliana BAC F15O4 from chromosome I	Genomic	AC007887	0.138		unknown	
At4g14370 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 38	At4g14370	AL161538	0.138	disease resistance protein (TIR-NBS-LRR class), putative,	unknown	
At5g07520 A.thaliana mRNA encoding glycine rich protein	At5g07520	Z11869	0.139	glycine-rich protein (GRP18), Oleosin; glycine-rich protein 18 (GRP18) PMID:11431566, encodes a glycine-rich protein that is expressed only in flowers during a specific developmental stage (flower stage 12).	unknown	
At3g23770 Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MYM9	At3g23770	AP000377	0.14	glycosyl hydrolase family 17 protein, similar to A6 anther-specific protein SP:Q06915 (Arabidopsis thaliana) , hydrolase activity, hydrolyzing O-glycosyl compounds, carbohydrate metabolism, endomembrane system	Metabolism; Glycan Biosynthesis and Metabolism; N-Glycan	
Arabidopsis thaliana chromosome II section 107 of 255 of the complete sequence. Sequence from clones T30D6, F24H14		AC006439	0.14		unknown	
At4g10620 Arabidopsis thaliana DNA chromosome 4, BAC clone T4F9 (ESSA project)	At4g10620	AL049523	0.14	expressed	unknown	
At3g28290 Arabidopsis thaliana At14a protein mRNA, complete cds	At3g28290	AF126374	0.141	Possesses a transmembrane domain and a small region that has sequence similarities to integrins from fungi, insects and humans. Is localized to plasma membrane and cytoplasm. Integrin-related protein 14a, identical to At14a protein (also hits At3g28310), extracellular matrix and adhesion functions?	Cellular Processes and Signaling; Cell adhesion	Environmental Information Processing; Signaling Molecules

At5g13630 A.thaliana CHLH gene	At5g13630	Z68495	0.141	magnesium-chelatase subunit chlH, chloroplast, putative / Mg-protoporphyrin IX chelatase, putative (CHLH), Pfam profile: PF02514 CobN/magnesium chelatase family protein	Metabolism; Metabolism of Cofactors and Vitamins; Porphyrin	
At1g31850 Arabidopsis thaliana chromosome 1 BAC F5M6 genomic sequence	At1g31850	AC079041	0.141	dehydration-responsive protein, putative, contains Pfam profile PF03141: Putative methyltransferase	Metabolism; other methyltransferase	
At5g40200 Arabidopsis thaliana putative serine protease (MSN9.10) mRNA, complete cds	At5g40200	AY046023	0.141	DegP protease, putative	Metabolism; Peptidases	
Arabidopsis thaliana AT4g16190/dl4135w mRNA, complete cds	AT4g16190	AY039556	0.141	cysteine proteinase, putative, contains similarity to papain-like cysteine proteinase , cysteine-type peptidase activity, proteolysis, endomembrane system	Metabolism; peptide	
Arabidopsis thaliana chromosome 3 BAC F24K9 genomic sequence	Arabidopsis	AC008153	0.141		unknown	
At5g14690 Arabidopsis thaliana DNA chromosome 5, BAC clone T15N1 (ESSA project)	At5g14690	AL163792	0.141	expressed	unknown	
At3g01480 Arabidopsis thaliana AT3g01480/F4P13_3 mRNA, complete cds	At3g01480	AC009325	0.142	peptidyl-prolyl cis-trans isomerase, putative / cyclophilin, putative / rotamase, putative, similar to peptidyl-prolyl cis-trans isomerase, chloroplast precursor	Environmental Information Processing; Signal Transduction; Calcium	
Arabidopsis thaliana putative ubiquitin_/ ribosomal protein CEP52 (F22O6_30/AT3g52590) mRNA, complete cds	AT3g52590	AY035148	0.142	ubiquitin extension protein 1 (UBQ1) / 60S ribosomal protein L40 (RPL40B), EARLY-RESPONSIVE TO DEHYDRATION 16, ribosome, structural constituent of ribosome, protein ubiquitination	Genetic Information Processing; Folding, Sorting and Degradation; proteolysis?	Genetic Information Processing; Translation; Ribosome
At3g09710 Arabidopsis thaliana chromosome 3 BAC F11F8 genomic sequence	At3g09710	AC016661	0.143	calmodulin-binding family protein, PF00612:	Environmental Information Processing; Signal Transduction	
At1g23420 Arabidopsis thaliana INNER NO OUTER (INO) mRNA, complete cds	At1g23420	AF195047	0.143	inner no outer protein (INO), Essential for formation and asymmetric growth of the ovule outer integument. Member of the YABBY protein family of putative transcription factors that contain apparent Cys(2)-Cys(2) zinc-finger domains and regions of similarity to the high mobility group (HMG) transcription factors	Genetic Information Processing; Transcription	

At1g62370 Genomic sequence for Arabidopsis thaliana BAC F24O1 from chromosome I	At1g62370	AC003113	0.143	zinc finger (C3HC4-type RING finger) family protein	Genetic Information Processing; Transcription	
At1g52230 Arabidopsis thaliana mRNA for photosystem I subunit VI precursor (psaH2 gene)	At1g52230	AC022354	0.143	photosystem I reaction center subunit VI, chloroplast, putative / PSI-H, putative (PSAH2), Pfam profile PF03244	Metabolism; energy	
At3g12145 Arabidopsis thaliana leucine-rich repeat protein FLR1 (FLR1) mRNA, complete cds	At3g12145	AF136588	0.143	polygalacturonase inhibitor, putative / leucine-rich repeat protein (FLR1), A novel leucine-rich repeat protein. Interacts directly with MADS domain transcription factor.	Metabolism; Peptidases	
At2g24320 Arabidopsis thaliana chromosome II section 137 of 255 of the complete sequence. Sequence from clones F27D4, T28I24, F25P17	At2g24320	AC006403	0.143	expressed	unknown	
At3g48600 Arabidopsis thaliana DNA chromosome 3, BAC clone T8P19	At3g48600	AL133315	0.143	SWIB complex BAF60b domain-containing protein, contains Pfam profile PF02201	unknown	
At5g26617 Arabidopsis thaliana BAC F21E10	At5g26617	AF058914	0.143	expressed	unknown	
Arabidopsis thaliana ubiquitin-like protein (K5J14.10) mRNA, complete cds	At5g42300	AF370527	0.144	ubiquitin family protein, contains INTERPRO:IPR000626 ubiquitin domain	Genetic Information Processing; Folding, Sorting and Degradation; proteolysis?	
A.thaliana mRNA for putative dTDP-glucose 4-6-dehydratases	A.thaliana	Z49239	0.144		Metabolism; carbohydrate	
At3g12580 Arabidopsis thaliana mRNA for heat shock protein 70	At3g12580	AJ002551	0.145	heat shock protein 70, putative / HSP70, putative	Genetic Information Processing; Folding, Sorting and Degradation	Environmental Information Processing; Signal Transduction
Arabidopsis thaliana heat shock protein 70 (Hsc70-7) mRNA, complete cds; nuclear gene for chloroplas	At5g49910	AF217459	0.145	heat shock protein 70 / HSP70 (HSC70-7), identical to heat shock protein 70 (Arabidopsis thaliana) GI:6746592 , plastid stroma, ATP binding, protein folding CPHSC70-2	Genetic Information Processing; Folding, Sorting and Degradation	Environmental Information Processing; Signal Transduction
At2g36160 Arabidopsis thaliana chromosome II section 197 of 255 of the complete sequence. Sequence from clones F11F19, F9C22	At2g36160	AC007135	0.145	40S ribosomal protein S14 (RPS14A)	Genetic Information Processing; Translation; Ribosome	
At4g00360 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 1	At4g00360	AL161471	0.145	cytochrome p450, putative, Encodes a member of the CYP86A subfamily of cytochrome p450 genes. Expressed at moderate levels in flowers, leaves, roots and stems.	Metabolism; Cytochrome P450	
At5g59260 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MNC17	At5g59260	AB016890	0.145	lectin protein kinase, putative, contains protein kinase domain, Pfam:PF00069; contains legume lectins alpha and beta domains, Pfam:PF00138 and Pfam:PF00139	Metabolism; kinase	Cellular Processes and Signaling; CAM ligands

At1g19650 Arabidopsis thaliana chromosome I BAC F14P1 genomic sequence	At1g19650	AC024609	0.145	SEC14 cytosolic factor, putative / phosphoglyceride transfer protein, putative, contains Pfam PF00650 : CRAL/TRIO domain; contains Pfam PF03765 : CRAL/TRIO, N-terminus	Metabolism; other; phosphoglyceride transferase	
At4g39090 Arabidopsis thaliana DNA chromosome 4, BAC clone F19H22 (ESSA project)	At4g39090	AL035679	0.145	cysteine proteinase RD19a (RD19A) / thiol protease,	Metabolism; Peptidases	
At5g13320 Arabidopsis thaliana DNA chromosome 5, BAC clone T31B5 (ESSA project)	At5g13320	AL163491	0.145	auxin-responsive GH3 family protein, similar to auxin-responsive GH3 product (Glycine max) GI:18591; contains Pfam profile PF03321: GH3 auxin-responsive promoter	unknown	
At1g60480 Arabidopsis thaliana BAC F8A5	At1g60480	AC002292	0.146	pseudogene, putative ADP-ribosylation factor	Cellular Processes and Signaling; GTP-binding	
Arabidopsis thaliana ZW10 mRNA, partial cds		AB028195	0.146	centromere/kinetochore protein, putative (ZW10), identical to centromere/kinetochore protein zw10 homolog SP:O48626 from (Arabidopsis thaliana)	Genetic Information Processing; cell cycle	
Arabidopsis thaliana heat shock protein 70 (Hsc70-7) mRNA, complete cds; nuclear gene for chloroplas	At5g49910	AF217459	0.146	heat shock protein 70 / HSP70 (HSC70-7), identical to heat shock protein 70 (Arabidopsis thaliana) GI:6746592 , plastid stroma, ATP binding, protein folding CPHSC70-2	Genetic Information Processing; Folding, Sorting and Degradation	Environmental Information Processing; Signal Transduction
Arabidopsis thaliana heat shock protein 70 (Hsc70-7) mRNA, complete cds; nuclear gene for chloroplas	At5g49910	AF217459	0.146	heat shock protein 70 / HSP70 (HSC70-7), identical to heat shock protein 70 (Arabidopsis thaliana) GI:6746592 , plastid stroma, ATP binding, protein folding CPHSC70-2	Genetic Information Processing; Folding, Sorting and Degradation	Environmental Information Processing; Signal Transduction
ESTs, Highly similar to [Segment 1 of 2] 60S RIBOSOMAL PROTEIN L5 [A.thaliana]		T46713	0.146	ribosomal	Genetic Information Processing; Translation; Ribosome	
At3g16870 Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:MUH15	At3g16870	AP001308	0.146	aldose 1-epimerase family protein, Pfam profile PF01263 (also hits At3g16870, zinc finger (GATA type) family protein, contains Pfam profile:PF00320	Metabolism; Carbohydrate Metabolism; Glycolysis	
At5g47050 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MQD22	At5g47050	AB013394	0.146	ubiquitin expressed protein (possible ubq ligase)	Metabolism; Peptidases	
At2g25680 Arabidopsis thaliana chromosome II section 144 of 255 of the complete sequence. Sequence from clones F13B15, F3N11, F17H15	At2g25680	AC006053	0.146	expressed	unknown	

At3g63020 Arabidopsis thaliana DNA chromosome 3, BAC clone T20O10	At3g63020	AL163816	0.146	hypothetical protein	unknown
At3g56620 Arabidopsis thaliana DNA chromosome 3, BAC clone T5P19	At3g56620	AL163972	0.147	integral membrane family protein / nodulin MtN21-related	unknown
Arabidopsis thaliana DNA chromosome 3, BAC clone T17J13		AL138651	0.147	unk	unknown
At3g13520 Arabidopsis thaliana arabinogalactan protein (AGP12) mRNA, complete cds	At3g13520	AF195893	0.148	Encodes a GPI-anchored arabinogalactan (AG) peptide with a short 'classical' backbone of 10 amino acids, seven of which are conserved among the 4 other Arabidopsis AG peptides. These peptides may be involved in cell signaling (hits AGP12), plant growth and development	Cellular Processes and Signaling; Transporters
At2g03670 Arabidopsis thaliana chromosome II section 15 of 255 of the complete sequence. Sequence from clones F19B11, T18C20	At2g03670	AC006836	0.148	CDC48 - like protein AAA-type ATPase family protein, contains Pfam domain	Genetic Information Processing; Folding, Sorting and Degradation
At1g19310 Genomic sequence for Arabidopsis thaliana BAC F18O14 from chromosome I	At1g19310	AC025808	0.148	zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger) , protein binding, zinc ion binding	Genetic Information Processing; Transcription
At5g41350 Arabidopsis thaliana AT5g41350/MYC6_6 mRNA, complete cds	At5g41350	AY048293	0.148	zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097	Genetic Information Processing; transcription
At5g41400 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MYC6	At5g41400	AB006707	0.148	zinc finger (C3HC4-type RING finger) family protein, similar to RING-H2 finger protein RHA1a (Arabidopsis thaliana) GI:3790554; contains Pfam profile PF00097: Zinc finger, C3HC4 type (RING finger)	Genetic Information Processing; transcription
At4g16720 Arabidopsis thaliana putative ribosomal protein (AT4g16720) mRNA, complete cds	At4g16720	AF370352	0.148	60S ribosomal protein L15 (RPL15A)	Genetic Information Processing; Translation
At2g15800 Arabidopsis thaliana chromosome II section 92 of 255 of the complete sequence. Sequence from clones F19G14, F7H1	At2g15800	AC006438	0.148	expressed	unknown
At3g55690 Arabidopsis thaliana DNA chromosome 3, BAC clone F1I16	At3g55690	AL161667	0.148	expressed	unknown
At4g34265 ESTs	At4g34265	AV533864	0.148	expressed	unknown
At1g32630 Genomic sequence for Arabidopsis thaliana BAC F6N18 from chromosome I	At1g32630	AC017118	0.149	expressed	unknown
At1g53260 Genomic sequence for Arabidopsis thaliana BAC F12M16 from chromosome I	At1g53260	AC008007	0.149	expressed	unknown
At1g69630 Arabidopsis thaliana chromosome 1 BAC F24J1 genomic sequence	At1g69630	AC021046	0.149	F-box family protein, contains F-box domain Pfam:PF00646	unknown

At5g03700 Arabidopsis thaliana DNA chromosome 5, BAC clone F17C15 (ESSA project)	At5g03700	AL162506	0.149	PAN domain-containing protein, contains Pfam profile: PF00024, found in many types of proteins	unknown	
Arabidopsis thaliana BAC F19G10, complete sequence		AF000657	0.149	pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat. Gene continues on the 3' end of BAC F19G10 gb|AF000657 gene F19G10.21	unknown	
At2g44840 Arabidopsis thaliana putative ethylene response element binding protein; EREBP (At2g44840; T13E15.15) mRNA, complete cds	At2g44840	AF370540	0.15	member of the ERF (ethylene response factor) subfamily B-3 of ERF/AP2 transcription factor family	Genetic Information Processing; transcription	
ESTs, Moderately similar to T00456 protein kinase homolog T14N5.13 - Arabidopsis thaliana [A.thaliana]	At1g77280	AV524106	0.15	protein kinase family protein, contains Pfam domain, PF00069: Protein kinase domain	Metabolism; kinase	
At1g52870 Arabidopsis thaliana At1g52870/F14G24_14 mRNA, complete cds	At1g52870	AF385726	0.151	peroxisomal membrane protein-related	Cellular Processes and Signaling; Transporters	
Arabidopsis thaliana proline iminopeptidase mRNA, complete cds		U72711	0.151		Metabolism; Amino Acid Metabolism; Arginine and proline metabolism	Metabolism; Peptidases
At5g49080 Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K20J1	At5g49080	AB023028	0.151	proline-rich extensin-like family protein,	Metabolism; other	
At1g05460 Genomic sequence for Arabidopsis thaliana BAC T25N20 from chromosome I	At1g05460	AF339908	0.152	RNA helicase SDE3 (SDE3), Encodes a protein with similarity to RNA helicases. Mutants are defective in post-transcriptional gene silencing.	Genetic Information Processing; Replication and Repair;	
At4g15770 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 42	At4g15770	AL161542	0.152	60S ribosome subunit biogenesis protein, putative	Genetic Information Processing; Translation	
Arabidopsis thaliana cytosolic phosphoglycerate kinase (PGK) mRNA, complete cds	At1g79550 (?)	AF247560	0.152	cytosolic phosphoglycerate kinase (PGK) mRNA, complete cds , cytosol, phosphoglycerate kinase activity	Metabolism; Carbohydrate Metabolism; Glycolysis /	Metabolism; Energy metab
Arabidopsis thaliana DNA chromosome 4, BAC clone F6I18 (ESSA project)		AL022198	0.152		unknown	

Arabidopsis thaliana membrane associated protein mRNA, complete cds	At5g54110	U83655	0.154	vesicle-associated membrane family protein / VAMP family protein, Encodes a highly polar protein with more than 60% hydrophilic amino acid residues that is associated with the plasma membrane. It has limited secondary structure similarity to VAP-33 from Aplysia, which may be involved in membrane trafficking. AtMAMI (membrane assoc, manitol induced) plasma membrane, response to osmotic stress	Genetic Information Processing; Folding, Sorting and Degradation	
At5g41700 Arabidopsis thaliana putative ubiquitin-conjugating enzyme (MBK23.24/AT5g41700) mRNA, complete cds	At5g41700	AF370257	0.154	ubiquitin-conjugating enzyme 8 (UBC8), E2, One of the polypeptides that constitute the ubiquitin-conjugating enzyme E2	Genetic Information Processing; Folding, Sorting and Degradation; proteolysis?	
At1g07810 Arabidopsis thaliana ER-type calcium pump (ACA3) mRNA, complete cds	At1g07810	U96455	0.154	calcium-transporting ATPase 1, endoplasmic reticulum-type (ECA1), response to manganese ion	Metabolism; Energy Metabolism; ATPases	
Arabidopsis thaliana DNA chromosome 4, BAC clone F27B13 (ESSA project)		AL050352	0.154		unknown	
Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MKM21		AB016876	0.154		unknown	
At2g18410 Arabidopsis thaliana chromosome II section 107 of 255 of the complete sequence. Sequence from clones T30D6, F24H14	At2g18410	AC006439	0.154	expressed	unknown	
At2g39070 Arabidopsis thaliana chromosome II section 210 of 255 of the complete sequence. Sequence from clones F13I13, T7F6, T16B24	At2g39070	AC005770	0.154	expressed	unknown	
At5g54600 A.thaliana mRNA for plastid ribosomal protein	At5g54600	Y09635	0.155	50S ribosomal protein L24, chloroplast (CL24),	Genetic Information processing; translation	
At3g29670 Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:MOD1	At3g29670	AB028618	0.155	transferase family protein, Pfam profile PF02458	Metabolism; other; transferase	
Arabidopsis thaliana chromosome 1 BAC F13N6 genomic sequence	Arabidopsis	AC058785	0.155		unknown	
Arabidopsis thaliana DNA chromosome 5, BAC clone F8F6 (ESSA project)		AL162873	0.155		unknown	
A.thaliana mRNA for ADP-ribosylation factor 3	A.thaliana	X77385	0.156		Cellular Processes and Signaling; GTP-binding	
Arabidopsis thaliana heat shock protein 70 (Hsc70-7) mRNA, complete cds; nuclear gene for chloroplas	At5g49910	AF217459	0.156	heat shock protein 70 / HSP70 (HSC70-7), identical to heat shock protein 70 (Arabidopsis thaliana) GI:6746592 , plastid stroma, ATP binding, protein folding CPHSC70-2	Genetic Information Processing; Folding, Sorting and Degradation	Environmental Information Processing; Signal Transduction
Arabidopsis thaliana DNA chromosome 3, BAC clone T10K17		AL132977	0.156		unknown	

Arabidopsis thaliana DNA chromosome 5, BAC clone F8F6 (ESSA project)		AL162873	0.156		unknown	
At1g51080 Arabidopsis thaliana chromosome 1 BAC F23H24 genomic sequence	At1g51080	AC079828	0.156	expressed	unknown	
At5g35160 Arabidopsis thaliana genomic DNA, chromosome 5, BAC clone:T13C12	At5g35160	AP000421	0.156	endomembrane protein 70, putative - integral to membrane	unknown	
Arabidopsis thaliana DNA chromosome 3, BAC clone T8M16		AL390921	0.156	unk	unknown	
At4g02340 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6	At4g02340	AL161494	0.157	epoxide hydrolase, putative, PF00561: hydrolase, alpha/beta fold family	Metabolism; Lipid Metabolism;	Metabolism; Xenobiotics Biodegradation and Metabolism
Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDJ14		AB016889	0.157		unknown	
At1g23060 Arabidopsis thaliana chromosome I BAC T26J12 genomic sequence	At1g23060	AC002311	0.157	expressed	unknown	
At4g07470 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 17	At4g07470	AL161505	0.157	expressed	unknown	
At5g44550 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MFC16	At5g44550	AB017065	0.157	integral membrane family protein, similar to unknown protein (pir||T10581)	unknown	
At5g54650 Arabidopsis thaliana Unknown protein (MRB17.15) mRNA, complete cds	At5g54650	AY042801	0.158	formin homology 2 domain-containing protein / FH2 domain-containing protein, contains formin homology 2 domain, Pfam:PF02181, regulator of actin filaments	Cellular Processes; Development;	
Arabidopsis thaliana chromosome 1 BAC T12P18 genomic sequence	Arabidopsis	AC010852	0.158		unknown	
At1g75500 Arabidopsis thaliana unknown protein (F10A5.28) mRNA, complete cds	At1g75500	AY045896	0.158	nodulin MtN21 family protein, contains Pfam profile PF00892: Integral membrane protein	unknown	
Arabidopsis thaliana beta-2 tubulin (TUB2) gene, complete cds	beta-2 tubulin	M84701	0.159	beta-2 tubulin	Cellular Processes; Cell Communication; Gap junction	
At1g14380 Sequence of BAC F14L17 from Arabidopsis thaliana chromosome 1	At1g14380	AC012188	0.159	calmodulin-binding family protein, contains Pfam profile PF00612: IQ calmodulin-binding motif	Environmental Information Processing; Signal Transduction	
At4g00300 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 1	At4g00300	AL161471	0.159	fringe-related protein, Fringe encodes an extracellular protein that regulates Notch signalling.	Environmental Information Processing; Signal Transduction;	
Arabidopsis thaliana mRNA for nuclear protein HCF136	At5g23120	Y15628	0.159	encodes a stability and/or assembly factor of photosystem II , chloroplast stromal thylakoid, protein binding, plastid organization and biogenesis, protein complex assembly	Metabolism; Energy Metabolism; Photosynthesis	
At4g02420 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6	At4g02420	AL161494	0.159	lectin protein kinase, putative	Metabolism; kinase	Cellular Processes and Signaling; CAM ligands

ESTs, Weakly similar to T10681 hypothetical protein F3L17.80 - Arabidopsis thaliana [A.thaliana]	At4g31510	AV540175	0.159	expressed protein, low similarity to MTD1 (Medicago truncatula) GI:9294810 , chloroplast	unknown	
Arabidopsis thaliana AT5g58570/mzn1_20 mRNA, complete cds	AT5g58570	AB020755	0.159	expressed	unknown	
At1g51450 Arabidopsis thaliana chromosome 1 BAC F5D21 genomic sequence	At1g51450	AC024261	0.16	SPla/RYanodine receptor (SPRY) domain-containing protein, Pfam profile PF00622: SPRY domain	Environmental Information Processing; Signal Transduction; Calcium	
At2g35920 Arabidopsis thaliana chromosome II section 196 of 255 of the complete sequence. Sequence from clones T20F21, F11F19	At2g35920	AC007017	0.16	helicase domain-containing protein	Genetic Information Processing; translation	
At5g41520 Arabidopsis thaliana AT5g41520/MBK23_4 mRNA, complete cds	At5g41520	AY037240	0.16	40S ribosomal protein S10	Genetic Information processing; translation	
At3g26650 Arabidopsis thaliana glyceraldehyde-3-phosphate dehydrogenase A subunit (GapA) mRNA, complete cds	At3g26650	M64117	0.16	glyceraldehyde 3-phosphate dehydrogenase A, chloroplast (GAPA	Metabolism; Carbohydrate Metabolism; Glycolysis / Gluconeogenesis	Metabolism; Energy Metabolism; Carbon fixation
Arabidopsis thaliana chromosome 1 BAC F2P9 genomic sequence	Arabidopsis	AC016662	0.16		unknown	
At5g59390 Arabidopsis thaliana genomic DNA, chromosome 5, BAC clone:F2O15	At5g59390	AB025604	0.16	XH/XS domain-containing protein, contains Pfam domain PF03469: XH domain and PF03468: XS domain	unknown	
At5g07310 Arabidopsis thaliana DNA chromosome 5, BAC clone T2I1 (ESSA project)	At5g07310	AL163912	0.161	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.	Genetic Information Processing; Transcription	
At1g16870 Arabidopsis thaliana chromosome I BAC F6I1 genomic sequence	At1g16870	AC051629	0.161	mitochondrial 28S ribosomal protein S29-related, contains weak similarity to Swiss-Prot:P51398 mitochondrial 28S ribosomal protein S29 (MRP-S29, Death-associated protein 3, DAP-3) (Homo sapiens) , mitochondrion, molecular function unknown, biological process unknown	Genetic Information Processing; Translation	
At2g36730 Arabidopsis thaliana chromosome II section 200 of 255 of the complete sequence. Sequence from clones F13K3, T1J8	At2g36730	AC006282	0.161	pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535	unknown	
At5g47380 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MQL5	At5g47380	AB018117	0.161	expressed	unknown	
At1g72120 Arabidopsis thaliana chromosome 1 BAC F28P5 genomic sequence	At1g72120	AC069273	0.162	proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854	Cellular processes and signaling; transporters	

At2g35800 Arabidopsis thaliana chromosome II section 196 of 255 of the complete sequence. Sequence from clones T20F21, F11F19	At2g35800	AC007017	0.162	mitochondrial substrate carrier family protein, calcium-binding EF-hand domain	Environmental Information Processing; Membrane Transport; Other	
At4g01350 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 3	At4g01350	AL161491	0.162	DC1 domain-containing protein, contains Pfam profile PF03107	Genetic Information Processing; Transcription	
At5g08290 Arabidopsis thaliana putative cis-trans isomerase protein (F8L15_20) mRNA, complete cds	At5g08290	AF326857	0.162	yellow-leaf-specific protein 8 (YLS8) / mitosis protein DIM1, putative, contains Pfam domain, spliceosome complex, catalytic activity, mitosis	Genetic Information processing; translation	
At1g24170 Arabidopsis thaliana chromosome I BAC F3I6 genomic sequence	At1g24170	AC002396	0.162	Encodes a protein with putative galacturonosyltransferase activity. transferase activity, transferring hexosyl groups, carbohydrate biosynthesis, endomembrane system, transferase activity, transferring glycosyl groups, polygalacturonate 4-alpha-galacturonosyltransferase activity	Metabolism; carbohydrate Metabolism	Cellular Processes and Signaling;
At2g29890 Arabidopsis thaliana villin 1 (VLN1) mRNA, complete cds	At2g29890	AF081201	0.163	villin 1 (VLN1) actin binding	Cellular Processes and Signaling; Membrane and structural molecules	
At5g33320 Arabidopsis thaliana phosphate/phosphoenolpyruvate translocator (PPT1) gene, complete cds	At5g33320	AF209210	0.163	triose phosphate/phosphate translocator, putative	Cellular Processes; Transport	
At3g50670 Arabidopsis thaliana 70kDa small nuclear ribonucleoprotein U1 (RNU1) mRNA, partial cds	At3g50670	U52910	0.163	U1 small nuclear ribonucleoprotein 70 (U1-70k), Encodes U1 snRNP 70K	Genetic Information Processing; Translation	
At1g47200 Arabidopsis thaliana chromosome 1 BAC F2G19 genomic sequence	At1g47200	AC083835	0.164	MFP1 attachment factor, putative–filament like protein	Cellular Processes; Cell Growth and Death; Cell division	
At1g14900 A.thaliana mRNA for HMG-I/Y protein	At1g14900	X99116	0.164	high-mobility-group protein / HMG-I/Y protein, nearly identical to high-mobility-group protein HMG-I/Y protein (Arabidopsis thaliana) GI:1429211; contains Pfam profiles PF00538: linker histone H1 and H5 family, PF02178: AT hook motif , nucleus, DNA binding, regulation of transcription, DNA-dependent	Genetic Information Processing; Transcription	
At1g69910 Arabidopsis thaliana chromosome 1 BAC T17F3 genomic sequence	At1g69910	AC010675	0.164	protein kinase family protein	Metabolism; kinase	
Arabidopsis thaliana chromosome 1 BAC F2J7 genomic sequence	Arabidopsis	AC079281	0.164		unknown	
At1g15010 Arabidopsis thaliana unknown protein (T15D22.5) mRNA, complete cds	At1g15010	AC012189	0.164	expressed, chloro	unknown	

At5g66400 A.thaliana rab18 gene	At5g66400	X68042	0.164	dehydrin (RAB18), ABA- and drought-induced glycine-rice dehydrin protein	unknown			
At5g52060 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MSG15	At5g52060	AB015478	0.165	BAG domain-containing protein, contains Pfam:PF02179 (also hits At5g62100), mitochondrion, protein binding, apoptosis, regulation of apoptosis	Cellular Processes; Cell Growth and Death; Apoptosis			
At3g42060 Arabidopsis thaliana DNA chromosome 3, BAC clone F4M19	At3g42060	AL356013	0.165	myosin heavy chain-related	Cellular Processes; Cell Motility; Regulation of actin			
At2g28740 Arabidopsis thaliana chromosome II section 164 of 255 of the complete sequence. Sequence from clones T11P11, F8N16, T9I4	At2g28740	AC005727	0.165	histone H4	Genetic Information Processing; Transcription			
At1g61600 Arabidopsis thaliana chromosome I BAC T25B24 genomic sequence	At1g61600	AC005850	0.165	expressed	unknown			
Arabidopsis thaliana unknown protein (AT3g24100) mRNA, complete cds	AT3g24100	AF370331	0.165	four F5 family protein / 4F5 family protein, contains Pfam PF04419: 4F5 protein family , mito	unknown			
At4g23870 Arabidopsis thaliana DNA chromosome 4, BAC clone T32A16 (ESSA project)	At4g23870	AL078468	0.165	expressed	unknown			
At5g04820 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MUK11	At5g04820	AB008271	0.165	ovate family protein, 62% similar to ovate protein (GI:23429649) (Lycopersicon esculentum); contains TIGRFAM TIGR01568 : uncharacterized plant-specific domain TIGR01568	unknown			
A.thaliana alpha-1-tubulin gene, complete cds	alpha-1-tubulin	M21414	0.166	alpha-1-tubulin	Cellular Processes; Cell Communication; Gap junction			
At1g04310 Arabidopsis thaliana putative ethylene receptor (ERS2) gene, complete cds	At1g04310	AF047976	0.166	ethylene receptor-related, similar to ethylene receptor CS-ETR2 (Cucumis sativus), encodes an ethylene receptor related to bacterial two-component histidine kinases, glycogen synthase kinase 3 activity, protein histidine kinase activity, ethylene binding , membrane, receptor activity, endomembrane system, negative regulation of ethylene mediated signaling pathway	Environmental Information Processing; Signal Transduction		Metabolism; Protein kinases	Cellular Processes and Signaling; Two-component
At1g26800 Genomic sequence for Arabidopsis thaliana BAC T24P13 from chromosome I	At1g26800	AC006535	0.166	zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097	Genetic Information Processing; Transcription			
At4g01850 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 5	At4g01850	M33217	0.166	S-adenosylmethionine synthetase 2 (SAM2),	Metabolism; amino acid			

Arabidopsis thaliana chromosome I BAC F28G4 genomic sequence	Arabidopsis	AC007843	0.166		unknown		
At4g04920 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 14	At4g04920	AL161502	0.166	expressed	unknown		
At4g11870 Arabidopsis thaliana DNA chromosome 4, BAC clone T26M18 (ESSA project)	At4g11870	AL078606	0.166	expressed	unknown		
At4g18420 Arabidopsis thaliana DNA chromosome 4, BAC clone F28J12 (ESSAII project)	At4g18420	AL021710	0.166	expressed	unknown		
Arabidopsis thaliana heat shock protein 70 (Hsc70-7) mRNA, complete cds; nuclear gene for chloroplas	At5g49910	AF217459	0.167	heat shock protein 70 / HSP70 (HSC70-7), identical to heat shock protein 70 (Arabidopsis thaliana) GI:6746592 , plastid stroma, ATP binding, protein folding CPHSC70-2	Genetic Information Processing; Folding, Sorting and Degradation	Environmental Information Processing; Signal Transduction	
At4g38140 Arabidopsis thaliana DNA chromosome 4, BAC clone F20D10 (ESSA project)	At4g38140	AL035538	0.167	zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097	Genetic Information Processing; transcription		
Arabidopsis thaliana mRNA for Ara6, complete cds		AB007766	0.167	GTPase, G protein function, (thiazole biosynthetic enzyme, chloroplast (ARA6) (THI1) (THI4)), Encodes a novel Rab-like GTP-ase that is localized to the peripheral membrane of the endosome.	Metabolism of Cofactors and Vitamins; Thiamine	Environmental Information Processing; Signal Transduction	Cellular Processes; Cell Communication
At5g01530 Arabidopsis thaliana AT5g01530/F7A7_50 mRNA, complete cds	At5g01530	X71878	0.167	chlorophyll A-B binding protein CP29 (LHCB4), identical to CP29 (Arabidopsis thaliana) GI:298036; contains Pfam profile: PF00504	Metabolism; energy; photosynthesis		
Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MXK3		AB019236	0.167		unknown		
At1g18850 Arabidopsis thaliana chromosome I BAC F6A14 genomic sequence	At1g18850	AC011809	0.167	expressed	unknown		
At2g44060 Arabidopsis thaliana chromosome II section 237 of 255 of the complete sequence. Sequence from clones F6E13, F4I1	At2g44060	AC004005	0.167	late embryogenesis abundant family protein / LEA family protein, PF03168	unknown		
At3g23760 Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MYM9	At3g23760	AP000377	0.167	expressed	unknown		
At2g37430 A.thaliana mRNA for ZAT11 protein	At2g37430	X98672	0.168	zinc finger (C2H2 type) family protein (ZAT11), contains Pfam domain	Genetic Information Processing; transcription		
At3g62160 Arabidopsis thaliana DNA chromosome 3, BAC clone T17J13	At3g62160	AL138651	0.168	transferase family protein, PF02458	Metabolism; other; transferase		
At5g44160 Arabidopsis thaliana AT5g44160/MLN1_8 mRNA, complete cds	At5g44160	AY037202	0.169	zinc finger (C2H2 type) family protein, contains Pfam domain, PF00096	Genetic Information Processing; transcription		
A. THALIANA AT-LS1 CDNA	A.	X58827	0.169		unknown		
At2g07090 Arabidopsis thaliana chromosome II section 40 of 255 of the complete sequence. Sequence from clones T4E14, T25N22	At2g07090	AC005693	0.169	expressed	unknown		

Arabidopsis thaliana Ran binding protein 1 homolog (RanBP1) mRNA, complete cds	At5g58590	U62742	0.17	Ran-binding protein 1, putative / RanBP1, putative, strong similarity to Ran binding proteins from Arabidopsis thaliana atranbp1a (Arabidopsis thaliana) GI:2058282, atranbp1b (Arabidopsis thaliana) GI:2058284; contains Pfam profile PF00638: RanBP1 domain , Ran binding protein 1 homolog (RanBP1) mRNA, complete cds , cellular component unknown, protein binding, protein import into nucleus, translocation, meristem	Cellular processes and signaling; transport	
At3g24190 Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:MUJ8	At3g24190	AB028621	0.17	ABC1 family protein, contains Pfam domain, PF03109: ABC1 family (also hits locus At3g15200, PRR protein)	Cellular Processes and Signaling; Transporters	Environmental Information Processing; Membrane Transport
At2g32700 Arabidopsis thaliana chromosome II section 183 of 255 of the complete sequence. Sequence from clones T26B15, F24L7	At2g32700	AC003974	0.17	WD-40 repeat family protein, contains 7 WD-40 repeats	Metabolism; Peptidases	
Arabidopsis thaliana chromosome III P1 MLP3 genomic sequence	Arabidopsis	AC009176	0.17		unknown	
At3g47820 Arabidopsis thaliana DNA chromosome 3, BAC clone T23J7	At3g47820	AL049746	0.171	armadillo/beta-catenin repeat family protein / U-box domain-containing protein, contains Pfam domain, PF00514, PF04564	Genetic Information Processing; Folding, sorting, deg	
At3g54850 Arabidopsis thaliana DNA chromosome 3, BAC clone F28P10	At3g54850	AL049655	0.171	armadillo/beta-catenin repeat family protein / U-box domain-containing family protein	Genetic information processing; folding, sorting, degredation	
Arabidopsis thaliana ribosomal protein S6 (rps6) mRNA, complete cds		AF034217	0.171		Genetic Information Processing; Translation; Ribosome	
At1g74470 Arabidopsis thaliana mRNA for geranylgeranyl reductase	At1g74470	AC011765	0.171	geranylgeranyl reductase (involvement: chlorophyll, the tocopherol and the phylloquinone pathways)	Metabolism; energy; photosynthesis	Metabolism; Biosynthesis of Secondary Metabolites;
At1g69820 Arabidopsis thaliana chromosome 1 BAC T17F3 genomic sequence	At1g69820	AC010675	0.171	gamma-glutamyltranspeptidase family protein, PF01019, part of the g -glutamyl cycle involving the degradation and neo-synthesis of glutathione, peptidase, membrane protein	Metabolism; Peptidases	
At1g73030 Arabidopsis thaliana chromosome I BAC F3N23 genomic sequence	At1g73030	AC008017	0.171	SNF7 family protein	Metabolism; Protein kinases	
Arabidopsis thaliana chromosome 1 BAC F4F7 genomic sequence	Arabidopsis	AC079374	0.171		unknown	
At5g44490 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MFC16	At5g44490	AB017065	0.171	F-box family protein, contains F-box domain Pfam:PF00646	unknown	

Arabidopsis thaliana ubiquitin-like protein (K5J14.10) mRNA, complete cds	At5g42300	AF370527	0.172	ubiquitin family protein, contains INTERPRO:IPR000626 ubiquitin domain	Genetic Information Processing; Folding, Sorting and Degradation; proteolysis?	
Arabidopsis thaliana ubiquitin-like protein (K5J14.10) mRNA, complete cds	At5g42300	AF370527	0.172	ubiquitin family protein, contains INTERPRO:IPR000626 ubiquitin domain	Genetic Information Processing; Folding, Sorting and Degradation; proteolysis?	
At2g04840 Arabidopsis thaliana chromosome II section 23 of 255 of the complete sequence. Sequence from clones F28I8	At2g04840	AC006955	0.172	F-box family protein	unknown	
Arabidopsis thaliana chromosome II section 24 of 255 of the complete sequence. Sequence from clones F28I8, F1O13		AC007211	0.172	unk	unknown	
At5g59950 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MMN10	At5g59950	AB015475	0.173	RNA and export factor-binding protein, putative	Genetic information and processing; translation	
Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MWF20		AB025638	0.173		unknown	
At3g43980 Arabidopsis thaliana ribosomal protein S29-like protein (T15B3_150) mRNA, complete cds	At3g43980	AF326888	0.174	40S ribosomal protein S29 (RPS29A),	Genetic Information Processing; Translation	
Sequence of BAC T20H2 from Arabidopsis thaliana chromosome 1	Sequence	AC022472	0.174		unknown	
At2g32890 Arabidopsis thaliana chromosome II section 184 of 255 of the complete sequence. Sequence from clones F24L7, T21L14, F25I18	At2g32890	AC003033	0.174	expressed	unknown	
Arabidopsis thaliana putative metallothionein-I gene transcription activator protein (MEE6.8/AT5g41010) mRNA, complete cds	AT5g41010	AY045954	0.175	DNA-directed RNA polymerases I, II, and III 7 kDa subunit, putative, similar to SP|P53803 DNA-directed RNA polymerases I, II, and III 7.0 kDa polypeptide (EC 2.7.7.6) (ABC10-alpha) (RPB7.0) (RPB10alpha) {Homo sapiens}; contains Pfam profile PF03604: DNA directed RNA polymerase, 7 kDa subunit , nucleus, DNA binding, DNA-directed RNA polymerase activity, transcription	Genetic Information Processing; Transcription; RNA polymerase	
At3g01260 Arabidopsis thaliana chromosome III BAC T4P13 genomic sequence	At3g01260	AC008261	0.175	aldose 1-epimerase family protein,	Metabolism; Carbohydrate Metabolism; Glycolysis / Gluconeogenesis	
At4g21960 A.thaliana mRNA for peroxidase, prxr1	At4g21960	X98313	0.175	peroxidase 42 (PER42) (P42) (PRXR1),	Metabolism; Energy Metabolism;	Metabolism; Biosynthesis of Secondary Metabolites;
Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:MVA11		AP001311	0.175		unknown	

At5g52740 Arabidopsis thaliana genomic DNA, chromosome 5, BAC clone:F6N7	At5g52740	AB025606	0.176	heavy-metal-associated domain-containing protein, contains Pfam profile PF00403	Environmental Information Processing; Membrane Transport;
Arabidopsis thaliana ubiquitin-like protein (K5J14.10) mRNA, complete cds	At5g42300	AF370527	0.176	ubiquitin family protein, contains INTERPRO:IPR000626 ubiquitin domain	Genetic Information Processing; Folding, Sorting and Degradation; proteolysis?
At3g52100 Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15	At3g52100	AL049711	0.176	PHD finger family protein, contains Pfam profile PF00628, protein binding, zinc ion binding, regulation of transcription, DNA-dependent, endomembrane system	Genetic Information Processing; transcription
Arabidopsis thaliana chromosome 3 BAC T9J14 genomic sequence	Arabidopsis	AC009465	0.176		unknown
At1g27740 Genomic sequence for Arabidopsis thaliana BAC T22C5 from chromosome I	At1g27740	AC012375	0.177	basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	Genetic Information Processing; Transcription
At3g14600 Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MIE1	At3g14600	AB023038	0.177	60S ribosomal protein L18A	Genetic Information Processing; Translation
At4g10050 Arabidopsis thaliana DNA chromosome 4, BAC clone T5L19 (ESSA project)	At4g10050	AL049481	0.177	hydrolase, alpha/beta fold family protein, similar to protein phosphatase methylesterase-1 (Homo sapiens) GI:5533003; contains Pfam profile PF00561	Metabolism; other
At4g18670 Arabidopsis thaliana DNA chromosome 4, BAC clone F28A21 (ESSA project)	At4g18670	AL035526	0.177	leucine-rich repeat family protein / extensin family protein, PF00560	Metabolism; other
Arabidopsis thaliana chromosome I BAC F3N23 genomic sequence	Arabidopsis	AC008017	0.177		unknown
Sequence of BAC F5I14 from Arabidopsis thaliana chromosome 1	Sequence	AC001229	0.177		unknown
Sequence of BAC F7G19 from Arabidopsis thaliana chromosome 1	Sequence	AC000106	0.177		unknown
Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K18L3		AB012241	0.177		unknown
A.thaliana mRNA for LEA D113 type1 protein	A.thaliana	X91915	0.177	unknown	unknown
Arabidopsis thaliana mRNA for bZIP transcription factor (AtbZIP21 gene)	Arabidopsis	AC011438	0.178	bZIP TF	Genetic Information Processing; Transcription
At3g03080 Arabidopsis thaliana chromosome III BAC T17B22 genomic sequence	At3g03080	AC012328	0.178	NADP-dependent oxidoreductase, putative,	Metabolism; energy
Arabidopsis thaliana chromosome III BAC F13E7 genomic sequence	Arabidopsis	AC018363	0.178		unknown
At3g15040 Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:K15M2	At3g15040	AP000370	0.178	expressed	unknown
At5g08210 Arabidopsis thaliana DNA chromosome 5, BAC clone T22D6 (ESSA project)	At5g08210	AL357612	0.178	expressed	unknown

At3g12850 Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MBK21	At3g12850	AB024033	0.179	COP9 signalosome complex-related / CSN complex-related	Environmental Information Processing; Signal Transduction
At3g27360 Arabidopsis thaliana AT3g27360/K1G2_6 mRNA, complete cds	At3g27360	AY037250	0.179	histone H3, Pfam profile PF00125 Core histone H2A/H2B/H3/H4	Genetic Information Processing; Transcription
At5g59910 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MMN10	At5g59910	AB015475	0.179	histone H2B	Genetic Information Processing; Transcription
At5g11880 Arabidopsis thaliana AT5g11880/F14F18_50 mRNA, complete cds	At5g11880	AY049266	0.179	diaminopimelate decarboxylase, putative / DAP carboxylase, putative, similar to diaminopimelate decarboxylase (Arabidopsis thaliana) GI:6562332; contains Pfam profiles PF02784: Pyridoxal-dependent decarboxylase pyridoxal binding domain, PF00278: Pyridoxal-dependent decarboxylase C-terminal sheet domain	Metabolism; Amino Acid Metabolism; Lysine biosynthesis
At5g63180 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MDC12	At5g63180	AB008265	0.179	pectate lyase family protein	Metabolism; Carbohydrate Metabolism; Starch and sucrose metabolism
EST	EST	F15227	0.179		unknown
At3g57450 Arabidopsis thaliana DNA chromosome 3, BAC clone T8H10	At3g57450	AL133248	0.179	expressed	unknown
Sequence of BAC F13K23 from Arabidopsis thaliana chromosome 1	Sequence	AC012187	0.18		unknown
At2g17040 Arabidopsis thaliana chromosome II section 98 of 255 of the complete sequence. Sequence from clones F12A24, F6P23	At2g17040	AC002354	0.18	no apical meristem (NAM) family protein, contains Pfam PF02365	unknown
At3g60980 Arabidopsis thaliana DNA chromosome 3, BAC clone T27I15	At3g60980	AL358732	0.18	pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535:	unknown
At4g00410 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 1	At4g00410	AL161471	0.18	expressed	unknown
At4g20470 Arabidopsis thaliana DNA chromosome 4, BAC clone F9F13 (ESSA project)	At4g20470	AL080253	0.18	expressed	unknown
At3g29030 Arabidopsis thaliana expansin At-EXP5 (At-EXP5) mRNA, complete cds	At3g29030	U30478	0.181	expansin At-EXP5 (At-EXP5)	Metabolism; other
At5g40800 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MHK7	At5g40800	AB011477	0.181	expressed	unknown
At1g24510 Genomic sequence for Arabidopsis thaliana BAC F21J9 from chromosome I	At1g24510	AC000103	0.182	T-complex protein 1 epsilon subunit, putative / TCP-1-epsilon, putative / chaperonin, putative,Pfam:PF00118 domain	Genetic Information Processing; Folding, sorting, deg

At1g32540 Arabidopsis thaliana chromosome 1 BAC T9G5 genomic sequence	At1g32540	AC055769	0.182	zinc finger protein, putative, similar to zinc-finger protein Lsd1 (hits LOL1, Encodes a protein with 3 plant-specific zinc finger domains that acts as a positive regulator of cell death)	Genetic Information Processing; transcription
At1g32580 Arabidopsis thaliana chromosome 1 BAC T9G5 genomic sequence	At1g32580	AC055769	0.182	putative plastid developmental protein DAG, putative	unknown
At3g59660 Arabidopsis thaliana DNA chromosome 3, BAC clone T16L24	At3g59660	AL138659	0.183	C2 domain-containing protein / GRAM domain-containing protein	Environmental Information Processing; signal transduction
Arabidopsis thaliana ubiquitin-like protein (K5J14.10) mRNA, complete cds	At5g42300	AF370527	0.183	ubiquitin family protein, contains INTERPRO:IPR000626 ubiquitin domain	Genetic Information Processing; Folding, Sorting and Degradation; proteolysis?
At1g60800 Arabidopsis thaliana BAC F8A5	At1g60800	AC002292	0.183	leucine-rich repeat family protein / protein kinase family protein, contains Pfam domains PF00560	Metabolism; kinase
At4g04460 Arabidopsis thaliana AT4g04460/T26N6_7 mRNA, complete cds	At4g04460	AF372974	0.183	aspartyl protease family protein, contains Pfam profiles: PF00026 eukaryotic aspartyl protease, PF03489 surfactant protein B, PF05184 saposin-like type B, region 1	Metabolism; Peptidases
At3g04510 Arabidopsis thaliana chromosome III BAC T27C4 genomic sequence	At3g04510	AC022287	0.183	expressed	unknown
At1g69410 Arabidopsis thaliana At1g69410/F10D13.8 mRNA, complete cds	At1g69410	AC073178	0.184	eukaryotic translation initiation factor 5A, putative / eIF-5A, putative	Genetic Information Processing; Translation
At5g55340 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MTE17	At5g55340	AB015479	0.184	long-chain-alcohol O-fatty-acyltransferase family protein / wax synthase family protein	Metabolism; Lipid Metabolism
Arabidopsis thaliana chromosome II section 104 of 255 of the complete sequence. Sequence from clones T13L16	Arabidopsis	AC003952	0.184		unknown
Arabidopsis thaliana DNA chromosome 5, BAC clone T7H20 (ESSA project)		AL162508	0.184		unknown
At4g03600 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 9	At4g03600	AL161497	0.184	expressed	unknown
At4g29520 Arabidopsis thaliana DNA chromosome 4, BAC clone T16L4 (ESSA project)	At4g29520	AL079344	0.184	expressed	unknown
At4g17800 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 47	At4g17800	AL161547	0.185	DNA-binding protein-related	Genetic Information Processing; transcription
At1g57860 Arabidopsis thaliana chromosome 1 BAC F12K22 genomic sequence	At1g57860	AC079732	0.185	60S ribosomal protein L21	Genetic information processing; translation

At2g48080 Arabidopsis thaliana chromosome II section 255 of 255 of the complete sequence. Sequence from clones T9J23, F11L15, pAtT51	At2g48080	AC006072	0.185	oxidoreductase, 2OG-Fe(II) oxygenase family protein, contains Pfam domain PF03171	Metabolism; Energy Metabolism; Reductive carboxylate cycle
At1g67860 Arabidopsis thaliana chromosome 1 BAC T23K23 genomic sequence	At1g67860	AC012563	0.185	expressed	unknown
At1g80970 Arabidopsis thaliana chromosome 1 BAC F23A5 sequence	At1g80970	AC011713	0.185	XH domain-containing protein, contains Pfam profile: PF03469	unknown
At3g09030 Arabidopsis thaliana chromosome III P1 MZB10 genomic sequence	At3g09030	AC009326	0.186	potassium channel tetramerisation domain-containing protein	Cellular Processes and Signaling; Receptors
At1g16690 Arabidopsis thaliana chromosome I BAC F19K19 genomic sequence	At1g16690	AC011808	0.186	transcription factor-related, similar to enhancer of polycomb (GI:11907923)(Homo sapiens) , transcription factor activity, regulation of transcription	Genetic Information Processing; Transcription
At2g19680 Arabidopsis thaliana copia-like retroelement pol polyprotein (At2g19680; F6F22.29) mRNA, complete cds	At2g19680	AF370542	0.186	mitochondrial ATP synthase g subunit family protein	Metabolism; Energy Metabolism; Oxidative phosphorylation
At3g17750 Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MIG5	At3g17750	AB026646	0.186	protein kinase family protein, contains Pfam profile: PF00069	Metabolism; kinase
Arabidopsis thaliana DNA chromosome 4, BAC clone T22F8 (ESSA project)		AL050351	0.186		unknown
At3g46630 Arabidopsis thaliana DNA chromosome 3, BAC clone F12A12	At3g46630	AL133314	0.186	expressed protein, contains similarity to defective chloroplasts and leaves protein - chloroplast development	unknown
At3g14415 Arabidopsis thaliana glycolate oxidase mRNA, partial cds	At3g14415	AB028617	0.187	(S)-2-hydroxy-acid oxidase, peroxisomal, putative / glycolate oxidase, putative / short chain alpha-hydroxy acid oxidase, putative	Metabolism; Carbohydrate Metabolism; Glyoxylate and dicarboxylate
At4g38210 Arabidopsis thaliana DNA chromosome 4, BAC clone F20D10 (ESSA project)	At4g38210	AL035538	0.187	EXPA20, alpha-expansin 3, alpha-expansin gene family, PMID:11641069	Metabolism; other
At1g80310 Arabidopsis thaliana chromosome 1 BAC F5I6 genomic sequence	At1g80310	AC018848	0.187	expressed	unknown

At1g44575 Arabidopsis thaliana PsbS protein (PsbS) mRNA, complete cds	At1g44575	AC084807	0.188	photosystem II 22kDa protein, chloroplast / CP22 (PSBS), (NPQ4, Encoding PSII-S (CP22), a ubiquitous pigment-binding protein associated with photosystem II (PSII) of higher plants. Involved in nonphotochemical quenching rather than in photosynthesis. Mutant has a normal violaxanthin cycle but has a limited capacity of quenching singlet excited chlorophylls and is tolerant to lipid peroxidation.)	Metabolism; energy; photosynthesis
At3g25160 Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MJL12	At3g25160	AB026647	0.188	ER lumen protein retaining receptor family protein, PF00810	unknown
At3g60200 Arabidopsis thaliana DNA chromosome 3, BAC clone T2O9	At3g60200	AL138658	0.188	expressed	unknown
At1g57680 Arabidopsis thaliana chromosome 1 BAC T8L23 genomic sequence	At1g57680	AC079730	0.189	expressed	unknown
At2g32690 Arabidopsis thaliana chromosome II section 183 of 255 of the complete sequence. Sequence from clones T26B15, F24L7	At2g32690	AC003974	0.189	pseudogene, glycine-rich protein	unknown
At4g30700 Arabidopsis thaliana mRNA for DYW9 protein, partial	At4g30700	AL109787	0.189	pentatricopeptide (PPR) repeat-containing protein	unknown
At1g15100 Arabidopsis thaliana RING-H2 finger protein RHA2a mRNA, complete cds	At1g15100	AF078822	0.19	zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger) , RING-H2 finger protein RHA2a mRNA, complete cds , protein binding, zinc ion binding, endomembrane system	Genetic Information Processing; Transcription
At3g51830 Arabidopsis thaliana putative transmembrane protein G5p (AtG5) mRNA, complete cds	At3g51830	U72504	0.19	putative transmembrane protein G5p (AtG5), phosphoinositide phosphatase family protein, PF02383: SacI homology domain	Metabolism; other
Arabidopsis thaliana chromosome 1 BAC T24P22 genomic sequence	Arabidopsis	AC084242	0.19		unknown
Arabidopsis thaliana ubiquitin-like protein (K5J14.10) mRNA, complete cds	At5g42300	AF370527	0.192	ubiquitin family protein, contains INTERPRO:IPR000626 ubiquitin domain	Genetic Information Processing; Folding, Sorting and Degradation; proteolysis?
At1g16910 Arabidopsis thaliana chromosome I BAC F6I1 genomic sequence	At1g16910	AC051629	0.192	expressed protein, contains Pfam profile PF04852: Protein of unknown function (DUF640)	unknown

At1g76590 Arabidopsis thaliana chromosome 1 BAC F14G6 genomic sequence	At1g76590	AC015450	0.193	zinc-binding family protein, PF04640 : Protein of unknown function, DUF597	Genetic Information Processing; transcription
At4g20460 Arabidopsis thaliana DNA chromosome 4, BAC clone F9F13 (ESSA project)	At4g20460	AL080253	0.193	NAD-dependent epimerase/dehydratase family protein	Metabolism; Carbohydrate Metabolism
Arabidopsis thaliana DNA chromosome 3, BAC clone T8M16		AL390921	0.193		unknown
At4g25800 Arabidopsis thaliana DNA chromosome 4, BAC clone F14M19 (ESSA project)	At4g25800	AL049480	0.194	calmodulin-binding protein	Environmental Information Processing; signal transduction
Arabidopsis thaliana chromosome 1 BAC T24D18 sequence	Arabidopsis	AC010924	0.194		unknown
A.thaliana mRNA for RAP-1 protein	At1g23640	X99548	0.195	Encodes a 68 kD MYC-related transcriptional activator with a typical DNA binding domain of a basic region helix-loop-helix leucine zipper motif. Its transcription is induced by dehydration stress and ABA treatment and precedes the induction of rd22, whose expression ATMYC2 can activate. Negative regulator of blue light–mediated photomorphogenic growth and blue and far-red-light–regulated gene expression. Positive regulator of lateral root formation. Interacts with the Z- and G-box light-responsive elements of minimal light–regulated promoters.	Genetic Information Processing; Transcription
At3g46620 Arabidopsis thaliana DNA chromosome 3, BAC clone F12A12	At3g46620	AL133314	0.195	zinc finger (C3HC4-type RING finger) family protein, contains Pfam domain, PF00097	Genetic Information Processing; transcription
At3g63210 Arabidopsis thaliana DNA chromosome 3, BAC clone F16M2	At3g63210	AL138648	0.195	MARD1, encodes a novel zinc-finger protein with a proline-rich N-terminus, identical to senescence-associated protein SAG102 , PF04570: Protein of unknown function (DUF581)	Genetic Information Processing; transcription
Arabidopsis thaliana mRNA for sterile apetala	Arabidopsis	AJ223125	0.195		unknown
At1g31240 Arabidopsis thaliana chromosome 1 BAC F28K20 sequence	At1g31240	AC007654	0.195	expressed	unknown
At2g32130 Arabidopsis thaliana chromosome II section 180 of 255 of the complete sequence. Sequence from clones F20M17, F22D22	At2g32130	AC006223	0.195	expressed	unknown

At2g40210 Arabidopsis thaliana ABA-regulated gene cluster, complete sequence	At2g40210	AF085279	0.196	MADS-box family protein, contains Pfam profile: PF00319 SRF-type transcription factor (DNA-binding and dimerisation domain)	Genetic Information Processing; transcription	
At3g46130 Arabidopsis thaliana putative transcription factor (MYB48) mRNA, complete cds	At3g46130	AL355775	0.196	myb family transcription factor	Genetic Information Processing; transcription	
At3g13784 Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:MMM17	At3g13784	AP001307	0.196	beta-fructosidase, putative / beta-fructofuranosidase, putative / cell wall invertase, putative	Metabolism; Carbohydrate Metabolism; Fructose and mannose	
At4g15150 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40	At4g15150	AL161540	0.196	glycine-rich protein	unknown	
At5g56330 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MCD7	At5g56330	AB009049	0.197	carbonic anhydrase family protein	Metabolism; Energy Metabolism; Nitrogen metabolism	
At1g28290 Arabidopsis thaliana chromosome I BAC F3H9 genomic sequence	At1g28290	AC021044	0.197	pollen Ole e 1 allergen and extensin family protein	Metabolism; other	
Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MDC12		AB008265	0.197		unknown	
At5g67040 Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K8A10	At5g67040	AB026640	0.197	expressed	unknown	
Arabidopsis thaliana heat shock protein 70 (Hsc70-7) mRNA, complete cds; nuclear gene for chloroplas	At5g49910	AF217459	0.198	heat shock protein 70 / HSP70 (HSC70-7), identical to heat shock protein 70 (Arabidopsis thaliana) GI:6746592 , plastid stroma, ATP binding, protein folding CPHSC70-2	Genetic Information Processing; Folding, Sorting and Degradation	Environmental Information Processing; Signal Transduction
Arabidopsis thaliana mRNA for HMG gamma protein	At2g15760	AF370150	0.198	Encodes a protein belonging to the subgroup of HMGB (high mobility group B) proteins that have a distinctive DNA-binding motif, the HMG-box domain. The motif confers non-sequence specific interaction with linear DNA and structure-specific binding to distorted DNA sites. The HMGB proteins are involved in the assembly of nucleoprotein complexes. Can be phosphorylated by CK2alpha. transcription factor activity	Genetic Information Processing; Transcription	
Arabidopsis thaliana vacuolar ATP synthase subunit C (DET3) mRNA, complete cds		AF208261	0.198		Metabolism; Energy Metabolism; Oxidative phosphorylation	

At1g14720 Arabidopsis thaliana EXGT-A2 mRNA for endoxyloglucan transferase related protein, complete cds	At1g14720	AF385714	0.198	xyloglucan:xyloglucosyl transferase / xyloglucan endotransglycosylase / endo-xyloglucan transferase (XTR2), identical to endoxyloglucan transferase (Arabidopsis thaliana), member of Glycoside Hydrolase Family 16 , hydrolase activity, acting on glycosyl bonds, carbohydrate metabolism, endomembrane system	Metabolism; Other enzymes	
At1g26760 Genomic sequence for Arabidopsis thaliana BAC T24P13 from chromosome I	At1g26760	AC006535	0.198	SET domain-containing protein, contains Pfam profiles PF00856: SET domain, PF00515: tetratricopeptide repeat (TPR) domain	unknown	
At2g39950 Arabidopsis thaliana chromosome II section 215 of 255 of the complete sequence. Sequence from clones T5I7, T28M21, F27I1	At2g39950	AF002109	0.198	expressed	unknown	
At3g63160 Arabidopsis thaliana DNA chromosome 3, BAC clone F16M2	At3g63160	BE039458	0.198	expressed	unknown	
Arabidopsis thaliana immunophilin (FKBP12) mRNA, complete cds	At5g64350	U96924	0.199	FK506 binding, peptidyl-prolyl cis-trans isomerase activity, protein folding	Genetic Information Processing; Folding, Sorting and Degradation;	
At5g58420 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MQJ2	At5g58420	AB025632	0.199	40S ribosomal protein S4 (RPS4D),	Genetic Information processing; translation	
Arabidopsis thaliana genomic DNA, chromosome 3, BAC clone: T23B7		AC069473	0.199		unknown	
At3g47490 Arabidopsis thaliana DNA chromosome 3, BAC clone F1P2	At3g47490	AL132955	0.2	HNH endonuclease domain-containing protein	Genetic Information Processing; Replication and Repair;	
At1g51220 Arabidopsis thaliana chromosome I BAC F11M15 genomic sequence	At1g51220	AC006085	0.2	zinc finger (C2H2 type) protein (WIP5),Pfam domain, PF00096	Genetic Information Processing; Transcription	
At1g62080 A.thaliana mRNA for unknown protein (clone YAP007)	At1g62080	X91953	0.2	expressed	unknown	
At5g29771 Arabidopsis thaliana putative ribosomal protein S1 (F19I11_30/AT5g30510) mRNA, complete cds	At5g29771	AF370232	0.201	ribosomal protein S1 (obsolete)	Genetic Information processing; translation	
At1g62840 Genomic sequence for Arabidopsis thaliana BAC F23N19 from chromosome I	At1g62840	AC007190	0.201	expressed	unknown	
At5g49910 Arabidopsis thaliana heat shock protein 70 (Hsc70-7) mRNA, complete cds; nuclear gene for chloroplast product	At5g49910	AF217459	0.202	heat shock protein 70 (Hsc70-7), heat shock protein 70 / HSP70 (HSC70-7), chloro	Genetic Information Processing; Folding, Sorting and Degradation	Environmental Information Processing; Signal Transduction
Arabidopsis thaliana mRNA for ZIM, complete cds		AB035310	0.202	ZIM, TF	Genetic Information Processing; Transcription; Other transcription	

Arabidopsis thaliana chromosome II section 122 of 255 of the complete sequence. Sequence from clones F7O24, F3K23, F2G1		AC006841	0.202		unknown
At1g03370 Arabidopsis thaliana chromosome 1 BAC F15K9 sequence	At1g03370	AC005278	0.203	C2 domain-containing protein / GRAM domain-containing protein, contains Pfam profiles PF00168: C2 domain; contains PF02893: GRAM domain; similar to Chain A, Crystal Structure Of Synaptotagmin Iii C2aC2B Length	Environmental Information Processing; signal transduction
At5g46760 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MZA15	At5g46760	AB016882	0.203	basic helix-loop-helix (bHLH) family protein	Genetic Information and Processing; transcription
Arabidopsis thaliana ubiquitin-like protein (K5J14.10) mRNA, complete cds	At5g42300	AF370527	0.203	ubiquitin family protein, contains INTERPRO:IPR000626 ubiquitin domain	Genetic Information Processing; Folding, Sorting and Degradation; proteolysis?
At1g68460 Arabidopsis thaliana AtIPT1 mRNA for cytokinin synthase, complete cds	At1g68460	AB061400	0.203	adenylate isopentenyltransferase 1 / cytokinin synthase (IPT1), Encodes a putative adenylate isopentenyltransferase which catalyzes the formation of isopentenyladenosine 5'-monophosphate (iPMP) from AMP and dimethylallylpyrophosphate (DMAPP). Involved in cytokinin biosynthesis	Metabolism; other molecules
At4g28150 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68	At4g28150	AL161572	0.203	expressed	unknown
At1g47270 Arabidopsis thaliana chromosome 1 BAC F8G22 genomic sequence	At1g47270	AC079677	0.204	F-box family protein / tubby family protein, contains Pfam profiles: PF00646 F-box domain, PF01167 Tub family	unknown
At4g18780 Arabidopsis thaliana cellulose synthase catalytic subunit (IRX1) mRNA, complete cds	At4g18780	AF267742	0.205	CESA8, cellulose synthase, catalytic subunit (IRX1–irregular xylem1), member of Cellulose Synthase; AtCesA	Metabolism; Carbohydrate Metabolism; Starch and sucrose metabolism
Arabidopsis thaliana ubiquitin-like protein (K5J14.10) mRNA, complete cds	At5g42300	AF370527	0.206	ubiquitin family protein, contains INTERPRO:IPR000626 ubiquitin domain	Genetic Information Processing; Folding, Sorting and Degradation; proteolysis?
At3g60580 Arabidopsis thaliana DNA chromosome 3, BAC clone T8B10	At3g60580	AL138646	0.206	zinc finger (C2H2 type) family protein, contains Pfam domain, PF00096	Genetic Information Processing; transcription
At2g13290 Arabidopsis thaliana chromosome II section 73 of 255 of the complete sequence. Sequence from clones T17A11, F15O11	At2g13290	AC006446	0.206	glycosyl transferase family 17 protein, PF04724	Metabolism; Glycan Biosynthesis and Metabolism; N-Glycan

At1g11740 Arabidopsis thaliana chromosome 1 BAC F25C20 sequence	At1g11740	AC007296	0.208	ankyrin repeat family protein, contains ankyrin repeats, Pfam domain PF00023	Genetic Information Processing; Transcription
At5g63620 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MBK5	At5g63620	AB005234	0.208	oxidoreductase, zinc-binding dehydrogenase family protein	Metabolism; Energy Metabolism; Reductive carboxylate cycle
At3g54980 Arabidopsis thaliana DNA chromosome 3, BAC clone F28P10	At3g54980	AL049655	0.208	pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535	unknown
At5g67070 Arabidopsis thaliana unknown protein (K21H1.3/AT5g67070) mRNA, complete cds	At5g67070	AF370212	0.208	rapid alkalinization factor (RALF) family protein	unknown
Arabidopsis thaliana chromosome 1 BAC T16O9 genomic sequence	Arabidopsis	AC027035	0.209		unknown
At3g09450 Arabidopsis thaliana chromosome III BAC F3L24 genomic sequence	At3g09450	AC011436	0.209	expressed	unknown
At3g53490 Arabidopsis thaliana DNA chromosome 3, BAC clone F4P12	At3g53490	AL132966	0.21	expressed protein, ADAM 13, Xenopus laevis, protease, developmental?	Metabolism; peptide
At2g41730 Arabidopsis thaliana chromosome II section 226 of 255 of the complete sequence. Sequence from clones T32G6, T11A7	At2g41730	AC002339	0.21	expressed	unknown
At4g18810 Arabidopsis thaliana DNA chromosome 4, BAC clone F28A21 (ESSA project)	At4g18810	AL035526	0.211	expressed protein, similar to UV-B and ozone similarly regulated protein 1 UOS1	unknown
At2g22330 Arabidopsis thaliana chromosome II section 127 of 255 of the complete sequence. Sequence from clones F14M13	At2g22330	AC006592	0.212	cytochrome P450, putative	Metabolism; Cytochrome P450
At5g01090 Arabidopsis thaliana DNA chromosome 5, BAC clone F7J8 (ESSA project)	At5g01090	AL137189	0.213	lectin family protein, contains Pfam domain, PF00139: Legume lectins beta domain	Cellular Processes and Signaling; CAM ligands
At5g50120 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MPF21	At5g50120	AB026650	0.213	transducin family protein / WD-40 repeat family protein, Similar to En/Spm-like transposon protein (gi:2739374)(Arabidopsis thaliana); similar to GTP-binding regulatory protein and WD-repeat protein; contains 7 WD-40 repeats	Metabolism; Peptidases
EST	EST	F15400	0.213		unknown
At1g03475 Arabidopsis thaliana LIN2 mRNA for coproporphyrinogen III oxidase, complete cds	At1g03475	AB044394	0.214	Encodes a protein (AtCPO-I) with coproporphyrinogen III oxidase activity. plastid, coproporphyrinogen oxidase activity, porphyrin biosynthesis	Metabolism; Metabolism of Cofactors and Vitamins; Porphyrin
Arabidopsis thaliana chromosome I BAC T13M11 genomic sequence	Arabidopsis	AC005882	0.214		unknown
Arabidopsis thaliana DNA chromosome 4, BAC clone T5K18 (ESSA project)		AL022580	0.214		unknown

At1g74510 Arabidopsis thaliana chromosome 1 BAC F1M20 genomic sequence	At1g74510	AC011765	0.214	kelch repeat-containing F-box family protein, contains Pfam:PF01344 Kelch motif, Pfam:PF00646 F-box domain	unknown		
At3g27200 Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:K17E12	At3g27200	AP000381	0.215	plastocyanin-like domain-containing protein	Metabolism; Energy Metabolism; Photosynthesis		
At1g69700 Arabidopsis thaliana AtHVA22c mRNA, complete cds	At1g69700	AF141661	0.215	ABA-responsive protein (HVA22c),	unknown		
At1g59675 Genomic sequence for Arabidopsis thaliana BAC T30E16 from chromosome I	At1g59675	AC009317	0.216	F-box family protein, similar to SKP1 interacting partner 2 (SKIP2)	Genetic Information Processing; Folding, Sorting and Degradation	Environmental Information Processing; Signal Transduction	Cellular Processes; Cell Growth and Death; Cell cycle
At3g12630 Arabidopsis thaliana chromosome 3 BAC T2E22 genomic sequence	At3g12630	AC069474	0.218	zinc finger (AN1-like) family protein, contains Pfam domain, PF01428	Genetic Information Processing; Transcription		
At3g49160 Arabidopsis thaliana DNA chromosome 3, BAC clone F2K15	At3g49160	AL132956	0.218	pyruvate kinase family protein	Metabolism; Carbohydrate Metabolism; Pyruvate metabolism		
EST	EST	AF067462	0.218		unknown		
At3g28550 Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MZN14	At3g28550	AP000420	0.219	proline-rich extensin-like family protein	Metabolism; other		
Arabidopsis thaliana chromosome III BAC F24P17 genomic sequence	Arabidopsis	AC011623	0.219		unknown		
Arabidopsis thaliana chromosome II section 10 of 255 of the complete sequence. Sequence from clones T16F16, T8K22		AC004136	0.219		unknown		
At2g05380 Arabidopsis thaliana At2g05380/F16J10.7 mRNA, complete cds	At2g05380	AY049267	0.219	glycine-rich protein (GRP3S),	unknown		
At4g38130 Arabidopsis thaliana histone deacetylase mRNA, complete cds	At4g38130	AF014824	0.22	histone deacetylase (HD1, RPD3A), encodes a protein whose sequence is similar to histone deacetylases in other organisms.	Genetic Information Processing; Transcription		
At1g07240 Arabidopsis thaliana putative flavonol 3-o-glucosyltransferase protein (F10K1.5) mRNA, complete cds	At1g07240	AC067971	0.22	UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase, cellular component unknown, UDP-glycosyltransferase activity, metabolism, transferase activity, transferring glycosyl groups	Metabolism; carbohydrate; glycosytransferase		
At1g48870 Arabidopsis thaliana chromosome 1 BAC F27K7 genomic sequence	At1g48870	AC084414	0.22	WD-40 repeat family protein	Metabolism; Peptidases		
At1g59500 Genomic sequence for Arabidopsis thaliana BAC T30E16 from chromosome I	At1g59500	AC009317	0.221	IAA-amido synthase that conjugates Asp and other amino acids to auxin in vitro	Metabolism; other; auxin		

At5g51680 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MIO24	At5g51680	AB010074	0.222	hydroxyproline-rich glycoprotein family protein	Environmental Information Processing; Signaling Molecules	Cellular Processes and Signaling; CD molecules
At3g02760 Arabidopsis thaliana chromosome III BAC F13E7 genomic sequence	At3g02760	AC018363	0.222	histidyl-tRNA synthetase, putative / histidine–tRNA ligase, putative, Pfam profiles PF00587: tRNA synthetase class II core domain (G, H, P, S and T), PF03129: Anticodon binding domain	Genetic Information Processing; Translation; Aminoacyl-tRNA	Metabolism; Amino Acid Metabolism; Histidine metabolism
At5g04630 Arabidopsis thaliana DNA chromosome 5, BAC clone T32M21 (ESSA project)	At5g04630	AL162875	0.222	cytochrome P450, putative, cytochrome P450 77A3p, Glycine max, PIR:T05948, member of CYP77A, electron transport, oxygen binding, endomembrane system	Metabolism; Cytochrome P450	
At1g26240 Arabidopsis thaliana chromosome 1 BAC F28B23 genomic sequence	At1g26240	AC079829	0.222	proline-rich extensin-like family protein	Metabolism; other	
At1g06980 Sequence of BAC F10K1 from Arabidopsis thaliana chromosome 1	At1g06980	AC067971	0.222	expressed protein, similar to hypothetical protein GI:2347189 from (Arabidopsis thaliana) , endomembrane	unknown	
At1g31130 Arabidopsis thaliana unknown protein (F28K20.6) mRNA, complete cds	At1g31130	AC004793	0.223	expressed	unknown	
Arabidopsis thaliana photolyase/blue light photoreceptor PHR2 (PHR2) mRNA, complete cds	At2g47590	AC002535	0.225	photolyase/blue light photoreceptor (PHR2), identical to photolyase/blue light photoreceptor PHR2 (Arabidopsis thaliana) GI:3319288; contains Pfam domain, PF00875: deoxyribodipyrimidine photolyase , DNA repair	Genetic Information Processing; Replication and Repair;	
Arabidopsis thaliana DNA chromosome 4, BAC clone F25G13, partial sequence (ESSA project)		AL079349	0.225		unknown	
At1g62350 Genomic sequence for Arabidopsis thaliana BAC F24O1 from chromosome I	At1g62350	AC003113	0.225	pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat	unknown	
Arabidopsis thaliana putative leucine rich protein (F7H2.8) mRNA, complete cds	At1g15740	AF360339	0.226	leucine rich protein	Cellular Processes and Signaling; Signal transduction	
At3g46230 Arabidopsis thaliana DNA chromosome 3, BAC clone F12M12	At3g46230	X17293	0.226	heat shock protein (HSP17.4-CI),17.4 kDa class I	Genetic Information Processing; Folding, Sorting and Degradation	Environmental Information Processing; Signal Transduction
Arabidopsis thaliana sterol delta-7 reductase (ST7R) mRNA, complete cds		U49398	0.226		Metabolism; Lipid Metabolism; Biosynthesis of steroids	
At1g69900 Arabidopsis thaliana chromosome 1 BAC T17F3 genomic sequence	At1g69900	AC010675	0.226	expressed	unknown	

At1g24130 Arabidopsis thaliana chromosome I BAC F3I6 genomic sequence	At1g24130	AC002396	0.227	transducin family protein / WD-40 repeat family protein, contains 7 WD-40 repeats (PF00400);	Environmental Information Processing; Signal Transduction		
At5g43940 A.thaliana mRNA for Class III ADH	At5g43940	X82647	0.227	alcohol dehydrogenase class III / glutathione-dependent formaldehyde dehydrogenase	Metabolism; Carbohydrate Metabolism; Glycolysis	Metabolism; Lipid Metabolism; Fatty acid metabolism	
At5g13780 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MXE10	At5g13780	AB011484	0.228	GCN5-related N-acetyltransferase, putative, similar to SP|P07347 N-terminal acetyltransferase complex ARD1 subunit (Arrest-defective protein 1) {Saccharomyces cerevisiae}; contains Pfam profile PF00583: acetyltransferase, GNAT family	Metabolism; lipid		
At3g52130 Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15	At3g52130	AL049711	0.228	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein, PF00234	Metabolism; Peptidases	Metabolism; lipid	Genetic Information Processing; Folding, Sorting and Degradation
At5g05950 Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K18J17	At5g05950	AB017060	0.229	expressed	unknown		
At3g51030 A.thaliana mRNA for thioredoxin H	At3g51030	Z14084	0.23	thioredoxin H-type 1 (TRX-H-1), -electron transport, cytochrome assembly	Genetic Information Processing; Folding, Sorting and Degradation		
At5g16960 Arabidopsis thaliana DNA chromosome 5, BAC clone F2K13 (ESSA project)	At5g16960	AL391141	0.23	NADP-dependent oxidoreductase, putative, similar to probable NADP-dependent oxidoreductase (zeta-crystallin homolog) P1 (SP|Q39172)(gi:886428) and P2 (SP|Q39173)(gi:886430), Arabidopsis thaliana	Metabolism; energy		
At4g04770 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13	At4g04770	AL161501	0.231	ABC 1, ATP-binding-cassette transporter, an iron-estimulated ATPase. A member of the NAP subfamily of ABC transporters. Involved in Fe-S cluster assembly. Similar to SufB. Involved in the regulation of iron homeostasis. Able to form homedimers. Intyeracts with AtNAP7 inside the chloroplast.	Cellular Processes and Signaling; Transporters	Environmental Information Processing; Membrane Transport	
At2g27590 Arabidopsis thaliana chromosome II section 156 of 255 of the complete sequence. Sequence from clones F15K20, T1E2	At2g27590	AC005824	0.231	expressed protein	unknown		
At3g54780 Arabidopsis thaliana DNA chromosome 3, BAC clone T5N23	At3g54780	AL138650	0.232	zinc finger (C3HC4-type RING finger) family protein	Genetic Information Processing; transcription		

At3g51190 Arabidopsis thaliana DNA chromosome 3, BAC clone F24M12	At3g51190	AL132980	0.232	60S ribosomal protein L8 (RPL8B), ribosomal protein L8, cytosolic	Genetic Information Processing; Translation		
At4g37900 Arabidopsis thaliana DNA chromosome 4, BAC clone F20D10 (ESSA project)	At4g37900	AL035538	0.232	glycine-rich protein	unknown		
At5g05840 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MJJ3	At5g05840	AB005237	0.232	expressed	unknown		
At1g79620 Genomic sequence for Arabidopsis thaliana BAC F20B17 from chromosome I	At1g79620	AC010793	0.233	leucine-rich repeat transmembrane protein kinase	Metabolism; kinase	Environmental Information Processing; Signal Transduction	
At1g43930 Genomic sequence for Arabidopsis thaliana BAC F9C16 from chromosome I	At1g43930	AC022314	0.233	Mutator-like transposase family, has a 1.2e-56 P-value blast match to GB:AAA21566 mudrA of transposon="MuDR" (MuDr-element) (Zea mays)	unknown	TRANSPOSON	
At3g15640 Arabidopsis thaliana AT3g15640/MSJ11_4 mRNA, complete cds	At3g15640	AF367258	0.234	cytochrome c oxidase family protein, contains Pfam domain, PF01215: Cytochrome c oxidase subunit Vb	Metabolism; energy		
Arabidopsis thaliana ubiquitin-like protein (K5J14.10) mRNA, complete cds	At5g42300	AF370527	0.235	ubiquitin family protein, contains INTERPRO:IPR000626 ubiquitin domain	Genetic Information Processing; Folding, Sorting and Degradation; proteolysis?		
At2g26200 Arabidopsis thaliana chromosome II section 147 of 255 of the complete sequence. Sequence from clones T19L18, T1D16, T9J22	At2g26200	AC004484	0.235	expressed	unknown		
At5g39220 Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K3K3	At5g39220	AB010694	0.236	hydrolase, alpha/beta fold family protein, contains Pfam profile: PF00561 alpha/beta hydrolase fold	Metabolism; other		
At3g22540 Arabidopsis thaliana genomic DNA, chromosome 3, BAC clone:F16J14	At3g22540	AP000731	0.236	expressed	unknown		
At3g63150 Arabidopsis thaliana DNA chromosome 3, BAC clone T20O10	At3g63150	AL163816	0.237	GTP-binding protein-related, PF00036: EF hand (domain)	Cellular Processes and Signaling; GTP-binding		
At5g09900 Arabidopsis thaliana putative 26S proteasome p55 protein (MYH9.11/AT5g09900) mRNA, complete cds	At5g09900	AY034908	0.237	26S proteasome regulatory subunit, putative (RPN5), p55 protein-like	Metabolism; Peptidases		
EST	EST	AV540446	0.238	unk	unknown		
At2g06040 Arabidopsis thaliana chromosome II section 33 of 255 of the complete sequence. Sequence from clones T6P5, F5K7	At2g06040	AC006413	0.238	expressed	unknown		
At5g59050 Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K18B18	At5g59050	AB024027	0.238	expressed	unknown		
At5g64080 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MHJ24	At5g64080	AB008266	0.239	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein, PF00234	Metabolism; Peptidases	Metabolism; lipid	Genetic Information Processing; Folding, Sorting and Degradation

At1g44890 Sequence of BAC T12C22 from Arabidopsis thaliana chromosome 1	At1g44890	AC020576	0.239	expressed	unknown		
At1g26880 Arabidopsis thaliana chromosome I BAC T2P11 genomic sequence	At1g26880	AC005508	0.24	60S ribosomal protein L34	Genetic Information Processing; Translation; Ribosome		
EST, Moderately similar to T10540 hypothetical protein F3I3.20 - Arabidopsis thaliana [A.thaliana]	At4g01000	AV535472	0.241	ubiquitin family protein, low similarity to SP|P13117 Ubiquitin. {Neurospora crassa}; contains Pfam profile PF00240: Ubiquitin family	Genetic Information Processing; Folding, Sorting and Degradation; proteolysis?		
At3g43850 Arabidopsis thaliana DNA chromosome 3, BAC clone T28A8	At3g43850	AL162691	0.242	hypothetical protein, similar to MTD1, NAD-dependent 5,10-methylenetetrahydrafolate dehydrogenase	Metabolism; other		
At2g46940 Arabidopsis thaliana chromosome II section 250 of 255 of the complete sequence. Sequence from clones F19D11, F14M4, T3D7	At2g46940	AC004411	0.242	expressed	unknown		
Arabidopsis thaliana AT5g04590 (AT5g04590/T32M21_190) mRNA, complete cds	AT5g04590	AF325027	0.243	sulfite reductase / ferredoxin (SIR), identical, electron transport, sulfite reductase (ferredoxin) activity	Metabolism; Energy Metabolism; Sulfur metabolism		
At1g31350 Genomic sequence for Arabidopsis thaliana BAC T19E23 from chromosome I	At1g31350	AC007654	0.244	F-box family protein, similar to SKP1 interacting partner 2 (SKIP2)	Genetic Information Processing; Folding, Sorting and Degradation	Environmental Information Processing; Signal Transduction	Cellular Processes; Cell Growth and Death; Cell cycle
Arabidopsis thaliana ubiquitin-like protein (K5J14.10) mRNA, complete cds	At5g42300	AF370527	0.244	ubiquitin family protein, contains INTERPRO:IPR000626 ubiquitin domain	Genetic Information Processing; Folding, Sorting and Degradation; proteolysis?		
At1g20330 Arabidopsis thaliana putative 24-sterol C-methyltransferase (F14O10.7) mRNA, complete cds	At1g20330	AY046042	0.244	S-adenosyl-methionine-sterol-C-methyltransferase	Metabolism; other; sterol		
Arabidopsis thaliana chromosome 3 BAC F24K9 genomic sequence	Arabidopsis	AC008153	0.244	unk	unknown		
Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MNJ7		AB025628	0.245	unk	unknown		
At1g07610 Arabidopsis thaliana Columbia ecotype metallothionein (MT1c) gene, complete cds	At1g07610	U11255	0.246	metallothionein-like protein 1C (MT-1C), identical to Metallothionein-like protein 1C (MT-1C). (SP:Q38804) (Arabidopsis thaliana), copper ion binding, response to copper ion, root, leaf, seedling growth	Cellular Processes and Signaling; Inorganic ion trasport		
Arabidopsis thaliana unknown protein (F20N2.22) mRNA, complete cds	At1g55780	AY035010	0.246	heavy-metal-associated domain-containing protein, contains Pfam profile PF00403: Heavy-metal-associated domain , metal ion transport, metal ion binding	Environmental Information Processing; Membrane Transport;		
At3g43430 Arabidopsis thaliana DNA chromosome 3, BAC clone T5C2	At3g43430	AL138664	0.246	zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097	Genetic Information Processing; transcription		

At2g13660 Arabidopsis thaliana chromosome II section 77 of 255 of the complete sequence. Sequence from clones F13J11, F17L24	At2g13660	AC006436	0.246	AGT1 encodes peroxisomal alanine : glyoxylate aminotransferase. It is involved in photorespiration. serine-glyoxylate aminotransferase-related	Metabolism; amino acid	
At4g22560 Arabidopsis thaliana DNA chromosome 4, BAC clone F7K2 (ESSA project)	At4g22560	AL033545	0.246	expressed	unknown	
At2g27810 Arabidopsis thaliana chromosome II section 156 of 255 of the complete sequence. Sequence from clones F15K20, T1E2	At2g27810	AC005824	0.247	xanthine/uracil permease family protein, contains Pfam profile: PF00860	Cellular Processes and Signaling; Transporters	
At4g11680 Arabidopsis thaliana DNA chromosome 4, BAC clone T5C23 (ESSA project)	At4g11680	AL049500	0.248	zinc finger (C3HC4-type RING finger) family protein, PF00097	Genetic Information Processing; transcription	
At1g60200 Arabidopsis thaliana chromosome 1 BAC T13D8	At1g60200	AC004473	0.248	splicing factor PWI domain-containing protein / RNA recognition motif (RRM)-containing protein	Genetic information processing; translation	
At1g71490 Arabidopsis thaliana chromosome 1 BAC F26A9 genomic sequence	At1g71490	AC016163	0.249	pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535	unknown	
At1g06400 Arabidopsis thaliana mRNA for small GTP-binding protein (ara-2), complete cds	At1g06400	D01024	0.251	mRNA for small GTP-binding protein (ara-2), complete cds , Ras-related GTP-binding protein (ARA-2), exosome (RNase complex), intracellular, GTP binding, intracellular protein transport, protein transport, small GTPase mediated signal transduction	Environmental Information Processing; Signal Transduction	Cellular Processes and Signaling; transport
At1g80920 Arabidopsis thaliana putative J8 protein (F23A5.28) mRNA, complete cds	At1g80920	AY040017	0.251	J8 mRNA, nuclear gene encoding plastid protein, PF00226, unknown function, DNAJ heat shock N-terminal domain-containing protein, similar to SP|Q05646 Chaperone protein dnaJ Erysipelothrix rhusiopathiae, SP|P45555 Chaperone protein dnaJ (HSP40) Staphylococcus aureus; contains Pfam profile PF00226 DnaJ domain	Genetic Information Processing; Folding, Sorting and Degradation;	
Arabidopsis thaliana chromosome 1 BAC F3I17 genomic sequence	Arabidopsis	AC016162	0.251		unknown	
At4g38340 Arabidopsis thaliana DNA chromosome 4, BAC clone F22I13 (ESSA project)	At4g38340	AL035539	0.251	RWP-RK domain-containing protein, similar to nodule inception protein GI:6448579 from (Lotus japonicus); contains Pfam profile: PF02042, nitrogen sensing?	unknown	
At5g64480 Arabidopsis thaliana genomic DNA, chromosome 5, BAC clone:T12B11	At5g64480	AB025640	0.251	expressed	unknown	

At1g31790 Arabidopsis thaliana chromosome 1 BAC F5M6 genomic sequence	At1g31790	AC079041	0.252	pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535	unknown
At1g26410 Sequence of BAC T1K7 from Arabidopsis thaliana chromosome 1	At1g26410	AC013427	0.253	FAD-binding domain-containing protein, contains PF01565	unknown
At3g46050 Arabidopsis thaliana DNA chromosome 3, BAC clone F12M12	At3g46050	AL355775	0.253	kelch repeat-containing F-box family protein	unknown
Genomic sequence for Arabidopsis thaliana BAC F27F5 from chromosome I	Genomic	AC007915	0.255		unknown
At5g64410 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MSJ1	At5g64410	AB008268	0.256	OPT4, oligopeptide transporter OPT family protein	Environmental Information Processing; Membrane Transport;
At1g65250 Arabidopsis thaliana chromosome 1 BAC T8F5 sequence	At1g65250	AC004512	0.256	protein kinase family protein, contains protein kinase domain, Pfam:PF00069	Metabolism; kinase
At5g05090 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MUG13	At5g05090	AB005245	0.257	myb family transcription factor	Genetic Information Processing; transcription
Arabidopsis thaliana chromosome III BAC T1B9 genomic sequence	Arabidopsis	AC012395	0.258		unknown
Genomic sequence for Arabidopsis thaliana BAC T4O12 from chromosome I	Genomic	AC007396	0.261		unknown
At2g17980 Arabidopsis thaliana chromosome II section 105 of 255 of the complete sequence. Sequence from clones T13L16, T27K22, F8D23	At2g17980	AC006201	0.264	sec1 family protein, PF00995. mitochondrion, protein transporter activity, protein secretion	Genetic Information Processing; Folding, Sorting and Degradation
At4g16280 A.thaliana mRNA for FCA gamma	At4g16280	Z82989	0.264	flowering time control protein / FCA gamma (FCA), Involved in the promotion of the transition of the vegetative meristem to reproductive development. Four forms of the protein (alpha, beta, delta and gamma) are produced by alternative splicing. RNA binding, regulation of flower development	Genetic information processing; translation
At1g34420 Genomic sequence for Arabidopsis thaliana BAC F12K21 from chromosome I	At1g34420	AC023279	0.265	leucine-rich repeat family protein / protein kinase family protein	Metabolism; kinase
At5g56380 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MCD7	At5g56380	AB009049	0.265	F-box family protein,	unknown

Arabidopsis thaliana mRNA for 3-hydroxy-3-methylglutaryl CoA reductase (EC 1.1.1.34)	At1g76490	X15032	0.266	Encodes a 3-hydroxy-3-methylglutaryl coenzyme A reductase, which is involved in melavonate biosynthesis and performs the first committed step in isoprenoid biosynthesis. Expression is activated in dark in leaf tissue but not controlled by light in the root , membrane, isoprenoid biosynthesis, whole plant	Metabolism; Lipid Metabolism; Biosynthesis of steroids			
At3g25960 Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MPE11	At3g25960	AB023041	0.267	pyruvate kinase, putative	Metabolism; Carbohydrate Metabolism; Glycolysis	Metabolism; Energy Metabolism; Carbon fixation	Metabolism; Nucleotide Metabolism; Purine metabolism	Metabolism; kinase
At3g20850 Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MOE17	At3g20850	AB025629	0.268	proline-rich family protein, extensin domains,	metabolism; other			
At1g20790 Genomic sequence for Arabidopsis thaliana BAC F2D10 from chromosome I	At1g20790	AC069251	0.268	F-box family protein, contains Pfam:PF00646	unknown			
At3g04420 Arabidopsis thaliana chromosome III BAC T27C4 genomic sequence	At3g04420	AC022287	0.268	no apical meristem (NAM) family protein	unknown			
Arabidopsis thaliana chromosome 1 BAC T17H3 sequence	Arabidopsis	AC005916	0.269		unknown			
At1g79110 Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence, complete sequence	At1g79110	AC002986	0.269	expressed	unknown			
At2g40970 Arabidopsis thaliana chromosome II section 221 of 255 of the complete sequence. Sequence from clones T20B5	At2g40970	AC002409	0.271	myb family transcription factor	Genetic Information Processing; transcription			
Arabidopsis thaliana mRNA for microbody NAD-dependent malate dehydrogenase	Arabidopsis	AY037252	0.272	malate metabolism	Metabolism; Carbohydrate; malate			
At3g26310 Arabidopsis thaliana genomic DNA, chromosome 3, BAC clone:F20C19	At3g26310	AP001298	0.276	cytochrome P450 family protein	Metabolism; Cytochrome P450			
At1g01710 Sequence of BAC T1N6 from Arabidopsis thaliana chromosome 1	At1g01710	AC009273	0.279	acyl-CoA thioesterase family protein, contains Pfam profiles: PF02551 acyl-CoA thioesterase, PF00027 cyclic nucleotide-binding domain , cellular component unknown, acyl-CoA thioesterase activity, acyl-CoA metabolism, cyclic nucleotide binding	Metabolim; lipid			
EST	EST	AA728500	0.28	expressed?, Arabidopsis thaliana mRNA for hypothetical protein, no hits are functioning genes	unknown			
At3g56430 Arabidopsis thaliana DNA chromosome 3, BAC clone T5P19	At3g56430	AL163972	0.281	expressed	unknown			
Arabidopsis thaliana DNA chromosome 4, contig fragment No. 42		AL161542	0.282		unknown			

At4g37450 Arabidopsis thaliana arabinogalactan protein AGP18 mRNA, complete cds	At4g37450	AF305940	0.287	arabinogalactan-protein, extracellular proteoglycans implicated in plant growth and development	Metabolism; other
Genomic sequence for Arabidopsis thaliana BAC T32E20 from chromosome I	Genomic	AC020646	0.287	unk	unknown
At2g25720 Arabidopsis thaliana chromosome II section 144 of 255 of the complete sequence. Sequence from clones F13B15, F3N11, F17H15	At2g25720	AC006053	0.292	expressed	unknown
At3g20350 Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MQC12	At3g20350	AB024036	0.292	expressed	unknown
At1g03330 Arabidopsis thaliana chromosome 1 BAC F15K9 sequence	At1g03330	AC005278	0.293	small nuclear ribonucleoprotein D, putative / snRNP core SM-like protein, putative / U6 snRNA-associated Sm-like protein, putative, nucleus, small nucleolar ribonucleoprotein complex, molecular function unknown, mRNA metabolism	Genetic Information and Processing; Translation
At1g14360 Arabidopsis thaliana putative UDP-galactose transporter MSS4 (F14L17.13) mRNA, partial cds	At1g14360	AC012188	0.295	UDP-galactose/UDP-glucose transporter, putative, very similar to UDP-galactose/UDP-glucose transporter, pyrimidine nucleotide sugar transporter activity, endomembrane system	Cellular Processes and Signaling; Transporters
At4g21930 Arabidopsis thaliana DNA chromosome 4, BAC clone T8O5 (ESSAII project)	At4g21930	AL021890	0.296	expressed	unknown
At1g70150 Sequence of BAC F20P5 from Arabidopsis thaliana chromosome 1	At1g70150	AC002062	0.297	zinc finger (MYND type) family protein, contains Pfam profile PF01753: MYND finger	Genetic Information Processing; Transcription
At1g36070 Genomic sequence for Arabidopsis thaliana BAC F5J5	At1g36070	AC006228	0.299	WD-40 repeat family protein, contains 2 WD-40 repeats (PF0400);	Metabolism; Peptidases
Arabidopsis thaliana DNA chromosome 4, BAC clone F4D11 (ESSAII project)		AL022537	0.3		unknown
Arabidopsis thaliana DNA chromosome 3, BAC clone T28A8		AL162691	0.306		unknown
At2g01920 Arabidopsis thaliana chromosome II section 6 of 255 of the complete sequence. Sequence from clones F23I14	At2g01920	AC007265	0.306	epsin N-terminal homology (ENTH) domain-containing protein / clathrin assembly protein-related	unknown
At4g24050 Arabidopsis thaliana chromosome IV BAC T19F6 genomic sequence	At4g24050	AC002343	0.31	short-chain dehydrogenase/reductase (SDR) family protein	Metabolism; Other energy metabolism

At4g08170 Arabidopsis thaliana DNA chromosome 4, BAC clone T12G13, partial sequence (ESSA project)	At4g08170	AL080252	0.311	inositol 1,3,4-trisphosphate 5/6-kinase family protein, similar to inositol phosphate kinase (GI:27549256) (Zea mays); similar to inositol 1,3,4-trisphosphate 5/6-kinase (GI:3396079) (Arabidopsis thaliana) , cytoplasm, nucleus, catalytic activity, biological process unknown	Metabolism; Carbohydrate Metabolism; Inositol phosphate metabolism	
Arabidopsis thaliana chromosome I BAC T14L22 genomic sequence	Arabidopsis	AC015448	0.311		unknown	
At1g28520 Genomic sequence for Arabidopsis thaliana BAC F3M18 from chromosome I	At1g28520	AC010155	0.311	expressed	unknown	
At1g36440 Arabidopsis thaliana chromosome 1 BAC F28J9 sequence	At1g36440	AC007918	0.32	expressed	unknown	
At4g31130 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 74	At4g31130	AL161578	0.336	expressed	unknown	
At1g17720 Arabidopsis thaliana At1g17720/F11A6_14 mRNA, complete cds	At1g17720	AY045665	0.337	type 2A protein serine/threonine phosphatase 55 kDa B , protein phosphatase type 2A complex, protein phosphatase type 2A regulator activity, protein amino acid dephosphorylation, cotyledon, root, flower, leaf, stem	Environmental Information Processing; Signal Transduction	
At2g20260 Arabidopsis thaliana mRNA for photosystem I subunit IV precursor (psaE2 gene)	At2g20260	AJ245909	0.338	photosystem I reaction center subunit IV, chloroplast, putative	Metabolism; energy; photosynthesis	
Arabidopsis thaliana vacuolar type ATPase subunit A mRNA, complete cds		U65638	0.341		Metabolism; Energy Metabolism; Oxidative phosphorylation	
At3g23830 Arabidopsis thaliana genomic DNA, chromosome 3, BAC clone:F14O13	At3g23830	AP001297	0.343	glycine-rich RNA-binding protein, putative, contains Pfam profile: PF00076 RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	Genetic Information Processing; translation	
At5g12480 Arabidopsis thaliana calmodulin-domain protein kinase CDPK isoform 7 (CPK7) mRNA, complete cds	At5g12480	U31836	0.344	calmodulin-domain protein kinase isoform 7 (CPK7), chloro	Metabolism; kinase	Environmental Information Processing; signal transduction
At1g78815 Arabidopsis thaliana chromosome 1 BAC F9K20 sequence, complete sequence	At1g78815	AC005679	0.356	expressed	unknown	
EST	EST	T21937	0.368		unknown	
Arabidopsis thaliana chromosome 1 BAC F28B23 genomic sequence	Arabidopsis	AC079829	0.404		unknown	
At2g16500 Arabidopsis thaliana arginine decarboxylase (ARGdc) mRNA, complete cds	At2g16500	U52851	0.411	Arabidopsis arginine decarboxylase paralogue (ADC1	Metabolism; amino acid	
At1g64740 A.thaliana alpha-1-tubulin gene, complete cds	At1g64740	M21414	0.426	tubulin alpha-1 chain (TUA1),	Cellular Processes; Cell Communication; Gap junction	
At4g03580 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 9	At4g03580	AL161497	0.46	expressed	unknown	

At1g23080 Arabidopsis thaliana auxin transport protein (PIN7) mRNA, complete cds	At1g23080	AF087820	0.463	auxin efflux carrier protein, putative, similar to efflux carrier of polar auxin transport	Cellular Processes; Transport	
At1g52310 Arabidopsis thaliana chromosome 1 BAC F19K6 genomic sequence	At1g52310	AC037424	0.464	protein kinase family protein / C-type lectin domain-containing protein, contains protein kinase domain, Pfam:PF00069, PF00059	Cellular Processes and Signaling; CAM ligands	Metabolism; kinase
ESTs	ESTs	AV440826	0.478		unknown	
At4g35320 Arabidopsis thaliana AT4g35320/F23E12_120 gene, complete cds	At4g35320	AF361581	0.483	expressed	unknown	
At2g43710 Arabidopsis thaliana At2g43710/F18O19.18 mRNA, complete cds	At2g43710	AY048233	0.511	acyl-(acyl-carrier-protein) desaturase / stearoyl-ACP desaturase (SSI2), PF03405	Metabolism; lipid Metabolism;	
At5g14610 Arabidopsis thaliana DNA chromosome 5, BAC clone T15N1 (ESSA project)	At5g14610	AL163792	0.525	DEAD box RNA helicase, putative, similar to RNA helicase DRH1 (Arabidopsis thaliana) GI:3149952	Genetic Information Processing; Replication and Repair;	
At2g06190 Arabidopsis thaliana chromosome II section 33 of 255 of the complete sequence. Sequence from clones T6P5, F5K7	At2g06190	AC006413	0.535	gypsy-like retrotransposon family	unknown	TRANSPOSON
At5g01580 Arabidopsis thaliana DNA chromosome 5, BAC clone F7A7 (ESSA project)	At5g01580	AL161946	0.767	gamma interferon responsive lysosomal thiol reductase family protein	Genetic Information Processing; Folding, Sorting and Degradation	Environmental Information Processing; Signal Transduction
At3g19640 Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MMB12	At3g19640	AP000417	0.785	magnesium transporter CorA-like family protein (MRS2-3), Pfam profile PF01544	Environmental Information Processing; Membrane Transport	
At4g27390 Arabidopsis thaliana AT4g27390/M4I22_200 mRNA, complete cds	At4g27390	AY037265	0.801	expressed	unknown	
At1g31730 Arabidopsis thaliana chromosome 1 BAC F27M3 genomic sequence	At1g31730	AC074360	1.05	epsilon-adaptin, putative, Pfam profile: PF01602 Adaptin N terminal region - vesicular transport	Environmental Information Processing; Signal Transduction	Cellular Processes; transport
At2g27730 Arabidopsis thaliana unknown protein (F15K20.17/At2g27730) mRNA, complete cds	At2g27730	AY035140	1.065	expressed protein, contains 1 transmembrane domain - mito	unknown	
At3g09610 Arabidopsis thaliana chromosome 3 BAC F11F8 genomic sequence	At3g09610	AC016661	1.144	myb family transcription factor, contains Pfam profile: PF00249	Genetic Information Processing; transcription	
At1g29010 Genomic sequence for Arabidopsis thaliana BAC F1K23 from chromosome I	At1g29010	AC007508	1.166	expressed	unknown	
Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MTH12		AB006705	1.186		unknown	
At4g27590 Arabidopsis thaliana DNA chromosome 4, BAC clone T29A15 (ESSA project)	At4g27590	AL035602	1.191	copper-binding protein-related, low similarity to copper homeostasis factor gi:3168840 from Arabidopsis thaliana; contains Pfam profile PF00403: Heavy-metal-associated domain	unknown	

At1g19870 Arabidopsis thaliana chromosome I BAC F6F9 genomic sequence	At1g19870	AC007797	1.326	calmodulin-binding family protein	Environmental Information Processing; Signal Transduction	
At4g39660 Arabidopsis thaliana alanine:glyoxylate aminotransferase 2 homolog (AGT2) mRNA, complete cds	At4g39660	AF166351	1.499	alanine–glyoxylate aminotransferase, putative	Metabolism; amino acid	
At4g22980 Arabidopsis thaliana DNA chromosome 4, BAC clone F7H19 (ESSA project)	At4g22980	AL031018	1.654	expressed	unknown	
At3g25580 Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:MWL2	At3g25580	AB025639	1.701	thioredoxin-related	Genetic Information Processing; Folding, Sorting and Degradation	
At1g05540 Genomic sequence for Arabidopsis thaliana BAC T25N20 from chromosome I	At1g05540	AC005106	1.766	expressed protein, contains Pfam profile PF03478: Protein of unknown function (DUF295)	unknown	
At1g19890 Arabidopsis thaliana chromosome I BAC F6F9 genomic sequence	At1g19890	AC007797	2.06	histone H3, putative	Genetic Information Processing; Transcription	
At3g29170 Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MXE2	At3g29170	AB018121	2.237	expressed	unknown	
At4g08610 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 24	At4g08610	AL161512	2.25	Mutator-like transposase family, has a 1.9e-87 P-value blast match to O22278 /203-375 Pfam PF03108 MuDR family transposase (MuDr-element domain)	unknown	TRANSPOSON
At3g43690 Arabidopsis thaliana DNA chromosome 3, BAC clone F23N14	At3g43690	AL138638	2.255	copia-like retrotransposon family protein, putative envelope protein (Endovir1-1)	unknown	TRANSPOSON
At3g28630 Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MZN14	At3g28630	AP000420	2.427	expressed	unknown	
At3g20730 Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MOE17	At3g20730	AB025629	2.43	pentatricopeptide (PPR) repeat-containing protein	unknown	
At3g57600 Arabidopsis thaliana DNA chromosome 3, BAC clone F15B8	At3g57600	AL049660	2.504	encodes a member of the DREB subfamily A-2 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are eight members in this subfamily including DREB2A AND DREB2B that are involved in response to drought.	Genetic Information Processing; transcription	
At1g56570 Arabidopsis thaliana chromosome I BAC F25P12 genomic sequence	At1g56570	AC009323	2.711	pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats	unknown	
Genomic sequence for Arabidopsis thaliana BAC F15H18 from chromosome I	Genomic	AC013354	2.812		unknown	
At2g28410 Arabidopsis thaliana chromosome II section 160 of 255 of the complete sequence. Sequence from clones T1B3, T17D12	At2g28410	AC006283	2.954	expressed	unknown	

Arabidopsis thaliana mRNA for photosystem I subunit XI precursor	Arabidopsis	AJ245867	3.421	photosystem I subunit XI precursor	Metabolism; Energy Metabolism; Photosynthesis	
At4g11740 Arabidopsis thaliana Unknown protein (T5C23.170) mRNA, complete cds	At4g11740	AB007767	3.458	ara4-interacting protein, (SAY1), PF00789: UBX domain, PF02809: Ubiquitin interaction motif , A novel protein with a small region of similarity to coil-coiled domain of yeast VSP27 protein.	Genetic Information Processing; Folding, sorting, degredation	
Arabidopsis thaliana chromosome I BAC F15H11 genomic sequence	Arabidopsis	AC008148	3.474	unk	unknown	
Arabidopsis thaliana chromosome II section 236 of 255 of the complete sequence. Sequence from clones F18O19, F6E13		AC002333	3.524		unknown	
At3g26830 Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDJ14	At3g26830	AB016889	3.596	cytochrome P450 71B15, putative (CYP71B15) - endomembrane system	Metabolism; Cytochrome P450	
At1g02140 Arabidopsis thaliana BAC T7I23, complete sequence	At1g02140	U89959	3.702	mago nashi family protein, similar to Mago Nashi, Genbank Accession Number U03559; contains Pfam PF02792: Mago nashi protein domain , nucleus, molecular function unknown, sex determination	unknown	
At1g07473 Genomic sequence for Arabidopsis thaliana BAC F22G5 from chromosome I	At1g07473	AC022464	4.104	expressed, chloro	unknown	
At2g23110 Arabidopsis thaliana similar to late embryogenesis abundant proteins (At2g23110; F21P24.17) mRNA, complete cds	At2g23110	AF386989	4.154	expressed	unknown	
Arabidopsis thaliana DNA chromosome 4, contig fragment No. 24		AL161512	4.535		unknown	
At2g35730 Arabidopsis thaliana chromosome II section 195 of 255 of the complete sequence. Sequence from clones T32F12, T20F21	At2g35730	AC006068	4.562	heavy-metal-associated domain-containing protein, PF00403: metal ion transport, endomembrane system, metal ion binding	Environmental Information Processing; Membrane Transport;	
At1g73690 Arabidopsis thaliana cak3At mRNA for CDK-activating kinase 3, complete cds	At1g73690	AC012679	4.836	cyclin dependent kinase activator CDKD;1. Nuclear localization. Involved in cell cycle regulation and cell differentiation.	Cellular Processes; Cell Growth and Death; Cell cycle	
Genomic sequence for Arabidopsis thaliana BAC T30E16 from chromosome I	Genomic	AC009317	4.885		unknown	
At1g17240 Arabidopsis thaliana chromosome I BAC F20D23 genomic sequence	At1g17240	AC007651	5.093	leucine-rich repeat family protein, contains leucine rich-repeat (LRR) domains Pfam:PF00560, mitochondrion, protein binding, protein kinase activity, signal transduction	Environmental Information Processing; Signal Transduction	Metabolism; kinase

At1g57770 Arabidopsis thaliana chromosome 1 BAC T8L23 genomic sequence	At1g57770	AC079730	5.362	amine oxidase family, contains Pfam profile PF01593 amine oxidase, flavin-containing	Metabolism; Amino Acid Metabolism;
At2g30010 Arabidopsis thaliana chromosome II section 169 of 255 of the complete sequence. Sequence from clones F23F1, T27E13	At2g30010	AC004680	5.443	expressed	unknown
At2g39770 Arabidopsis thaliana CYT1 protein (cyt1) mRNA, complete cds	At2g39770	AF076484	5.478	GDP-mannose pyrophosphorylase (GMP1),	Metabolism; Carbohydrate Metabolism;
Arabidopsis thaliana DNA chromosome 4, BAC clone F18F4 (ESSA project)		AL021637	5.562		unknown
At4g28780 Arabidopsis thaliana DNA chromosome 4, BAC clone F16A16 (ESSAII project)	At4g28780	AL035353	5.818	GDSL-motif lipase/hydrolase family protein, similar to family II lipase EXL3 (GI:15054386), EXL1 (GI:15054382), EXL2 (GI:15054384) (Arabidopsis thaliana); contains Pfam profile PF00657: Lipase/Acylhydrolase with GDSL-like motif	Metabolism; Lipid Metabolism; Glycerolipid metabolism
At5g36110 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MAB16	At5g36110	AB018112	6.351	cytochrome P450 family protein, similar to taxane 13-alpha-hydroxylase (GI:17148242) {Taxus cuspidata}; contains Pfam profile: PF00067: Cytochrome P450	Metabolism; Cytochrome P450
At3g19480 Arabidopsis thaliana phosphoglycerate dehydrogenase (MLD14.22) mRNA, partial cds	At3g19480	AB025624	7.584	D-3-phosphoglycerate dehydrogenase, putative / 3-PGDH, putative, serine biosynthesis	Metabolism; Amino Acid Metabolism; Glycine, serine and threonine
At1g80230 Arabidopsis thaliana chromosome I BAC F18B13 genomic sequence	At1g80230	AC009322	8.403	cytochrome c oxidase family protein, contains Pfam domain, PF01215: Cytochrome c oxidase subunit Vb	Metabolism; Energy Metabolism; Oxidative phosphorylation
At3g50790 Arabidopsis thaliana DNA chromosome 3, BAC clone F18B3	At3g50790	AL049862	8.627	late embryogenesis abundant protein, putative / LEA protein, putative, contains Pfam profile hydrolase	unknown
At2g04680 Arabidopsis thaliana chromosome II section 23 of 255 of the complete sequence. Sequence from clones F28I8	At2g04680	AC006955	9.86	DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain , protein binding, zinc ion binding, regulation of transcription, DNA-dependent	Genetic Information Processing; Transcription
At1g61280 Arabidopsis thaliana BAC T1F9 chromosome 1, complete sequence	At1g61280	AC004255	10.403	expressed	unknown
At1g65180 Arabidopsis thaliana chromosome 1 BAC T23K8 sequence	At1g65180	AC007230	11.818	DC1 domain-containing protein, histidine and cystine rich, probably binds Zn	unknown
EST	(At1g27150	AA394730	15.456	expressed	unknown

At2g02710 Arabidopsis thaliana At2g02710/T20F6.15 mRNA, complete cds	At2g02710	AY045642	15.968	PAC motif-containing protein, Pfam profile PF00785:possible relation to signal transduction, binding molecule	Environmental Information Processing; signal transduction	
At1g65840 Arabidopsis thaliana putative protein kinase gb|AAD22129 (F1E22.18) mRNA, complete cds	At1g65840	AF370508	16.05	amine oxidase family protein	Metabolism; Amino Acid Metabolism;	
Arabidopsis thaliana chromosome II section 177 of 255 of the complete sequence. Sequence from clones T28P16, T9H9		AC007169	16.801		unknown	
At1g41825 Arabidopsis thaliana chromosome 1 BAC T4I21 genomic sequence	At1g41825	AC022456	17.333	gypsy-like retrotransposon family (Athila), has a 1.9e-98 P-value blast match to gb|AAL06422.1|AF378081_1 reverse transcriptase (Athila4) (Arabidopsis thaliana) (Gypsy_Ty3-family)	unknown	TRANSPOSON
At5g54180 Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K18G13	At5g54180	AB013387	17.363	mitochondrial transcription termination factor-related / mTERF-related, contains Pfam profile PF02536, located in chloro?, plastid chromosome, molecular function unknown, biological process unknown	Genetic Information Processing; Transcription; Other transcription	
At4g12600 Arabidopsis thaliana DNA chromosome 4, BAC clone T1P17 (ESSA project)	At4g12600	AL049730	18.303	ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein, protein biosynthesis, ribosome biogenesis and assembly, structural component of ribosome	Genetic Information Processing; Translation; Ribosome	
At1g27060 Genomic sequence for Arabidopsis thaliana BAC T7N9 from chromosome I	At1g27060	AC000348	18.412	regulator of chromosome condensation (RCC1) family protein, low similiarity to UVB-resistance protein UVR8 (Arabidopsis thaliana) GI:5478530; contains Pfam profile PF00415: Regulator of chromosome condensation (RCC1) , cellular component unknown, Ran GTPase binding, biological process unknown	Cellular Processes; Cell Growth and Death	
At2g15980 Arabidopsis thaliana chromosome II section 92 of 255 of the complete sequence. Sequence from clones F19G14, F7H1	At2g15980	AC006438	18.421	pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat	unknown	
At2g03580 Arabidopsis thaliana chromosome II section 15 of 255 of the complete sequence. Sequence from clones F19B11, T18C20	At2g03580	AC006836	18.746	F-box family protein-related, supported by tandem duplication of F-box protein family, AtFBX7	unknown	

At5g15950 Arabidopsis thaliana adometDC2 gene for S-adenosylmethionine decarboxylase, exons 1-3	At5g15950	AJ252212	19.952	adenosylmethionine decarboxylase family protein, contains Pfam profile: PF01536 adenosylmethionine decarboxylase , cellular component unknown, adenosylmethionine decarboxylase activity, polyamine biosynthesis, spermidine biosynthesis, spermine biosynthesis	Metabolism; Amino Acid Metabolism; Methionine, arginine, proline metabolism
At5g17190 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MKP11	At5g17190	AB005238	20.206	expressed protein, similar to unknown protein (gb|AAF26109.1) - endomembrane	unknown
At3g16260 Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MYA6	At3g16260	AB023046	21.21	metallo-beta-lactamase family protein	Metabolism; other
Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MBL20		AP002544	22.2	unk	unknown
At5g13440 Arabidopsis thaliana ubiquinol–cytochrome-c reductase-like protein (T22N19_90) mRNA, complete cds	At5g13440	AF370533	25.639	ubiquinol-cytochrome C reductase iron-sulfur subunit, mitochondrial, putative / Rieske iron-sulfur protein, putative, –electron transport	Metabolism; Energy Metabolism; Oxidative phosphorylation
At1g04200 Arabidopsis thaliana chromosome 1 BAC F20D22 sequence	At1g04200	AC002411	26.057	multi-copper oxidase type I family protein, similar to SP|P07788 Spore coat protein A {Bacillus subtilis}; contains Pfam profile PF00394: Multicopper oxidase , copper ion binding, biological process unknown, endomembrane system	Metabolism; Energy Metabolism; Oxidative phosphorylation
Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MPO12		AB006702	26.905	unk	unknown
At2g01260 Arabidopsis thaliana chromosome II section 2 of 255 of the complete sequence. Sequence from clones F23H14, F10A8	At2g01260	AC006200	28.783	expressed protein - mito	unknown
At4g19450 Arabidopsis thaliana DNA chromosome 4, BAC clone T5K18 (ESSA project)	At4g19450	AL022580	29.383	nodulin-related, weak similarity to nodule-specific protein Nlj70 (Lotus japonicus) GI:3329366 (similar to beta and gamma crystalines of the eye lens–may be involved in osmotic/stress response)	unknown

At4g08040 Arabidopsis thaliana ACS11 (T17A2_2/AT4g08040) mRNA, complete cds	At4g08040	AL161509	36.298	encodes an aminotransferase that belongs to ACC synthase gene family structurally ACS11, 1-aminocyclopropane-1-carboxylate synthase, putative / ACC synthase, putative, similar to ACC synthase from Malus sylvestris (SP|P37821), Solanum tuberosum (GI:520914) , 1-aminocyclopropane-1-carboxylate synthase activity, ethylene biosynthesis	Metabolism; amino acid; hormone (ethylene)
Genomic sequence for Arabidopsis thaliana BAC F21D18 from chromosome I	Genomic	AC023673	37.275	unk	unknown
At2g15290 Arabidopsis thaliana chromosome II section 89 of 255 of the complete sequence. Sequence from clones F15A23, F27O10, F26H6	At2g15290	AC007267	40.842	expressed protein - chloro	unknown
Arabidopsis thaliana chromosome II section 219 of 255 of the complete sequence. Sequence from clones T3G21, T2P4		AC002336	42.015		unknown
At5g50510 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MBA10	At5g50510	AB025619	43.118	hypothetical	unknown
At3g07640 Arabidopsis thaliana chromosome III P1 MLP3 genomic sequence	At3g07640	AC009176	44.329	expressed	unknown
At1g62490 Genomic sequence for Arabidopsis thaliana BAC T3P18 from Chromosome 1	At1g62490	AC005698	44.455	mitochondrial transcription termination factor-related / mTERF-related, contains Pfam profile PF02536: mTERF	Genetic Information Processing; Transcription
At3g24000 Arabidopsis thaliana genomic DNA, chromosome 3, BAC clone:F14O13	At3g24000	AP001297	62.231	pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat , mito	unknown
Arabidopsis thaliana AtFruct5 mRNA for beta-fructofuranosidase, complete cds	AT1G55120.1	AB029310	62.517	beta-fructosidase, putative / beta-fructofuranosidase, putative, similar to beta-fructofuranosidase GI:402740 , hydrolase activity, hydrolyzing O-glycosyl compounds, carbohydrate metabolism, endomembrane system, sucrose catabolism, using beta-fructofuranosidase	Metabolism; Carbohydrate Metabolism; Fructose and mannose
At5g13620 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MSH12	At5g13620	AB006704	63.509	expressed protein	unknown
At2g42820 Arabidopsis thaliana chromosome II section 231 of 255 of the complete sequence. Sequence from clones F14N22, F7D19	At2g42820	AC006931	64.056	abscisic acid-responsive HVA22 family protein, endomembrane, stress induced	unknown

At1g16390 Arabidopsis thaliana chromosome 1 BAC F3O9 sequence	At1g16390	AC006341	68.177	organic cation transporter-related, Pfam profile PF00083: major facilitator superfamily protein, low similarity to Organic cation/carnitine transporter 2 , integral to membrane, membrane, carbohydrate transporter activity,	Cellular Processes and Signaling; Transporters
At3g06340 Arabidopsis thaliana chromosome III BAC F24P17 genomic sequence	At3g06340	AC011623	69.836	DNAJ heat shock N-terminal domain-containing protein, contains Pfam profile PF00226 DnaJ domain , cellular component unknown, protein folding, unfolded protein binding, heat shock protein binding	Genetic Information Processing; Folding, Sorting and Degradation
Arabidopsis thaliana DNA chromosome 3, BAC clone T22E16		AL132975	75.765	unk	unknown
Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MRI1		AB018118	78.444	unk	unknown
Sequence of BAC F16N3 from Arabidopsis thaliana chromosome 1	Sequence	AC007519	80.155	unk	unknown
At3g49150 Arabidopsis thaliana DNA chromosome 3, BAC clone F2K15	At3g49150	AL132956	101.293	F-box family protein, contains F-box domain Pfam:PF00646, cyclin like Fbox (cell cycle, proteolysis?)	Genetic Information Processing; Folding, Sorting and Degradation
At5g45340 Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K9E15	At5g45340	AB020744	102.234	cytochrome P450 family protein, similar to SP|Q42569|C901_ARATH Cytochrome P450 90A1 (SP:Q42569) (Arabidopsis thaliana); contains Pfam profile: PF00067: Cytochrome P450 , Encodes a protein with ABA 8'-hydroxylase activity; involved in ABA catabolism. Mutant analyses show that disruption in the gene results in more drought tolerance whereas overexpression results in increased transpiration rate and reduced drought tolerance. Gene involved in postgermination growth. CYP707A3 , response to water deprivation, abscisic acid catabolism, fruit, pericarp, embryo, root, flower, stem, rosette leaf , oxygen binding, endomembrane system	Metabolism; Cytochrome P450
Arabidopsis thaliana BAC TM021B04	Arabidopsis	AF007271	103.91	unk	unknown

At3g17480 Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MKP6	At3g17480	AB022219	104.277	F-box family protein, contains F-box domain Pfam:PF00646 (cell cycle, proteolysis)	Genetic Information Processing; Folding, Sorting and Degradation
Arabidopsis thaliana triosephosphate isomerase (TIM) mRNA, complete cds; nuclear gene for chloroplast product		AF247559	104.349	glycolysis (DHAP<->GAP)	Metabolism; Carbohydrate Metabolism; Glycolysis / Gluconeogenesis
Arabidopsis thaliana chromosome II section 96 of 255 of the complete sequence. Sequence from clones T24I21, F12A24		AC005825	121.369		unknown
At4g30630 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 73	At4g30630	AL161577	125.956	expressed protein	unknown
Arabidopsis thaliana putative ADP-ribosylation factor 1 protein (F24J13.6) mRNA, complete cds		AF360164	134.075	*putative ADP-ribosylation factor (monomeric G protein)*	Cellular Processes and Signaling
At1g23010 Arabidopsis thaliana BAC F19G10, complete sequence	At1g23010	AF000657	153.249	multi-copper oxidase type I family protein, Pfam profile PF00394	Metabolism; Energy Metabolism; Oxidative phosphorylation
EST	EST	AV558082	190.957		unknown

Table S2. Corrected gene ratios, functional annotation and p-values for 547 spots passing filtering criteria in the competition experiments

Centaurea maculosa plants were grown alone (control) or with a strong competitor (Gaillardia aristata) or a weak competitor (Festuca idahoensis). Roots were collected from Centaurea plants grown in each of these conditions and resulting cDNAs were used to probe the Arabidopsis OAR27K microarray chip. Duplicate microarrays were performed for each test condition. Accession numbers for each gene identified in the microarray analysis were used to query the Arabidopsis gene database to determine function, and genes were then grouped into functional categories based on the Kyoto Encyclopedia of Genes and Genomics (KEGG) Ontology System. Functional (KEGG) categories in table are as follows: CPS, Cell processing and signaling; GIP, Genetic information processing; EIP, Environmental information processing; M, Metabolism; U, Unknown. Reported categories that did not fall into one of these major functional categories are considered as unknown. Average C–G (average ratio of Centaurea–Gaillardia to Centaurea alone) and average C–F (average ratio of Centaurea–Festuca to Centaurea alone) were calculated and gene ratios were further normalized as described in Materials and Methods. The log base two of the corrected ratios was calculated, one sample t-tests were performed for the two replicates of each separate C–G and C–F comparison, and the fold change was noted (D, down over two fold; U, up over two fold; NS, not significant, regulated less than two fold). A two sample t-test was performed to compare C–G to C–F ratios and the significance was noted (ns, not significant; s

ID	Name	Function	Functional category			Raw ratios				Corrected ratios				log base 2 of corrected ratios				Ave log base 2 of corrected ratios		SD log base 2 of corrected		1 sample t-test T-value for each		1 sample t test P value for each experiment				2 sample t-test	
			KEGG	KEGG 2	KEGG 3	Average C–G	Average C–F	SD C–G	SD C–F	C–G Chip 618	C–G Chip 623	C–F Chip 720	C–F Chip 723	log 2 C–G Chip 618	log 2 C–G Chip 623	log 2 C–F Chip 720	log 2 C–F Chip 723	Avg log C–G 618–623	Avg log C–F 720–723	SD log C–G 618–623	SD log C–F 720–723	ABS T C–G	ABS T C–F	*P* value C–G	Regulation C–G	*P* value C–F	Regulation C–G	*P* value C–G v C–F	
AL050351	Arabidopsis thaliana DNA chromosome 4, BAC clone T22F8 (ESSA project)	unknown	unknown			0.01440	0.01441	0.00172	0.00508	0.01562	0.01318	0.01082	0.01801	-6.00059	-6.24554	-6.53000	-5.79521	-6.12307	-6.16260	0.17321	0.51958	49.99461	16.77375	0.01273	D	0.03791	D	0.92800	ns
AL162874	At5g02330 Arabidopsis thaliana DNA chromosome 5, BAC clone T1E22 (ESSA project)	DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain , protein binding, zinc ion binding, regulation of transcription, DNA-dependent	GIP, TF			0.01707	0.01647	0.00793	0.00722	0.01146	0.02268	0.01137	0.02158	-6.44738	-5.46243	-6.45848	-5.53425	-5.95490	-5.99637	0.69646	0.65353	12.09179	12.97585	0.05253	NS	0.04897	D	0.95663	ns
AB016875	At5g43580 Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K9D7	protease inhibitor, putative, similar to SP|P19873 Inhibitor of trypsin and hageman factor (CMTI-V) {Cucurbita maxima}; contains Pfam profile PF00280: Potato inhibitor I family , serine-type endopeptidase inhibitor activity, response to wounding	M, peptidase inhibitor			0.01131	0.01659	0.00121	0.00913	0.01046	0.01217	0.01013	0.02305	-6.57940	-6.36042	-6.62498	-5.43927	-6.46991	-6.03212	0.15484	0.83842	59.09165	10.17472	0.01077	D	0.06237	NS	0.54323	ns
AB015479	At5g55360 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MTE17	long-chain-alcohol O-fatty-acyltransferase family protein / wax synthase family protein, contains similarity to wax synthase, acyltransferase activity,	M, lipid, wax			0.02001	0.01676	0.01152	0.00538	0.01187	0.02815	0.02057	0.01295	-6.39714	-5.15059	-5.60346	-6.27057	-5.77386	-5.93702	0.88144	0.47172	9.26376	17.79930	0.06846	NS	0.03573	D	0.83894	ns
AC006284	At2g03360 Arabidopsis thaliana chromosome II section 14 of 255 of the complete sequence. Sequence from clones T18E12, T4M8, F19B11	expressed protein, contains Pfam domain, PF04577: Protein of unknown function (DUF563)	unknown			0.01668	0.01728	0.00651	0.00230	0.01208	0.02128	0.01891	0.01565	-6.37140	-5.55412	-5.72503	-5.99771	-5.96276	-5.86137	0.57790	0.19281	14.59176	42.99093	0.04356	D	0.01481	D	0.83583	ns
AB016886	At5g47920 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MCA23	expressed protein, similar to unknown protein (emb|CAB67623.1)	unknown			0.01313	0.01874	0.00491	0.00267	0.00966	0.01660	0.02063	0.01685	-6.69375	-5.91284	-5.59929	-5.89141	-6.30330	-5.74535	0.55219	0.20656	16.14332	39.33606	0.03939	D	0.01618	D	0.31263	ns
AB023029	At5g56260 Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K24C1	dimethylmenaquinone methyltransferase family protein, similar to bacterial S-adenosylmethionine:2-demethylmenaquinone methyltransferases; contains Pfam profile PF03737: Dimethylmenaquinone methyltransferase	M, amino acid?			0.03063	0.01875	0.02267	0.00753	0.01460	0.04666	0.01343	0.02408	-6.09804	-4.42182	-6.21842	-5.37631	-5.25993	-5.79737	1.18527	0.59546	6.27594	13.76866	0.10059	NS	0.04616	D	0.62448	ns
AC004411	At2g46870 Arabidopsis thaliana chromosome II section 250 of 255 of the complete sequence. Sequence from clones F19D11, F14M4, T3D7	DNA-binding protein, putative, transcription factor activity, flower development, leaf development (NGA1)	GIP, TF			0.05580	0.01969	0.04185	0.00723	0.08539	0.02621	0.01458	0.02481	-3.54978	-5.25382	-6.09954	-5.33319	-4.40180	-5.71637	1.20494	0.54189	5.16630	14.91846	0.12172	NS	0.04261	D	0.29467	ns
AB015472	At5g60790 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MAE1	ABC transporter family protein, similar to ABC transporter homolog PnATH GI:7573600 from (Populus nigra) , member of GCN subfamily (ARABIDOPSIS THALIANA GENERAL CONTROL NON-REPRESSIBLE 1), transporter activity	EIP, transport	CPS, transport		0.02011	0.02017	0.00545	0.00256	0.01625	0.02396	0.01836	0.02198	-5.94313	-5.38314	-5.76743	-5.50759	-5.66313	-5.63751	0.39597	0.18373	20.22587	43.39308	0.03145	D	0.01467	D	0.94140	ns
AC020580	At3g06620 Arabidopsis thaliana chromosome 3 BAC F5E6 genomic sequence	protein kinase family protein, contains Pfam domain, PF00069: Protein kinase domain, kinase activity, protein threonine/tyrosine kinase activity, protein amino acid phosphorylation, signal transduction	M, kinase			0.07926	0.02152	0.08398	0.00472	0.01988	0.13864	0.01818	0.02486	-5.65249	-2.85057	-5.78183	-5.33031	-4.25153	-5.55607	1.98126	0.31927	3.03473	24.61082	0.20264	NS	0.02585	D	0.45498	ns
AB015479	At5g55340 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MTE17	long-chain-alcohol O-fatty-acyltransferase family protein / wax synthase family protein, contains similarity to wax synthase similarity to wax synthase wax synthase - Simmondsia chinensis, PID:g5020219 similar to wax synthase (gi:5020219) from Simmondsia chinensis , acyltransferase activity,	M, lipid, wax			0.01817	0.02190	0.00029	0.01125	0.01838	0.01796	0.01394	0.02985	-5.76571	-5.79869	-6.16441	-5.06609	-5.78220	-5.61525	0.02332	0.77663	350.68049	10.22520	0.00182	D	0.06206	NS	0.78993	ns
AY034929	At1g50600 Arabidopsis thaliana putative scarecrow-like protein (F17J6.12) mRNA, complete cds	scarecrow-like transcription factor 5 (SCL5), similar to SCARECROW GB:AAB06318 GI:1497987 from (Arabidopsis thaliana) , transcription factor activity, regulation of transcription	GIP, TF			0.01846	0.02211	0.00862	0.00192	0.01236	0.02455	0.02076	0.02347	-6.33821	-5.34792	-5.59031	-5.41308	-5.84306	-5.50170	0.70024	0.12532	11.80067	62.08502	0.05382	NS	0.01025	D	0.56737	ns
AP002543	At5g06550 Arabidopsis thaliana genomic DNA, chromosome 5, BAC clone:F15M7	similar to transcription factor jumonji (jmjC) domain-containing protein [Arabidopsis thaliana] (TAIR:At1g78280.1); similar to hypothetical protein [Neurospora crassa] (GB:XP_327705.1); contains InterPro domain Cyclin-like F-box (InterPro:IPR001810); contains InterPro domain Transcription factor jumonji, jmjC (InterPro:IPR003347) , cell surface receptor linked signal transduction	GIP, TF	EIP, signal transduction		0.03916	0.02388	0.03530	0.00169	0.01421	0.06412	0.02269	0.02507	-6.13733	-3.96302	-5.46183	-5.31769	-5.05018	-5.38976	1.53747	0.10192	4.64531	74.78361	0.13499	NS	0.00851	D	0.78478	ns
AL132956	At3g49160 Arabidopsis thaliana DNA chromosome 3, BAC clone F2K15	pyruvate kinase family protein, similar to SP|Q92122 Pyruvate kinase, muscle isozyme (EC 2.7.1.40) (Cytosolic thyroid hormone binding protein) (CTHBP) {Xenopus laevis}; contains Pfam profile PF00224: Pyruvate kinase, barrel domain , pyruvate kinase activity, glycolysis	M, carbohydrate, kinase			0.06416	0.02436	0.06601	0.00918	0.01748	0.11084	0.01787	0.03085	-5.83798	-3.17349	-5.80592	-5.01856	-4.50574	-5.41224	1.88408	0.55675	3.38206	13.74787	0.18302	NS	0.04623	D	0.58103	ns
AB007766	AT3G54840 Arabidopsis thaliana mRNA for Ara6, complete cds	Encodes a novel Rab-like GTP-ase that is localized to the peripheral membrane of the endosome. GTPase activity, early endosome to late endosome transport, external side of endosome membrane	CPS, Gprotein			0.05195	0.02457	0.04289	0.01480	0.02162	0.08227	0.01410	0.03503	-5.53145	-3.60348	-6.14789	-4.83506	-4.56746	-5.49147	1.36328	0.92831	4.73810	8.36588	0.13242	NS	0.07574	NS	0.51124	ns
AC004261	At2g41040 Arabidopsis thaliana chromosome II section 222 of 255 of the complete sequence. Sequence from clones T20B5, T3K9	methyltransferase-related, eak similarity to C5-O-methyltransferase (GI:5921167) (Streptomyces avermitilis); weak similarity to Probable menaquinone biosynthesis methyltransferase (EC 2.1.1.-) (gerC2 protein homolog) (Swiss-Prot:P49016) (Lactococcus lactis)	M, menaquinone			0.06365	0.02803	0.06601	0.00372	0.01697	0.11032	0.02540	0.03065	-5.88069	-3.18020	-5.29921	-5.02781	-4.53044	-5.16351	1.90953	0.19191	3.35527	38.05074	0.18440	NS	0.01673	D	0.68673	ns

U96455	At1g07810 Arabidopsis thaliana ER-type calcium pump (ACA3) mRNA, complete cds	calcium-transporting ATPase 1, endoplasmic reticulum-type (ECA1), identical to SP|P92939 Calcium-transporting ATPase 1, endoplasmic reticulum-type (EC 3.6.3.8) {Arabidopsis thaliana); contains InterPro Accession IPR006069: Cation transporting ATPase , Encodes an ER-type Ca2+-pumping ATPase. calcium-transporting ATPase activity, manganese ion homeostasis, response to manganese ion	M, energy			0.04735	0.03012	0.04456	0.01391	0.01584	0.07885	0.02029	0.03995	-5.98024	-3.66465	-5.62329	-4.64552	-4.82245	-5.13441	1.63737	0.69139	4.16521	10.50220	0.15000	NS	0.06044	NS	0.82712	ns
AB011483	At5g60530 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MUF9	late embryogenesis abundant protein-related / LEA protein-related, similar to late embryogenesis abundant protein (Picea glauca) GI:1350543	LEA			0.11991	0.03351	0.09193	0.01602	0.05490	0.18492	0.02218	0.04484	-4.18692	-2.43505	-5.49461	-4.47908	-3.31099	-4.98685	1.23876	0.71809	3.77995	9.82115	0.16465	NS	0.06460	NS	0.23971	ns
AP001298	At3g26310 Arabidopsis thaliana genomic DNA, chromosome 3, BAC clone:F20C19	cytochrome P450 family protein, contains Pfam profile: PF00067 cytochrome P450 , CYTOCHROME P450, FAMILY 71, SUBFAMILY B, POLYPEPTIDE 35, electron transport, oxygen binding, endomembrane system	M, cytP450			0.02606	0.04255	0.01192	0.03006	0.01764	0.03449	0.06380	0.02129	-5.82533	-4.85760	-3.97029	-5.55354	-5.34147	-4.76192	0.68428	1.11953	11.03923	6.01537	0.05751	NS	0.10487	NS	0.59596	ns
AL049482	At4g09840 Arabidopsis thaliana DNA chromosome 4, BAC clone F17A8 (ESSA project)	expressed protein	unknown			0.12946	0.05135	0.05767	0.01999	0.17024	0.08868	0.03722	0.06548	-2.55438	-3.49521	-4.74790	-3.93270	-3.02479	-4.34030	0.66527	0.57643	6.43005	10.64847	0.09822	NS	0.05961	NS	0.16890	ns
AC007661	At2g37970 Arabidopsis thaliana Unknown protein (At2g37970; T8P21.12) mRNA, complete cds	SOUL heme-binding family protein, weak similarity to SOUL protein (Mus musculus) GI:4886906; contains Pfam profile PF04832: SOUL heme-binding protein , N-terminal protein myristoylation	EIP transport	Myristoylation		0.25940	0.05475	0.34421	0.03302	0.01601	0.50279	0.03140	0.07810	-5.96513	-0.99197	-4.99310	-3.67849	-3.47855	-4.33580	3.51655	0.92957	1.39893	6.59633	0.39509	NS	0.09578	NS	0.77061	ns
AL021637	At4g20040 Arabidopsis thaliana DNA chromosome 4, BAC clone F18F4 (ESSA project)	expressed protein, C70DMY30S	unknown			0.15688	0.05635	0.03673	0.02852	0.13090	0.18285	0.03618	0.07652	-2.93346	-2.45126	-4.78857	-3.70804	-2.69236	-4.24831	0.34097	0.76405	11.16697	7.86335	0.05686	NS	0.08053	NS	0.11926	ns
AL163816	At3g63150 Arabidopsis thaliana DNA chromosome 3, BAC clone T20O10	GTP-binding protein-related, low similarity to SP|Q38912 RAC-like GTP binding protein ARAC3 (GTP-binding protein ROP6) {Arabidopsis thaliana}; contains Pfam profile PF00036: EF hand (domain), intracellular, mitochondrion, ATP binding, GTP binding, calcium ion binding, protein transport, small GTPase mediated signal transduction	EIP, signal transduction	CPS, signal transduction		0.08183	0.05688	0.09533	0.02577	0.01442	0.14924	0.03866	0.07510	-6.11567	-2.74434	-4.69313	-3.73495	-4.43001	-4.21404	2.38389	0.67753	2.62804	8.79595	0.23147	NS	0.07207	NS	0.91319	ns
AC009325	At3g01490 Arabidopsis thaliana chromosome III BAC F4P13 genomic sequence	protein kinase, putative, similar to ATMRK1 (Arabidopsis thaliana) gi|2351097|dbj|BAA22079 , kinase activity, protein threonine/tyrosine kinase activity, protein amino acid phosphorylation	M, kinase			0.21257	0.06460	0.10637	0.04549	0.28779	0.13736	0.03243	0.09677	-1.79692	-2.86397	-4.94636	-3.36927	-2.33044	-4.15781	0.75452	1.11517	4.36800	5.27278	0.14328	NS	0.11932	NS	0.19493	ns
AB006705	At5g59740 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MTH12	UDP-galactose/UDP-glucose transporter-related, weak similarity to UDP-galactose/UDP-glucose transporter (Arabidopsis thaliana) GI:22651763 , galactose transporter activity	CPS, transport	EIP, transport		0.20125	0.06497	0.18250	0.04104	0.07220	0.33029	0.03594	0.09399	-3.79184	-1.59818	-4.79809	-3.41141	-2.69501	-4.10475	1.55115	0.98053	2.45709	5.92025	0.24606	NS	0.10653	NS	0.39080	ns
AC006434	At1g75710 Genomic sequence for Arabidopsis thaliana BAC F10A5	zinc finger (C2H2 type) family protein, contains zinc finger, C2H2 type, domain, PROSITE:PS00028 , intracellular, nucleic acid binding, transcription factor activity, zinc ion binding	GIP, TF			0.12391	0.07267	0.12719	0.01419	0.03398	0.21385	0.06263	0.08271	-4.87932	-2.22533	-3.99690	-3.59586	-3.55233	-3.79638	1.87666	0.28358	2.67696	18.93273	0.22760	NS	0.03359	D	0.87246	ns
AP000377	At3g23710 Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MYM9	chloroplast inner membrane import protein Tic22, putative, similar to Tic22 (Pisum sativum) gi|3769671|gb|AAC64606; contains Pfam domain PF04278: Tic22-like family	CPS, transport			0.40852	0.07387	0.26692	0.04461	0.21978	0.59726	0.04233	0.10541	-2.18585	-0.74356	-4.56215	-3.24588	-1.46470	-3.90401	1.01985	0.93074	2.03109	5.93197	0.29126	NS	0.10632	NS	0.12974	ns
AC002391	At2g23320 Arabidopsis thaliana WRKY DNA-binding protein 15 (WRKY15) mRNA, complete cds	WRKY family transcription factor, identical to WRKY DNA-binding protein 15 GI:13506742 from (Arabidopsis thaliana) , WRKY DNA-BINDING PROTEIN 15, transcription factor activity, regulation of transcription, DNA-dependent , calmodulin binding	GIP, TF	EIP, signal transduction	CPS, signal transduction	0.22623	0.07927	0.28220	0.01923	0.02668	0.42577	0.06567	0.09286	-5.22809	-1.23184	-3.92854	-3.42875	-3.22997	-3.67865	2.82577	0.35340	1.61650	14.72082	0.35269	NS	0.04318	D	0.84437	ns
AL132966	At3g53490 Arabidopsis thaliana DNA chromosome 3, BAC clone F4P12	expressed protein, ADAM 13, Xenopus laevis, EMBL:XLU66003 , metalloproteinase family containing disintegrin-like domains	M, peptide			0.02765	0.08397	0.01726	0.07079	0.01545	0.03986	0.13402	0.03392	-6.01651	-4.64896	-2.89943	-4.88188	-5.33273	-3.89066	0.96700	1.40180	7.79898	3.92510	0.08119	NS	0.15881	NS	0.35377	ns
AL353912	At3g52760 Arabidopsis thaliana DNA chromosome 3, BAC clone F3C22	integral membrane Yip1 family protein, contains Pfam domain, PF04893: Yip1 domain	GIP, FSD			0.10781	0.13288	0.10310	0.00626	0.03491	0.18071	0.13730	0.12845	-4.84019	-2.46822	-2.86456	-2.96068	-3.65420	-2.91262	1.67724	0.06797	3.08115	60.60386	0.19979	NS	0.01050	D	0.59589	ns
AL078464	At4g30030 Arabidopsis thaliana DNA chromosome 4, BAC clone F6G3 (ESSA project)	aspartyl protease family protein, contains Pfam domain, PF00026: eukaryotic aspartyl protease , pepsin A activity, proteolysis, endomembrane system	M, peptide			0.18940	0.15604	0.04755	0.10004	0.15578	0.22303	0.08530	0.22677	-2.68243	-2.16471	-3.55129	-2.14068	-2.42357	-2.84598	0.36609	0.99745	9.36236	4.03513	0.06774	NS	0.15465	NS	0.63056	ns
AC007152	At1g67035 Arabidopsis thaliana chromosome I BAC F1O19 genomic sequence	expressed protein, ; expression supported by MPSS	unknown			0.39967	0.18256	0.12585	0.22711	0.31068	0.48866	0.02197	0.34315	1.68651	-1.03310	-5.50826	-1.54307	-1.35981	-3.52567	0.46203	2.80381	4.16216	1.77831	0.15011	NS	0.32612	NS	0.39381	ns
AC079284	At1g50900 Arabidopsis thaliana chromosome 1 BAC F8A12 genomic sequence	expressed protein	unknown			0.11600	0.18463	0.02298	0.09790	0.13225	0.09975	0.11541	0.25386	-2.91865	-3.32557	-3.11521	-1.97789	-3.12211	-2.54655	0.28773	0.80421	15.34520	4.47815	0.04143	D	0.13987	NS	0.44118	ns
AL163002	At5g03030 Arabidopsis thaliana DNA chromosome 5, BAC clone F15A17 (ESSA project)	DNAJ heat shock N-terminal domain-containing protein, contains Pfam profile PF00226 DnaJ domain; DNAJ domain-containing protein, Homo sapiens, EMBL:AF126743 , protein folding, heat shock protein binding	GIP, FSD	EIP, signal transduction		0.25132	0.21205	0.22741	0.04793	0.09052	0.41213	0.24595	0.17816	-3.46565	-1.27882	-2.02358	-2.48878	-2.37224	-2.25618	1.54632	0.32894	2.16957	9.69995	0.27495	NS	0.06540	NS	0.92679	ns
AC006264	At2g21040 Arabidopsis thaliana chromosome II section 120 of 255 of the complete sequence. Sequence from clones F26H11, F7O24	C2 domain-containing protein, low similarity to phloem protein (Cucurbita maxima) GI:4164541; contains Pfam profile PF00168: C2 domain	CPS, signal transduction			0.57019	0.22567	0.23031	0.18732	0.40733	0.73304	0.09322	0.35813	-1.29572	-0.44803	-3.42321	-1.48145	-0.87188	-2.45233	0.59941	1.37304	2.05707	2.52588	0.28806	NS	0.23999	NS	0.27425	ns
AL132957	At3g54270 Arabidopsis thaliana DNA chromosome 3, BAC clone F24B22	sucrose-phosphatase 3 (SPP3), nearly identical to sucrose-phosphatase (SPP3) (Arabidopsis thaliana) GI:16904077 , sucrose biosynthetic process, sucrose-phosphatase activity	M, carbohydrate, sucrose			0.33289	0.23510	0.12589	0.24169	0.24387	0.42191	0.06420	0.40600	-2.03580	-1.24500	-3.96130	-1.30044	-1.64040	-2.63087	0.55918	1.88151	4.14872	1.97746	0.15058	NS	0.29806	NS	0.54950	ns
AP002057	At3g28720 Arabidopsis thaliana genomic DNA, chromosome 3, BAC clone: T19N8	expressed protein	unknown			0.35151	0.23530	0.17967	0.08072	0.47856	0.22447	0.29238	0.17822	-1.06323	-2.15543	-1.77410	-2.48830	-1.60933	-2.13120	0.77230	0.50501	2.94696	5.96812	0.20826	NS	0.10569	NS	0.50772	ns
AL163972	At3g56410 Arabidopsis thaliana DNA chromosome 3, BAC clone T5P19	expressed protein	unknown			0.28177	0.23722	0.02723	0.04191	0.30103	0.26252	0.20759	0.26686	-1.73202	-1.92951	-2.26820	-1.90587	-1.83076	-2.08704	0.13965	0.25621	18.54010	11.51997	0.03430	D	0.05512	NS	0.34011	ns

X91915	Arabidopsis thaliana mRNA for LEA D113 type1 protein	late embryogenesis abundant domain-containing protein / embryonic development	LEA			0.37815	0.24555	0.26476	0.03241	0.19094	0.56537	0.22264	0.26846	-2.38883	-0.82274	-2.16725	-1.89720	-1.60578	-2.03222	1.10740	0.19095	2.05068	15.05082	0.28884	NS	0.04224	D	0.64521	ns
AC016041	At1g49150 Genomic sequence for Arabidopsis thaliana BAC F27J15 from chromosome I	expressed protein	unknown			0.68585	0.24725	0.77693	0.06933	0.13648	1.23522	0.19823	0.29627	-2.87327	0.30477	-2.33476	-1.75501	-1.28425	-2.04488	2.24721	0.40995	0.80820	7.05433	0.56727	NS	0.08965	NS	0.68407	ns
AL162459	At3g45910 Arabidopsis thaliana DNA chromosome 3, BAC clone F16L2	expressed protein	unknown			0.33148	0.25389	0.14876	0.08755	0.22630	0.43667	0.19199	0.31579	-2.14372	-1.19539	-2.38092	-1.66294	-1.66956	-2.02193	0.67057	0.50769	3.52106	5.63225	0.17616	NS	0.11187	NS	0.61358	ns
X90387	At1g74650 Arabidopsis thaliana DNA for cY13 gene	myb family transcription factor (cY13), similar to myb protein cY13 GI:928930 from (Arabidopsis thaliana); contains Pfam profile: PF00249 myb DNA-binding domain; identical to cDNA cY13 gene GI:928929 , DNA binding, transcription factor activity, regulation of transcription, DNA-dependent, response to gibberellic acid stimulus, response to salicylic acid stimulus	GIP, TF			0.16776	0.25525	0.01988	0.17364	0.15371	0.18182	0.13247	0.37803	-2.70172	-2.45943	-2.91627	-1.40342	-2.58057	-2.15984	0.17132	1.06975	21.30208	2.85532	0.02986	D	0.21446	NS	0.63799	ns
M84701	AT5G62700 Arabidopsis thaliana beta-2 tubulin (TUB2) gene, complete cds	encodes tubulin beta-2/beta-3 chain , response to cold, tubulin complex	CPS, cell structure			0.32091	0.25810	0.02607	0.05224	0.30247	0.33934	0.22115	0.29504	-1.72512	-1.55921	-2.17687	-1.76102	-1.64216	-1.96895	0.11731	0.29405	19.79604	9.46942	0.03213	D	0.06698	NS	0.28178	ns
AC007727	At1g21700 Arabidopsis thaliana chromosome 1 BAC F8K7 sequence	SWIRM domain-containing protein / DNA-binding family protein, a member of the Arabidopsis SWI3 gene family. Protein physically interacts with ATSWI3B and ATSWI3A, the other two members of the SWI3 family. Homologous to yeast SWI3 & RSC8, components of the SWI/SNF and RSC chromatin remodeling complexes. Referred to as CHB3 in Zhou et al (2003). SWI/SNF complex, chromatin remodeling complex, chromatin remodeling	GIP, chromatin remodeling			0.27284	0.26515	0.04194	0.15073	0.24318	0.30249	0.15857	0.37173	-2.03988	-1.72504	-2.65685	-1.42768	-1.88246	-2.04226	0.22263	0.86916	11.95806	3.32299	0.05311	NS	0.18609	NS	0.82465	ns
AL022141	At4g36260 Arabidopsis thaliana DNA chromosome 4, BAC clone F23E13 (ESSAII project)	zinc finger protein-related, similar to lateral root primordium 1 (LRP1), A member of SHI gene family. Arabidopsis thaliana has ten members that encode proteins with a RING finger-like zinc finger motif. SHI RELATED SEQUENCE 2 (STY2), nucleus, transcription factor activity, negative regulation of gibberellic acid mediated signaling, vascular tissue pattern formation (sensu Tracheophyta), stigma development, style development, leaf trichome, cotyledon, stigma, style, hydathode, lateral root primordium, gynoecium primordium, leaf primordium, shoot apex, auxin homeostasis	GIP, TF			0.34745	0.26529	0.08192	0.11342	0.28953	0.40538	0.18509	0.34549	-1.78824	-1.30265	-2.43372	-1.53328	-1.54544	-1.98350	0.34337	0.63671	6.36517	4.40558	0.09921	NS	0.14210	NS	0.48201	ns
AC010793	At1g79760 Genomic sequence for Arabidopsis thaliana BAC F20B17 from chromosome I	Identified as target of the AGL15 binding motif CArG. DOWNSTREAM TARGET OF AGL15-4 (DTA4)	CPS, signal transduction			0.73553	0.26952	0.37369	0.29480	0.47129	0.99977	0.06106	0.47798	-1.08530	-0.00034	-4.03352	-1.06498	-0.54282	-2.54925	0.76719	2.09908	1.00062	1.71751	0.49980	NS	0.33566	NS	0.33195	ns
AC000107	At1g30910 Genomic sequence for Arabidopsis thaliana BAC F17F8 from chromosome I	molybdenum cofactor sulfurase family protein, weak similarity to molybdenum cofactor sulfurase (LOS5/ABA3) (Arabidopsis thaliana) GI:15407262; contains Pfam profiles PF03476: MOSC N-terminal beta barrel domain, PF03473: MOSC domain , Mo-molybdopterin cofactor sulfurase activity,	M, hormone synth, ABA			0.33381	0.27437	0.13176	0.17672	0.24064	0.42698	0.14941	0.39933	-2.05503	-1.22776	-2.74261	-1.32434	-1.64140	-2.03348	0.58497	1.00287	3.96823	2.86755	0.15716	NS	0.21361	NS	0.68005	ns
AL132972	At3g52300 Arabidopsis thaliana DNA chromosome 3, BAC clone T25B15	ATP synthase D chain-related, contains weak similarity to ATP synthase D chain, mitochondrial	M, energy, ox phos			0.24455	0.29381	0.12052	0.07701	0.15933	0.32977	0.23936	0.34827	-2.64991	-1.60048	-2.06274	-1.52173	-2.12519	-1.79223	0.74206	0.38255	4.05018	6.62560	0.15410	NS	0.09536	NS	0.62956	ns
AC008113	At1g67650 Genomic sequence for Arabidopsis thaliana BAC F12A21 from chromosome I	expressed protein	unknown			0.60812	0.29783	0.28805	0.18239	0.40444	0.81180	0.16886	0.42680	-1.30599	-0.30080	-2.56608	-1.22837	-0.80339	-1.89723	0.71078	0.94591	1.59849	2.83651	0.35589	NS	0.21578	NS	0.32117	ns
AL161540	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40	unknown	unknown			0.42719	0.29979	0.39079	0.00605	0.15086	0.70352	0.29551	0.30407	-2.72868	-0.50734	-1.75873	-1.71753	-1.61801	-1.73813	1.57073	0.02913	1.45679	84.37130	0.38297	NS	0.00755	D	0.92376	ns
AL138647	At3g59770 Arabidopsis thaliana DNA chromosome 3, BAC clone F24G16	phosphoinositide phosphatase. The sac9 null mutant accumulates elevated levels of PtdIns(4,5)P2 and Ins(1,4,5)P3. sacI homology domain-containing protein / WW domain-containing protein, contains Pfam profiles PF00397: WW domain, PF02383: SacI homology domain; identical to cDNA SAC domain protein 9 (SAC9) GI:31415734, inositol or phosphatidylinositol phosphatase activity, response to cold, response to osmotic stress, response to high light intensity, phosphoinositide-mediated signaling, phosphatidylinositol metabolic process	M, phosphatase, carbohydrate, glycan	EIP, signal transduction	CPS, signal transduction	0.39318	0.30010	0.23103	0.30568	0.22982	0.55654	0.08395	0.51625	-2.12144	-0.84545	-3.57430	-0.95386	-1.48344	-2.26408	0.90226	1.85293	2.32517	1.72802	0.25857	NS	0.33398	NS	0.64578	ns
AP000377	At3g23770 Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MYM9	glycosyl hydrolase family 17 protein, similar to A6 anther-specific protein SP:Q06915 (Arabidopsis thaliana) , hydrolase activity, hydrolyzing O-glycosyl compounds, carbohydrate metabolic process, endomembrane system	M, glycosyltransferase			0.45670	0.31087	0.26967	0.21500	0.26601	0.64738	0.15884	0.46291	-1.91043	-0.62732	-2.65432	-1.11121	-1.26888	-1.88277	0.90730	1.09114	1.97781	2.44022	0.29802	NS	0.24760	NS	0.60296	ns
AC009398	At1g10800 Genomic sequence for Arabidopsis thaliana BAC F20B24 from chromosome I	expressed protein	unknown			0.31170	0.31642	0.06862	0.05782	0.36023	0.26318	0.27553	0.35730	-1.47303	-1.92588	-1.85971	-1.48479	-1.69945	-1.67225	0.32021	0.26510	7.50558	8.92076	0.08432	NS	0.07107	NS	0.93471	ns
AL138659	At3g59680 Arabidopsis thaliana DNA chromosome 3, BAC clone T16L24	similar to unknown [Zea mays] (GB:AAV64233.1)	unknown			0.30006	0.32175	0.07090	0.06515	0.24993	0.35020	0.27568	0.36782	-2.00041	-1.51376	-1.85892	-1.44294	-1.75709	-1.65093	0.34411	0.29414	7.22125	7.93756	0.08760	NS	0.07978	NS	0.77170	ns
AL138659	At3g59710 Arabidopsis thaliana DNA chromosome 3, BAC clone T16L24	short-chain dehydrogenase/reductase (SDR) family protein, contains INTERPRO family IPR002198 short chain dehydrogenase/reductase SDR family, oxidoreductase activity, metabolic process, endomembrane system	M, oxidoreductase			0.33770	0.33324	0.04802	0.08014	0.37165	0.30374	0.27658	0.38991	-1.42797	-1.71908	-1.85425	-1.35878	-1.57352	-1.60652	0.20584	0.35035	10.81071	6.48483	0.05872	NS	0.09740	NS	0.91907	ns

AY045940	At3g46560 Arabidopsis thaliana putative zinc finger protein TIM9 (F12A12.80/AT3g46560) mRNA, complete cds	mitochondrial import inner membrane translocase (TIM9), identical to mitochondrial import inner membrane translocase subunit Tim9 (Arabidopsis thaliana) Swiss-Prot:Q9XGX9; contains Pfam domain, PF02953: Tim10/DDP family zinc finger , small zinc finger-like protein (TIM9) mRNA, complete cds , protein translocase activity, protein targeting to mitochondrion,	CPS, transport		0.25474	0.33353	0.00929	0.14714	0.26131	0.24818	0.22949	0.43757	-1.93618	-2.01057	-2.12349	-1.19240	-1.97337	-1.65795	0.05260	0.65838	53.05759	3.56129	0.01200	D	0.17427	NS	0.56905	ns
AF360196	At4g14210 Arabidopsis thaliana phytoene dehydrogenase precursor protein (AT4g14210) mRNA, complete cds	Encodes phytoene desaturase (phytoene dehydrogenase), an enzyme that catalyzes the desaturation of phytoene to zeta-carotene during carotenoid biosynthesis. Processed protein is localized to the plastid. phytoene dehydrogenase activity, carotenoid biosynthetic process	M, caretenoid		0.31868	0.33674	0.24495	0.07525	0.14548	0.49189	0.28353	0.38995	-2.78115	-1.02360	-1.81844	-1.35864	-1.90237	-1.58854	1.24278	0.32513	2.16480	6.90971	0.27549	NS	0.09150	NS	0.76267	ns
AL035526	At4g18660 Arabidopsis thaliana DNA chromosome 4, BAC clone F28A21 (ESSA project)	expressed protein, weak similarity to tumor-related protein (Nicotiana glauca x Nicotiana langsdorffii) GI:688423	unknown		0.38480	0.34347	0.24623	0.14812	0.21069	0.55891	0.23874	0.44820	-2.24681	-0.83931	-2.06651	-1.15777	-1.54306	-1.61214	0.99525	0.64258	2.19263	3.54809	0.27241	NS	0.17489	NS	0.94179	ns
AL138643	At3g31540 Arabidopsis thaliana DNA chromosome 3, BAC clone F7M19	expressed protein, similar to hypothetical protein [Arabidopsis thaliana] (TAIR:At3g31540.1); similar to hypothetical protein [Arabidopsis thaliana] (TAIR:At1g40133.1); similar to hypothetical protein [Arabidopsis thaliana] (TAIR:At1g34590.1); similar to expressed protein [Arabidopsis thaliana] (TAIR:At4g06603.1)	unknown		0.28549	0.35194	0.04776	0.08364	0.25172	0.31926	0.29280	0.41108	-1.99010	-1.64720	-1.77203	-1.28249	-1.81865	-1.52726	0.24247	0.34615	10.60754	6.23964	0.05984	NS	0.10117	NS	0.43237	ns
AJ010500	AT1G16460 (ATRDH2) Arabidopsis thaliana mRNA for thiosulfate sulfurtransferase (RDH2 gene)	encodes a cytoplasmic thiosulfate:cyanide sulfurtransferase, activity of which increased the rhodanese activity of transgenic yeast. Can also act as a mercaptopyruvate sulfurtransferase. cytoplasm, cytosol, 3-mercaptopyruvate sulfurtransferase activity, thiosulfate sulfurtransferase activity	M, amino acid, cysteine		0.26351	0.35219	0.11049	0.13541	0.34163	0.18538	0.25644	0.44794	-1.54948	-2.43142	-1.96330	-1.15863	-1.99045	-1.56097	0.62362	0.56899	4.51381	3.87976	0.13880	NS	0.16059	NS	0.54656	ns
AP000736	At3g29796 Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:K17E7	hypothetical protein	unknown		0.33353	0.36390	0.06991	0.08425	0.38296	0.28409	0.30433	0.42347	-1.38473	-1.81558	-1.71629	-1.23966	-1.60015	-1.47798	0.30466	0.33703	7.42793	6.20172	0.08519	NS	0.10178	NS	0.74031	ns
AP002061	At3g14810 Arabidopsis thaliana genomic DNA, chromosome 3, BAC clone: T21E2	mechanosensitive ion channel domain-containing protein / MS ion channel domain-containing protein, contains Pfam profile PF00924: Mechanosensitive ion channel	EIP, transport	CPS, transport	0.23381	0.37361	0.02816	0.08121	0.25373	0.21390	0.31618	0.43103	-1.97866	-2.22497	-1.66117	-1.21412	-2.10181	-1.43765	0.17416	0.31611	17.06671	6.43172	0.03726	D	0.09819	NS	0.12135	ns
AL132964	At3g49590 Arabidopsis thaliana DNA chromosome 3, BAC clone T9C5	expressed protein	unknown		0.06967	0.37474	0.08824	0.11076	0.13207	0.00728	0.29642	0.45306	-2.92062	-7.10271	-1.75427	-1.14223	-5.01167	-1.44825	2.95718	0.43278	2.39673	4.73255	0.25164	NS	0.13257	NS	0.23381	ns
AL133314	At3g46600 Arabidopsis thaliana DNA chromosome 3, BAC clone F12A12	scarecrow transcription factor family protein, scarecrow-like 11 - Arabidopsis thaliana, EMBL:AF036307 , transcription factor activity, regulation of transcription	GIP, TF		0.16746	0.37510	0.02075	0.10249	0.18214	0.15279	0.30263	0.44758	-2.45688	-2.71039	-1.72438	-1.15980	-2.58364	-1.44209	0.17926	0.39922	20.38248	5.10853	0.03121	D	0.12306	NS	0.06626	ns
AP002051	At3g28330 Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MZF16	F-box family protein-related, contains TIGRFAM TIGR01640: F-box protein interaction domain	Fbox		0.38039	0.37535	0.13063	0.14774	0.28801	0.47276	0.27088	0.47982	-1.79580	-1.08083	-1.88426	-1.05945	-1.43831	-1.47185	0.50556	0.58323	4.02341	3.56894	0.15509	NS	0.17392	NS	0.95658	ns
AL035605	At4g37540 Arabidopsis thaliana DNA chromosome 4, BAC clone F19F18 (ESSA project)	LOB domain protein 39 / lateral organ boundaries domain protein 39 (LBD39), identical to SP|Q9SZE8 LOB domain protein 39 {Arabidopsis thaliana}	CPS, cell structure		0.69483	0.37954	0.08656	0.41516	0.75603	0.63362	0.08597	0.67310	-0.40348	-0.65830	-3.53994	-0.57110	-0.53089	-2.05552	0.18019	2.09929	4.16671	1.38473	0.14995	NS	0.39817	NS	0.41378	ns
AL162691	Arabidopsis thaliana DNA chromosome 3, BAC clone T28A8	unknown	unknown		0.33214	0.38128	0.16507	0.09931	0.21542	0.44887	0.31106	0.45151	-2.21480	-1.15565	-1.68473	-1.14718	-1.68522	-1.41595	0.74894	0.38011	3.18220	5.26818	0.19384	NS	0.11942	NS	0.69470	ns
AL049660	At3g57580 Arabidopsis thaliana DNA chromosome 3, BAC clone F15B8	F-box family protein, contains Pfam PF00646: F-box domain; contains TIGRFAM TIGR01640 : F-box protein interaction domain; similar to F-box protein family, AtFBX8 (GI:20197464) (Arabidopsis thaliana)	Fbox		0.29475	0.38145	0.09464	0.08198	0.22783	0.36167	0.32348	0.43942	-2.13397	-1.46724	-1.62826	-1.18633	-1.80061	-1.40729	0.47145	0.31249	5.40131	6.36880	0.11654	NS	0.09915	NS	0.42909	ns
AY045844	At1g29850 Arabidopsis thaliana putative apoptosis related protein 19 (F1N18.11) mRNA, complete cds	double-stranded DNA-binding family protein, contains Pfam profile: PF01984 double-stranded DNA-binding domain	GIP		0.32483	0.38265	0.24141	0.04910	0.15413	0.49553	0.41738	0.34793	-2.69782	-1.01296	-1.26058	-1.52311	-1.85539	-1.39185	1.19138	0.18564	2.20242	10.60327	0.27134	NS	0.05986	NS	0.64116	ns
AL049487	At4g10130 Arabidopsis thaliana DNA chromosome 4, BAC clone F28M11 (ESSA project)	DNAJ heat shock N-terminal domain-containing protein, low similarity to SP|Q9QYI7 DnaJ homolog subfamily B member 8 Mus musculus, SP|P50025 Chaperone protein dnaJ Legionella pneumophila; contains Pfam profile PF00226 DnaJ domain , protein folding, heat shock protein binding	GIP, FSD	EIP, signal transduction	0.28136	0.38296	0.09165	0.21165	0.21656	0.34617	0.23330	0.53262	-2.20719	-1.53044	-2.09977	-0.90883	-1.86881	-1.50430	0.47853	0.84212	5.52290	2.52625	0.11403	NS	0.23995	NS	0.64778	ns
AL132966	At3g53430 Arabidopsis thaliana DNA chromosome 3, BAC clone F4P12	60S ribosomal protein L12 (RPL12B), 60S RIBOSOMAL PROTEIN L12, Prunus armeniaca, SWISSPROT:RL12_PRUAR , cytosolic large ribosomal subunit (sensu Bacteria), ribosome, structural constituent of ribosome, ribosome biogenesis and assembly	GIP, translation, ribosome		0.30533	0.39544	0.01609	0.10834	0.29395	0.31670	0.31884	0.47205	-1.76635	-1.65880	-1.64911	-1.08298	-1.71258	-1.36605	0.07605	0.40031	31.84668	4.82599	0.01998	D	0.13007	NS	0.35215	ns
AP002057	At3g28770 Arabidopsis thaliana genomic DNA, chromosome 3, BAC clone: T19N8	expressed protein	unknown		0.22148	0.40029	0.11299	0.41413	0.14159	0.30138	0.10746	0.69312	-2.82025	-1.73036	-3.21816	-0.52882	-2.27531	-1.87349	0.77067	1.90165	4.17530	1.39327	0.14965	NS	0.39631	NS	0.80782	ns
AY048228	At1g70600 Arabidopsis thaliana At1g70600/F5A18_22 mRNA, complete cds	60S ribosomal protein L27A (RPL27aC), identical to 60S ribosomal protein L27A GB:P49637 (Arabidopsis thaliana) , ribosome, structural constituent of ribosome, translation	GIP, translation, ribosome		0.36822	0.40203	0.08563	0.05468	0.42877	0.30767	0.44070	0.36337	-1.22172	-1.70055	-1.18213	-1.46050	-1.46113	-1.32132	0.33858	0.19684	6.10302	9.49319	0.10339	NS	0.06681	NS	0.66378	ns
AB020749	At3g18160 Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MRC8	peroxin-3 family protein, contains Pfam domain, PF04882: Peroxin-3, peroxisome, molecular_function, peroxisome organization and biogenesis	CPS, cell structure		0.47807	0.40228	0.01142	0.23831	0.47000	0.48614	0.23377	0.57079	-1.08927	-1.04054	-2.09682	-0.80897	-1.06491	-1.45290	0.03446	0.91065	43.70611	2.25631	0.01456	D	0.26559	NS	0.60827	ns

AY045964	At1g42990 Arabidopsis thaliana putative bZIP transcription factor (F13A11.5) mRNA, complete cds	AtbZIP60 consists of a bZIP DNA binding domain followed by a putative transmembrane domain. GFP fusions containing the first 260 amino acids (AtbZIP60deltaC) are nuclear-localized. can activate the promoters of the ER chaperones BiP1, BiP2 and BiP3 and CNX1 and CNX2 via binding to the ER stress response element (ERSE) and the plant unfolded protein response element(P-UPRE). It can also activate its own transcription. nucleus, DNA binding, transcription factor activity, regulation of transcription, DNA-dependent, unfolded protein response	GIP, TF		0.84966	0.40841	0.22660	0.14701	0.68943	1.00989	0.30446	0.51236	-0.53653	0.01420	-1.71566	-0.96477	-0.26116	-1.34021	0.38943	0.53096	0.94842	3.56964	0.51685	NS	0.17389	NS	0.14638	ns
AC017118	At1g32760 Genomic sequence for Arabidopsis thaliana BAC F6N18 from chromosome I	glutaredoxin family protein, chloroplast, electron carrier activity, protein disulfide oxidoreductase activity, electron transport	GIP, FSD	M, energy	0.32071	0.41158	0.25937	0.29560	0.13730	0.50411	0.20256	0.62060	-2.86457	-0.98818	-2.30357	-0.68826	-1.92637	-1.49592	1.32681	1.14220	2.05328	1.85217	0.28853	NS	0.31517	NS	0.76124	ns
AL031986	At4g35870 Arabidopsis thaliana DNA chromosome 4, BAC clone F4B14 (ESSA project)	expressed protein	unknown		0.37767	0.41800	0.04843	0.10552	0.41191	0.34342	0.34338	0.49261	-1.27960	-1.54194	-1.54211	-1.02148	-1.41077	-1.28179	0.18550	0.36814	10.75545	4.92404	0.05902	NS	0.12755	NS	0.70140	ns
AB013396	At5g57910 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MTI20	expressed protein, similar to unknown protein (emb|CAB79781.1)	unknown		0.27014	0.42264	0.14047	0.27966	0.17082	0.36947	0.62038	0.22489	-2.54948	-1.43647	-0.68877	-2.15272	-1.99298	-1.42075	0.78702	1.03517	3.58124	1.94097	0.17335	NS	0.30287	NS	0.59722	ns
AC003113	At1g62370 Genomic sequence for Arabidopsis thaliana BAC F24O1 from chromosome I	zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger) , protein binding, zinc ion binding	ZINC		0.48907	0.42378	0.10947	0.11659	0.41167	0.56648	0.34134	0.50622	-1.28046	-0.81990	-1.55074	-0.98215	-1.05018	-1.26644	0.32566	0.40205	4.56044	4.45474	0.13742	NS	0.14058	NS	0.61434	ns
AL132909	Arabidopsis thaliana DNA chromosome 3, BAC clone T14K23	unknown	unknown		0.34710	0.43449	0.07176	0.19546	0.29636	0.39784	0.29628	0.57270	-1.75460	-1.32974	-1.75497	-0.80416	-1.54217	-1.27956	0.30042	0.67232	7.25969	2.69152	0.08714	NS	0.22647	NS	0.66411	ns
AL049482	At4g09850 Arabidopsis thaliana DNA chromosome 4, BAC clone F17A8 (ESSA project)	expressed protein,	unknown		0.24942	0.43953	0.02922	0.18338	0.22876	0.27008	0.30985	0.56920	-2.12812	-1.88854	-1.69034	-0.81300	-2.00833	-1.25167	0.16941	0.62038	16.76512	2.85332	0.03793	D	0.21460	NS	0.23803	ns
AP001306	At3g22190 Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:MKA23	calmodulin-binding family protein, contains Pfam profile PF00612: IQ calmodulin-binding motif	EIP, signal transduction	CPS, signal transduction	0.38473	0.44515	0.03387	0.24704	0.36078	0.40868	0.27047	0.61983	-1.47081	-1.29096	-1.88649	-0.69004	-1.38089	-1.28826	0.12717	0.84601	15.35634	2.15350	0.04140	D	0.27676	NS	0.89236	ns
AB022216	At3g17220 Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGD8	invertase/pectin methylesterase inhibitor family protein, similar to SP|P83326 Pectinesterase inhibitor (Pectin methylesterase inhibitor) (PMEI) {Actinidia chinensis}; contains Pfam profile PF04043: Plant invertase/pectin methylesterase inhibitor , pectinesterase inhibitor activity	M, lipid INHIBITOR		0.28210	0.45059	0.08291	0.19617	0.22347	0.34073	0.31187	0.58930	-2.16182	-1.55329	-1.68097	-0.76293	-1.85756	-1.22195	0.43030	0.64916	6.10507	2.66207	0.10336	NS	0.22876	NS	0.36772	ns
AC007654	Genomic sequence for Arabidopsis thaliana BAC T19E23 from chromosome I	unknown	unknown		0.40586	0.45214	0.29433	0.23892	0.19773	0.61398	0.28320	0.62108	-2.33837	-0.70373	-1.82013	-0.68715	-1.52105	-1.25364	1.15586	0.80114	1.86102	2.21301	0.31390	NS	0.27019	NS	0.81321	ns
AL138659	At3g59650 Arabidopsis thaliana DNA chromosome 3, BAC clone T16L24	mitochondrial ribosomal protein L51/S25/CI-B8 family protein, low similarity to mitochondrial ribosomal protein bMRP36a (Mus musculus) GI:13559406; contains Pfam profile PF05047: Mitochondrial ribosomal protein L51 / S25 / CI-B8 domain	GIP, translation, ribosome		0.30976	0.45629	0.14010	0.27157	0.21069	0.40883	0.26426	0.64831	-2.24681	-1.29044	-1.91996	-0.62524	-1.76863	-1.27260	0.67626	0.91551	3.69861	1.96582	0.16810	NS	0.29958	NS	0.60049	ns
AC003033	At2g32960 Arabidopsis thaliana chromosome II section 184 of 255 of the complete sequence. Sequence from clones F24L7, T21L14, F25I18	tyrosine specific protein phosphatase family protein, protein amino acid dephosphorylation	M, kinase		0.60091	0.46185	0.30577	0.16086	0.38470	0.81712	0.34811	0.57560	-1.37819	-0.29138	-1.52240	-0.79686	-0.83478	-1.15963	0.76849	0.51303	1.53622	3.19660	0.36736	NS	0.19302	NS	0.66833	ns
AC010675	At1g69960 Arabidopsis thaliana type 2A serine/threonine protein phosphatase (PP2A) mRNA, complete cds	serine/threonine protein phosphatase PP2A-5 catalytic subunit (PP2A5), identical to SP|O04951|P2A5_ARATH Serine/threonine protein phosphatase PP2A-5 catalytic subunit (EC 3.1.3.16) {Arabidopsis thaliana}; contains Pfam profile PF00149: Ser/Thr protein phosphatase , type 2A serine/threonine protein phosphatase (PP2A) mRNA, protein phosphatase type 2A activity, auxin polar transport	M, phosphatase	CPS, transport	0.35075	0.46283	0.06874	0.27727	0.30214	0.39936	0.65889	0.26677	-1.72670	-1.32424	-0.60189	-1.90632	-1.52547	-1.25410	0.28458	0.92238	7.58066	1.92283	0.08350	NS	0.30531	NS	0.72936	ns
AL035678	At4g33410 Arabidopsis thaliana DNA chromosome 4, BAC clone F17M5 (ESSA project)	signal peptide peptidase family protein, contains Pfam domain PF04258: Membrane protein of unknown function (DUF435) , D-alanyl-D-alanine endopeptidase activity,	M, peptide		0.36275	0.47301	0.08630	0.07296	0.30173	0.42377	0.42142	0.52460	-1.72868	-1.23864	-1.24667	-0.93071	-1.48366	-1.08869	0.34651	0.22341	6.05525	6.89147	0.10419	NS	0.09174	NS	0.30822	ns
AF370220	At4g25700 Arabidopsis thaliana putative beta-carotene hydroxylase (AT4g25700) mRNA, complete cds	similar to beta-carotene hydroxylase, putative [Arabidopsis thaliana] (TAIR:At5g52570.1); similar to beta-carotene hydroxylase [Citrus unshiu] (GB:AAG10793.1); contains InterPro domain Carotene hydroxylase (InterPro:IPR005596); contains InterPro domain SUR2-type hydroxylase/desaturase, catalytic domain (InterPro:IPR006087) , Converts beta-carotene to zeaxanthin via cryptoxanthin, beta hydroxylase 1 (BETA-OHASE1), carotene metabolic process, xanthophyll biosynthetic process, beta-carotene hydroxylase activity, leaf	M, caretenoid/xanthophyll		0.19718	0.48123	0.06269	0.40196	0.15285	0.24150	0.19701	0.76546	-2.70979	-2.04988	-2.34369	-0.38561	-2.37983	-1.36465	0.46662	1.38458	7.21264	1.39386	0.08771	NS	0.39619	NS	0.42940	ns
AC010675	At1g69900 Arabidopsis thaliana chromosome 1 BAC T17F3 genomic sequence	expressed protein, contains Pfam profile: PF04601 protein of unknown function (DUF569	unknown		0.38752	0.49521	0.05937	0.15307	0.42950	0.34554	0.38698	0.60345	-1.21927	-1.53309	-1.36969	-0.72870	-1.37618	-1.04919	0.22190	0.45325	8.77057	3.27367	0.07227	NS	0.18874	NS	0.45622	ns
AL161572	At4g28300 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68	hydroxyproline-rich glycoprotein family protein, predicted location cell wall	CPS, cell wall		0.53071	0.53047	0.27891	0.14233	0.33349	0.72792	0.42983	0.63112	-1.58429	-0.45814	-1.21816	-0.66402	-1.02122	-0.94109	0.79631	0.39184	1.81364	3.39658	0.32079	NS	0.18228	NS	0.91008	ns
AF078822	At1g15100 Arabidopsis thaliana RING-H2 finger protein RHA2a mRNA, complete cds	zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger) , RING-H2 finger protein RHA2a mRNA, complete cds (RHA2A) protein binding, zinc ion binding, endomembrane system	ZINC		0.53642	0.53071	0.15691	0.44805	0.42547	0.64737	0.21389	0.84753	-1.23288	-0.62733	-2.22505	-0.23867	-0.93011	-1.23186	0.42819	1.40458	3.07194	1.24030	0.20035	NS	0.43197	NS	0.79871	ns
AF370527	AT5G42300 Arabidopsis thaliana ubiquitin-like protein (K5J14.10) mRNA, complete cds	ubiquitin family protein, contains INTERPRO:IPR000626 ubiquitin domain	GIP, FSD	EIP, signal transduction	0.41198	0.53154	0.00326	0.21219	0.40967	0.41428	0.38150	0.68158	-1.28746	-1.27132	-1.39023	-0.55304	-1.27939	-0.97164	0.01141	0.59199	158.60117	2.32116	0.00401	D	0.25897	NS	0.53881	ns

U70478	At4g22880 Arabidopsis thaliana putative leucoanthocyanidin dioxygenase (LDOX) mRNA, complete cds	leucoanthocyanidin dioxygenase, which is involved in proanthocyanin biosynthesis. Mutant analysis suggests that this gene is also involved in vacuole formation. (LDOX), similar to flavonol synthase 1 (FLS1) [Arabidopsis thaliana] (TAIR:At5g08640.1); similar to anthocyanidin synthase , organization and biogenesis, leucoanthocyanidin dioxygenase activity, proanthocyanidin biosynthetic process	M, anthocyanin biosynth		1.28729	0.53163	1.28568	0.15283	2.19640	0.37817	0.42356	0.63970	1.13514	-1.40288	-1.23936	-0.64454	-0.13387	-0.94195	1.79465	0.42060	0.10549	3.16718	0.93309	NS	0.19470	NS	0.59850	ns
AC016041	At1g49000 Genomic sequence for Arabidopsis thaliana BAC F27J15 from chromosome I	expressed protein	unknown		0.37826	0.53295	0.20205	0.01228	0.23539	0.52113	0.54164	0.52427	-2.08686	-0.94027	-0.88459	-0.93162	-1.51356	-0.90811	0.81076	0.03326	2.64012	38.61658	0.23050	NS	0.01648	NC	0.40198	ns
AF370527	AT5G42300 Arabidopsis thaliana ubiquitin-like protein (K5J14.10) mRNA, complete cds	ubiquitin family protein, contains INTERPRO:IPR000626 ubiquitin domain	GIP, FSD	EIP, signal transduction	0.41263	0.53512	0.32474	0.17364	0.18300	0.64226	0.41234	0.65789	-2.45005	-0.63878	-1.27810	-0.60407	-1.54442	-0.94109	1.28076	0.47661	1.70534	2.79241	0.33763	NS	0.21892	NS	0.59612	ns
AC005724	At2g18700 Arabidopsis thaliana Unknown protein (At2g18700) mRNA, complete cds	glycosyl transferase family 20 protein / trehalose-phosphatase family protein, similar to trehalose-6-phosphate synthase SL-TPS/P, Encodes an enzyme putatively involved in trehalose biosynthesis. The protein has a trehalose synthase (TPS)-like domain that may or may not be active as well as a trehalose phosphatase (TPP)-like domain. metabolic process, trehalose biosynthetic process, transferase activity, transferring glycosyl groups (ATTPS11)	M, glycosyltransferase , threhalose synth		0.43509	0.54097	0.30873	0.25022	0.21679	0.65339	0.36403	0.71790	-2.20565	-0.61398	-1.45786	-0.47814	-1.40981	-0.96800	1.12548	0.69277	1.77149	1.97608	0.32716	NS	0.29824	NS	0.68295	ns
M84701	AT5G62700 Arabidopsis thaliana beta-2 tubulin (TUB2) gene, complete cds	encodes tubulin beta-2/beta-3 chain , response to cold, tubulin complex	CPS, cell structure		0.38103	0.54761	0.08390	0.22749	0.44036	0.32170	0.38675	0.70847	-1.18325	-1.63620	-1.37053	-0.49721	-1.40973	-0.93387	0.32029	0.61753	6.22458	2.13867	0.10141	NS	0.27844	NS	0.43541	ns
U39480	Arabidopsis thaliana AT3g53750/F5K20_50 mRNA, complete cds	Member of the Actin gene family. Expressed in mature pollen. actin 3 (ACT3), identical to SP|P53493 Actin 3 {Arabidopsis thaliana}; supported by full-length cDNA: Ceres: 19581. cytoskeleton, structural constituent of cytoskeleton, cytoskeleton organization and biogenesis, M germinated pollen stage	CPS, cell structure		0.38583	0.54839	0.07749	0.23797	0.44062	0.33104	0.38013	0.71666	-1.18238	-1.59492	-1.39545	-0.48064	-1.38865	-0.93805	0.29171	0.64687	6.73228	2.05079	0.09388	NS	0.28883	NS	0.46394	ns
AC005851	At2g28050 Arabidopsis thaliana chromosome II section 158 of 255 of the complete sequence. Sequence from clones T1E2, F24D13	pentatricopeptide (PPR) repeat-containing protein,	PRR		0.22733	0.56666	0.10075	0.08307	0.15609	0.29857	0.62540	0.50792	-2.67951	-1.74384	-0.67716	-0.97732	-2.21167	-0.82724	0.66162	0.21225	4.72747	5.51187	0.13271	NS	0.11426	NS	0.10625	ns
AL080253	At4g20390 Arabidopsis thaliana DNA chromosome 4, BAC clone F9F13 (ESSA project)	integral membrane family protein, contains TIGRFAM TIGR01569 : plant integral membrane protein TIGR01569; contains Pfam PF04535 : Domain of unknown function (DUF588)	unknown		0.44836	0.58152	0.20547	0.29749	0.30307	0.59365	0.37117	0.79188	-1.72226	-0.75231	-1.42985	-0.33665	-1.23728	-0.88325	0.68586	0.77301	2.55123	1.61589	0.23782	NS	0.35279	NS	0.67590	ns
AL162873	At5g03870 Arabidopsis thaliana DNA chromosome 5, BAC clone F8F6 (ESSA project)	glutaredoxin family protein, contains Pfam profile PF00462: Glutaredoxin , cellular_component, electron carrier activity, protein disulfide oxidoreductase activity, electron transport, N-terminal protein myristoylation	GIP, FSD	M, energy	0.73027	0.59560	0.07267	0.05412	0.67889	0.78166	0.55733	0.63387	-0.55876	-0.35538	-0.84339	-0.65773	-0.45707	-0.75056	0.14381	0.13128	4.49490	8.08531	0.13936	NS	0.07834	NS	0.16672	ns
U95973	At1g11060 Arabidopsis thaliana chromosome 1 BAC T19D16 genomic sequence	expressed protein	unknown		0.51357	0.60228	0.26013	0.13870	0.32963	0.69751	0.70035	0.50420	-1.60107	-0.51971	-0.51384	-0.98793	-1.06039	-0.75088	0.76464	0.33523	1.96122	3.16772	0.30018	NS	0.19467	NS	0.65240	ns
AF325019	At4g27960 A.thaliana UBC9 mRNA for ubiquitin conjugating enzyme homolog	ubiquitin-conjugating enzyme E2-17 kDa 9 (UBC9), E2; identical to gi:297883, SP:P35132; identical to cDNA UBC9 for ubiquitin, ubiquitin conjugating enzyme activity, ubiquitin-dependent protein catabolic process, endomembrane system UBIQUITIN-PROTEIN LIGASE , UBIQUITIN CONJUGATING ENZYME 9	GIP, FSD	EIP, signal transduction	0.55302	0.60527	0.48492	0.04431	0.89591	0.21013	0.57394	0.63660	-0.15858	-2.25063	-0.80104	-0.65153	-1.20460	-0.72629	1.47931	0.10572	1.15160	9.71552	0.45522	NS	0.06530	NS	0.69305	ns
AC009991	AT3G61010 Arabidopsis thaliana chromosome III BAC F9F8 genomic sequence	glycosyl hydrolase family protein 85, hypothetical protein F9F8.14 - Arabidopsis thaliana, EMBL:AC009991 , hydrolase activity, acting on glycosyl bonds, biological_process	M, glycosyltransferase		0.65604	0.60557	0.07076	0.26114	0.70608	0.60601	0.42092	0.79023	-0.50210	-0.72259	-1.24839	-0.33966	-0.61234	-0.79402	0.15591	0.64257	5.55431	1.74754	0.11340	NS	0.33088	NS	0.73506	ns
AL161472	At4g00700 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2	C2 domain-containing protein, contains INTERPRO:IPR000008 C2 domain	CPS, signal transduction		0.44203	0.61459	0.01758	0.07568	0.45446	0.42960	0.66811	0.56108	-1.13777	-1.21894	-0.58185	-0.83373	-1.17836	-0.70779	0.05740	0.17811	29.03360	5.62004	0.02192	D	0.11210	NS	0.07078	ns
U02949	AT3G55440 Arabidopsis thaliana Columbia cytosolic triose phosphate isomerase (Atctimc) mRNA, complete cds	Columbia cytosolic triose phosphate isomerase (Atctimc)	M, carbohydrate		0.94730	0.62152	1.01409	0.01140	1.66437	0.23023	0.61346	0.62958	0.73497	-2.11886	-0.70496	-0.66753	-0.69194	-0.68624	2.01796	0.02647	0.48492	36.66738	0.71256	NS	0.01736	NC	0.99718	ns
AC006919	At2g36400 Arabidopsis thaliana chromosome II section 199 of 255 of the complete sequence. Sequence from clones F2H17, F1O11, F13K3	expressed protein, nearly identical to transcription activator GRL3, Growth regulating factor encoding transcription activator. One of the nine members of a GRF gene family, containing nuclear targeting domain. Mutants result in smaller leaves indicating the role of the gene in leaf development. Expressed in root, shoot and flower. (ATGRF3), transcriptional activator activity, leaf development, root, elongation zone, floral meristem, flower, juvenile leaf, apical meristem, seedling growth, B reproductive growth	GIP, trans activator		0.34681	0.62606	0.14978	0.17451	0.24090	0.45272	0.74946	0.50266	-2.05352	-1.14332	-0.41608	-0.99233	-1.59842	-0.70421	0.64361	0.40747	3.51223	2.44407	0.17659	NS	0.24725	NS	0.23876	ns
AC016447	At1g68360 Arabidopsis thaliana chromosome 1 BAC T22E19 genomic sequence	zinc finger protein-related, similar to zinc finger protein GI:790683 from (Arabidopsis thaliana) , intracellular, transcription factor activity, regulation of transcription	GIP, TF		0.48094	0.63524	0.19090	0.24789	0.34595	0.61592	0.45995	0.81052	-1.53135	-0.69918	-1.12044	-0.30308	-1.11527	-0.71176	0.58843	0.57796	2.68038	1.74160	0.22733	NS	0.33182	NS	0.56055	ns
AC007212	At2g18190 Arabidopsis thaliana chromosome II section 106 of 255 of the complete sequence. Sequence from clones F8D23, T30D6	AAA-type ATPase family protein, contains Pfam profile: ATPase family PF00004 , ATP binding, ATPase activity, endomembrane system	M, energy, ATPase		0.47589	0.63799	0.17337	0.02112	0.35330	0.59848	0.62306	0.65293	-1.50104	-0.74064	-0.68256	-0.61500	-1.12084	-0.64878	0.53769	0.04777	2.94800	19.20788	0.20820	NS	0.03311	NC	0.34171	ns

AY046048	At3g56800 Arabidopsis thaliana putative calmodulin-3 protein (T8M16_130/AT3g56800) mRNA, complete cds	calmodulin-2/3/5 (CAM3), identical to calmodulin GI:474183 from (Arabidopsis thaliana); almost identical to calmodulin-2/3/5 SP:P25069 (Arabidopsis thaliana) , calcium ion binding, calcium-mediated signaling , ACAM3	EIP, signal transduction	CPS, signal transduction	0.76213	0.64256	0.49552	0.16172	1.11251	0.41174	0.75692	0.52820	0.15382	-1.28020	-0.40180	-0.92083	-0.56319	-0.66131	1.01400	0.36701	0.78547	2.54823	0.57613	NS	0.23807	NS	0.90938	ns
AC069251	At1g20790 Genomic sequence for Arabidopsis thaliana BAC F2D10 from chromosome I	F-box family protein, contains Pfam:PF00646 F-box domain	Fbox		0.27338	0.65549	0.20660	0.22492	0.12729	0.41946	0.81453	0.49644	-2.97379	-1.25339	-0.29595	-1.01030	-2.11359	-0.65313	1.21651	0.50512	2.45708	1.82860	0.24606	NS	0.31859	NS	0.25741	ns
M84701	AT5G62700 Arabidopsis thaliana beta-2 tubulin (TUB2) gene, complete cds	encodes tubulin beta-2/beta-3 chain , response to cold, tubulin complex	CPS, cell structure		0.38260	0.65844	0.06931	0.21839	0.33359	0.43161	0.50401	0.81287	-1.58385	-1.21221	-0.98846	-0.29891	-1.39803	-0.64368	0.26279	0.48759	7.52353	1.86695	0.08412	NS	0.31306	NS	0.19396	ns
AC009176	At3g07710 Arabidopsis thaliana chromosome III P1 MLP3 genomic sequence	expressed protein	unknown		0.59853	0.66261	0.41367	0.12821	0.89104	0.30603	0.57195	0.75326	-0.16644	-1.70827	-0.80604	-0.40877	-0.93735	-0.60740	1.09024	0.28091	1.21590	3.05794	0.43817	NS	0.20121	NS	0.71876	ns
AC026875	At1g08170 Genomic sequence for Arabidopsis thaliana BAC T6D22 from chromosome I	histone H2B family protein, similar to histone H2B from Chlamydomonas reinhardtii (SP|P54347, SP|P54346, SP|P50565), Volvox carteri (SP|P16867, SP|P16868); contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4, nucleus, DNA binding, chromosome organization and biogenesis (sensu Eukaryota), nucleosome assembly, nucleosome	GIP, chromosome		0.68878	0.66487	0.15374	0.15248	0.58006	0.79749	0.55705	0.77269	-0.78572	-0.32646	-0.84412	-0.37204	-0.55609	-0.60808	0.32475	0.33381	2.42170	2.57615	0.24930	NS	0.23572	NS	0.88906	ns
AC003680	Arabidopsis thaliana At2g45640/F17K2.17 mRNA, complete cds	Involved in the regulation of salt stress. Expression of AtSAP18 is induced by NaCl, cold, drought, ABA, and ethylene treatment. AtSAP18 and HDA19 associate with ERF3 and ERF4 both in vitro and in vivo. SIN3 ASSOCIATED POLYPEPTIDE P18 (SAP18), mitochondrion, protein binding, response to salt stress, transcription regulator activity, response to abscisic acid stimulus,	GIP, Transcription regulator		0.38541	0.66959	0.15338	0.31399	0.27695	0.49387	0.44757	0.89162	-1.85229	-1.01781	-1.15983	-0.16550	-1.43505	-0.66266	0.59007	0.70310	3.43937	1.33288	0.18013	NS	0.40977	NS	0.35614	ns
D01024	At1g06400 Arabidopsis thaliana mRNA for small GTP-binding protein (ara-2), complete cds	mRNA for small GTP-binding protein (ara-2), complete cds, Ras-related GTP-binding protein (ARA-2), identical to Ras-related protein ARA-2 SP:P28185 from (Arabidopsis thaliana) exosome (RNase complex), intracellular, GTP binding, intracellular protein transport, protein transport, small GTPase mediated signal transduction	CPS, transport, signal transduction	EIP, signal transduction	0.55756	0.67831	0.19884	0.00247	0.41695	0.69816	0.67656	0.68005	-1.26204	-0.51837	-0.56371	-0.55628	-0.89021	-0.56000	0.52585	0.00526	2.39411	150.62440	0.25189	NS	0.00423	NC	0.46822	ns
N65439	ESTs	unknown	unknown		0.37146	0.68823	0.39660	0.07167	0.09102	0.65190	0.63755	0.73892	-3.45761	-0.61728	-0.64938	-0.43652	-2.03745	-0.54295	2.00841	0.15052	1.43466	5.10135	0.38753	NS	0.12323	NS	0.40410	ns
AF275664	AT3G19980 Arabidopsis thaliana serine/threonine protein phosphatase (STPP) mRNA, complete cds	Encodes catalytic subunit of serine/threonine protein phosphatase 2A. It can associate with phytochromes A and B in vitro. Mutant plants display an accelerated flowering phenotype. protein phosphatase type 2A complex, protein binding, protein serine/threonine kinase activity, negative regulation of flower development (STPP)	M, kinase		0.41790	0.70737	0.17203	0.25012	0.53954	0.29625	0.88423	0.53050	-0.89019	-1.75510	-0.17750	-0.91456	-1.32265	-0.54603	0.61159	0.52118	3.05842	1.48164	0.20118	NS	0.37796	NS	0.30504	ns
AL035679	At4g39020 Arabidopsis thaliana DNA chromosome 4, BAC clone F19H22 (ESSA project)	SH3 domain-containing protein, similar to SH3 domain-containing protein 2 (SH3, found in a great variety of intracellular or membrane-associated proteins)	unknown		0.51446	0.71066	0.22477	0.20949	0.35553	0.67340	0.56253	0.85879	-1.49197	-0.57046	-0.82999	-0.21962	-1.03122	-0.52480	0.65160	0.43159	2.23811	1.71963	0.26750	NS	0.33532	NS	0.45623	ns
AC079286	At1g33980 Arabidopsis thaliana chromosome 1 BAC T15K4 genomic sequence	Involved in mRNA surveillance, detects exported mRNAs with truncated open reading frames and initiates nonsense-mediated mRNA decay (NMD)	GIP, replication and repair		0.25239	0.71321	0.15034	0.39136	0.35870	0.14609	0.98994	0.43647	-1.47915	-2.77511	-0.01458	-1.19604	-2.12713	-0.60531	0.91638	0.83541	3.28273	1.02469	0.18824	NS	0.49224	NS	0.22477	ns
AL031018	At4g22980 Arabidopsis thaliana DNA chromosome 4, BAC clone F7H19 (ESSA project)	expressed protein,	unknown		0.73313	0.71912	0.09759	0.55775	0.66413	0.80214	0.32473	1.11351	-0.59047	-0.31808	-1.62267	0.15511	-0.45427	-0.73378	0.19261	1.25708	3.33544	0.82550	0.18544	NS	0.56067	NS	0.78534	ns
AC083891	At1g66920 Arabidopsis thaliana chromosome 1 BAC T4O24 genomic sequence	serine/threonine protein kinase, putative, similar to receptor serine/threonine kinase PR55K gi|1235680|gb|AAC49208; contains protein kinase domain, Pfam:PF00069; contains serine/threonine protein kinase domain, INTERPRO:IPR002290 , kinase activity, protein amino acid phosphorylation, endomembrane system	M, kinase		0.41762	0.72266	0.32576	0.18617	0.18728	0.64797	0.59102	0.85430	-2.41674	-0.62600	-0.75873	-0.22718	-1.52137	-0.49296	1.26624	0.37586	1.69915	1.85479	0.33864	NS	0.31479	NS	0.38565	ns
AB009053	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MQB2	unknown	unknown		0.34858	0.74000	0.23717	0.68751	0.18088	0.51629	0.25385	1.22614	-2.46693	-0.95375	-1.97793	0.29413	-1.71034	-0.84190	1.06998	1.60658	2.26059	0.74109	0.26514	NS	0.59398	NS	0.58971	ns
AC083859	At1g41750 Arabidopsis thaliana chromosome 1 BAC F9M8 genomic sequence	expressed protein	unknown		0.46425	0.74097	0.43135	0.02481	0.15925	0.76926	0.72343	0.75851	-2.65068	-0.37845	-0.46707	-0.39875	-1.51456	-0.43291	1.60671	0.04831	1.33311	12.67304	0.40972	NS	0.05013	NC	0.44172	ns
AF370464	At1g33055 Arabidopsis thaliana Unknown protein mRNA, complete cds	Expressed protein	unknown		0.59377	0.74187	0.33881	0.55811	0.35420	0.83335	0.34722	1.13651	-1.49736	-0.26301	-1.52607	0.18461	-0.88018	-0.67073	0.87282	1.20963	1.42615	0.78417	0.38931	NS	0.57664	NS	0.86095	ns
AC013354	Genomic sequence for Arabidopsis thaliana BAC F15H18 from chromosome I	unknown	unknown		0.66371	0.74275	0.15824	0.23007	0.55182	0.77561	0.90543	0.58006	-0.85774	-0.36661	-0.14333	-0.78572	-0.61217	-0.46452	0.34728	0.45424	2.49290	1.44625	0.24286	NS	0.38513	NS	0.74998	ns
AC007168	At2g22320 Arabidopsis thaliana chromosome II section 126 of 255 of the complete sequence. Sequence from clones T16B14, T26C19, F14M13	hypothetical protein	unknown		0.60368	0.75560	0.20785	0.61948	0.45671	0.75066	0.31756	1.19363	-1.13066	-0.41378	-1.65489	0.25536	-0.77222	-0.69977	0.50692	1.35075	2.15437	0.73264	0.27666	NS	0.59747	NS	0.94984	ns
AL033545	At4g22560 Arabidopsis thaliana DNA chromosome 4, BAC clone F7K2 (ESSA project)	expressed protein	unknown		0.51717	0.75610	0.08686	0.22158	0.45576	0.57859	0.59942	0.91278	-1.13367	-0.78938	-0.73836	-0.13166	-0.96152	-0.43501	0.24345	0.42900	5.58563	1.43403	0.11278	NS	0.38766	NS	0.27023	ns
AC005698	At1g62520 Genomic sequence for Arabidopsis thaliana BAC T3P18 from Chromosome 1	expressed protein	unknown		0.41089	0.75643	0.20067	0.17469	0.26899	0.55278	0.63290	0.87995	-1.89436	-0.85521	-0.65995	-0.18450	-1.37479	-0.42223	0.73479	0.33620	2.64598	1.77610	0.23004	NS	0.32645	NS	0.23742	ns
AF325000	At1g54410 Arabidopsis thaliana At1g54410 (At1g54410/F20D21_23) mRNA, complete cds	dehydrin family protein, contains Pfam domain, PF00257: Dehydrin , response to stress, response to water	EIP, signal transduction		0.86121	0.75835	1.06445	0.11475	0.10853	1.61389	0.67721	0.83949	-3.20378	0.69055	-0.56233	-0.25242	-1.25662	-0.40738	2.75371	0.21914	0.64536	2.62896	0.63515	NS	0.23140	NS	0.70614	ns

AF326881	At4g38580 Arabidopsis thaliana putative farnesylated protein (ATFP6) (F20M13.140/AT4g38580) mRNA, complete cds	heavy-metal-associated domain-containing protein / copper chaperone (CCH)-related, low similarity to copper homeostasis factor (PMID:9701579)(GI:3168840); nearly identical to farnesylated protein TFP6 (GI:4097553); contains Heavy-metal-associated domain PF00403 , metal ion binding, heat acclimation (ATPF6)	EIP, signal transduction		0.53175	0.76393	0.01348	0.83342	0.52222	0.54128	0.17462	1.35325	-0.93727	-0.88555	-2.51772	0.43643	-0.91141	-1.04065	0.03657	2.08890	35.24522	0.70453	0.01806	NC	0.60927	NS	0.93826	ns
AL392145	At5g24740 Arabidopsis thaliana DNA chromosome 5, BAC clone T4C12 (ESSA project)	expressed protein	unknown		0.42900	0.76935	0.20391	0.23169	0.57319	0.28482	0.60552	0.93318	-0.80291	-1.81189	-0.72375	-0.09977	-1.30740	-0.41176	0.71346	0.44122	2.59153	1.31979	0.23445	NS	0.41279	NS	0.27014	ns
AF386979	At3g13740 Arabidopsis thaliana Unknown protein (MMM17.15) mRNA, complete cds	URF 4-related, similar to URF 4 (GI:49224) (Swiss-Prot:Q05370)(Synechococcus sp.) , chloroplast, RNA binding, ribonuclease III activity, RNA processing	GIP, translation//rep and repair		0.42682	0.77492	0.08928	0.04195	0.36369	0.48995	0.80458	0.74525	-1.45922	-1.02930	-0.31370	-0.42420	-1.24426	-0.36895	0.30400	0.07814	5.78835	6.67780	0.10891	NS	0.09463	NS	0.05869	ns
AC005508	At1g26910 Arabidopsis thaliana chromosome I BAC T2P11 genomic sequence	60S ribosomal protein L10 (RPL10B), ribosome, structural constituent of ribosome, protein biosynthesis	GIP, translation, ribosome		0.47127	0.78534	0.16849	0.49064	0.35213	0.59041	0.43841	1.13227	-1.50581	-0.76020	-1.18966	0.17922	-1.13301	-0.50522	0.52722	0.96794	3.03916	0.73815	0.20237	NS	0.59519	NS	0.50508	ns
AC022472	At1g19960 Arabidopsis thaliana unknown protein (T20H2.25) mRNA, complete cds	expressed protein	unknown		0.39296	0.80965	0.32141	0.73119	0.16569	0.62023	0.29262	1.32668	-2.59348	-0.68913	-1.77290	0.40782	-1.64130	-0.68254	1.34658	1.54200	1.72374	0.62597	0.33466	NS	0.64394	NS	0.57588	ns
AL050300	Arabidopsis thaliana DNA chromosome 3, BAC clone F22O6	unknown	unknown		0.61028	0.82053	0.28679	0.42487	0.81306	0.40749	0.52009	1.12096	-0.29856	-1.29518	-0.94315	0.16473	-0.79687	-0.38921	0.70471	0.78339	1.59914	0.70262	0.35577	NS	0.61008	NS	0.63919	ns
AL138652	At3g44650 Arabidopsis thaliana DNA chromosome 3, BAC clone T18B22	non-LTR retrotransposon family (LINE), has a 5.1e-43 P-value blast match to GB:NP_038605 L1 repeat, Tf subfamily, member 30 (LINE-element) (Mus musculus), RNA-directed DNA polymerase activity	TRANS		1.63122	0.82152	1.40546	0.38170	2.62503	0.63741	0.55162	1.09143	1.39233	-0.64970	-0.85827	0.12622	0.37132	-0.36602	1.44393	0.69613	0.36368	0.74359	0.77794	NS	0.59295	NS	0.58211	ns
AF224701	At2g03340 Arabidopsis thaliana WRKY DNA-binding protein 3 (WRKY3) mRNA, complete cds	WRKY family transcription factor, contains Pfam profile: PF03106 WRKY DNA -binding domain , transcription factor activity, regulation of transcription, DNA-dependent , AF224701 Arabidopsis thaliana WRKY DNA-binding protein 3 (WRKY3)	GIP, TF		0.19366	0.82990	0.18423	0.62953	0.06339	0.32393	0.38476	1.27505	-3.97966	-1.62626	-1.37799	0.35055	-2.80296	-0.51372	1.66411	1.22226	2.38205	0.59440	0.25303	NS	0.65859	NS	0.25742	ns
AF325030	At1g28480 Arabidopsis thaliana At1g28480 (At1g28480/F3M18_8) mRNA, complete cds	glutaredoxin family protein, contains INTERPRO Domain IPR002109, Glutaredoxin (thioltransferase) , cellular_component, electron transport, thiol-disulfide exchange intermediate activity	GIP, FSD	M, energy	0.59135	0.83342	0.29764	0.07562	0.38088	0.80181	0.77995	0.88689	-1.39258	-0.31866	-0.35855	-0.17318	-0.85562	-0.26586	0.75938	0.13108	1.59345	2.86838	0.35679	NS	0.21356	NS	0.39224	ns
AC079677	At1g47270 Arabidopsis thaliana chromosome 1 BAC F8G22 genomic sequence	Member of TLP family, TLP6, TUBBY LIKE PROTEIN 6 , phosphoric diester hydrolase activity, transcription factor activity, regulation of transcription	GIP, TF		0.67629	0.84791	0.47224	0.65572	0.34237	1.01022	0.38425	1.31158	-1.54637	0.01467	-1.37987	0.39130	-0.76585	-0.49429	1.10382	1.25241	0.98121	0.55814	0.50604	NS	0.67591	NS	0.83944	ns
AL022604	At4g35390 Arabidopsis thaliana DNA chromosome 4, BAC clone F23E12 (ESSA project)	DNA-binding protein-related, contains Pfam domain PF03479: Domain of unknown function (DUF296), found in AT-hook motifs Pfam:PF02178	GIP		0.51032	0.86664	0.31704	0.04654	0.28614	0.73450	0.83374	0.89955	-1.80520	-0.44517	-0.26233	-0.15272	-1.12518	-0.20753	0.96169	0.07750	1.65464	3.78675	0.34608	NS	0.16437	NS	0.31082	ns
N37162	ESTs, Highly similar to T05255 RNA-binding protein homolog F18A5.250 (AT4G13860)- Arabidopsis thaliana [A.thaliana]	glycine-rich RNA-binding protein, putative, similar to Glycine-rich RNA-binding protein 2, mitochondrial precursor (AtGRP2) (Swiss-Prot:Q9SVM8) (Arabidopsis thaliana) ; contains InterPro entry IPR000504: RNA-binding region RNP 1 (RNA recognition motif) (RRM)	GIP		0.45804	0.87190	0.33589	0.34651	0.22053	0.69555	0.62688	1.11692	-2.18095	-0.52378	-0.67373	0.15953	-1.35236	-0.25710	1.17180	0.58920	1.63213	0.61710	0.34995	NS	0.64802	NS	0.35903	ns
AC008016	At1g52720 Arabidopsis thaliana chromosome 1 BAC F6D8 sequence	expressed protein	unknown		0.46607	0.87524	0.40959	0.25034	0.17644	0.75569	0.69822	1.05226	-2.50272	-0.40414	-0.51824	0.07349	-1.45343	-0.22238	1.48393	0.41841	1.38515	0.75162	0.39808	NS	0.58968	NS	0.37604	ns
AC079041	At1g31850 Arabidopsis thaliana chromosome 1 BAC F5M6 genomic sequence	dehydration-responsive protein, putative, strong similarity to early-responsive to dehydration stress ERD3 protein (Arabidopsis thaliana) GI:15320410; contains Pfam profile PF03141: Putative methyltransferase	EIP, signal transduction	M, methyltransferase	0.42826	0.87554	0.34310	0.54491	0.18565	0.67086	0.49022	1.26085	-2.42936	-0.57591	-1.02849	0.33440	-1.50264	-0.34705	1.31059	0.96371	1.62144	0.50928	0.35182	NS	0.70012	NS	0.42088	ns
AC012679	At1g73690 Arabidopsis thaliana cak3At mRNA for CDK-activating kinase 3, complete cds	cyclin dependent kinase activator CDKD;1. Nuclear localization. Involved in cell cycle regulation and cell differentiation. kinase activity, regulation of progression through cell cycle, cell differentiation	CPS, cell cycle	M, kinase	0.62873	0.88336	0.68799	0.39524	1.11521	0.14225	1.16283	0.60388	0.15732	-2.81355	0.21764	-0.72766	-1.32812	-0.25501	2.10072	0.66843	0.89409	0.53953	0.53556	NS	0.68502	NS	0.56232	ns
AB017068	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MJG14	unknown	unknown		0.49104	0.92073	0.06705	0.20736	0.44363	0.53845	1.06736	0.77410	-1.17257	-0.89312	0.09404	-0.36940	-1.03285	-0.13768	0.19760	0.32771	7.39196	0.59415	0.08560	NS	0.65870	NS	0.08049	ns
AL133452	At3g51380 Arabidopsis thaliana DNA chromosome 3, BAC clone F26O13	calmodulin-binding family protein	EIP, signal transduction	CPS, signal transduction	0.36941	0.92668	0.39151	0.26575	0.09258	0.64625	0.73877	1.11459	-3.43323	-0.62983	-0.43680	0.15652	-2.03153	-0.14014	1.98230	0.41954	1.44933	0.47240	0.38450	NS	0.71905	NS	0.31763	ns
AL161471	At4g00360 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 1	Encodes a member of the CYP86A subfamily of cytochrome p450 genes. Expressed at moderate levels in flowers, leaves, roots and stems. , fatty acid (omega-1)-hydroxylase activity, fatty acid metabolic process, fruit, flower, leaf, stem	M, Cytp450		0.44662	0.94203	0.25997	0.66717	0.26279	0.63045	0.47027	1.41379	-1.92799	-0.66554	-1.08844	0.49957	-1.29677	-0.29443	0.89269	1.12289	2.05436	0.37082	0.28839	NS	0.77394	NS	0.42723	ns
M84701	AT5G62700 Arabidopsis thaliana beta-2 tubulin (TUB2) gene, complete cds	encodes tubulin beta-2/beta-3 chain , response to cold, tubulin complex	CPS, cell structure		0.31379	0.94959	0.21745	0.59069	0.16002	0.46755	0.53191	1.36727	-2.64365	-1.09681	-0.91073	0.45130	-1.87023	-0.22972	1.09378	0.96310	2.41813	0.33731	0.24964	NS	0.79289	NS	0.25239	ns
AL132972	At3g52270 Arabidopsis thaliana DNA chromosome 3, BAC clone T25B15	expressed protein	unknown		0.18717	0.95950	0.06626	0.39075	0.23403	0.14032	0.68319	1.23580	-2.09526	-2.83320	-0.54963	0.30544	-2.46423	-0.12210	0.52180	0.60463	6.67867	0.28558	0.09462	NS	0.82291	NS	0.05352	ns
AL022603	At4g21550 Arabidopsis thaliana DNA chromosome 4, BAC clone F18E5 (ESSAII project)	transcriptional factor B3 family protein, low similarity to SP|Q01593 Abscisic acid-insensitive protein 3 {Arabidopsis thaliana}, SP|P37398 Viviparous protein homolog {Oryza sativa}; contains Pfam profile PF02362: B3 DNA binding domain , transcription factor activity, regulation of transcription, DNA-dependent, endomembrane system	GIP, TF		0.37106	0.97705	0.23043	0.37954	0.20813	0.53400	0.70867	1.24543	-2.26447	-0.90510	-0.49681	0.31664	-1.58478	-0.09008	0.96122	0.57520	2.33164	0.22149	0.25793	NS	0.86124	NS	0.19978	ns
AC005882	Arabidopsis thaliana chromosome I BAC T13M11 genomic sequence	unknown	unknown		0.38371	0.99497	0.17671	0.62482	0.25876	0.50866	0.55315	1.43678	-1.95034	-0.97524	-0.85425	0.52284	-1.46279	-0.16571	0.68950	0.97375	3.00029	0.24066	0.20481	NS	0.84965	NS	0.26402	ns
AB026643	At5g36000 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MEE13	expressed protein, strong similarity to unknown protein (emb|CAB71103.1)	unknown		0.48104	0.99957	0.13264	0.41061	0.38725	0.57483	0.70922	1.28991	-1.36865	-0.79879	-0.49570	0.36727	-1.08372	-0.06421	0.40296	0.61021	3.80342	0.14882	0.16368	NS	0.90595	NS	0.18741	ns

AC084414	At1g48920 Arabidopsis thaliana At1g48920/F27K7_6 mRNA sequence	nucleolin, putative, similar to nuM1 protein GI:1279562 from (Medicago sativa) , nucleic acid binding	GIP, chromatin remodeling		0.35131	1.00059	0.34983	0.35488	0.10394	0.59867	0.74966	1.25153	-3.26618	-0.74016	-0.41570	0.32369	-2.00317	-0.04600	1.78617	0.52283	1.58603	0.12443	0.35813	NS	0.92119	NS	0.27533	ns
AB017061	At5g49010 Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K19E20	DNA replication protein-related, similar to Sld5 (Xenopus laevis) GI:29365477; contains Pfam profile PF05916: Eukaryotic protein of unknown function (DUF873)	GIP, replication		0.44867	1.01990	0.26571	0.82408	0.26079	0.63656	0.43719	1.60261	-1.93903	-0.65164	-1.19367	0.68043	-1.29533	-0.25662	0.91032	1.32518	2.01234	0.27386	0.29360	NS	0.82983	NS	0.45733	ns
AL049660	At3g57600 Arabidopsis thaliana DNA chromosome 3, BAC clone F15B8	encodes a member of the DREB subfamily A-2 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are eight members in this subfamily including DREB2A AND DREB2B that are involved in response to drought. DNA binding, transcription factor activity, regulation of transcription, DNA-dependent	GIP, TF		1.00089	1.02197	0.72866	0.28295	0.48565	1.51613	0.82189	1.22204	-1.04201	0.60039	-0.28298	0.28929	-0.22081	0.00316	1.16135	0.40466	0.26888	0.01104	0.83278	NS	0.99297	NS	0.82084	ns
AC002391	At2g23200 Arabidopsis thaliana chromosome II section 132 of 255 of the complete sequence. Sequence from clones F21P24, T20D16, F26B6	protein kinase family protein, contains protein kinase domain, Pfam:PF00069, kinase activity, protein amino acid phosphorylation, endomembrane system	M, kinase		0.60767	1.02691	0.14872	0.38726	0.71283	0.50250	0.75307	1.30074	-0.48837	-0.99279	-0.40915	0.37933	-0.74058	-0.01491	0.35668	0.55754	2.93634	0.03781	0.20896	NS	0.97594	NS	0.26116	ns
AC022492	Genomic sequence for Arabidopsis thaliana BAC F1L3 from chromosome I	unknown	unknown		0.50237	1.03116	0.42394	1.01536	0.20260	0.80214	0.31319	1.74913	-2.30330	-0.31808	-1.67490	0.80663	-1.31069	-0.43413	1.40376	1.75471	1.32044	0.34989	0.41264	NS	0.78573	NS	0.63659	ns
AL162459	At3g45870 Arabidopsis thaliana DNA chromosome 3, BAC clone F16L2	integral membrane family protein / nodulin MtN21-related, simlar to MtN21 GI:2598575 (root nodule development) Medicago truncatula, EMBL:MTY15293	EIP, signal transduction		0.71446	1.04686	0.31307	0.31169	0.49309	0.93583	0.82646	1.26726	-1.02009	-0.09568	-0.27498	0.34171	-0.55789	0.03337	0.65365	0.43607	1.20702	0.10821	0.44046	NS	0.93138	NS	0.39874	ns
AB016879	At5g54540 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MRB17	expressed protein	unknown		0.33849	1.04702	0.25713	0.02811	0.15667	0.52031	1.06690	1.02715	-2.67423	-0.94257	0.09342	0.03864	-1.80840	0.06603	1.22447	0.03874	2.08862	2.41068	0.28427	NS	0.25033	NS	0.16293	ns
AL353995	At5g10570 Arabidopsis thaliana DNA chromosome 5, BAC clone F12B17 (ESSA project)	basic helix-loop-helix (bHLH) family protein, bHLH transcription factor, Arabidopsis thaliana, EMBL:AC005167 , nucleus, DNA binding, transcription factor activity, regulation of transcription	GIP, TF		0.87599	1.04926	0.41206	0.65352	1.16735	0.58462	0.58715	1.51137	0.22324	-0.77443	-0.76819	0.59586	-0.27560	-0.08617	0.70546	0.96453	0.55248	0.12634	0.67867	NS	0.91999	NS	0.84343	ns
AL031004	Arabidopsis thaliana DNA chromosome 4, BAC clone F28M20 (ESSAII project)	unknown	unknown		0.68913	1.05248	0.18807	0.21223	0.55615	0.82211	0.90241	1.20255	-0.84645	-0.28259	-0.14814	0.26610	-0.56452	0.05898	0.39871	0.29291	2.00233	0.28475	0.29487	NS	0.82339	NS	0.21665	ns
AL163527	At3g59060 Arabidopsis thaliana DNA chromosome 3, BAC clone F17J16	encodes a novel Myc-related bHLH transcription factor, which physically associated with APRR1/TOC1 and is a member of PIF3 transcription factor family. similar to phytochrome-interacting factor 4 (PIF4) / basic helix-loop-helix protein 9 (bHLH9) / short under red-light 2 (SRL2) [Arabidopsis thaliana] (TAIR:At2g43010.1); similar to BP-5 protein [Oryza sativa] (GB:CAD32238.1); contains InterPro domain Basic helix-loop-helix dimerization domain bHLH (InterPro:IPR001092) , DNA binding, transcription factor activity	GIP, TF		0.66984	1.05750	0.33010	0.28210	0.43643	0.90326	0.85802	1.25697	-1.19619	-0.14679	-0.22091	0.32995	-0.67149	0.05452	0.74204	0.38952	1.27976	0.19795	0.42227	NS	0.87559	NS	0.34523	ns
AF326857	At5g08290 Arabidopsis thaliana putative cis-trans isomerase protein (F8L15_20) mRNA, complete cds	yellow-leaf-specific protein 8 (YLS8) / mitosis protein DIM1, putative, contains Pfam domain PF02966: Mitosis protein DIM1; identical to cDNA YLS8 mRNA for Dim1 homolog GI:13122293 , spliceosome complex, catalytic activity, mitosis	GIP, translation		0.36029	1.06394	0.21197	0.19470	0.21040	0.51017	0.92627	1.20161	-2.24880	-0.97094	-0.11049	0.26497	-1.60987	0.07724	0.90358	0.26549	2.51964	0.41143	0.24053	NS	0.75151	NS	0.12683	ns
AB016889	At3g26830 Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDJ14	cytochrome P450 71B15, Mutations in pad3 (phytoalexin deficient 3) are defective in biosynthesis of the indole derived phytoalexin camalexin. Encodes a cytochrome P450 enzyme that catalyzes the conversion of dihydrocamalexic acid to camalexin. monooxygenase activity, indole phytoalexin biosynthesis, camalexin biosynthesis, response to ABA	M, CytP450, camalexin		0.20693	1.07226	0.08611	0.66258	0.14604	0.26782	1.54078	0.60375	-2.77552	-1.90066	0.62366	-0.72799	-2.33809	-0.05216	0.61862	0.95576	5.34510	0.07718	0.11774	NS	0.95096	NS	0.10487	ns
AF217458	At4g32210 Arabidopsis thaliana heat shock protein 70 (Hsc70-5) mRNA, complete cds; nuclear gene for mitochondrial product	retrotransposon family, weak similarity to heat shock protein 70 (Arabidopsis thaliana) GI:6746590, succinate dehydrogenase subunit 3 (Gossypium hirsutum) GI:14861484; contains Pfam profiles PF01127: Succinate dehydrogenase cytochrome b subunit, PF03732: Retrotransposon gag protein ; mitochondrion, respiratory chain complex II (sensu Eukaryota), succinate dehydrogenase activity, mitochondrial electron transport, succinate to ubiquinone, (SDH3-2)	TRANS		0.42142	1.07289	0.34077	0.13421	0.18046	0.66238	1.16779	0.97800	-2.47022	-0.59426	0.22378	-0.03210	-1.53224	0.09584	1.32650	0.18094	1.63355	0.74910	0.34970	NS	0.59070	NS	0.22761	ns
X63443	At5g12020 A.thaliana mRNA for heat shock protein hsp 17.6 - II	17.6 kDa class II heat shock protein (HSP17.6-CII), identical to 17.6 kDa class II heat shock protein SP:P29830 from (Arabidopsis thaliana)	GIP, FSD	EIP, signal transduction	0.48479	1.07768	0.22426	0.60584	0.32622	0.64336	0.64929	1.50608	-1.61609	-0.63629	-0.62307	0.59080	-1.12619	-0.01614	0.69282	0.85834	2.29883	0.02659	0.26121	NS	0.98307	NS	0.29066	ns
AC006922	At2g36880 Arabidopsis thaliana chromosome II section 201 of 255 of the complete sequence. Sequence from clones T1J8	S-adenosylmethionine synthetase, putative, similar to S-adenosylmethionine synthetase 3 (Methionine adenosyltransferase 3, AdoMet synthetase 3) (Lycopersicon esculentum) SWISS-PROT:P43282 , methionine adenosyltransferase activity, S-adenosylmethionine biosynthesis	M, amino acid		0.49484	1.08697	0.29466	0.08497	0.28649	0.70320	1.02689	1.14705	-1.80346	-0.50799	0.03828	0.19793	-1.15573	0.11811	0.91603	0.11289	1.78426	1.47961	0.32521	NS	0.37837	NS	0.19022	ns
U72711	AT2G14260 Arabidopsis thaliana proline iminopeptidase mRNA, complete cds	encodes proline iminopeptidase , prolyl aminopeptidase activity, aromatic compound metabolic process, proteolysis	M, peptide		0.78861	1.09905	0.38026	0.87199	1.05750	0.51973	0.48246	1.71564	0.08065	-0.94418	-1.05151	0.77875	-0.43176	-0.13638	0.72466	1.29419	0.84260	0.14903	0.55425	NS	0.90582	NS	0.80469	ns

AY035013	At3g27380 Arabidopsis thaliana putative succinate dehydrogenase iron-protein subunit (K1G2.9) mRNA, complete cds	succinate dehydrogenase, iron-sulphur subunit, mitochondrial (SDH2-1),One of three isoforms of the iron-sulfur component of the succinate dehydrogenase complex, a component of the mitochondrial respiratory chain complex II. The product of the nuclear encoded gene is imported into the mitochondrion. Expressed during germination and post-germinative growth. electron carrier activity, succinate dehydrogenase activity, mitochondrial electron transport, succinate to ubiquinone, succinate dehydrogenase complex,	M, carbohydrate, energy		0.53952	1.09994	0.42634	0.20292	0.23805	0.84099	0.95645	1.24343	-2.07066	-0.24984	-0.06423	0.31433	-1.16025	0.12505	1.28751	0.26768	1.27443	0.66065	0.42356	NS	0.62833	NS	0.30103	ns
AB016472	At4g16110 Arabidopsis thaliana mRNA for receiver-like protein 5	Encodes a pollen-specific transcription factor involved in the expression of nuclear genes for components of mitochondrial complex I in Arabidopsis. Acts in concert with other type-B ARRs in the cytokinin signaling pathway. AHK3 mediates cytokinin-induced phosphorylation of ARR2 on the Asp-80 residue. This phosphorylation plays a positive role of ARR2 in cytokinin-mediated control of leaf longevity. two-component responsive regulator family protein / response regulator family protein, two-component response regulator activity, ethylene mediated signaling pathway, response to cytokinin stimulus, response to ethylene stimulus, regulation of stomatal movement, leaf senescence	GIP, TF	CPS, signal transduction, cytokinin	0.62802	1.11577	0.75441	0.17332	0.09457	1.16147	1.23832	0.99322	-3.40245	0.21595	0.30838	-0.00982	-1.59325	0.14928	2.55860	0.22501	0.88064	0.93827	0.54035	NS	0.52027	NS	0.43858	ns
U39449	At2g37620 Arabidopsis thaliana actin (ACT1) gene, complete cds	Member of the actin gene family. Expressed in mature pollen, cytoskeleton, structural constituent of cytoskeleton, cytoskeleton organization and biogenesis, M germinated pollen stage	CPS, cell structure		0.44997	1.11899	0.05655	1.04416	0.48995	0.40998	0.38065	1.85732	-1.02929	-1.28637	-1.39345	0.89322	-1.15783	-0.25011	0.18178	1.61692	9.00764	0.21876	0.07039	NS	0.86289	NS	0.51281	ns
AL162507	At3g62400 Arabidopsis thaliana DNA chromosome 3, BAC clone T12C14	expressed protein, cytochrome c oxidase subunit 5c - Oryza sativa, EMBL:AB027123	M, cytcox		0.38211	1.13360	0.07859	0.68848	0.43768	0.32654	0.64677	1.62043	-1.19204	-1.61467	-0.62867	0.69638	-1.40335	0.03385	0.29884	0.93695	6.64107	0.05110	0.09515	NS	0.96750	NS	0.17472	ns
AB023044	At5g51200 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MWD22	expressed protein	unknown		0.84000	1.14041	0.12128	0.56743	0.92575	0.75424	0.73918	1.54165	-0.11130	-0.40691	-0.43601	0.62447	-0.25910	0.09423	0.20903	0.74987	1.75301	0.17772	0.33003	NS	0.88803	NS	0.58669	ns
U39449	AT2G37620 Arabidopsis thaliana actin (ACT1) gene, complete cds	Member of the actin gene family (ACT1). Expressed in mature pollen. cytoskeleton, structural constituent of cytoskeleton, cytoskeleton organization and biogenesis, M germinated pollen stage	CPS, cell structure		0.51750	1.15675	0.11002	0.69742	0.43971	0.59530	0.66360	1.64989	-1.18539	-0.74832	-0.59162	0.72237	-0.96685	0.06538	0.30906	0.92913	4.42421	0.09951	0.14152	NS	0.93686	NS	0.27450	ns
AL137081	At3g58220 Arabidopsis thaliana DNA chromosome 3, BAC clone F9D24	similar to meprin and TRAF homology domain-containing protein / MATH domain-containing protein [Arabidopsis thaliana] (TAIR:At3g58270.1); similar to putative ubiquitin-specific protease [Oryza sativa (japonica cultivar-group)] (GB:XP_476711.1); contains InterPro domain Meprin/TRAF-like MATH (InterPro:IPR002083)	GIP, FSD	EIP, signal transduction	0.50929	1.16223	0.04518	0.90660	0.47734	0.54124	0.52117	1.80329	-1.06690	-0.88566	-0.94018	0.85063	-0.97628	-0.04477	0.12816	1.26629	10.77286	0.05000	0.05893	NS	0.96819	NS	0.40940	ns
AL365234	At5g10980 Arabidopsis thaliana DNA chromosome 5, BAC clone T30N20 (ESSA project)	histone H3, identical to HISTONE H3.2, MINOR, Medicago sativa, SWISSPROT:P11105, histone H3 variant H3.3 Lycopersicon esculentum GI:1435157; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4 , chloroplast, nucleus, DNA binding, chromosome organization and biogenesis (sensu Eukaryota), nucleosome assembly, nucleosome, root, inflorescence, flower, leaf, K second mitotic division stage, seedling growth	GIP, chromosome		0.48431	1.18438	0.19466	0.80245	0.34667	0.62195	0.61696	1.75180	-1.52838	-0.68512	-0.69674	0.80884	-1.10675	0.05605	0.59628	1.06461	2.62493	0.07445	0.23172	NS	0.95269	NS	0.31013	ns
AC006841	At2g21300 Arabidopsis thaliana chromosome II section 122 of 255 of the complete sequence. Sequence from clones F7O24, F3K23, F2G1	similar to kinesin motor family protein, microtubule associated complex, microtubule motor activity, microtubule-based movement	CPS, cell structure		0.38548	1.18727	0.19191	0.46995	0.24978	0.52118	0.85497	1.51958	-2.00128	-0.94015	-0.22606	0.60367	-1.47071	0.18881	0.75033	0.58671	2.77199	0.45510	0.22041	NS	0.72811	NS	0.13270	ns
AC008148	Arabidopsis thaliana chromosome I BAC F15H11 genomic sequence	unknown	unknown		0.56614	1.19255	0.34512	0.63754	0.81018	0.32210	1.64336	0.74174	-0.30369	-1.63442	0.71665	-0.43102	-0.96905	0.14282	0.94097	0.81152	1.45642	0.24888	0.38305	NS	0.84471	NS	0.33317	ns
AL109619	At4g24110 Arabidopsis thaliana DNA chromosome 4, BAC clone T19F6, partial sequence (ESSA project)	expressed protein	unknown		0.31723	1.19338	0.13702	0.46182	0.22034	0.41412	0.86682	1.51994	-2.18219	-1.27189	-0.20619	0.60401	-1.72704	0.19891	0.64368	0.57290	3.79445	0.49102	0.16405	NS	0.70942	NS	0.08720	ns
L14844	At4g38740 Arabidopsis thaliana cytosolic cyclophilin (ROC1) mRNA, complete cds	peptidyl-prolyl cis-trans isomerase / cyclophilin / rotamase / cyclosporin A-binding protein (ROC1), identical to SP|P34790 Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8) (PPIase) (Rotamase) (Cyclophilin) (Cyclosporin A-binding protein) {Arabidopsis thaliana} , cytosol, peptidyl-prolyl cis-trans isomerase activity, signal transduction	M, amino acid	CPS, signal transduction	0.25751	1.19750	0.08274	0.75920	0.19901	0.31601	0.66066	1.73434	-2.32910	-1.66194	-0.59801	0.79439	-1.99552	0.09819	0.47175	0.98457	5.98216	0.14104	0.10544	NS	0.91080	NS	0.11331	ns
AC006423	At1g43800 Arabidopsis thaliana chromosome I BAC F28H19 genomic sequence	acyl-(acyl-carrier-protein) desaturase, putative / stearoyl-ACP desaturase, mitochondrion, fatty acid biosynthesis, acyl-[acyl-carrier protein] desaturase activity	M, lipid		0.49751	1.21306	0.15371	0.32114	0.38882	0.60620	1.44014	0.98597	-1.36284	-0.72214	0.52620	-0.02038	-1.04249	0.25291	0.45304	0.38649	3.25420	0.92544	0.18980	NS	0.52464	NS	0.09141	ns
AC005169	At2g19750 Arabidopsis thaliana chromosome II section 114 of 255 of the complete sequence. Sequence from clones F3P11, F6F22	40S ribosomal protein S30 (RPS30A) , ribosome, structural constituent of ribosome, protein biosynthesis	GIP, translation, ribosome		0.83824	1.22221	0.61097	0.00325	1.27026	0.40622	1.22450	1.21991	0.34512	-1.29966	0.29219	0.28677	-0.47727	0.28948	1.16304	0.00383	0.58034	106.80218	0.66524	NS	0.00596	NC	0.44959	ns
AC007135	At2g36160 Arabidopsis thaliana chromosome II section 197 of 255 of the complete sequence. Sequence from clones F11F19, F9C22	40S ribosomal protein S14 (RPS14A) , cytosolic small ribosomal subunit (sensu Eukaryota), structural constituent of ribosome, translation	GIP, translation, ribosome		0.29375	1.23074	0.10610	0.89283	0.36878	0.21873	0.59942	1.86207	-1.43918	-2.19279	-0.73836	0.89691	-1.81598	0.07927	0.53288	1.15631	4.81942	0.09695	0.13025	NS	0.93847	NS	0.16991	ns
AC005278	At1g03370 Arabidopsis thaliana chromosome 1 BAC F15K9 sequence	C2 domain-containing protein / GRAM domain-containing protein,	CPS, signal transduction		0.41274	1.23234	0.33426	0.11534	0.17638	0.64910	1.15078	1.31389	-2.50323	-0.62348	0.20261	0.39385	-1.56335	0.29823	1.32918	0.13523	1.66337	3.11891	0.34460	NS	0.19752	NS	0.18758	ns
AL353993	At5g15120 Arabidopsis thaliana DNA chromosome 5, BAC clone F8M21 (ESSA project)	unknown	unknown		0.50263	1.24178	0.38617	1.47961	0.22957	0.77569	0.19554	2.28802	-2.12302	-0.36644	-2.35448	1.19410	-1.24473	-0.58019	1.24209	2.50923	1.41722	0.32700	0.39119	NS	0.79880	NS	0.76907	ns
AV518995	ESTs	unknown	unknown		0.43100	1.27081	0.25889	0.10365	0.24794	0.61406	1.34411	1.19752	-2.01193	-0.70354	0.42665	0.26005	-1.35774	0.34335	0.92517	0.11781	2.07544	4.12179	0.28584	NS	0.15152	NS	0.12314	ns

AL138651	Arabidopsis thaliana DNA chromosome 3, BAC clone T17J13	unknown	unknown	0.21322	1.27394	0.14295	1.06338	0.11214	0.31430	0.52201	2.02586	-3.15663	-1.66978	-0.93784	1.01854	-2.41320	0.04035	1.05136	1.38337	3.24607	0.04125	0.19025	NS	0.97376	NS	0.18391	ns
M82883	At5g66055 Arabidopsis thaliana ankyrin repeat-containing protein (akr) gene, complete cds	ankyrin repeat protein / AKRP (AKR), identical to ankyrin repeat protein (AKRP), chloroplast, protein binding, embryonic development (sensu Magnoliophyta)	Ankyrin	0.48403	1.27982	0.34830	0.39048	0.23774	0.73031	1.00371	1.55593	-2.07253	-0.45341	0.00534	0.63778	-1.26297	0.32156	1.14489	0.44720	1.56008	1.01689	0.36288	NS	0.49467	NS	0.20985	ns
AB025632	At5g58500 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MQJ2	expressed protein,	unknown	1.02114	1.29048	0.57608	0.32591	1.42849	0.61379	1.52094	1.06003	0.51449	-0.70419	0.60496	0.08410	-0.09485	0.34453	0.86174	0.36831	0.15566	1.32292	0.90169	NS	0.41206	NS	0.57549	ns
AC002339	At2g41780 Arabidopsis thaliana chromosome II section 226 of 255 of the complete sequence. Sequence from clones T32G6, T11A7	expressed protein	unknown	0.47694	1.29085	0.20615	0.25024	0.33116	0.62271	1.46780	1.11391	-1.59438	-0.68338	0.55365	0.15563	-1.13888	0.35464	0.64418	0.28144	2.50027	1.78202	0.24221	NS	0.32555	NS	0.09521	ns
AC006304	At2g14240 Arabidopsis thaliana chromosome II section 82 of 255 of the complete sequence. Sequence from clones T1O16, T13P21	hypothetical protein,	unknown	0.36819	1.29088	0.29723	0.99948	0.15802	0.57836	0.58414	1.99762	-2.66185	-0.78996	-0.77560	0.99828	-1.72591	0.11134	1.32362	1.25433	1.84403	0.12553	0.31634	NS	0.92050	NS	0.29025	ns
X69373	At4g09320 Arabidopsis thaliana Unknown protein mRNA, complete cds	nucleoside diphosphate kinase type 1 (NDPK1) gene, ATP binding, nucleoside diphosphate kinase activity, CTP biosynthetic process, GTP biosynthetic process, UTP biosynthetic process, nucleotide metabolic process, pyrimidine ribonucleotide metabolic process, pyrimidine deoxyribonucleoside interconversion	M, kinase, nucleotide	0.30276	1.29416	0.08224	0.81386	0.24461	0.36092	0.71868	1.86965	-2.03143	-1.47026	-0.47659	0.90277	-1.75085	0.21309	0.39681	0.97535	6.23998	0.30897	0.10116	NS	0.80922	NS	0.11868	ns
AF386921	Arabidopsis thaliana Metallothionein (F24B9.34) mRNA, complete cds	metallothionein, binds to and detoxifies excess copper and other metals, limiting oxidative damage. ?? one of the five metallothioneins (MTs) genes identified in Arabidopsis. MTs are cysteine-rich proteins required for heavy metal tolerance	M, oxidoreductase	0.56734	1.29977	0.25626	0.16177	0.38613	0.74854	1.18538	1.41416	-1.37283	-0.41785	0.24535	0.49994	-0.89534	0.37265	0.67527	0.18002	1.87510	2.92741	0.31190	NS	0.20956	NS	0.12421	ns
U76501	At3g42960 Arabidopsis thaliana alcohol dehydrogenase (ATA1) mRNA, complete cds	alcohol dehydrogenase (ATA1), identical to alcohol dehydrogenase (ATA1) GI:2501781 from (Arabidopsis thaliana) , oxidoreductase activity, flower development, Arabidopsis homolog of TASSELSEED2. Expressed specifically in tapetal cells.	M, oxidoreductase	0.73470	1.30074	0.34312	0.30618	0.49208	0.97732	1.08424	1.51724	-1.02304	-0.03310	0.11668	0.60145	-0.52807	0.35907	0.69999	0.34278	1.06687	1.48140	0.47941	NS	0.37801	NS	0.24876	ns
AC003028	At2g38190 Arabidopsis thaliana chromosome II section 206 of 255 of the complete sequence. Sequence from clones F16M14	no hit	unknown	0.47744	1.30781	0.08276	0.84977	0.53596	0.41892	1.90869	0.70694	-0.89979	-1.25525	0.93258	-0.50035	-1.07752	0.21612	0.25134	1.01324	6.06278	0.30164	0.10407	NS	0.81349	NS	0.22179	ns
AF326899	At3g06130 Arabidopsis thaliana unknown protein (F28L1.7) mRNA, complete cds	heavy-metal-associated domain-containing protein, contains Pfam heavy metal associated domain PF00403 , metal ion transport, metal ion binding	EIP, transport	0.72414	1.31185	0.33927	1.19500	0.48424	0.96404	0.46685	2.15684	-1.04620	-0.05284	-1.09896	1.10892	-0.54952	0.00498	0.70242	1.56120	1.10638	0.00451	0.46788	NS	0.99713	NS	0.69186	ns
AC034107	At1g18140 Genomic sequence for Arabidopsis thaliana BAC T10O22 from chromosome I	putative laccase, a member of laccase family of genes (with 17 members in Arabidopsis). copper ion binding, endomembrane system	M, oxidoreductase	0.60073	1.31218	0.17973	0.46590	0.47364	0.72782	0.98274	1.64162	-1.07813	-0.45835	-0.02512	0.71512	-0.76824	0.34500	0.43825	0.52343	2.47906	0.93212	0.24409	NS	0.52236	NS	0.14752	ns
AB015479	At5g55320 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MTE17	membrane bound O-acyl transferase (MBOAT) family protein / wax synthase-related, similar to wax synthase (Simmondsia chinensis) GI:5020219 (EC 2.3.1.75) , acyltransferase activity	M, lipid, wax	0.49787	1.32575	0.17012	0.23551	0.37758	0.61816	1.15921	1.49228	-1.40513	-0.69394	0.21315	0.57752	-1.04954	0.39533	0.50289	0.25765	2.95149	2.16995	0.20797	NS	0.27491	NS	0.06868	ns
AC002343	At4g24050 Arabidopsis thaliana chromosome IV BAC T19F6 genomic sequence	short-chain dehydrogenase/reductase (SDR) family protein, contains INTERPRO family IPR002198 Short-chain dehydrogenase/reductase (SDR) superfamily, oxidoreductase activity, metabolic process	M, oxidoreductase	0.39145	1.32796	0.27071	0.65692	0.20003	0.58287	1.79247	0.86344	-2.32172	-0.77876	0.84195	-0.21183	-1.55024	0.31506	1.09104	0.74513	2.00943	0.59797	0.29397	NS	0.65691	NS	0.18397	ns
AC005693	At2g07090 Arabidopsis thaliana chromosome II section 40 of 255 of the complete sequence. Sequence from clones T4E14, T25N22	expressed protein	unknown	0.55262	1.32813	0.40233	1.29433	0.26813	0.83711	0.41290	2.24336	-1.89899	-0.25652	-1.27613	1.16566	-1.07775	-0.05523	1.16140	1.72661	1.31236	0.04524	0.41452	NS	0.97122	NS	0.55898	ns
AF360327	Arabidopsis thaliana putative metal-binding protein (MLE2.16/AT5g63530) mRNA, complete cds	copper chaperone (CCH)-related, low similarity to copper homeostasis factor (GI:3168840); nearly identical to farnesylated protein ATFP3 (GI:4097547); contains Pfam profile PF00403: Heavy-metal-associated domain , Farnesylated protein that binds metals (ATFP3), transition metal ion binding, transition metal ion homeostasis	EIP, signal transduction	0.43004	1.33909	0.30960	0.54731	0.21112	0.64896	0.95208	1.72609	-2.24388	-0.62380	-0.07084	0.78751	-1.43384	0.35833	1.14557	0.60695	1.77009	0.83493	0.32738	NS	0.55712	NS	0.18977	ns
AB012243	At5g39570 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MIJ24	expressed protein	unknown	0.34518	1.34433	0.16363	0.37848	0.22948	0.46089	1.07670	1.61196	-2.12354	-1.11752	0.10662	0.68881	-1.62053	0.39772	0.71136	0.41167	3.22166	1.36627	0.19160	NS	0.40223	NS	0.07385	ns
AC007017	At2g35960 Arabidopsis thaliana chromosome II section 196 of 255 of the complete sequence. Sequence from clones T20F21, F11F19	harpin-induced family protein / HIN1 family protein / harpin-responsive family protein, similar to harpin-induced protein hin1 (GI:1619321) (Nicotiana tabacum) , Encodes a protein whose sequence is similar to tobacco hairpin-induced gene (HIN1) and Arabidopsis non-race specific disease resistance gene (NDR1). Expression is not altered in response to cucumber mosaic virus or spermine. (NHL12)	EIP, signal transduction	0.41117	1.38160	0.27830	0.80587	0.21439	0.60796	0.81176	1.95144	-2.22172	-0.71794	-0.30088	0.96454	-1.46983	0.33183	1.06333	0.89478	1.95485	0.52446	0.30102	NS	0.69250	NS	0.20819	ns
AL133298	At3g46300 Arabidopsis thaliana DNA chromosome 3, BAC clone F18L15	expressed protein	unknown	0.44200	1.39215	0.30616	0.28793	0.22551	0.65849	1.59574	1.18855	-2.14872	-0.60276	0.67423	0.24921	-1.37574	0.46172	1.09316	0.30054	1.77979	2.17269	0.32589	NS	0.27461	NS	0.14896	ns
AL035527	Arabidopsis thaliana DNA chromosome 4, BAC clone F17L22 (ESSAII project)	unknown	unknown	0.28519	1.39298	0.16539	1.06580	0.16825	0.40214	2.14662	0.63935	-2.57136	-1.31423	1.10206	-0.64533	-1.94280	0.22837	0.88892	1.23560	3.09086	0.26138	0.19920	NS	0.83724	NS	0.18118	ns
AC005169	At2g19740 Arabidopsis thaliana chromosome II section 114 of 255 of the complete sequence. Sequence from clones F3P11, F6F22	60S ribosomal protein L31 (RPL31A) , ribosome, structural constituent of ribosome, translation, ribosome biogenesis and assembly	GIP, translation, ribosome	0.35593	1.40123	0.02032	0.81687	0.37030	0.34157	0.82361	1.97884	-1.43323	-1.54976	-0.27997	0.98466	-1.49149	0.35234	0.08240	0.89422	25.59773	0.55723	0.02486	D	0.67636	NS	0.10096	ns
AC013428	At3g10525 Arabidopsis thaliana chromosome III BAC F18K10 genomic sequence	expressed protein	unknown	0.84483	1.40130	0.26450	0.80052	0.65780	1.03186	1.96736	0.83525	-0.60427	0.04525	0.97626	-0.25972	-0.27951	0.35827	0.45928	0.87397	0.86068	0.57973	0.54758	NS	0.66553	NS	0.45738	ns
AC006418	At2g46620 Arabidopsis thaliana chromosome II section 247 of 255 of the complete sequence. Sequence from clones F13A10	AAA-type ATPase family protein, contains Pfam profile: ATPase family PF00004 , ATP binding, ATPase activity,	M, energy, ATPase	0.23133	1.42026	0.20639	1.14649	0.08539	0.37726	0.60957	2.23095	-3.54982	-1.40635	-0.71414	1.15765	-2.47809	0.22176	1.51566	1.32356	2.31222	0.23695	0.25986	NS	0.85189	NS	0.19820	ns

AL049482	At4g09790 Arabidopsis thaliana DNA chromosome 4, BAC clone F17A8 (ESSA project)	F-box family protein, hypothetical protein - Arabidopsis thaliana;PID:g2245079; contains Pfam PF00646: F-box domain; contains TIGRFAM TIGR01640: F-box protein interaction domain	Fbox		0.44693	1.42176	0.27606	0.28277	0.25172	0.64213	1.22181	1.62171	-1.99010	-0.63906	0.28902	0.69752	-1.31458	0.49327	0.95533	0.28885	1.94602	2.41506	0.30219	NS	0.24992	NS	0.12455	ns
AF361581	At4g35320 Arabidopsis thaliana AT4g35320/F23E12_120 gene, complete cds	expressed protein, predicted protein, Arabidopsis thaliana	unknown		0.63063	1.44683	0.27583	0.14276	0.82567	0.43559	1.34588	1.54778	-0.27636	-1.19897	0.42855	0.63020	-0.73766	0.52937	0.65239	0.14259	1.59908	5.25048	0.35578	NS	0.11981	NS	0.11535	ns
AL161545	At4g17160 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 45	Ras-related GTP-binding protein, putative, similar to GTP-binding protein GI:1208537 from (Glycine max), exosome (RNase complex), intracellular, GTP binding, intracellular protein transport, protein transport, small GTPase mediated signal transduction	EIP, transport, signal transduction	CPS, signal transduction	0.58954	1.45050	0.33574	0.24856	0.35213	0.82695	1.27474	1.62626	-1.50581	-0.27413	0.35020	0.70156	-0.88997	0.52588	0.87093	0.24844	1.44514	2.99346	0.38536	NS	0.20525	NS	0.15760	ns
AC004793	At1g31175 Arabidopsis thaliana chromosome 1 BAC F28K20 sequence	expressed protein	unknown		0.58704	1.46386	0.52187	0.74198	0.21802	0.95607	0.93920	1.98852	-2.19744	-0.06482	-0.09050	0.99170	-1.13113	0.45060	1.50799	0.76523	1.06079	0.83275	0.48123	NS	0.55793	NS	0.31689	ns
AL353865	Arabidopsis thaliana DNA chromosome 3, BAC clone T10D17	unknown	unknown		0.42815	1.47557	0.13869	1.37276	0.33008	0.52622	2.44626	0.50489	-1.59912	-0.92626	1.29058	-0.98597	-1.26269	0.15231	0.47578	1.60976	3.75325	0.13380	0.16577	NS	0.91532	NS	0.35548	ns
AC006446	At2g13330 Arabidopsis thaliana chromosome II section 73 of 255 of the complete sequence. Sequence from clones T17A11, F15O11	gypsy-like retrotransposon family, has a 2.0e-156 P-value blast match to GB:AAD11615 prpol (gypsy_Ty3-element) (Zea mays), RNA binding, RNA-directed DNA polymerase activity, RNA-dependent DNA replication	TRANS		0.70440	1.48296	0.65407	0.35509	0.24190	1.16690	1.23188	1.73405	-2.04750	0.22268	0.30086	0.79414	-0.91241	0.54750	1.60527	0.34880	0.80382	2.21982	0.56897	NS	0.26945	NS	0.33571	ns
AL161547	At4g17800 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 47	DNA-binding protein-related, contains Pfam domain PF03479: Domain of unknown function (DUF296), found in AT-hook motifs Pfam:PF02178	GIP		0.50896	1.49086	0.33806	0.73123	0.26992	0.74801	0.97380	2.00791	-1.88940	-0.41888	-0.03830	1.00570	-1.15414	0.48370	1.03982	0.73822	1.56970	0.92662	0.36111	NS	0.52424	NS	0.21096	ns
AB023044	At5g51180 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MWD22	expressed protein	unknown		0.29451	1.49166	0.27166	0.40784	0.10241	0.48660	1.20327	1.78004	-3.28750	-1.03919	0.26696	0.83191	-2.16335	0.54943	1.58980	0.39948	1.92442	1.94505	0.30509	NS	0.30232	NS	0.14412	ns
AC006053	At2g25680 Arabidopsis thaliana chromosome II section 144 of 255 of the complete sequence. Sequence from clones F13B15, F3N11, F17H15	sulfate transporter activity	EIP, transport	CPS, transport	0.50569	1.50874	0.16853	0.27776	0.38652	0.62486	1.31234	1.70515	-1.37139	-0.67839	0.39214	0.76990	-1.02489	0.58102	0.49002	0.26712	2.95786	3.07611	0.20755	NS	0.20010	NS	0.05542	ns
AJ010472	At1g72730 Arabidopsis thaliana mRNA for DEAD box RNA helicase, RH23	eukaryotic translation initiation factor 4A, putative / eIF-4A, putative, similar to Eukaryotic initiation factor 4A-10 GB:P41382 (Nicotiana tabacum); identical to (putative) RNA helicase GB:CAA09211 (Arabidopsis thaliana) (Nucleic Acids Res. 27 (2), 628-636 (1999)) , cell wall (sensu Magnoliophyta), ATP-dependent helicase activity, biological_process	GIP, replication and repair		0.39460	1.51646	0.23802	1.47032	0.22630	0.56290	0.47679	2.55613	-2.14372	-0.82904	-1.06858	1.35396	-1.48638	0.14269	0.92962	1.71300	2.26120	0.11780	0.26508	NS	0.92535	NS	0.35868	ns
AB026654	At3g18800 Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MVE11	expressed protein	unknown		0.51625	1.51863	0.25569	0.13654	0.33545	0.69706	1.42208	1.61518	-1.57583	-0.52065	0.50800	0.69169	-1.04824	0.59985	0.74612	0.12989	1.98685	6.53095	0.29685	NS	0.09673	NS	0.09135	ns
AL035679	At4g38940 Arabidopsis thaliana DNA chromosome 4, BAC clone F19H22 (ESSA project)	kelch repeat-containing F-box family protein, low similarity to SKP1 interacting partner 6 (Arabidopsis thaliana) GI:10716957; contains Pfam profiles PF01344: Kelch motif, PF00646: F-box domain	Fbox		0.69822	1.52096	0.06574	0.44766	0.65173	0.74470	1.20442	1.83751	-0.61765	-0.42527	0.26834	0.87775	-0.52146	0.57304	0.13604	0.43092	5.42095	1.88065	0.11613	NS	0.31112	NS	0.07568	ns
Y13648	At3g24050 Arabidopsis thaliana mRNA for GATA transcription factor 1	GATA transcription factor 1 (GATA-1), identical to GATA transcription factor 1 (AtGATA-1), nucleus, transcription factor activity, regulation of transcription, DNA-dependent	GIP, TF		0.37505	1.53636	0.18786	0.39664	0.24222	0.50789	1.81683	1.25590	-2.04563	-0.97741	0.86142	0.32872	-1.51152	0.59507	0.75535	0.37668	2.82998	2.23416	0.21624	NS	0.26792	NS	0.07174	ns
AF385696	At4g38680 Glycine-rich protein {clone atGRP-2} [Arabidopsis thaliana, C24, mRNA, 965 nt]	cold-shock DNA-binding family protein, contains Pfam domains PF00313: 'Cold-shock' DNA-binding domain and PF00098: Zinc knuckle (GRP2, encodes a glycine-rich protein that is present as several copies in the genome. It is expressed equally abundantly in all tissues examined.), nucleic acid binding, regulation of transcription, DNA-dependent	GIP, FSD? Or TF		0.39791	1.55419	0.28150	0.33685	0.19885	0.59696	1.31600	1.79238	-2.33021	-0.74429	0.39616	0.84187	-1.53725	0.61901	1.12142	0.31517	1.93862	2.77761	0.30318	NS	0.22000	NS	0.12018	ns
AC021046	At1g69630 Arabidopsis thaliana chromosome 1 BAC F24J1 genomic sequence	F-box family protein,	Fbox		0.45296	1.55446	0.23994	0.25018	0.28329	0.62262	1.37756	1.73137	-1.81962	-0.68358	0.46211	0.79191	-1.25160	0.62701	0.80330	0.23320	2.20345	3.80239	0.27122	NS	0.16372	NS	0.08646	ns
AB005237	At5g05840 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MJJ3	expressed protein, contains Pfam profile PF04788: Protein of unknown function (DUF620); expression supported by MPSS	unknown		0.46810	1.56739	0.49102	1.00156	0.12090	0.81530	0.85919	2.27560	-3.04814	-0.29459	-0.21896	1.18625	-1.67137	0.48365	1.94705	0.99363	1.21397	0.68836	0.43866	NS	0.61620	NS	0.29795	ns
AC069251	AT1G20690 Arabidopsis thaliana unknown protein (F2D10.18) mRNA, complete cds	expressed protein	unknown		0.73605	1.57098	0.21009	0.44214	0.58750	0.88461	1.88363	1.25834	-0.76734	-0.17688	0.91351	0.33152	-0.47211	0.62252	0.41752	0.41153	1.59914	2.13928	0.35577	NS	0.27837	NS	0.11846	ns
AL161505	At4g07470 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 17	hypothetical protein	unknown		0.50481	1.57173	0.22339	0.86227	0.34685	0.66277	0.96201	2.18145	-1.52760	-0.59342	-0.05587	1.12528	-1.06051	0.53471	0.66056	0.83521	2.27047	0.90539	0.26412	NS	0.53158	NS	0.16828	ns
AL391144	At5g15820 Arabidopsis thaliana DNA chromosome 5, BAC clone F14F8 (ESSA project)	zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger) , protein binding, zinc ion binding	ZINC		0.40963	1.57960	0.24488	0.28234	0.23647	0.58279	1.37995	1.77925	-2.08029	-0.77896	0.46462	0.83127	-1.42963	0.64794	0.92018	0.25926	2.19718	3.53444	0.27191	NS	0.17553	NS	0.09156	ns
AC006234	At2g20710 Arabidopsis thaliana chromosome II section 119 of 255 of the complete sequence. Sequence from clones F5H14, F26H11	pentatricopeptide (PPR) repeat-containing protein, low similarity to DNA-binding protein	PRR		0.39811	1.58274	0.24512	0.16900	0.22478	0.57143	1.46324	1.70224	-2.15340	-0.80735	0.54917	0.76744	-1.48038	0.65830	0.95180	0.15434	2.19959	6.03204	0.27164	NS	0.10459	NS	0.08837	ns
AB020744	At5g45280 Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K9E15	pectinacetylesterase, putative, similar to pectinacetylesterase precursor GI:1431629 from (Vigna radiata) , carboxylic ester hydrolase activity, biological_process, endomembrane system	M, lipid		0.61562	1.60525	0.12073	1.53465	0.53025	0.70099	0.52009	2.69041	-0.91524	-0.51254	-0.94315	1.42783	-0.71389	0.24234	0.28476	1.67654	3.54545	0.20442	0.17501	NS	0.87163	NS	0.50987	ns
AJ245867	Arabidopsis thaliana mRNA for photosystem I subunit XI precursor	photosystem I subunit XI precursor	M, energy		0.72215	1.60671	0.28259	0.12497	0.92197	0.52232	1.69507	1.51834	-0.11720	-0.93699	0.76135	0.60249	-0.52709	0.68192	0.57967	0.11233	1.28594	8.58559	0.42078	NS	0.07382	NS	0.10143	ns
AF386989	At2g23110 Arabidopsis thaliana similar to late embryogenesis abundant proteins (At2g23110; F21P24.17) mRNA, complete cds	expressed protein	unknown		1.05803	1.60808	0.17473	0.15088	0.93448	1.18159	1.71477	1.50139	-0.09777	0.24073	0.77802	0.58630	0.07148	0.68216	0.23935	0.13556	0.42232	7.11641	0.74561	NS	0.08888	NS	0.08823	ns
AL049658	At3g48120 Arabidopsis thaliana DNA chromosome 3, BAC clone T17F15	expressed protein	unknown		0.52935	1.64761	0.42620	0.13030	0.22798	0.83072	1.55547	1.73974	-2.13299	-0.26757	0.63735	0.79887	-1.20028	0.71811	1.31906	0.11421	1.28687	8.89176	0.42056	NS	0.07130	NS	0.17698	ns

AC007519	At1g47655 Sequence of BAC F16N3 from Arabidopsis thaliana chromosome 1	Dof-type zinc finger domain-containing protein , cellular component unknown, DNA binding, transcription factor activity, regulation of transcription	GIP, TF		0.36392	1.68220	0.36265	0.44292	0.10749	0.62035	1.36901	1.99539	-3.21779	-0.68886	0.45313	0.99667	-1.95332	0.72490	1.78823	0.38434	1.54478	2.66735	0.36574	NS	0.22835	NS	0.17420	ns
AC009273	At1g01725 Arabidopsis thaliana unknown protein (T1N6.13) mRNA, complete cds	expressed protein	unknown		0.48441	1.68342	0.36831	0.85822	0.22398	0.74484	1.07657	2.29027	-2.15855	-0.42499	0.10645	1.19552	-1.29177	0.65098	1.22581	0.77009	1.49031	1.19548	0.37624	NS	0.44347	NS	0.19814	ns
AB025606	At5g52650 Arabidopsis thaliana genomic DNA, chromosome 5, BAC clone:F6N7	40S ribosomal protein S10 (RPS10C), contains similarity to 40S ribosomal protein S10 , cytosolic small ribosomal subunit (sensu Eukaryota), structural constituent of ribosome, protein biosynthesis	GIP, translation, ribosome		0.52959	1.68732	0.20821	0.48786	0.38237	0.67682	1.34235	2.03229	-1.38696	-0.56316	0.42477	1.02311	-0.97506	0.72394	0.58252	0.42309	2.36721	2.41981	0.25446	NS	0.24948	NS	0.07926	ns
AB016886	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MCA23	unknown	unknown		0.29498	1.68877	0.23435	0.86279	0.12927	0.46069	1.07869	2.29885	-2.95154	-1.11813	0.10927	1.20091	-2.03484	0.65509	1.29642	0.77190	2.21973	1.20020	0.26946	NS	0.44223	NS	0.12783	ns
AC079829	At1g26240 Arabidopsis thaliana chromosome 1 BAC F28B23 genomic sequence	proline-rich extensin-like family protein, similar to hydroxyproline-rich glycoprotein precursor gi|727264|gb|AAA87902; contains proline-rich extensin domains, INTERPRO:IPR002965 , structural constituent of cell wall, cell wall organization and biogenesis (sensu Magnoliophyta), endomembrane system, cell surface (sensu Magnoliophyta)	CPS, cell wall		0.47891	1.69713	0.22795	0.39132	0.64009	0.31772	1.42043	1.97384	-0.64365	-1.65416	0.50632	0.98101	-1.14890	0.74366	0.71454	0.33565	2.27390	3.13332	0.26376	NS	0.19667	NS	0.07708	ns
AB023042	At5g57070 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MUL3	hydroxyproline-rich glycoprotein family protein,	M, glycan biosynthesis		0.53759	1.71114	0.33356	0.38656	0.30173	0.77345	1.43779	1.98448	-1.72868	-0.37062	0.52386	0.98876	-1.04965	0.75631	0.96030	0.32874	1.54581	3.25363	0.36555	NS	0.18983	NS	0.12825	ns
AL163817	At5g14290 Arabidopsis thaliana DNA chromosome 5, BAC clone F18O22 (ESSA project)	hypothetical protein	unknown		0.50315	1.73117	0.35963	0.96732	0.24885	0.75745	1.04717	2.41516	-2.00664	-0.40079	0.06650	1.27212	-1.20371	0.66931	1.13551	0.85250	1.49916	1.11031	0.37450	NS	0.46675	NS	0.20310	ns
AB030250	Arabidopsis thaliana mRNA for AtRAD17, complete cds	cell cycle checkpoint protein-related, weak similarity to cell cycle checkpoint protein RAD17 (Radiation sensitive)	CPS, cell cycle		0.43043	1.73238	0.37345	0.64408	0.16636	0.69449	1.27694	2.18781	-2.58761	-0.52597	0.35269	1.12949	-1.55679	0.74109	1.45780	0.54928	1.51024	1.90807	0.37234	NS	0.30732	NS	0.17229	ns
AL161497	At4g03600 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 9	expressed protein	unknown		0.57326	1.74862	0.42469	0.69400	0.27295	0.87356	1.25789	2.23935	-1.87327	-0.19502	0.33100	1.16308	-1.03414	0.74704	1.18670	0.58837	1.23241	1.79560	0.43396	NS	0.32349	NS	0.19756	ns
AV557234	EST, Moderately similar to T00448 hypothetical protein T14N5.5 - Arabidopsis thaliana [A.thaliana]	chromatin protein family, contains Pfam domain, PF02731: SKIP/SNW domain found in chromatin proteins. similar to RNA recognition motif (RRM)-containing protein [Arabidopsis thaliana] (TAIR:At2g16940.1); similar to WD-40 repeat family protein [Arabidopsis thaliana] (TAIR:At5g67320.1); similar to GAMYB-binding protein [Hordeum vulgare subsp. vulgare] (GB:AAO25542.1); contains InterPro domain SKIP/SNW domain (InterPro:IPR004015)	GIP, chromosome	WD40	0.44083	1.75720	0.28457	0.30342	0.23961	0.64205	1.54265	1.97175	-2.06126	-0.63923	0.62541	0.97948	-1.35024	0.80245	1.00552	0.25036	1.89904	4.53276	0.30856	NS	0.13823	NS	0.09896	ns
AC008017	At1g73030 Arabidopsis thaliana chromosome I BAC F3N23 genomic sequence	SNF7 family protein, contains Pfam domain, PF03357: SNF7 family , , protein transport	CPS, transport		0.40551	1.76057	0.18842	0.54220	0.27228	0.53874	1.37718	2.14396	-1.87683	-0.89234	0.46172	1.10028	-1.38459	0.78100	0.69614	0.45153	2.81278	2.44611	0.21746	NS	0.24706	NS	0.06620	ns
AL132966	Arabidopsis thaliana DNA chromosome 3, BAC clone F4P12	unknown	unknown		0.32881	1.76354	0.01904	1.11941	0.34228	0.31535	0.97200	2.55508	-1.54677	-1.66500	-0.04097	1.35337	-1.60588	0.65620	0.08360	0.98595	27.16661	0.94124	0.02342	D	0.51927	NS	0.08382	ns
AL161589	At4g36390 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 85	radical SAM domain-containing protein / TRAM domain-containing protein, similar to CDK5 activator-binding protein (Rattus norvegicus) GI:7330738; contains Pfam profiles PF00919: UPF0004 family protein, PF01938: TRAM domain, PF04055: radical SAM domain protein , chloroplast, catalytic activity, iron ion binding, biological_process	CPS, cell cyle		0.43408	1.76730	0.29606	1.53382	0.22473	0.64342	0.68273	2.85188	-2.15370	-0.63616	-0.55062	1.51191	-1.39493	0.48064	1.07306	1.45843	1.83841	0.46607	0.31715	NS	0.72235	NS	0.28055	ns
AC069474	At3g12510 Arabidopsis thaliana chromosome 3 BAC T2E22 genomic sequence	expressed protein	unknown		0.47536	1.76983	0.33831	0.88062	0.23613	0.71458	1.14714	2.39252	-2.08232	-0.48483	0.19804	1.25853	-1.28358	0.72828	1.12959	0.74988	1.60700	1.37349	0.35437	NS	0.40064	NS	0.17074	ns
AL163816	At3g63020 Arabidopsis thaliana DNA chromosome 3, BAC clone T20O10	expressed protein, predicted protein, Arabidopsis thaliana	unknown		0.52499	1.77262	0.22547	1.74394	0.36555	0.68442	0.53947	3.00577	-1.45184	-0.54705	-0.89037	1.58774	-0.99944	0.34868	0.63979	1.75229	2.20921	0.28141	0.27060	NS	0.82537	NS	0.41426	ns
AC008047	At1g63360 Genomic sequence for Arabidopsis thaliana BAC F2K11 from chromosome I	disease resistance protein (CC-NBS-LRR class), putative, domain signature CC-NBS-LRR exists, suggestive of a disease resistance protein. ATP binding, transferase activity, defense response, N-terminal protein myristoylation	EIP, signal transduction	Myristoylation	0.42975	1.77709	0.31279	0.13889	0.20857	0.65093	1.67888	1.87530	-2.26137	-0.61943	0.74750	0.90712	-1.44040	0.82731	1.16103	0.11287	1.75450	10.36559	0.32979	NS	0.06123	NS	0.11075	ns
AC003033	At2g32890 Arabidopsis thaliana chromosome II section 184 of 255 of the complete sequence. Sequence from clones F24L7, T21L14, F25I18	expressed protein	unknown		0.82504	1.78014	0.21293	0.03881	0.67448	0.97561	1.80759	1.75270	-0.56816	-0.03562	0.85407	0.80958	-0.30189	0.83182	0.37656	0.03146	1.13379	37.39406	0.46014	NS	0.01702	NC	0.05131	ns
AL353992	Arabidopsis thaliana DNA chromosome 3, BAC clone F14D17	unknown	unknown		0.48667	1.79129	0.04917	0.93522	0.52144	0.45190	2.45259	1.12998	-0.93943	-1.14594	1.29431	0.17630	-1.04268	0.73530	0.14602	0.79055	10.09859	1.31539	0.06284	NS	0.41381	NS	0.08881	ns
AF385726	At1g52870 Arabidopsis thaliana At1g52870/F14G24_14 mRNA, complete cds	peroxisomal membrane protein-related, contains weak similarity to Swiss-Prot:Q07066 22 kDa peroxisomal membrane protein (Rattus norvegicus) , chloroplast, integral to membrane,	CPS, cell structure		0.71367	1.80914	0.32922	0.34960	0.48088	0.94646	2.05635	1.56194	-1.05626	-0.07938	1.04008	0.64334	-0.56782	0.84171	0.69076	0.28054	1.16252	4.24305	0.45225	NS	0.14735	NS	0.11604	ns
AB009051	At5g63010 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MJH22	WD-40 repeat family protein (transducin), contains 4 WD-40 repeats (PF00400);low similarity to photomorphogenesis repressor (COP1), nucleotide binding	WD40		0.53517	1.84128	0.39565	0.47118	0.25540	0.81493	1.50811	2.17445	-1.96916	-0.29525	0.59274	1.12065	-1.13221	0.85670	1.18363	0.37329	1.35277	3.24562	0.40525	NS	0.19027	NS	0.15163	ns
AF370527	At5g42300 Arabidopsis thaliana ubiquitin-like protein (K5J14.10) mRNA, complete cds	ubiquitin family protein, contains INTERPRO:IPR000626 ubiquitin domain ; ubiquitin cycle	GIP, FSD	EIP, signal transduction	0.46076	1.84325	0.17281	0.77908	0.58296	0.33856	1.29236	2.39414	-0.77854	-1.56252	0.37000	1.25951	-1.17053	0.81476	0.55436	0.62897	2.98613	1.83193	0.20572	NS	0.31810	NS	0.07878	ns
U89959	At1g02140 Arabidopsis thaliana BAC T7I23, complete sequence	mago nashi family protein, similar to Mago Nashi, Genbank Accession Number U03559; contains Pfam PF02792: Mago nashi protein domain , nucleus, molecular_function, sex determination	unknown		0.76691	1.85991	0.46202	0.43550	1.09361	0.44022	2.16785	1.55196	0.12910	-1.18372	1.11627	0.63409	-0.52731	0.87518	0.92830	0.34095	0.80332	3.63013	0.56916	NS	0.17113	NS	0.18274	ns
AL078468	At4g23870 Arabidopsis thaliana DNA chromosome 4, BAC clone T32A16 (ESSA project)	expressed protein, predicted proteins, Arabidopsis thaliana	unknown		0.37002	1.86071	0.32553	0.81500	0.13983	0.60020	1.28441	2.43700	-2.83825	-0.73648	0.36111	1.28511	-1.78737	0.82311	1.48618	0.65336	1.70082	1.78163	0.33837	NS	0.32561	NS	0.15082	ns

AB007651	At5g22260 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MWD9	DNA binding, regulation of transcription, DNA-dependent, male sterility 1 protein, putative (MS1), Sporophytic factor controlling anther and pollen development. Mutants fail to make functional pollen;pollen degeneration occurs after microspore release and the tapetum also appears abnormally vacuolated. Similar to PHD-finger motif transcription factors.	GIP, TF		0.51166	1.86857	0.28855	0.02215	0.30762	0.71569	1.88423	1.85291	-1.70078	-0.48259	0.91398	0.88979	-1.09168	0.90188	0.86139	0.01710	1.79230	74.59242	0.32399	NS	0.00853	NC	0.08206	ns
AL161471	At4g00270 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 1	DNA-binding storekeeper protein-related, contains similarity to storekeeper protein (Solanum tuberosum) gi|14268476|emb|CAC39398; contains PF04504: Protein of unknown function, DUF573 , transcription regulator activity	GIP, Transcription regulator		0.28304	1.87724	0.27017	0.18812	0.09200	0.47407	1.74422	2.01026	-3.44224	-1.07681	0.80258	1.00738	-2.25953	0.90498	1.67261	0.14482	1.91046	8.83773	0.30699	NS	0.07173	NS	0.11662	ns
Y12807	At5g64620 Arabidopsis thaliana mRNA for invertase inhibitor homolog	Plant cell wall (CWI) and vacuolar invertases (VI) play important roles in carbohydrate metabolism, stress responses and sugar signaling. invertase/pectin methylesterase inhibitor family protein, pectinesterase inhibitor activity. CELL WALL / VACUOLAR INHIBITOR OF FRUCTOSIDASE 2.	M, carbohydrate, inhibitor		0.32939	1.88197	0.32146	0.23210	0.10209	0.55670	2.04609	1.71785	-3.29211	-0.84503	1.03287	0.78061	-2.06857	0.90674	1.73035	0.17838	1.69065	7.18879	0.34004	NS	0.08799	NS	0.13672	ns
AB018112	At5g36110 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MAB16	cytochrome P450 family protein, similar to taxane 13-alpha-hydroxylase (GI:17148242) {Taxus cuspidata}; contains Pfam profile: PF00067: Cytochrome P450 , member of CYP716A , electron transport, oxygen binding, endomembrane system, CYTOCHROME P450, FAMILY 716, SUBFAMILY A, POLYPEPTIDE 1	M, cytP450		2.14447	1.89358	0.47975	0.63519	1.80523	2.48370	1.44444	2.34273	0.85218	1.31249	0.53051	1.22819	1.08234	0.87935	0.32549	0.49334	4.70266	2.52077	0.13339	NS	0.24043	NS	0.67517	ns
AC006224	At2g43050 Arabidopsis thaliana chromosome II section 233 of 255 of the complete sequence. Sequence from clones MFL8	pectinesterase family protein, cell wall (sensu Magnoliophyta), pectinesterase activity, cell wall modification	CPS, cell wall		0.35543	1.89383	0.32468	0.69602	0.12584	0.58501	1.40167	2.38598	-2.99031	-0.77346	0.48714	1.25458	-1.88189	0.87086	1.56755	0.54266	1.69780	2.26953	0.33887	NS	0.26421	NS	0.14349	ns
AL161514	At4g09130 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 26	zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097: Zinc finger, C3HC4 type (RING finger)	ZINC		0.46846	1.89499	0.27167	0.21424	0.27636	0.66056	1.74350	2.04648	-1.85537	-0.59823	0.80199	1.03314	-1.22680	0.91756	0.88893	0.16345	1.95173	7.93888	0.30143	NS	0.07977	NS	0.07851	ns
AF102823	AT2G16700 Arabidopsis thaliana actin depolymerizing factor 5 (ADF5) mRNA, complete cds	actin depolymerizing factor 5 (ADF5) mRNA, intracellular, actin binding,	CPS, cell structure		0.40698	1.89672	0.31181	0.62156	0.18650	0.62747	1.45722	2.33623	-2.42278	-0.67239	0.54321	1.22418	-1.54758	0.88370	1.23771	0.48152	1.76827	2.59542	0.32766	NS	0.23413	NS	0.12240	ns
AB009049	At5g56420 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MCD7	F-box family protein, contains F-box domain	Fbox		0.58848	1.89860	0.15717	0.70545	0.47734	0.69961	1.39978	2.39743	-1.06690	-0.51538	0.48520	1.26149	-0.79114	0.87334	0.38999	0.54892	2.86891	2.25003	0.21352	NS	0.26625	NS	0.07298	ns
AB018107	At5g37670 Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K12B20	15.7 kDa class I-related small heat shock protein-like (HSP15.7-CI), Hsp20/alpha crystallin family;	GIP, FSD	EIP, signal transduction	0.40647	1.90261	0.35059	0.52413	0.15856	0.65437	1.53200	2.27323	-2.65687	-0.61182	0.61542	1.18474	-1.63434	0.90008	1.44607	0.40257	1.59834	3.16192	0.35591	NS	0.19500	NS	0.13959	ns
AL163491	At5g13320 Arabidopsis thaliana DNA chromosome 5, BAC clone T31B5 (ESSA project)	auxin-responsive GH3 family protein, similar to auxin-responsive GH3 product (Glycine max) GI:18591; contains Pfam profile PF03321: GH3 auxin-responsive promoter (PBS3, signaling gene in disease-resistance involved in restricting the spread of both virulent and avirulent pathogens), defense response, detection of fungus , response to auxin stimulus	EIP, signal transduction	CPS, signal transduction	0.38177	1.90474	0.33487	0.24815	0.14498	0.61856	1.72927	2.08021	-2.78605	-0.69302	0.79016	1.05673	-1.73954	0.92345	1.47999	0.18849	1.66222	6.92848	0.34479	NS	0.09125	NS	0.12759	ns
AL049711	At3g52100 Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15	PHD finger family protein, contains Pfam profile PF00628: PHD-finger , protein binding, zinc ion binding, regulation of transcription, DNA-dependent, endomembrane system	GIP, Transcription regulator		0.49766	1.91155	0.47992	1.70882	0.15831	0.83701	0.70323	3.11987	-2.65916	-0.25668	-0.50792	1.64149	-1.45792	0.56678	1.69881	1.51986	1.21367	0.52738	0.43874	NS	0.69104	NS	0.33591	ns
AB012243	At5g39650 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MIJ24	expressed protein,	unknown		0.45747	1.91200	0.31403	0.24985	0.23541	0.67952	1.73533	2.08867	-2.08675	-0.55741	0.79521	1.06258	-1.32208	0.92890	1.08140	0.18907	1.72896	6.94817	0.33383	NS	0.09100	NS	0.10120	ns
AC051629	At1g16870 Arabidopsis thaliana chromosome I BAC F6I1 genomic sequence	mitochondrial 28S ribosomal protein S29-related, contains weak similarity to Swiss-Prot:P51398 mitochondrial 28S ribosomal protein S29 (MRP-S29, Death-associated protein 3, DAP-3) (Homo sapiens)	GIP, translation, ribosome		0.46377	1.91807	0.40246	0.84462	0.17919	0.74836	1.32083	2.51530	-2.48047	-0.41820	0.40145	1.33073	-1.44934	0.86609	1.45824	0.65710	1.40558	1.86399	0.39367	NS	0.31348	NS	0.17722	ns
AY045846	At3g11940 Arabidopsis thaliana putative 40S ribosomal protein S5 (F26K24.23/AT3g11940) mRNA, complete cds	40S ribosomal protein S5 (RPS5B), similar to 40S ribosomal protein S5 GB:AAC98068 GI:4056502 from (Arabidopsis thaliana) , One of two genes encoding the ribosomal protein S5, cytosolic ribosome (sensu Eukaryota), cytosolic small ribosomal subunit (sensu Eukaryota), ribosome, structural constituent of ribosome, translation	GIP, translation, ribosome		0.32396	1.92440	0.09553	1.64464	0.25642	0.39151	0.76146	3.08733	-1.96344	-1.35288	-0.39316	1.62636	-1.65816	0.61660	0.43173	1.42802	5.43161	0.61064	0.11591	NS	0.65100	NS	0.16379	ns
AB007727	At5g12120 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MXC9	ubiquitin-associated (UBA)/TS-N domain-containing protein, contains Pfam profile PF00627: UBA/TS-N domain	GIP, FSD	EIP, signal transduction	0.32579	1.93179	0.31463	1.43558	0.10331	0.54826	0.91668	2.94689	-3.27496	-0.86706	-0.12551	1.55920	-2.07101	0.71684	1.70265	1.19127	1.72018	0.85100	0.33523	NS	0.55114	NS	0.19823	ns
AF000657	At1g22850 Arabidopsis thaliana BAC F19G10, complete sequence	expressed protein	unknown		0.40333	1.94195	0.30014	1.07863	0.19109	0.61556	2.70465	1.17925	-2.38765	-0.70003	1.43544	0.23786	-1.54384	0.83665	1.19332	0.84682	1.82961	1.39724	0.31844	NS	0.39546	NS	0.14808	ns
AL161572	At4g28150 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68	expressed protein	unknown		0.51353	1.94486	0.24376	0.20611	0.34117	0.68590	1.79912	2.09060	-1.55145	-0.54393	0.84729	1.06392	-1.04769	0.95561	0.71243	0.15318	2.07973	8.82266	0.28533	NS	0.07185	NS	0.06024	ns
AF372908	At4g31985 Arabidopsis thaliana AT4g31981/F13D4.162 mRNA, complete cds	60S ribosomal protein L39 (RPL39C) ; ribosome, structural constituent of ribosome, protein biosynthesis	GIP, translation, ribosome		0.48672	1.94498	0.18119	0.99675	0.61484	0.35860	1.24017	2.64979	-0.70172	-1.47954	0.31053	1.40588	-1.09063	0.85821	0.55000	0.77453	2.80430	1.56701	0.21807	NS	0.36160	NS	0.10110	ns
AB016884	At5g24360 Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K16H17	protein kinase family protein / Ire1 homolog-1 (IRE1-1), kinase activity, protein amino acid phosphorylation, ser/thr/tyr kinase, inositol-requiring 1 protein kinase, senses unfolded proteins	M, kinase	CPS, signal transduction	1.79889	1.94600	0.27775	0.10642	1.60250	1.99529	1.87075	2.02125	0.68032	0.99660	0.90361	1.01525	0.83846	0.95943	0.22364	0.07894	5.30205	17.18912	0.11868	NS	0.03699	NC	0.54562	ns
AL353992	Arabidopsis thaliana DNA chromosome 3, BAC clone F14D17	unknown	unknown		0.45234	1.95684	0.40171	2.26798	0.16829	0.73639	0.35314	3.56055	-2.57097	-0.44146	-1.50169	1.83210	-1.50622	0.16520	1.50579	2.35735	1.41461	0.09911	0.39174	NS	0.93711	NS	0.48707	ns
AC002131	At1g11850 Arabidopsis thaliana chromosome 1 BAC F12F1 sequence, complete sequence	expressed protein	unknown		0.37892	1.95883	0.18088	0.86180	0.25102	0.50682	1.34945	2.56821	-1.99414	-0.98045	0.43237	1.36076	-1.48730	0.89657	0.71679	0.65648	2.93442	1.93143	0.20909	NS	0.30414	NS	0.07401	ns

AC006434	At1g75590 Genomic sequence for Arabidopsis thaliana BAC F10A5	auxin-responsive family protein, similar to auxin-induced protein TGSAUR22, molecular function unknown, response to auxin stimulus	CPS, signal transduction		0.45724	1.97895	0.41804	0.60981	0.16164	0.75284	1.54774	2.41015	-2.62915	-0.40959	0.63017	1.26912	-1.51937	0.94965	1.56947	0.45181	1.36907	2.97249	0.40161	NS	0.20660	NS	0.16596	ns
AL163912	At5g07510 Glycine-rich protein {clone atGRP-4} [Arabidopsis thaliana, C24, mRNA Partial, 498 nt]	glycine-rich protein (GRP14), oleosin; glycine-rich protein 14 (GRP14) PMID:11431566; PIR:JQ1063 , extracellular region, membrane, sequestering of lipid, sexual reproduction, nutrient reservoir activity	CPS, resivor		0.38080	1.98398	0.33456	0.58664	0.14423	0.61737	1.56916	2.39880	-2.79353	-0.69579	0.64999	1.26231	-1.74466	0.95615	1.48333	0.43297	1.66337	3.12306	0.34460	NS	0.19728	NS	0.13202	ns
AL138646	At3g60480 Arabidopsis thaliana DNA chromosome 3, BAC clone T8B10	expressed protein	unknown		0.43929	2.00465	0.36947	0.61858	0.17803	0.70054	1.56725	2.44206	-2.48981	-0.51346	0.64823	1.28810	-1.50163	0.96817	1.39749	0.45245	1.51960	3.02617	0.37053	NS	0.20318	NS	0.14052	ns
AC007576	At1g14170 Arabidopsis thaliana chromosome I BAC F7A19 genomic sequence	KH domain-containing protein, nucleic acid binding,	GIP		0.50177	2.00902	0.51459	0.58365	0.13790	0.86564	1.59631	2.42172	-2.85832	-0.20816	0.67475	1.27603	-1.53324	0.97539	1.87394	0.42517	1.15709	3.24435	0.45372	NS	0.19034	NS	0.20613	ns
AC004680	At2g30010 Arabidopsis thaliana chromosome II section 169 of 255 of the complete sequence. Sequence from clones F23F1, T27E13	expressed protein	unknown		1.82152	2.01253	0.36139	0.48580	2.07706	1.56597	1.66902	2.35604	1.05454	0.64706	0.73900	1.23636	0.85080	0.98768	0.28813	0.35169	4.17588	3.97169	0.14963	NS	0.15703	NS	0.71171	ns
AC007017	At2g35920 Arabidopsis thaliana chromosome II section 196 of 255 of the complete sequence. Sequence from clones T20F21, F11F19	helicase domain-containing protein, similar to DEIH-box RNA/DNA helicase, cellular component unknown, ATP binding, helicase activity, nucleic acid binding,	GIP, replication and repair		0.32583	2.01404	0.19434	0.61211	0.18841	0.46325	1.58121	2.44686	-2.40803	-1.11015	0.66103	1.29093	-1.75909	0.97598	0.91774	0.44541	2.71071	3.09884	0.22499	NS	0.19872	NS	0.06305	ns
AB010068	At5g24510 Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K18P6	60s acidic ribosomal protein P1, putative , ribosome, structural constituent of ribosome, translational elongation	GIP, translation, ribosome		0.53753	2.01538	0.28014	1.82467	0.33944	0.73562	0.72515	3.30562	-1.55876	-0.44298	-0.46365	1.72492	-1.00087	0.63063	0.78898	1.54755	1.79402	0.57630	0.32373	NS	0.66717	NS	0.31539	ns
AV557031	EST, Moderately similar to T08583 cellulose synthase [A.thaliana]	cellulose synthase	M, carbohydrate, cellulose		0.30660	2.02735	0.31709	1.21995	0.08238	0.53082	1.16471	2.88998	-3.60153	-0.91371	0.21998	1.53106	-2.25762	0.87552	1.90058	0.92708	1.67989	1.33556	0.34183	NS	0.40916	NS	0.17112	ns
AB026639	At5g65610 Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K21L13	expressed protein,	unknown		0.39903	2.02851	0.29084	0.78303	0.19338	0.60469	1.47483	2.58220	-2.37049	-0.72573	0.56055	1.36860	-1.54811	0.96457	1.16302	0.57138	1.88248	2.38741	0.31087	NS	0.25252	NS	0.11122	ns
AL138656	At3g54590 Arabidopsis thaliana DNA chromosome 3, BAC clone T14E10	proline-rich extensin-like family protein, contains proline-rich extensin domains, INTERPRO:IPR002965 , AB022782 Arabidopsis thaliana mRNA for hydroxyproline-rich glycoprotein, complete cds (ATHRGP1), structural constituent of cell wall, cell wall organization and biogenesis (sensu Magnoliophyta), endomembrane system, cell surface (sensu Magnoliophyta)	CPS, cell wall		0.49094	2.03430	0.25661	1.01388	0.30949	0.67239	1.31738	2.75122	-1.69202	-0.57262	0.39767	1.46007	-1.13232	0.92887	0.79154	0.75123	2.02309	1.74863	0.29225	NS	0.33071	NS	0.11622	ns
AC005679	Arabidopsis thaliana chromosome 1 BAC F9K20 sequence, complete sequence	unknown	unknown		0.38647	2.03867	0.20891	0.97396	0.23875	0.53419	1.34997	2.72736	-2.06644	-0.90458	0.43293	1.44750	-1.48551	0.94022	0.82156	0.71741	2.55712	1.85342	0.23732	NS	0.31499	NS	0.08796	ns
AC010797	At3g02000 Arabidopsis thaliana chromosome III BAC F28J7 genomic sequence	glutaredoxin family protein, contains INTERPRO Domain IPR002109, Glutaredoxin (thioltransferase), Roxy1 encodes a glutaredoxin belonging to a subgroup specific to higher plants. It is required for proper petal initiation and organogenesis. thiol-disulfide exchange intermediate activity, petal formation, sepal formation, stamen formation, petal development, stamen morphogenesis, fruit, root, inflorescence, flower,	GIP, FSD	M, energy	0.43674	2.05656	0.40385	1.70723	0.15117	0.72231	0.84937	3.26375	-2.72571	-0.46931	-0.23554	1.70653	-1.59751	0.73549	1.59551	1.37325	1.41598	0.75743	0.39145	NS	0.58732	NS	0.25756	ns
AB028607	At3g25790 Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:K13N2	myb family transcription factor, nucleus, DNA binding, transcription factor activity, regulation of transcription	GIP, TF		0.41851	2.06230	0.42351	0.01491	0.11904	0.71797	2.07284	2.05176	-3.07045	-0.47800	1.05161	1.03686	-1.77423	1.04423	1.83314	0.01043	1.36877	141.59906	0.40168	NS	0.00450	U	0.16171	ns
AF360132	At1g55460 Arabidopsis thaliana putative Kin17 protein (T5A14.13) mRNA, complete cds	Kin17 DNA-binding protein-related (chromatin associated), contains similarity to zinc finger protein rts2 GB:U16133 GI:563244 from (Saccharomyces cerevisiae)	GIP, chromatin		0.45247	2.10039	0.37503	1.63668	0.18728	0.71765	0.94308	3.25770	-2.41674	-0.47864	-0.08454	1.70385	-1.44769	0.80966	1.37044	1.26459	1.49393	0.90546	0.37553	NS	0.53156	NS	0.22904	ns
AF149841	At3g11670 Arabidopsis thaliana digalactosyldiacylglycerol synthase (DGD1) mRNA, complete cds	digalactosyldiacylglycerol synthase 1 (DGD1) / MGDG:MGDG galactosyltransferase / galactolipid galactosyltransferase,Responsible for the final assembly of galactolipids in photosynthetic membranes. Provides stability to the PS I core complex (e.g. subunits PsaD, PsaE). galactolipid biosynthetic process, chloroplast outer membrane, photosystem I stabilization, transferase activity, transferring glycosyl groups, UDP-galactosyltransferase activity	M, glycosyltransferase		0.66990	2.10546	0.33019	1.05093	0.43643	0.90338	1.36234	2.84858	-1.19619	-0.14660	0.44609	1.51024	-0.67139	0.97817	0.74217	0.75247	1.27934	1.83840	0.42237	NS	0.31716	NS	0.15800	ns
AC006233	At2g27380 Arabidopsis thaliana chromosome II section 154 of 255 of the complete sequence. Sequence from clones T22O13, F12K2	proline-rich family protein, contains proline-rich extensin domains, structural constituent of cell wall, cell wall modification (sensu Magnoliophyta), seed germination, micropylar endosperm (ATEPR1, Encodes an extensin like gene involved in seed germination.)	CPS, cell wall		0.44712	2.11695	0.17148	0.83257	0.32587	0.56837	1.52824	2.70567	-1.61765	-0.81509	0.61187	1.43599	-1.21637	1.02393	0.56750	0.58274	3.03123	2.48490	0.20286	NS	0.24357	NS	0.06004	ns
AB016884	At5g24350 Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K16H17	expressed protein, weak similarity to neuroblastoma-amplified protein (Homo sapiens) GI:4337460	unknown		0.47912	2.11916	0.42117	0.34605	0.18131	0.77693	1.87447	2.36385	-2.46351	-0.36414	0.90648	1.24114	-1.41383	1.07381	1.48448	0.23664	1.34691	6.41732	0.40657	NS	0.09841	NS	0.14413	ns
AB008266	At5g64090 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MHJ24	expressed protein	unknown		0.44941	2.12503	0.22514	0.54048	0.29021	0.60861	1.74285	2.50721	-1.78483	-0.71641	0.80145	1.32608	-1.25062	1.06377	0.75548	0.37097	2.34107	4.05527	0.25700	NS	0.15392	NS	0.06021	ns
AF360270	At3g06250 Arabidopsis thaliana unknown protein (F28L1.19) mRNA, complete cds	far-red impaired responsive protein, putative, similar to far-red impaired response protein FAR1 (Arabidopsis thaliana) gi|5764395|gb|AAD51282; contains Pfam:PF03101 domain: FAR1 family ; zinc ion binding, response to red or far red light	EIP, signal transduction		0.39012	2.12800	0.39837	0.44564	0.10843	0.67181	1.81288	2.44312	-3.20512	-0.57387	0.85828	1.28872	-1.88949	1.07350	1.86058	0.30437	1.43619	4.98795	0.38721	NS	0.12596	NS	0.15631	ns

AY035065	At5g14570 Arabidopsis thaliana putative high affinity nitrate transporter protein (T15N1_60/AT5g14570) mRNA, complete cds	member of High affinity nitrate transporter family, transporter, putative, similar to trans-membrane nitrate transporter protein AtNRT2:1 (Arabidopsis thaliana) GI:3747058, high-affinity nitrate transporter ACH1 (Arabidopsis thaliana) GI:3608362; contains Pfam profile PF00083: Sugar (and other) transporter , chloroplast, integral to membrane, nitrate transporter activity, transport	EIP, transport	CPS, transport		0.38798	2.13250	0.38968	0.08223	0.11243	0.66352	2.19064	2.07435	-3.15294	-0.59178	1.13135	1.05266	-1.87236	1.09201	1.81101	0.05564	1.46212	27.75431	0.38189	NS	0.02293	U	0.14676	ns
AF385727	At3g03980 Arabidopsis thaliana AT3g03980/T11I18_9 mRNA, complete cds	short-chain dehydrogenase/reductase (SDR) family protein, similar to short-chain type dehydrogenase/reductase SP:Q08632 (Picea abies) ; chloroplast, oxidoreductase activity, metabolism	M, oxidoreductase			0.35782	2.14113	0.38341	1.25557	0.08672	0.62893	1.25331	3.02896	-3.52755	-0.66902	0.32574	1.59882	-2.09829	0.96228	2.02129	0.90020	1.46809	1.51174	0.38068	NS	0.37205	NS	0.18961	ns
AC000098	At1g05130 Arabidopsis thaliana chromosome 1 YAC yUP8H12 complete sequence	unknown protein , obsolete	unknown			0.51828	2.14473	0.32529	0.52766	0.28827	0.74830	1.77162	2.51784	-1.79453	-0.41831	0.82507	1.33219	-1.10642	1.07863	0.97314	0.35859	1.60791	4.25394	0.35421	NS	0.14699	NS	0.09660	ns
AC074228	At1g44190 Arabidopsis thaliana chromosome 1 BAC T7O23 genomic sequence	pseudogene, hypothetical protein	unknown			0.47147	2.14719	0.37046	1.21105	0.20952	0.73343	1.29085	3.00353	-2.25486	-0.44727	0.36832	1.58666	-1.35107	0.97749	1.27815	0.86149	1.49489	1.60463	0.37534	NS	0.35479	NS	0.16614	ns
AB015475	At5g59990 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MMN10	expressed protein,	unknown			0.52270	2.15023	0.34428	0.44491	0.27926	0.76615	1.83563	2.46483	-1.84033	-0.38431	0.87627	1.30149	-1.11232	1.08888	1.02956	0.30067	1.52789	5.12155	0.36894	NS	0.12276	NS	0.10104	ns
AC007047	At2g16340 Arabidopsis thaliana chromosome II section 94 of 255 of the complete sequence. Sequence from clones F7H1, F16F14, F1P15	hypothetical protein	unknown			0.38403	2.15390	0.31416	0.21764	0.16189	0.60618	2.00000	2.30780	-2.62693	-0.72218	1.00000	1.20652	-1.67456	1.10326	1.34686	0.14603	1.75830	10.68451	0.32920	NS	0.05941	NS	0.10120	ns
AB006703	At5g44060 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MRH10	expressed protein,	unknown			0.35671	2.15555	0.31998	0.00332	0.13045	0.58297	2.15790	2.15320	-2.93840	-0.77852	1.10963	1.10648	-1.85846	1.10805	1.52727	0.00222	1.72089	704.57870	0.33512	NS	0.00090	U	0.11091	ns
AL162873	At5g03850 Arabidopsis thaliana DNA chromosome 5, BAC clone F8F6 (ESSA project)	40S ribosomal protein S28 (RPS28B), ribosomal protein S28, Arabidopsis thaliana, EMBL:ATRP28A , ribosome, structural constituent of ribosome, translation, ribosome biogenesis and assembly	GIP, translation, ribosome			0.45219	2.16575	0.25828	1.16548	0.26956	0.63482	1.34163	2.98987	-1.89133	-0.65557	0.42399	1.58008	-1.27345	1.00204	0.87381	0.81748	2.06101	1.73349	0.28759	NS	0.33311	NS	0.11492	ns
Z54137	At3g50060 A.thaliana mRNA for MYB-related protein (1107 bp)	myb family transcription factor, contains Pfam profile: PF00249 myb-like DNA-binding domain; identical to cDNA MYB-related protein, nucleus, DNA binding, transcription factor activity, response to salt stress, regulation of transcription, DNA-dependent, response to abscisic acid stimulus, response to ethylene stimulus, response to gibberellic acid stimulus, response to jasmonic acid stimulus, response to salicylic acid stimulus, response to cadmium ion	GIP, TF			0.47285	2.18677	0.19346	0.96500	0.33605	0.60965	1.50441	2.86913	-1.57326	-0.71395	0.58919	1.52061	-1.14361	1.05490	0.60762	0.65861	2.66171	2.26516	0.22879	NS	0.26467	NS	0.07397	ns
AV566828	ESTs	unknown	unknown			0.36226	2.19367	0.31411	0.44465	0.14015	0.58437	1.87925	2.50808	-2.83498	-0.77505	0.91016	1.32659	-1.80501	1.11837	1.45659	0.29446	1.75250	5.37123	0.33011	NS	0.11718	NS	0.10856	ns
U75187	At1g18970 Arabidopsis thaliana germin-like protein (GLP4) mRNA, complete cds	germin-like protein (GLP1) (GLP4), identical to germin-like protein subfamily T member 1 (SP|P92995) , Encodes a germin-like protein with possible oxalate oxidase activity , manganese ion binding, nutrient reservoir activity, metal ion binding, apoplast	M, carbohydrate, oxalate oxidase			0.57388	2.21183	0.22731	0.70474	0.41315	0.73462	2.71016	1.71350	-1.27526	-0.44493	1.43838	0.77695	-0.86010	1.10766	0.58713	0.46770	2.07170	3.34932	0.28629	NS	0.18471	NS	0.06567	ns
F19940	EST	unknown	unknown			0.34378	2.22499	0.33329	0.10770	0.10811	0.57945	2.30114	2.14883	-3.20947	-0.78723	1.20235	1.10355	-1.99835	1.15295	1.71278	0.06986	1.65000	23.33865	0.34687	NS	0.02726	U	0.12156	ns
AL133363	Arabidopsis thaliana DNA chromosome 3, BAC clone T20E23	unknown	unknown			0.34079	2.23242	0.21709	0.37690	0.18728	0.49429	1.96591	2.49893	-2.41674	-1.01656	0.97520	1.32131	-1.71665	1.14825	0.99008	0.24474	2.45204	6.63511	0.24652	NS	0.09523	NS	0.05791	ns
F15227	EST	unknown	unknown			0.46389	2.24928	0.23125	0.54509	0.30037	0.62741	1.86384	2.63472	-1.73518	-0.67253	0.89828	1.39765	-1.20385	1.14797	0.75141	0.35311	2.26574	4.59766	0.26461	NS	0.13634	NS	0.05703	ns
AL049751	At4g13150 Arabidopsis thaliana DNA chromosome 4, BAC clone F17N18 (ESSA project)	expressed protein	unknown			0.50742	2.24948	0.40185	0.13811	0.22327	0.79157	2.15182	2.34715	-2.16314	-0.33721	1.10556	1.23091	-1.25017	1.16823	1.29113	0.08863	1.36935	18.63980	0.40155	NS	0.03412	U	0.11831	ns
AB015473	At5g17980 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MCM23	C2 domain-containing protein, The C2 domain is a Ca2+-dependent membrane-targeting module found in many cellular proteins involved in signal transduction or membrane trafficking.	CPS, signal transduction			0.57558	2.25215	0.40616	0.60789	0.28838	0.86278	1.82230	2.68199	-1.79397	-0.21294	0.86576	1.42331	-1.00346	1.14453	1.11796	0.39424	1.26937	4.10563	0.42479	NS	0.15210	NS	0.12448	ns
Z35474	At5g42980 A.thaliana (GIF1) mRNA for thioredoxin	thioredoxin H-type 3 (TRX-H-3) (GIF1), encodes a cytosolic thioredoxin that reduces disulfide bridges of target proteins by the reversible formation of a disulfide bridge between two neighboring Cys residues present in the active site. Thioredoxins have been found to regulate a variety of biological reactions in prokaryotic and eukaryotic cells. cytosol, oxidoreductase activity, acting on sulfur group of donors, disulfide as acceptor, response to hydrogen peroxide	GIP, FSD	M, energy		0.49465	2.26094	0.35532	0.97292	0.24340	0.74590	1.57298	2.94890	-2.03862	-0.42296	0.65350	1.56017	-1.23079	1.10684	1.14245	0.64112	1.52357	2.44153	0.36977	NS	0.24748	NS	0.12765	ns
AL049711	At3g51930 Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15	transducin family protein / WD-40 repeat family protein, contains 7 WD-40 repeats (PF00400); myosin heavy chain kinase B (SP:P90648)(GI:1903458) (Dictyostelium discoideum) , chloroplast, nucleotide binding	M, kinase	CPS, cell structure	WD40	0.63668	2.26135	0.29459	0.12805	0.42837	0.84499	2.17081	2.35190	-1.22305	-0.24299	1.11823	1.23383	-0.73302	1.17603	0.69301	0.08174	1.49588	20.34714	0.37514	NS	0.03126	U	0.06078	ns
AL161542	At4g15770 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 42	60S ribosome subunit biogenesis protein, putative, contains similarity to 60S ribosome subunit biogenesis protein NIP7 (Swiss-Prot:Q08962) (Saccharomyces cerevisiae) , cellular_component, RNA binding, ribosome biogenesis and assembly	GIP, translation, ribosome			0.48142	2.26610	0.34849	1.02760	0.23500	0.72783	1.53947	2.99272	-2.08927	-0.45832	0.62244	1.58146	-1.27380	1.10195	1.15326	0.67813	1.56203	2.29807	0.36252	NS	0.26129	NS	0.12866	ns
AL163491	At5g13310 Arabidopsis thaliana DNA chromosome 5, BAC clone T31B5 (ESSA project)	expressed protein	unknown			0.44286	2.26641	0.35735	0.76491	0.19017	0.69554	1.72554	2.80729	-2.39464	-0.52379	0.78705	1.48918	-1.45921	1.13811	1.32289	0.49648	1.55995	3.24189	0.36291	NS	0.19048	NS	0.12157	ns
AC017118	At1g32630 Genomic sequence for Arabidopsis thaliana BAC F6N18 from chromosome I	expressed protein	unknown			0.50055	2.28183	0.45281	0.84324	0.18037	0.82073	1.68556	2.87809	-2.47098	-0.28501	0.75323	1.52511	-1.37800	1.13917	1.54571	0.54580	1.26077	2.95168	0.42689	NS	0.20795	NS	0.16203	ns
Z14991	At5g53300 A.thaliana UBC10 mRNA for ubiquitin conjugating enzyme homolog	ubiquitin-conjugating enzyme 10 (UBC10), E2; identical to gi:297877, SP:P35133 , ubiquitin conjugating enzyme activity, ubiquitin-dependent protein catabolic process	GIP, FSD	EIP, signal transduction		0.54259	2.31629	0.12140	2.86379	0.45675	0.62843	0.29129	4.34129	-1.13052	-0.67017	-1.77949	2.11812	-0.90035	0.16932	0.32552	2.75603	3.91157	0.08688	0.15934	NS	0.94483	NS	0.64035	ns
AB011482	At5g57480 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MUA2	AAA-type ATPase family protein, ATPase activity, endomembrane system	M, energy, ATPase			0.54276	2.31916	0.36363	0.74521	0.28563	0.79988	1.79222	2.84610	-1.80778	-0.32214	0.84175	1.50899	-1.06496	1.17537	1.05051	0.47181	1.43367	3.52306	0.38774	NS	0.17607	NS	0.11062	ns

AB007651	At5g22310 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MWD9	expressed protein	unknown		0.46804	2.32569	0.30322	1.40714	0.25363	0.68245	1.33069	3.32069	-1.97919	-0.55119	0.41218	1.73148	-1.26519	1.07183	1.00975	0.93289	1.77198	1.62484	0.32709	NS	0.35122	NS	0.13807	ns
AC006951	At2g04390 Arabidopsis thaliana chromosome II section 21 of 255 of the complete sequence. Sequence from clones T1O3, F7D11	40S ribosomal protein S17 (RPS17A) , ribosome, structural constituent of ribosome, translation	GIP, translation, ribosome		0.35898	2.33197	0.33857	1.58843	0.11957	0.59839	1.20878	3.45516	-3.06404	-0.74084	0.27355	1.78875	-1.90244	1.03115	1.64275	1.07141	1.63778	1.36107	0.34897	NS	0.40339	NS	0.16867	ns
AL049480	At4g25890 Arabidopsis thaliana DNA chromosome 4, BAC clone F14M19 (ESSA project)	60S acidic ribosomal protein P3 (RPP3A), acidic ribosomal protein P3a - maize, PIR2:T02037 , ribosome, structural constituent of ribosome, translational elongation	GIP, translation, ribosome		0.55215	2.33614	0.37161	0.53962	0.28938	0.81492	1.95458	2.71771	-1.78896	-0.29527	0.96686	1.44239	-1.04211	1.20462	1.05619	0.33625	1.39536	5.06639	0.39586	NS	0.12406	NS	0.10320	ns
AC004697	At2g39170 Arabidopsis thaliana chromosome II section 211 of 255 of the complete sequence. Sequence from clones T16B24, F12L6	expressed protein	unknown		0.30089	2.34485	0.28626	0.62998	0.09848	0.50330	1.89938	2.79032	-3.34409	-0.99050	0.92553	1.48043	-2.16729	1.20298	1.66424	0.39237	1.84170	4.33587	0.31668	NS	0.14430	NS	0.10821	ns
AL132969	At3g53020 Arabidopsis thaliana DNA chromosome 3, BAC clone F8J2	RPL24B encodes ribosomal protein L24, homolog of cytosolic RPL24, found in archaea and higher eukaryotes. Arabidopsis has two RPL24 homologs, RPL24A (AT2G36620) and RPL24B (STV1, SHORT VALVE1). Regulated by TCP20. ribosome, structural constituent of ribosome, translation, ribosome biogenesis and assembly , auxin mediated signaling pathway, gynoecium development	GIP, translation, ribosome		0.44899	2.34684	0.39083	1.33417	0.17264	0.72535	1.40344	3.29024	-2.53420	-0.46325	0.48897	1.71819	-1.49872	1.10358	1.46438	0.86919	1.44738	1.79557	0.38490	NS	0.32349	NS	0.16324	ns
AA651363	EST	unknown	unknown		0.74897	2.36525	0.12225	1.23588	0.66253	0.83542	1.49135	3.23914	-0.59395	-0.25943	0.57662	1.69561	-0.42669	1.13612	0.23654	0.79125	2.55107	2.03060	0.23783	NS	0.29132	NS	0.11586	ns
AB023041	At3g25900 Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MPE11	homocysteine S-methyltransferase 1 (HMT-1), homocysteine S-methyltransferase activity, methionine biosynthesis	M, amino acid		0.52113	2.36571	0.40848	0.62791	0.23229	0.80997	1.92171	2.80971	-2.10602	-0.30406	0.94239	1.49042	-1.20504	1.21641	1.27418	0.38751	1.33748	4.43920	0.40872	NS	0.14105	NS	0.12379	ns
AL035353	At4g28780 Arabidopsis thaliana DNA chromosome 4, BAC clone F16A16 (ESSAII project)	GDSL-motif lipase/hydrolase family protein, similar to family II lipase EXL3 (GI:15054386), EXL1 (GI:15054382), EXL2 (GI:15054384) (Arabidopsis thaliana); contains Pfam profile PF00657: Lipase/Acylhydrolase with GDSL-like motif , carboxylic ester hydrolase activity, lipid metabolic process,	M, lipid		1.84652	2.37303	0.18910	0.19260	1.98024	1.71281	2.23684	2.50921	0.98567	0.77636	1.16146	1.32724	0.88102	1.24435	0.14800	0.11722	8.41839	15.01241	0.07527	NS	0.04234	U	0.11265	ns
AY037250	At3g27360 Arabidopsis thaliana AT3g27360/K1G2_6 mRNA, complete cds	histone H3, identical to histone H3 from Zea mays SP|P05203, Medicago sativa GI:166384, Encephalartos altensteinii SP|P08903, Pisum sativum SP|P02300; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4 , chloroplast, nucleus, DNA binding, chromosome organization and biogenesis (sensu Eukaryota), nucleosome assembly, nucleosome, root, inflorescence, flower, leaf, seedling growth	GIP, chromosome		0.72725	2.37310	0.12782	1.84149	0.81764	0.63687	1.07097	3.67523	-0.29047	-0.65093	0.09892	1.87784	-0.47070	0.98838	0.25489	1.25788	2.61163	1.11121	0.23280	NS	0.46650	NS	0.24915	ns
AB022222	At5g40040 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MUD12	60S acidic ribosomal protein P2 (RPP2E), acidic ribosomal protein P2, ribosome, structural constituent of ribosome, translational elongation	GIP, translation, ribosome		0.44128	2.37347	0.43268	0.32811	0.13533	0.74723	2.14146	2.60548	-2.88549	-0.42037	1.09860	1.38155	-1.65293	1.24007	1.74310	0.20008	1.34106	8.76518	0.40790	NS	0.07232	NS	0.14496	ns
AC004521	At2g44300 Arabidopsis thaliana chromosome II section 238 of 255 of the complete sequence. Sequence from clones F4I1	lipid transfer protein-related, low similarity to lipid transfer protein Picea abies GI:2627141; contains Pfam profile: PF00234: Protease inhibitor/seed storage/LTP family , lipid binding, lipid transport, anchored to membrane	M, protease inhibitor	CPS, transport	0.49038	2.38006	0.41212	0.67207	0.19896	0.78179	1.90483	2.85528	-2.32943	-0.35514	0.92966	1.51363	-1.34228	1.22165	1.39603	0.41293	1.35977	4.18394	0.40368	NS	0.14936	NS	0.13040	ns
AY034973	At3g28200 Arabidopsis thaliana putative peroxidase (T19D11.1/AT3g28200) mRNA, complete cds	peroxidase, putative, similar to peroxidase ATP26a GB:CAA72487 GI:1890317 (Arabidopsis thaliana) , cell wall (sensu Magnoliophyta), peroxidase activity, response to oxidative stress	M, oxidoreductase		0.53014	2.40835	0.33660	2.63307	0.29213	0.76815	0.54649	4.27021	-1.77533	-0.38054	-0.87174	2.09431	-1.07794	0.61128	0.98627	2.09731	1.54566	0.41219	0.36558	NS	0.75110	NS	0.41099	ns
AA394613	EST	unknown	unknown		0.44129	2.41298	0.37142	0.69117	0.17865	0.70392	2.90171	1.92425	-2.48476	-0.50651	1.53691	0.94429	-1.49563	1.24060	1.39883	0.41904	1.51208	4.18689	0.37198	NS	0.14925	NS	0.11777	ns
AY049267	At2g05380 Arabidopsis thaliana At2g05380/F16J10.7 mRNA, complete cds	glycine-rich protein (GRP3S), identical to cDNA glycine-rich protein 3 short isoform (GRP3S) GI:4206766 , (GRP3 responds to hormone, and abiotic stimuli)	GLYCINE		0.54288	2.44567	0.24887	1.08567	0.36690	0.71886	1.67799	3.21336	-1.44655	-0.47622	0.74674	1.68408	-0.96139	1.21541	0.68612	0.66280	1.98158	2.59330	0.29753	NS	0.23430	NS	0.08409	ns
AC016041	At1g48930 Genomic sequence for Arabidopsis thaliana BAC F27J15 from chromosome I	endo-1,4-beta-glucanase, putative / cellulase, putative, similar to endo-beta-1,4-glucanase GI:4972236 from (Fragaria x ananassa) , hydrolase activity, hydrolyzing O-glycosyl compounds, carbohydrate metabolic process, endomembrane system	M, glycosyltransferase		0.47254	2.44821	0.34630	1.67424	0.22766	0.71741	1.26435	3.63208	-2.13503	-0.47913	0.33839	1.86079	-1.30708	1.09959	1.17090	1.07650	1.57869	1.44455	0.35946	NS	0.38548	NS	0.16573	ns
AP002048	At3g24480 Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MXP5	leucine-rich repeat family protein / extensin family protein, similar to extensin-like protein (Lycopersicon esculentum) gi|5917664|gb|AAD55979; contains leucine-rich repeats, Pfam:PF00560; contains proline rich extensin domains, INTERPRO:IPR002965 , cell wall (sensu Magnoliophyta), structural constituent of cell wall, protein binding	CPS, cell wall		0.41958	2.45117	0.30293	0.40299	0.20538	0.63379	2.16622	2.73613	-2.28365	-0.65793	1.11518	1.45214	-1.47079	1.28366	1.14956	0.23827	1.80939	7.61902	0.32142	NS	0.08308	NS	0.08007	ns
U60445	AT3G02520 Arabidopsis thaliana 14-3-3 protein isoform GF14 nu mRNA, complete cds	Encodes GF14 ν, a 14-3-3 protein isoform (14-3-3ν).cytoplasm, nuclear envelope, plasma membrane, protein binding	PB14-3-3		0.71888	2.45769	0.45640	0.91324	0.39616	1.04160	1.81193	3.10345	-1.33585	0.05881	0.85753	1.63387	-0.63852	1.24570	0.98617	0.54896	0.91567	3.20915	0.52801	NS	0.19231	NS	0.14213	ns
AC009853	At3g07560 Arabidopsis thaliana chromosome III BAC F21O3 genomic sequence	Encodes peroxin 13 (PEX13) involved in protein transport into peroxisomes. peroxisomal membrane, protein binding, protein import into peroxisome matrix (APM2)	CPS, transport		0.34582	2.46889	0.35152	0.26262	0.09726	0.59438	2.65459	2.28318	-3.36194	-0.75053	1.40849	1.19105	-2.05624	1.29977	1.84655	0.15375	1.57481	11.95509	0.36017	NS	0.05313	NS	0.12457	ns
T21937	EST	unknown	unknown		0.60362	2.48461	0.54106	1.00630	0.22103	0.98620	1.77305	3.19617	-2.17767	-0.02004	0.82623	1.67634	-1.09885	1.25129	1.52567	0.60112	1.01858	2.94382	0.49414	NS	0.20847	NS	0.17990	ns
X83369	At1g70210 A.thaliana mRNA for cyclin delta-1	Encodes a D-type cyclin that physically interacts with CDC2A. Its expression is upregulated early during germination. nucleus, cyclin-dependent protein kinase regulator activity, regulation of progression through cell cycle	CPS, cell cycle		0.55708	2.49146	0.42305	0.05916	0.25794	0.85622	2.53329	2.44962	-1.95489	-0.22395	1.34101	1.29256	-1.08942	1.31679	1.22396	0.03426	1.25876	54.35414	0.42739	NS	0.01171	U	0.10876	ns

L22568	At5g52310 Arabidopsis thaliana cor78 protein mRNA, complete cds	low-temperature-responsive protein 78 (LTI78) / desiccation-responsive protein 29A (RD29A) , cold regulated gene, the 5' region of cor78 has cis-acting regulatory elements that can impart cold-regulated gene expression COLD REGULATED 78, response to desiccation, response to osmotic stress, response to abscisic acid stimulus, hyperosmotic salinity response	EIP, signal transduction	0.40402	2.49575	0.39417	0.40333	0.12530	0.68274	2.21056	2.78094	-2.99657	-0.55059	1.14441	1.47557	-1.77358	1.30999	1.72957	0.23417	1.45020	7.91139	0.38432	NS	0.08004	NS	0.12973	ns
AL132978	At3g50080 Arabidopsis thaliana DNA chromosome 3, BAC clone F3A4	F-box family protein (FBL16), contains similarity to SKP1 interacting partner 2 GI:10716949 from (Arabidopsis thaliana); contains Pfam profile: PF00646 F-box domain , VIER F-BOX PROTEINE 2 (VFB2)	Fbox	0.44598	2.51543	0.31756	1.30443	0.22144	0.67053	1.59306	3.43780	-2.17504	-0.57663	0.67180	1.78149	-1.37583	1.22664	1.13025	0.78467	1.72150	2.21079	0.33502	NS	0.27043	NS	0.11595	ns
AC002376	At1g04610 Sequence of BAC T1G11 from Arabidopsis thaliana chromosome 1	flavin-containing monooxygenase / FMO (YUCCA3), disulfide oxidoreductase activity, oxidoreductase activity, auxin biosynthesis	M, oxidoreductase, hormone synth, ABA	0.62063	2.54086	0.59871	0.71926	0.19728	1.04398	2.03227	3.04945	-2.34166	0.06210	1.02309	1.60855	-1.13978	1.31582	1.69971	0.41398	0.94833	4.49499	0.51688	NS	0.13936	NS	0.18555	ns
AC004218	Arabidopsis thaliana chromosome II section 212 of 255 of the complete sequence. Sequence from clones F12L6	unknown	unknown	0.41847	2.54631	0.37968	1.30903	0.15000	0.68695	3.47193	1.62069	-2.73701	-0.54172	1.79574	0.69661	-1.63936	1.24617	1.55230	0.77720	1.49353	2.26756	0.37561	NS	0.26442	NS	0.14312	ns
AC012328	At3g03230 Arabidopsis thaliana chromosome III BAC T17B22 genomic sequence	esterase/lipase/thioesterase family protein, contains Interpro entry IPR000379	M, lipid	0.38959	2.54835	0.32595	0.86927	0.15911	0.62007	1.93368	3.16302	-2.65187	-0.68949	0.95135	1.66130	-1.67068	1.30633	1.38761	0.50201	1.70271	3.68006	0.33806	NS	0.16891	NS	0.10403	ns
AL161541	At4g15500 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 41	UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase , cellular_component, UDP-glycosyltransferase activity, transferase activity, transferring hexosyl groups, metabolic process, transferase activity, transferring glycosyl groups	M, glycosyltransferase	0.54122	2.56068	0.43902	1.31962	0.23078	0.85165	1.62757	3.49380	-2.11539	-0.23166	0.70272	1.80480	-1.17353	1.25376	1.33200	0.77929	1.24596	2.27526	0.43056	NS	0.26362	NS	0.15611	ns
AJ249598	At5g12110 Arabidopsis thaliana mRNA for elongation factor 1B alpha-subunit (eEF1Balpha1 gene)	elongation factor 1B alpha-subunit 1 (eEF1Balpha1), eukaryotic translation elongation factor 1 complex, translation elongation factor activity, translational elongation	GIP, translation, regulation	0.52588	2.56802	0.36143	0.28843	0.27031	0.78145	2.36407	2.77197	-1.88730	-0.35578	1.24127	1.47091	-1.12154	1.35609	1.08295	0.16238	1.46461	11.81055	0.38138	NS	0.05377	NS	0.08535	ns
AC055769	At1g32570 Arabidopsis thaliana chromosome 1 BAC T9G5 genomic sequence	hypothetical protein	unknown	0.65202	2.58280	0.21080	0.96672	0.50297	0.80108	1.89922	3.26637	-0.99147	-0.31998	0.92541	1.70769	-0.65572	1.31655	0.47481	0.55316	1.95304	3.36592	0.30126	NS	0.18385	NS	0.06202	ns
AC005623	At2g27110 Arabidopsis thaliana chromosome II section 151 of 255 of the complete sequence. Sequence from clones T20P8, F20F1	far-red impaired responsive protein, putative, similar to far-red impaired response protein FAR1, contains InterPro domain SWIM Zn-finger (InterPro:IPR007527); contains InterPro domain Zn-finger, PMZ type, zinc ion binding, response to red or far red light	EIP, signal transduction	0.61172	2.58881	0.12952	1.28680	0.52013	0.70330	1.67891	3.49872	-0.94305	-0.50779	0.74752	1.80683	-0.72542	1.27717	0.30778	0.74904	3.33328	2.41134	0.18555	NS	0.25027	NS	0.07293	ns
AV533809	EST	unknown	unknown	0.50239	2.59812	0.35045	0.11553	0.25458	0.75019	2.67981	2.51643	-1.97379	-0.41467	1.42213	1.33138	-1.19423	1.37676	1.10247	0.06417	1.53192	30.34033	0.36817	NS	0.02098	U	0.08118	ns
AL049500	At4g11680 Arabidopsis thaliana DNA chromosome 4, BAC clone T5C23 (ESSA project)	zinc finger (C3HC4-type RING finger) family protein, low similarity to SP|Q9WTV7 RING finger protein 12 (LIM domain interacting RING finger protein) {Mus musculus}; contains Pfam profile PF00097: Zinc finger, C3HC4 type (RING finger), chloroplast, protein binding, zinc ion binding	ZINC	0.48502	2.61922	0.37562	0.70443	0.21942	0.75062	2.12112	3.11733	-2.18824	-0.41384	1.08483	1.64031	-1.30104	1.36257	1.25469	0.39279	1.46646	4.90587	0.38101	NS	0.12801	NS	0.10329	ns
U37281	AT5G09810 Arabidopsis thaliana actin-2 mRNA, complete cds	Member of Actin gene family.Mutants are defective in germination and root growth.(ACT2/7) cytoskeleton, structural constituent of cytoskeleton, cytoskeleton organization and biogenesis, response to light stimulus, response to wounding, seed germination, response to auxin stimulus, root development, seed coat, seedling growth	CPS, cell structure	0.62483	2.63014	0.08072	1.36689	0.56776	0.68191	1.66360	3.59668	-0.81665	-0.55234	0.73431	1.84667	-0.68450	1.29049	0.18690	0.78655	5.17945	2.32028	0.12142	NS	0.25906	NS	0.07454	ns
AB020745	At5g48470 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MJE7	expressed protein	unknown	0.55996	2.63766	0.56520	0.54161	0.16030	0.95962	2.25468	3.02063	-2.64111	-0.05947	1.17293	1.59485	-1.35029	1.38389	1.82549	0.29835	1.04607	6.55989	0.48567	NS	0.09631	NS	0.17173	ns
AC074360	At1g31630 Arabidopsis thaliana chromosome 1 BAC F27M3 genomic sequence	MADS-box family protein, similar to MADS-box protein NMH 7 GI:2827300 from (Medicago sativa) , mitochondrion, nucleus, DNA binding, transcription factor activity, regulation of transcription, DNA-dependent	GIP, TF	0.51450	2.64330	0.25957	0.66336	0.33096	0.69805	3.11237	2.17423	-1.59528	-0.51860	1.63801	1.12051	-1.05694	1.37926	0.76133	0.36593	1.96332	5.33039	0.29991	NS	0.11806	NS	0.05518	ns
AB019235	At5g62400 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MMI9	expressed protein	unknown	0.43558	2.66928	0.32193	0.98252	0.20795	0.66322	1.97453	3.36402	-2.26571	-0.59244	0.98151	1.75019	-1.42907	1.36585	1.18318	0.54354	1.70812	3.55377	0.33718	NS	0.17462	NS	0.09354	ns
AL132972	AT3G52280 Arabidopsis thaliana DNA chromosome 3, BAC clone T25B15	Bromodomain containing nuclear-localized protein involved in leaf development. GTE6 binds to the promoter and intron of AS1 and regulates its expression via histone acetylation. GENERAL TRANSCRIPTION FACTOR GROUP E6, nucleus, H3/H4 histone acetyltransferase activity, chromatin remodeling	GIP, TF	0.77307	2.67677	0.36755	1.39942	0.51317	1.03297	3.66631	1.68723	-0.96248	0.04681	1.87433	0.75466	-0.45784	1.31449	0.71367	0.79173	0.90725	2.34800	0.53093	NS	0.25632	NS	0.14304	ns

AY034978	AT1G74030 Arabidopsis thaliana putative enolase (F2P9.10) mRNA, complete cds	enolase, putative, similar to Swiss-Prot:P15007 enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase)(2-phospho-D- glycerate hydro-lyase) (Drosophila melanogaster) , chloroplast, phosphopyruvate hydratase complex, phosphopyruvate hydratase activity, anaerobic respiration, gluconeogenesis, glycolysis, serine-isocitrate lyase pathway, glyceraldehyde-3-phosphate catabolic process, aerobic glycerol catabolic process, anaerobic glycolysis, non-phosphorylated glucose catabolic process, acetate fermentation, glucose catabolic process to D-lactate and ethanol, glucose catabolic process to butanediol, glucose catabolic process to lactate and acetate	M, carbohydrate		0.54478	2.70919	0.09069	2.83799	0.48065	0.60890	4.71595	0.70243	-1.05694	-0.71572	2.23755	-0.50958	-0.88633	0.86398	0.24127	1.94251	5.19516	0.62901	0.12106	NS	0.64255	NS	0.33343	ns
AC006228	At1g36035 Genomic sequence for Arabidopsis thaliana BAC F5J5	copia-like retrotransposon family, has a 0. P-value blast match to gb|AAO73523.1| gag-pol polyprotein (Glycine max) (SIRE1) (Ty1_Copia-family)	TRANS		0.57134	2.72187	0.27198	0.97548	0.37902	0.76366	2.03210	3.41164	-1.39966	-0.38899	1.02297	1.77046	-0.89432	1.39672	0.71465	0.52855	1.76977	3.73709	0.32743	NS	0.16645	NS	0.06771	ns
AC004680	At2g29950 Arabidopsis thaliana chromosome II section 169 of 255 of the complete sequence. Sequence from clones F23F1, T27E13	unknown protein , obsolete	unknown		0.53610	2.72314	0.18210	1.44196	0.40733	0.66486	1.70352	3.74276	-1.29572	-0.58887	0.76852	1.90410	-0.94230	1.33631	0.49982	0.80298	2.66618	2.35352	0.22844	NS	0.25578	NS	0.07641	ns
AC002332	At2g33510 Arabidopsis thaliana chromosome II section 186 of 255 of the complete sequence. Sequence from clones F25I18, F4P9	expressed protein	unknown		0.36775	2.72874	0.34006	0.54640	0.12729	0.60820	2.34238	3.11511	-2.97379	-0.71738	1.22797	1.63928	-1.84559	1.43363	1.59553	0.29084	1.63585	6.97105	0.34931	NS	0.09070	NS	0.10364	ns
AC006438	At2g15880 Arabidopsis thaliana chromosome II section 92 of 255 of the complete sequence. Sequence from clones F19G14, F7H1	leucine-rich repeat family protein / extensin family protein, similar to extensin-like protein. structural constituent of cell wall, protein binding, endomembrane system	CPS, cell wall		0.52329	2.73379	0.38555	0.14782	0.25067	0.79592	2.83832	2.62927	-1.99616	-0.32930	1.50504	1.39466	-1.16273	1.44985	1.17865	0.07805	1.39512	26.27172	0.39592	NS	0.02422	U	0.08881	ns
AC069143	At1g19190 Sequence of BAC T29M8 from Arabidopsis thaliana chromosome 1	expressed protein, contains similarity to anther-specific and pathogenesis response protein (PrMC3) GI:5487873 from (Pinus radiata)	unknown		0.51032	2.73436	0.35843	1.21338	0.25688	0.76377	1.87637	3.59235	-1.96086	-0.38879	0.90795	1.84493	-1.17482	1.37644	1.11162	0.66255	1.49462	2.93803	0.37539	NS	0.20885	NS	0.10817	ns
AY037220	At4g24060 Arabidopsis thaliana AT4g24060/T19F6_50 mRNA, complete cds	Dof-type zinc finger domain-containing protein, Dof zinc finger protein - Oryza sativa,PID:d1042342 , cellular_component, DNA binding, transcription factor activity, regulation of transcription	GIP, TF		0.56641	2.75987	0.50666	0.48735	0.20815	0.92467	2.41526	3.10447	-2.26434	-0.11299	1.27218	1.63435	-1.18866	1.45326	1.52123	0.25609	1.10504	8.02525	0.46826	NS	0.07892	NS	0.13644	ns
AC007127	At2g17230 Arabidopsis thaliana chromosome II section 99 of 255 of the complete sequence. Sequence from clones F6P23, T23A1	phosphate-responsive 1 family protein, similar to phi-1 (phosphate-induced gene) (Nicotiana tabacum) GI:3759184; contains Pfam profile PF04674: Phosphate-induced protein 1 conserved region	EIP, signal transduction		0.42480	2.75995	0.29520	0.85593	0.21606	0.63354	2.15471	3.36518	-2.21051	-0.65850	1.10750	1.75069	-1.43451	1.42909	1.09744	0.45480	1.84858	4.44377	0.31568	NS	0.14091	NS	0.07633	ns
AF380632	At4g16515 Arabidopsis thaliana AT4g16511 mRNA, complete cds	expressed protein	unknown		0.46647	2.77648	0.28642	2.05745	0.26394	0.66900	1.32164	4.23132	-1.92173	-0.57991	0.40233	2.08111	-1.25082	1.24172	0.94880	1.18707	1.86437	1.47932	0.31342	NS	0.37842	NS	0.14618	ns
AL132955	At3g47620 Arabidopsis thaliana DNA chromosome 3, BAC clone F1P2	TCP family transcription factor, putative, auxin-induced basic helix-loop-helix transcription factor - Gossypium hirsutum, EMBL:AF165924 ; transcription factor activity, regulation of transcription	GIP, TF		0.51959	2.78776	0.47297	0.22696	0.18515	0.85403	2.62727	2.94824	-2.43323	-0.22765	1.39357	1.55985	-1.33044	1.47671	1.55958	0.11758	1.20643	17.76089	0.44061	NS	0.03581	U	0.12644	ns
AB006706	At5g17670 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MVA3	expressed protein	unknown		0.52039	2.79150	0.15602	1.55035	0.41007	0.63072	1.69523	3.88776	-1.28607	-0.66494	0.76148	1.95894	-0.97551	1.36021	0.43921	0.84673	3.14105	2.27183	0.19622	NS	0.26398	NS	0.07422	ns
AL353994	At5g09750 Arabidopsis thaliana DNA chromosome 5, BAC clone F17I14 (ESSA project)	basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain, nucleus, DNA binding, transcription factor activity, regulation of transcription	GIP, TF		0.35146	2.79176	0.25477	0.66420	0.17131	0.53161	2.32210	3.26142	-2.54534	-0.91155	1.21543	1.70550	-1.72844	1.46047	1.15526	0.34653	2.11587	5.96022	0.28107	NS	0.10583	NS	0.06467	ns
AC006217	At2g07320 Arabidopsis thaliana chromosome II section 41 of 255 of the complete sequence. Sequence from clones T25N22, T13E11	SWIM zinc finger family protein, contains Pfam profile PF04434: SWIM zinc finger , zinc ion binding, biological process unknown	ZINC		0.47969	2.79573	0.35583	0.64161	0.22808	0.73129	2.34204	3.24942	-2.13239	-0.45147	1.22777	1.70018	-1.29193	1.46397	1.18858	0.33405	1.53718	6.19783	0.36717	NS	0.10184	NS	0.08740	ns
AC006068	At2g35640 Arabidopsis thaliana chromosome II section 195 of 255 of the complete sequence. Sequence from clones T32F12, T20F21	transcription factor activity, regulation of transcription, hydroxyproline-rich glycoprotein family protein, contains proline-rich extensin domains,	CPS, cell wall	CPS, cell wall	0.57364	2.79630	0.13919	2.01713	0.47522	0.67206	1.36997	4.22263	-1.07333	-0.57333	0.45415	2.07814	-0.82333	1.26614	0.35355	1.14834	3.29334	1.55929	0.18767	NS	0.36303	NS	0.13311	ns
AC004684	AT5G02450 Arabidopsis thaliana chromosome II section 204 of 255 of the complete sequence. Sequence from clones F3G5, F13M22	60S ribosomal protein L36 (RPL36C), 60S ribosomal protein L36, Arabidopsis thaliana, EMBL:AC004684 , ribosome, structural constituent of ribosome, protein biosynthesis	GIP, translation, ribosome		0.33228	2.81066	0.01047	1.79576	0.32488	0.33968	1.54086	4.08046	-1.62204	-1.55774	0.62374	2.02873	-1.58989	1.32624	0.04547	0.99348	49.44755	1.88789	0.01287	D	0.31011	NS	0.05353	ns
AB010693	At5g44860 Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K21C13	expressed protein,	unknown		0.46617	2.81508	0.38495	1.23536	0.19397	0.73836	3.68861	1.94155	-2.36611	-0.43760	1.88308	0.95721	-1.40185	1.42014	1.36367	0.65469	1.45382	3.06770	0.38358	NS	0.20061	NS	0.11864	ns
AF378888	At3g17020 Arabidopsis thaliana AT3g17020/K14A17_14 mRNA, complete cds	universal stress protein (USP) family protein, similar to early nodulin ENOD18 (Vicia faba) GI:11602747; contains Pfam profile PF00582: universal stress protein family , response to cold, response to stress	EIP, signal transduction		0.62225	2.83037	0.39873	1.56624	0.34030	0.90419	1.72287	3.93787	-1.55511	-0.14529	0.78481	1.97742	-0.85020	1.38111	0.99689	0.84330	1.20612	2.31613	0.44069	NS	0.25947	NS	0.13692	ns
AC006955	At2g04850 Arabidopsis thaliana chromosome II section 23 of 255 of the complete sequence. Sequence from clones F28I8	auxin-responsive protein-related, related to auxin-induced protein AIR12 GI:11357190 (Arabidopsis thaliana) , membrane, dopamine beta-monooxygenase activity	M, amino acid, tyrosine		0.48710	2.84478	0.32273	1.43967	0.25890	0.71531	1.82678	3.86277	-1.94955	-0.48337	0.86930	1.94964	-1.21646	1.40947	1.03674	0.76391	1.65936	2.60932	0.34528	NS	0.23299	NS	0.10216	ns
AP000372	At5g48290 Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K23F3	heavy-metal-associated domain-containing protein, strong similarity to farnesylated proteins ATFP4 (GI:4097549) and ATFP5 (GI:4097551); contains Pfam profile PF00403: Heavy-metal-associated domain , cellular_component, metal ion transport, metal ion binding	EIP, transport	CPS, transport	0.44175	2.85100	0.37078	0.22706	0.17957	0.70393	2.69045	3.01155	-2.47741	-0.50650	1.42785	1.59051	-1.49196	1.50918	1.39364	0.11502	1.51398	18.55601	0.37161	NS	0.03427	U	0.09357	ns
AC004521	At2g44290 Arabidopsis thaliana YLS3 mRNA for non-specific lipid transfer protein (nLTP) like protein, partial cds	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein (YLS3), lipid binding, lipid transport, anchored to membrane	M, protease inhibitor	CPS, transport	0.55722	2.86047	0.46641	0.40657	0.22742	0.88703	2.57298	3.14796	-2.13658	-0.17295	1.36344	1.65442	-1.15476	1.50893	1.38849	0.20575	1.17616	10.37155	0.44858	NS	0.06119	NS	0.11532	ns

AF326862	AT4G25100 A.thaliana iron superoxide dismutase (FeSOD) mRNA, 3' end	superoxide dismutase (Fe), chloroplast (SODB) / iron superoxide dismutase (FSD1), chloroplast, mitochondrion, iron superoxide dismutase activity, response to oxidative stress, removal of superoxide radicals	M, oxidoreductase		0.54999	2.87926	0.29263	0.65873	0.34307	0.75691	2.41346	3.34505	-1.54341	-0.40180	1.27111	1.74203	-0.97260	1.50657	0.80724	0.33299	1.70391	6.39837	0.33787	NS	0.09870	NS	0.05680	ns
AB005245	At5g05100 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MUG13	expressed protein, nucleic acid binding	GIP		0.50456	2.89171	0.32809	1.44808	0.27256	0.73655	1.86776	3.91566	-1.87533	-0.44115	0.90131	1.96926	-1.15824	1.43528	1.01412	0.75515	1.61519	2.68794	0.35292	NS	0.22674	NS	0.10113	ns
AL391711	At5g13100 Arabidopsis thaliana DNA chromosome 5, BAC clone T19L5 (ESSA project)	expressed protein	unknown		0.43826	2.90615	0.32970	0.54809	0.20513	0.67140	3.29371	2.51859	-2.28538	-0.57476	1.71971	1.33262	-1.43007	1.52617	1.20959	0.27372	1.67200	7.88524	0.34315	NS	0.08031	NS	0.07786	ns
AC002329	At2g17310 Arabidopsis thaliana chromosome II section 100 of 255 of the complete sequence. Sequence from clones T23A1, F5J6, MJB20	F-box family protein, Encodes an F-Box protein that regulates a novel induced defense response independent of both salicylic acid and systemic acquired resistance (SUPPRESSOR OF NIM1-1 1), protein ubiquitination, response to bacterium, response to fungus, SCF ubiquitin ligase complex	GIP, FSD	EIP, signal transduction	0.33436	2.92520	0.28173	0.27948	0.13515	0.53357	3.12282	2.72758	-2.88738	-0.90625	1.64285	1.44762	-1.89682	1.54524	1.40087	0.13805	1.91489	15.82968	0.30638	NS	0.04016	U	0.07441	ns
AB023033	At5g49610 Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K6M13	F-box family protein,	Fbox		0.46211	2.92523	0.31466	0.24531	0.23961	0.68461	2.75177	3.09870	-2.06126	-0.54665	1.46036	1.63166	-1.30395	1.54601	1.07099	0.12113	1.72183	18.05033	0.33497	NS	0.03523	U	0.06465	ns
AB009052	At5g40490 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MNF13	RNA recognition motif (RRM)-containing protein, ribonucleoprotein, RNA-binding region RNP-1 (RNA recognition motif) (RRM)	GIP, transcription, FSD		0.40161	2.94313	0.36845	0.42887	0.14108	0.66214	2.63987	3.24639	-2.82546	-0.59480	1.40047	1.69883	-1.71013	1.54965	1.57731	0.21098	1.53329	10.38760	0.36791	NS	0.06110	NS	0.10136	ns
AL161572	At4g28220 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68	NADH dehydrogenase-related, similar to 64 kDa mitochondrial NADH dehydrogenase (Neurospora crassa) GI:4753821, alternative NADH-dehydrogenase (Yarrowia lipolytica) GI:3718005; contains Pfam profile PF00070: Pyridine nucleotide-disulphide oxidoreductase , NADH dehydrogenase activity, disulfide oxidoreductase activity, electron transport , NAD(P)H DEHYDROGENASE B1, NDB1	M, energy		0.57131	2.94440	0.06486	1.90308	0.61717	0.52545	1.59872	4.29008	-0.69626	-0.92837	0.67692	2.10100	-0.81232	1.38896	0.16413	1.00698	6.99932	1.95067	0.09034	NS	0.30157	NS	0.09272	ns
AB005234	At5g63650 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MBK5	encodes a member of SNF1-related protein kinases (SnRK2) whose activity is activated by ionic (salt) and non-ionic (mannitol) osmotic stress. SUCROSE NONFERMENTING 1-RELATED PROTEIN KINASE 2-5, kinase activity, response to osmotic stress, response to salt stress, cultured cell, seedling growth	M, kinase	EIP, signal transduction	0.49445	2.95602	0.34887	1.42865	0.24777	0.74114	1.94581	3.96623	-2.01293	-0.43218	0.96037	1.98777	-1.22256	1.47407	1.11776	0.72648	1.54681	2.86952	0.36536	NS	0.21348	NS	0.10356	ns
AP002049	At3g28920 Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MYI13	zinc finger homeobox family protein / ZF-HD homeobox family protein, contains Pfam PF04770: ZF-HD protein dimerisation region;	ZINC		0.37274	2.97683	0.29275	0.43694	0.16573	0.57975	2.66786	3.28579	-2.59308	-0.78650	1.41568	1.71624	-1.68979	1.56596	1.27744	0.21253	1.87071	10.42036	0.31252	NS	0.06091	NS	0.07081	ns
AB013389	At5g66580 Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K1F13	expressed protein	unknown		0.50084	2.99979	0.42956	0.62459	0.19710	0.80459	2.55813	3.44144	-2.34303	-0.31367	1.35509	1.78301	-1.32835	1.56905	1.43497	0.30259	1.30913	7.33335	0.41528	NS	0.08628	NS	0.10778	ns
AC006586	At2g10020 Arabidopsis thaliana chromosome II section 50 of 255 of the complete sequence. Sequence from clones F7B19, T15D9	expressed protein	unknown		0.35311	3.03819	0.25540	0.15249	0.17252	0.53370	2.93036	3.14602	-2.53519	-0.90590	1.55108	1.65353	-1.72054	1.60230	1.15208	0.07244	2.11201	31.27977	0.28152	NS	0.02035	U	0.05538	ns
AC006220	At2g05540 Arabidopsis thaliana chromosome II section 28 of 255 of the complete sequence. Sequence from clones F16J10, T20G20, T3P4	glycine-rich protein	GLYCINE		0.59618	3.03834	0.46315	1.55505	0.26869	0.92368	1.93876	4.13793	-1.89599	-0.11454	0.95513	2.04891	-1.00527	1.50202	1.25968	0.77342	1.12859	2.74648	0.46159	NS	0.22230	NS	0.13856	ns
AF326903	At4g02520 A.thaliana Atpm24.1 mRNA for glutathione S-transferase	Encodes glutathione transferase belonging to the phi class of GSTs (ATGSTF2). Naming convention according to Wagner et al. (2002). The expression of this gene is upregulated by herbicide safeners such as benoxacor and fenclorim. glutathione transferase activity, toxin catabolism, seedling growth	M, glutathione transferase, detox		0.62337	3.03861	0.34872	1.82161	0.37678	0.86995	1.75053	4.32668	-1.40820	-0.20100	0.80780	2.11326	-0.80460	1.46053	0.85362	0.92310	1.33299	2.23756	0.40974	NS	0.26756	NS	0.12566	ns
AF020715	At3g46100 Arabidopsis thaliana histidyl-tRNA synthetase mRNA, complete cds	histidyl-tRNA synthetase / histidine-tRNA ligase, identical to histidyl-tRNA synthetase (Arabidopsis thaliana) GI:3659909 , histidine-tRNA ligase activity, histidyl-tRNA aminoacylation	GIP, translation		0.46881	3.04371	0.41167	0.41407	0.17771	0.75990	2.75091	3.33650	-2.49237	-0.39611	1.45991	1.73834	-1.44424	1.59912	1.48228	0.19688	1.37793	11.48693	0.39966	NS	0.05528	NS	0.10248	ns
AC006585	At2g24990 Arabidopsis thaliana chromosome II section 140 of 255 of the complete sequence. Sequence from clones F27A10, F27C12, F13D4	RIO1 family protein, similar to extragenic suppressor of the bimD6 mutation (SUDD), ATP binding, protein serine/threonine kinase activity	M, kinase		0.42062	3.09899	0.26045	1.00195	0.23645	0.60479	2.39050	3.80747	-2.08037	-0.72550	1.25731	1.92883	-1.40293	1.59307	0.95804	0.47484	2.07095	4.74468	0.28638	NS	0.13224	NS	0.05818	ns
AL161539	At4g14540 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 39	CCAAT-box binding transcription factor subunit B (NF-YB) (HAP3) (AHAP3) family, contains Pfam PF00808 : Histone-like transcription factor (CBF/NF-Y) and archaeal histone; similar to LEC1-like protein (GI:22536010) (Phaseolus coccineus) , intracellular, nucleus, transcription factor activity, regulation of transcription, DNA-dependent	GIP, TF		0.56926	3.12312	0.35648	1.21350	0.31718	0.82133	2.26505	3.98119	-1.65660	-0.28397	1.17954	1.99320	-0.97029	1.58637	0.97060	0.57534	1.41376	3.89935	0.39192	NS	0.15982	NS	0.08513	ns
AF361624	At4g00810 Arabidopsis thaliana AT4g00810/A_TM018A10_9 gene, complete cds	60S acidic ribosomal protein P1 (RPP1B), similar to acidic ribosomal protein p1 , ribosome, structural constituent of ribosome, translational elongation	GIP, translation, ribosome		0.37723	3.13234	0.28382	0.64270	0.17654	0.57792	2.67788	3.58679	-2.50191	-0.79106	1.42109	1.84269	-1.64648	1.63189	1.20976	0.29812	1.92475	7.74139	0.30504	NS	0.08178	NS	0.06523	ns
AL161514	At4g09100 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 26	zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger) , protein binding, zinc ion binding, endomembrane system	ZINC		0.49488	3.16085	0.34471	0.06359	0.25113	0.73863	3.20582	3.11589	-1.99348	-0.43708	1.68069	1.63964	-1.21528	1.66017	1.10054	0.02903	1.56165	80.89001	0.36259	NS	0.00787	U	0.06611	ns

AJ002295	AT1G05630 (1 of 3 hits, but most specific) Arabidopsis thaliana mRNA for inositol-1,4,5-trisphosphate 5-phosphatase	Encodes an inositol polyphosphate 5-phosphatase with phosphatase activity toward only Ins(1,4,5)P3. Induced in response to ABA and wounding treatments. Expressed in young seedlings and flowers, while no transcripts were detectable in maturated roots, stems, and rosette leaves Modulates the development of cotyledon veins through its regulation of auxin homeostasis; inositol or phosphatidylinositol phosphatase activity, response to wounding, response to abscisic acid stimulus, vascular tissue development (sensu Tracheophyta), cotyledon, root, flower, stem, rosette leaf, auxin homeostasis, seedling growth , contains InterPro domain G-protein beta WD-40 repeat	M, kinase	EIP, signal transduction	CPS, signal transduction	0.38570	3.16244	0.36659	0.77765	0.12648	0.64492	2.61256	3.71232	-2.98297	-0.63282	1.38547	1.89232	-1.80789	1.63889	1.66181	0.35840	1.53853	6.46689	0.36692	NS	0.09767	NS	0.10315	ns
AB028622	At3g22070 Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:MZN24	proline-rich family protein, contains proline-rich extensin domains,	CPS, cell wall			0.45320	3.17659	0.36920	0.48704	0.19214	0.71426	2.83220	3.52098	-2.37979	-0.48548	1.50192	1.81598	-1.43263	1.65895	1.33948	0.22207	1.51257	10.56471	0.37189	NS	0.06008	NS	0.08441	ns
J04185	AT1G76030 Arabidopsis thaliana nucleotide-binding subunit of vacuolar ATPase mRNA, complete cds	Encodes the vacuolar ATP synthase subunit B1. This subunit was shown to interact with the gene product of hexokinase1 (ATHXK1). This interaction, however, is solely restricted to the nucleus. cytoplasm, hydrogen-transporting two-sector ATPase complex, hydrogen ion transporting ATP synthase activity, rotational mechanism, glucose mediated signaling	M, energy	CPS, signal transduction		0.26411	3.19343	0.24768	0.22651	0.08898	0.43925	3.03326	3.35360	-3.49037	-1.18689	1.60087	1.74571	-2.33863	1.67329	1.62880	0.10242	2.03052	23.10523	0.29133	NS	0.02754	U	0.07371	ns
AL079347	At4g34910 Arabidopsis thaliana mRNA for DEAD box RNA helicase, RH16	DEAD/DEAH box helicase, putative (RH16), identical to cDNA DEAD box RNA helicase, RH16 GI:3776006 , cellular_component, ATP-dependent helicase activity	GIP, replication and repair			0.44381	3.20067	0.36495	0.71391	0.18575	0.70187	2.69586	3.70548	-2.42853	-0.51072	1.43075	1.88966	-1.46963	1.66020	1.35610	0.32450	1.53261	7.23539	0.36804	NS	0.08743	NS	0.08655	ns
U81293	At4g15550 Arabidopsis thaliana UDP-glucose:indole-3-acetate beta-D-glucosyltransferase (iaglu) mRNA, complete cds	UDP-glucose:indole-3-acetate beta-D-glucosyltransferase (IAGLU), chloroplast, UDP-glycosyltransferase activity, metabolic process, transferase activity, transferring glycosyl groups	M, glycosyltransferase			0.50639	3.20199	0.37977	0.35605	0.23786	0.77493	2.95023	3.45376	-2.07183	-0.36786	1.56083	1.78817	-1.21985	1.67450	1.20488	0.16076	1.43177	14.73108	0.38813	NS	0.04315	U	0.07801	ns
AB012248	At5g50400 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MXI22	calcineurin-like phosphoesterase family protein, acid phosphatase activity, protein serine/threonine phosphatase activity, biological process unknown, endomembrane system, fruit, root, flower, leaf, stem	M, kinase	EIP, signal transduction		0.52212	3.21714	0.38375	1.19799	0.25076	0.79347	2.37004	4.06425	-1.99562	-0.33375	1.24491	2.02299	-1.16469	1.63395	1.17512	0.55018	1.40166	4.19996	0.39451	NS	0.14881	NS	0.09277	ns
AC007661	At2g37830 Arabidopsis thaliana chromosome II section 205 of 255 of the complete sequence. Sequence from clones F13M22, T8P21, F16M14	glycine-rich protein, pseudogene,	GLYCINE			0.48041	3.22264	0.35156	0.60105	0.23181	0.72900	2.79763	3.64764	-2.10895	-0.45601	1.48421	1.86696	-1.28248	1.67558	1.16881	0.27065	1.55176	8.75531	0.36443	NS	0.07240	NS	0.07332	ns
AF285105	At5g10930 Arabidopsis thaliana CBL-interacting protein kinase 5 (CIPK5) mRNA, complete cds	CBL-interacting protein kinase 5 (CIPK5) mRNA, kinase activity, protein amino acid phosphorylation, signal transduction	M, kinase	CPS, signal transduction		0.49404	3.22832	0.34047	0.86462	0.25329	0.73478	2.61694	3.83970	-1.98114	-0.44461	1.38788	1.94099	-1.21287	1.66444	1.08649	0.39111	1.57872	6.01842	0.35946	NS	0.10482	NS	0.07195	ns
U91995	AT1G48410 Arabidopsis thaliana Argonaute protein (AGO1) mRNA, complete cds	Encodes an RNA Slicer that selectively recruits microRNAs and siRNAs. There is currently no evidence that AGO1 Slicer is in a high molecular weight RNA-induced silencing complex (RISC). Mutants are defective in post-transcriptional gene silencing and have pleiotropic developmental and morphological defects. Through its action on the regulation of ARF17 expression, the protein regulates genes involved at the cross talk between auxin and light signaling during adventitious root development. endoribonuclease activity, posttranscriptional gene silencing, auxin metabolic process, response to auxin stimulus,	GIP, silencing			0.41912	3.25558	0.28893	1.10019	0.21482	0.62342	2.47762	4.03353	-2.21880	-0.68172	1.30896	2.01204	-1.45026	1.66050	1.08688	0.49716	1.88703	4.72346	0.31023	NS	0.13282	NS	0.06653	ns
AB005233	At5g41680 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MBK23	similar to receptor-like protein kinase, mitochondrion, kinase activity, protein amino acid phosphorylation	M, kinase	EIP, signal transduction		0.55393	3.26107	0.32794	0.37700	0.32204	0.78581	2.99448	3.52765	-1.63471	-0.34774	1.58231	1.81871	-0.99122	1.70051	0.91002	0.16716	1.54040	14.38674	0.36657	NS	0.04418	U	0.05431	ns
AJ286344	At3g28550 Arabidopsis thaliana partial mRNA for extensin-like protein (DiDi 4T-2 gene)	proline-rich extensin-like family protein, contains proline-rich extensin domains, structural constituent of cell wall, cell wall organization and biogenesis (sensu Magnoliophyta), endomembrane system, cell surface (sensu Magnoliophyta)	CPS, cell wall			0.43399	3.27486	0.48700	2.31932	0.08963	0.77835	1.63485	4.91487	-3.47983	-0.36151	0.70916	2.29715	-1.92067	1.50316	2.20498	1.12288	1.23186	1.89315	0.43410	NS	0.30938	NS	0.18951	ns
AB005246	At5g60630 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MUP24	expressed protein,	unknown			0.53435	3.29613	0.25699	1.44510	0.35264	0.71607	2.27429	4.31797	-1.50374	-0.48182	1.18542	2.11035	-0.99278	1.64789	0.72261	0.65403	1.94297	3.56324	0.30260	NS	0.17418	NS	0.06186	ns
AL138656	At3g54530 Arabidopsis thaliana DNA chromosome 3, BAC clone T14E10	expressed protein	unknown			0.66019	3.31896	0.36557	1.59237	0.40169	0.91869	2.19298	4.44493	-1.31583	-0.12235	1.13289	2.15216	-0.71909	1.64253	0.84392	0.72073	1.20503	3.22296	0.44097	NS	0.19153	NS	0.09495	ns
AL162973	At5g02890 Arabidopsis thaliana DNA chromosome 5, BAC clone F9G14 (ESSA project)	transferase family protein, contains Pfam profile PF02458: Transferase family	M			0.38804	3.40501	0.38309	0.32622	0.11715	0.65892	3.17433	3.63568	-3.09353	-0.60182	1.66645	1.86223	-1.84768	1.76434	1.76191	0.13843	1.48306	18.02428	0.37768	NS	0.03528	U	0.10176	ns
AC011765	At1g74510 Arabidopsis thaliana chromosome 1 BAC F1M20 genomic sequence	kelch repeat-containing F-box family protein, contains Pfam:PF01344 Kelch motif, Pfam:PF00646 F-box domain	Fbox			0.38790	3.44153	0.34561	0.70884	0.14352	0.63228	3.94275	2.94030	-2.80065	-0.66136	1.97920	1.55596	-1.73100	1.76758	1.51271	0.29928	1.61829	8.35259	0.35237	NS	0.07586	NS	0.08494	ns
AF370237	At3g24450 Arabidopsis thaliana unknown protein (MXP5.2/AT3g24450) mRNA, complete cds	copper-binding family protein, similar to copper homeostasis factor gi:3168840 from Arabidopsis thaliana; contains Pfam profile PF00403: Heavy-metal-associated domain ; copper ion binding, copper ion transport, endomembrane system	EIP, transport			0.39411	3.47328	0.27223	0.73640	0.20162	0.58661	3.99399	2.95257	-2.31032	-0.76953	1.99783	1.56197	-1.53993	1.77990	1.08950	0.30820	1.99888	8.16727	0.29531	NS	0.07756	NS	0.05353	ns
AB008270	At5g16590 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MTG13	leucine-rich repeat transmembrane protein kinase, cell wall (sensu Magnoliophyta), ATP binding, kinase activity, protein serine/threonine kinase activity, protein amino acid phosphorylation, transmembrane receptor protein tyrosine kinase signaling pathway	M, kinase	CPS, signal transduction		0.53168	3.51990	0.41005	0.44056	0.24172	0.82163	3.20838	3.83142	-2.04856	-0.28345	1.68184	1.93788	-1.16600	1.80986	1.24813	0.18104	1.32117	14.13759	0.41247	NS	0.04496	U	0.07927	ns

AB012241	At5g37880 Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K18L3	expressed protein,	unknown		0.45537	3.52948	0.41451	0.90847	0.16227	0.74848	2.88709	4.17186	-2.62356	-0.41797	1.52962	2.06069	-1.52076	1.79515	1.55959	0.37553	1.37901	6.76044	0.39942	NS	0.09349	NS	0.09981	ns
AL021960	At4g21140 Arabidopsis thaliana DNA chromosome 4, BAC clone F7J7 (ESSA project)	expressed protein	unknown		0.39131	3.54628	0.27830	0.92750	0.19453	0.58810	2.89044	4.20212	-2.36197	-0.76586	1.53129	2.07112	-1.56391	1.80120	1.12862	0.38172	1.95966	6.67325	0.30039	NS	0.09469	NS	0.05734	ns
AB026644	At3g28420 Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MFJ20	expressed protein	unknown		0.61494	3.54999	0.38605	0.58943	0.34196	0.88792	3.13320	3.96678	-1.54811	-0.17150	1.64764	1.98797	-0.85981	1.81780	0.97341	0.24065	1.24916	10.68254	0.42976	NS	0.05942	NS	0.06351	ns
AL096859	At3g46890 Arabidopsis thaliana DNA chromosome 3, BAC clone T6H20	expressed protein, hypothetical protein F2I9.20 - Arabidopsis thaliana,PID:g3785987	unknown		0.47543	3.57252	0.30007	1.72891	0.26324	0.68761	2.34999	4.79505	-1.92554	-0.54034	1.23266	2.26154	-1.23294	1.74710	0.97949	0.72753	1.78015	3.39610	0.32583	NS	0.18230	NS	0.07456	ns
AC013427	At1g26410 Sequence of BAC T1K7 from Arabidopsis thaliana chromosome 1	FAD-binding domain-containing protein, similar to SP|P30986 reticuline oxidase precursor (Berberine-bridge-forming enzyme) (BBE) (Tetrahydroprotoberberine synthase) (Eschscholzia californica); contains PF01565 FAD binding domain, electron carrier activity, electron transport	M, energy, 2ndary metab		0.39930	3.57281	0.29701	2.38028	0.18928	0.60931	1.88970	5.25592	-2.40140	-0.71474	0.91816	2.39394	-1.55807	1.65605	1.19265	1.04354	1.84752	2.24429	0.31584	NS	0.26685	NS	0.10309	ns
AB012239	At5g61550 Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K11J9	protein kinase family protein, ubiquitin ligase complex, kinase activity, protein amino acid phosphorylation, protein ubiquitination, Eukaryotic protein kinase domain; protein kinase 1, PnPK1	GIP, FSD	EIP, signal transduction	0.55109	3.57331	0.36914	1.32959	0.29007	0.81212	2.63315	4.51348	-1.78553	-0.30024	1.39679	2.17424	-1.04289	1.78551	1.05026	0.54974	1.40429	4.59325	0.39394	NS	0.13647	NS	0.07773	ns
AY048276	At5g37780 Arabidopsis thaliana AT5g37780/K22F20_20 mRNA, complete cds	calmodulin-1/4 (CAM1), identical to calmodulin 4 (Arabidopsis thaliana) GI:16223, SP|P25854 Calmodulin-1/4 {Arabidopsis thaliana} , encodes a calmodulin that is involved in thigmomorphogenesis. Gene expression is rapidly induced upon a variety of abiotic stimuli, including water spray, subirrigation, wind, touch, wounding, or darkness. calcium ion binding, detection of calcium ion, response to mechanical stimulus	EIP, signal transduction	CPS, signal transduction	0.77046	3.58255	0.10322	2.03311	0.84345	0.69748	2.14493	5.02018	-0.24563	-0.51978	1.10093	2.32774	-0.38270	1.71433	0.19386	0.86749	2.79187	2.79478	0.21896	NS	0.21875	NS	0.07930	ns
AB026636	At3g17050 A.thaliana gene encoding a glycine-rich protein	glycine-rich protein, pseudogene,	GLYCINE		0.50799	3.60919	0.31917	0.43005	0.28231	0.73368	3.30510	3.91328	-1.82465	-0.44678	1.72469	1.96838	-1.13571	1.84654	0.97430	0.17231	1.64850	15.15521	0.34713	NS	0.04195	U	0.05087	ns
X74604	AT5G02500 A.thaliana hsc70 mRNA for heat shock cognate protein	encodes a member of heat shock protein 70 family. response to heat, response to virus AT-HSC70-1	GIP, FSD	EIP, signal transduction	0.70933	3.62619	0.34306	2.57725	0.95191	0.46674	1.80380	5.44857	-0.07111	-1.09930	0.85104	2.44588	-0.58520	1.64846	0.72704	1.12772	1.13831	2.06724	0.45888	NS	0.28683	NS	0.14277	ns
AB015469	At5g62440 Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K19B1	expressed protein	unknown		0.47124	3.66125	0.39630	0.56699	0.19102	0.75147	3.26033	4.06217	-2.38820	-0.41222	1.70502	2.02225	-1.40021	1.86364	1.39723	0.22432	1.41723	11.74934	0.39119	NS	0.05405	NS	0.08253	ns
AL161513	At4g08910 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 25	expressed protein	unknown		0.59976	3.66674	0.55289	0.68896	0.20881	0.99071	3.17958	4.15391	-2.25973	-0.01346	1.66884	2.05447	-1.13660	1.86165	1.58835	0.27268	1.01199	9.65502	0.49621	NS	0.06570	NS	0.11918	ns
AC009177	At3g05220 Arabidopsis thaliana chromosome III BAC T12H1 genomic sequence	heavy-metal-associated domain-containing protein, similar to farnesylated protein 1, ATP binding, metal ion transport, metal ion binding	EIP, transport	CPS, transport	0.47114	3.73016	0.38213	0.03905	0.20094	0.74135	3.70254	3.75777	-2.31518	-0.43178	1.88852	1.90988	-1.37348	1.89920	1.33177	0.01510	1.45851	177.83825	0.38262	NS	0.00358	U	0.07376	ns
AL161493	At4g02120 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 5	CTP synthase, putative / UTP-ammonia ligase, putative, similar to SP|P17812 CTP synthase (EC 6.3.4.2) (UTP-ammonia ligase) {Homo sapiens}; contains Pfam profile PF00117: glutamine amidotransferase class-I , CTP synthase activity, pyrimidine nucleotide biosynthetic process, pyrimidine ribonucleotide metabolic process, endomembrane system	M, nucleotide		0.51605	3.76379	0.41354	0.49823	0.22363	0.80846	3.41149	4.11610	-2.16079	-0.30675	1.77040	2.04128	-1.23377	1.90584	1.31101	0.19154	1.33090	14.07172	0.41022	NS	0.04517	U	0.07868	ns
AB012242	At5g48860 Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:K24G6	hypothetical protein	unknown		0.55308	3.80312	0.34068	1.13107	0.31219	0.79398	3.00333	4.60290	-1.67951	-0.33283	1.58656	2.20254	-1.00617	1.89455	0.95225	0.43556	1.49429	6.15133	0.37545	NS	0.10260	NS	0.05941	ns
AF195893	At3g13520 Arabidopsis thaliana arabinogalactan protein (AGP12) mRNA, complete cds	Encodes a GPI-anchored arabinogalactan (AG) peptide with a short 'classical' backbone of 10 amino acids, seven of which are conserved among the 4 other Arabidopsis AG peptides. These peptides may be involved in cell signaling. arabinogalactan-protein (AGP12),	EIP, signal transduction	CPS, signal transduction	0.46177	3.82015	0.33031	1.21344	0.22821	0.69533	2.96212	4.67819	-2.13157	-0.52423	1.56663	2.22595	-1.32790	1.89629	1.13656	0.46621	1.65229	5.75226	0.34648	NS	0.10958	NS	0.06553	ns
AC007109	At2g20530 Arabidopsis thaliana chromosome II section 117 of 255 of the complete sequence. Sequence from clones F11A3, T13C7, F23N11	prohibitin, putative, similar to SP|P24142 Prohibitin (B-cell receptor associated protein 32) (BAP 32) {Rattus norvegicus}; contains Pfam profile PF01145: SPFH domain / Band 7 family , inhibits DNA synthesis.	GIP, replication inhibitor		0.41901	3.89029	0.32284	0.19481	0.19072	0.64729	4.02804	3.75254	-2.39044	-0.62752	2.01008	1.90787	-1.50898	1.95897	1.24658	0.07228	1.71190	38.33090	0.33657	NS	0.01660	U	0.05913	ns
AL138650	At3g54700 Arabidopsis thaliana DNA chromosome 3, BAC clone T5N23	phosphate transporter, putative, strong similarity to phosphate transporter (AtPT2) (Arabidopsis thaliana) GI:1502430 , carbohydrate transporter activity, phosphate transporter activity, sugar porter activity, transport	EIP, transport	CPS, transport	0.45255	3.90128	0.22295	1.97919	0.29490	0.61020	2.50178	5.30078	-1.76170	-0.71264	1.32295	2.40620	-1.23717	1.86458	0.74180	0.76597	2.35863	3.44256	0.25529	NS	0.17997	NS	0.05432	ns
AF144386	At5g16400 Arabidopsis thaliana thioredoxin f2 mRNA, complete cds	thioredoxin, putative, similar to SP|P29450 Thioredoxin F-type, chloroplast precursor (TRX-F) {Pisum sativum};chloroplast, thiol-disulfide exchange intermediate activity (ATF2, TRXF2)	GIP, FSD	M, energy	0.55653	3.91229	0.53882	1.22440	0.17553	0.93753	4.77808	3.04651	-2.51024	-0.09307	2.25643	1.60716	-1.30165	1.93179	1.70920	0.45911	1.07700	5.95063	0.47641	NS	0.10599	NS	0.12280	ns
AB026632	At5g60200 Arabidopsis thaliana genomic DNA, chromosome 5, BAC clone:F15L12	Transcription factor, Dof-type zinc finger domain-containing protein, similar to dof6, nucleus, DNA binding, transcription factor activity, regulation of transcription, primary root differentiation zone, primary root elongation zone, root stele, pericycle, phloem	GIP, TF		0.47934	3.92094	0.33167	1.45240	0.24481	0.71387	2.89394	4.94794	-2.03028	-0.48628	1.53304	2.30683	-1.25828	1.91993	1.09178	0.54715	1.62989	4.96240	0.35034	NS	0.12659	NS	0.06654	ns
X12853	At5g20620 Arabidopsis thaliana UBQ4 gene for polyubiquitin	polyubiquitin (UBQ4), identical to GI:17677 , protein binding, protein modification, protein ubiquitination during ubiquitin-dependent protein catabolic process	GIP, FSD	EIP, signal transduction	3.55580	3.93030	3.84669	0.86182	6.27581	0.83578	4.53969	3.32090	2.64980	-0.25881	2.18259	1.73157	1.19550	1.95708	2.05670	0.31892	0.82204	8.67847	0.56198	NS	0.07303	NS	0.65636	ns

AL161591	At4g37340 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 87	CYP81D3, CYTOCHROME P450, FAMILY 81, SUBFAMILY D, POLYPEPTIDE 3, cytochrome P450 family protein, Similar to Cytochrome P450 91A1 (SP:Q9FG65) (Arabidopsis thaliana); chloroplast, electron transport, oxygen binding	M, Cytp450		0.44286	3.93639	0.27128	2.02300	0.25104	0.63469	2.50591	5.36687	-1.99401	-0.65588	1.32533	2.42408	-1.32495	1.87471	0.94620	0.77693	1.98030	3.41245	0.29770	NS	0.18148	NS	0.06604	ns
AC007323	Genomic sequence for Arabidopsis thaliana BAC T25K16 from chromosome I	unknown	unknown		0.40657	3.95451	0.07399	3.43657	0.35425	0.45888	1.52449	6.38454	-1.49716	-1.12380	0.60833	2.67458	-1.31048	1.64145	0.26401	1.46106	7.01983	1.58882	0.09008	NS	0.35762	NS	0.10664	ns
X69377	A.thaliana mRNA for glycine-rich RNA-binding protein	glycine-rich RNA-binding	GIP		0.44803	3.98399	0.34152	0.54968	0.20653	0.68952	4.37267	3.59530	-2.27555	-0.53634	2.12851	1.84611	-1.40594	1.98731	1.22981	0.19969	1.61676	14.07450	0.35264	NS	0.04516	U	0.06128	ns
AB008104	At5g47220 Arabidopsis thaliana AtERF-2 mRNA for ethylene responsive element binding factor 2, complete cds	Encodes a member of the ERF (ethylene response factor) subfamily B-3 of ERF/AP2 transcription factor family (ATERF-2). The protein contains one AP2 domain. Functions as activator of GCC box-dependent transcription. Positive regulator of JA-responsive defense genes and resistance to F. oxysporum and enhances JA inhibition of root elongation. regulation of transcription, DNA-dependent, induced systemic resistance, jasmonic acid mediated signaling pathway, ethylene mediated signaling pathway,	GIP, TF		0.52936	3.99568	0.43547	1.48340	0.22144	0.83728	2.94676	5.04460	-2.17502	-0.25622	1.55913	2.33474	-1.21562	1.94693	1.35680	0.54844	1.26706	5.02039	0.42535	NS	0.12517	NS	0.09246	ns
AB022215	At3g22310 Arabidopsis thaliana mRNA for DEAD box RNA helicase, RH9	DEAD box RNA helicase, putative (RH9), ATP-dependent helicase activity	GIP, replication and repair		0.50263	4.00054	0.31259	1.33034	0.28160	0.72367	3.05984	4.94123	-1.82830	-0.46659	1.61346	2.30487	-1.14745	1.95917	0.96287	0.48890	1.68531	5.66713	0.34093	NS	0.11119	NS	0.05544	ns
AL161591	At4g37240 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 87	expressed protein	unknown		0.55214	4.04524	0.32978	1.14052	0.31895	0.78533	3.23877	4.85171	-1.64858	-0.34862	1.69545	2.27849	-0.99860	1.98697	0.91920	0.41228	1.53637	6.81582	0.36733	NS	0.09274	NS	0.05249	ns
AL033545	At4g22480 Arabidopsis thaliana DNA chromosome 4, BAC clone F7K2 (ESSA project)	glycine-rich protein, similar to uncharacterized glycine-rich protein (GI:7269047) {Arabidopsis thaliana}; blastp match of 29% identity and 9.2e-28 P-value to GP|603857|emb|CAA87091.1||Z46970 secreted acid phosphatase 2 (SAP2) {Leishmania mexicana} , pseudogene,	GLYCINE		0.46211	4.18540	0.35980	0.71612	0.20770	0.71653	3.67902	4.69177	-2.26743	-0.48090	1.87932	2.23013	-1.37417	2.05473	1.26327	0.24806	1.53837	11.71413	0.36695	NS	0.05421	NS	0.06381	ns
AF360336	At4g21620 Arabidopsis thaliana unknown protein (AT4g21620) mRNA, complete cds	glycine-rich protein	GLYCINE		0.55367	4.25597	0.36351	0.56997	0.29664	0.81071	3.85294	4.65900	-1.75323	-0.30274	1.94596	2.22002	-1.02798	2.08299	1.02566	0.19379	1.41742	15.20088	0.39115	NS	0.04182	U	0.05194	ns
AP001306	At3g22160 Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:MKA23	VQ motif-containing protein, contains PF05678: VQ motif , might be involved in modulating plastid sigma factors.	GIP, Transcription regulator		0.49386	4.39711	0.41766	0.84144	0.19853	0.78919	3.80212	4.99210	-2.33256	-0.34155	1.92680	2.31965	-1.33705	2.12322	1.40786	0.27778	1.34309	10.80950	0.40744	NS	0.05873	NS	0.07628	ns
AC009324	Arabidopsis thaliana chromosome I BAC T18A20 genomic sequence	unknown	unknown		0.54032	4.49165	0.44474	3.09039	0.22584	0.85479	6.67689	2.30641	-2.14663	-0.22635	2.73918	1.20565	-1.18649	1.97241	1.35784	1.08437	1.23575	2.57239	0.43312	NS	0.23604	NS	0.12382	ns
AV565888	ESTs	unknown	unknown		0.48648	4.50105	0.48040	0.87703	0.14679	0.82617	3.88089	5.12120	-2.76821	-0.27548	1.95639	2.35648	-1.52185	2.15644	1.76262	0.28291	1.22103	10.77967	0.43685	NS	0.05889	NS	0.10036	ns
X68042	At5g66400 A.thaliana rab18 gene	dehydrin (RAB18), Belongs to the dehydrin protein family, which contains highly conserved stretches of 7-17 residues that are repetitively scattered in their sequences, the K-, S-, Y- and lysine rich segments. ABA- and drought-induced glycine-rice dehydrin protein. The ABA-induced expression of RAB18 was reduced following ACC application, indicating that ethylene inhibits the ABA signaling pathway. RAB18 is also expressed in response to the formation of the phospholipid diacylglycerol pyrophosphate. COR47 and RAB18 double overexpressor plants are cold tolerant. Expressed in guard cells. cold acclimation, response to water deprivation, response to stress, response to abscisic acid stimulus, response to 1-Aminocyclopropane-1-carboxylic Acid	EIP, signal transduction		0.47468	4.92856	0.39530	2.38742	0.19516	0.75419	3.24040	6.61672	-2.35728	-0.40699	1.69617	2.72612	-1.38214	2.21114	1.37906	0.72828	1.41737	4.29372	0.39116	NS	0.14567	NS	0.08267	ns
AL022141	At4g36230 Arabidopsis thaliana DNA chromosome 4, BAC clone F23E13 (ESSAII project)	glycine-rich protein, glycine-rich protein GRP22, rape, PIR2:S31415 , pseudogene,	GLYCINE		0.62670	5.05162	0.54547	1.57192	0.24099	1.01240	3.94011	6.16313	-2.05295	0.01778	1.97824	2.62366	-1.01759	2.30095	1.46423	0.45639	0.98283	7.12999	0.50551	NS	0.08871	NS	0.09226	ns
AL353032	At3g58690 Arabidopsis thaliana DNA chromosome 3, BAC clone T20N10	protein kinase family protein, contains protein kinase domain, Pfam:PF00069 , kinase activity, protein amino acid phosphorylation, endomembrane system	M, kinase		0.51465	5.95009	0.37674	2.18169	0.24825	0.78104	7.49278	4.40740	-2.01014	-0.35652	2.90550	2.13993	-1.18333	2.52271	1.16928	0.54134	1.43121	6.59039	0.38825	NS	0.09587	NS	0.05546	ns
AC005508	At1g26880 Arabidopsis thaliana chromosome I BAC T2P11 genomic sequence	60S ribosomal protein L34 (RPL34A), identical to GB:Q42351, location of EST 105E2T7, gb|T22624 , ribosome, structural constituent of ribosome, translation, ribosome biogenesis and assembly	GIP, translation, ribosome		0.39440	6.04329	0.05421	4.94423	0.43274	0.35607	2.54720	9.53939	-1.20844	-1.48978	1.34891	3.25390	-1.34911	2.30140	0.19894	1.34703	9.59050	2.41619	0.06614	NS	0.24982	NS	0.06306	ns
AB005240	At5g03240 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MOK16	polyubiquitin (UBQ3), encodes ubiquitin that is attached to proteins destined for degradation. UBQ3 is most homologous with UBQ4, and is expressed in higher levels in vegetative tissue but lower levels in flowers than UBQ4. UBQ3 encodes different number of ubiquitins in different ecotypes. UBQ3 transcript level is modulated by UV-B and light/dark treatments. intracellular, protein binding, ubiquitin-dependent protein catabolism, response to UV-B,	GIP, FSD	EIP, signal transduction	0.83694	6.10151	0.69871	0.99896	1.33100	0.34288	5.39514	6.80788	0.41251	-1.54424	2.43166	2.76721	-0.56586	2.59943	1.38363	0.23727	0.57837	15.49373	0.66618	NS	0.04103	U	0.08587	ns
AF062485	At5g64740 Arabidopsis thaliana cellulose synthase mRNA, partial cds	cellulose synthase, catalytic subunit, CESA6, Encodes a cellulase synthase. Mutants are defective in hypocotyl elongation dark-grown plants. Normal hypocotyl elongation is restored in plants grown in white, blue or red light. primary cell wall biosynthesis (sensu Magnoliophyta), cortical microtubule (sensu Viridiplantae) , transferring glycosyl groups	M, glycosyltransferase , cellulose	CPS, cell wall	1.67485	9.69286	1.18719	2.80364	2.51431	0.83538	7.71039	11.67533	1.33016	-0.25950	2.94680	3.54539	0.53533	3.24610	1.12406	0.42327	0.67352	10.84584	0.62266	NS	0.05853	NS	0.08573	ns
AP000420	At3g28630 Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MZN14	expressed protein, contains Pfam profile: PF04601 protein of unknown function (DUF569	unknown		4.30845	11.45943	3.23806	11.78569	6.59810	2.01879	3.12569	19.79317	2.72205	1.01349	1.64418	4.30693	1.86777	2.97555	1.20813	1.88285	2.18637	2.23494	0.27309	NS	0.26784	NS	0.55624	ns

AC006200	At2g01260 Arabidopsis thaliana chromosome II section 2 of 255 of the complete sequence. Sequence from clones F23H14, F10A8	expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g15030.1); similar to hypothetical protein [Oryza sativa (japonica cultivar-group)] (GB:XP_477257.1); contains InterPro domain Protein of unknown function DUF789 (InterPro:IPR008507)	unknown		24.60532	13.64231	11.78222	4.56083	32.93661	16.27403	16.86730	10.41731	5.04162	4.02450	4.07616	3.38091	4.53306	3.72853	0.71921	0.49161	8.91351	10.72580	0.07112	NS	0.05918	NS	0.32156	ns
AF076484	At2g39770 Arabidopsis thaliana CYT1 protein (cyt1) mRNA, complete cds	GDP-mannose pyrophosphorylase (GMP1), Encodes a GDP-mannose pyrophosphorylase/ mannose-1-pyrophosphatase. This enzyme provides GDP-mannose, which is used for cell wall carbohydrate biosynthesis and protein glycosylation as well as for ascorbate (vitamin C) biosynthesis. CYTOKINESIS DEFECTIVE 1 (CYT1), mannose-1-phosphate guanylyltransferase activity, response to heat, response to salt stress, cellulose biosynthetic process, L-ascorbic acid biosynthetic process, response to jasmonic acid stimulus, defense response to bacterium, response to ozone	M, glycosyltransferase, GDP mannose	CPS, cell wall	5.14883	14.43965	1.05330	17.09224	5.89363	4.40404	2.35361	26.52569	2.55916	2.13883	1.23487	4.72932	2.34899	2.98210	0.29722	2.47095	11.17687	1.70676	0.05681	NS	0.33740	NS	0.75347	ns
AF087820	At1g23080 Arabidopsis thaliana auxin transport protein (PIN7) mRNA, complete cds	auxin efflux carrier protein, putative, similar to efflux carrier of polar auxin transport (Brassica juncea) gi|12331173|emb|CAC24691 (PIN7) Encodes a novel component of auxin efflux that is located apically in the basal cell and is involved during embryogenesis in setting up the apical-basal axis in the embryo. It is also involved in pattern specification during root development. In roots, The action of PINs in auxin efflux is distinct from PGPs, rate-limiting, specific to auxins and sensitive to auxin transport inhibitors. PINs are directly involved of in catalyzing cellular auxin efflux. plasma membrane, pattern specification process, auxin polar transport, longitudinal axis specification, root development, root hair, primary root apical meristem	EIP, signal transduction	CPS, signal transduction (auxin trasport)	0.95117	17.11623	0.23345	18.00589	1.11625	0.78610	29.84832	4.38415	0.15866	-0.34722	4.89958	2.13230	-0.09428	3.51594	0.35771	1.95676	0.37275	2.54108	0.77286	NS	0.23868	NS	0.12415	ns
AY039975	At3g20015 Arabidopsis thaliana putative nucleoid chloroplast DNA-binding protein (MZE19.7/AT3g20015) mRNA, complete cds	similar to aspartyl protease family protein [Arabidopsis thaliana] (TAIR:At3g18490.1); similar to putative aspartic proteinase nepenthesin I [Oryza sativa (japonica cultivar-group)] (GB:NP_909181.1); contains InterPro domain Aspartic protease A1, pepsin (InterPro:IPR001461) , pepsin A activity, proteolysis, endomembrane system	M, peptide		4.68383	25.32632	5.02103	16.62316	8.23424	1.13343	37.08066	13.57197	3.04164	0.18069	5.21260	3.76256	1.61116	4.48758	2.02299	1.02533	1.12632	6.18960	0.46223	NS	0.10197	NS	0.21474	ns
AC005825	Arabidopsis thaliana chromosome II section 96 of 255 of the complete sequence. Sequence from clones T24I21, F12A24	unknown	unknown		118.43366	64.26507	129.31634	32.35757	209.87412	26.99319	87.14532	41.38481	7.71338	4.75452	6.44535	5.37103	6.23395	5.90819	2.09223	0.75966	4.21376	10.99892	0.14834	NS	0.05772	NS	0.85519	ns
AF360164	AT1G70490 Arabidopsis thaliana putative ADP-ribosylation factor 1 protein (F24J13.6) mRNA, complete cds	A member of ARF GTPase family. A thaliana has 21 members of this family, known to be essential for vesicle coating and uncoating and functions in GTP-binding. Gene encoding ADP-ribosylation factor and similar to other ARFs and ARF-like proteins. The gene is shown to play a role in cell division, cell expansion and cellulose production using antisense construct. intracellular, mitochondrion, GTP binding, phospholipase activator activity, protein binding, N-terminal protein myristoylation	EIP, signal transduction	CPS, signal transduction	150.60572	84.81553	60.95864	28.39948	107.50146	193.70999	104.89699	64.73407	6.74821	7.59775	6.71283	6.01645	7.17298	6.36464	0.60072	0.49241	16.88671	18.27932	0.03766	U	0.03479	U	0.27894	ns
Y09823	At1g22750 A.thaliana mRNA matching EST 34f9	expressed protein	unknown		0.54898	0.14878	0.01395	0.01200	0.53912	0.55885	0.14029	0.15726	-0.89133	-0.83947	-2.83350	-2.66875	-0.86540	-2.75112	0.03667	0.11649	33.37482	33.39812	0.01907	NC	0.01906	D	0.00209	s
AY039896	Arabidopsis thaliana At1g71810/F14O23_17 mRNA, complete cds	ABC1 family protein, contains Pfam domain, PF03109: ABC1 family , plastoglobule (chaperone?)	GIP, FSD		0.22078	0.28954	0.01140	0.01022	0.22884	0.21272	0.29677	0.28231	-2.12760	-2.23296	-1.75260	-1.82462	-2.18028	-1.78861	0.07450	0.05093	41.38767	49.67063	0.01538	D	0.01282	D	0.02553	s
AC005322	At1g05120 Arabidopsis thaliana chromosome 1 BAC T7A14 sequence	SNF2 domain-containing protein / helicase domain-containing protein / RING finger domain-containing protein, similar to SP|P79051 DNA repair protein rhp16 (RAD16 homolog), ATP binding, DNA binding Zinc finger, C3HC4 type (RING finger)	GIP, replication and repair		0.21885	0.36938	0.01659	0.02089	0.20712	0.23058	0.35461	0.38416	-2.27148	-2.11663	-1.49570	-1.38023	-2.19405	-1.43796	0.10949	0.08165	28.33932	24.90687	0.02245	D	0.02555	D	0.01593	s
AC010155	At1g28400 Genomic sequence for Arabidopsis thaliana BAC F3M18 from chromosome I	expressed protein, similar to E6 (GI:1000090) (Gossypium barbadense)	unknown		0.18877	0.55760	0.00736	0.02122	0.19397	0.18356	0.54259	0.57260	-2.36611	-2.44564	-0.88207	-0.80439	-2.40588	-0.84323	0.05623	0.05492	60.50394	21.71199	0.01052	D	0.02930	NC	0.00126	s
Y10116	At2g43640 A.thaliana mRNA for signal recognition particle subunit 14	signal recognition particle 14 kDa family protein / SRP14 family protein, signal recognition particle (sensu Eukaryota), RNA binding, protein targeting	GIP, translation		0.33069	0.64362	0.00923	0.06510	0.33722	0.32417	0.59758	0.68966	-1.56825	-1.62519	-0.74279	-0.53605	-1.59672	-0.63942	0.04026	0.14618	56.08787	6.18589	0.01135	D	0.10203	NS	0.01231	s
U39449	Arabidopsis thaliana actin (ACT1) gene, complete cds		CPS, cell structure		0.27646	0.64554	0.05718	0.08255	0.23603	0.31689	0.70391	0.58717	-2.08297	-1.65793	-0.50654	-0.76816	-1.87045	-0.63735	0.30055	0.18499	8.80127	4.87246	0.07202	NS	0.12887	NS	0.03860	s
AB006700	At5g06440 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MHF15	expressed protein,	unknown		0.49453	0.72810	0.03833	0.02923	0.46743	0.52164	0.70743	0.74877	-1.09718	-0.93888	-0.49934	-0.41741	-1.01803	-0.45838	0.11193	0.05794	12.86254	11.18883	0.04939	D	0.05675	NS	0.02443	s
AY042814	At3g08580 Arabidopsis thaliana putative adenylate translocator (F17O14.5/AT3g08580) mRNA, complete cds	ADP, ATP carrier protein 1, mitochondrial / ADP/ATP translocase 1 / adenine nucleotide translocator 1 (ANT1), identical to SWISS-PROT:P31167 ADP,ATP carrier protein 1 (Adenine nucleotide translocator 1) (Arabidopsis thaliana) , mitochondrial envelope, ATP:ADP antiporter activity, purine nucleotide transport	CPS, transport		0.48968	0.96811	0.01188	0.12453	0.49808	0.48128	0.88005	1.05617	-1.00555	-1.05504	-0.18434	0.07884	-1.03030	-0.05275	0.03499	0.18609	41.63752	0.40088	0.01529	D	0.75728	NS	0.01825	s

AF361622	At2g20690 Arabidopsis thaliana At2g20690/F5H14.34 gene, complete cds	lumazine-binding family protein, SP|P50854 Riboflavin synthase alpha chain (EC 2.5.1.9) {Actinobacillus pleuropneumoniae}; contains Pfam profile PF00677: Lumazine binding domain	M, vitamim, riboflavin	0.46503	1.13008	0.03613	0.05583	0.49058	0.43949	1.09061	1.16956	-1.02743	-1.18611	0.12513	0.22596	-1.10677	0.17555	0.11220	0.07130	13.94995	3.48185	0.04556	D	0.17805	NS	0.00533	s
AL021710	At4g18420 Arabidopsis thaliana DNA chromosome 4, BAC clone F28J12 (ESSAII project)	hypothetical protein	unknown	0.45456	1.13822	0.00982	0.30371	0.44762	0.46150	0.92346	1.35297	-1.15966	-1.11560	-0.11487	0.43613	-1.13763	0.16063	0.03116	0.38962	51.63602	0.58304	0.01233	D	0.66396	NS	0.04246	s
AB013392	At5g56670 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MIK19	40S ribosomal protein S30 (RPS30C) , ribosome, structural constituent of ribosome, protein biosynthesis	GIP, translation, ribosome	0.39019	1.14084	0.00035	0.28031	0.38994	0.39044	0.94263	1.33905	-1.35866	-1.35682	-0.08523	0.42121	-1.35774	0.16799	0.00130	0.35811	1479.05316	0.66341	0.00043	D	0.62710	NS	0.02646	s
AL161514	Arabidopsis thaliana DNA chromosome 4, BAC clone T30A10 (ESSA project)	unknown	unknown	0.37704	1.28013	0.03946	0.36668	0.34914	0.40494	1.02085	1.53941	-1.51812	-1.30420	0.02977	0.62238	-1.41116	0.32607	0.15126	0.41904	13.19384	1.10046	0.04816	D	0.46958	NS	0.03134	s
AC025416	At1g12430 Genomic sequence for Arabidopsis thaliana BAC F5O11 from chromosome I	armadillo/beta-catenin repeat family protein / kinesin motor family protein , Encodes the kinesin-like protein PAK has an Armadillo motif tail and is involved RT in guard cell development in Arabidopsis (from Genbank record AF159052). microtubule associated complex, microtubule motor activity, microtubule-based movement	CPS, cell structure	0.57408	1.28820	0.11581	0.13956	0.49219	0.65597	1.18951	1.38689	-1.02270	-0.60830	0.25037	0.47185	-0.81550	0.36111	0.29303	0.15661	3.93572	3.26091	0.15840	NS	0.18943	NS	0.03763	s
AB011484	At5g13770 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MXE10	pentatricopeptide (PPR) repeat-containing protein,	PRR	0.65932	1.29614	0.13393	0.04759	0.56462	0.75403	1.32979	1.26248	-0.82465	-0.40731	0.41120	0.33626	-0.61598	0.37373	0.29510	0.05298	2.95195	9.97533	0.20794	NS	0.06361	NS	0.04295	s
AL163975	At3g44010 Arabidopsis thaliana DNA chromosome 3, BAC clone T15B3	40S ribosomal protein S29 (RPS29B), ribosomal protein S29, rat, PIR:S30298 , ribosome, structural constituent of ribosome, translation	GIP, translation, ribosome	0.20482	1.47804	0.03212	0.81858	0.22753	0.18210	0.89922	2.05687	-2.13588	-2.45717	-0.15326	1.04045	-2.29652	0.44359	0.22719	0.84408	14.29566	0.74322	0.04446	D	0.59311	NS	0.04730	s
AF152555	AT5G66350 Arabidopsis thaliana putative zinc finger protein SHI (SHI) mRNA, complete cds	A member of SHI (SHORT INTERNODES) gene family. Arabidopsis thaliana has ten members that encode proteins with a RING finger-like zinc finger motif. Putative zinc finger protein. Involved in the response to gibberellic acid. protein binding, response to gibberellic acid stimulus, protein heterodimerization activity	ZINC	0.41131	1.54615	0.05057	0.23321	0.44707	0.37556	1.71105	1.38124	-1.16142	-1.41290	0.77489	0.46597	-1.28716	0.62043	0.17782	0.21844	10.23679	4.01675	0.06199	NS	0.15533	NS	0.01073	s
AL391146	At5g14970 Arabidopsis thaliana DNA chromosome 5, BAC clone F2G14 (ESSA project)	expressed protein	unknown	0.63165	1.56062	0.15536	0.08239	0.52179	0.74150	1.61887	1.50236	-0.93846	-0.43148	0.69499	0.58723	-0.68497	0.64111	0.35849	0.07620	2.70213	11.89918	0.22565	NS	0.05338	NS	0.03614	s
AB017067	At5g42120 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MJC20	lectin protein kinase family protein, kinase activity, protein amino acid phosphorylation,	M, kinase	0.47209	1.62758	0.15470	0.15900	0.36269	0.58148	1.51515	1.74001	-1.46318	-0.78220	0.59946	0.79910	-1.12269	0.69928	0.48152	0.14116	3.29730	7.00553	0.18746	NS	0.09026	NS	0.03590	s
AY048232	At3g12390 Arabidopsis thaliana AT3g12390/T2E22_130 mRNA, complete cds	nascent polypeptide associated complex alpha chain protein, putative / alpha-NAC, putative, similar to alpha-NAC, non-muscle form (Mus musculus) GI:1666690; contains Pfam profiles PF01849: NAC domain, PF00627: UBA/TS-N domain	GIP	0.21655	1.68657	0.11052	0.17710	0.13840	0.29470	1.56134	1.81181	-2.85307	-1.76268	0.64279	0.85743	-2.30787	0.75011	0.77102	0.15177	4.23310	6.98939	0.14768	NS	0.09047	NS	0.03147	s
AL138654	At3g42850 Arabidopsis thaliana DNA chromosome 3, BAC clone F18P9	galactokinase, putative, contains some similarity to galactokinase (Pasteurella multocida) SWISS-PROT:P57899 , ATP binding, galactokinase activity, metabolic process, phosphorylation	M, carbohydrate, kinase	0.38216	1.69097	0.07961	0.69785	0.32587	0.43845	1.19752	2.18443	-1.61765	-1.18952	0.26005	1.12726	-1.40359	0.69365	0.30273	0.61321	6.55686	1.59974	0.09635	NS	0.35566	NS	0.04927	s
AC018364	At1g69310 Arabidopsis thaliana chromosome 1 BAC F23O10 genomic sequence	WRKY family transcription factor, contains Pfam profile: PF03106 WRKY DNA -binding domain , member of WRKY Transcription Factor; Group II-c , nucleus, transcription factor activity, regulation of transcription, DNA-dependent	GIP, TF	0.52573	1.71561	0.12629	0.17315	0.43643	0.61503	1.59318	1.83804	-1.19619	-0.70127	0.67190	0.87817	-0.94873	0.77504	0.34996	0.14585	3.83390	7.51490	0.16243	NS	0.08422	NS	0.02334	s
AB005234	At5g63620 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MBK5	oxidoreductase, zinc-binding dehydrogenase family protein, mitochondrion, zinc ion binding	M, oxidoreductase	0.38037	1.73802	0.17789	0.30120	0.25458	0.50615	1.52503	1.95100	-1.97379	-0.98236	0.60884	0.96421	-1.47808	0.78653	0.70105	0.25129	2.98170	4.42651	0.20600	NS	0.14145	NS	0.05005	s
AF268090	AT4G23600 Arabidopsis thaliana coronatine-regulated tyrosine aminotransferase (F9D16.70) mRNA, complete cds	Coronotine induced gene (COR13) belonging to the tyrosine aminotransferase family but recent work proved that it functions as cystine lyase. mRNA levels are elevated in response to wounding. cystathionine beta-lyase activity, transaminase activity, response to wounding, response to abscisic acid stimulus, response to jasmonic acid stimulus, hyperosmotic salinity response, response to microbial phytotoxin ; encodes cystine lyase which is expected to be involved in amino acid metabolism, providing the plant with cysteine and the generation of precursors of ethylene biosynthesis	M, amino acid , ethylene synth	0.22762	1.77977	0.00589	0.56204	0.22346	0.23178	2.17719	1.38234	-2.16192	-2.10915	1.12247	0.46711	-2.13554	0.79479	0.03732	0.46340	80.92379	2.42554	0.00787	D	0.24895	NS	0.01235	s
AL161578	At4g31130 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 74	expressed protein	unknown	0.69196	1.81226	0.08303	0.20152	0.63325	0.75067	1.66977	1.95476	-0.65916	-0.41375	0.73965	0.96699	-0.53645	0.85332	0.17353	0.16076	4.37183	7.50688	0.14316	NS	0.08431	NS	0.01418	s
AC018748	At1g53620 Sequence of BAC T3F20 from Arabidopsis thaliana chromosome 1	glycine rich protein, similar to hypothetical protein [Arabidopsis thaliana] (TAIR:At1g53610.1); similar to hypothetical protein [Neurospora crassa] (GB:XP_330065.1); similar to Hypothetical protein E02A10.2 [Caenorhabditis elegans] (GB:CAB02877.1); similar to ORF; able to induce HR-like lesions [Nicotiana tabacum] (GB:AAC49971.1); contains domain GLY_RICH (PS50315)	GLYCINE	0.48860	1.84329	0.13392	0.31805	0.39390	0.58329	1.61839	2.06819	-1.34409	-0.77772	0.69456	1.04837	-1.06090	0.87146	0.40048	0.25018	3.74633	4.92621	0.16606	NS	0.12750	NS	0.02858	s
AF262042	At3g33073 Arabidopsis thaliana BAC T15F17	expressed protein	unknown	0.49210	1.89921	0.09273	0.18575	0.42653	0.55767	1.76787	2.03055	-1.22930	-0.84252	0.82201	1.02187	-1.03591	0.92194	0.27349	0.14132	5.35659	9.22576	0.11750	NS	0.06874	NS	0.01214	s

AY045954	Arabidopsis thaliana putative metallothionein-I gene transcription activator protein (MEE6.8/AT5g41010) mRNA, complete cds	DNA-directed RNA polymerases I, II, and III 7 kDa subunit, putative, similar to SP|P53803 DNA-directed RNA polymerases I, II, and III 7.0 kDa polypeptide (EC 2.7.7.6) (ABC10-alpha) (RPB7.0) (RPB10alpha) {Homo sapiens}; contains Pfam profile PF03604: DNA directed RNA polymerase, 7 kDa subunit , nucleus, DNA binding, DNA-directed RNA polymerase activity, transcription	GIP, transcription, polymerase		0.69141	1.93157	0.03505	0.44118	0.66663	0.71620	1.61961	2.24353	-0.58503	-0.48157	0.69565	1.16577	-0.53330	0.93071	0.07316	0.33243	10.30957	3.95944	0.06156	NS	0.15749	NS	0.02598	s
AF360339	AT1G15740 Arabidopsis thaliana putative leucine rich protein (F7H2.8) mRNA, complete cds	leucine-rich repeat family protein	LRR		0.74233	1.94467	0.13619	0.35598	0.83862	0.64603	1.69295	2.19638	-0.25390	-0.63033	0.75954	1.13513	-0.44212	0.94733	0.26618	0.26558	2.34900	5.04449	0.25622	NS	0.12459	NS	0.03472	s
AY035133	At2g17870 Arabidopsis thaliana putative glycine-rich zinc-finger DNA-binding protein (T13L16.11/At2g17870) mRNA, complete cds	cold-shock DNA-binding family protein, contains Pfam domains, PF00313: 'Cold-shock' DNA-binding domain and PF00098: Zinc knuckle , cellular_component, nucleic acid binding, regulation of transcription, DNA-dependent	GIP, TF		0.31612	2.05509	0.13528	0.84766	0.22046	0.41178	1.45571	2.65447	-2.18139	-1.28004	0.54172	1.40843	-1.73071	0.97507	0.63735	0.61285	3.84026	2.25006	0.16217	NS	0.26624	NS	0.04946	s
AB026650	At5g50120 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MPF21	transducin family protein / WD-40 repeat family protein, Similar to En/Spm-like transposon protein (gi:2739374)(Arabidopsis thaliana); similar to GTP-binding regulatory protein and WD-repeat protein; contains 7 WD-40 repeats, heterotrimeric G-protein complex, nucleotide binding,	CPS, Gprotein	WD40	0.44935	2.14756	0.15649	0.14329	0.33869	0.56000	2.04624	2.24888	-1.56196	-0.83650	1.03297	1.16920	-1.19923	1.10109	0.51298	0.09633	3.30614	16.16521	0.18699	NS	0.03933	U	0.02479	s
AL161542	At4g15590 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 42	non-LTR retrotransposon family (LINE), has a 1.5e-50 P-value blast match to GB:AAA67727 reverse transcriptase (LINE-element) (Mus musculus)	TRANS		0.38756	2.20688	0.09405	0.85831	0.32105	0.45406	1.59997	2.81379	-1.63913	-1.13904	0.67804	1.49252	-1.38909	1.08528	0.35362	0.57592	5.55535	2.66498	0.11338	NS	0.22853	NS	0.03533	s
AF386978	AT3G06700 Arabidopsis thaliana ribosomal protein L29, putative; 3222-3503 (T8E24.8) mRNA, complete cds	60S ribosomal protein L29 (RPL29A), similar to ribosomal protein L29 GI:7959366 (Panax ginseng) , ribosome, structural constituent of ribosome, protein biosynthesis, ribosome biogenesis	GIP, translation, ribosome		0.53655	2.33392	0.11764	0.39858	0.61973	0.45337	2.05208	2.61576	-0.69029	-1.14125	1.03709	1.38723	-0.91577	1.21216	0.31888	0.24759	4.06143	6.92382	0.15369	NS	0.09131	NS	0.01753	s
AL162971	At5g02490 A.thaliana mRNA for Hsc70-G8 protein, partial	heat shock cognate 70 kDa protein 2 (HSC70-2) (HSP70-2), identical to SP|P22954 Heat shock cognate 70 kDa protein 2 (Hsc70.2) {Arabidopsis thaliana} , cytosol, ATP binding, response to heat, protein folding	GIP, FSD	EIP, signal transduction	0.77805	2.33908	0.11760	0.55602	0.69489	0.86120	2.73224	1.94592	-0.52514	-0.21558	1.45008	0.96045	-0.37036	1.20527	0.21889	0.34622	2.39281	4.92312	0.25201	NS	0.12758	NS	0.03217	s
AC006438	At2g15800 Arabidopsis thaliana chromosome II section 92 of 255 of the complete sequence. Sequence from clones F19G14, F7H1	expressed protein	unknown		0.58237	2.40931	0.23719	0.42670	0.41465	0.75008	2.10759	2.71103	-1.27004	-0.41488	1.07559	1.43884	-0.84246	1.25722	0.60469	0.25685	1.97030	6.92211	0.29899	NS	0.09134	NS	0.04563	s
AP000421	At5g35090 Arabidopsis thaliana genomic DNA, chromosome 5, BAC clone:T13C12	expressed protein	unknown		0.33155	2.46972	0.13850	0.80419	0.23362	0.42949	1.90107	3.03837	-2.09778	-1.21930	0.92681	1.60330	-1.65854	1.26506	0.62118	0.47834	3.77591	3.74011	0.16482	NS	0.16632	NS	0.03413	s
AV441101	ESTs, Weakly similar to T49123 hypothetical protein F26G5.20 - Arabidopsis thaliana [A.thaliana]	expressed protein	unknown		0.56674	2.58687	0.26911	0.04463	0.37644	0.75703	2.61843	2.55532	-1.40949	-0.40158	1.38870	1.35350	-0.90554	1.37110	0.71270	0.02489	1.79685	77.90859	0.32330	NS	0.00817	U	0.04572	s
AL035394	At4g23620 Arabidopsis thaliana DNA chromosome 4, BAC clone F9D16 (ESSAII project)	50S ribosomal protein-related, contains weak similarity to 50S ribosomal protein L25 (TL5). (Swiss-Prot:P56930) (Thermus thermophilus) , ribosome, 5S rRNA binding, structural constituent of ribosome, translation	GIP, translation, ribosome		0.53463	2.68808	0.12794	0.92671	0.44417	0.62510	2.03280	3.34336	-1.17083	-0.67785	1.02347	1.74130	-0.92434	1.38238	0.34859	0.50758	3.74997	3.85154	0.16591	NS	0.16172	NS	0.03383	s
AB028608	At3g16830 Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:K20I9	WD-40 repeat family protein, contains 10 WD-40 repeats, TOPLESS-RELATED PROTEINS (TPRs), thought to be involved in transcriptional repression of root-promoting genes in the top help of the embryo during the transition stage of embryogenesis. (TPR-2)	GIP, TF	WD40	0.45396	2.68920	0.04328	1.25369	0.42335	0.48456	1.80271	3.57569	-1.24007	-1.04525	0.85017	1.83822	-1.14266	1.34420	0.13776	0.69866	11.73001	2.72090	0.05414	NS	0.22422	NS	0.03864	s
AC002291	At1g76930 Arabidopsis thaliana chromosome I BAC F22K20 genomic sequence	proline-rich extensin-like family protein, contains extensin-like region, Encodes an Arabidopsis extensin gene that belongs to cell-wall hydroxyproline-rich glycoproteins. The cross-link of extensins enforces cell wall strength. Transgenic plants overexpressing this gene show an increase in stem thickness (ATEXT1, ORG5, Extensin4). structural constituent of cell wall, response to wounding, response to abscisic acid stimulus, response to jasmonic acid stimulus, response to salicylic acid stimulus	CPS, cell wall		0.36161	2.74360	0.08544	0.47321	0.30120	0.42203	3.07821	2.40899	-1.73122	-1.24460	1.62209	1.26843	-1.48791	1.44526	0.34410	0.25008	6.11517	8.17303	0.10319	NS	0.07751	NS	0.01035	s
AB025632	At5g58420 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MQJ2	40S ribosomal protein S4 (RPS4D), ribosomal protein S4, Arabidopsis thaliana, PIR:T48480, cytosolic ribosome (sensu Eukaryota), cytosolic small ribosomal subunit (sensu Eukaryota), structural constituent of ribosome, translation	GIP, translation, ribosome		0.59498	2.80173	0.19011	0.71794	0.46055	0.72941	2.29408	3.30939	-1.11857	-0.45519	1.19791	1.72657	-0.78688	1.46224	0.46908	0.37381	2.37235	5.53195	0.25396	NS	0.11385	NS	0.03377	s
AJ223125	AT5G35770 Arabidopsis thaliana mRNA for sterile apetala	sterile apetala (SAP), transcription regulator activity, megasporogenesis, flower development, ovule primordium, petal primordium , A recessive mutation in the Arabidopsis STERILE APETALA (SAP) causes severe aberrations in inflorescence and flower and ovule development.	GIP, TF		0.46273	2.88395	0.14649	0.21854	0.35914	0.56631	2.72942	3.03848	-1.47737	-0.82034	1.44860	1.60335	-1.14885	1.52597	0.46459	0.10943	3.49710	19.72118	0.17731	NS	0.03225	U	0.01555	s
AL355775	At3g46050 Arabidopsis thaliana DNA chromosome 3, BAC clone F12M12	kelch repeat-containing F-box family protein, contains F-box domain Pfam:PF00646 and Kelch motif Pfam:PF01344	Fbox		0.57362	2.95443	0.26299	0.57866	0.38766	0.75959	2.54525	3.36360	-1.36714	-0.39672	1.34781	1.75001	-0.88193	1.54891	0.68619	0.28440	1.81762	7.70226	0.32020	NS	0.08219	NS	0.04365	s
AL353995	At5g10390 Arabidopsis thaliana DNA chromosome 5, BAC clone F12B17 (ESSA project)	histone H3, identical to histone H3 from Zea mays SP|P05203, Medicago sativa GI:166384, Encephalartos altensteinii SP|P08903, Pisum sativum SP|P02300; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4 , DNA binding, chromosome organization and biogenesis (sensu Eukaryota), nucleosome assembly,	GIP, chromosome		0.61836	2.97453	0.02120	0.95555	0.63335	0.60337	2.29885	3.65020	-0.65892	-0.72889	1.20091	1.86798	-0.69391	1.53444	0.04948	0.47169	19.83386	4.60059	0.03207	NC	0.13626	NS	0.02191	s

AF370142	At2g39710 Arabidopsis thaliana unknown protein (T5I7.1/At2g39710) mRNA, complete cds	aspartyl protease family protein, contains profile Pfam PF00026: Eukaryotic aspartyl protease; contains Prosite PS00141: Eukaryotic and viral aspartyl proteases active site.; chloroplast, pepsin A activity, proteolysis	M, protease		0.59957	2.99120	0.24484	0.38939	0.42645	0.77270	2.71586	3.26654	-1.22956	-0.37202	1.44141	1.70776	-0.80079	1.57459	0.60637	0.18834	1.86765	11.82325	0.31296	NS	0.05372	NS	0.03392	s
AL163527	Arabidopsis thaliana DNA chromosome 3, BAC clone F17J16	unknown	unknown		0.38869	3.05011	0.22121	0.01951	0.23227	0.54511	3.06390	3.03631	-2.10613	-0.87538	1.61537	1.60232	-1.49075	1.60884	0.87027	0.00923	2.42252	246.61447	0.24923	NS	0.00258	U	0.03723	s
AF389283	At1g76540 Arabidopsis thaliana mRNA for cyclin dependent kinase (CDKB2;1 gene)	Encodes a cyclin-dependent protein kinase (CDKB2;1) involved in regulation of the G2/M transition of the mitotic cell cycle. Specifically binds to the cyclin CYCD4;1, expressed in shoot meristem, young leaves and vascular tissue during the G2/M phase. cyclin-dependent protein kinase activity, protein binding, G2/M transition of mitotic cell cycle, histone phosphorylation, cyclin-dependent protein kinase holoenzyme complex,	CPS, cell cycle	M, kinase	0.56664	3.09087	0.30927	0.01591	0.34796	0.78533	3.10212	3.07962	-1.52302	-0.34862	1.63325	1.62275	-0.93582	1.62800	0.83043	0.00742	1.59371	310.09310	0.35674	NS	0.00205	U	0.04866	s
AC007591	At1g15460 Arabidopsis thaliana chromosome 1 BAC F9L1 sequence	anion exchange family protein, member of the PF|00955 Anion exchanger family, membrane, anion exchanger activity, anion transport	EIP, transport	CPS, transport	0.50445	3.10675	0.27963	0.53812	0.30673	0.70218	2.72624	3.48726	-1.70498	-0.51009	1.44691	1.80209	-1.10753	1.62450	0.84491	0.25115	1.85378	9.14746	0.31493	NS	0.06932	NS	0.04831	s
AL138659	At3g59540 Arabidopsis thaliana DNA chromosome 3, BAC clone T16L24	60S ribosomal protein L38 (RPL38B), 60S RIBOSOMAL PROTEIN L38 - Lycopersicon esculentum, EMBL:X69979 , ribosome, structural constituent of ribosome, translation, ribosome biogenesis and assembly	GIP, translation, ribosome		0.33454	3.13287	0.08756	0.93632	0.27263	0.39645	3.79495	2.47079	-1.87500	-1.33478	1.92408	1.30497	-1.60489	1.61453	0.38199	0.43778	5.94159	5.21564	0.10615	NS	0.12060	NS	0.01590	s
AC022492	At1g17640 Genomic sequence for Arabidopsis thaliana BAC F1L3 from chromosome I	RNA recognition motif (RRM)-containing protein, similar to GB:L02953 from (Xenopus laevis) (Nucleic Acids Res. 21, 999-1006 (1993)); contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)	GIP, translation		0.43518	3.21906	0.22859	1.16712	0.27354	0.59682	2.39378	4.04434	-1.87019	-0.74464	1.25929	2.01590	-1.30742	1.63760	0.79589	0.53501	2.32315	4.32877	0.25877	NS	0.14453	NS	0.04914	s
AF367321	Arabidopsis thaliana chromosome II section 230 of 255 of the complete sequence. Sequence from clones F14N22	unknown	unknown		0.43123	3.32602	0.10487	0.28578	0.35708	0.50539	3.12394	3.52810	-1.48569	-0.98454	1.64337	1.81889	-1.23512	1.73113	0.35437	0.12411	4.92905	19.72557	0.12743	NS	0.03225	U	0.00792	s
AL391712	At5g09510 Arabidopsis thaliana DNA chromosome 5, BAC clone T5E8 (ESSA project)	40S ribosomal protein S15 (RPS15A), cytosolic ribosome (sensu Eukaryota), cytosolic small ribosomal subunit (sensu Eukaryota), structural constituent of ribosome, translation	GIP, translation, ribosome		0.54733	3.34756	0.14105	0.94551	0.44759	0.64707	2.67899	4.01614	-1.15974	-0.62802	1.42169	2.00581	-0.89388	1.71375	0.37598	0.41304	3.36220	5.86778	0.18404	NS	0.10746	NS	0.02218	s
AL391151	At5g17600 Arabidopsis thaliana DNA chromosome 5, BAC clone K10A8 (ESSA project)	zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)	ZINC		0.58439	3.36359	0.24479	0.77598	0.41130	0.75748	2.81489	3.91229	-1.28175	-0.40073	1.49308	1.96801	-0.84124	1.73055	0.62298	0.33583	1.90969	7.28748	0.30710	NS	0.08682	NS	0.03584	s
AB016879	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MRB17	unknown	unknown		0.51648	3.37150	0.19157	0.73450	0.38102	0.65194	2.85213	3.89087	-1.39207	-0.61719	1.51204	1.96009	-1.00463	1.73607	0.54793	0.31682	2.59299	7.74939	0.23433	NS	0.08170	NS	0.02564	s
AA394491	EST	unknown	unknown		0.53101	3.50338	0.27275	0.02081	0.33815	0.72388	3.51809	3.48866	-1.56427	-0.46618	1.81479	1.80267	-1.01523	1.80873	0.77647	0.00857	1.84908	298.50656	0.31561	NS	0.00213	U	0.03579	s
AC006592	At2g22350 Arabidopsis thaliana chromosome II section 127 of 255 of the complete sequence. Sequence from clones F14M13	RNase H domain-containing protein, low similarity to reverse transcriptase, nuclease activity	GIP, replication and repair		0.50508	3.52637	0.28648	0.69656	0.30251	0.70765	4.01891	3.03383	-1.72495	-0.49890	2.00681	1.60114	-1.11192	1.80397	0.86695	0.28685	1.81383	8.89390	0.32076	NS	0.07128	NS	0.04570	s
AL109819	At4g08400 Arabidopsis thaliana DNA chromosome 4, BAC clone T28D5, partial sequence (ESSA project)	proline-rich extensin-like family protein, contains proline-rich extensin domains, INTERPRO:IPR002965 ; mitochondrion, structural constituent of cell wall, cell wall organization and biogenesis (sensu Magnoliophyta), cell surface (sensu Magnoliophyta)	CPS, cell wall		0.34383	3.55511	0.23143	1.00053	0.18018	0.50747	2.84763	4.26259	-2.47250	-0.97860	1.50976	2.09173	-1.72555	1.80075	1.05635	0.41152	2.31013	6.18843	0.26007	NS	0.10199	NS	0.04799	s
AB005239	At5g44190 Arabidopsis thaliana golden2-like transcription factor (GLK2) mRNA, complete cds	myb family transcription factor (GLK2), Encodes a protein containing a GARP DNA-binding domain which interacts with the Pro-rich regions of GBF1. Transactivates transcription in yeast, similar to the yeast Golden2 transcription factor that is required for photosynthetic differentiation. nucleus, DNA binding, transcription factor activity, transcriptional regulator	GIP, TF		0.51904	3.55578	0.22866	0.27528	0.35735	0.68072	3.36112	3.75043	-1.48459	-0.55486	1.74894	1.90706	-1.01973	1.82800	0.65742	0.11180	2.19360	23.12272	0.27230	NS	0.02752	U	0.02634	s
AY042826	At2g21660 A.thaliana mRNA for glycine rich protein	small glycine-rich protein (GRPs) that is part of a negative-feedback loop through which AtGRP7 regulates the circadian oscillations of its own transcript , encodes a glycine-rich RNA binding protein. Gene expression is induced by cold. nucleus, RNA binding, circadian rhythm	GLYCINE		0.49798	3.59324	0.28287	0.97060	0.29796	0.69799	2.90693	4.27956	-1.74680	-0.51871	1.53949	2.09746	-1.13276	1.81848	0.86839	0.39454	1.84475	6.51823	0.31624	NS	0.09691	NS	0.04846	s
AB019231	At5g60120 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MGO3	AP2 domain-containing transcription factor, putative, Similar to Floral homeotic protein APETALA2 protein, nucleus, DNA binding, transcription factor activity, regulation of transcription, DNA-dependent ; TOE2	GIP, TF		0.47950	3.60551	0.29010	0.10248	0.27437	0.68464	3.67798	3.53304	-1.86581	-0.54659	1.87891	1.82091	-1.20620	1.84991	0.93283	0.04101	1.82866	63.78873	0.31858	NS	0.00998	U	0.04364	s
AC007293	Arabidopsis thaliana chromosome II section 19 of 255 of the complete sequence. Sequence from clones T16B23, T23O15	unknown	unknown		0.33056	3.64039	0.19498	0.23360	0.19269	0.46843	3.80557	3.47522	-2.37562	-1.09409	1.92811	1.79710	-1.73485	1.86261	0.90618	0.09264	2.70746	28.43456	0.22524	NS	0.02238	U	0.03059	s
AL162971	At5g02570 Arabidopsis thaliana DNA chromosome 5, BAC clone T22P11 (ESSA project)	histone H2B, putative, similar to histone H2B-2 Lycopersicon esculentum GI:3021483, nucleus, DNA binding, chromosome organization and biogenesis (sensu Eukaryota), nucleosome assembly, nucleosome	GIP, chromosome		0.38146	3.68707	0.23887	0.16049	0.21255	0.55037	3.57359	3.80056	-2.23409	-0.86152	1.83737	1.92621	-1.54781	1.88179	0.97056	0.06282	2.25533	42.36513	0.26569	NS	0.01502	U	0.03794	s
AP001297	At3g23840 Arabidopsis thaliana genomic DNA, chromosome 3, BAC clone:F14O13	transferase family protein, low similarity to hypersensitivity-related gene (Nicotiana tabacum) GI:1171577, acetyl-CoA:benzylalcohol acetyltranferase (Clarkia concinna) GI:6166330; contains Pfam profile PF02458: Transferase family	M, lipid, acetyltransferase		0.50607	3.68813	0.21819	0.60625	0.35179	0.66035	3.25945	4.11682	-1.50723	-0.59870	1.70463	2.04153	-1.05296	1.87308	0.64243	0.23823	2.31795	11.11942	0.25929	NS	0.05710	NS	0.02634	s
AB017064	At5g47980 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MDN11	transferase family protein, similar to alcohol acyltransferase	M, lipid, acyltransferase		0.41966	3.69687	0.26285	0.01681	0.23380	0.60553	3.70876	3.68498	-2.09665	-0.72373	1.89094	1.88166	-1.41019	1.88630	0.97080	0.00656	2.05429	406.53478	0.28840	NS	0.00157	U	0.04073	s

AC009755	At3g02190 Arabidopsis thaliana chromosome III BAC F14P3 genomic sequence	60S ribosomal protein L39 (RPL39B), similar to ribosomal protein L39 GB:P51424 (Arabidopsis thaliana) , ribosome, structural constituent of ribosome, protein biosynthesis	GIP, translation, ribosome		0.52399	3.69787	0.06311	0.54746	0.56861	0.47936	3.31076	4.08498	-0.81449	-1.06082	1.72716	2.03033	-0.93765	1.87875	0.17418	0.21437	7.61297	12.39414	0.08315	NS	0.05125	NS	0.00477	s
AY035140	At2g27730 Arabidopsis thaliana unknown protein (F15K20.17/At2g27730) mRNA, complete cds	expressed protein, contains 1 transmembrane domain; similar to Unknown mitochondrial protein At2g27730 (Swiss-Prot:Q9ZUX4) (Arabidopsis thaliana) similar to F1F0-ATPase inhibitor protein (GI:5821432) (Oryza sativa) , mitochondrion, molecular_function, photorespiration, NADH dehydrogenase complex (ubiquinone), mitochondrial membrane	M, energy		0.69503	3.69792	0.19114	0.22994	0.55988	0.83019	3.53533	3.86052	-0.83681	-0.26849	1.82184	1.94879	-0.55265	1.88532	0.40186	0.08977	1.94487	29.70186	0.30234	NS	0.02143	U	0.01397	s
AL390921	At3g56770 Arabidopsis thaliana DNA chromosome 3, BAC clone T8M16	basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain , nucleus, DNA binding, transcription factor activity, regulation of transcription	GIP, TF		0.41745	3.70486	0.19494	0.87701	0.27961	0.55530	3.08473	4.32500	-1.83852	-0.84866	1.62514	2.11270	-1.34359	1.86892	0.69993	0.34476	2.71472	7.66646	0.22469	NS	0.08257	NS	0.02825	s
AL049608	At4g13340 Arabidopsis thaliana DNA chromosome 4, BAC clone T9E8, partial sequence (ESSA project)	leucine-rich repeat family protein / extensin family protein, similar to extensin-like protein (Lycopersicon esculentum) gi|5917664|gb|AAD55979; contains leucine-rich repeats, Pfam:PF00560; contains proline rich extensin domains, INTERPRO:IPR002965 , cell wall (sensu Magnoliophyta), structural constituent of cell wall, protein binding	CPS, cell wall		0.53330	3.75647	0.30176	0.93494	0.31992	0.74668	3.09536	4.41757	-1.64423	-0.42144	1.63011	2.14325	-1.03283	1.88668	0.86464	0.36285	1.68932	7.35342	0.34026	NS	0.08605	NS	0.04790	s
AF109376	At2g27760 Arabidopsis thaliana tRNA isopentenyl transferase mRNA, complete cds	tRNA isopentenyltransferase 2 / IPP transferase 2 (IPT2), cytosol, tRNA isopentenyltransferase activity, cytokinin biosynthesis, adenylate dimethylallyltransferase activity, whole plant, A vegetative growth, B reproductive growth	M, hormone synth, cytokinin		0.46966	3.75744	0.19566	0.33277	0.33131	0.60801	3.52214	3.99274	-1.59374	-0.71782	1.81645	1.99738	-1.15578	1.90692	0.61937	0.12793	2.63901	21.07935	0.23059	NS	0.03018	U	0.02066	s
AC016827	At3g07030 Arabidopsis thaliana chromosome III BAC F17A9 genomic sequence	pseudogene, similar to OSJNBa0042L16.13, blastp match of 56% identity and 1.3e-39 P-value to GP|21740825|emb|CAD41015.1||AL606632 OSJNBa0042L16.13 {Oryza sativa (japonica cultivar-group)}	unknown		0.58747	3.77977	0.28967	0.21715	0.38265	0.79230	3.93332	3.62623	-1.38592	-0.33588	1.97575	1.85847	-0.86090	1.91711	0.74249	0.08293	1.63974	32.69348	0.34863	NS	0.01947	U	0.03431	s
AA728481	EST	unknown	unknown		0.50232	3.83892	0.28277	0.53052	0.30238	0.70227	3.46379	4.21405	-1.72559	-0.50991	1.79235	2.07521	-1.11775	1.93378	0.85961	0.20001	1.83889	13.67319	0.31708	NS	0.04648	U	0.03937	s
AL391150	At5g17490 Arabidopsis thaliana DNA chromosome 5, BAC clone K3M16 (ESSA project)	gibberellin response modulator, putative / gibberellin-responsive modulator, putative, putative member of the VHIID domain transcription factor family RGAL - Arabidopsis thaliana, EMBL:AJ224957 (RGL3, DELLA subfamily member involved in GA signal transduction) nucleus, transcription factor activity, gibberellic acid mediated signaling	GIP, TF	CPS, signal transduction	0.54366	3.85914	0.26184	0.65485	0.35851	0.72881	3.39610	4.32219	-1.47990	-0.45638	1.76388	2.11176	-0.96814	1.93782	0.72374	0.24599	1.89178	11.14056	0.30957	NS	0.05699	NS	0.03290	s
AB027153	At3g23000 Arabidopsis thaliana ATSRPK1 mRNA for SNF1 related protein kinase, complete cds	CBL-interacting protein kinase 7 (CIPK7), Encodes a serine/threonine protein kinase with similarities to CBL-interacting protein kinases, SNF1 and SOS2. interact with calcineurin B-like calcium sensor proteins (CBLs).	M, kinase		0.58175	3.89087	0.31981	0.62584	0.35561	0.80789	3.44834	4.33341	-1.49164	-0.30777	1.78590	2.11550	-0.89971	1.95070	0.83712	0.23306	1.51994	11.83671	0.37046	NS	0.05366	NS	0.04346	s
S47405	Glycine-rich protein {clone atGRP-1} [Arabidopsis thaliana, C24, mRNA Partial, 740 nt]	Glycine-rich protein, lipid binding	GLYCINE		0.53507	3.89800	0.25235	1.21886	0.35663	0.71351	3.03614	4.75986	-1.48750	-0.48699	1.60224	2.25092	-0.98724	1.92658	0.70747	0.45869	1.97349	5.93997	0.29858	NS	0.10618	NS	0.03941	s
AC005309	At2g47810 Arabidopsis thaliana chromosome II section 254 of 255 of the complete sequence. Sequence from clones T30B22, F17A22, T9J23	histone-like transcription factor (CBF/NF-Y) family protein, transcription factor activity, regulation of transcription, DNA-dependent, similar to LEC1	GIP, TF		0.47086	3.90802	0.20706	1.08611	0.32445	0.61728	3.14003	4.67602	-1.62392	-0.69601	1.65078	2.22528	-1.15997	1.93803	0.65613	0.40624	2.50016	6.74678	0.24222	NS	0.09368	NS	0.02965	s
AP000368	Arabidopsis thaliana genomic DNA, chromosome 5, BAC clone:F6B6	unknown	unknown		0.45350	3.91144	0.19302	0.56230	0.31701	0.58999	4.30905	3.51383	-1.65739	-0.76124	2.10737	1.81305	-1.20931	1.96021	0.63367	0.20812	2.69892	13.32008	0.22590	NS	0.04770	U	0.02143	s
AL049523	At4g10620 Arabidopsis thaliana DNA chromosome 4, BAC clone T4F9 (ESSA project)	expressed protein	unknown		0.43110	3.91246	0.26264	0.77840	0.24538	0.61681	3.36205	4.46286	-2.02691	-0.69710	1.74934	2.15797	-1.36200	1.95365	0.94032	0.28895	2.04842	9.56196	0.28912	NS	0.06634	NS	0.04130	s
AC004411	At2g46850 Arabidopsis thaliana chromosome II section 250 of 255 of the complete sequence. Sequence from clones F19D11, F14M4, T3D7	expressed protein , ATP binding, protein kinase activity, protein serine/threonine kinase activity, protein-tyrosine kinase activity, protein amino acid phosphorylation, endomembrane system	M, kinase		0.57706	3.99807	0.34001	0.69346	0.33664	0.81748	3.50772	4.48842	-1.57073	-0.29075	1.81053	2.16621	-0.93074	1.98837	0.90508	0.25150	1.45430	11.18087	0.38348	NS	0.05679	NS	0.04808	s
AC006446	At2g13320 Arabidopsis thaliana chromosome II section 73 of 255 of the complete sequence. Sequence from clones T17A11, F15O11	expressed protein,	unknown		0.50267	4.10578	0.27906	0.24172	0.30534	0.70000	3.93486	4.27670	-1.71150	-0.51458	1.97631	2.09650	-1.11304	2.03640	0.84635	0.08498	1.85984	33.88736	0.31407	NS	0.01878	U	0.03459	s
AJ002892	AT4G13850 (?, 1 0f 9) Arabidopsis thaliana mRNA for glycine-rich RNA-binding protein (AtGRP2)	encodes a glycine-rich RNA-binding protein. Gene expression is induced by cold. RNA binding, double-stranded DNA binding, single-stranded DNA binding ; GLYCINE-RICH RNA-BINDING PROTEIN (AtGRP2)	GIP, translation		0.47283	4.15861	0.27743	0.59137	0.27666	0.66900	4.57677	3.74045	-1.85383	-0.57992	2.19433	1.90321	-1.21688	2.04877	0.90079	0.20585	1.91046	14.07515	0.30699	NS	0.04515	U	0.03778	s
X65549	Arabidopsis thaliana putative adenylate translocator (F17O14.5/AT3g08580) mRNA, complete cds	ADP, ATP carrier protein 1, mitochondrial / ADP/ATP translocase 1 / adenine nucleotide translocator 1 (ANT1), mitochondrial envelope, ATP:ADP antiporter activity, purine nucleotide transport	CPS, transport		0.43096	4.17206	0.02033	2.41591	0.41659	0.44534	2.46376	5.88037	-1.26332	-1.16703	1.30086	2.55591	-1.21517	1.92838	0.06809	0.88745	25.24063	3.07300	0.02521	D	0.20028	NS	0.03782	s
AC023912	Arabidopsis thaliana chromosome 3 BAC T8E24 genomic sequence	unknown	unknown		0.70502	4.27699	0.01638	0.14326	0.71660	0.69344	4.37829	4.17569	-0.48075	-0.52816	2.13037	2.06201	-0.50446	2.09619	0.03352	0.04833	21.28148	61.33347	0.02989	NC	0.01038	U	0.00026	s
AF325037	At4g13940 Arabidopsis thaliana AT4g13940 (AT4g13940/dl3010w) mRNA, complete cds	adenosylhomocysteinase / S-adenosyl-L-homocysteine hydrolase / AdoHcyase (SAHH), Encodes a S-adenosyl-L-homocysteine hydrolase required for DNA methylation-dependent gene silencing. (HOG1, HOMOLOGY-DEPENDENT GENE SILENCING 1), cellular component unknown, adenosylhomocysteinase activity, methylation-dependent chromatin silencing, posttranscriptional gene silencing	M, amino acid	GIP, silencing	0.51661	4.57976	0.20850	2.05729	0.36918	0.66404	3.12503	6.03448	-1.43759	-0.59065	1.64387	2.59323	-1.01412	2.11855	0.59888	0.67130	2.39480	4.46312	0.25182	NS	0.14032	NS	0.03885	s

AB016892	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MXF12	unknown	unknown		0.40909	4.62930	0.25123	0.11386	0.23144	0.58673	4.70981	4.54879	-2.11130	-0.76922	2.23567	2.18548	-1.44026	2.21058	0.94899	0.03549	2.14632	88.09692	0.27757	NS	0.00723	U	0.03221	s
AY040013	Arabidopsis thaliana putative spermidine synthase (MFH8.5/AT5g53120) mRNA, complete cds	spermidine synthase, putative / putrescine aminopropyltransferase, putative, encodes a novel spermine synthase and is a paralog of previously characterized spermidine synthases, SPDS1 and SPDS2. SPDS3 forms heterodimers with SDPS2, which in turn forms heterodimers with SDPS1 in vivo. cytoplasm, spermidine synthase activity, spermine synthase activity, polyamine biosynthetic process	M, polyamine		0.46893	4.64568	0.26115	0.13742	0.28427	0.65359	4.74285	4.54850	-1.81467	-0.61353	2.24575	2.18539	-1.21410	2.21557	0.84933	0.04268	2.02158	73.41065	0.29244	NS	0.00867	U	0.02939	s
AC005170	At2g24060 Arabidopsis thaliana chromosome II section 135 of 255 of the complete sequence. Sequence from clones F27L4, T29E15	translation initiation factor 3 (IF-3) family protein, translational initiation	GIP, translation		0.46660	4.81142	0.33321	0.61710	0.23099	0.70222	4.37506	5.24777	-2.11412	-0.51001	2.12930	2.39171	-1.31206	2.26050	1.13428	0.18555	1.63587	17.22922	0.34930	NS	0.03691	U	0.04805	s
AY042884	At4g02890 Arabidopsis thaliana Unknown protein mRNA, complete cds	polyubiquitin (UBQ14), identical to GI:166795; similar to N. sylvestris hexameric polyubiquitin, GenBank accession number M74101 , Polyubiquitin gene containing 4 ubiquitin repeats. protein binding, protein modification	GIP, FSD	EIP, signal transduction	0.77112	5.33320	0.10038	2.99358	0.84210	0.70014	3.21642	7.44998	-0.24794	-0.51428	1.68545	2.89724	-0.38111	2.29135	0.18833	0.85686	2.86190	3.78178	0.21400	NS	0.16457	NS	0.04989	s
AL162971	At5g02460 Arabidopsis thaliana DNA chromosome 5, BAC clone T22P11 (ESSA project)	Dof-type zinc finger domain-containing protein, zinc finger protein OBP3, Arabidopsis thaliana, EMBL:AF155818 , cellular_component, DNA binding, transcription factor activity, regulation of transcription	GIP, TF		0.83862	5.46556	0.29646	1.63361	1.04825	0.62899	4.31042	6.62069	0.06798	-0.66890	2.10783	2.72698	-0.30046	2.41741	0.52105	0.43781	0.81549	7.80875	0.56448	NS	0.08109	NS	0.02995	s
AF159255	At4g27330 Arabidopsis thaliana sporocyteless (SPL) mRNA, complete cds	sporocyteless (SPL), identical to sporocyteless SPL (MADS-box related protein), Encodes a putative transcription factor that is required for the initiation of both micro- and megagametogenesis and is expressed in the sporogenous tissue of the anther and the ovule.nucleus, protein binding, transcription factor activity, megasporogenesis, microsporogenesis, sporocyte differentiation	GIP, TF		0.55169	5.67633	0.36686	0.41984	0.29228	0.81110	5.37946	5.97320	-1.77459	-0.30205	2.42746	2.57850	-1.03832	2.50298	1.04124	0.10680	1.41025	33.14262	0.39267	NS	0.01920	U	0.04101	s
AL161502	At4g05050 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 14	polyubiquitin (UBQ11), identical to GI:304117, polyubiquitin gene, belongs to a subtype group with UBQ10 and UBQ14. Various ecotypes of Arabidopsis have different numbers of ubiquitin repeats within this gene. protein binding, ubiquitin-dependent protein catabolic process	GIP, FSD	EIP, signal transduction	0.49197	5.81052	0.04108	1.18312	0.52103	0.46292	6.64711	4.97393	-0.94057	-1.11115	2.73273	2.31439	-1.02586	2.52356	0.12062	0.29581	12.02799	12.06462	0.05281	NS	0.05265	NS	0.00403	s
L05361	At4g05320 Arabidopsis thaliana polyubiquitin (ubq10) mRNA, complete cds	polyubiquitin (UBQ10) (SEN3), senescence-associated protein; identical to GI:870791 , One of five polyubiquitin genes in A. thaliana. These genes encode the highly conserved 76-amino acid protein ubiquitin that is covalently attached to substrate proteins targeting most for degradation. Polyubiquitin genes are characterized by the presence of tandem repeats of the 228 bp that encode a ubiquitin monomer. Induced by salicylic acid. Independent of NPR1 for their induction by salicylic acid.	GIP, FSD	EIP, signal transduction	0.54466	6.27004	0.07886	0.39613	0.60042	0.48890	5.98993	6.55014	-0.73595	-1.03240	2.58254	2.71153	-0.88417	2.64703	0.20962	0.09121	5.96514	41.04378	0.10574	NS	0.01551	U	0.00209	s
AL353814	At3g44140 Arabidopsis thaliana DNA chromosome 3, BAC clone F26G5	expressed protein	unknown		0.46532	6.69128	0.31892	2.66847	0.23981	0.69083	4.80439	8.57818	-2.06003	-0.53360	2.26435	3.10067	-1.29681	2.68251	1.07935	0.59137	1.69914	6.41506	0.33865	NS	0.09845	NS	0.04465	s
AY026254	At5g27350 Arabidopsis thaliana sugar-porter family protein 1 (SFP1) mRNA, complete cds	sugar-porter family protein 1 (SFP1), identical to sugar-porter family protein 1 (Arabidopsis thaliana) GI:14585699 , membrane, carbohydrate transporter activity, sugar porter activity, response to nematode, root	EIP, transport	CPS, transport	0.56797	9.91983	0.01673	3.29641	0.55614	0.57980	12.25075	7.58892	-0.84649	-0.78638	3.61480	2.92389	-0.81644	3.26935	0.04250	0.48854	27.16605	9.46399	0.02342	NC	0.06702	NS	0.00713	s