Utility of *Amborella trichopoda* and *Nuphar advena* expressed sequence tags for comparative sequence analysis

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Expressed sequence tags (ESTs) for the basal angiosperms *Amborella trichopoda* (Amborellaceae) and the water lily *Nuphar advena* (Nymphaeaceae) have proven valuable in identification of gene pairs to study the timing of duplication events relative to the most recent common ancestor (MRCA) of all extant angiosperms. Here we discuss how ESTs for these taxa are also useful for deducing gene families that were present in the MRCA of all flowering plants. For example, 4,572 gene clusters identified in an analysis of the rice and *Arabidopsis* proteomes contained putative orthologs of *Amborella* or *Nuphar*. Homologs of many developmentally important genes were identified from *Amborella* or *Nuphar* in these gene clusters. This number of ancestral genes is expected to increase as the number of *Amborella* and water lily ESTs increases. Genes found unduplicated in the rice and *Arabidopsis* genomes may be especially useful for phylogenetic analyses including diverse angiosperm lineages. We identify 595 of these single copy genes with putative orthologs in *Amborella* or *Nuphar*. Phylogenetic analysis of one of these nuclear single-copy genes encoding the enzyme carboxymethylenebutenolidase yields a topology that places *Amborella* and *Nuphar* as the sisters to all other extant lineages of angiosperms and is generally consistent with current angiosperm phylogenies based mainly on chloroplast, mitochondrial, and nuclear ribosomal sequences.

KEYWORDS: basal angiosperms, ESTs, MADS box, single copy gene, transcription factors, transcriptome

INTRODUCTION

Since their introduction, expressed sequence tags (ESTs) have proven to be the most efficient way to characterize the expressed gene set in plants and other organisms. The initial utility of ESTs, and still their most common use, is to leverage research within a species, such as genome mapping, gene and genome annotation, estimation of the number of expressed genes (Wang & al., 2005), building microarrays for expression analysis, and finding genes associated with particular traits. Although most ESTs are derived from model and crop species in the Poaceae and core eudicots, the availability of large EST sets from a diverse array of angiosperms (215 have over 5,000 ESTs; see http://plantta.tigr.org/) has enabled a wide range of analyses that focus on the utility of ESTs for comparative studies in these plants. These studies include analyses of gene families in multiple organisms (Kim & al., 2004, 2005, 2006; Zahn & al., 2005a, b, 2006a, b; Yoo & al., 2006); comparative studies of genome history and duplication (Blanc & Wolfe, 2004; Cui & al., 2006; Schlueter & al., 2004); and the identification of nuclear genes for phylogenetic analysis of organismal relationships (De la Torre & al., 2006; Whittall & al., 2006).

Amborella trichopoda Baill. is a small, evergreen, dioecious shrub endemic to the island of New Caledonia and the sole living representative of the monotypic Amborellaceae (Stevens, 2001). *Nuphar advena* (Aiton) W.T. Aiton is a member of the water lily family (Nymphaeaceae) and is commonly known as spatterdock or yellow pond lily, with a geographic range extending throughout eastern North America (Wiersema & Hellquist, 1997). *Nuphar advena* has a genome size of 2,772 MB/1C, while that of *Amborella trichopoda* is only 870 MB/1C (Cui & al., 2006). Nearly all molecular phylogenetic studies have placed *Amborella* and Nymphaeales as basal lineages of angiosperms with either *Amborella* alone, or

Amborella + Nymphaeaceae as sister to all other angiosperms (Mathews & Donoghue, 1999; Parkinson & al., 1999; Qiu & al., 1999; Soltis & al., 1999; Barkman & al., 2000; Graham & Olmstead, 2000; Zanis & al., 2002; Borsch & al., 2003; Hilu & al., 2003; Stefanovic & al., 2004; Leebens-Mack & al., 2005). *Nuphar* is sister to the rest of Nymphaeaceae (Les & al., 1999; see also Yoo & al., 2005).

A striking observation stemming from phylogenetic analyses has been the identification of numerous mitochondrial sequences from *Amborella* that have apparently been acquired through horizontal transfer from plants as diverse as eudicots, monocots, and mosses (Bergthorsson & al., 2003, 2004). Analyses of mitochondrial sequences of water lilies (and other basal angiosperms) have shown no similar evidence for horizontal transfer (Bergthorsson & al., 2004). There has not yet been an evaluation of the possibility that horizontal gene transfer has impacted expressed nuclear genes in these species.

By studying the genetic diversity present in the basalmost angiosperm lineages, we can gain insights into the genetic characteristics of the most recent common ancestor of all extant angiosperms. Evidence from floral transcriptome sequencing in *Amborella* and *Nuphar* provides important information on potential genome duplications that occurred early in angiosperm history, identification of the common set of angiosperm genes, the potential for functional horizontal gene transfer of nuclear-encoded genes, and single-copy phylogenetic markers from the nuclear genome. In addition, by studying the basalmost angiosperm lineages, we will be able to polarize the direction of changes observed in genes and gene families in monocot and eudicot lineages to infer whether characters are ancestral or derived.

In this paper we demonstrate the utility of the *Amborella* and *Nuphar* ESTs in comparative genomics and phylogenetic analysis, as well as review previous research using these ESTs in comparative sequence analysis to detect genome duplication and improve gene family analysis by providing a root to angiosperm clades.

MATERIALS AND METHODS

Tissue sampling and collection. — EST libraries were built from RNAs isolated from premeitoc flower buds (Albert & al., 2005). *Nuphar* flower buds were collected from a single population of *Nuphar advena* plants growing at Black Moshannon Lake, Black Moshannon State Park, Centre County, Pennsylvania. Buds were sampled from the smallest sizes obtainable (ca. 0.3 mm) through initiation of meiosis (13 mm diameter).

Premeiotic (< 2 mm in diameter) flower buds of *Amborella* were collected from plants maintained at the National Tropical Botanical Garden, Kauai, Hawaii, U.S.A. Buds of male flowers were collected from plants 980644-018, 980631-019, 980631-013, 980647-010, and 980647-008, which correspond to NTBG vouchers DL8346, TF6481, and DHL8350, for 980644, 980631, and 980647, respectively. Buds of female flowers were collected from plants 980631-019, 980631-015, 980647-002, 980647-005, and 980647-006, which correspond to NTBG vouchers TF6481 and DHL8350 for 980631 and 980647, respectively.

EST sequences and unigene assembly. — Complementary DNA (cDNA) libraries were constructed from RNAs isolated from premeiotic flower buds of *Amborella trichopoda* and *Nuphar advena*, and EST sequencing was performed as described in Albert & al. (2005). ESTs and unigenes (assembled contigs of ESTs) for *Amborella trichopoda* and *Nuphar advena* are available through the Plant Genome Network (PGN) website (http://www.pgn.cornell.edu), and are indicated there as build #4 for *Amborella* and build #2 for *Nuphar*.

Classification of *Amborella* and *Nuphar* unigenes using PlantTribes and INPARANOID groups. — In this study, we used two classification systems to provide putative homology groups at two levels of resolution to aid in the tentative identification of the sequences captured in the study. Tribes (Enright & al., 2002, 2003; Albert & al., 2005; Wall & al., 2008) approximate gene families, while INPARANOID groups (Remm & al., 2001) represent a finer-grained analysis intended to recover putative sets of orthologs. *Amborella* and *Nuphar* unigenes were sorted into putative homology groups using tBLASTx. “Best hits” with e-values stronger than 10^{-5} (Altschul & al., 1990) were used to assign unigenes into PlantTribes (http://fgp.huck.psu.edu/tribe.php) and INPARANOID groups composed of *Arabidopsis* and rice proteins using a similar BLASTx approach.

PlantTribes is a database of putative gene families based on TribeMCL clustering of the *Arabidopsis* and rice proteomes (Enright & al., 2002, 2003; Albert & al., 2005; Wall & al., 2008). For this analysis, we used the *Arabidopsis thaliana* genome version 5 and *Oryza sativa* version 3 (http://fgp.huck.psu.edu/tribe.php)INPARANOID groups are putative orthologous groups of genes, based on pairwise comparison of two genomes, in this case *Arabidopsis thaliana* and *Oryza sativa* (Remm & al., 2001). TribeMCL and INPARANOID clustering both use blast e-values as a distance metric. Whereas TribeMCL clusters genes irrespective of the taxon from which genes are sampled, the INPARANOID algorithm identifies gene pairs sampled from two focal taxa with minimal distances and then grows clusters by including all genes within each taxon that have smaller distances than the minimal cross-species distance. As a consequence, INPARANOID clusters only include genes for which cross-species gene pairs are found with an e-value below some threshold (10^{-5} in this study).

Table 1. Reproductive development genes present in the *Amborella* and *Nuphar* unigenes. A subset of the PlantTribe and INPARANOID gene clusters listed in the Appendix (Taxon online issue) shows unique *Nuphar* and *Amborella* genes assembled from Floral Genome Project EST sequences with PGN unigene IDs (see http://pgn.cornell.edu). Deduced gene sequences are organized by PlantTribe and INPARANOID cluster identity based on the placement of the best BLAST hit in *Arabidopsis*. #ESTS = number of EST sequences comprising the unigene; INPAR = INPARANOID, or putative orthologous group assignment; #ATH or #OSA = number or *Arabidopsis thaliana* or *Oryza sativa* genes assigned to the indicated INPARALOG group; BEST ATH = identity of *Arabidopsis thaliana* best BLAST hit; E-VALUE = probability of best BLAST best hit by random occurrence; Description = brief annotation for putative ortholog in *Arabidopsis thaliana*.

UNI ID	Taxon	# ESTS	INPAR	#ATH	#OSA	BEST ATH	E-VALUE	Description
AP2 (tribe 34)								
197035	*Amborella*	1	645	1	1	At1g15130	4.00E–50	Hydroxyproline-rich glycoprotein family protein
359307	*Nuphar*	1	645	1	1	At1g15130	1.00E–91	Hydroxyproline-rich glycoprotein family protein
195946	*Amborella*	2	6,860	1	1	At1g44835	4.00E–11	YbaK/prolyl-tRNA synthetase family protein contains Pfam PF04073
195738	*Amborella*	2	7,435	1	2	At1g15360	2.00E–48	AP2 domain-containing transcription factor family protein similar to SP|P16146 PPLZ02 protein {*Lupinus polyphyllus*}
200316	*Amborella*	1				At3g16770	2.00E–17	AP2 domain-containing protein RAP2.3 (RAP2.3) identical to GI:2281631 [*Arabidopsis thaliana*]
BEL-1 like Homeobox (tribe 319)								
196074	*Amborella*	2	5,278	1	1	At2g35940	4.00E–08	Homeodomain-containing protein contains “Homeobox” domain signature, Prosite:PS00027
199304	*Amborella*	1	5,278	1	1	At2g35940	5.00E–46	Homeodomain-containing protein contains “Homeobox” domain signature, Prosite:PS00027
198226	*Amborella*	1	5,479	2	3	At2g16400	10.00E–68	Homeodomain-containing protein
355770	*Nuphar*	1	5,479	2	3	At4g34610	1.00E–39	Homeodomain-containing protein similaritry to homeotic protein BEL1, *Arabidopsis thaliana*, PIR2:A57632
199146	*Amborella*	1				At1g75410	2.00E–17	BEL1-like homeodomain 3 protein (BLH3) identical to BEL1-like homeodomain 3 (GI:13877515) [*Arabidopsis thaliana*]
HEN2-like (tribe 383)								
199223	*Amborella*	1	172	1	1	At2g06990	2.00E–101	HUA enhancer 2 (HEN2) / DExH-box RNA helicase, putative nearly identical to HUA enhancer 2 [*Arabidopsis thaliana*] GI:16024936
HUA1-like (tribe 270)								
197734	*Amborella*	1	795	1	1	At3g60240	3.00E–81	Eukaryotic translation initiation factor 4F, putative / eIF-4F, similar to SP|Q03387 eIF-(iso)4F subunit P82-34 {*Triticum aestivum*}; contains Pfam profiles PF02854, PF02847
199465	*Amborella*	1	795	1	1	At3g60240	1.00E–30	Eukaryotic translation initiation factor 4F, putative / eIF-4F, similar to SP|Q03387 eIF-(iso)4F subunit P82-34 {*Triticum aestivum*}; contains Pfam profiles PF02854, PF02847
353520	*Nuphar*	2	795	1	1	At3g60240	3.00E–25	Eukaryotic translation initiation factor 4F, putative / eIF-4F, similar to SP|Q03387 eIF-(iso)4F subunit P82-34 {*Triticum aestivum*}; contains Pfam profiles PF02854, PF02847

Table 1. Continued.

UNI ID	Taxon	# ESTS	INPAR	#ATH	#OSA	BEST ATH	EVALUE	Description
356799	*Nuphar*	1	795	1	1	At3g60240	7.00E–24	Eukaryotic translation initiation factor 4F, putative / eIF-4F, similar to SP|Q03387 eIF-(iso)4F subunit P82-34 {*Triticum aestivum*}; contains Pfam profiles PF02854, PF02847
357998	*Nuphar*	1	795	1	1	At3g60240	1.00E–23	Eukaryotic translation initiation factor 4F, putative / eIF-4F, similar to SP|Q03387 eIF-(iso)4F subunit P82-34 {*Triticum aestivum*}; contains Pfam profiles PF02854, PF02847
195721	*Amborella*	2	1,214	1	2	At5g57870	4.00E–58	Eukaryotic translation initiation factor 4F, putative / eIF-4F, similar to SP|Q03387 eIF-(iso)4F subunit P82-34 {*Triticum aestivum*}; contains Pfam profiles PF02854, PF02847
198740	*Amborella*	1	4,694	1	1	At3g12680	6.00E–68	Floral homeotic protein (HUA1) identical to floral homeotic protein HUA1 [*Arabidopsis thaliana*] gi|16797661|gb|AAK01470
359956	*Nuphar*	1	4,694	1	1	At3g12680	5.00E–16	Floral homeotic protein (HUA1) identical to floral homeotic protein HUA1 [*Arabidopsis thaliana*] gi|16797661|gb|AAK01470 KNAT-like Homeobox (tribe 364)
196230	*Amborella*	2	641	1	1	At5g45380	2.00E–108	Sodium:solute symporter family protein contains Pfam profile: PF00474
352987	*Nuphar*	2	641	1	1	At5g45380	3.00E–50	Sodium:solute symporter family protein contains Pfam profile: PF00474
195913	*Amborella*	2	4,123	2	1	At5g25220	10.00E–122	Homeobox protein knotted-1 like 3 (KNAT3) SP:P48000 from [*Arabidopsis thaliana*]
200829	*Amborella*	1				At1g62990	5.00E–55	Homeodomain transcription factor (KNAT7) contains Pfam profiles: PF03789, PF03790, PF03791; GI:11878229
353349	*Nuphar*	2				At1g62990	2.00E–77	Homeodomain transcription factor (KNAT7) contains Pfam profiles: PF03789, PF03790, PF03791; GI:11878229
354722	*Nuphar*	1				At1g62990	2.00E–59	Homeodomain transcription factor (KNAT7) contains Pfam profiles: PF03789, PF03790, PF03791; GI:11878229
Late embryogenesis abundant (LEA) protein genes								
(tribe 1183)								
199266	*Amborella*	1	4,239	1	2	At2g44060	4.00E–43	LEA family protein similar to ethylene-responsive late embryogenesis-like protein [*Lycopersicon esculentum*] GI:1684830; contains Pfam profile PF03168
353849	*Nuphar*	2	4,239	1	2	At2g44060	9.00E–32	LEA family protein similar to ethylene-responsive late embryogenesis-like protein [*Lycopersicon esculentum*] GI:1684830; contains Pfam profile PF03168
(tribe 1226)								
201407	*Amborella*	1	3,446	1	1	At3g50790	2.00E–31	LEA protein, putative similar to *Picea glauca* late embryogenesis abundant protein (EMB8), PID:g1350545 SP|Q40863; contains Pfam profile PF00561

Table 1. Continued.

UNI ID	Taxon	# ESTS	INPAR	#ATH	#OSA	BEST ATH	EVALUE	Description
(tribe 1962)								
359931	*Nuphar*	1	9,059	2	2	At3g15670	8.00E–11	LEA protein, putative similar to SP|P13934 Late embryogenesis abundant protein 76 (LEA 76) {*Brassica napus*}; contains Pfam profile PF02987
MADS (tribe 54)								
196124	*Amborella*	2	7,104	2	2	At2g45650	3.00E–81	MADS-box protein (AGL6)
353948	*Nuphar*	2	7,104	2	2	At2g45650	1.00E–72	MADS-box protein (AGL6)
196122	*Amborella*	6	7,150	3	1	At5g15800	1.00E–70	Developmental protein SEPALLATA1 / floral homeotic protein (AGL2) (SEP1) SP:P29382 from [*Arabidopsis thaliana*]
198461	*Amborella*	1	7,150	3	1	At5g15800	3.00E–28	Developmental protein SEPALLATA1 / floral homeotic protein (AGL2) (SEP1) SP:P29382 from [*Arabidopsis thaliana*]
199780	*Amborella*	1	7,150	3	1	At5g15800	7.00E–50	Developmental protein SEPALLATA1 / floral homeotic protein (AGL2) (SEP1) SP:P29382 from [*Arabidopsis thaliana*]
353945	*Nuphar*	2	7,150	3	1	At5g15800	5.00E–57	Developmental protein SEPALLATA1 / floral homeotic protein (AGL2) (SEP1) SP:P29382 from [*Arabidopsis thaliana*]
356714	*Nuphar*	1	7,150	3	1	At5g15800	5.00E–55	Developmental protein SEPALLATA1 / floral homeotic protein (AGL2) (SEP1) SP:P29382 from [*Arabidopsis thaliana*]
197826	*Amborella*	1	7,165	2	2	At1g26310	2.00E–08	MADS-box protein, putative strong similarity to DNA-binding protein [*Brassica rapa* subsp. *pekinensis*] GI:6469345, SP|Q41276 Floral homeotic protein APETALA1 (MADS C) {Sinapis alba}; contains InterPro accession IPR002100
357070	*Nuphar*	1	7,165	2	2	At1g69120	1.00E–29	Floral homeotic protein APETALA1 (AP1) / agamous-like MADS box protein (AGL7) identical to SP|P35631 Floral homeotic protein APETALA1 (AGL7 protein) {*Arabidopsis thaliana*}
197771	*Amborella*	1	7,352	3	1	At4g18960	4.00E–49	Floral homeotic protein AGAMOUS (AG) contains an ACG start codon
199356	*Amborella*	1	7,352	3	1	At4g18960	3.00E–82	Floral homeotic protein AGAMOUS (AG) contains an ACG start codon
354351	*Nuphar*	5	7,352	3	1	At4g18960	8.00E–70	Floral homeotic protein AGAMOUS (AG) contains an ACG start codon
196610	*Amborella*	2	7,688	3	1	At3g57230	4.00E–31	MADS-box protein (AGL16) MADS-box transcription factor Pfam domain PF00319, PF01480.25K
353295	*Nuphar*	5	8,089	1	2	At5g20240	1.00E–22	Floral homeotic protein PISTILLATA (PI) contains Pfam profiles PF01486: K-box region and PF00319: SRF-type transcription factor
353627	*Nuphar*	12	8,089	1	2	At5g20240	2.00E–57	Floral homeotic protein PISTILLATA (PI) contains Pfam profiles PF01486: K-box region and PF00319: SRF-type transcription factor
196410	*Amborella*	2	8,530	1	1	At3g54340	6.00E–16	Floral homeotic protein APETALA3 (AP3)
198366	*Amborella*	1	8,530	1	1	At3g54340	9.00E–12	Floral homeotic protein APETALA3 (AP3)

Table 1. Continued.

UNI ID	Taxon	# ESTS	INPAR	#ATH	#OSA	BEST ATH	EVALUE	Description
356264	*Nuphar*	1	8,530	1	1	At3g54340	1.00E–21	Floral homeotic protein APETALA3 (AP3)
358723	*Nuphar*	1	8,530	1	1	At3g54340	5.00E–10	Floral homeotic protein APETALA3 (AP3)
198454	*Amborella*	1				At5g60910	6.00E–28	Agamous-like MADS box protein AGL8 (Floral homeotic protein AGL8) (FRUITFULL)
199447	*Amborella*	1				At5g60910	8.00E–29	Agamous-like MADS box protein AGL8 (Floral homeotic protein AGL8) (FRUITFULL)
354424	*Nuphar*	2				At5g13790	7.00E–19	Floral homeotic protein AGL-15 (AGL15)
358550	*Nuphar*	1				At5g52550	1.00E–07	Expressed protein
NAC (tribe 40)								
359836	*Nuphar*	1	5,184	1	1	At1g65910	3.00E–11	No apical meristem (NAM) family protein similar to jasmonic acid 2 GI:6175246 from [*Lycopersicon esculentum*]; similar to NAC2 (GI:6456751) {*Arabidopsis thaliana*}
200647	*Amborella*	1	6,674	2	2	At3g10500	1.00E–57	No apical meristem (NAM) family protein similar to to NAC2 (GI:645671) [*Arabidopsis thaliana*]; contains Pfam PF02365
353976	*Nuphar*	2	6,674	2	2	At3g10500	2.00E–47	No apical meristem (NAM) family protein similar to to NAC2 (GI:645671) [*Arabidopsis thaliana*]; contains Pfam PF02365
198513	*Amborella*	1	7,263	2	1	At4g35580	5.00E–39	No apical meristem (NAM) family protein similar to TIP [*Arabidopsis thaliana*] GI:9408601; contains Pfam profile PF02365
354384	*Nuphar*	2	8,211	1	2	At5g64530	2.00E–13	No apical meristem (NAM) family protein contains Pfam PF02365
359550	*Nuphar*	1	8,211	1	2	At5g64530	2.00E–13	No apical meristem (NAM) family protein contains Pfam PF02365
198860	*Amborella*	1				At5g17260	10.00E–35	No apical meristem (NAM) family protein contains Pfam PF02365: No apical meristem (NAM) domain;
199787	*Amborella*	1				At1g69490	5.00E–68	No apical meristem (NAM) family protein similar to N-term half of NAC domain protein NAM [*Arabidopsis thaliana*] GI:4325282
354376	*Nuphar*	2				At1g69490	1.00E–35	No apical meristem (NAM) family protein similar to N-term half of NAC domain protein NAM [*Arabidopsis thaliana*] GI:4325282 Scarecrow (tribe 75)
201039	*Amborella*	1	2,631	2	1	At2g01570	4.00E–24	Gibberellin response modulator (RGA1) / gibberellin-responsive modulator identical to GB:Y11336, member of SCARECROW family
353821	*Nuphar*	2	6,625	3	4	At4g00150	6.00E–51	Scarecrow-like transcription factor 6 (SCL6)
355941	*Nuphar*	1	6,625	3	4	At2g45160	1.00E–10	Scarecrow transcription factor family protein
357635	*Nuphar*	1				At3g03450	1.00E–19	Gibberellin response modulator, putative / gibberellin-responsive modulator, putative similar to GAI (GI:2569938), RGA1 (GB:AAC67333) and RGA2 (GI:2339980) [*Arabidopsis thaliana*]

Table 1. Continued.

UNI ID	Taxon	# ESTS	INPAR	#ATH	#OSA	BEST ATH	EVALUE	Description
YABBY (tribe 807)								
200518	*Amborella*	1	7,720	2	3	At2g45190	4.00E–55	Axial regulator YABBY1 (YABBY1) / abnormal floral organs protein (AFO) / filamentous flower protein (FIL)
352904	*Nuphar*	2	7,720	2	3	At2g45190	4.00E–53	Axial regulator YABBY1 (YABBY1) / abnormal floral organs protein (AFO) / filamentous flower protein (FIL)
353882	*Nuphar*	6	7,720	2	3	At2g45190	3.00E–57	Axial regulator YABBY1 (YABBY1) / abnormal floral organs protein (AFO) / filamentous flower protein (FIL)
195711	*Amborella*	2	8,500	1	2	At2g26580	2.00E–34	Plant-specific transcription factor YABBY family protein contains Pfam profile: PF04690
353063	*Nuphar*	4	8,500	1	2	At2g26580	2.00E–40	Plant-specific transcription factor YABBY family protein contains Pfam profile: PF04690

In our experience, INPARANOID clusters are typically, but not always, nested within TribeMCL clusters (e.g., see Table 1; and the Appendix in Taxon online issue).

Phylogenetic analysis using a single copy nuclear gene. — To illustrate the utility of the *Amborella* and *Nuphar* ESTs in phylogenetic analysis, we chose a single-copy nuclear gene for which sequences are available from both *Amborella* and *Nuphar*, and also for a diversity of eudicot and monocot species. Clones for ESTs from this gene were sequenced on both strands to obtain a high-quality finished sequence for phylogenetic analysis. Internal primers were designed using MacVector (Accelrys, San Diego, California) when necessary. Additional sequences for phylogenetic analysis were obtained from the TIGR gene indices (Lee & al., 2005) and additional FGP unigenes from PGN (http://pgn.cornell.edu).

Amino acid sequences were aligned using MUSCLE (Edgar, 2004), and nucleotide alignments were created by forcing the DNA sequence onto the protein alignment using CLUSTAL W (Higgins & al., 1994). Alignments were manually inspected and adjusted. Nucleotide alignments were used to produce phylogenies using maximum parsimony (MP), neighbor-joining (NJ), and maximum likelihood (ML). Appropriate models of sequence evolution for NJ and ML analyses were determined using MODELTEST (Posada & Crandall, 1998). Phylogenetic analyses were performed using PAUP 4.0b10 (Swofford, 2001). All MP and ML analyses were based on a heuristic search with 10 random sequence additions and tree bisection-reconnection branch swapping. Bootstrapping was also performed with 1,000 replicates for MP and NJ and 250 replicates for ML analyses using a heuristic search with random sequence addition.

RESULTS

Description of *Amborella* and *Nuphar* EST sequences. — A general description of the *Amborella* and *Nuphar* EST sets is provided in Albert & al. (2005). From these species, floral EST sequencing yielded a total of 8,489 and 8,442 ESTs from *Amborella* and *Nuphar*, respectively (Albert & al., 2005). Clustering these ESTs to combine sequences putatively derived from the same gene reduced these to 6,099 and 6,205 unigene (putative gene) sequences, respectively (Albert & al., 2005). Of the 6,099 *Amborella* unigenes, 3,970 were sorted into a PlantTribe using BLAST, and 3,478 have a BLAST best hit (with e-value greater than 10^{-5}) into an *Arabidopsis* and rice INPARANOID group. Of the 6,205 *Nuphar* Unigenes, 4,445 belong to a PlantTribe, and 3,898 were classified using BLAST into an *Arabidopsis* and rice INPARANOID group (Appendix in Taxon online issue). By comparing the non-redundant set of INPARANOID groups identified in *Amborella* and/or *Nuphar*, we estimated that there was a minimal set of 4,572 genes in the ancestral angiosperm that have orthologs in *Arabidopsis* and rice (Fig. 1D; Appendix in Taxon online issue). In addition, by comparing the non-redundant set of PlantTribes identified in *Amborella* and/or *Nuphar*, we estimated that of those gene families that existed in the common ancestor of all angiosperms, a minimal set of 2,857 gene families has been retained in both monocots and eudicots (Fig. 1D). The putative functional categories of the non-redundant set of INPARANOID groups from *Amborella* and *Nuphar* (ancestral orthologs of genes present in *Arabidopsis* and rice) were deduced using the Gene Ontology (GO) information for *Arabidopsis* best BLAST hits (Fig. 1A–C). Because Tribes approximate gene families and INPARANOID groups approximate orthologous groups present in both monocot (rice) and eudicot (*Arabidopsis*) genomes, their presence in the basal angiosperms could be used to root a gene tree or infer anestral characteristics of that group of genes. MADS-box genes are critical floral regulators (Becker & Theissen, 2003; Irish, 2003; Zahn & al., 2006b), and their evolution has been analyzed, including sequences from *Amborella* and *Nuphar* (Becker & Theissen, 2003; Irish, 2003; Kim & al., 2004, 2005; Zahn & al., 2005a, b). In addition, several other families with important plant and floral developmental function were identified in the EST sets (Table 1). Members of the *AP2* (Reichmann & Meyerowitz, 1998; Kim & al., 2006) and *NAC* families (Olsen

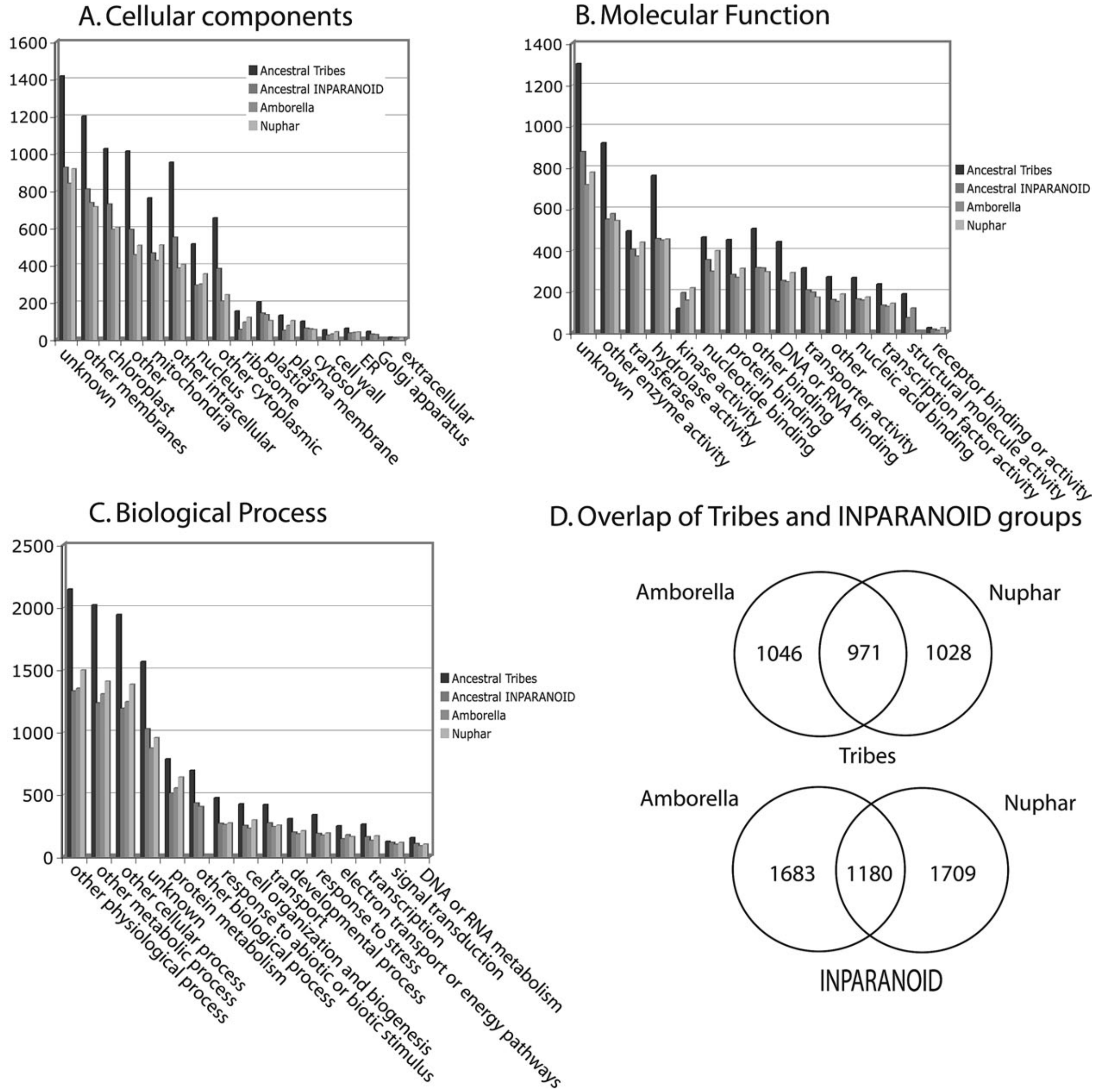

Fig. 1. Characterization of the *Amborella* and *Nuphar* ESTs and insights into the ancestral angiosperm. The classification of the nonredundant set of *Amborella* and/or *Nuphar* Tribe and INPARANOID groups into slim Gene Ontology (GO) categories is shown in Fig. 1A–C. The best BLAST hit into *Arabidopsis* was used to classify the *Amborella* and *Nuphar* unigenes into slim GO categories. Each histogram provides four values per functional category, based on the presence of at least one gene from *Amborella* and/or *Nuphar* in a plant tribe ("Ancestral Tribes") or INPARANOID group ("Ancestral INPARANOID"). INPARANOID groups with at least one *Amborella* or *Nuphar* gene, irrespective of the other taxon, are counted as "*Amborella*" or "*Nuphar*". The number of *Amborella* and *Nuphar* Unigenes sorted into INPARANOID groups and PlantTribes, along with overlap is shown in 1D.

& al., 2005) are involved in floral development, among other functions. Homologs were also found for several genes involved in RNA processing and silencing such as members of the *ARGONAUTE*, *HEN1*, *HUA1*, *HUA2*, and other families; many of these regulate genes involved in floral and developmental function (Ma, 2005; Zahn & al., 2006b). Many genes that are homologous to those involved in hormone signaling such as *PINOID*, *PIN1*, *BRI1*, *ARFs*, *SCARECROW*, *IAAs*, *ERFs* and *ETR1* (Gazzarrini & McCourt, 2003) were also detected among the *Amborella* and *Nuphar* unigenes. Several genes encoding proteins that may function in seed and embryo development were also identified, including *LEA*, *PcG* (polycomb-group), endo-1,4-beta-glucanase and members of the *YABBY* family (Eshed & al., 2001; Yamada & al., 2001, 2004; Chanvivattana & al., 2004; Ingouff & al., 2005). The identification of homologs of known regulators of development and signal responses suggests that many of these processes are conserved in basal angiosperms. Some *Amborella* or *Nuphar* unigenes were assigned to Tribes (gene families) but not to any INPARANOID group with probability stronger than 10^{-5}. These could represent novel gene lineages in these basal angiosperms, or be a reflection of assignment uncertainty for unigenes that are less than full length.

In addition to the identification of putative homologs of genes with known regulatory functions, other *Amborella* and *Nuphar* unigenes were found to encode proteins that contain domains known to be important for development, including the DNA-binding homeodomain, MYB, bZIP, bHLH, and WRKY domains, as well as protein-protein and other interaction motifs WD-40, F-box, zinc fingers and zinc knuckles. Moreover, *Amborella* and *Nuphar* genes might also be involved in cell-cell signaling such as the putative receptors containing an LRR domain, which might function as receptors for plant peptides, including members of the CLAVATA3 family (Ito & al., 2006).

There are 353 *Amborella* and 342 *Nuphar* unigenes with a best BLAST hit (threshold of 10^{-5}) to one of the 1574 *Arabidopsis* and rice 1:1 PlantTribes that contain a single member from *Arabidopsis* and rice (Appendix in Taxon online issue). These 1 : 1 PlantTribes represent gene families that have not expanded despite the genome duplications that likely occurred during angiosperm history, including those on the specific lineages leading to *Arabidopsis* (Vision & al., 2000; Simillion & al., 2002; Vandepoele & al., 2002) and rice (Paterson & al., 2004; Yu, 2005). There are 100 pairs of *Amborella* and *Nuphar* unigenes that were sorted by BLAST to these 1 : 1 PlantTribes.

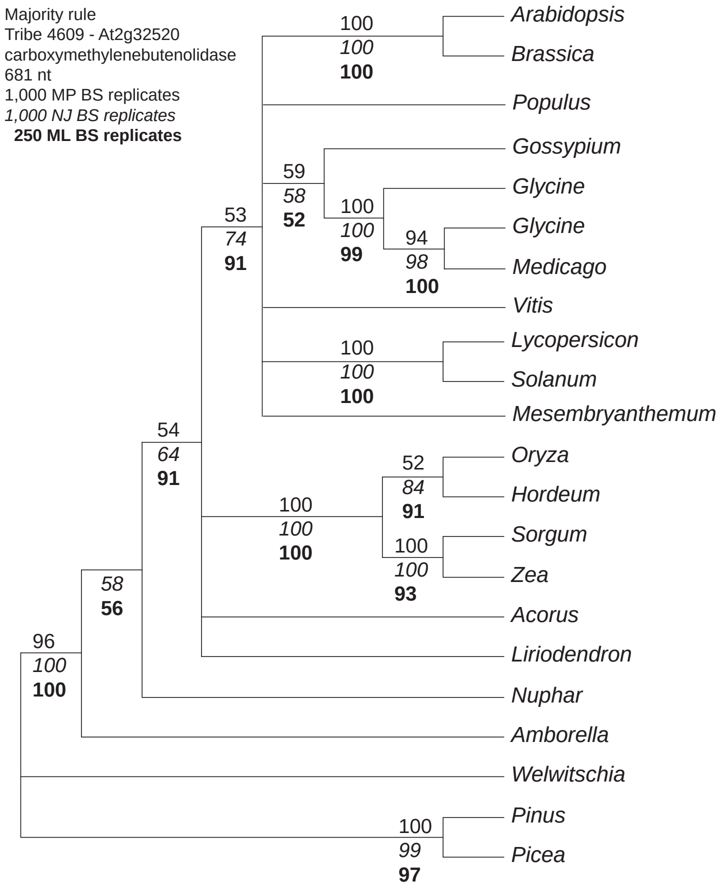

Fig. 2. Using single copy nuclear genes for organismal phylogeny. The gene used to construct the tree shown, carboxymethylenebutenolidase, is an example of a single copy nuclear gene identified using a comparative genomic approach to the proteomes of *Arabidopsis* and rice. Unigenes sampled from throughout the angiosperms were used to illustrate their potential in elucidating organismal phylogeny as well as the conservation of single or low copy throughout the angiosperms, in spite of repeated rounds of duplication in the angiosperm tree of life, as inferred by other studies (Blanc & Wolfe, 2004; Schlueter & al., 2004; Lee & al., 2005; Cui & al., 2006). While the information contained in this one gene is not sufficient to provide an entirely resolved tree, especially at the base of the angiosperms, it provides resolution similar to other single-gene analyses from other markers.

These nuclear protein-coding genes have the potential to be used for phylogenetic analysis across all angiosperms, as illustrated in Fig. 2. However, current sequence data from a single nuclear gene are not sufficient for resolving the branching order of *Amborella* and *Nuphar* or several internal nodes (Fig. 2; data not shown for other genes).

DISCUSSION

Utility of *Amborella* and *Nuphar* ESTs in comparative sequence analyses. — *Amborella* and the water lilies (Nymphaeales) either form a clade, sister to all other extant flowering plant lineages, or *Amborella* and then the water lilies are successive sisters to all other angiosperms (Mathews & Donoghue, 1999; Parkinson & al., 1999; Qiu & al., 1999; Soltis & al., 1999; Barkman & al., 2000; Graham & Olmstead, 2000; Zanis & al., 2002; Borsch & al., 2003; Hilu & al., 2003; Stefanovic & al., 2004; Leebens-Mack & al., 2005). The EST sequences described in this paper are being mined for genes that may allow us to resolve the positions of the *Amborella* and water lily lineages at the base of the angiosperm phylogeny (see discussion of 1 : 1 PlantTribes, below). Regardless of their relationship to each other relative to the rest of the angiosperms, however, the placement of *Amborella* and *Nuphar* genes in gene family phylogenies can elucidate duplication events early in angiosperm history. The placement of *Amborella* or *Nuphar* sequences in gene-family phylogenies can reveal whether duplication events predate or postdate the most recent common ancestor of *Amborella*, the water lilies, and all other angiosperms by the identification of duplicated gene clades and whether *Amborella* or *Nuphar* sequences are located within the clade (duplication prior to the diversification of the basal angiosperms) or are placed sister to a set of clades (duplication after the diversification of the basal angiosperms). Further, meta-analyses of gene families can be used to test hypotheses of when gene and whole-genome duplication events occurred. More refined molecular evolutionary analyses and expanded sequence datasets from basal angiosperms may be able to test the hypothesis that gene and genome duplications spawned the evolutionary innovations associated with the early radiation of flowering plants (Darwin, 1903).

The MADS-box transcription factor gene family has been the focus of much research on the genetic basis of floral evolution (Zahn & al., 2006b). Except for *AP2*, *Arabidopsis* genes specifying the genetically defined functions in the classical ABC model of floral development (Coen & Meyerowitz, 1991) are MIKC-type MADS-box genes: *APETALA1* (A class), *PISTILLATA* and *APETALA3* (B class, *GLOBOSA* and *DEFICIENS* in *Antirrhinum*), and *AGAMOUS* (C class; *PLENA* in *Antirrhinum*). According to the quartet model (Theissen & Saedler, 2001), these ABC-function MADS-domain proteins interact with each other and with the MADS-domain SEPALLATA proteins to form quaternary complexes (Honma & Goto, 2001) that regulate specification of floral organ identity. These and other MIKC-type MADS-box genes have been classified based on clade membership (Becker & Theissen, 2003). The placement of *Amborella* and water lily homologs in phylogenetic analyses of *PISTILLATA* + *APETALA3* (Aoki & al., 2004; Kim & al., 2004), *AGAMOUS* (Kramer & al., 2004; Zahn & al., 2006a), and *SEPALLATA* (Zahn & al., 2005a) clades reveal gene duplications predating the diversification of the angiosperm crown group. Given the role of these genes in floral development, these duplication events, particularly of the *SEPALLATA* subfamily, are hypothesized to have played a role in the origin of the flower (Zahn & al., 2005a). Whether duplication events in the *PISTILLATA* + *APETALA3*, *AGAMOUS*, and *SEPALLATA* clades occurred simultaneously through a single ancient whole-genome duplication (Buzgo & al., 2005) remains an open question.

Phylogenies of nuclear genes also provide a means of assessing the possible acquisition of functional nuclear-encoded genes through horizontal transfer, as has been proposed for mitochondrial sequences in *Amborella*, but not water lilies (Bergthorsson & al., 2004). In published gene family phylogenies to date, including those for phytochromes (Mathews & Donoghue, 1999), numerous MADS-box genes (Aoki & al., 2004; Kim & al., 2004; Zahn & al., 2005a), the *AP2* family (Kim & al., 2006), RNA polymerase II (Nickerson & Drouin, 2004), *YABBY* genes (Fourquin & al., 2005), *Amborella* and water lilies are found in a phylogenetic position consistent with a basal position among extant angiosperm lineages. This is true as well in the tree presented in this paper. This observation is consistent with vertical (standard) inheritance of each of the genes examined above and highlights the very different dynamic observed for *mitochondrial* sequences in *Amborella*. The mechanism by which apparently xenologous sequences are taken up and then incorporated into the mitochondrial genome of this species remains a fundamental problem in plant genetics and genomics (Bergthorsson & al., 2004). However, the evidence at this point suggests that these dynamics may not extend to the expressed nuclear genes that have been studied thus far, as well as additional single-copy nuclear genes we have examined (data not shown).

Detecting ancient genome duplications. — Studies in *Arabidopsis* indicate that there were at least two and possibly three or more whole genome duplications in the evolutionary history of *Arabidopsis* (Vision & al., 2000; Blanc & al., 2003; Bowers & al., 2003). Additional studies utilizing EST sequences for the identification of genome duplication have inferred whole genome duplications throughout the evolutionary history of diverse angiosperms (Blanc & Wolfe, 2004; Schlueter & al., 2004; Cui & al., 2006).

Recent work using ESTs from *Amborella* and *Nuphar* indicated that there was a concentration of duplicate gene pairs consistent with ancient genome duplication in the *Nuphar* lineage, but no detectable signal of a similar ancient genome duplication event in *Amborella* (Cui & al., 2006). This provides evidence for an ancient paleopolyploidy event shared by all angiosperms except *Amborella*.

Single-copy nuclear genes for organismal phylogeny. — As a result of pervasive gene duplication, most nuclear genes in angiosperms are part of gene families. This has often deterred researchers from using nuclear genes (other than RNA genes) in phylogenetic reconstruction in angiosperms because of the difficulty of isolating all members of a gene family in each taxon for accurate phylogenetic reconstruction (e.g., Sang, 2002; Crawford & Mort, 2004; Small & al., 2004; Hughes & al., 2006). In addition, there is evidence from yeast that phylogenies based on paralogous genes with asymmetric divergence are misrepresentations of the organismal phylogeny (Fares & al., 2005). These difficulties in using nuclear genes in phylogeny reconstruction are relieved by adopting a high-throughput approach for the identification of single- or low-copy nuclear genes. Using PlantTribes, we have identified 1,574 putative single- or low-copy nuclear genes that contain only one member from *Arabidopsis* and only one member from rice. By adding unigenes from a wide variety of flowering plants to these 1 : 1 PlantTribes, we can identify putative single-copy gene families and construct multiple sequence alignments for phylogenetic analysis. Including unigenes from basal lineages aids in the identification of single- or very low-copy nuclear genes that would be widely distributed among all flowering plants and permits using sequences from *Amborella* and *Nuphar* as outgroups for angiosperm-wide analysis if corresponding sequence data from gymnosperms are missing. Although individual gene trees do not provide sufficient resolution across the entire tree, we hypothesize that these single-copy genes will be valuable phylogenetic markers, especially given that we already have sequences from the basal angiosperms for rooting the tree (Fig. 2). The addition of basal taxa improves the ability to properly root the angiosperm phylogeny (Leebens-Mack & al., 2005).

The applications featured in this paper reflect the many uses of *Amborella trichopoda* and *Nuphar advena* ESTs and the importance of these organisms in the study of the evolution of flowering plants. The genes identified by the ESTs suggest possible molecular bases for the evolution of floral structure and development. Future work will develop comprehensive search strategies for finding genes in EST sets that may be most useful for organismal phylogeny reconstruction and comparative sequence analysis, using the basal position of these two lineages to elucidate the mysteries of the ancestral angiosperm and the origin of the flower.

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Appendix. For explanation see Table 1.

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
353673	2	0	1144	1825	108	2	1	At3g13530	2,00E-21	68416.m01701 MAP3K epsilon protein kinase identical to MAP3K epsilon protein kinase [Arabidopsis thaliana] gi|3549652|emb|CAA12272
356026	1	0	1144	1825	108	2	1	At3g13530	5,00E-42	68416.m01701 MAP3K epsilon protein kinase identical to MAP3K epsilon protein kinase [Arabidopsis thaliana] gi|3549652|emb|CAA12272
357204	1	0	1144	1825	230	1	1	At2g26330	6,00E-39	68415.m03159 leucine-rich repeat protein kinase, putative (ERECTA) identical to uncharacterized receptor protein kinase ERECTA [Arabidopsis thaliana] gi|1389566|dbj|BAA11869; contains Pfam domains PF00560: Leucine Rich Repeat and PF00069: Protein kinase domain
358137	1	0	1144	1825	233	1	1	At3g17850	2,00E-78	68416.m02275 protein kinase, putative similar to IRE (incomplete root hair elongation) [Arabidopsis thaliana] gi|6729346|dbj|BAA89783; contains protein kinase domain Pfam:PF00069
357371	1	0	1144	1825	249	2	2	At3g49670	9,00E-29	68416.m05429 leucine-rich repeat transmembrane protein kinase, putative CLAVATA1 receptor kinase, Arabidopsis thaliana, EMBL:ATU96879
355967	1	0	1144	1825	317	2	2	At4g26540	4,00E-15	68417.m03823 protein kinase family protein Three false introns were added with non-consensus splice sites to circumenvent frameshifts likely due to sequencing errors; this is extremely unusual and is under investigation.
355376	1	0	1144	1825	404	1	2	At3g45780	1,00E-09	68416.m04953 protein kinase / nonphototropic hypocotyl protein 1 (NPH1) / phototropin identical to SP|O48963 Nonphototropic hypocotyl protein 1 (EC 2.7.1.37) (Phototropin) {Arabidopsis thaliana}, cDNA nonphototropic hypocotyl 1 (NPH1) GI:2832240; contains Pfam profiles PF00069:Protein kinase domain and PF00785:PAC motif
357366	1	0	1144	1825	404	1	2	At3g45780	2,00E-115	68416.m04953 protein kinase / nonphototropic hypocotyl protein 1 (NPH1) / phototropin identical to SP|O48963 Nonphototropic hypocotyl protein 1 (EC 2.7.1.37) (Phototropin) {Arabidopsis thaliana}, cDNA nonphototropic hypocotyl 1 (NPH1) GI:2832240; contains Pfam profiles PF00069:Protein kinase domain and PF00785:PAC motif
357868	1	0	1144	1825	414	1	1	At1g28440	6,00E-53	68414.m03496 leucine-rich repeat transmembrane protein kinase, putative similar to receptor kinase GI:4105699 from [Arabidopsis thaliana]

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
353955	4	0	1144	1825	430	2	1	At1g73460	9,00E-141	68414.m08504 protein kinase family protein contains protein kinase domain Pfam:PF00069
354711	1	0	1144	1825	455	1	1	At4g39400	2,00E-26	68417.m05577 brassinosteroid insensitive 1 (BRI1) identical to GI:2392895
359820	1	0	1144	1825	455	1	1	At4g39400	2,00E-30	68417.m05577 brassinosteroid insensitive 1 (BRI1) identical to GI:2392895
353445	2	0	1144	1825	519	1	1	At1g66150	1,00E-45	68414.m07508 leucine-rich repeat protein kinase, putative (TMK1) identical to protein kinase TMK1 gi|166888|gb|AAA32876, SP|P43298 Putative receptor protein kinase TMK1 precursor (EC 2.7.1.-) {Arabidopsis thaliana}
359599	1	0	1144	1825	590	1	2	At3g02130	5,00E-40	68416.m00180 leucine-rich repeat transmembrane protein kinase, putative contains Pfam profile: Eukaryotic protein kinase domain
354263	3	0	1144	1825	630	4	8	At1g56140	2,00E-124	68414.m06446 leucine-rich repeat family protein / protein kinase family protein contains Pfam domains PF00560: Leucine Rich Repeat and PF00069: Protein kinase domain
359539	1	0	1144	1825	653	1	1	At2g02220	3,00E-94	68415.m00159 leucine-rich repeat transmembrane protein kinase, putative
353750	2	0	1144	1825	668	1	1	At5g10020	1,00E-49	68418.m01161 leucine-rich repeat transmembrane protein kinase, putative receptor-like protein kinase ERECTA, Arabidopsis thaliana, EMBL:AC004484
358664	1	0	1144	1825	717	1	2	At1g79620	1,00E-46	68414.m09283 leucine-rich repeat transmembrane protein kinase, putative similar to receptor protein kinase GI:1389566 from [Arabidopsis thaliana]
355841	1	0	1144	1825	740	2	2	At1g73080	8,00E-30	68414.m08450 leucine-rich repeat transmembrane protein kinase, putative similar to receptor protein kinase GI:1389566 from [Arabidopsis thaliana]
356445	1	0	1144	1825	762	1	2	At3g61130	4,00E-28	68416.m06841 glycosyl transferase family 8 protein contains Pfam profile: PF01501 glycosyl transferase family 8
353174	3	0	1144	1825	847	2	2	At3g13690	9,00E-131	68416.m01729 protein kinase family protein contains protein kinase domain, Pfam:PF00069
355064	1	0	1144	1825	872	2	2	At3g46290	5,00E-08	68416.m05010 protein kinase, putative similar to receptor-like protein kinase [Catharanthus roseus] gi|1644291|emb|CAA97692
352969	3	0	1144	1825	874	1	1	At3g28040	1,00E-70	68416.m03500 leucine-rich repeat transmembrane protein kinase, putative contains Pfam profiles: PF00560 leucine rich repeat, PF00069 eukaryotic protein kinase domain

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
353158	2	0	1144	1825	1016	2	2	At5g10290	2,00E-114	68418.m01194 leucine-rich repeat family protein / protein kinase family protein contains Pfam domains PF00560: Leucine Rich Repeat and PF00069: Protein kinase domain
355879	1	0	1144	1825	1016	2	2	At5g10290	2,00E-30	68418.m01194 leucine-rich repeat family protein / protein kinase family protein contains Pfam domains PF00560: Leucine Rich Repeat and PF00069: Protein kinase domain
359348	1	0	1144	1825	1075	1	1	At3g50530	5,00E-78	68416.m05526 calcium-dependent protein kinase, putative / CDPK, putative similar to calcium/calmodulin-dependent protein kinase CaMK3 [Nicotiana tabacum] gi|16904226|gb|AAL30820
358688	1	0	1144	1825	1178	2	2	At5g12180	5,00E-77	68418.m01429 calcium-dependent protein kinase, putative / CDPK, putative
355203	1	0	1144	1825	1180	1	1	At1g50240	1,00E-53	68414.m05633 armadillo/beta-catenin repeat family protein contains Pfam profile: PF00514 armadillo/beta-catenin-like repeat
353707	2	0	1144	1825	1200	2	1	At1g31420	6,00E-43	68414.m03848 leucine-rich repeat transmembrane protein kinase, putative contains Pfam profile: PF00069: Eukaryotic protein kinase domain
358302	1	0	1144	1825	1200	2	1	At2g35620	7,00E-29	68415.m04368 leucine-rich repeat transmembrane protein kinase, putative similar to somatic embryogenesis receptor-like kinase 1 (SERK1) [Zea mays] gi|13897318|emb|CAC37640; contains leucine rich repeat (LRR) domains, Pfam:PF00560; contains protein kinase domain, Pfam:PF00069
357134	1	0	1144	1825	1207	1	2	At2g19130	2,00E-40	68415.m02233 S-locus lectin protein kinase family protein contains Pfam domains PF00954: S-locus glycoprotein family, PF00069: Protein kinase domain and PF01453: Lectin (probable mannose binding)
355732	1	0	1144	1825	1240	1	1	At5g57610	2,00E-31	68418.m07197 protein kinase family protein similar to protein kinase [Glycine max] GI:170047, MAP3K delta-1 protein kinase [Arabidopsis thaliana] GI:2253010; contains Pfam profile: PF00069 Eukaryotic protein kinase domain
359656	1	0	1144	1825	1250	1	1	At1g16900	8,00E-80	68414.m02047 curculin-like (mannose-binding) lectin family protein very low similarity to Ser Thr protein kinase GI:2598067 from (Zea mays); contains Pfam lectin (probable mannose binding) domain PF01453

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
357194	1	0	1144	1825	1266	2	1	At5g12480	7,00E-34	68418.m01466 calmodulin-domain protein kinase isoform 7 (CPK7) identical to calmodulin-domain protein kinase CDPK isoform 7 [Arabidopsis thaliana] gi|1399277|gb|AAB03247
358725	1	0	1144	1825	1276	1	1	At3g51850	4,00E-60	68416.m05686 calcium-dependent protein kinase, putative / CDPK, putative similar to calcium-dependent protein kinase [Arabidopsis thaliana] gi|836942|gb|AAA67655; contains protein kinase domain, Pfam:PF00069; contains EF hand domain (calcium-binding EF-hand), Pfam:PF00036, INTERPRO:IPR002048
358838	1	0	1144	1825	1276	1	1	At3g51850	4,00E-41	68416.m05686 calcium-dependent protein kinase, putative / CDPK, putative similar to calcium-dependent protein kinase [Arabidopsis thaliana] gi|836942|gb|AAA67655; contains protein kinase domain, Pfam:PF00069; contains EF hand domain (calcium-binding EF-hand), Pfam:PF00036, INTERPRO:IPR002048
357797	1	0	1144	1825	1277	2	2	At1g53730	1,00E-66	68414.m06114 leucine-rich repeat transmembrane protein kinase, putative similar to GI:3360289 from [Zea mays] (Plant Mol. Biol. 37 (5), 749-761 (1998))
353588	2	0	1144	1825	1311	1	2	At3g03770	1,00E-30	68416.m00383 leucine-rich repeat transmembrane protein kinase, putative may contain C-terminal ser/thr protein kinase domain, similar to serine/threonine protein kinase Pto GB:AAB47421 [Lycopersicon esculentum]
355961	1	0	1144	1825	1311	1	2	At3g03770	7,00E-28	68416.m00383 leucine-rich repeat transmembrane protein kinase, putative may contain C-terminal ser/thr protein kinase domain, similar to serine/threonine protein kinase Pto GB:AAB47421 [Lycopersicon esculentum]
358390	1	0	1144	1825	1311	1	2	At3g03770	1,00E-50	68416.m00383 leucine-rich repeat transmembrane protein kinase, putative may contain C-terminal ser/thr protein kinase domain, similar to serine/threonine protein kinase Pto GB:AAB47421 [Lycopersicon esculentum]
354548	1	0	1144	1825	1354	1	1	At1g28340	2,00E-60	68414.m03481 leucine-rich repeat family protein contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001611; contains some similarity to receptor-like protein kinases
355021	1	0	1144	1825	1354	1	1	At1g28340	4,00E-77	68414.m03481 leucine-rich repeat family protein contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001611; contains some similarity to receptor-like protein kinases

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
353522	2	0	1144	1825	1376	2	2	At4g14350	4,00E-50	68417.m02211 protein kinase family protein contains similarity to Swiss-Prot:O13310 serine/threonine-protein kinase orb6 [Schizosaccharomyces pombe]
355099	1	0	1144	1825	1384	2	1	At2g01210	4,00E-61	68415.m00033 leucine-rich repeat transmembrane protein kinase, putative
358685	1	0	1144	1825	1397	1	2	At4g23650	3,00E-20	68417.m03405 calcium-dependent protein kinase, putative / CDPK, putative similar to calcium-dependent protein kinase [Marchantia polymorpha] gi|5162877|dbj|BAA81748; contains protein kinase domain, Pfam:PF00069; contains EF hand domain (calcium-binding EF-hand), Pfam:PF00036, INTERPRO:IPR002048
354863	1	0	1144	1825	1403	1	3	At5g47750	2,00E-07	68418.m05899 protein kinase, putative similar to protein kinase G11A [Oryza sativa] SWISS-PROT:P47997
354962	1	0	1144	1825	1403	1	3	At5g47750	8,00E-70	68418.m05899 protein kinase, putative similar to protein kinase G11A [Oryza sativa] SWISS-PROT:P47997
359286	1	0	1144	1825	1403	1	3	At5g47750	8,00E-70	68418.m05899 protein kinase, putative similar to protein kinase G11A [Oryza sativa] SWISS-PROT:P47997
355790	1	0	1144	1825	1407	1	1	At4g35230	1,00E-73	68417.m05007 protein kinase family protein contains protein kinase domain, Pfam:PF00069
357186	1	0	1144	1825	1448	1	1	At5g46570	7,00E-09	68418.m05734 protein kinase family protein contains protein kinase domain, Pfam:PF00069
359435	1	0	1144	1825	1448	1	1	At5g46570	2,00E-63	68418.m05734 protein kinase family protein contains protein kinase domain, Pfam:PF00069
359738	1	0	1144	1825	1459	3	1	At4g21940	3,00E-42	68417.m03174 calcium-dependent protein kinase, putative / CDPK, putative similar to calcium-dependent protein kinase [Nicotiana tabacum] gi|3283996|gb|AAC25423
356932	1	0	1144	1825	1518	1	1	At5g62710	3,00E-68	68418.m07869 leucine-rich repeat family protein / protein kinase family protein contains protein kinase domain, Pfam:PF00069; contains leucine-rich repeats, Pfam:PF00560
354101	4	0	1144	1825	1568	2	2	At4g09570	9,00E-69	68417.m01575 calcium-dependent protein kinase, putative / CDPK, putative similar to calcium-dependent protein kinase [Arabidopsis thaliana] gi|604881|dbj|BAA04830; contains protein kinase domain, Pfam:PF00069; contains EF hand domain (calcium-binding EF-hand), Pfam:PF00036, INTERPRO:IPR002048
353223	2	0	1144	1825	1599	1	2	At5g58300	2,00E-42	68418.m07298 leucine-rich repeat transmembrane protein kinase, putative

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
353478	2	0	1144	1825	1668	2	1	At5g26751	9,00E-85	68418.m03187 shaggy-related protein kinase alpha / ASK-alpha (ASK1) identical to shaggy-related protein kinase alpha SP:P43288 GI:460832 from [Arabidopsis thaliana]
354260	3	0	1144	1825	1714	1	1	At1g69220	3,00E-44	68414.m07926 serine/threonine protein kinase, putative identical to serine/threonine kinase [Arabidopsis thaliana] gi|2352084|gb|AAB68776
353704	3	0	1144	1825	1747	1	1	At5g14720	2,00E-26	68418.m01727 protein kinase family protein contains eukaryotic protein kinase domain, INTERPRO:IPR000719
357626	1	0	1144	1825	1747	1	1	At5g14720	2,00E-06	68418.m01727 protein kinase family protein contains eukaryotic protein kinase domain, INTERPRO:IPR000719
358379	1	0	1144	1825	1810	1	2	At1g54610	2,00E-65	68414.m06228 protein kinase family protein contains Pfam domain, PF00069: Protein kinase domain
356568	1	0	1144	1825	1819	1	1	At1g30270	5,00E-39	68414.m03702 CBL-interacting protein kinase 23 (CIPK23) identical to CBL-interacting protein kinase 23 [Arabidopsis thaliana] gi|14486386|gb|AAK61494
358765	1	0	1144	1825	1819	1	1	At1g30270	5,00E-86	68414.m03702 CBL-interacting protein kinase 23 (CIPK23) identical to CBL-interacting protein kinase 23 [Arabidopsis thaliana] gi|14486386|gb|AAK61494
359107	1	0	1144	1825	1819	1	1	At1g30270	4,00E-19	68414.m03702 CBL-interacting protein kinase 23 (CIPK23) identical to CBL-interacting protein kinase 23 [Arabidopsis thaliana] gi|14486386|gb|AAK61494
358495	1	0	1144	1825	1833	1	2	At3g44200	2,00E-19	68416.m04739 protein kinase family protein contains protein kinase domain, Pfam:PF00069; contains serine/threonine protein kinase domain, INTERPRO:IPR002290
356194	1	0	1144	1825	1909	1	2	At5g48380	6,00E-54	68418.m05978 leucine-rich repeat family protein / protein kinase family protein contains protein kinase domain, Pfam:PF00069; contains leucine-rich repeats, Pfam:PF00560
357724	1	0	1144	1825	1910	1	1	At3g53570	5,00E-33	68416.m05915 protein kinase (AFC1) (AME2) identical to protein kinase AFC1 (EC 2.7.1.-) [Arabidopsis thaliana]
353767	2	0	1144	1825	1927	2	1	At1g57870	2,00E-28	68414.m06566 shaggy-related protein kinase kappa, putative / ASK-kappa, putative similar to shaggy-related protein kinase kappa SP:Q39019 GI:717180 from [Arabidopsis thaliana]
354586	1	0	1144	1825	1927	2	1	At1g57870	1,00E-12	68414.m06566 shaggy-related protein kinase kappa, putative / ASK-kappa, putative similar to shaggy-related protein kinase kappa SP:Q39019 GI:717180 from [Arabidopsis thaliana]

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
358733	1	0	1144	1825	1927	2	1	At1g09840	4,00E-97	68414.m01108 shaggy-related protein kinase kappa / ASK-kappa (ASK10) identical to shaggy-related protein kinase kappa SP:Q39019 GI:717180 from [Arabidopsis thaliana]
354293	3	0	1144	1825	1928	2	1	At3g25140	9,00E-94	68416.m03139 glycosyl transferase family 8 protein contains Pfam profile: PF01501 glycosyl transferase family 8
355566	1	0	1144	1825	2013	1	1	At3g10540	1,00E-15	68416.m01265 3-phosphoinositide-dependent protein kinase, putative similar to 3-phosphoinositide-dependent protein kinase-1 [Oryza sativa] gi|5001830|gb|AAD37166
353735	5	0	1144	1825	2029	2	1	At2g30980	2,00E-118	68415.m03778 shaggy-related protein kinase delta / ASK-delta / ASK-dzeta (ASK4) identical to shaggy-related protein kinase delta (ASK-delta) (ASK- dzeta) [Arabidopsis thaliana] SWISS-PROT:Q39010
355577	1	0	1144	1825	2073	1	1	At3g24550	7,00E-26	68416.m03083 protein kinase family protein contains Pfam domain PF00069: Protein kinase domain
353925	2	0	1144	1825	2083	1	2	At5g18610	1,00E-05	68418.m02203 protein kinase family protein contains eukaryotic protein kinase domain, PROSITE:PS00107
357104	1	0	1144	1825	2099	1	1	At2g43790	2,00E-102	68415.m05443 mitogen-activated protein kinase, putative / MAPK, putative (MPK6) identical to mitogen-activated protein kinase homolog 6 (AtMPK6)[Arabidopsis thaliana] SWISS-PROT:Q39026; PMID:12119167
360081	1	0	1144	1825	2099	1	1	At2g43790	7,00E-50	68415.m05443 mitogen-activated protein kinase, putative / MAPK, putative (MPK6) identical to mitogen-activated protein kinase homolog 6 (AtMPK6)[Arabidopsis thaliana] SWISS-PROT:Q39026; PMID:12119167
356891	1	0	1144	1825	2114	5	1	At5g49470	3,00E-57	68418.m06121 protein kinase family protein contains Pfam domain, PF00069: Protein kinase domain
354475	3	0	1144	1825	2163	1	1	At1g52310	5,00E-135	68414.m05902 protein kinase family protein / C-type lectin domain-containing protein contains protein kinase domain, Pfam:PF00069, PF00059 Lectin C-type domain
358769	1	0	1144	1825	2185	1	1	At3g04910	8,00E-32	68416.m00533 protein kinase family protein contains protein kinase domain, Pfam:PF00069
359304	1	0	1144	1825	2185	1	1	At3g04910	7,00E-25	68416.m00533 protein kinase family protein contains protein kinase domain, Pfam:PF00069
355526	1	0	1144	1825	2198	1	1	At5g40440	1,00E-41	68418.m04904 mitogen-activated protein kinase kinase (MAPKK), putative (MKK3) similar to NPK2 [Nicotiana tabacum] gi|862342|dbj|BAA06731; mitogen-activated protein kinase kinase (MAPKK) family, PMID:12119167

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
357451	1	0	1144	1825	2222	1	1	At5g06940	2,00E-39	68418.m00784 leucine-rich repeat family protein contains protein kinase domain, Pfam:PF00069; contains leucine-rich repeats, Pfam:PF00560
358574	1	0	1144	1825	2235	2	2	At1g59580	7,00E-41	68414.m06701 mitogen-activated protein kinase, putative / MAPK, putative (MPK2) identical to mitogen-activated protein kinase homolog 2 (AtMPK2)[Arabidopsis thaliana] SWISS-PROT:Q39022; PMID:12119167
353252	2	0	1144	1825	2284	2	2	At1g48480	2,00E-29	68414.m05419 leucine-rich repeat transmembrane protein kinase, putative contains similarity to many predicted protein kinases
359581	1	0	1144	1825	2284	2	2	At3g17840	6,00E-29	68416.m02274 leucine-rich repeat transmembrane protein kinase, putative similar to receptor kinase GB:AAA33715 from [Petunia integrifolia]
354650	1	0	1144	1825	2327	2	1	At3g04810	7,00E-17	68416.m00521 protein kinase, putative similar to LSTK-1-like kinase [Lycopersicon esculentum] GI:15637110; contains Pfam profile: PF00069 Eukaryotic protein kinase domain
359622	1	0	1144	1825	2327	2	1	At3g04810	1,00E-35	68416.m00521 protein kinase, putative similar to LSTK-1-like kinase [Lycopersicon esculentum] GI:15637110; contains Pfam profile: PF00069 Eukaryotic protein kinase domain
355974	1	0	1144	1825	2338	2	2	At5g15080	7,00E-37	68418.m01767 protein kinase, putative similar to protein kinase APK1A [Arabidopsis thaliana] Swiss-Prot:Q06548
354835	1	0	1144	1825	2346	2	1	At5g59010	9,00E-59	68418.m07392 protein kinase-related low similarity to serine/threonine/tyrosine-specific protein kinase APK1, Arabidopsis thaliana, SP|Q06548 PIR:S28615; contains Pfam profile: PF00069 Eukaryotic protein kinase domain
358855	1	0	1144	1825	2383	1	1	At4g01370	6,00E-57	68417.m00177 mitogen-activated protein kinase, putative / MAPK, putative (MPK4) identical to mitogen-activated protein kinase homolog (AtMPK4)[Arabidopsis thaliana] SWISS-PROT:Q39024; PMID:12119167
353425	2	0	1144	1825	2461	2	1	At1g26150	8,00E-77	68414.m03192 protein kinase family protein similar to Pto kinase interactor 1 GI:3668069 from [Lycopersicon esculentum]
359055	1	0	1144	1825	2466	1	1	At5g02070	2,00E-73	68418.m00128 protein kinase-related contains eukaryotic protein kinase domain, INTERPRO:IPR000719
359479	1	0	1144	1825	2509	1	1	At2g36570	3,00E-38	68415.m04485 leucine-rich repeat transmembrane protein kinase, putative

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
354452	2	0	1144	1825	2521	1	1	At3g24660	8,00E-33	68416.m03096 leucine-rich repeat transmembrane protein kinase, putative identical to putative kinase-like protein TMKL1 precursor GB:P33543 from [Arabidopsis thaliana], (Plant Mol. Biol. 23 (2), 415-421 (1993))
356374	1	0	1144	1825	2521	1	1	At3g24660	2,00E-59	68416.m03096 leucine-rich repeat transmembrane protein kinase, putative identical to putative kinase-like protein TMKL1 precursor GB:P33543 from [Arabidopsis thaliana], (Plant Mol. Biol. 23 (2), 415-421 (1993))
355194	1	0	1144	1825	2546	1	2	At3g01490	3,00E-65	68416.m00073 protein kinase, putative similar to ATMRK1 [Arabidopsis thaliana] gi|2351097|dbj|BAA22079
357394	1	0	1144	1825	2546	1	2	At3g01490	1,00E-31	68416.m00073 protein kinase, putative similar to ATMRK1 [Arabidopsis thaliana] gi|2351097|dbj|BAA22079
355572	1	0	1144	1825	2555	1	2	At5g13160	2,00E-68	68418.m01507 protein kinase family protein contains protein kinase domain, Pfam:PF00069
358886	1	0	1144	1825	2556	1	2	At5g01020	7,00E-138	68418.m00004 protein kinase family protein contains protein kinase domain, Pfam:PF00069
358738	1	0	1144	1825	2564	2	2	At2g24360	1,00E-72	68415.m02911 serine/threonine/tyrosine kinase, putative similar to serine/threonine/tyrosine kinase [Arachis hypogaea] gi|13124865|gb|AAK11734
359644	1	0	1144	1825	2564	2	2	At2g24360	1,00E-99	68415.m02911 serine/threonine/tyrosine kinase, putative similar to serine/threonine/tyrosine kinase [Arachis hypogaea] gi|13124865|gb|AAK11734
359588	1	0	1144	1825	2614	1	1	At1g68400	4,00E-13	68414.m07814 leucine-rich repeat transmembrane protein kinase, putative similar to receptor kinase GB:AAA33715 from [Petunia integrifolia]
353749	2	0	1144	1825	2648	3	1	At5g03640	1,00E-22	68418.m00323 protein kinase family protein contains serine/threonine protein kinase domain, INTERPRO:IPR002290
354852	1	0	1144	1825	2651	1	1	At2g23450	1,00E-28	68415.m02800 protein kinase family protein contains protein kinase domain, Pfam:PF00069
358397	1	0	1144	1825	2651	1	1	At2g23450	3,00E-91	68415.m02800 protein kinase family protein contains protein kinase domain, Pfam:PF00069
354699	1	0	1144	1825	2719	2	3	At5g58380	2,00E-33	68418.m07311 CBL-interacting protein kinase 10 (CIPK10) identical to CBL-interacting protein kinase 10 [Arabidopsis thaliana] gi|13249119|gb|AAK16685; contains Pfam profiles PF00069: Protein kinase domain and PF03822: NAF domain; identical to cDNA CBL-interacting protein kinase 10 (CIPK10) GI:13249118

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
355565	1	0	1144	1825	2719	2	3	At5g07070	1,00E-14	68418.m00800 CBL-interacting protein kinase 2 (CIPK2) identical to CBL-interacting protein kinase 2 [Arabidopsis thaliana] gi|9280636|gb|AAF86506
359132	1	0	1144	1825	2733	1	1	At1g01540	9,00E-12	68414.m00071 protein kinase family protein contains protein kinase domain, Pfam:PF00069; contains serine/threonine protein kinase domain, INTERPRO:IPR002290
355368	1	0	1144	1825	2765	2	1	At1g63430	1,00E-50	68414.m07173 leucine-rich repeat transmembrane protein kinase, putative contains Pfam profiles: PF00069 Eukaryotic protein kinase domain, PF00560 Leucine Rich Repeat; contains 1 predicted transmembrane domain
358552	1	0	1144	1825	2765	2	1	At1g63430	3,00E-44	68414.m07173 leucine-rich repeat transmembrane protein kinase, putative contains Pfam profiles: PF00069 Eukaryotic protein kinase domain, PF00560 Leucine Rich Repeat; contains 1 predicted transmembrane domain
353284	3	0	1144	1825	2808	2	2	At1g10940	1,00E-134	68414.m01256 serine/threonine protein kinase, putative similar to serine/threonine-protein kinase ASK1 [Arabidopsis thaliana] SWISS-PROT:P43291
358316	1	0	1144	1825	3014	1	2	At3g06030	3,00E-27	68416.m00688 NPK1-related protein kinase, putative (ANP3) similar to protein kinase [Nicotiana tabacum] gi|456309|dbj|BAA05648; identical to cDNA NPK1-related protein kinase 3 GI:2342426
359148	1	0	1144	1825	3167	1	1	At5g50180	5,00E-45	68418.m06214 protein kinase, putative similar to protein kinase ATN1 [Arabidopsis thaliana] gi|1054633|emb|CAA63387
353737	2	0	1144	1825	3183	4	2	At3g59350	2,00E-72	68416.m06618 serine/threonine protein kinase, putative similar to Pto kinase interactor 1 (Pti1)[Lycopersicon esculentum] gi|3668069|gb|AAC61805
358011	1	0	1144	1825	3259	12	16	At4g23250	1,00E-18	68417.m03352 protein kinase family protein contains Pfam domain PF00069: Protein kinase domain
355222	1	0	1144	1825	3339	3	1	At3g53030	2,00E-31	68416.m05845 protein kinase family protein contains eukaryotic protein kinase domain, INTERPRO:IPR000719
357401	1	0	1144	1825	3340	1	2	At2g38650	2,00E-16	68415.m04747 glycosyl transferase family 8 protein contains Pfam profile: PF01501 glycosyl transferase family 8
357571	1	0	1144	1825	3412	1	1	At1g70520	1,00E-21	68414.m08116 protein kinase family protein contains Pfam domain, PF00069: Protein kinase domain
357760	1	0	1144	1825	3412	1	1	At1g70520	2,00E-54	68414.m08116 protein kinase family protein contains Pfam domain, PF00069: Protein kinase domain

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
353071	2	0	1144	1825	3522	1	2	At1g53570	1,00E-19	68414.m06081 mitogen-activated protein kinase kinase kinase (MAPKKK), putative (MAP3Ka) identical to MEK kinase (MAP3Ka)[Arabidopsis thaliana] gi|4204912|gb|AAD10848
354420	3	0	1144	1825	3531	2	1	At1g49160	1,00E-29	68414.m05512 protein kinase family protein contains protein kinase domain, Pfam:PF00069
354853	1	0	1144	1825	3611	2	1	At4g32830	1,00E-68	68417.m04669 protein kinase, putative similar to protein kinase p46XlEg22 [Xenopus laevis] gi|609280|emb|CAA78914; contains protein kinase domain, Pfam:PF00069
358086	1	0	1144	1825	3611	2	1	At4g32830	6,00E-127	68417.m04669 protein kinase, putative similar to protein kinase p46XlEg22 [Xenopus laevis] gi|609280|emb|CAA78914; contains protein kinase domain, Pfam:PF00069
354417	2	0	1144	1825	3717	1	2	At3g48750	1,00E-100	68416.m05324 cell division control protein 2 homolog A (CDC2A) identical to cell division control protein 2 homolog A [Arabidopsis thaliana] SWISS-PROT:P24100
359439	1	0	1144	1825	3717	1	2	At3g48750	6,00E-07	68416.m05324 cell division control protein 2 homolog A (CDC2A) identical to cell division control protein 2 homolog A [Arabidopsis thaliana] SWISS-PROT:P24100
354228	2	0	1144	1825	3745	1	1	At5g56580	2,00E-54	68418.m07061 mitogen-activated protein kinase kinase (MAPKK), putative (MKK6) similar to NQK1 MAPKK [Nicotiana tabacum] gi|12718822|dbj|BAB32405; mitogen-activated protein kinase kinase (MAPKK) family, PMID:12119167
354750	1	0	1144	1825	3858	2	2	At3g17510	4,00E-87	68416.m02236 CBL-interacting protein kinase 1 (CIPK1) identical to CBL-interacting protein kinase 1 [Arabidopsis thaliana] gi|11066952|gb|AAG28776; contains Pfam profiles PF00069: Protein kinase domain and PF03822: NAF domain; identical to cDNA CBL-interacting protein kinase 1 (CIPK1) GI:11066951
353235	2	0	1144	1825	3883	2	1	At1g76540	2,00E-25	68414.m08907 cell division control protein, putative similar to SWISS-PROT:Q38775, cell division control protein 2 homolog D [Antirrhinum majus]; contains protein kinase domain, Pfam:PF00069
354716	1	0	1144	1825	3883	2	1	At1g20930	7,00E-59	68414.m02621 cell division control protein, putative cdc2MsF [Medicago sativa] gi|1806146|emb|CAA65982
355425	1	0	1144	1825	3889	1	1	At2g28250	3,00E-39	68415.m03429 protein kinase family protein contains protein kinase domain, Pfam:PF00069

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
352899	2	0	1144	1825	3969	2	2	At1g66880	1,00E-38	68414.m07601 serine/threonine protein kinase family protein contains protein kinase domain, Pfam:PF00069; contains serine/threonine protein kinase domain, INTERPRO:IPR002290
359724	1	0	1144	1825	3969	2	2	At5g38210	4,00E-22	68418.m04606 serine/threonine protein kinase family protein contains protein kinase domain, Pfam:PF00069; contains serine/threonine protein kinase domain, INTERPRO:IPR002290
355943	1	0	1144	1825	4047	1	1	At5g61240	1,00E-59	68418.m07681 leucine-rich repeat family protein contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001611; contains similarity to Hcr2-0B [Lycopersicon esculentum] gi|3894387|gb|AAC78593
358951	1	0	1144	1825	4047	1	1	At5g61240	1,00E-101	68418.m07681 leucine-rich repeat family protein contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001611; contains similarity to Hcr2-0B [Lycopersicon esculentum] gi|3894387|gb|AAC78593
359381	1	0	1144	1825	4047	1	1	At5g61240	1,00E-32	68418.m07681 leucine-rich repeat family protein contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001611; contains similarity to Hcr2-0B [Lycopersicon esculentum] gi|3894387|gb|AAC78593
357999	1	0	1144	1825	4082	1	1	At2g11520	7,00E-19	68415.m01242 protein kinase family protein contains protein kinase domain, Pfam:PF00069
357557	1	0	1144	1825	4112	2	3	At2g25220	3,00E-45	68415.m03018 protein kinase family protein contains protein kinase domain, Pfam:PF00069
359237	1	0	1144	1825	4112	2	3	At4g32000	9,00E-90	68417.m04556 protein kinase family protein contains protein kinase domain, Pfam:PF00069
353682	2	0	1144	1825	4354	1	1	At3g58690	7,00E-61	68416.m06541 protein kinase family protein contains protein kinase domain, Pfam:PF00069
357355	1	0	1144	1825	4427	1	3	At1g18390	4,00E-50	68414.m02297 protein kinase family protein contains protein kinase domain, Pfam:PF00069
356339	1	0	1144	1825	4429	2	2	At5g05850	5,00E-30	68418.m00643 leucine-rich repeat family protein contains Pfam PF00560: Leucine Rich Repeat domains; similar to (SP:Q9UQ13) Leucine-rich repeat protein SHOC-2 (Ras-binding protein Sur-8) (SP:Q9UQ13) {Homo sapiens}
353842	2	0	1144	1825	4592	1	2	At2g34650	9,00E-72	68415.m04256 protein kinase PINOID (PID) identical to protein kinase PINOID [Arabidopsis thaliana] gi|7208442|gb|AAF40202; contains protein kinase domain, Pfam:PF00069

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
353589	2	0	1144	1825	4611	1	1	At3g54180	5,00E-125	68416.m05989 cell division control protein 2 homolog B (CDC2B) identical to cell division control protein 2 homolog B [Arabidopsis thaliana] SWISS-PROT:P25859
354301	2	0	1144	1825	4687	1	1	At2g18890	1,00E-65	68415.m02204 protein kinase family protein contains protein kinase domain, Pfam:PF00069
358359	1	0	1144	1825	4705	1	1	At1g80870	2,00E-18	68414.m09489 protein kinase family protein contains eukaryotic protein kinase domain, INTERPRO:IPR000719
357827	1	0	1144	1825	4706	1	1	At5g15730	2,00E-33	68418.m01840 serine/threonine protein kinase, putative similar to protein-serine/threonine kinase [Nicotiana tabacum] gi|505146|dbj|BAA06538
358054	1	0	1144	1825	4903	1	1	At5g63610	1,00E-109	68418.m07986 protein kinase, putative similar to cyclin-dependent kinase cdc2MsE [Medicago sativa] gi|1806144|emb|CAA65981; contains protein kinase domain, Pfam:PF00069
358774	1	0	1144	1825	5145	1	1	At1g12680	1,00E-66	68414.m01472 protein kinase family protein contains protein kinase domain, Pfam:PF00069
357491	1	0	1144	1825	5442	2	3	At1g70250	3,00E-09	68414.m08082 receptor serine/threonine kinase, putative similar to to receptor serine/threonine kinase PR5K gi|1235680|gb|AAC49208
357189	1	0	1144	1825	5816	1	5	At4g18250	1,00E-39	68417.m02710 receptor serine/threonine kinase, putative similar to to receptor serine/threonine kinase PR5K gi|1235680|gb|AAC49208
358061	1	0	1144	1825	6090	2	1	At5g21090	4,00E-62	68418.m02511 leucine-rich repeat protein, putative similar to leucine rich repeat protein (LRP) GI:1619300 from [Lycopersicon esculentum]; contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001611
356943	1	0	1144	1825	7219	2	3	At5g06870	7,00E-48	68418.m00777 polygalacturonase inhibiting protein 2 (PGIP2) identical to polygalacturonase inhibiting protein 2 (PGIP2) [Arabidopsis thaliana] gi|7800201|gb|AAF69828; contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001611
357587	1	0	1144	1825	7219	2	3	At5g06860	2,00E-59	68418.m00776 polygalacturonase inhibiting protein 1 (PGIP1) identical to polygalacturonase inhibiting protein 1 (PGIP1) [Arabidopsis thaliana] gi|7800199|gb|AAF69827; contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001611
359024	1	0	1144	1825	7219	2	3	At5g06860	4,00E-31	68418.m00776 polygalacturonase inhibiting protein 1 (PGIP1) identical to polygalacturonase inhibiting protein 1 (PGIP1) [Arabidopsis thaliana] gi|7800199|gb|AAF69827; contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001611

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
353117	3	0	1144	1825				At1g12580	2,00E-53	68414.m01461 protein kinase family protein contains protein kinase domain, Pfam:PF00069; contains similarity to calcium-dependent protein kinase GI:5162877 from [Marchantia polymorpha]
353347	4	0	1144	1825				At5g14640	2,00E-77	68418.m01715 protein kinase family protein similar to glycogen synthase kinase-3 homolog MsK-3 SP:P51139 from [Medicago sativa]; contains Pfam profile PF00069: Protein kinase domain
353793	3	0	1144	1825				At2g23070	6,00E-83	68415.m02750 casein kinase II alpha chain, putative similar to casein kinase II, alpha chain (CK II) [Zea mays] SWISS-PROT:P28523; contains protein kinase domain, Pfam:PF00069
354465	4	0	1144	1825				At1g12580	4,00E-101	68414.m01461 protein kinase family protein contains protein kinase domain, Pfam:PF00069; contains similarity to calcium-dependent protein kinase GI:5162877 from [Marchantia polymorpha]
354928	1	0	1144	1825				At5g14640	5,00E-70	68418.m01715 protein kinase family protein similar to glycogen synthase kinase-3 homolog MsK-3 SP:P51139 from [Medicago sativa]; contains Pfam profile PF00069: Protein kinase domain
355700	1	0	1144	1825				At5g62310	5,00E-08	68418.m07822 incomplete root hair elongation (IRE) / protein kinase, putative nearly identical to IRE (incomplete root hair elongation) [Arabidopsis thaliana] gi|6729346|dbj|BAA89783
355718	1	0	1144	1825				At4g30000	4,00E-32	68417.m04268 dihydropterin pyrophosphokinase, putative / dihydropteroate synthase, putative / DHPS, putative similar to dihydropterin pyrophosphokinase /dihydropteroate synthase [Pisum sativum] gi|1934972|emb|CAA69903
355800	1	0	1144	1825				At3g17410	2,00E-65	68416.m02224 serine/threonine protein kinase, putative similar to Pto kinase interactor 1 GB:AAC61805 from [Lycopersicon esculentum]
356009	1	0	1144	1825				At4g13020	4,00E-43	68417.m02032 serine/threonine protein kinase (MHK) identical to serine/threonine-protein kinase MHK [Arabidopsis thaliana] SWISS-PROT:P43294
356221	1	0	1144	1825				At1g72760	6,00E-29	68414.m08413 protein kinase family protein contains protein kinase domain, Pfam:PF00069
356278	1	0	1144	1825				At3g27580	4,00E-29	68416.m03446 protein kinase, putative similar to serine/threonine protein kinase [Arabidopsis thaliana] gi|217861|dbj|BAA01715

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
356313	1	0	1144	1825				At5g62310	1,00E-07	68418.m07822 incomplete root hair elongation (IRE) / protein kinase, putative nearly identical to IRE (incomplete root hair elongation) [Arabidopsis thaliana] gi|6729346|dbj|BAA89783
356320	1	0	1144	1825				At4g30000	2,00E-60	68417.m04268 dihydropterin pyrophosphokinase, putative / dihydropteroate synthase, putative / DHPS, putative similar to dihydropterin pyrophosphokinase /dihydropteroate synthase [Pisum sativum] gi|1934972|emb|CAA69903
356694	1	0	1144	1825				At1g29740	5,00E-46	68414.m03636 leucine-rich repeat family protein / protein kinase family protein contains Pfam domains PF00560: Leucine Rich Repeat and PF00069: Protein kinase domain
356834	1	0	1144	1825				At2g23070	5,00E-19	68415.m02750 casein kinase II alpha chain, putative similar to casein kinase II, alpha chain (CK II) [Zea mays] SWISS-PROT:P28523; contains protein kinase domain, Pfam:PF00069
356871	1	0	1144	1825				At5g02800	7,00E-96	68418.m00222 protein kinase family protein contains protein kinase domain, Pfam:PF00069
356949	1	0	1144	1825				At4g18710	2,00E-31	68417.m02766 shaggy-related protein kinase eta / ASK-eta (ASK7) identical to shaggy-related protein kinase eta (ASK-eta) [Arabidopsis thaliana] SWISS-PROT:Q39011
357214	1	0	1144	1825				At1g03920	3,00E-93	68414.m00377 protein kinase, putative contains protein kinase domain, Pfam:PF00069
357903	1	0	1144	1825				At4g29180	1,00E-14	68417.m04175 leucine-rich repeat protein kinase, putative similar to light repressible receptor protein kinase [Arabidopsis thaliana] gi|1321686|emb|CAA66376; contains leucine rich repeat (LRR) domains, Pfam:PF00560; contains protein kinase domain, Pfam:PF00069
358143	1	0	1144	1825				At4g40010	3,00E-72	68417.m05665 serine/threonine protein kinase, putative similar to serine-threonine protein kinase [Triticum aestivum] gi|2055374|gb|AAB58348
358208	1	0	1144	1825				At2g35050	3,00E-71	68415.m04300 protein kinase family protein contains Pfam profile: PF00069 Eukaryotic protein kinase domain
358279	1	0	1144	1825				At2g26730	2,00E-73	68415.m03206 leucine-rich repeat transmembrane protein kinase, putative
358549	1	0	1144	1825				At4g22130	4,00E-14	68417.m03199 protein kinase family protein contains protein kinase domain, Pfam:PF00069

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
358986	1	0	1144	1825				At4g36450	3,00E-16	68417.m05177 mitogen-activated protein kinase, putative / MAPK, putative (MPK14) mitogen-activated protein kinase (MAPK)(AtMPK14), PMID:12119167
359214	1	0	1144	1825				At2g26980	8,00E-13	68415.m03240 CBL-interacting protein kinase 3 (CIPK3) identical to CBL-interacting protein kinase 3 [Arabidopsis thaliana] gi|9280638|gb|AAF86507
359232	1	0	1144	1825				At1g53430	4,00E-47	68414.m06056 leucine-rich repeat family protein / protein kinase family protein contains Pfam domains PF00560: Leucine Rich Repeat and PF00069: Protein kinase domain
359310	1	0	1144	1825				At3g19100	4,00E-15	68416.m02427 calcium-dependent protein kinase, putative / CDPK, putative similar to calcium/calmodulin-dependent protein kinase CaMK3 [Nicotiana tabacum] gi|16904226|gb|AAL30820; contains protein kinase domain, Pfam:PF00069; contains serine/threonine protein kinase domain, INTERPRO:IPR002290
359578	1	0	1144	1825				At3g55450	2,00E-25	68416.m06158 protein kinase, putative similar to protein kinase APK1B [Arabidopsis thaliana] SWISS-PROT:P46573
359618	1	0	1144	1825				At4g24740	3,00E-69	68417.m03540 protein kinase (AFC2) identical to protein kinase AFC2 [Arabidopsis thaliana] SWISS-PROT:P51567
359669	1	0	1144	1825				At1g48210	1,00E-37	68414.m05382 serine/threonine protein kinase, putative similar to Pto kinase interactor 1 [Lycopersicon esculentum] gi|3668069|gb|AAC61805; contains protein kinase domain, Pfam:PF00069
359740	1	0	1144	1825				At4g22130	8,00E-60	68417.m03199 protein kinase family protein contains protein kinase domain, Pfam:PF00069
358538	1	1	4	2780	699	1	2	At3g18730	1,00E-11	68416.m02378 tetratricopeptide repeat (TPR)-containing protein contains Pfam profile PF00515: TPR Domain
354442	20	1	4	2780				At3g01410	7,00E-33	68416.m00064 RNase H domain-containing protein low similarity to GAG-POL precursor [Oryza sativa (japonica cultivar-group)] GI:5902445; contains Pfam profile: PF00075 RNase H
357020	1	1	4	2780				At3g01410	7,00E-11	68416.m00064 RNase H domain-containing protein low similarity to GAG-POL precursor [Oryza sativa (japonica cultivar-group)] GI:5902445; contains Pfam profile: PF00075 RNase H
357276	1	1	4	2780				At3g01410	1,00E-07	68416.m00064 RNase H domain-containing protein low similarity to GAG-POL precursor [Oryza sativa (japonica cultivar-group)] GI:5902445; contains Pfam profile: PF00075 RNase H

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
359271	1	1	4	2780				At3g01410	5,00E-39	68416.m00064 RNase H domain-containing protein low similarity to GAG-POL precursor [Oryza sativa (japonica cultivar-group)] GI:5902445; contains Pfam profile: PF00075 RNase H
357590	1	3	18	2169	5716	1	1	At1g06070	4,00E-23	68414.m00636 bZIP transcription factor, putative (bZIP69) similar to transcriptional activator RF2a GB:AF005492 GI:2253277 from [Oryza sativa]; contains Pfam profile PF00170: bZIP transcription factor
357846	1	3	18	2169	5716	1	1	At1g06070	2,00E-21	68414.m00636 bZIP transcription factor, putative (bZIP69) similar to transcriptional activator RF2a GB:AF005492 GI:2253277 from [Oryza sativa]; contains Pfam profile PF00170: bZIP transcription factor
360003	1	3	18	2169	7310	2	1	At3g58120	6,00E-15	68416.m06481 bZIP transcription factor family protein contains Pfam profile: PF00170 bZIP transcription factor ;supported by cDNA gi|15100054|gb|AF401300.1|AF401300
354026	3	3	18	2169	7610	1	1	At1g58110	1,00E-40	68414.m06587 bZIP family transcription factor similar to bZIP transcriptional activator RSG GI:8777512 from [Nicotiana tabacum]; contains PFAM profile: bZIP transcription factor PF00170
356416	1	3	18	2169	7610	1	1	At1g58110	3,00E-09	68414.m06587 bZIP family transcription factor similar to bZIP transcriptional activator RSG GI:8777512 from [Nicotiana tabacum]; contains PFAM profile: bZIP transcription factor PF00170
352933	2	4	33	1896	3259	12	16	At4g23160	1,00E-21	68417.m03342 protein kinase family protein contains Pfam domain PF00069: Protein kinase domain
353576	2	4	33	1896	3259	12	16	At4g23160	1,00E-36	68417.m03342 protein kinase family protein contains Pfam domain PF00069: Protein kinase domain
353898	2	4	33	1896	3259	12	16	At4g23160	1,00E-33	68417.m03342 protein kinase family protein contains Pfam domain PF00069: Protein kinase domain
354193	2	4	33	1896	3259	12	16	At4g23160	6,00E-34	68417.m03342 protein kinase family protein contains Pfam domain PF00069: Protein kinase domain
354194	2	4	33	1896	3259	12	16	At4g23160	8,00E-21	68417.m03342 protein kinase family protein contains Pfam domain PF00069: Protein kinase domain
354499	1	4	33	1896	3259	12	16	At4g23160	3,00E-19	68417.m03342 protein kinase family protein contains Pfam domain PF00069: Protein kinase domain
354813	1	4	33	1896	3259	12	16	At4g23160	2,00E-18	68417.m03342 protein kinase family protein contains Pfam domain PF00069: Protein kinase domain
354895	1	4	33	1896	3259	12	16	At4g23160	9,00E-42	68417.m03342 protein kinase family protein contains Pfam domain PF00069: Protein kinase domain
354916	1	4	33	1896	3259	12	16	At4g23160	5,00E-53	68417.m03342 protein kinase family protein contains Pfam domain PF00069: Protein kinase domain

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
355075	1	4	33	1896	3259	12	16	At4g23160	5,00E-24	68417.m03342 protein kinase family protein contains Pfam domain PF00069: Protein kinase domain
355095	1	4	33	1896	3259	12	16	At4g23160	5,00E-34	68417.m03342 protein kinase family protein contains Pfam domain PF00069: Protein kinase domain
355291	1	4	33	1896	3259	12	16	At4g23160	2,00E-22	68417.m03342 protein kinase family protein contains Pfam domain PF00069: Protein kinase domain
355335	1	4	33	1896	3259	12	16	At4g23160	4,00E-31	68417.m03342 protein kinase family protein contains Pfam domain PF00069: Protein kinase domain
355517	1	4	33	1896	3259	12	16	At4g23160	4,00E-39	68417.m03342 protein kinase family protein contains Pfam domain PF00069: Protein kinase domain
355530	1	4	33	1896	3259	12	16	At4g23160	1,00E-11	68417.m03342 protein kinase family protein contains Pfam domain PF00069: Protein kinase domain
355737	1	4	33	1896	3259	12	16	At4g23160	1,00E-20	68417.m03342 protein kinase family protein contains Pfam domain PF00069: Protein kinase domain
355739	1	4	33	1896	3259	12	16	At4g23160	4,00E-18	68417.m03342 protein kinase family protein contains Pfam domain PF00069: Protein kinase domain
355812	1	4	33	1896	3259	12	16	At4g23160	2,00E-24	68417.m03342 protein kinase family protein contains Pfam domain PF00069: Protein kinase domain
355892	1	4	33	1896	3259	12	16	At4g23160	9,00E-15	68417.m03342 protein kinase family protein contains Pfam domain PF00069: Protein kinase domain
356083	1	4	33	1896	3259	12	16	At4g23160	1,00E-10	68417.m03342 protein kinase family protein contains Pfam domain PF00069: Protein kinase domain
356152	1	4	33	1896	3259	12	16	At4g23160	7,00E-10	68417.m03342 protein kinase family protein contains Pfam domain PF00069: Protein kinase domain
356252	1	4	33	1896	3259	12	16	At4g23160	5,00E-26	68417.m03342 protein kinase family protein contains Pfam domain PF00069: Protein kinase domain
356717	1	4	33	1896	3259	12	16	At4g23160	3,00E-21	68417.m03342 protein kinase family protein contains Pfam domain PF00069: Protein kinase domain
357132	1	4	33	1896	3259	12	16	At4g23160	8,00E-06	68417.m03342 protein kinase family protein contains Pfam domain PF00069: Protein kinase domain
357153	1	4	33	1896	3259	12	16	At4g23160	1,00E-32	68417.m03342 protein kinase family protein contains Pfam domain PF00069: Protein kinase domain
357185	1	4	33	1896	3259	12	16	At4g23160	2,00E-12	68417.m03342 protein kinase family protein contains Pfam domain PF00069: Protein kinase domain
357665	1	4	33	1896	3259	12	16	At4g23160	1,00E-36	68417.m03342 protein kinase family protein contains Pfam domain PF00069: Protein kinase domain
357697	1	4	33	1896	3259	12	16	At4g23160	1,00E-10	68417.m03342 protein kinase family protein contains Pfam domain PF00069: Protein kinase domain
357863	1	4	33	1896	3259	12	16	At4g23160	3,00E-07	68417.m03342 protein kinase family protein contains Pfam domain PF00069: Protein kinase domain
357949	1	4	33	1896	3259	12	16	At4g23160	7,00E-13	68417.m03342 protein kinase family protein contains Pfam domain PF00069: Protein kinase domain

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
357967	1	4	33	1896	3259	12	16	At4g23160	2,00E-16	68417.m03342 protein kinase family protein contains Pfam domain PF00069: Protein kinase domain
358050	1	4	33	1896	3259	12	16	At4g23160	4,00E-13	68417.m03342 protein kinase family protein contains Pfam domain PF00069: Protein kinase domain
358171	1	4	33	1896	3259	12	16	At4g23160	3,00E-13	68417.m03342 protein kinase family protein contains Pfam domain PF00069: Protein kinase domain
358253	1	4	33	1896	3259	12	16	At4g23160	1,00E-19	68417.m03342 protein kinase family protein contains Pfam domain PF00069: Protein kinase domain
358275	1	4	33	1896	3259	12	16	At4g23160	3,00E-33	68417.m03342 protein kinase family protein contains Pfam domain PF00069: Protein kinase domain
358473	1	4	33	1896	3259	12	16	At4g23160	5,00E-43	68417.m03342 protein kinase family protein contains Pfam domain PF00069: Protein kinase domain
358542	1	4	33	1896	3259	12	16	At4g23160	3,00E-14	68417.m03342 protein kinase family protein contains Pfam domain PF00069: Protein kinase domain
358713	1	4	33	1896	3259	12	16	At4g23160	3,00E-12	68417.m03342 protein kinase family protein contains Pfam domain PF00069: Protein kinase domain
358749	1	4	33	1896	3259	12	16	At4g23160	5,00E-26	68417.m03342 protein kinase family protein contains Pfam domain PF00069: Protein kinase domain
358801	1	4	33	1896	3259	12	16	At4g23160	4,00E-08	68417.m03342 protein kinase family protein contains Pfam domain PF00069: Protein kinase domain
359163	1	4	33	1896	3259	12	16	At4g23160	9,00E-19	68417.m03342 protein kinase family protein contains Pfam domain PF00069: Protein kinase domain
359188	1	4	33	1896	3259	12	16	At4g23160	2,00E-32	68417.m03342 protein kinase family protein contains Pfam domain PF00069: Protein kinase domain
359225	1	4	33	1896	3259	12	16	At4g23160	4,00E-52	68417.m03342 protein kinase family protein contains Pfam domain PF00069: Protein kinase domain
359332	1	4	33	1896	3259	12	16	At4g23160	6,00E-45	68417.m03342 protein kinase family protein contains Pfam domain PF00069: Protein kinase domain
359394	1	4	33	1896	3259	12	16	At4g23160	6,00E-20	68417.m03342 protein kinase family protein contains Pfam domain PF00069: Protein kinase domain
359589	1	4	33	1896	3259	12	16	At4g23160	1,00E-21	68417.m03342 protein kinase family protein contains Pfam domain PF00069: Protein kinase domain
359670	1	4	33	1896	3259	12	16	At4g23160	2,00E-10	68417.m03342 protein kinase family protein contains Pfam domain PF00069: Protein kinase domain
359773	1	4	33	1896	3259	12	16	At4g23160	5,00E-15	68417.m03342 protein kinase family protein contains Pfam domain PF00069: Protein kinase domain
359791	1	4	33	1896	3259	12	16	At4g23160	1,00E-08	68417.m03342 protein kinase family protein contains Pfam domain PF00069: Protein kinase domain
359803	1	4	33	1896	3259	12	16	At4g23160	9,00E-17	68417.m03342 protein kinase family protein contains Pfam domain PF00069: Protein kinase domain
359823	1	4	33	1896	3259	12	16	At4g23160	4,00E-24	68417.m03342 protein kinase family protein contains Pfam domain PF00069: Protein kinase domain

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
359960	1	4	33	1896	3259	12	16	At4g23160	3,00E-31	68417.m03342 protein kinase family protein contains Pfam domain PF00069: Protein kinase domain
360053	1	4	33	1896	3259	12	16	At4g23160	4,00E-14	68417.m03342 protein kinase family protein contains Pfam domain PF00069: Protein kinase domain
358949	1	4	33	1896				At5g48050	8,00E-08	68418.m05937 hypothetical protein low similarity to copia-like polyprotein [Arabidopsis thaliana] GI:13872712
359166	1	4	33	1896				At5g48050	6,00E-07	68418.m05937 hypothetical protein low similarity to copia-like polyprotein [Arabidopsis thaliana] GI:13872712
359285	1	4	33	1896				At5g48050	2,00E-09	68418.m05937 hypothetical protein low similarity to copia-like polyprotein [Arabidopsis thaliana] GI:13872712
359686	1	4	33	1896				At1g21280	3,00E-06	68414.m02659 expressed protein
359170	1	6	492	550	859	1	1	At4g02750	2,00E-56	68417.m00375 pentatricopeptide (PPR) repeat-containing protein contains INTERPRO:IPR002885 PPR repeats
358536	1	6	492	550	953	1	1	At4g13650	2,00E-33	68417.m02123 pentatricopeptide (PPR) repeat-containing protein contains Pfam profile PF01535: PPR repeat
353741	2	6	492	550	1002	2	1	At1g74750	2,00E-82	68414.m08661 pentatricopeptide (PPR) repeat-containing protein low similarity to post-transcriptional control of chloroplast gene expression CRP1 [Zea mays] GI:3289002; contains Pfam profile PF01535: PPR repeat
354129	2	6	492	550	1164	1	1	At1g11290	1,00E-27	68414.m01297 pentatricopeptide (PPR) repeat-containing protein contains Pfam profile PF01535: PPR repeat
358584	1	6	492	550	1342	2	1	At1g09410	7,00E-21	68414.m01052 pentatricopeptide (PPR) repeat-containing protein contains INTERPRO:IPR002885 PPR repeats
359387	1	6	492	550	1372	1	1	At3g53700	1,00E-11	68416.m05931 pentatricopeptide (PPR) repeat-containing protein low similarity to fertility restorer [Petunia x hybrida] GI:22128587; contains Pfam profile PF01535: PPR repeat
355891	1	6	492	550	1527	1	1	At3g02010	4,00E-62	68416.m00162 pentatricopeptide (PPR) repeat-containing protein contains Pfam profile PF01535: PPR repeat
357040	1	6	492	550	1560	1	1	At2g13600	5,00E-14	68415.m01499 pentatricopeptide (PPR) repeat-containing protein contains INTERPRO:IPR002885 PPR repeats

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
356457	1	6	492	550	1603	1	1	At3g13770	1,00E-25	68416.m01737 pentatricopeptide (PPR) repeat-containing protein contains Pfam profile PF01535: PPR repeat
356407	1	6	492	550	1709	1	1	At3g63370	3,00E-11	68416.m07133 pentatricopeptide (PPR) repeat-containing protein contains Pfam profile PF01535: PPR repeat
354088	2	6	492	550	2023	1	1	At2g35130	3,00E-122	68415.m04309 pentatricopeptide (PPR) repeat-containing protein contains Pfam profile PF01535: PPR repeat
355118	1	6	492	550	2026	1	1	At3g59040	2,00E-52	68416.m06580 pentatricopeptide (PPR) repeat-containing protein contains Pfam profile PF01535: PPR repeat
359385	1	6	492	550	2063	1	1	At3g46790	2,00E-65	68416.m05079 pentatricopeptide (PPR) repeat-containing protein contains INTERPRO:IPR002885 PPR repeats
356652	1	6	492	550	2091	1	1	At2g33680	1,00E-26	68415.m04128 pentatricopeptide (PPR) repeat-containing protein contains INTERPRO:IPR002885 PPR repeats
359345	1	6	492	550	2091	1	1	At2g33680	2,00E-35	68415.m04128 pentatricopeptide (PPR) repeat-containing protein contains INTERPRO:IPR002885 PPR repeats
357037	1	6	492	550	2095	1	1	At5g42310	2,00E-58	68418.m05149 pentatricopeptide (PPR) repeat-containing protein contains Pfam profile PF01535: PPR repeat
353104	4	6	492	550	2335	1	1	At5g46580	6,00E-47	68418.m05735 pentatricopeptide (PPR) repeat-containing protein contains similarity to 67kD chloroplastic RNA-binding protein, P67.1 [Raphanus sativus] GI:9755886; contains Pfam profile PF01535: PPR repeat
359456	1	6	492	550	2381	1	1	At4g21070	5,00E-33	68417.m03047 BRCT domain-containing protein / zinc finger (C3HC4-type RING finger) family protein (BRCA1) contains Pfam profiles PF00533: BRCA1 C Terminus (BRCT) domain, PF00097: Zinc finger, C3HC4 type (RING finger), PF01535: PPR repeat; identical to cDNA BRCA1 GI:28372473
358558	1	6	492	550	2419	1	1	At4g37170	2,00E-36	68417.m05262 pentatricopeptide (PPR) repeat-containing protein contains Pfam profile PF01535: PPR repeat
358791	1	6	492	550	2768	1	1	At5g55840	3,00E-41	68418.m06958 pentatricopeptide (PPR) repeat-containing protein low similarity to fertility restorer [Petunia x hybrida] GI:22128587; contains Pfam profile PF01535: PPR repeat

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
352923	2	6	492	550	2813	1	1	At1g77360	9,00E-23	68414.m09009 pentatricopeptide (PPR) repeat-containing protein contains Pfam profile PF01535: PPR repeat
358358	1	6	492	550	2840	1	1	At2g37230	4,00E-16	68415.m04568 pentatricopeptide (PPR) repeat-containing protein contains Pfam profile PF01535: PPR repeat
359869	1	6	492	550	2848	1	1	At1g60770	7,00E-33	68414.m06841 pentatricopeptide (PPR) repeat-containing protein low similarity to DNA-binding protein [Triticum aestivum] GI:6958202; contains Pfam profile PF01535: PPR repeat
353009	5	6	492	550	2893	1	1	At4g01320	2,00E-17	68417.m00172 CAAX protease, putative (STE24) contains Pfam domain, PF01435: Peptidase family M48
356182	1	6	492	550	2893	1	1	At4g01320	2,00E-43	68417.m00172 CAAX protease, putative (STE24) contains Pfam domain, PF01435: Peptidase family M48
352966	3	6	492	550	2993	1	1	At1g73400	2,00E-14	68414.m08498 pentatricopeptide (PPR) repeat-containing protein contains Pfam profile PF01535: PPR repeat
355886	1	6	492	550	3050	1	1	At1g59720	1,00E-13	68414.m06720 pentatricopeptide (PPR) repeat-containing protein contains Pfam profile PF01535: PPR repeat
356987	1	6	492	550	3073	1	1	At4g01400	2,00E-61	68417.m00180 pentatricopeptide (PPR) repeat-containing protein contains Pfam profile PF01535: PPR repeat
357199	1	6	492	550	3356	2	2	At1g15480	2,00E-50	68414.m01862 DNA-binding protein, putative similar to DNA-binding protein [Triticum aestivum] GI:6958202; contains Pfam profile PF01535: PPR repeat
357291	1	6	492	550	3356	2	2	At1g15480	2,00E-39	68414.m01862 DNA-binding protein, putative similar to DNA-binding protein [Triticum aestivum] GI:6958202; contains Pfam profile PF01535: PPR repeat
358258	1	6	492	550	3473	1	1	At2g20540	2,00E-35	68415.m02399 pentatricopeptide (PPR) repeat-containing protein contains INTERPRO:IPR002885 PPR repeats
356689	1	6	492	550	3506	1	1	At5g50390	2,00E-24	68418.m06241 pentatricopeptide (PPR) repeat-containing protein contains INTERPRO:IPR002885 PPR repeats
358210	1	6	492	550	3662	1	1	At3g53170	9,00E-85	68416.m05859 pentatricopeptide (PPR) repeat-containing protein low similarity to fertility restorer [Petunia x hybrida] GI:22128587; contains Pfam profile PF01535: PPR repeat
358368	1	6	492	550	3767	1	1	At3g47840	2,00E-06	68416.m05215 pentatricopeptide (PPR) repeat-containing protein contains Pfam profile PF01535: PPR repeat

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
357434	1	6	492	550	4549	1	1	At1g02060	4,00E-30	68414.m00126 pentatricopeptide (PPR) repeat-containing protein contains Pfam profile PF01535: PPR repeat
357391	1	6	492	550	4553	1	1	At5g15010	1,00E-13	68418.m01760 pentatricopeptide (PPR) repeat-containing protein contains Pfam profile PF01535: PPR repeat
357537	1	6	492	550	4851	2	1	At2g25580	1,00E-52	68415.m03064 pentatricopeptide (PPR) repeat-containing protein contains Pfam profile PF01535: PPR repeat
356157	1	6	492	550	5170	1	1	At3g02650	4,00E-29	68416.m00256 pentatricopeptide (PPR) repeat-containing protein contains Pfam profile PF01535: PPR repeat
356702	1	6	492	550	5170	1	1	At3g02650	2,00E-47	68416.m00256 pentatricopeptide (PPR) repeat-containing protein contains Pfam profile PF01535: PPR repeat
356033	1	6	492	550	6839	1	1	At3g59300	3,00E-19	68416.m06610 expressed protein hypothetical protein T2J13.20 - Arabidopsis thaliana, PIR:T46116
354118	2	6	492	550	8034	1	1	At1g05805	4,00E-33	68414.m00607 basic helix-loop-helix (bHLH) family protein
355740	1	6	492	550	8607	1	1	At5g14030	2,00E-11	68418.m01640 translocon-associated protein beta (TRAPB) family protein low similarity to SP|P23438 Translocon-associated protein, beta subunit precursor (TRAP-beta) (Signal sequence receptor beta subunit) {Canis familiaris}; contains Pfam profile PF05753: Translocon-associated protein beta (TRAPB)
356172	1	6	492	550				At4g09180	3,00E-18	68417.m01519 basic helix-loop-helix (bHLH) family protein contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain
356250	1	6	492	550				At1g06140	2,00E-30	68414.m00645 pentatricopeptide (PPR) repeat-containing protein contains INTERPRO:IPR002885 PPR repeats
356773	1	6	492	550				At2g20180	5,00E-27	68415.m02360 basic helix-loop-helix (bHLH) family protein contains Pfam domain, PF00010: Helix-loop-helix DNA-binding domain
357687	1	6	492	550				At1g68920	5,00E-29	68414.m07888 basic helix-loop-helix (bHLH) family protein contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain
358228	1	6	492	550				At1g06150	5,00E-66	68414.m00646 pentatricopeptide (PPR) repeat-containing protein contains Pfam profile PF01535: PPR repeat

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
358998	1	6	492	550				At5g24830	9,00E-24	68418.m02934 pentatricopeptide (PPR) repeat-containing protein contains Pfam profile PF01535: PPR repeat
359498	1	6	492	550				At4g33170	2,00E-43	68417.m04725 pentatricopeptide (PPR) repeat-containing protein contains Pfam profile PF01535: PPR repeat
359527	1	6	492	550				At5g15980	3,00E-42	68418.m01868 pentatricopeptide (PPR) repeat-containing protein contains Pfam profile PF01535: PPR repeat
356745	1	7	89	886	6428	3	1	At4g32150	1,00E-83	68417.m04573 synaptobrevin family protein similar to Synaptobrevin-like protein 1 (SP:P51809) [Homo sapiens]
358014	1	7	89	886	9122	7	41	At5g52065	1,00E-05	68418.m06463 hypothetical protein
356396	1	7	89	886				At1g43730	1,00E-08	68414.m05028 hypothetical protein
357286	1	7	89	886				At2g02520	2,00E-08	68415.m00192 hypothetical protein
358144	1	7	89	886				At4g15780	1,00E-80	68417.m02402 synaptobrevin-related family protein similar to Vesicle-associated membrane protein 722 (AtVAMP722) Synaptobrevin-related protein 1 (SP:P47192) {Arabidopsis thaliana}
354310	5	8	16	803	7245	2	1	At3g52560	1,00E-73	68416.m05785 ubiquitin-conjugating enzyme family protein similar to DNA-binding protein CROC-1B [Homo sapiens] GI:1066082; contains Pfam profile PF00179: Ubiquitin-conjugating enzyme
356035	1	8	16	803	7245	2	1	At3g52560	5,00E-37	68416.m05785 ubiquitin-conjugating enzyme family protein similar to DNA-binding protein CROC-1B [Homo sapiens] GI:1066082; contains Pfam profile PF00179: Ubiquitin-conjugating enzyme
353463	2	8	16	803	7332	1	199	At4g02450	3,00E-31	68417.m00332 glycine-rich protein similar to several proteins containing a tandem repeat region such as Plasmodium falciparum GGM tandem repeat protein (GB:U27807)
355225	1	8	16	803	7332	1	199	At4g02450	4,00E-16	68417.m00332 glycine-rich protein similar to several proteins containing a tandem repeat region such as Plasmodium falciparum GGM tandem repeat protein (GB:U27807)
355690	1	8	16	803	7519	2	1	At1g23260	8,00E-52	68414.m02910 ubiquitin-conjugating enzyme family protein similar to TRAF6-regulated IKK activator 1 beta Uev1A [Homo sapiens] GI:10880969; contains Pfam profile PF00179: Ubiquitin-conjugating enzyme
357543	1	8	16	803	8596	3	159	At1g64260	1,00E-14	68414.m07281 zinc finger protein-related contains Pfam profiles PF03108: MuDR family transposase, PF04434: SWIM zinc finger

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
354348	2	8	16	803				At1g17930	2,00E-06	68414.m02219 expressed protein similar to hypothetical protein GI:4559351 from [Arabidopsis thaliana]
354870	1	8	16	803				At1g17930	8,00E-09	68414.m02219 expressed protein similar to hypothetical protein GI:4559351 from [Arabidopsis thaliana]
355914	1	8	16	803				At5g42300	1,00E-37	68418.m05148 ubiquitin family protein contains INTERPRO:IPR000626 ubiquitin domain
359172	1	8	16	803				At1g17930	6,00E-08	68414.m02219 expressed protein similar to hypothetical protein GI:4559351 from [Arabidopsis thaliana]
359436	1	8	16	803				At1g17930	5,00E-06	68414.m02219 expressed protein similar to hypothetical protein GI:4559351 from [Arabidopsis thaliana]
357554	1	9	245	382	1503	1	1	At1g11680	3,00E-50	68414.m01341 obtusifoliol 14-demethylase (CYP51) identical to obtusifoliol 14-demethylase (GI:14624983) [Arabidopsis thaliana]
359687	1	9	245	382	2540	1	1	At4g15110	1,00E-56	68417.m02322 cytochrome P450 97B3, putative (CYP97B3) identical to Cytochrome P450 97B3 (SP:O23365) [Arabidopsis thaliana]
353236	2	9	245	382	2561	1	1	At5g07990	2,00E-47	68418.m00930 flavonoid 3'-monooxygenase / flavonoid 3'-hydroxylase (F3'H) / cytochrome P450 75B1 (CYP75B1) / transparent testa 7 protein (TT7) identical to SP|Q9SD85 Flavonoid 3'-monooxygenase (EC 1.14.13.21) (Flavonoid 3'-hydroxylase) (AtF3'H) (Cytochrome P450 75B1) (TRANSPARENT TESTA 7 protein) {Arabidopsis thaliana}; similar to gi:10334806, gi:10334808
359169	1	9	245	382	2878	2	1	At5g38970	2,00E-21	68418.m04714 cytochrome P450, putative similar to Cytochrome P450 85 (SP:Q43147) {Lycopersicon esculentum};
354993	1	9	245	382	3037	1	4	At5g25900	4,00E-31	68418.m03075 ent-kaurene oxidase, putative (GA3) / cytochrome P450 identical to GA3 [Arabidopsis thaliana] GI:3342249; similar to ent-kaurene oxidase [Cucurbita maxima] GI:11934675; contains Pfam profile PF00067: Cytochrome P450
359963	1	9	245	382	3124	8	13	At3g14680	4,00E-42	68416.m01857 cytochrome P450, putative similar to GB:Q05047 from [Catharanthus roseus]
355199	1	9	245	382	3834	2	1	At5g08250	1,00E-37	68418.m00969 cytochrome P450 family protein contains Pfam profile: PF00067 cytochrome P450
359583	1	9	245	382	3834	2	1	At5g23190	5,00E-28	68418.m02712 cytochrome P450 family protein contains Pfam profile: PF00067 cytochrome P450
353752	4	9	245	382				At4g31940	5,00E-82	68417.m04539 cytochrome P450, putative cytochrome P450 monooxygenase, Pisum sativum, PATCHX:G894153
354982	1	9	245	382				At2g35320	8,00E-53	68415.m04331 expressed protein

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
359713	1	9	245	382				At2g35320	1,00E-15	68415.m04331 expressed protein
359856	1	9	245	382				At3g52970	2,00E-34	68416.m05839 cytochrome P450 family protein cytochrome P450 76A2, eggplant, PIR:S38534
357264	1	10	57	555	2152	4	1	At5g47280	6,00E-28	68418.m05829 disease resistance protein (NBS-LRR class), putative domain signature NBS-LRR exists, suggestive of a disease resistance protein.
359376	1	10	57	555	4504	1	2	At3g07040	2,00E-34	68416.m00836 disease resistance protein RPM1 (CC-NBS-LRR class), putative domain signature CC-NBS-LRR exists, suggestive of a disease resistance protein. Identical to RPM1 (gi:1361985)
359929	1	10	57	555	4504	1	2	At3g07040	1,00E-25	68416.m00836 disease resistance protein RPM1 (CC-NBS-LRR class), putative domain signature CC-NBS-LRR exists, suggestive of a disease resistance protein. Identical to RPM1 (gi:1361985)
356148	1	10	57	555				At1g61180	6,00E-37	68414.m06894 disease resistance protein (CC-NBS-LRR class), putative domain signature CC-NBS-LRR exists, suggestive of a disease resistance protein.
356589	1	10	57	555				At4g27190	6,00E-12	68417.m03905 disease resistance protein (NBS-LRR class), putative domain signature NBS-LRR exists, suggestive of a disease resistance protein.
353822	3	11	40	496	1864	1	1	At4g34350	1,00E-85	68417.m04881 LytB family protein contains Pfam profile: PF02401 LytB protein
358454	1	11	40	496	1864	1	1	At4g34350	7,00E-37	68417.m04881 LytB family protein contains Pfam profile: PF02401 LytB protein
359813	1	11	40	496	1864	1	1	At4g34350	4,00E-70	68417.m04881 LytB family protein contains Pfam profile: PF02401 LytB protein
356853	1	11	40	496	3529	2	4	At3g48670	1,00E-30	68416.m05314 XH/XS domain-containing protein / XS zinc finger domain-containing protein contains Pfam domains PF03469: XH domain, PF03468: XS domain and PF03470: XS zinc finger domain
357943	1	11	40	496	6226	3	1	At5g41210	3,00E-37	68418.m05008 glutathione S-transferase (GST10) identical to glutathione transferase AtGST 10 [Arabidopsis thaliana] GI:4049401
359298	1	12	2	389	3520	2	1	At5g40810	6,00E-39	68418.m04955 cytochrome c1, putative cytochrome c1, heme protein, mitochondrial precursor (Clone PC13III) [Solanum tuberosum] SWISS-PROT:P25076
355306	1	14	162	204	3395	1	1	At3g47990	6,00E-49	68416.m05232 zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
353413	2	14	162	204	4035	3	2	At1g12760	7,00E-53	68414.m01481 zinc finger (C3HC4-type RING finger) family protein low similarity to SP|Q9NVW2 RING finger protein 12 (LIM domain interacting RING finger protein) {Homo sapiens}; contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)
355908	1	14	162	204	4035	3	2	At4g11680	3,00E-46	68417.m01866 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)
353636	4	14	162	204	4489	1	1	At1g71980	7,00E-90	68414.m08320 protease-associated zinc finger (C3HC4-type RING finger) family protein identical to ReMembR-H2 protein JR702 [Arabidopsis thaliana] gi|6942149|gb|AAF32326; contains Pfam domain, PF02225: protease-associated (PA) domain and Pfam domain, PF00097: Zinc finger, C3HC4 type (RING finger); identical to cDNA ReMembR-H2 protein JR702 mRNA, partial cds GI:6942148
358586	1	14	162	204	4489	1	1	At1g71980	2,00E-13	68414.m08320 protease-associated zinc finger (C3HC4-type RING finger) family protein identical to ReMembR-H2 protein JR702 [Arabidopsis thaliana] gi|6942149|gb|AAF32326; contains Pfam domain, PF02225: protease-associated (PA) domain and Pfam domain, PF00097: Zinc finger, C3HC4 type (RING finger); identical to cDNA ReMembR-H2 protein JR702 mRNA, partial cds GI:6942148
357584	1	14	162	204	5430	2	1	At4g17910	1,00E-09	68417.m02669 zinc finger (C3HC4-type RING finger) family protein / pentatricopeptide (PPR) repeat-containing protein contains Pfam domains PF01535: PPR repeat and PF00097: Zinc finger, C3HC4 type (RING finger)
356317	1	14	162	204	6501	1	1	At5g45290	3,00E-57	68418.m05560 zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)
359050	1	14	162	204	6501	1	1	At5g45290	5,00E-29	68418.m05560 zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)
356227	1	14	162	204	7383	1	2	At5g01980	8,00E-32	68418.m00117 zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
359675	1	14	162	204	7476	1	1	At3g19950	1,00E-19	68416.m02525 zinc finger (C3HC4-type RING finger) family protein contains Pfam domain, PF00097: Zinc finger, C3HC4 type (RING finger)
353470	2	14	162	204	9628	3	1	At3g02340	1,00E-37	68416.m00217 zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 Zinc finger, C3HC4 type (RING finger)
357161	1	14	162	204				At2g34990	3,00E-18	68415.m04293 zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097: Zinc finger, C3HC4 type (RING finger)
353990	8	15	180	173	1974	1	2	At5g22060	1,00E-112	68418.m02569 DNAJ heat shock protein, putative strong similarity to SP|O60884 DnaJ homolog subfamily A member 2 (Dnj3) Homo sapiens, several plant DnaJ proteins from PGR; contains Pfam profiles PF00226 DnaJ domain, PF00684 DnaJ central domain (4 repeats), PF01556 DnaJ C terminal region
358654	1	15	180	173	1974	1	2	At5g22060	3,00E-15	68418.m02569 DNAJ heat shock protein, putative strong similarity to SP|O60884 DnaJ homolog subfamily A member 2 (Dnj3) Homo sapiens, several plant DnaJ proteins from PGR; contains Pfam profiles PF00226 DnaJ domain, PF00684 DnaJ central domain (4 repeats), PF01556 DnaJ C terminal region
360074	1	15	180	173	1974	1	2	At5g22060	2,00E-23	68418.m02569 DNAJ heat shock protein, putative strong similarity to SP|O60884 DnaJ homolog subfamily A member 2 (Dnj3) Homo sapiens, several plant DnaJ proteins from PGR; contains Pfam profiles PF00226 DnaJ domain, PF00684 DnaJ central domain (4 repeats), PF01556 DnaJ C terminal region
354268	2	15	180	173	2647	2	3	At2g22360	1,00E-61	68415.m02653 DNAJ heat shock family protein similar to SP|Q9S5A3 Chaperone protein dnaJ {Listeria monocytogenes}; contains Pfam profiles PF00226 DnaJ domain, PF01556 DnaJ C terminal region, PF00684 DnaJ central domain (4 repeats)
353716	2	15	180	173	3256	1	1	At3g62600	5,00E-46	68416.m07032 DNAJ heat shock family protein similar to DnaJ homolog subfamily B member 11 precursor (SP:Q99KV1){Mus musculus}; contains Pfam PF00226: DnaJ domain; contains PfaPF01556: DnaJ C terminal regionm
355158	1	15	180	173	3770	2	2	At5g11510	3,00E-18	68418.m01343 myb family transcription factor (MYB3R4) contains Pfam profile: PF00249 myb-like DNA-binding domain

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
354240	2	15	180	173	4544	2	2	At1g24120	4,00E-70	68414.m03043 DNAJ heat shock protein, putative similar to Altered Response to Gravity [Arabidopsis thaliana] GI:4249662; contains Pfam profile PF00226 DnaJ domain
353142	2	15	180	173	4575	2	2	At4g39150	5,00E-90	68417.m05545 DNAJ heat shock N-terminal domain-containing protein similar to SP|P39101 CAJ1 protein, Saccharomyces cerevisiae, PIR2:S48085; contains Pfam profile PF00226 DnaJ domain
356774	1	15	180	173	5269	1	1	At3g57340	8,00E-21	68416.m06383 DNAJ heat shock N-terminal domain-containing protein similar to SP|Q9QYI4 DnaJ homolog subfamily B member 12 Mus musculus; contains Pfam profile PF00226 DnaJ domain
355019	1	15	180	173	6527	1	2	At4g38620	1,00E-73	68417.m05465 myb family transcription factor (MYB4) contains Pfam profile: PF00249 myb-like DNA-binding domain
359557	1	15	180	173	6527	1	2	At4g38620	1,00E-61	68417.m05465 myb family transcription factor (MYB4) contains Pfam profile: PF00249 myb-like DNA-binding domain
356349	1	15	180	173	6644	3	2	At3g47600	1,00E-69	68416.m05182 myb family transcription factor (MYB94) contains Pfam profile: PF00249 myb-like DNA-binding domain; identical to cDNA putative transcription factor (MYB94) GI:3941527
356133	1	15	180	173	7011	1	2	At3g61250	3,00E-59	68416.m06855 myb family transcription factor (MYB17) contains PFAM profile: Myb-like DNA-binding domain PF00249
357013	1	15	180	173	7122	1	2	At3g06490	3,00E-44	68416.m00753 myb family transcription factor (MYB108) identical to transcription factor MYB108 GI:15375290 from [Arabidopsis thaliana]
358360	1	15	180	173	7134	1	1	At5g57620	4,00E-56	68418.m07198 myb family transcription factor (MYB36) contains PFAM profile: myb DNA binding domain PF00249
353554	2	15	180	173	8945	1	1	At1g56300	4,00E-23	68414.m06472 DNAJ heat shock N-terminal domain-containing protein similar to SP|Q9QYI7 DnaJ homolog subfamily B member 8 Mus musculus; contains Pfam profile: PF00226: DnaJ domain
354910	1	15	180	173				At3g44110	3,00E-67	68416.m04728 DNAJ heat shock protein, putative (J3) identical to AtJ3 [Arabidopsis thaliana] GI:2641638, strong similarity to several plant DnaJ proteins from PGR; contains Pfam profiles PF00226 DnaJ domain, PF00684 DnaJ central domain (4 repeats), PF01556 DnaJ C terminal region

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
355162	1	15	180	173				At3g08910	2,00E-66	68416.m01037 DNAJ heat shock protein, putative similar to SP|P25685 DnaJ homolog subfamily B member 1 (Heat shock 40 kDa protein 1) {Homo sapiens}; contains Pfam profile PF00226: DnaJ domain
358099	1	15	180	173				At5g17610	4,00E-16	68418.m02065 expressed protein
358717	1	15	180	173				At4g09460	1,00E-61	68417.m01557 myb family transcription factor
354622	1	16	115	234	3182	6	7	At1g22360	4,00E-59	68414.m02797 UDP-glucoronosyl/UDP-glucosyl transferase family protein contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase
354282	2	16	115	234	5397	3	1	At2g22590	1,00E-31	68415.m02678 glycosyltransferase family protein contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase
358775	1	16	115	234	5973	4	6	At1g05560	2,00E-17	68414.m00573 UDP-glucose transferase (UGT75B2) similar to UDP-glucose:indole-3-acetate beta-D-glucosyltransferase GI:2149127 from (Arabidopsis thaliana); identical to cDNA UDP-glucosyltransferase (UGT75B2) GI:13661274
357182	1	18	31	302	11	1	2	At4g35800	1,00E-11	68417.m05087 DNA-directed RNA polymerase II largest subunit (RPB205) (RPII) (RPB1) nearly identical to P|P18616 DNA-directed RNA polymerase II largest subunit (EC 2.7.7.6) {Arabidopsis thaliana}
356120	1	18	31	302	1224	3	1	At1g12360	8,00E-54	68414.m01428 cytokinesis-related Sec1 protein (KEULE) similar to cytokinesis-related Sec1 protein KEULE [Arabidopsis thaliana] gi|12659318|gb|AAK01291; contains Pfam domain, PF00995: Sec1 family
356404	1	18	31	302	1661	1	1	At2g17980	6,00E-54	68415.m02090 sec1 family protein similar to SWISS-PROT:P22213 SLY1 protein [Saccharomyces cerevisiae]; contains Pfam domain, PF00995: Sec1 family
359954	1	18	31	302	1661	1	1	At2g17980	8,00E-10	68415.m02090 sec1 family protein similar to SWISS-PROT:P22213 SLY1 protein [Saccharomyces cerevisiae]; contains Pfam domain, PF00995: Sec1 family
356180	1	18	31	302	4925	1	1	At5g04460	7,00E-24	68418.m00443 expressed protein

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
357212	1	18	31	302	7351	2	3	At1g16340	1,00E-06	68414.m01955 2-dehydro-3-deoxyphosphooctonate aldolase, putative / phospho-2-dehydro-3-deoxyoctonate aldolase, putative / 3-deoxy-D-manno-octulosonic acid 8-phosphate synthetase, putative similar to Swiss-Prot:Q9AV97 2-dehydro-3-deoxyphosphooctonate aldolase (EC 4.1.2.16) (Phospho-2-dehydro-3-deoxyoctonate aldolase) (3-deoxy-D-manno-octulosonic acid 8-phosphate synthetase) (KDO-8-phosphate synthetase) (KDO 8-P synthase) [Arabidopsis thaliana]
353253	4	18	31	302	7513	1	14	At5g41980	9,00E-53	68418.m05111 expressed protein
354736	1	18	31	302	8869	2	9	At2g28230	6,00E-21	68415.m03427 expressed protein
360010	1	19	39	270	3690	1	2	At3g52870	2,00E-53	68416.m05826 calmodulin-binding family protein contains Pfam profile PF00612: IQ calmodulin-binding motif
356684	1	19	39	270	4663	2	3	At1g52520	3,00E-16	68414.m05929 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
356215	1	19	39	270	5067	5	1	At2g32250	1,00E-12	68415.m03942 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
356900	1	19	39	270	5067	5	1	At3g22170	1,00E-35	68416.m02798 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
359507	1	19	39	270	5067	5	1	At4g15090	4,00E-08	68417.m02318 far-red impaired response protein (FAR1) / far-red impaired responsive protein (FAR1) identical to far-red impaired response protein FAR1 [Arabidopsis thaliana] gi|5764395|gb|AAD51282; contains Pfam:PF03101 domain: FAR1 family
357757	1	19	39	270				At4g38170	8,00E-28	68417.m05389 far-red impaired responsive protein, putative / SWIM zinc finger family protein similar to far-red impaired response protein [Arabidopsis thaliana] GI:5764395; contains Pfam profile PF04434: SWIM zinc finger
358204	1	20	4	259	1492	2	1	At4g07410	7,00E-46	68417.m01136 transducin family protein / WD-40 repeat family protein contains 7 WD-40 repeats (PF00400) (2 weak); similar to Vegetatible incompatibility protein HET-E-1 (SP:Q00808) {Podospora anserina}
355586	1	20	4	259	5090	2	2	At5g10010	3,00E-40	68418.m01159 expressed protein

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
356726	1	21	195	52	470	2	1	At5g42140	9,00E-32	68418.m05130 zinc finger protein, putative / regulator of chromosome condensation (RCC1) family protein similar to zinc finger protein [Arabidopsis thaliana] gi|15811367|gb|AAL08940
357681	1	21	195	52	485	1	1	At3g03790	9,00E-08	68416.m00389 ankyrin repeat family protein / regulator of chromosome condensation (RCC1) family protein similar to hect domain and RLD 2 GB:NP_004658 [Homo sapiens]; contains Pfam PF00415: Regulator of chromosome condensation (RCC1); contains Pfam PF00023: Ankyrin repeat; similar to rjs (GI:3414809) [Mus musculus]; similar to HERC2 (GI:4079809) [Homo sapiens]
356669	1	21	195	52	1814	1	1	At3g26100	7,00E-80	68416.m03250 regulator of chromosome condensation (RCC1) family protein weak similarity to UVB-resistance protein UVR8 [Arabidopsis thaliana] GI:5478530; contains Pfam profile PF00415: Regulator of chromosome condensation (RCC1)
356887	1	21	195	52	1814	1	1	At3g26100	3,00E-12	68416.m03250 regulator of chromosome condensation (RCC1) family protein weak similarity to UVB-resistance protein UVR8 [Arabidopsis thaliana] GI:5478530; contains Pfam profile PF00415: Regulator of chromosome condensation (RCC1)
352956	3	21	195	52	2020	1	2	At5g63860	4,00E-69	68418.m08016 UVB-resistance protein (UVR8) identical to UVB-resistance protein UVR8 (GI:5478530, GB:AAD43920.1) [Arabidopsis thaliana]; contains Pfam 00415: Regulator of chromosome condensation (RCC1)
354275	2	21	195	52	2020	1	2	At5g63860	2,00E-51	68418.m08016 UVB-resistance protein (UVR8) identical to UVB-resistance protein UVR8 (GI:5478530, GB:AAD43920.1) [Arabidopsis thaliana]; contains Pfam 00415: Regulator of chromosome condensation (RCC1)
359253	1	21	195	52	2267	1	1	At1g19270	6,00E-62	68414.m02397 ubiquitin interaction motif-containing protein / LIM domain-containing protein weak similarity to LIM-homeobox protein [Mus musculus] GI:2149584, Hic-5 [Mus musculus] GI:664955; contains Pfam profiles PF02809: Ubiquitin interaction motif, PF00412: LIM domain
356563	1	21	195	52	2504	2	1	At5g16040	2,00E-64	68418.m01875 regulator of chromosome condensation (RCC1) family protein similar to UVB-resistance protein UVR8 [Arabidopsis thaliana] GI:5478530; contains Pfam profile PF00415: Regulator of chromosome condensation (RCC1)

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
356354	1	21	195	52	3615	1	1	At2g39830	3,00E-85	68415.m04892 LIM domain-containing protein contains Pfam profile PF00412: LIM domain
355960	1	21	195	52	4843	1	1	At5g45550	9,00E-102	68418.m05594 mob1/phocein family protein contains Pfam profile: PF03637 Mob1/phocein family
353078	3	21	195	52	6752	8	1	At1g69545	2,00E-21	68414.m07997 leucine-rich repeat family protein contains Pfam PF00560: Leucine Rich Repeat domains; similar to disease resistance protein RPP1-WsA (GI:3860163)[Arabidopsis thaliana]
353127	2	21	195	52	6752	8	1	At1g69545	5,00E-10	68414.m07997 leucine-rich repeat family protein contains Pfam PF00560: Leucine Rich Repeat domains; similar to disease resistance protein RPP1-WsA (GI:3860163)[Arabidopsis thaliana]
353269	2	21	195	52	6752	8	1	At2g14080	1,00E-12	68415.m01566 disease resistance protein (TIR-NBS-LRR class), putative domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.
353632	2	21	195	52	6752	8	1	At1g69545	2,00E-27	68414.m07997 leucine-rich repeat family protein contains Pfam PF00560: Leucine Rich Repeat domains; similar to disease resistance protein RPP1-WsA (GI:3860163)[Arabidopsis thaliana]
354377	4	21	195	52	6752	8	1	At1g69545	2,00E-45	68414.m07997 leucine-rich repeat family protein contains Pfam PF00560: Leucine Rich Repeat domains; similar to disease resistance protein RPP1-WsA (GI:3860163)[Arabidopsis thaliana]
356626	1	21	195	52	6752	8	1	At1g69545	1,00E-21	68414.m07997 leucine-rich repeat family protein contains Pfam PF00560: Leucine Rich Repeat domains; similar to disease resistance protein RPP1-WsA (GI:3860163)[Arabidopsis thaliana]
357968	1	21	195	52	6752	8	1	At1g69545	1,00E-13	68414.m07997 leucine-rich repeat family protein contains Pfam PF00560: Leucine Rich Repeat domains; similar to disease resistance protein RPP1-WsA (GI:3860163)[Arabidopsis thaliana]
358067	1	21	195	52	6752	8	1	At5g44510	2,00E-21	68418.m05453 disease resistance protein (TIR-NBS-LRR class), putative domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.
358128	1	21	195	52	6752	8	1	At1g69545	2,00E-24	68414.m07997 leucine-rich repeat family protein contains Pfam PF00560: Leucine Rich Repeat domains; similar to disease resistance protein RPP1-WsA (GI:3860163)[Arabidopsis thaliana]
359951	1	21	195	52	6752	8	1	At5g44510	2,00E-14	68418.m05453 disease resistance protein (TIR-NBS-LRR class), putative domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
353534	2	21	195	52				At5g36930	7,00E-34	68418.m04427 disease resistance protein (TIR-NBS-LRR class), putative domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.
354049	2	21	195	52				At5g40060	7,00E-08	68418.m04860 disease resistance protein (TIR-NBS-LRR class), putative domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein. False intron created at intron 2 to escape a frameshift in the BAC sequence.
354994	1	21	195	52				At1g17615	1,00E-21	68414.m02177 disease resistance protein (TIR-NBS class), putative domain signature TIR exists, suggestive of a disease resistance protein.
355404	1	21	195	52				At1g27170	4,00E-21	68414.m03310 disease resistance protein (TIR-NBS-LRR class), putative domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.
355469	1	21	195	52				At1g72890	2,00E-30	68414.m08431 disease resistance protein (TIR-NBS class), putative domain signature TIR-NBS exists, suggestive of a disease resistance protein.
355874	1	21	195	52				At3g04220	8,00E-13	68416.m00446 disease resistance protein (TIR-NBS-LRR class), putative domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.
356137	1	21	195	52				At1g27170	6,00E-10	68414.m03310 disease resistance protein (TIR-NBS-LRR class), putative domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.
356523	1	21	195	52				At1g27170	7,00E-12	68414.m03310 disease resistance protein (TIR-NBS-LRR class), putative domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.
356826	1	21	195	52				At5g36930	3,00E-07	68418.m04427 disease resistance protein (TIR-NBS-LRR class), putative domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.
356835	1	21	195	52				At1g27170	2,00E-18	68414.m03310 disease resistance protein (TIR-NBS-LRR class), putative domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.
356937	1	21	195	52				At5g45200	2,00E-12	68418.m05548 disease resistance protein (TIR-NBS-LRR class), putative domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.
357250	1	21	195	52				At1g27170	4,00E-08	68414.m03310 disease resistance protein (TIR-NBS-LRR class), putative domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.
358249	1	21	195	52				At5g36930	4,00E-22	68418.m04427 disease resistance protein (TIR-NBS-LRR class), putative domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
358434	1	21	195	52				At5g36930	1,00E-25	68418.m04427 disease resistance protein (TIR-NBS-LRR class), putative domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.
359545	1	21	195	52				At1g27170	1,00E-21	68414.m03310 disease resistance protein (TIR-NBS-LRR class), putative domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.
359613	1	21	195	52				At1g27170	5,00E-26	68414.m03310 disease resistance protein (TIR-NBS-LRR class), putative domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.
357303	1	22	83	161	3835	1	1	At1g77490	2,00E-44	68414.m09024 L-ascorbate peroxidase, thylakoid-bound (tAPX) identical to thylakoid-bound ascorbate peroxidase GB:CAA67426 [Arabidopsis thaliana]
354084	2	22	83	161	4159	1	1	At5g66390	2,00E-98	68418.m08372 peroxidase 72 (PER72) (P72) (PRXR8) identical to SP|Q9FJZ9 Peroxidase 72 precursor (EC 1.11.1.7) (Atperox P72) (PRXR8) (ATP6a) {Arabidopsis thaliana}
354618	1	22	83	161	4284	1	2	At4g35000	1,00E-50	68417.m04963 L-ascorbate peroxidase 3 (APX3) identical to ascorbate peroxidase 3 [Arabidopsis thaliana] GI:2444019, L-ascorbate peroxidase [Arabidopsis thaliana] gi|1523791|emb|CAA66926; similar to ascorbate peroxidase [Gossypium hirsutum] gi|1019946|gb|AAB52954
354679	1	22	83	161	4586	1	1	At2g22420	3,00E-40	68415.m02658 peroxidase 17 (PER17) (P17) identical to SP|Q9SJZ2 Peroxidase 17 precursor (EC 1.11.1.7) (Atperox P17) (ATP25a) {Arabidopsis thaliana}
353130	2	22	83	161	4742	1	2	At1g07890	5,00E-64	68414.m00858 L-ascorbate peroxidase 1, cytosolic (APX1) identical to SP|Q05431 L-ascorbate peroxidase, cytosolic (EC 1.11.1.11) (AP) {Arabidopsis thaliana}, L-ascorbate peroxidase [Arabidopsis thaliana] gi|16173|emb|CAA42168; strong similarity to cytosolic ascorbate peroxidase [Spinacia oleracea] gi|1384110|dbj|BAA12890
353690	6	22	83	161	4742	1	2	At1g07890	2,00E-117	68414.m00858 L-ascorbate peroxidase 1, cytosolic (APX1) identical to SP|Q05431 L-ascorbate peroxidase, cytosolic (EC 1.11.1.11) (AP) {Arabidopsis thaliana}, L-ascorbate peroxidase [Arabidopsis thaliana] gi|16173|emb|CAA42168; strong similarity to cytosolic ascorbate peroxidase [Spinacia oleracea] gi|1384110|dbj|BAA12890

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
352928	2	22	83	161	4841	1	2	At5g05340	5,00E-65	68418.m00575 peroxidase, putative similar to peroxidase [Nicotiana tabacum] gi|5381253|dbj|BAA82306; similar to Peroxidase P7 [Brassica rapa (Turnip)] SWISS-PROT:P00434
353964	8	22	83	161				At4g21960	7,00E-149	68417.m03178 peroxidase 42 (PER42) (P42) (PRXR1) identical to SP|Q9SB81 Peroxidase 42 precursor (EC 1.11.1.7) (Atperox P42) (PRXR1) (ATP1a/ATP1b) {Arabidopsis thaliana}
354050	10	22	83	161				At4g21960	2,00E-98	68417.m03178 peroxidase 42 (PER42) (P42) (PRXR1) identical to SP|Q9SB81 Peroxidase 42 precursor (EC 1.11.1.7) (Atperox P42) (PRXR1) (ATP1a/ATP1b) {Arabidopsis thaliana}
354335	2	22	83	161				At5g40150	2,00E-60	68418.m04872 peroxidase, putative identical to peroxidase ATP26a {Arabidopsis thaliana} GP|1890317|emb|CAA72487
355667	1	22	83	161				At3g28200	4,00E-15	68416.m03523 peroxidase, putative similar to peroxidase ATP26a GB:CAA72487 GI:1890317 [Arabidopsis thaliana]
356883	1	22	83	161				At4g21960	1,00E-26	68417.m03178 peroxidase 42 (PER42) (P42) (PRXR1) identical to SP|Q9SB81 Peroxidase 42 precursor (EC 1.11.1.7) (Atperox P42) (PRXR1) (ATP1a/ATP1b) {Arabidopsis thaliana}
354463	2	23	52	189	1122	2	2	At1g62740	5,00E-98	68414.m07081 stress-inducible protein, putative similar to sti (stress inducible protein) [Glycine max] GI:872116; contains Pfam profile PF00515 TPR Domain
355863	1	23	52	189	2318	1	1	At5g14230	2,00E-29	68418.m01663 ankyrin repeat family protein contains ankyrin repeats, Pfam:PF00023
357839	1	23	52	189	2318	1	1	At5g14230	7,00E-07	68418.m01663 ankyrin repeat family protein contains ankyrin repeats, Pfam:PF00023
358393	1	23	52	189	2318	1	1	At5g14230	4,00E-23	68418.m01663 ankyrin repeat family protein contains ankyrin repeats, Pfam:PF00023
358751	1	23	52	189	2758	1	1	At5g57740	3,00E-34	68418.m07218 zinc finger (C3HC4-type RING finger) family protein / ankyrin repeat family protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger) and Pfam profile: PF00023 ankyrin repeat
353172	2	23	52	189	2976	1	1	At2g28840	4,00E-57	68415.m03506 ankyrin repeat family protein contains ankyrin repeats, Pfam:PF00023
354296	2	23	52	189	2976	1	1	At2g28840	1,00E-39	68415.m03506 ankyrin repeat family protein contains ankyrin repeats, Pfam:PF00023
353958	5	23	52	189	3358	1	2	At3g01750	5,00E-65	68416.m00112 ankyrin repeat family protein contains ankyrin repeats, Pfam:PF00023

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
355601	1	23	52	189	3358	1	2	At3g01750	2,00E-11	68416.m00112 ankyrin repeat family protein contains ankyrin repeats, Pfam:PF00023
357408	1	23	52	189	3358	1	2	At3g01750	2,00E-40	68416.m00112 ankyrin repeat family protein contains ankyrin repeats, Pfam:PF00023
356725	1	23	52	189	3432	1	1	At3g04710	3,00E-65	68416.m00505 ankyrin repeat family protein contains Pfam profile: PF00023 ankyrin repeat
353058	2	23	52	189				At4g12400	1,00E-71	68417.m01960 stress-inducible protein, putative similar to sti (stress inducible protein) [Glycine max] GI:872116; contains Pfam profile PF00515 TPR Domain
357078	1	23	52	189				At2g24600	6,00E-18	68415.m02939 ankyrin repeat family protein contains ankyrin repeats, Pfam:PF00023
356531	1	24	106	135	3666	1	1	At2g23540	2,00E-61	68415.m02809 GDSL-motif lipase/hydrolase family protein similar to family II lipase EXL1 GI:15054382 from [Arabidopsis thaliana]; contains Pfam profile PF00657: GDSL-like Lipase/Acylhydrolase
353416	2	24	106	135	3946	4	2	At1g29670	6,00E-36	68414.m03626 GDSL-motif lipase/hydrolase family protein similar to family II lipase EXL1 GI:15054382 from [Arabidopsis thaliana]; contains Pfam profile: PF00657 Lipase/Acylhydrolase with GDSL-like motif
353527	5	24	106	135	3946	4	2	At1g29660	8,00E-49	68414.m03625 GDSL-motif lipase/hydrolase family protein low similarity to family II lipase EXL1 [Arabidopsis thaliana] GI:15054382; contains InterPro Entry IPR001087 Lipolytic enzyme, G-D-S-L family
354207	7	24	106	135	3946	4	2	At1g29660	1,00E-67	68414.m03625 GDSL-motif lipase/hydrolase family protein low similarity to family II lipase EXL1 [Arabidopsis thaliana] GI:15054382; contains InterPro Entry IPR001087 Lipolytic enzyme, G-D-S-L family
354415	3	24	106	135	3946	4	2	At4g18970	2,00E-39	68417.m02794 GDSL-motif lipase/hydrolase family protein similar to family II lipases EXL3 GI:15054386, EXL1 GI:15054382, EXL2 GI:15054384 from [Arabidopsis thaliana]; contains Pfam profile PF00657: GDSL-like Lipase/Acylhydrolase
354712	1	24	106	135	3946	4	2	At4g18970	3,00E-17	68417.m02794 GDSL-motif lipase/hydrolase family protein similar to family II lipases EXL3 GI:15054386, EXL1 GI:15054382, EXL2 GI:15054384 from [Arabidopsis thaliana]; contains Pfam profile PF00657: GDSL-like Lipase/Acylhydrolase
355693	1	24	106	135	3946	4	2	At5g45670	9,00E-45	68418.m05615 GDSL-motif lipase/hydrolase family protein similar to family II lipases EXL3 GI:15054386, EXL1 GI:15054382, EXL2 GI:15054384 from [Arabidopsis thaliana]; contains Pfam profile PF00657: GDSL-like Lipase/Acylhydrolase

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
359542	1	24	106	135	3946	4	2	At4g18970	4,00E-46	68417.m02794 GDSL-motif lipase/hydrolase family protein similar to family II lipases EXL3 GI:15054386, EXL1 GI:15054382, EXL2 GI:15054384 from [Arabidopsis thaliana]; contains Pfam profile PF00657: GDSL-like Lipase/Acylhydrolase
359917	1	24	106	135	3946	4	2	At5g45670	1,00E-17	68418.m05615 GDSL-motif lipase/hydrolase family protein similar to family II lipases EXL3 GI:15054386, EXL1 GI:15054382, EXL2 GI:15054384 from [Arabidopsis thaliana]; contains Pfam profile PF00657: GDSL-like Lipase/Acylhydrolase
354952	1	24	106	135	4024	1	1	At3g16370	2,00E-43	68416.m02071 GDSL-motif lipase/hydrolase family protein similar to family II lipases EXL3 GI:15054386, EXL1 GI:15054382, EXL2 GI:15054384 from [Arabidopsis thaliana]; contains Pfam profile: PF00657 Lipase Acylhydrolase with GDSL-like motif
357211	1	24	106	135	4189	1	1	At1g54790	1,00E-54	68414.m06248 GDSL-motif lipase/hydrolase family protein similar to early nodulin ENOD8 [Medicago sativa] GI:304037, elicitor-induced glycoprotein iEP4 [Daucus carota] GI:1911765, lanatoside 15'-O-acetylesterase [Digitalis lanata] GI:3688284; contains InterPro Entry IPR001087 Lipolytic enzyme, G-D-S-L family
357082	1	24	106	135	4863	3	1	At5g22810	7,00E-47	68418.m02667 GDSL-motif lipase, putative similar to EXL3 (GP:15054386) [Arabidopsis thaliana]
359843	1	24	106	135	5413	1	1	At4g26790	2,00E-18	68417.m03859 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
355843	1	24	106	135				At5g45960	5,00E-30	68418.m05651 GDSL-motif lipase/hydrolase family protein
356173	1	24	106	135				At4g16230	2,00E-11	68417.m02463 GDSL-motif lipase/hydrolase family protein similar to SP|P40602 Anther-specific proline-rich protein APG precursor {Arabidopsis thaliana}; contains Pfam profile PF00657: GDSL-like Lipase/Acylhydrolase
357812	1	24	106	135				At5g14450	1,00E-34	68418.m01691 GDSL-motif lipase/hydrolase family protein similar to early nodulin ENOD8 [Medicago sativa] GI:304037, elicitor-induced glycoprotein iEP4 [Daucus carota] GI:1911765, pollen-expressed coil protein [Medicago sativa] GI:1110502; contains InterPro Entry IPR001087 Lipolytic enzyme, G-D-S-L family

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358566	1	24	106	135				At1g71250	2,00E-13	68414.m08223 GDSL-motif lipase/hydrolase family protein similar to family II lipases EXL3 GI:15054386, EXL1 GI:15054382, EXL2 GI:15054384 from [Arabidopsis thaliana]; contains Pfam profile: PF00657 lipase/acylhydrolase with GDSL-like motif
359706	1	24	106	135				At1g71250	6,00E-24	68414.m08223 GDSL-motif lipase/hydrolase family protein similar to family II lipases EXL3 GI:15054386, EXL1 GI:15054382, EXL2 GI:15054384 from [Arabidopsis thaliana]; contains Pfam profile: PF00657 lipase/acylhydrolase with GDSL-like motif
354836	1	25	104	127	51	1	8	At1g15520	3,00E-54	68414.m01867 ABC transporter family protein similar to ABC1 protein GI:14331118 from [Nicotiana plumbaginifolia]
357012	1	25	104	127	51	1	8	At1g15520	3,00E-24	68414.m01867 ABC transporter family protein similar to ABC1 protein GI:14331118 from [Nicotiana plumbaginifolia]
358569	1	25	104	127	59	1	1	At2g36910	9,00E-22	68415.m04527 multidrug resistance P-glycoprotein (PGP1) identical to P-glycoprotein GI:3849833 from [Arabidopsis thaliana]; homologous to mammalian mdr gene,contains ATP-binding cassette; related to multi drug resistance proteins
354002	2	25	104	127	68	2	1	At4g25960	1,00E-29	68417.m03735 multidrug resistance P-glycoprotein, putative similar to multidrug resistant P-glycoprotein GI:4204793 from [Solanum tuberosum]
354509	1	25	104	127	79	1	1	At2g26910	3,00E-72	68415.m03228 ABC transporter family protein similar to PDR5-like ABC transporter GI:1514643 from [Spirodela polyrhiza]
356415	1	25	104	127	105	4	1	At1g02520	2,00E-22	68414.m00203 multidrug resistance P-glycoprotein, putative similar to multidrug-resistant protein CjMDR1 GI:14715462 from [Coptis japonica]
354508	1	25	104	127	116	2	2	At3g53480	2,00E-47	68416.m05904 ABC transporter family protein PDR5-like ABC transporter, Spirodela polyrrhiza, EMBL:Z70524
358378	1	25	104	127	349	1	1	At2g07680	3,00E-12	68415.m00992 ABC transporter family protein
355242	1	25	104	127	544	1	2	At1g17840	3,00E-49	68414.m02208 ABC transporter family protein similar to ABC transporter GI:10280532 from [Homo sapiens]
355665	1	25	104	127	929	1	1	At5g39040	1,00E-25	68418.m04724 ABC transporter (TAP2) TAP-like ABC transporter, Rattus norvegicus, EMBL:AB027520; identical to cDNA transporter associated with antigen processing-like protein (TAP2); GI:19335723

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
358101	1	25	104	127	929	1	1	At5g39040	3,00E-52	68418.m04724 ABC transporter (TAP2) TAP-like ABC transporter, Rattus norvegicus, EMBL:AB027520; identical to cDNA transporter associated with antigen processing-like protein (TAP2); GI:19335723
358499	1	25	104	127	929	1	1	At5g39040	5,00E-42	68418.m04724 ABC transporter (TAP2) TAP-like ABC transporter, Rattus norvegicus, EMBL:AB027520; identical to cDNA transporter associated with antigen processing-like protein (TAP2); GI:19335723
353839	2	25	104	127				At2g13610	1,00E-46	68415.m01500 ABC transporter family protein
354547	1	26	62	166	2855	1	2	At5g48930	2,00E-53	68418.m06053 transferase family protein similar to anthranilate N-hydroxycinnamoyl/benzoyltransferase from Dianthus caryophyllus [GI:3288180, GI:2239091]; contains Pfam profile PF02458 transferase family
353457	2	26	62	166	5670	2	1	At4g26630	1,00E-19	68417.m03837 expressed protein
357808	1	26	62	166	5670	2	1	At4g26630	4,00E-13	68417.m03837 expressed protein
353905	2	26	62	166				At3g48710	6,00E-13	68416.m05319 expressed protein putative protein - Arabidopsis thaliana, EMBL:AL078465.1
354094	3	26	62	166				At3g48710	4,00E-16	68416.m05319 expressed protein putative protein - Arabidopsis thaliana, EMBL:AL078465.1
354643	1	26	62	166				At3g48710	2,00E-21	68416.m05319 expressed protein putative protein - Arabidopsis thaliana, EMBL:AL078465.1
355990	1	26	62	166				At4g31910	3,00E-16	68417.m04534 transferase family protein low similarity to anthranilate N-hydroxycinnamoyl/benzoyltransferase Dianthus caryophyllus GI:3288180, 10-deacetylbaccatin III-10-O-acetyl transferase Taxus cuspidata GI:6746554; contains Pfam profile PF02458 transferase family
357397	1	26	62	166				At3g48710	8,00E-24	68416.m05319 expressed protein putative protein - Arabidopsis thaliana, EMBL:AL078465.1
354652	1	28	214	2	5211	1	2	At2g38560	8,00E-30	68415.m04737 transcription factor S-II (TFIIS) domain-containing protein similar to SP|P49373 Transcription elongation factor S-II (TFIIS) {Schizosaccharomyces pombe}; contains Pfam profile PF01096: Transcription factor S-II (TFIIS)
357031	1	28	214	2	5211	1	2	At2g38560	1,00E-08	68415.m04737 transcription factor S-II (TFIIS) domain-containing protein similar to SP|P49373 Transcription elongation factor S-II (TFIIS) {Schizosaccharomyces pombe}; contains Pfam profile PF01096: Transcription factor S-II (TFIIS)

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
353270	2	29	5	211	2494	1	1	At1g18560	2,00E-11	68414.m02315 hAT dimerisation domain-containing protein / BED zinc finger domain-containing protein / transposase-related weak similarity to Tam3-transposase [Antirrhinum majus] GI:16064; contains Pfam profiles PF02892: BED zinc finger, PF05699: hAT family dimerisation domain
355339	1	29	5	211	2494	1	1	At1g18560	8,00E-42	68414.m02315 hAT dimerisation domain-containing protein / BED zinc finger domain-containing protein / transposase-related weak similarity to Tam3-transposase [Antirrhinum majus] GI:16064; contains Pfam profiles PF02892: BED zinc finger, PF05699: hAT family dimerisation domain
356555	1	29	5	211	2494	1	1	At1g18560	7,00E-08	68414.m02315 hAT dimerisation domain-containing protein / BED zinc finger domain-containing protein / transposase-related weak similarity to Tam3-transposase [Antirrhinum majus] GI:16064; contains Pfam profiles PF02892: BED zinc finger, PF05699: hAT family dimerisation domain
359841	1	30	99	115	5491	1	2	At4g22880	3,00E-29	68417.m03304 leucoanthocyanidin dioxygenase, putative / anthocyanidin synthase, putative similar to SP|P51091 [Malus domestica]; contains PF03171 2OG-Fe(II) oxygenase superfamily
359971	1	30	99	115	5491	1	2	At4g22880	4,00E-74	68417.m03304 leucoanthocyanidin dioxygenase, putative / anthocyanidin synthase, putative similar to SP|P51091 [Malus domestica]; contains PF03171 2OG-Fe(II) oxygenase superfamily
358196	1	30	99	115	6293	3	2	At1g17020	1,00E-78	68414.m02067 oxidoreductase, 2OG-Fe(II) oxygenase family protein similar to flavonol synthase [Petunia x hybrida][GI:311658], leucoanthocyanidin dioxygenase [Malus domestica][SP|P51091]; contains PF03171 2OG-Fe(II) oxygenase superfamily domain
356958	1	30	99	115				At3g50210	4,00E-68	68416.m05490 2-oxoacid-dependent oxidase, putative strong similarity to partial cds of 2-oxoacid-dependent oxidase (din11) from GI:10834554 [Arabidopsis thaliana]
354491	1	31	66	145	1063	1	1	At1g22060	8,00E-28	68414.m02759 expressed protein
355702	1	31	66	145	1375	2	2	At1g47900	5,00E-10	68414.m05334 expressed protein
353870	2	31	66	145	3359	2	1	At1g63300	5,00E-37	68414.m07156 expressed protein similar to Intracellular protein transport protein USO1 (Swiss-Prot:P25386) [Saccharomyces cerevisiae]; similar to Myosin II heavy chain, non muscle (Swiss-Prot:P08799) [Dictyostelium discoideum]

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
355495	1	31	66	145	3387	1	1	At1g24460	8,00E-10	68414.m03081 myosin-related contains TIGRFAM TIGR01612: reticulocyte binding protein; similar to Myosin heavy chain, non-muscle (Zipper protein) (Myosin II) (SP:Q99323) {Drosophila melanogaster} similar to EST gb|T76116
356279	1	31	66	145	3667	2	2	At1g58210	3,00E-11	68414.m06610 kinase interacting family protein similar to kinase interacting protein 1 (GI:13936326) {Petunia integrifolia}
357874	1	31	66	145	4850	1	2	At3g16000	6,00E-22	68416.m02024 matrix-localized MAR DNA-binding protein-related similar to matrix-localized MAR DNA binding protein MFP1 GI:1771158 from [Lycopersicon esculentum]
354757	1	31	66	145	5893	2	2	At1g77580	9,00E-26	68414.m09032 myosin heavy chain-related low similarity to SP|P08799 Myosin II heavy chain, non muscle {Dictyostelium discoideum}
358398	1	31	66	145	6452	1	1	At2g23360	4,00E-13	68415.m02790 transport protein-related contains Pfam PF05911: Plant protein of unknown function (DUF869) profile; weak similarity to Intracellular protein transport protein USO1 (Swiss-Prot:P25386) [Saccharomyces cerevisiae]
355513	1	31	66	145				At2g32240	2,00E-08	68415.m03940 expressed protein contains Pfam profile: PF04508 viral A-type inclusion protein repeat
354145	3	32	106	104	1098	1	1	At1g49760	6,00E-52	68414.m05580 polyadenylate-binding protein, putative / PABP, putative similar to poly(A)-binding protein GB:AAF66825 GI:7673359 from [Nicotiana tabacum]
355920	1	32	106	104	1098	1	1	At1g49760	3,00E-21	68414.m05580 polyadenylate-binding protein, putative / PABP, putative similar to poly(A)-binding protein GB:AAF66825 GI:7673359 from [Nicotiana tabacum]
356792	1	32	106	104	1098	1	1	At1g49760	6,00E-14	68414.m05580 polyadenylate-binding protein, putative / PABP, putative similar to poly(A)-binding protein GB:AAF66825 GI:7673359 from [Nicotiana tabacum]
353599	2	32	106	104	1637	1	1	At2g44710	7,00E-24	68415.m05564 RNA recognition motif (RRM)-containing protein
357217	1	32	106	104	1637	1	1	At2g44710	1,00E-09	68415.m05564 RNA recognition motif (RRM)-containing protein
354395	6	32	106	104	2796	3	1	At3g14100	2,00E-59	68416.m01782 oligouridylate-binding protein, putative similar to GB:CAB75429 (GI:6996560) from [Nicotiana plumbaginifolia], contains Pfam profiles: PF00076 RNA recognition motif (3 copies)

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
354930	1	32	106	104	2796	3	1	At3g14100	2,00E-10	68416.m01782 oligouridylate-binding protein, putative similar to GB:CAB75429 (GI:6996560) from [Nicotiana plumbaginifolia], contains Pfam profiles: PF00076 RNA recognition motif (3 copies)
356767	1	32	106	104	2796	3	1	At3g14100	1,00E-46	68416.m01782 oligouridylate-binding protein, putative similar to GB:CAB75429 (GI:6996560) from [Nicotiana plumbaginifolia], contains Pfam profiles: PF00076 RNA recognition motif (3 copies)
358653	1	32	106	104	2796	3	1	At1g17370	8,00E-36	68414.m02118 oligouridylate-binding protein, putative similar to oligouridylate binding protein [Nicotiana plumbaginifolia] GI:6996560; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)
353808	4	32	106	104	3908	1	2	At4g00830	3,00E-82	68417.m00114 RNA recognition motif (RRM)-containing protein similar to nucleolin protein; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)
352986	3	32	106	104	4182	1	1	At1g11650	6,00E-81	68414.m01337 RNA-binding protein 45 (RBP45), putative similar to gb|U90212 DNA binding protein ACBF from Nicotiana tabacum and contains 3 PF|00076 RNA recognition motif domains. ESTs gb|T44278, gb|R65195, gb|N65904, gb|H37499, gb|R90487, gb|N95952, gb|T44278, gb|Z20166, gb|N96891, gb|W43137, gb|F15504, gb|F1
354700	1	32	106	104	4413	1	1	At4g36960	3,00E-67	68417.m05238 RNA recognition motif (RRM)-containing protein similar to SP|P48809 Heterogeneous nuclear ribonucleoprotein 27C (hnRNP 48) {Drosophila melanogaster}; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM); non-consensus TA donor splice site at exon 6
357017	1	32	106	104	4518	1	2	At3g52660	1,00E-29	68416.m05801 RNA recognition motif (RRM)-containing protein heterogeneous nuclear ribonucleoprotein R, Homo sapiens, PIR:T02673; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)
359410	1	32	106	104	4518	1	2	At3g52660	9,00E-24	68416.m05801 RNA recognition motif (RRM)-containing protein heterogeneous nuclear ribonucleoprotein R, Homo sapiens, PIR:T02673; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
354387	4	32	106	104	4738	2	3	At1g47500	1,00E-82	68414.m05272 RNA-binding protein 47 (RBP47), putative similar to DNA binding protein GI:1899187 from [Nicotiana tabacum]
358707	1	32	106	104	4738	2	3	At1g47500	2,00E-13	68414.m05272 RNA-binding protein 47 (RBP47), putative similar to DNA binding protein GI:1899187 from [Nicotiana tabacum]
356001	1	32	106	104	5061	1	1	At1g48920	3,00E-18	68414.m05480 nucleolin, putative similar to nuM1 protein GI:1279562 from [Medicago sativa]
354626	1	32	106	104	5539	2	1	At3g56860	6,00E-39	68416.m06325 UBP1 interacting protein 2a (UBA2a) identical to UBP1 interacting protein 2a [Arabidopsis thaliana] GI:19682816; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)
359741	1	32	106	104	5539	2	1	At2g41060	7,00E-22	68415.m05070 RNA recognition motif (RRM)-containing protein similar to UBP1 interacting protein 1a [Arabidopsis thaliana] GI:19574236; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)
354872	1	32	106	104	5993	1	1	At3g15010	8,00E-13	68416.m01899 RNA recognition motif (RRM)-containing protein similar to UBP1 interacting protein 1a [Arabidopsis thaliana] GI:19574236; contains Pfam profile: PF00076 RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
359460	1	32	106	104	6736	2	2	At4g24770	1,00E-24	68417.m03546 31 kDa ribonucleoprotein, chloroplast, putative / RNA-binding protein RNP-T, putative / RNA-binding protein 1/2/3, putative / RNA-binding protein cp31, putative similar to SP|Q04836 31 kDa ribonucleoprotein, chloroplast precursor (RNA-binding protein RNP-T) (RNA-binding protein 1/2/3) (AtRBP33) (RNA-binding protein cp31) {Arabidopsis thaliana}; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)
355583	1	32	106	104	6925	1	1	At3g04500	6,00E-20	68416.m00477 RNA recognition motif (RRM)-containing protein similar to ssRNA-binding protein [Dictyostelium discoideum] GI:1546894; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)
357702	1	32	106	104	6925	1	1	At3g04500	9,00E-08	68416.m00477 RNA recognition motif (RRM)-containing protein similar to ssRNA-binding protein [Dictyostelium discoideum] GI:1546894; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
353625	2	32	106	104	6927	1	1	At3g20930	1,00E-36	68416.m02645 RNA recognition motif (RRM)-containing protein contains Pfam profile: PF00076 RNA recognition motif
353016	2	32	106	104	7850	1	2	At2g21660	3,00E-17	68415.m02578 glycine-rich RNA-binding protein (GRP7) SP|Q03250 Glycine-rich RNA-binding protein 7 {Arabidopsis thaliana}
353866	2	32	106	104	7850	1	2	At2g21660	7,00E-25	68415.m02578 glycine-rich RNA-binding protein (GRP7) SP|Q03250 Glycine-rich RNA-binding protein 7 {Arabidopsis thaliana}
357565	1	32	106	104	8958	2	1	At4g10170	4,00E-09	68417.m01665 synaptobrevin-related family protein similar to Vesicle-associated membrane protein 722 (AtVAMP722) Synaptobrevin-related protein 1 (SP:P47192) {Arabidopsis thaliana}; vesicle-associated membrane protein 7B, Arabidopsis thaliana, AF025333
353102	3	32	106	104	9192	1	2	At4g10110	1,00E-29	68417.m01654 RNA recognition motif (RRM)-containing protein contains INTERPRO:IPR000504 RNA-binding region RNP-1 (RNA recognition motif) domain
354236	2	32	106	104				At2g47310	1,00E-08	68415.m05906 flowering time control protein-related / FCA gamma-related
354756	1	32	106	104				At2g47310	2,00E-07	68415.m05906 flowering time control protein-related / FCA gamma-related
354923	1	32	106	104				At5g55550	2,00E-61	68418.m06922 RNA recognition motif (RRM)-containing protein similar to DAZ associated protein 1 [Homo sapiens] GI:8671754; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)
355942	1	32	106	104				At3g19130	2,00E-36	68416.m02429 RNA-binding protein, putative similar to RNA Binding Protein 47 [Nicotiana plumbaginifolia] GI:9663769, DNA binding protein ACBF GB:AAC49850 from [Nicotiana tabacum]; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)
356686	1	32	106	104				At5g40490	5,00E-12	68418.m04910 RNA recognition motif (RRM)-containing protein ribonucleoprotein, Xenopus laevis, PIR:S40778; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)
356992	1	32	106	104				At4g27840	3,00E-09	68417.m03998 expressed protein
357824	1	32	106	104				At1g22760	1,00E-22	68414.m02844 polyadenylate-binding protein 3 (PABP3)
355904	1	33	63	147	1343	2	1	At5g61000	3,00E-43	68418.m07652 replication protein, putative similar to replication protein A1 [Oryza sativa] GI:2258469; contains InterPro entry IPR004365: OB-fold nucleic acid binding domain

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
359307	1	34	102	107	645	1	1	At1g15130	1,00E-91	68414.m01807 hydroxyproline-rich glycoprotein family protein
358488	1	37	77	120	2875	1	1	At4g38520	2,00E-81	68417.m05451 protein phosphatase 2C family protein / PP2C family protein similar to Ser/Thr protein phosphatase 2C (PP2C6) (GI:15020818) [Arabidopsis thaliana]; similar to protein phosphatase 2C (GI:3608412) [Mesembryanthemum crystallinum]; contains Pfam PF00481 : Protein phosphatase 2C domain;
353364	2	37	77	120	3449	2	2	At1g68410	2,00E-60	68414.m07815 protein phosphatase 2C-related / PP2C-related similar to protein phosphatase-2C GB:AAC36697 from [Mesembryanthemum crystallinum]
354466	2	37	77	120	3542	1	2	At5g06750	4,00E-95	68418.m00763 protein phosphatase 2C family protein / PP2C family protein similar to Ser/Thr protein phosphatase 2C (PP2C6) (GI:15020818) [Arabidopsis thaliana]; similar to protein phosphatase 2C (GI:3608412) [Mesembryanthemum crystallinum]; contains Pfam PF00481 : Protein phosphatase 2C domain;
353829	3	37	77	120	3645	1	1	At3g16560	7,00E-70	68416.m02116 protein phosphatase 2C-related / PP2C-related contains protein phosphatase 2C domain
354221	3	37	77	120	3808	1	1	At2g25070	1,00E-132	68415.m02999 protein phosphatase 2C, putative / PP2C, putative
356497	1	37	77	120	4258	1	2	At5g53140	5,00E-19	68418.m06606 protein phosphatase 2C, putative / PP2C, putative
358416	1	37	77	120	4262	1	1	At3g17090	2,00E-18	68416.m02180 protein phosphatase 2C family protein / PP2C family protein similar to Ser/Thr protein phosphatase 2C (PP2C6) (GI:15020818) [Arabidopsis thaliana]; similar to protein phosphatase 2C (GI:3608412) [Mesembryanthemum crystallinum]; contains Pfam PF00481 : Protein phosphatase 2C domain;
358814	1	37	77	120	4262	1	1	At3g17090	3,00E-75	68416.m02180 protein phosphatase 2C family protein / PP2C family protein similar to Ser/Thr protein phosphatase 2C (PP2C6) (GI:15020818) [Arabidopsis thaliana]; similar to protein phosphatase 2C (GI:3608412) [Mesembryanthemum crystallinum]; contains Pfam PF00481 : Protein phosphatase 2C domain;

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
359930	1	37	77	120	4262	1	1	At3g17090	7,00E-62	68416.m02180 protein phosphatase 2C family protein / PP2C family protein similar to Ser/Thr protein phosphatase 2C (PP2C6) (GI:15020818) [Arabidopsis thaliana]; similar to protein phosphatase 2C (GI:3608412) [Mesembryanthemum crystallinum]; contains Pfam PF00481 : Protein phosphatase 2C domain;
358458	1	37	77	120	4366	3	1	At4g31750	2,00E-75	68417.m04506 protein phosphatase 2C, putative / PP2C, putative protein phosphatase 2C, Medicago sativa, PID:g2582800
356984	1	37	77	120	4855	1	1	At1g18030	2,00E-24	68414.m02230 protein phosphatase 2C, putative / PP2C, putative contains similarity to protein phosphatase 2C GI:3777604 from [Rattus norvegicus]
354198	2	37	77	120				At3g51370	2,00E-74	68416.m05627 protein phosphatase 2C, putative / PP2C, putative similar to Ser/Thr protein phosphatase 2C (PP2C6) (GI:15020818) [Arabidopsis thaliana]; similar to protein phosphatase 2C (GI:3608412) [Mesembryanthemum crystallinum]; contains Pfam PF00481 : Protein phosphatase 2C domain
355298	1	37	77	120				At3g06270	1,00E-06	68416.m00720 protein phosphatase 2C, putative / PP2C, putative similar to protein phosphatase-2C (PP2C) GB:AAC36699 [Mesembryanthemum crystallinum]; contains Pfam profile: PF00481 protein phosphatase 2C
355654	1	37	77	120				At1g34750	5,00E-57	68414.m04321 protein phosphatase 2C, putative / PP2C, putative similar to GB:AAD17805 from (Lotus japonicus) (Proc. Natl. Acad. Sci. U.S.A. 96 (4), 1738-1743 (1999))
355728	1	37	77	120				At2g46920	2,00E-30	68415.m05861 protein phosphatase 2C family protein / PP2C family protein similar to protein phosphatase-2c (GI:3608412) [Mesembryanthemum crystallinum]; contains Pfam PF00481 : Protein phosphatase 2C domain
356047	1	37	77	120				At1g22280	4,00E-39	68414.m02785 protein phosphatase 2C, putative / PP2C, putative similar to protein phosphatase type 2C GI:4336436 from [Lotus japonicus]
357339	1	37	77	120				At2g40180	4,00E-40	68415.m04941 protein phosphatase 2C, putative / PP2C, putative contains PF00481: Protein phosphatase 2C domain; identical to protein phosphatase 2C (GI:4587992) [Arabidopsis thaliana]

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
357833	1	37	77	120				At5g66080	1,00E-35	68418.m08325 protein phosphatase 2C family protein / PP2C family protein similar to Ser/Thr protein phosphatase 2C (PP2C6) (GI:15020818) [Arabidopsis thaliana]; similar to protein phosphatase 2C (GI:3608412) [Mesembryanthemum crystallinum]; contains Pfam PF00481 : Protein phosphatase 2C domain
358937	1	37	77	120				At1g34750	3,00E-68	68414.m04321 protein phosphatase 2C, putative / PP2C, putative similar to GB:AAD17805 from (Lotus japonicus) (Proc. Natl. Acad. Sci. U.S.A. 96 (4), 1738-1743 (1999))
354965	1	38	66	130	2412	1	1	At5g43100	3,00E-06	68418.m05261 aspartyl protease family protein low similarity to CND41, chloroplast nucleoid DNA binding protein [Nicotiana tabacum] GI:2541876; contains Pfam profile PF00026: Eukaryotic aspartyl protease
358471	1	38	66	130	3219	2	1	At5g22850	5,00E-77	68418.m02671 aspartyl protease family protein contains Pfam profile: PF00026 eukaryotic aspartyl protease
356739	1	38	66	130	3751	2	1	At3g54400	7,00E-40	68416.m06015 aspartyl protease family protein contains Pfam profile: PF00026 eukaryotic aspartyl protease
357255	1	38	66	130	3751	2	1	At3g54400	5,00E-25	68416.m06015 aspartyl protease family protein contains Pfam profile: PF00026 eukaryotic aspartyl protease
358016	1	38	66	130	3751	2	1	At5g07030	4,00E-33	68418.m00796 aspartyl protease family protein contains Pfam profile:PF00026 eukaryotic aspartyl protease
359110	1	38	66	130	3751	2	1	At5g07030	6,00E-12	68418.m00796 aspartyl protease family protein contains Pfam profile:PF00026 eukaryotic aspartyl protease
356080	1	38	66	130	3972	2	1	At1g25510	8,00E-38	68414.m03168 aspartyl protease family protein contains Pfam domain, PF00026: eukaryotic aspartyl protease
353490	2	38	66	130	4966	2	4	At1g03220	5,00E-35	68414.m00300 extracellular dermal glycoprotein, putative / EDGP, putative similar to extracellular dermal glycoprotein EDGP precursor [Daucus carota] GI:285741
356289	1	38	66	130	7053	2	1	At1g76010	5,00E-06	68414.m08825 expressed protein
359070	1	39	66	124	2040	1	1	At2g43330	4,00E-28	68415.m05388 sugar transporter family protein similar to SP|Q96QE2 Proton myo-inositol co-transporter (Hmit) [Homo sapiens], SP|Q01440 Membrane transporter D1 {Leishmania donovani}; contains Pfam profile PF00083: major facilitator superfamily protein
357638	1	39	66	124	2420	1	1	At5g59250	2,00E-64	68418.m07425 sugar transporter family protein similar to D-xylose-H+ symporter from Lactobacillus brevis GI:2895856, sugar-porter family protein 2 [Arabidopsis thaliana] GI:14585701; contains Pfam profile PF00083: major facilitator superfamily protein

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358872	1	39	66	124	2420	1	1	At5g59250	6,00E-51	68418.m07425 sugar transporter family protein similar to D-xylose-H+ symporter from Lactobacillus brevis GI:2895856, sugar-porter family protein 2 [Arabidopsis thaliana] GI:14585701; contains Pfam profile PF00083: major facilitator superfamily protein
355009	1	39	66	124	2838	1	1	At1g79740	2,00E-14	68414.m09302 hAT dimerisation domain-containing protein contains Pfam profiles: PF04937 domain of unknown function (DUF659), PF05699 hAT family dimerisation domain
357380	1	39	66	124	2838	1	1	At1g79740	2,00E-08	68414.m09302 hAT dimerisation domain-containing protein contains Pfam profiles: PF04937 domain of unknown function (DUF659), PF05699 hAT family dimerisation domain
353565	3	39	66	124	3654	1	1	At3g22220	2,00E-08	68416.m02803 hAT dimerisation domain-containing protein contains Pfam profiles PF04937: Protein of unknown function (DUF 659), PF05699 hAT family dimerisation domain
353800	4	39	66	124	3654	1	1	At3g22220	6,00E-18	68416.m02803 hAT dimerisation domain-containing protein contains Pfam profiles PF04937: Protein of unknown function (DUF 659), PF05699 hAT family dimerisation domain
356552	1	39	66	124	3654	1	1	At3g22220	2,00E-15	68416.m02803 hAT dimerisation domain-containing protein contains Pfam profiles PF04937: Protein of unknown function (DUF 659), PF05699 hAT family dimerisation domain
359505	1	39	66	124	9683	2	1	At1g27350	5,00E-11	68414.m03331 expressed protein contains 1 transmembrane domain; similar to ribosome associated membrane protein RAMP4 GI:4585827 [Rattus norvegicus]; similar to ESTs gb|T20610 and gb|AA586199
352940	2	39	66	124				At1g43260	3,00E-06	68414.m04987 hypothetical protein contains Pfam domain, PF04937: Protein of unknown function (DUF 659)
353535	3	39	66	124				At3g17450	3,00E-20	68416.m02228 hAT dimerisation domain-containing protein contains Pfam profile PF04937: Protein of unknown function (DUF 659)
354202	6	39	66	124				At5g33406	3,00E-09	68418.m03990 hAT dimerisation domain-containing protein low similarity to transposase [Fusarium oxysporum f. sp. lycopersici] GI:3126916; contains Pfam profile PF05699: hAT family dimerisation domain

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
355410	1	39	66	124				At5g33406	5,00E-47	68418.m03990 hAT dimerisation domain-containing protein low similarity to transposase [Fusarium oxysporum f. sp. lycopersici] GI:3126916; contains Pfam profile PF05699: hAT family dimerisation domain
355676	1	39	66	124				At3g17450	3,00E-15	68416.m02228 hAT dimerisation domain-containing protein contains Pfam profile PF04937: Protein of unknown function (DUF 659)
355685	1	39	66	124				At3g17450	1,00E-15	68416.m02228 hAT dimerisation domain-containing protein contains Pfam profile PF04937: Protein of unknown function (DUF 659)
355902	1	39	66	124				At3g17450	1,00E-06	68416.m02228 hAT dimerisation domain-containing protein contains Pfam profile PF04937: Protein of unknown function (DUF 659)
359028	1	39	66	124				At3g17450	2,00E-17	68416.m02228 hAT dimerisation domain-containing protein contains Pfam profile PF04937: Protein of unknown function (DUF 659)
359544	1	39	66	124				At2g48020	1,00E-28	68415.m06011 sugar transporter, putative similar to ERD6 protein {Arabidopsis thaliana} GI:3123712, sugar-porter family proteins 1 and 2 [Arabidopsis thaliana] GI:14585699, GI:14585701; contains Pfam profile PF00083: major facilitator superfamily protein
359685	1	39	66	124				At5g33406	8,00E-12	68418.m03990 hAT dimerisation domain-containing protein low similarity to transposase [Fusarium oxysporum f. sp. lycopersici] GI:3126916; contains Pfam profile PF05699: hAT family dimerisation domain
359836	1	40	91	92	5184	1	1	At1g65910	3,00E-11	68414.m07479 no apical meristem (NAM) family protein similar to jasmonic acid 2 GI:6175246 from [Lycopersicon esculentum]; similar to NAC2 (GI:6456751) {Arabidopsis thaliana}
353976	2	40	91	92	6674	2	2	At3g10500	2,00E-47	68416.m01260 no apical meristem (NAM) family protein similar to to NAC2 (GI:645671) [Arabidopsis thaliana]; contains Pfam PF02365: No apical meristem (NAM) protein
354384	2	40	91	92	8211	1	2	At5g64530	2,00E-13	68418.m08110 no apical meristem (NAM) family protein contains Pfam PF02365: No apical meristem (NAM) domain; similar to NAM (no apical meristem)
359550	1	40	91	92	8211	1	2	At5g64530	2,00E-13	68418.m08110 no apical meristem (NAM) family protein contains Pfam PF02365: No apical meristem (NAM) domain; similar to NAM (no apical meristem)
354376	2	40	91	92				At1g69490	1,00E-35	68414.m07985 no apical meristem (NAM) family protein similar to N-term half of NAC domain protein NAM [Arabidopsis thaliana] GI:4325282

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
359986	1	41	77	99	1009	2	1	At1g76390	1,00E-44	68414.m08877 armadillo/beta-catenin repeat family protein / U-box domain-containing protein contains Pfam domain, PF00514: Armadillo/beta-catenin-like repeats and Pfam, PF04564: U-box domain
360034	1	41	77	99	1172	2	1	At2g44900	1,00E-82	68415.m05589 armadillo/beta-catenin repeat family protein / F-box family protein contains similarity to F-box protein FBL2 GI:6010699 from [Rattus norvegicus]; contains Pfam profiles PF00514: Armadillo/beta-catenin-like repeat, PF00646: F-box domain
353309	2	41	77	99	2032	1	1	At2g23140	1,00E-50	68415.m02763 armadillo/beta-catenin repeat family protein / U-box domain-containing protein contains Pfam domain, PF00514: Armadillo/beta-catenin-like repeats and Pfam, PF04564: U-box domain
356798	1	41	77	99	2032	1	1	At2g23140	7,00E-52	68415.m02763 armadillo/beta-catenin repeat family protein / U-box domain-containing protein contains Pfam domain, PF00514: Armadillo/beta-catenin-like repeats and Pfam, PF04564: U-box domain
353649	2	41	77	99	2085	1	2	At2g45720	1,00E-87	68415.m05686 armadillo/beta-catenin repeat family protein contains Pfam profile PF00514: Armadillo/beta-catenin-like repeat
359584	1	41	77	99	2454	1	1	At3g06880	1,00E-21	68416.m00817 transducin family protein / WD-40 repeat family protein similar to PAK/PLC-interacting protein 1 (GI:4211689) {Homo sapiens}
358134	1	41	77	99	5113	2	2	At1g60190	1,00E-29	68414.m06780 armadillo/beta-catenin repeat family protein / U-box domain-containing protein contains Pfam domain, PF00514: Armadillo/beta-catenin-like repeats and Pfam, PF04564: U-box domain
354166	3	41	77	99				At5g13060	1,00E-86	68418.m01497 armadillo/beta-catenin repeat family protein / BTB/POZ domain-containing protein contains armadillo/beta-catenin-like repeats, Pfam:PF00514 and a BTB/POZ domain, Pfam:PF00651
355056	1	41	77	99				At4g12710	7,00E-53	68417.m01995 armadillo/beta-catenin repeat family protein contains Pfam profile: PF00514 armadillo/beta-catenin-like repeat
355230	1	41	77	99				At4g12710	1,00E-69	68417.m01995 armadillo/beta-catenin repeat family protein contains Pfam profile: PF00514 armadillo/beta-catenin-like repeat
355454	1	41	77	99				At5g13060	6,00E-14	68418.m01497 armadillo/beta-catenin repeat family protein / BTB/POZ domain-containing protein contains armadillo/beta-catenin-like repeats, Pfam:PF00514 and a BTB/POZ domain, Pfam:PF00651

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359939	1	41	77	99				At2g45920	9,00E-18	68415.m05710 U-box domain-containing protein contains Pfam profile PF04564: U-box domain
356737	1	42	85	91	2344	3	3	At2g19440	6,00E-30	68415.m02269 glycosyl hydrolase family 17 protein similar to elicitor inducible chitinase Nt-SubE76 GI:11071974 from [Nicotiana tabacum]; an isoform contains a non-consensus GA-AG intron
355817	1	42	85	91	2691	1	1	At1g79050	5,00E-38	68414.m09217 DNA repair protein recA identical to DNA repair protein recA, chloroplast [Precursor] SP:Q39199 from [Arabidopsis thaliana] ;contains Pfam profile: PF00154 recA bacterial DNA recombination protein
357882	1	42	85	91	4507	2	1	At3g55430	2,00E-35	68416.m06156 glycosyl hydrolase family 17 protein / beta-1,3-glucanase, putative similar to beta-1,3 glucanase GI:7414433 from [Pisum sativum]; contains Pfam profile PF00332: Glycosyl hydrolases family 17
357087	1	42	85	91	5961	1	1	At1g30970	2,00E-10	68414.m03792 zinc finger (C2H2 type) family protein contains Pfam domain PF00096: Zinc finger, C2H2 type
353072	4	42	85	91	8784	1	1	At5g67460	4,00E-43	68418.m08505 glycosyl hydrolase family protein 17 similar to beta-1,3-glucanase GI:6714534 from [Salix gilgiana]
353699	2	42	85	91	8784	1	1	At5g67460	1,00E-26	68418.m08505 glycosyl hydrolase family protein 17 similar to beta-1,3-glucanase GI:6714534 from [Salix gilgiana]
359129	1	42	85	91	8979	1	2	At1g18650	5,00E-15	68414.m02325 glycosyl hydrolase family protein 17 similar to beta-1,3-glucanase GI:15150341 from [Camellia sinensis]; C-terminal homology only
355973	1	42	85	91				At4g31140	5,00E-79	68417.m04420 glycosyl hydrolase family 17 protein similar to elicitor inducible chitinase Nt-SubE76 GI:11071974 from [Nicotiana tabacum]
357399	1	43	59	113	1356	2	1	At3g54140	7,00E-46	68416.m05985 proton-dependent oligopeptide transport (POT) family protein contains Pfam profile: PF00854 POT family
353992	2	44	78	92	413	2	1	At2g19170	8,00E-23	68415.m02237 subtilase family protein contains similarity to meiotic serine proteinase TMP GI:6468325 from [Lycopersicon esculentum]
357155	1	44	78	92	413	2	1	At2g19170	2,00E-19	68415.m02237 subtilase family protein contains similarity to meiotic serine proteinase TMP GI:6468325 from [Lycopersicon esculentum]
355115	1	44	78	92	603	2	1	At5g44530	6,00E-40	68418.m05455 subtilase family protein contains Pfam profiles: PF00082 subtilase family
359765	1	44	78	92	603	2	1	At5g44530	7,00E-08	68418.m05455 subtilase family protein contains Pfam profiles: PF00082 subtilase family

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359837	1	44	78	92	603	2	1	At4g20430	2,00E-66	68417.m02981 subtilase family protein contains Pfam profile: PF00082 subtilase family
353389	3	44	78	92	684	1	1	At5g51750	1,00E-67	68418.m06417 subtilase family protein similar to subtilisin-like protease GI:3687307 from [Lycopersicon esculentum]
354522	1	44	78	92	684	1	1	At5g51750	2,00E-55	68418.m06417 subtilase family protein similar to subtilisin-like protease GI:3687307 from [Lycopersicon esculentum]
357688	1	44	78	92	684	1	1	At5g51750	2,00E-40	68418.m06417 subtilase family protein similar to subtilisin-like protease GI:3687307 from [Lycopersicon esculentum]
355900	1	44	78	92	724	1	2	At5g67360	2,00E-29	68418.m08494 cucumisin-like serine protease (ARA12) Asp48; almost identical to cucumisin-like serine protease (ARA12) GI:3176874 from [Arabidopsis thaliana]
358362	1	44	78	92	1091	1	1	At2g04160	6,00E-44	68415.m00400 subtilisin-like protease (AIR3) almost identical to subtilisin-like protease AIR3 GI:4218991 from [Arabidopsis thaliana], missing 200 aa at N-terminus
353524	2	44	78	92	1920	15	1	At4g10510	8,00E-45	68417.m01723 subtilase family protein contains similarity to subtilase; SP1 GI:9957714 from [Oryza sativa]
353056	4	44	78	92	2784	1	2	At1g69420	4,00E-27	68414.m07975 zinc finger (DHHC type) family protein contains Pfam profile: PF01529: DHHC zinc finger domain
359849	1	44	78	92	2784	1	2	At1g69420	4,00E-11	68414.m07975 zinc finger (DHHC type) family protein contains Pfam profile: PF01529: DHHC zinc finger domain
357115	1	44	78	92	3007	2	3	At3g26935	7,00E-20	68416.m03371 zinc finger (DHHC type) family protein contains Pfam profile PF01529: DHHC zinc finger domain
359921	1	44	78	92	3007	2	3	At3g26935	2,00E-70	68416.m03371 zinc finger (DHHC type) family protein contains Pfam profile PF01529: DHHC zinc finger domain
353525	2	44	78	92	3059	2	1	At4g15080	6,00E-18	68417.m02317 zinc finger (DHHC type) family protein contains Pfam profile PF01529: DHHC zinc finger domain
356698	1	44	78	92	5272	1	1	At3g09320	1,00E-36	68416.m01106 zinc finger (DHHC type) family protein similar to Golgi-specific DHHC zinc figer protein [Mus musculus] GI:21728103; contains Pfam profile PF01529: DHHC zinc finger domain

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356495	1	44	78	92	5545	1	1	At3g18620	4,00E-31	68416.m02366 zinc finger (DHHC type) family protein contains Pfam profile: PF01529 DHHC zinc finger domain
358450	1	44	78	92	5939	1	2	At3g51390	2,00E-53	68416.m05629 zinc finger (DHHC type) family protein contains Pfam profile PF01529: DHHC zinc finger domain
357701	1	44	78	92				At5g59190	2,00E-21	68418.m07418 subtilase family protein contains similarity to prepro-cucumisin GI:807698 from [Cucumis melo]
359056	1	44	78	92				At2g14255	4,00E-19	68415.m01593 zinc finger (DHHC type) family protein contains Pfam profile PF01529: DHHC zinc finger domain; low similarity to SP:Q96GR4 Zinc finger DHHC domain containing protein 12 (Zinc finger protein 400) {Homo sapiens}
354728	1	45	151	19	3723	1	1	At5g47380	9,00E-13	68418.m05839 expressed protein contains Pfam profile PF04784: Protein of unknown function, DUF547
354413	2	45	151	19	4068	2	2	At5g66600	2,00E-39	68418.m08395 expressed protein contains Pfam profile PF04784: Protein of unknown function, DUF547; expression supported by MPSS
358524	1	45	151	19	4299	1	1	At4g37080	2,00E-86	68417.m05252 expressed protein contains Pfam profile PF04784: Protein of unknown function, DUF547
358570	1	46	72	97	4902	1	1	At4g26640	1,00E-11	68417.m03839 WRKY family transcription factor contains Pfam profile: PF03106 WRKY DNA -binding domain
359874	1	46	72	97	5180	2	2	At5g56270	3,00E-31	68418.m07022 WRKY family transcription factor
356459	1	46	72	97	9346	1	4	At5g26170	5,00E-25	68418.m03113 WRKY family transcription factor DNA-binding protein, WRKY1 Avena sativa, EMBL:AF140554
353084	2	46	72	97				At2g37260	6,00E-34	68415.m04571 WRKY family transcription factor (TTG2) contains Pfam profile: PF03106 WRKY DNA -binding domain
355795	1	46	72	97				At5g28650	3,00E-10	68418.m03508 WRKY family transcription factor DNA-binding protein WRKY3, parsley, PIR:S72445
353272	3	48	79	78	53	2	3	At1g62020	7,00E-127	68414.m06995 coatomer protein complex, subunit alpha, putative contains Pfam PF00400: WD domain, G-beta repeat; similar to Coatomer alpha subunit (Alpha-coat protein) (Alpha-COP) (HEPCOP) (HEP-COP) (SP:P53621) [Homo sapiens]
359111	1	48	79	78	53	2	3	At1g62020	5,00E-16	68414.m06995 coatomer protein complex, subunit alpha, putative contains Pfam PF00400: WD domain, G-beta repeat; similar to Coatomer alpha subunit (Alpha-coat protein) (Alpha-COP) (HEPCOP) (HEP-COP) (SP:P53621) [Homo sapiens]

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358988	1	48	79	78	156	3	1	At1g52360	2,00E-43	68414.m05909 coatomer protein complex, subunit beta 2 (beta prime), putative contains 7 WD-40 repeats (PF00400) (1 weak); similar to (SP:O55029) Coatomer beta' subunit (Beta'-coat protein) (Beta'-COP) (p102) (SP:O55029) [Mus musculus]; similar to GI:298096 from [Homo sapiens]
358372	1	48	79	78	305	2	1	At5g49430	3,00E-35	68418.m06116 transducin family protein / WD-40 repeat family protein similar to WD-repeat protein 9 (SP:Q9NSI6) {Homo sapiens}; contains Pfam PF00400: WD domain, G-beta repeat (4 copies)
357015	1	48	79	78	365	1	1	At3g44530	1,00E-55	68416.m04786 transducin family protein / WD-40 repeat family protein contains 6 (4 significant) WD-40 repeats (PF0400); nuclear protein HIRA, mouse, PIR:S68141
360022	1	48	79	78	365	1	1	At3g44530	5,00E-37	68416.m04786 transducin family protein / WD-40 repeat family protein contains 6 (4 significant) WD-40 repeats (PF0400); nuclear protein HIRA, mouse, PIR:S68141
355671	1	48	79	78	484	1	1	At3g21540	5,00E-46	68416.m02717 transducin family protein / WD-40 repeat family protein contains Pfam profile: PF00400 WD domain, G-beta repeat (10 copies); similar to WD-repeat protein 3 (SP:Q9UNX4) [Homo sapiens]
353763	3	48	79	78	623	1	1	At4g32551	7,00E-101	68417.m04633 WD-40 repeat family protein (LEUNIG) contains seven G-protein beta WD-40 repeats; beta transducin-like protein, Podospora anserina, gb:L28125; contains Pfam profiles PF04503: Single-stranded DNA binding protein, SSDP; PF00400:WD domain, G-beta repeat; identical to cDNA LEUNIG (LEUNIG) GI:11141604
357064	1	48	79	78	973	1	1	At5g25150	2,00E-55	68418.m02981 transducin family protein / WD-40 repeat family protein similar to TBP-associated factor (GI:1732075) [Homo sapiens] and to 100 kDa subunit of Pol II transcription factor (GI:1491718) {Homo sapiens]; contains Pfam PF00400: WD domain, G-beta repeat (6 copies)|8689032|gb|AV528749.1|AV528749
355277	1	48	79	78	993	1	1	At1g73720	3,00E-08	68414.m08536 transducin family protein / WD-40 repeat family protein contains 5 WD-40 repeats (PF00400); similar to Will die slowly protein (SP:Q9V3J8)[Drosophila melanogaster]
358728	1	48	79	78	993	1	1	At1g73720	1,00E-45	68414.m08536 transducin family protein / WD-40 repeat family protein contains 5 WD-40 repeats (PF00400); similar to Will die slowly protein (SP:Q9V3J8)[Drosophila melanogaster]

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358650	1	48	79	78	1023	1	1	At2g20330	1,00E-57	68415.m02374 transducin family protein / WD-40 repeat family protein similar to Transcriptional repressor rco-1 (SP:P78706) [Neurospora crassa]; similar to TUP1(GB:AF079369); contains 6 WD-40 repeats (PF00400)
354949	1	48	79	78	1576	1	1	At3g18860	3,00E-72	68416.m02396 transducin family protein / WD-40 repeat family protein contains seven G-protein beta WD-40 repeats; similar to phospholipase a-2-activating protein SP:P27612 from [Mus musculus]
357759	1	48	79	78	1591	1	2	At5g52820	1,00E-07	68418.m06556 WD-40 repeat family protein / notchless protein, putative similar to notchless [Xenopus laevis] GI:3687833; contains Pfam PF00400: WD domain, G-beta repeat (8 copies)
353135	2	48	79	78	1812	1	1	At5g08560	4,00E-67	68418.m01018 transducin family protein / WD-40 repeat family protein contains 7 WD-40 repeats (PF00400); similar to will die slowly protein (WDS) (SP:Q9V3J8) [Drosophila melanogaster]
357203	1	48	79	78	1926	1	1	At5g67320	2,00E-38	68418.m08490 WD-40 repeat family protein strong similarity to unknown protein (ref|NP_005638.1)
354041	2	48	79	78	2256	4	2	At4g33270	3,00E-48	68417.m04734 WD-40 repeat family protein contains 6 WD-40 repeats (PF00400); WD-repeat protein -Daucus carota,PID:g2253631
354172	2	48	79	78	2258	2	1	At4g15900	6,00E-130	68417.m02416 PP1/PP2A phosphatases pleiotropic regulator 1 (PRL1) identical to PP1/PP2A phosphatases pleiotropic regulator PRL1 (SP:Q42384) [Arabidopsis thaliana], PRL1 [Arabidopsis thaliana] GI:577733; contains Pfam PF00400: WD domain, G-beta repeat (7 copies)
355787	1	48	79	78	2425	1	1	At5g13840	2,00E-56	68418.m01618 WD-40 repeat family protein contains 6 WD-40 repeats (PF00400); similar to Fzr1 (GI:6463679){Homo sapiens}
355315	1	48	79	78	2544	1	2	At2g41500	8,00E-07	68415.m05127 WD-40 repeat family protein / small nuclear ribonucleoprotein Prp4p-related similar to U4/U6 small nuclear ribonucleoprotein hPrp4 (GP:2708305) {Homo sapiens}; contains Pfam PF00400: WD domain, G-beta repeat (7 copies)|19877698|gb|AU238529.1|AU238529

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
355438	1	48	79	78	2544	1	2	At2g41500	3,00E-40	68415.m05127 WD-40 repeat family protein / small nuclear ribonucleoprotein Prp4p-related similar to U4/U6 small nuclear ribonucleoprotein hPrp4 (GP:2708305) {Homo sapiens}; contains Pfam PF00400: WD domain, G-beta repeat (7 copies)|19877698|gb|AU238529.1|AU238529
358687	1	48	79	78	2984	1	1	At4g03020	2,00E-37	68417.m00410 transducin family protein / WD-40 repeat family protein contains 6 WD-40 repeats (PF00400); similar to L. erythrorhizon LEC14B, GenBank accession number Q40153
356084	1	48	79	78	3501	1	2	At2g46290	2,00E-10	68415.m05758 eukaryotic translation initiation factor 3 subunit 2, putative / eIF-3 beta, putative / eIF3i, putative strong similarity to SP|Q38884 Eukaryotic translation initiation factor 3 subunit 2 (eIF-3 beta) (eIF3 p36) (eIF3i) (TGF-beta receptor interacting protein 1) (TRIP-1) {Arabidopsis thaliana}; contains Pfam PF00400: WD domain, G-beta repeat (5 copies)|19799885|gb|AU231175.1|AU231175
357516	1	48	79	78	3549	1	1	At4g05410	3,00E-29	68417.m00823 transducin family protein / WD-40 repeat family protein contains 6 WD-40 repeats (PF00400); U3 snoRNP-associated 55-kDa protein, Homo sapiens, gb:NP_004695; Vegetatible incompatibility protein HET-E-1 (SP:Q00808) [Podospora anserina]
358513	1	48	79	78	3829	1	1	At5g56130	5,00E-21	68418.m07002 transducin family protein / WD-40 repeat family protein contains 5 WD-40 repeats (PF00400); similar to beta transducin-like protein HET-E2C*4 (GI:17225206) [Podospora anserina]
356301	1	48	79	78	3878	3	2	At3g18130	9,00E-30	68416.m02305 guanine nucleotide-binding family protein / activated protein kinase C receptor (RACK1) identical to guanine nucleotide-binding protein; activated protein kinase C receptor; RACK1 (GI:9294068) {Arabidopsis thaliana}; contains Pfam profile: PF00400 WD domain, G-beta repeat (7 copies)
358062	1	48	79	78	3878	3	2	At1g48630	2,00E-117	68414.m05440 guanine nucleotide-binding family protein / activated protein kinase C receptor, putative / RACK, putative contains 7 WD-40 repeats (PF00400); very similar to guanine nucleotide-binding protein; activated protein kinase C receptor; RACK1 (GI:9294068) {Arabidopsis thaliana}; similar to WD-40 repeat auxin-dependent protein ARCA (SP:O24456) [Arabidopsis thaliana];

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353274	2	48	79	78	4316	1	1	At5g64630	4,00E-41	68418.m08123 transducin family protein / WD-40 repeat family protein Similar to (SP:Q13112) Chromatin assembly factor 1 subunit B (CAF-1 subunit B) (CAF-Ip60) [Homo sapiens]
355959	1	48	79	78	4768	1	1	At1g71840	5,00E-36	68414.m08302 transducin family protein / WD-40 repeat family protein contains Pfam profile:PF00560 Leucine Rich Repeat (4 copies); Pfam profile:PF00069 Eukaryotic protein kinase domain; Pfam profile:PF00400 WD domain, G-beta repeat (7 copies)
356781	1	48	79	78	4768	1	1	At1g71840	4,00E-55	68414.m08302 transducin family protein / WD-40 repeat family protein contains Pfam profile:PF00560 Leucine Rich Repeat (4 copies); Pfam profile:PF00069 Eukaryotic protein kinase domain; Pfam profile:PF00400 WD domain, G-beta repeat (7 copies)
356570	1	48	79	78	5605	1	1	At5g02230	1,00E-53	68418.m00145 haloacid dehalogenase-like hydrolase family protein contains InterPro accession IPR005834: Haloacid dehalogenase-like hydrolase
358049	1	48	79	78				At2g46280	6,00E-37	68415.m05757 eukaryotic translation initiation factor 3 subunit 2 / TGF-beta receptor interacting protein 1 / eIF-3 beta / eIF3i / TRIP-1 (TIF3I1) identical to eukaryotic translation initiation factor 3 subunit 2 (SP:Q38884) {Arabidopsis thaliana}; contains Pfam PF00400: WD domain, G-beta repeat (5 copies)
355835	1	49	43	114	1614	1	1	At5g35570	1,00E-63	68418.m04232 expressed protein similar to axi 1 [Nicotiana tabacum] GI:559921; contains Pfam profile PF03138: Plant protein family
355270	1	49	43	114	1755	2	2	At5g15740	3,00E-64	68418.m01841 expressed protein contains Pfam PF03138: Plant protein family. The function of this family of plant proteins is unknown;
355781	1	49	43	114	1755	2	2	At5g15740	5,00E-09	68418.m01841 expressed protein contains Pfam PF03138: Plant protein family. The function of this family of plant proteins is unknown;
359324	1	49	43	114	1789	1	2	At1g04910	2,00E-99	68414.m00488 expressed protein contains Pfam PF03138: Plant protein family. The function of this family of plant proteins is unknown; previously annotated as 'growth regulator protein' based on similarity to axi 1 protein (GB:X80301) (GI:559920) from [Nicotiana tabacum], which, due to scienitific fraud was retracted. Retraction in: Schell J. EMBO J 1999 May 17;18(10):2908. PMID:10400497.

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
357922	1	49	43	114	1861	1	1	At4g24530	4,00E-71	68417.m03516 expressed protein contains Pfam PF03138: Plant protein family. The function of this family of plant proteins is unknown; previously annotated as 'PsRT17-1 like protein' based on similarity to PsRT17-1 (GP:1778376) [Pisum sativum] which was based upon similarity to axi 1 protein (GB:X80301) (GI:559920) from [Nicotiana tabacum], which, due to scienitific fraud was retracted. Retraction in: Schell J. EMBO J 1999 May 17;18(10):2908. PMID:10400497.
357280	1	49	43	114	2577	1	1	At5g64600	2,00E-80	68418.m08118 expressed protein similar to axi 1 [Nicotiana tabacum] GI:559921; contains Pfam profile PF03138: Plant protein family
357119	1	49	43	114	3364	1	1	At1g22460	7,00E-24	68414.m02807 expressed protein similar to axi 1 [Nicotiana tabacum] GI:559921; contains Pfam profile PF03138: Plant protein family
359186	1	49	43	114	3364	1	1	At1g22460	3,00E-63	68414.m02807 expressed protein similar to axi 1 [Nicotiana tabacum] GI:559921; contains Pfam profile PF03138: Plant protein family
355396	1	49	43	114	4969	2	1	At1g51630	1,00E-11	68414.m05817 expressed protein contains Pfam PF03138: Plant protein family. The function of this family of plant proteins is unknown;
355746	1	49	43	114	4969	2	1	At3g21190	1,00E-29	68416.m02678 expressed protein contains Pfam PF03138: Plant protein family. The function of this family of plant proteins is unknown;
360028	1	49	43	114	4969	2	1	At3g21190	2,00E-67	68416.m02678 expressed protein contains Pfam PF03138: Plant protein family. The function of this family of plant proteins is unknown;
358190	1	49	43	114				At5g65470	1,00E-81	68418.m08233 expressed protein contains Pfam PF03138: Plant protein family. The function of this family of plant proteins is unknown;
353814	2	50	73	79	5915	1	1	At5g61380	5,00E-08	68418.m07701 ABI3-interacting protein 1 (AIP1) identical to pseudo-response regulator 1 GI:7576354 from [Arabidopsis thaliana]; timing of CAB expression 1 protein (TOC1) GI:9247019; contains Pfam profile PF00072: Response regulator receiver domain; identical to cDNA ABI3-interacting protein 1 (aip1 gene) GI:6996312
355093	1	50	73	79	6295	1	2	At3g13040	4,00E-35	68416.m01625 myb family transcription factor contains Pfam profile: PF00249 myb-like DNA-binding domain
353314	2	50	73	79	7664	1	3	At2g01060	1,00E-25	68415.m00011 myb family transcription factor contains Pfam profile: PF00249 myb-like DNA-binding domain

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
357659	1	50	73	79	7664	1	3	At2g01060	4,00E-26	68415.m00011 myb family transcription factor contains Pfam profile: PF00249 myb-like DNA-binding domain
359516	1	50	73	79	7912	1	2	At5g16560	7,00E-07	68418.m01938 myb family transcription factor (KAN1) contains Pfam profile: PF00249 myb-like DNA-binding domain; identical to cDNA GARP-like putative transcription factor KANADI1 (KAN1) GI:15723590
355170	1	50	73	79	7973	2	1	At2g41310	5,00E-24	68415.m05101 two-component responsive regulator / response reactor 3 (RR3) identical to response reactor 3 GI:3273200 from [Arabidopsis thaliana]; contains Pfam profile: PF00072 response regulator receiver domain
356778	1	50	73	79	7973	2	1	At3g57040	2,00E-36	68416.m06349 two-component responsive regulator / response reactor 4 (RR4) identical to responce reactor4 GI:3273202 from [Arabidopsis thaliana]; contains Pfam profile: PF00072 response regulator receiver domain
359802	1	50	73	79	7973	2	1	At3g57040	3,00E-35	68416.m06349 two-component responsive regulator / response reactor 4 (RR4) identical to responce reactor4 GI:3273202 from [Arabidopsis thaliana]; contains Pfam profile: PF00072 response regulator receiver domain
353024	2	51	8	135	2997	1	1	At5g19000	2,00E-77	68418.m02257 speckle-type POZ protein-related contains Pfam PF00651 : BTB/POZ domain; contains Pfam PF00917: MATH domain; similar to Speckle-type POZ protein (SP:O43791) [Homo sapiens]
358737	1	52	78	59	1006	1	2	At5g27540	6,00E-35	68418.m03297 GTP-binding protein-related low similarity to Mig-2-like GTPase Mtl [Drosophila melanogaster] GI:7271872; contains Pfam profile PF00036: EF hand
354312	5	52	78	59	4379	2	1	At5g55190	5,00E-110	68418.m06880 Ras-related GTP-binding protein (RAN3) identical to atran3 [Arabidopsis thaliana] GI:2058280
357879	1	52	78	59	4379	2	1	At5g55190	7,00E-64	68418.m06880 Ras-related GTP-binding protein (RAN3) identical to atran3 [Arabidopsis thaliana] GI:2058280
357978	1	52	78	59	4379	2	1	At5g55190	4,00E-115	68418.m06880 Ras-related GTP-binding protein (RAN3) identical to atran3 [Arabidopsis thaliana] GI:2058280
354025	3	52	78	59	5070	2	2	At5g60860	4,00E-109	68418.m07634 Ras-related GTP-binding protein, putative similar to GTP-binding protein GI:303742 from [Pisum sativum]
354484	1	52	78	59	5279	3	3	At5g59840	9,00E-25	68418.m07503 Ras-related GTP-binding family protein contains Pfam profile: PF00071 Ras family
359051	1	52	78	59	5279	3	3	At5g59840	1,00E-23	68418.m07503 Ras-related GTP-binding family protein contains Pfam profile: PF00071 Ras family

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
358410	1	52	78	59	5407	2	1	At3g18820	4,00E-59	68416.m02390 Ras-related GTP-binding protein, putative similar to Ras-related protein RAB7 GI:1370186 from [Pisum sativum], Plant Mol. Biol. 21 (6), 1195-1199 (1993); contains Pfam profile: PF00071 Ras family
356493	1	52	78	59	5441	4	1	At4g35020	2,00E-33	68417.m04967 Rac-like GTP-binding protein (ARAC3) / Rho-like GTP-binding protein (ROP6) identical to SP|Q38912 RAC-like GTP binding protein ARAC3 (GTP-binding protein ROP6) {Arabidopsis thaliana}; identical to cDNA Rho-like GTP binding protein (Rop6) GI:2645642
359061	1	52	78	59	5495	1	1	At1g02130	1,00E-52	68414.m00139 Ras-related protein (ARA-5) / small GTP-binding protein, putative identical to Ras-related protein ARA-5 SP:P28188 from [Arabidopsis thaliana]
357975	1	52	78	59	5592	3	1	At1g07410	1,00E-91	68414.m00790 Ras-related GTP-binding protein, putative similar to GTP-binding protein RAB11C GI:1370146 from [Lotus japonicus]
353153	2	52	78	59	5646	2	2	At3g48040	1,00E-56	68416.m05237 Rac-like GTP-binding protein (ARAC8) identical to rac GTP binding protein Arac8 GI:3702966 from [Arabidopsis thaliana]
359352	1	52	78	59	5646	2	2	At5g62880	2,00E-21	68418.m07890 Rac-like GTP-binding protein (ARAC10) identical to rac GTP binding protein Arac10 [Arabidopsis thaliana] GI:3702964, rac-like GTP binding protein Arac10 [Arabidopsis thaliana] GI:7211193; contains Pfam profile: PF00071 Ras family
353708	3	52	78	59	5994	1	1	At1g09630	5,00E-79	68414.m01080 Ras-related GTP-binding protein, putative similar to GTP-binding protein GI:1370146 from [Lotus japonicus]
359375	1	52	78	59	5994	1	1	At1g09630	3,00E-88	68414.m01080 Ras-related GTP-binding protein, putative similar to GTP-binding protein GI:1370146 from [Lotus japonicus]
358639	1	52	78	59	6120	2	1	At5g65270	7,00E-13	68418.m08210 Ras-related GTP-binding family protein similar to GTP-binding protein RAB11A GI:1370142 from [Lotus japonicus]; contains Pfam profile: PF00071 Ras family
359210	1	52	78	59	6463	2	2	At4g19640	2,00E-74	68417.m02884 Ras-related GTP-binding protein, putative similar to GTP-binding protein RAB5A GI:1370178 from [Lotus japonicus]
359035	1	52	78	59	6490	3	2	At1g43890	4,00E-30	68414.m05059 Ras-related GTP-binding protein, putative similar to GTP-binding protein(RAB1Y) GI:1370173 from (Lotus japonicus)
359117	1	52	78	59	6490	3	2	At5g03530	4,00E-21	68418.m00309 Ras-related GTP-binding family protein contains Pfam profile: PF00071 Ras family

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
353094	3	52	78	59				At3g11730	9,00E-92	68416.m01439 Ras-related GTP-binding protein, putative similar to Rab1-like small GTP-binding protein GI:4096662 from [Petunia x hybrida]
353382	2	52	78	59				At1g75840	8,00E-95	68414.m08809 Rac-like GTP-binding protein (ARAC5) / Rho-like GTP-binding protein (ROP4) identical to RAC-like GTP-binding protein (ARAC5) SP:Q38937 [Arabidopsis thaliana], Rho-like GTP binding protein [Arabidopsis thaliana] GI:2654009; identical to cDNA Rho-like GTP binding protein (Rop4) GI:2654008
355159	1	52	78	59				At5g47200	6,00E-06	68418.m05820 Ras-related GTP-binding protein, putative similar to GTP-binding protein GI:303750 from [Pisum sativum]
359582	1	52	78	59				At4g18800	5,00E-58	68417.m02776 Ras-related GTP-binding family protein similar to ras-related GTP binding protein RIC2 SP:P40393 from [Oryza sativa]; contains Pfam profile: PF00071 Ras family
353948	2	54	61	70	7104	2	2	At2g45650	1,00E-72	68415.m05676 MADS-box protein (AGL6)
353945	2	54	61	70	7150	3	1	At5g15800	5,00E-57	68418.m01848 developmental protein SEPALLATA1 / floral homeotic protein (AGL2) (SEP1) identical to developmental protein SEPALLATA1 / floral homeotic protein (AGL2 / SEP1) SP:P29382 from [Arabidopsis thaliana]
356714	1	54	61	70	7150	3	1	At5g15800	5,00E-55	68418.m01848 developmental protein SEPALLATA1 / floral homeotic protein (AGL2) (SEP1) identical to developmental protein SEPALLATA1 / floral homeotic protein (AGL2 / SEP1) SP:P29382 from [Arabidopsis thaliana]
357070	1	54	61	70	7165	2	2	At1g69120	1,00E-29	68414.m07909 floral homeotic protein APETALA1 (AP1) / agamous-like MADS box protein (AGL7) identical to SP|P35631 Floral homeotic protein APETALA1 (AGL7 protein) {Arabidopsis thaliana}
354351	5	54	61	70	7352	3	1	At4g18960	8,00E-70	68417.m02793 floral homeotic protein AGAMOUS (AG) contains an ACG start codon (Riechmann, Ito, and Meyerowitz, Mol Cell Biol, 1999); supported by cDNA gi|16155|emb|X53579
353295	5	54	61	70	8089	1	2	At5g20240	1,00E-22	68418.m02409 floral homeotic protein PISTILLATA (PI) contains Pfam profiles PF01486: K-box region and PF00319: SRF-type transcription factor (DNA-binding and dimerisation domain)

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
353627	12	54	61	70	8089	1	2	At5g20240	2,00E-57	68418.m02409 floral homeotic protein PISTILLATA (PI) contains Pfam profiles PF01486: K-box region and PF00319: SRF-type transcription factor (DNA-binding and dimerisation domain)
356264	1	54	61	70	8530	1	1	At3g54340	1,00E-21	68416.m06005 floral homeotic protein APETALA3 (AP3)
358723	1	54	61	70	8530	1	1	At3g54340	5,00E-10	68416.m06005 floral homeotic protein APETALA3 (AP3)
354424	2	54	61	70				At5g13790	7,00E-19	68418.m01608 floral homeotic protein AGL-15 (AGL15)
358550	1	54	61	70				At5g52550	1,00E-07	68418.m06525 expressed protein
355543	1	55	68	60	85	1	1	At3g19050	6,00E-09	68416.m02420 kinesin motor protein-related contains Pfam profile: PF00225 Kinesin motor domain; contains non-consensus splice site (GC) at intron 12
353500	2	55	68	60	94	1	1	At5g65930	4,00E-39	68418.m08300 kinesin-like calmodulin-binding protein (ZWICHEL) identical to kinesin-like protein GI:2224925 from [Arabidopsis thaliana]
355612	1	55	68	60	194	2	1	At5g10470	1,00E-52	68418.m01213 kinesin motor protein-related TH65 protein, Arabidopsis thaliana, EMBL:AJ001729; contains Pfam profile PF00225: Kinesin motor domain
355088	1	55	68	60	373	1	1	At5g60930	9,00E-17	68418.m07643 chromosome-associated kinesin, putative microtubule-associated motor KIF4 , Mus musculus, PIR:A54803
353057	2	55	68	60	441	1	1	At1g18370	2,00E-45	68414.m02295 kinesin motor family protein (NACK1) similar to kinesin heavy chain isolog GB:AAB63609 GI:2262101 from [Arabidopsis thaliana]
354840	1	55	68	60	441	1	1	At1g18370	2,00E-40	68414.m02295 kinesin motor family protein (NACK1) similar to kinesin heavy chain isolog GB:AAB63609 GI:2262101 from [Arabidopsis thaliana]
355581	1	55	68	60	614	2	1	At4g39050	3,00E-35	68417.m05531 kinesin-related protein (MKRP2) kinesin motor protein - Ustilago maydis, PID:g2062750; identical to cDNA MKRP2 mRNA for kinesin-related protein GI:16902293, kinesin-related protein [Arabidopsis thaliana] GI:16902294
355761	1	55	68	60	614	2	1	At4g39050	7,00E-21	68417.m05531 kinesin-related protein (MKRP2) kinesin motor protein - Ustilago maydis, PID:g2062750; identical to cDNA MKRP2 mRNA for kinesin-related protein GI:16902293, kinesin-related protein [Arabidopsis thaliana] GI:16902294
357851	1	55	68	60	614	2	1	At4g39050	9,00E-18	68417.m05531 kinesin-related protein (MKRP2) kinesin motor protein - Ustilago maydis, PID:g2062750; identical to cDNA MKRP2 mRNA for kinesin-related protein GI:16902293, kinesin-related protein [Arabidopsis thaliana] GI:16902294

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
355537	1	55	68	60	658	1	1	At2g36200	2,00E-24	68415.m04444 kinesin motor protein-related
357946	1	55	68	60	782	1	1	At2g22610	2,00E-23	68415.m02680 kinesin motor protein-related
355188	1	55	68	60	810	1	1	At2g47500	3,00E-06	68415.m05929 kinesin motor protein-related
358919	1	55	68	60	810	1	1	At2g47500	1,00E-14	68415.m05929 kinesin motor protein-related
358672	1	55	68	60	933	2	2	At4g14150	2,00E-23	68417.m02183 phragmoplast-associated kinesin-related protein (PAKRP1)
359305	1	55	68	60	933	2	2	At4g14150	2,00E-24	68417.m02183 phragmoplast-associated kinesin-related protein (PAKRP1)
355044	1	55	68	60	994	1	1	At3g16630	2,00E-10	68416.m02126 kinesin motor family protein similar to mitotic centromere-associated kinesin GB:AAC27660 from [Homo sapiens]; contains Pfam profile PF00225: Kinesin motor domain
358490	1	55	68	60	994	1	1	At3g16630	3,00E-45	68416.m02126 kinesin motor family protein similar to mitotic centromere-associated kinesin GB:AAC27660 from [Homo sapiens]; contains Pfam profile PF00225: Kinesin motor domain
355729	1	55	68	60	1364	2	2	At1g63640	2,00E-26	68414.m07198 kinesin motor protein-related C-terminal region is similar to C-term region of kinesin motor protein GB:AAB51397 (Mus musculus); contains Pfam profile: PF00225 Kinesin motor domain
354683	1	55	68	60	2925	1	1	At5g27550	1,00E-52	68418.m03299 kinesin motor protein-related kinesin-like heavy chain - Arabidopsis thaliana, EMBL:AF080249
352996	3	55	68	60	3291	1	1	At5g02370	2,00E-27	68418.m00160 kinesin motor protein-related kinesin, Xenopus laevis, EMBL:XLA249840
353186	2	55	68	60	3291	1	1	At5g02370	1,00E-21	68418.m00160 kinesin motor protein-related kinesin, Xenopus laevis, EMBL:XLA249840
353769	3	55	68	60	4118	1	1	At5g27950	2,00E-51	68418.m03366 kinesin motor protein-related kinesin heavy chain-like protein, potato, PIR:T07397
354663	1	55	68	60	4118	1	1	At5g27950	1,00E-69	68418.m03366 kinesin motor protein-related kinesin heavy chain-like protein, potato, PIR:T07397
356418	1	55	68	60	6418	2	1	At2g30260	9,00E-30	68415.m03684 small nuclear ribonucleoprotein U2B, putative / spliceosomal protein, putative similar to spliceosomal protein [Solanum tuberosum] GI:169589
355107	1	55	68	60				At5g47820	3,00E-57	68418.m05908 kinesin-like protein (FRA1) identical to kinesin-like protein [Arabidopsis thaliana] GI:27260890; contains Pfam profile PF00225: Kinesin motor domain
356595	1	55	68	60				At5g27000	2,00E-22	68418.m03221 kinesin motor protein-related non-consensus AT donor splice site at exon 12; non-consensus AC acceptor splice site at exon 13
358661	1	55	68	60				At3g49650	2,00E-54	68416.m05426 kinesin motor protein-related several kinesin-like proteins

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358695	1	55	68	60				At3g17360	1,00E-26	68416.m02218 kinesin motor protein-related similar to KLP2 protein GB:CAA63826 from [Xenopus laevis]
359970	1	55	68	60				At2g47580	5,00E-61	68415.m05937 small nuclear ribonucleoprotein U1A / spliceosomal protein U1A / U1snRNP-specific protein identical to GB:Z49991 U1snRNP-specific protein [Arabidopsis thaliana]
358250	1	56	63	65	2932	1	1	At4g13250	2,00E-22	68417.m02060 short-chain dehydrogenase/reductase (SDR) family protein contains INTERPRO family IPR002198 Short-chain dehydrogenase/reductase (SDR) superfamily
358908	1	56	63	65	4339	1	1	At3g12800	2,00E-107	68416.m01597 short-chain dehydrogenase/reductase (SDR) family protein contains Pfam profile PF00106:oxidoreductase, short chain dehydrogenase/reductase family
353781	5	56	63	65	6297	1	1	At1g52340	1,00E-60	68414.m05908 short-chain dehydrogenase/reductase (SDR) family protein similar to stem secoisolariciresinol dehydrogenase GI:13752458 from [Forsythia x intermedia]
354290	2	56	63	65	6297	1	1	At1g52340	1,00E-16	68414.m05908 short-chain dehydrogenase/reductase (SDR) family protein similar to stem secoisolariciresinol dehydrogenase GI:13752458 from [Forsythia x intermedia]
354276	2	56	63	65				At5g04900	6,00E-31	68418.m00515 short-chain dehydrogenase/reductase (SDR) family protein contains INTERPRO family IPR002198 Short-chain dehydrogenase/reductase (SDR) superfamily
359088	1	57	71	53	3079	3	1	At2g47550	6,00E-12	68415.m05934 pectinesterase family protein contains Pfam profile: PF01095 pectinesterase
356325	1	57	71	53	3581	1	1	At5g19730	3,00E-55	68418.m02346 pectinesterase family protein contains Pfam profile: PF01095 pectinesterase
358319	1	57	71	53	3903	1	1	At3g29090	3,00E-86	68416.m03642 pectinesterase family protein similar to pectinesterase precursor GB:Q43043 [Petunia integrifolia]; contains Pfam profile: PF01095 pectinesterase
356727	1	57	71	53	4537	1	1	At2g26440	9,00E-40	68415.m03172 pectinesterase family protein contains Pfam profile: PF01095 pectinesterase
353444	5	57	71	53	6555	3	4	At4g30800	3,00E-49	68417.m04363 40S ribosomal protein S11 (RPS11B) ribosomal protein S11, Arabidopsis thaliana,PIR2:C35542
352973	2	57	71	53				At1g11580	3,00E-82	68414.m01329 pectin methylesterase, putative similar to pectin methylesterase GI:1617583 from [Lycopersicon esculentum]

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
353495	2	57	71	53				At4g02300	3,00E-104	68417.m00311 pectinesterase family protein contains Pfam profile: PF01095 pectinesterase
354864	1	57	71	53				At4g03930	2,00E-21	68417.m00556 pectin methylesterase, putative similar to pectin methylesterase GI:1617588 from [Lycopersicon esculentum]
354485	1	58	63	59	201	3	2	At3g53230	3,00E-85	68416.m05865 cell division cycle protein 48, putative / CDC48, putative very strong similarity to SP|P54609 Cell division cycle protein 48 homolog {Arabidopsis thaliana}; contains Pfam profiles PF00004: ATPase AAA family, PF02359: Cell division protein 48 (CDC48) N-terminal domain
359476	1	58	63	59	201	3	2	At3g53230	7,00E-48	68416.m05865 cell division cycle protein 48, putative / CDC48, putative very strong similarity to SP|P54609 Cell division cycle protein 48 homolog {Arabidopsis thaliana}; contains Pfam profiles PF00004: ATPase AAA family, PF02359: Cell division protein 48 (CDC48) N-terminal domain
354796	1	58	63	59	465	2	1	At4g02480	2,00E-56	68417.m00335 AAA-type ATPase family protein contains Pfam domain, PF00004: ATPase, AAA family; similar to Spastin (Swiss-Prot:Q9UBP0) [Homo sapiens] and Spastin (Fragment) (Swiss-Prot:Q9QYY8) [Mus musculus]; similar to mitochondrial sorting protein 1 (MSP1) protein (TAT-binding homolog 4) (Swiss-Prot:P28737) [Saccharomyces cerevisiae]
358020	1	58	63	59	465	2	1	At4g02480	2,00E-88	68417.m00335 AAA-type ATPase family protein contains Pfam domain, PF00004: ATPase, AAA family; similar to Spastin (Swiss-Prot:Q9UBP0) [Homo sapiens] and Spastin (Fragment) (Swiss-Prot:Q9QYY8) [Mus musculus]; similar to mitochondrial sorting protein 1 (MSP1) protein (TAT-binding homolog 4) (Swiss-Prot:P28737) [Saccharomyces cerevisiae]
358612	1	58	63	59	465	2	1	At4g02480	9,00E-19	68417.m00335 AAA-type ATPase family protein contains Pfam domain, PF00004: ATPase, AAA family; similar to Spastin (Swiss-Prot:Q9UBP0) [Homo sapiens] and Spastin (Fragment) (Swiss-Prot:Q9QYY8) [Mus musculus]; similar to mitochondrial sorting protein 1 (MSP1) protein (TAT-binding homolog 4) (Swiss-Prot:P28737) [Saccharomyces cerevisiae]

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359235	1	58	63	59	465	2	1	At1g02890	7,00E-36	68414.m00256 AAA-type ATPase family protein contains Pfam domain, PF00004: ATPase, AAA family; similar to mitochondrial sorting protein 1 (MSP1) (TAT-binding homolog 4) (Swiss-Prot:P28737) [Saccharomyces cerevisiae]
353502	2	58	63	59	662	1	2	At2g26140	5,00E-85	68415.m03137 FtsH protease, putative contains similarity to YME1 GI:295582, a member of the ftsH-SEC18-PAS1-CDC48 family of putative ATPase-encoding genes from [Saccharomyces cerevisiae]
354601	1	58	63	59	801	1	1	At4g04910	7,00E-92	68417.m00714 AAA-type ATPase family protein similar to SP|P18708 Vesicular-fusion protein NSF (N-ethylmaleimide-sensitive fusion protein) (NEM-sensitive fusion protein) {Cricetulus griseus}; contains Pfam profiles PF00004: ATPase AAA family, PF02359: Cell division protein 48 (CDC48) N-terminal domain; contains non-consensus AT-AC splice sites at intron 2
355447	1	58	63	59	801	1	1	At4g04910	5,00E-59	68417.m00714 AAA-type ATPase family protein similar to SP|P18708 Vesicular-fusion protein NSF (N-ethylmaleimide-sensitive fusion protein) (NEM-sensitive fusion protein) {Cricetulus griseus}; contains Pfam profiles PF00004: ATPase AAA family, PF02359: Cell division protein 48 (CDC48) N-terminal domain; contains non-consensus AT-AC splice sites at intron 2
357883	1	58	63	59	1190	1	1	At1g80350	1,00E-66	68414.m09406 katanin 1 (KTN1) identical to katanin 1 (KTN1) [Arabidopsis thaliana] GI:14133602
354997	1	58	63	59	1203	1	1	At1g53750	8,00E-93	68414.m06115 26S proteasome AAA-ATPase subunit (RPT1a) similar to 26S proteasome ATPase subunit GI:1395190 from [Spinacia oleracea]
358402	1	58	63	59	1203	1	1	At1g53750	7,00E-86	68414.m06115 26S proteasome AAA-ATPase subunit (RPT1a) similar to 26S proteasome ATPase subunit GI:1395190 from [Spinacia oleracea]
353640	3	58	63	59	1315	2	2	At4g29040	1,00E-128	68417.m04153 26S proteasome AAA-ATPase subunit (RPT2a) almost identical to 26S proteasome AAA-ATPase subunit RPT2a (GI:6652880) {Arabidopsis thaliana}; Drosophila melanogaster 26S proteasome subunit 4 ATPase, PID:g1066065
358326	1	58	63	59	1315	2	2	At2g20140	2,00E-60	68415.m02353 26S protease regulatory complex subunit 4, putative similar to Swiss-Prot:P48601 26S protease regulatory subunit 4 (P26S4) [Drosophila melanogaster]

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352944	4	58	63	59	1467	1	1	At3g05530	9,00E-173	68416.m00606 26S proteasome AAA-ATPase subunit (RPT5a) identical to GB:AAF22525 GI:6652886 from [Arabidopsis thaliana]
353136	9	58	63	59	1590	2	1	At5g19990	0	68418.m02379 26S proteasome AAA-ATPase subunit (RPT6a)
353874	2	58	63	59	1590	2	1	At5g19990	4,00E-74	68418.m02379 26S proteasome AAA-ATPase subunit (RPT6a)
354717	1	58	63	59	1590	2	1	At5g20000	8,00E-38	68418.m02380 26S proteasome AAA-ATPase subunit, putative almost identical to 26S proteasome AAA-ATPase subunit RPT6a GI:6652888 from [Arabidopsis thaliana]; almost identical to a member of conserved Sug1 CAD family AtSUG1 GI:13537115 from [Arabidopsis thaliana]
353283	6	58	63	59	1785	1	1	At5g58290	0	68418.m07297 26S proteasome AAA-ATPase subunit (RPT3) identical to 26S proteasome AAA-ATPase subunit RPT3 GI:6652882 from [Arabidopsis thaliana]
354288	3	58	63	59	3250	2	1	At4g27680	2,00E-131	68417.m03980 MSP1 protein, putative / intramitochondrial sorting protein, putative similar to Swiss-Prot:P28737 MSP1 protein (TAT-binding homolog 4) [Saccharomyces cerevisiae]; contains Pfam domain, PF00004: ATPase, AAA family
357448	1	58	63	59	3482	1	2	At2g34560	1,00E-77	68415.m04246 katanin, putative similar to katanin p60 subunit [Strongylocentrotus purpuratus] GI:3098603; contains Pfam profile PF00004: ATPase AAA family
358760	1	58	63	59	3482	1	2	At2g34560	4,00E-17	68415.m04246 katanin, putative similar to katanin p60 subunit [Strongylocentrotus purpuratus] GI:3098603; contains Pfam profile PF00004: ATPase AAA family
353790	2	58	63	59				At5g64580	8,00E-78	68418.m08116 AAA-type ATPase family protein similar to zinc dependent protease [Arabidopsis thaliana] GI:7650138; contains Pfam profile PF00004: ATPase AAA family
357735	1	58	63	59				At5g64580	4,00E-22	68418.m08116 AAA-type ATPase family protein similar to zinc dependent protease [Arabidopsis thaliana] GI:7650138; contains Pfam profile PF00004: ATPase AAA family
358906	1	58	63	59				At5g64580	2,00E-06	68418.m08116 AAA-type ATPase family protein similar to zinc dependent protease [Arabidopsis thaliana] GI:7650138; contains Pfam profile PF00004: ATPase AAA family

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352918	2	60	84	37	742	1	2	At5g57360	7,00E-69	68418.m07166 F-box family protein / LOV kelch protein 1 (LKP1) E3 ubiquitin ligase SCF complex F-box subunit; identical to clock-associated PAS protein ZTL; ZEITLUPE GI:7839456, LOV kelch protein 1 GI:11610573, Adagio 1 GI:13487068 from [Arabidopsis thaliana]; contains Pfam profile PF01344: Kelch motif; identical to cDNA Adagio 1 (ADO1) GI:13487067; identical to cDNA LKP1 mRNA for LOV kelch protein 1, GI:11610572
355539	1	60	84	37	1004	2	1	At3g05420	3,00E-32	68416.m00594 acyl-CoA binding family protein similar to PIR|S68824|S68824 rngB protein, cytosolic (Dictyostelium discoideum); contains Pfam profiles PF00887: Acyl CoA binding protein, PF01344: Kelch motif
354501	1	60	84	37	1290	1	1	At2g42810	7,00E-71	68415.m05300 serine/threonine protein phosphatase, putative similar to SP|P53042 Serine/threonine protein phosphatase 5 (EC 3.1.3.16) (PP5) (Protein phosphatase T) (PPT) {Rattus norvegicus}; contains Pfam profiles PF00149: Ser/Thr protein phosphatase, PF00515: TPR Domain
355811	1	60	84	37	1290	1	1	At2g42810	3,00E-11	68415.m05300 serine/threonine protein phosphatase, putative similar to SP|P53042 Serine/threonine protein phosphatase 5 (EC 3.1.3.16) (PP5) (Protein phosphatase T) (PPT) {Rattus norvegicus}; contains Pfam profiles PF00149: Ser/Thr protein phosphatase, PF00515: TPR Domain
354183	6	60	84	37	2594	1	1	At3g58500	8,00E-177	68416.m06520 serine/threonine protein phosphatase PP2A-4 catalytic subunit (PP2A4) identical to SP|P48578 Serine/threonine protein phosphatase PP2A-4 catalytic subunit (EC 3.1.3.16) (Protein phosphatase 2A isoform 4) {Arabidopsis thaliana}; contains Pfam profile PF00149: Ser/Thr protein phosphatase
358631	1	60	84	37	2649	1	2	At5g18590	3,00E-51	68418.m02198 kelch repeat-containing protein identical to RanGAP1 interacting protein (GI:21950739) [Arabidopsis thaliana]; similar to Tip elongation aberrant protein 1 (Cell polarity protein tea1) (SP:P87061) [Schizosaccharomyces pombe]; contains Pfam PF01344: Kelch motif (5 repeats)

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
358827	1	60	84	37	2649	1	2	At5g18590	3,00E-20	68418.m02198 kelch repeat-containing protein identical to RanGAP1 interacting protein (GI:21950739) [Arabidopsis thaliana]; similar to Tip elongation aberrant protein 1 (Cell polarity protein tea1) (SP:P87061) [Schizosaccharomyces pombe]; contains Pfam PF01344: Kelch motif (5 repeats)
353922	2	60	84	37	2680	2	1	At1g50370	2,00E-140	68414.m05646 serine/threonine protein phosphatase, putative nearly identical to serine/threonine protein phosphatase [Arabidopsis thaliana] GI:14582206
358966	1	60	84	37	3088	2	1	At4g11240	2,00E-18	68417.m01820 serine/threonine protein phosphatase PP1 isozyme 6 (PP1BG) (TOPP6) identical to SP|P48486 Serine/threonine protein phosphatase PP1 isozyme 6 (EC 3.1.3.16) {Arabidopsis thaliana}
356611	1	60	84	37	3323	2	1	At2g39840	2,00E-64	68415.m04893 serine/threonine protein phosphatase PP1 isozyme 4 (TOPP4) / phosphoprotein phosphatase 1 identical to SP|P48484 Serine/threonine protein phosphatase PP1 isozyme 4 (EC 3.1.3.16) {Arabidopsis thaliana}, phosphoprotein phosphatase 1 GI:166801 (Arabidopsis thaliana); contains a Ser/Thr protein phosphatase signature (PDOC00115); contains a metallo-phosphoesterase motif (QDOC50185)
358268	1	60	84	37	3323	2	1	At2g39840	2,00E-39	68415.m04893 serine/threonine protein phosphatase PP1 isozyme 4 (TOPP4) / phosphoprotein phosphatase 1 identical to SP|P48484 Serine/threonine protein phosphatase PP1 isozyme 4 (EC 3.1.3.16) {Arabidopsis thaliana}, phosphoprotein phosphatase 1 GI:166801 (Arabidopsis thaliana); contains a Ser/Thr protein phosphatase signature (PDOC00115); contains a metallo-phosphoesterase motif (QDOC50185)
354130	3	60	84	37	3673	1	1	At5g04420	1,00E-11	68418.m00435 kelch repeat-containing protein low similarity to rngB protein, Dictyostelium discoideum, PIR:S68824; contains Pfam profile PF01344: Kelch motif
357782	1	60	84	37				At3g46820	3,00E-30	68416.m05082 serine/threonine protein phosphatase PP1 isozyme 5 (TOPP5) / phosphoprotein phosphatase 1 identical to SP|P48485 Serine/threonine protein phosphatase PP1 isozyme 5 (EC 3.1.3.16) {Arabidopsis thaliana}, phosphoprotein phosphatase 1 GI:166803 {Arabidopsis thaliana}
352906	3	61	54	67	1905	2	1	At1g28110	3,00E-135	68414.m03444 serine carboxypeptidase S10 family protein similar to H.vulgare gene encoding serine carboxypeptidase II, CP-MII GI:1731989

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359248	1	61	54	67	2183	1	2	At3g10410	3,00E-106	68416.m01248 serine carboxypeptidase III, putative similar to serine carboxypeptidase III from Oryza sativa SP|P37891, Matricaria chamomilla GI:6960455, Hordeum vulgare SP|P21529, Triticum aestivum SP|P11515; contains Pfam profile PF0450 serine carboxypeptidase
357685	1	61	54	67	2724	1	2	At3g17180	6,00E-61	68416.m02191 serine carboxypeptidase S10 family protein similar to serine carboxypeptidase II SP:P08819 [Triticum aestivum] (Carlsberg Res. Commun. 52:297-311(1987))
359094	1	61	54	67	2724	1	2	At3g17180	3,00E-65	68416.m02191 serine carboxypeptidase S10 family protein similar to serine carboxypeptidase II SP:P08819 [Triticum aestivum] (Carlsberg Res. Commun. 52:297-311(1987))
358666	1	61	54	67	2795	3	1	At4g30610	1,00E-67	68417.m04342 serine carboxypeptidase S10 family protein similar to Serine carboxypeptidase II chains A and B (SP:P08819) (EC 3.4.16.6) [Triticum aestivum (Wheat)];
359092	1	61	54	67	3179	1	1	At4g30810	2,00E-59	68417.m04365 serine carboxypeptidase S10 family protein similar to serine-type carboxypeptidase (SP:P55748) [Hordeum vulgare]
356660	1	61	54	67	3806	1	1	At5g08260	2,00E-60	68418.m00971 serine carboxypeptidase S10 family protein similar to Serine carboxypeptidase II chains A and B (SP:P08819) (EC 3.4.16.6) [Triticum aestivum (Wheat)]; carboxypeptidase D - Triticum aestivum, PIR:A29639
354147	2	61	54	67	4632	19	3	At3g12203	1,00E-16	68416.m01522 serine carboxypeptidase S10 family protein contains Pfam profile: PF00450 serine carboxypeptidase; similar to serine carboxypeptidase I precursor (SP:P07519) [Hordeum vulgare]
353805	2	61	54	67	4712	1	5	At1g15000	1,00E-46	68414.m01792 serine carboxypeptidase S10 family protein similar to Serine carboxypeptidase precursor (SP:P32826) [Arabidopsis thaliana]; similar to GB:AAD42963 from [Matricaria chamomilla]
354611	1	61	54	67	4779	1	2	At2g27920	4,00E-10	68415.m03383 serine carboxypeptidase S10 family protein similar to retinoid-inducible serine carboxypeptidase precursor (GI:15146429) [Mus musculus]
356268	1	62	72	46	2012	2	1	At1g19170	3,00E-97	68414.m02386 glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein low similarity to SP|P27644 Polygalacturonase (EC 3.2.1.15) (Pectinase) {Agrobacterium tumefaciens}; contains PF00295: Glycosyl hydrolases family 28

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
359252	1	62	72	46	2012	2	1	At1g19170	4,00E-52	68414.m02386 glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein low similarity to SP|P27644 Polygalacturonase (EC 3.2.1.15) (Pectinase) {Agrobacterium tumefaciens}; contains PF00295: Glycosyl hydrolases family 28
353630	9	62	72	46	2483	1	1	At3g61490	8,00E-101	68416.m06887 glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein weak similarity to SP|P27644 Polygalacturonase (EC 3.2.1.15) (Pectinase) {Agrobacterium tumefaciens}; contains PF00295: Glycosyl hydrolases family 28
354568	1	62	72	46	2483	1	1	At3g61490	2,00E-58	68416.m06887 glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein weak similarity to SP|P27644 Polygalacturonase (EC 3.2.1.15) (Pectinase) {Agrobacterium tumefaciens}; contains PF00295: Glycosyl hydrolases family 28
354015	5	62	72	46	2533	2	3	At1g60590	9,00E-146	68414.m06820 polygalacturonase, putative / pectinase, putative similar to polygalacturonase PG1 (GI:5669846), PG2 (GI:5669848) from [Glycine max]; contains PF00295: Glycosyl hydrolases family 28 (polygalacturonases)
358885	1	62	72	46	2533	2	3	At1g10640	2,00E-44	68414.m01206 polygalacturonase, putative / pectinase, putative similar to polygalacturonase PG1 GI:5669846, PG2 GI:5669848 from [Glycine max]; contains PF00295: Glycosyl hydrolases family 28 (polygalacturonases)
358668	1	62	72	46	2588	1	1	At1g48100	4,00E-55	68414.m05368 glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein similar to polygalacturonase PG1 GI:5669846, PG2 GI:5669848 from [Glycine max]; contains PF00295: Glycosyl hydrolases family 28 (polygalacturonases)
356089	1	62	72	46	2752	1	2	At3g62110	7,00E-42	68416.m06978 glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein weak similarity to polygalacturonase [Lycopersicon esculentum] GI:4325090; contains PF00295: Glycosyl hydrolases family 28
355290	1	62	72	46	3123	1	1	At3g57790	1,00E-65	68416.m06438 glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein weak similarity to SP|P15922 Exo-poly-alpha-D-galacturonosidase precursor (EC 3.2.1.82) (Exo-PG) {Erwinia chrysanthemi}; contains PF00295: Glycosyl hydrolases family 28
357624	1	63	59	58	857	1	2	At5g51280	2,00E-51	68418.m06357 DEAD-box protein abstrakt, putative

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354223	2	63	59	58	1198	1	1	At5g26742	3,00E-28	68418.m03161 DEAD box RNA helicase (RH3) nearly identical to RNA helicase [Arabidopsis thaliana] GI:3775987; contains Pfam profiles PF00270: DEAD/DEAH box helicase, PF00271: Helicase conserved C-terminal domain, PF00098: Zinc knuckle
353070	2	63	59	58	1314	1	3	At4g00660	2,00E-81	68417.m00091 DEAD/DEAH box helicase, putative similar to ATP-dependent RNA helicases
353219	3	63	59	58	1314	1	3	At4g00660	9,00E-108	68417.m00091 DEAD/DEAH box helicase, putative similar to ATP-dependent RNA helicases
358742	1	63	59	58	1469	1	1	At5g62190	1,00E-44	68418.m07807 DEAD box RNA helicase (PRH75) nearly identical to RNA helicase [Arabidopsis thaliana] GI:1488521; contains Pfam profiles PF00270: DEAD/DEAH box helicase, PF00271: Helicase conserved C-terminal domain
354096	4	63	59	58	1570	1	2	At5g11200	1,00E-51	68418.m01309 DEAD/DEAH box helicase, putative
356458	1	63	59	58	1570	1	2	At5g11200	8,00E-100	68418.m01309 DEAD/DEAH box helicase, putative
357715	1	63	59	58	1570	1	2	At5g11200	5,00E-17	68418.m01309 DEAD/DEAH box helicase, putative
353740	3	63	59	58	1586	2	2	At3g13920	1,00E-162	68416.m01758 eukaryotic translation initiation factor 4A-1 / eIF-4A-1 eIF-4A-1 gi:15293046, gi:15450485; contains Pfam profile PF00270: DEAD/DEAH box helicase; contains Pfam profile PF00271: Helicase conserved C-terminal domain
353836	4	63	59	58	1586	2	2	At3g13920	3,00E-152	68416.m01758 eukaryotic translation initiation factor 4A-1 / eIF-4A-1 eIF-4A-1 gi:15293046, gi:15450485; contains Pfam profile PF00270: DEAD/DEAH box helicase; contains Pfam profile PF00271: Helicase conserved C-terminal domain
356952	1	63	59	58	1586	2	2	At3g13920	5,00E-14	68416.m01758 eukaryotic translation initiation factor 4A-1 / eIF-4A-1 eIF-4A-1 gi:15293046, gi:15450485; contains Pfam profile PF00270: DEAD/DEAH box helicase; contains Pfam profile PF00271: Helicase conserved C-terminal domain
353122	4	63	59	58	1939	1	2	At3g19760	3,00E-174	68416.m02501 eukaryotic translation initiation factor 4A, putative / eIF-4A, putative / DEAD box RNA helicase, putative contains DEAD/DEAH helicase domain; similar to RNA helicase GB:CAA09195 from [Arabidopsis thaliana]; identical to cDNA DEAD box RNA helicase, RH2 GI:3775984

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358262	1	63	59	58	2325	1	2	At1g12770	2,00E-25	68414.m01482 DEAD/DEAH box helicase family protein / pentatricopeptide (PPR) repeat-containing protein contains Pfam profiles: PF00271 helicase conserved C-terminal domain, PF01535 PPR repeat, PF00270: DEAD/DEAH box helicase
353489	2	63	59	58	2478	2	1	At5g65900	5,00E-101	68418.m08295 DEAD/DEAH box helicase, putative contains Pfam profiles PF00270:DEAD/DEAH box helicase and PF00271: Helicase conserved C-terminal domain; identical to cDNA RH27 helicase, partial GI:4033334
357973	1	63	59	58	2478	2	1	At3g18600	5,00E-40	68416.m02364 DEAD/DEAH box helicase, putative non-consensus acceptor splice site AT at exon 2; similar to DEAD box helicase protein GB:NP_006764 from [Homo sapiens], contains Pfam profile: PF00270 DEAD/DEAH box helicase
353481	2	63	59	58	3034	1	1	At4g15850	3,00E-55	68417.m02410 DEAD/DEAH box helicase, putative similar to D-E-A-D box protein [Drosophila melanogaster] GI:499204; contains Pfam profiles PF00270: DEAD/DEAH box helicase, PF00271: Helicase conserved C-terminal domain
357416	1	63	59	58	3102	1	2	At5g60990	1,00E-57	68418.m07651 DEAD/DEAH box helicase, putative (RH10) probable replication protein A1, Oryza sativa, EMBL:AF009179
352991	2	63	59	58	3644	1	1	At3g53110	3,00E-96	68416.m05853 DEAD/DEAH box helicase, putative RNA helicase, Mus musculus, PIR:I49731
357240	1	63	59	58	4702	1	1	At5g19210	3,00E-68	68418.m02287 DEAD/DEAH box helicase, putative EUKARYOTIC INITIATION FACTOR 4A-II (EIF-4A-II), Homo sapiens, SWISSPROT:IF42_HUMAN
357476	1	63	59	58	6775	1	1	At5g08290	8,00E-44	68418.m00976 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
356974	1	63	59	58				At1g72730	3,00E-116	68414.m08410 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))
354433	2	64	47	68	2986	2	2	At5g06700	4,00E-84	68418.m00757 expressed protein strong similarity to unknown protein (emb|CAB82953.1)
355248	1	64	47	68	3214	1	1	At5g20590	1,00E-25	68418.m02445 expressed protein various predicted proteins, Arabidopsis thaliana

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358075	1	64	47	68	3850	1	1	At3g62390	7,00E-65	68416.m07008 expressed protein several hypothetical proteins - Arabidopsis thaliana
356972	1	64	47	68	4268	1	2	At1g48880	8,00E-19	68414.m05476 hypothetical protein
356741	1	65	54	61	3077	1	3	At4g23030	7,00E-29	68417.m03321 MATE efflux protein-related contains Pfam profile PF01554: Uncharacterized membrane protein family
353133	2	65	54	61	3856	5	3	At3g26590	5,00E-54	68416.m03319 MATE efflux family protein similar to ripening regulated protein DDTFR18 [Lycopersicon esculentum] GI:12231296; contains Pfam profile: PF01554 uncharacterized membrane protein family
354664	1	65	54	61	3856	5	3	At5g38030	7,00E-74	68418.m04581 MATE efflux family protein similar to ripening regulated protein DDTFR18 [Lycopersicon esculentum] GI:12231296; contains Pfam profile PF01554: Uncharacterized membrane protein family; putative multidrug efflux protein NorM - Vibrio parahaemolyticus, EMBL:AB010463
354100	2	65	54	61	4063	1	1	At2g32230	3,00E-43	68415.m03938 pentatricopeptide (PPR) repeat-containing protein contains Pfam profile PF01535: PPR repeat
358409	1	65	54	61				At1g66780	3,00E-27	68414.m07591 MATE efflux family protein contains TIGRfam profile: TIGR00797: MATE efflux family protein, Pfam profile PF01554: Uncharacterized membrane protein family
359243	1	66	33	80	7261	2	1	At5g47310	2,00E-33	68418.m05832 expressed protein
358928	1	67	68	42	314	1	1	At5g47690	2,00E-50	68418.m05887 expressed protein
359293	1	67	68	42	2789	1	1	At1g67230	2,00E-42	68414.m07652 expressed protein
354911	1	67	68	42	4283	1	2	At4g27500	1,00E-58	68417.m03950 expressed protein non-consensus GA donor splice site at exon 6
354927	1	67	68	42	4752	3	1	At5g14270	7,00E-07	68418.m01669 DNA-binding bromodomain-containing protein contains bromodomain, INTERPRO:IPR001487
353342	3	67	68	42	5142	1	1	At4g39680	1,00E-09	68417.m05614 SAP domain-containing protein contains Pfam domain PF02037: SAP domain
354317	2	67	68	42	5142	1	1	At4g39680	1,00E-35	68417.m05614 SAP domain-containing protein contains Pfam domain PF02037: SAP domain
355599	1	67	68	42	5142	1	1	At4g39680	7,00E-33	68417.m05614 SAP domain-containing protein contains Pfam domain PF02037: SAP domain
356315	1	67	68	42	5770	1	1	At1g20970	1,00E-15	68414.m02625 adhesin-related contains TIGRFAM TIGR01612: reticulocyte binding protein; contains TIGRFAM TIGR00864: polycystin cation channel protein; similar to fimbriae-associated protein Fap1 [Streptococcus parasanguinis] (GI:3929312)

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
354972	1	67	68	42	6365	2	1	At3g55770	3,00E-50	68416.m06197 LIM domain-containing protein similar to pollen specific LIM domain protein 1b [Nicotiana tabacum] GI:6467905, PGPS/D1 [Petunia x hybrida] GI:4105772; contains Pfam profile PF00412: LIM domain
358663	1	67	68	42				At5g10950	1,00E-19	68418.m01271 cylicin-related low similarity to SP|Q28092 Cylicin II (Multiple-band polypeptide II) {Bos taurus}
354196	2	68	31	79	1131	4	2	At1g19260	3,00E-43	68414.m02396 hAT dimerisation domain-containing protein
354960	1	68	31	79	6932	1	3	At3g28007	2,00E-43	68416.m03496 nodulin MtN3 family protein contains Pfam PF03083 MtN3/saliva family; similar to LIM7 GI:431154 (induced in meiotic prophase in lily microsporocytes) from [Lilium longiflorum]
358024	1	68	31	79				At2g06500	1,00E-54	68415.m00720 hAT dimerisation domain-containing protein / transposase-related low similarity to transposase [Ipomoea purpurea] AB004906 GI:4063770
352979	5	69	51	55	2711	2	1	At3g08580	7,00E-55	68416.m00996 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]
353111	8	69	51	55	2935	1	1	At4g28390	9,00E-139	68417.m04063 ADP, ATP carrier protein, mitochondrial, putative / ADP/ATP translocase, putative / adenine nucleotide translocator, putative similar to mitochondrial ADP,ATP carrier protein SP:P12857 from [Zea mays]
353683	2	69	51	55	2935	1	1	At4g28390	3,00E-32	68417.m04063 ADP, ATP carrier protein, mitochondrial, putative / ADP/ATP translocase, putative / adenine nucleotide translocator, putative similar to mitochondrial ADP,ATP carrier protein SP:P12857 from [Zea mays]
355726	1	69	51	55	2935	1	1	At4g28390	2,00E-17	68417.m04063 ADP, ATP carrier protein, mitochondrial, putative / ADP/ATP translocase, putative / adenine nucleotide translocator, putative similar to mitochondrial ADP,ATP carrier protein SP:P12857 from [Zea mays]
357003	1	69	51	55	2935	1	1	At4g28390	3,00E-17	68417.m04063 ADP, ATP carrier protein, mitochondrial, putative / ADP/ATP translocase, putative / adenine nucleotide translocator, putative similar to mitochondrial ADP,ATP carrier protein SP:P12857 from [Zea mays]
357342	1	69	51	55	2935	1	1	At4g28390	3,00E-44	68417.m04063 ADP, ATP carrier protein, mitochondrial, putative / ADP/ATP translocase, putative / adenine nucleotide translocator, putative similar to mitochondrial ADP,ATP carrier protein SP:P12857 from [Zea mays]

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
359047	1	69	51	55	2995	1	1	At4g01100	7,00E-48	68417.m00148 mitochondrial substrate carrier family protein contains Pfam profile: PF00153 mitochondrial carrier protein
359299	1	69	51	55	2995	1	1	At4g01100	4,00E-66	68417.m00148 mitochondrial substrate carrier family protein contains Pfam profile: PF00153 mitochondrial carrier protein
353959	7	69	51	55	3729	1	2	At5g19760	4,00E-132	68418.m02349 dicarboxylate/tricarboxylate carrier (DTC) identical to dicarboxylate/tricarboxylate carrier [Arabidopsis thaliana] GI:19913113
354289	2	69	51	55	3729	1	2	At5g19760	2,00E-31	68418.m02349 dicarboxylate/tricarboxylate carrier (DTC) identical to dicarboxylate/tricarboxylate carrier [Arabidopsis thaliana] GI:19913113
357432	1	69	51	55	3729	1	2	At5g19760	4,00E-37	68418.m02349 dicarboxylate/tricarboxylate carrier (DTC) identical to dicarboxylate/tricarboxylate carrier [Arabidopsis thaliana] GI:19913113
355652	1	69	51	55	4450	1	1	At5g15640	1,00E-32	68418.m01830 mitochondrial substrate carrier family protein contains Pfam profile: PF00153 mitochondrial carrier protein
354257	2	69	51	55	5480	2	1	At1g07030	6,00E-35	68414.m00749 mitochondrial substrate carrier family protein contains Pfam profile: PF00153 mitochondrial carrier protein
359042	1	69	51	55	5980	1	1	At1g25380	9,00E-67	68414.m03150 mitochondrial substrate carrier family protein contains Pfam profile: PF00153 mitochondrial carrier protein
355323	1	69	51	55	7680	1	1	At2g33820	2,00E-37	68415.m04149 mitochondrial substrate carrier family protein (BAC1) contains Pfam profile: PF00153 mitochondrial carrier protein
354435	2	71	34	71	6502	1	1	At4g38210	1,00E-59	68417.m05393 expansin, putative (EXP20) similar to alpha-expansin 3 GI:6942322 from [Triphysaria versicolor]; alpha-expansin gene family, PMID:11641069
353499	13	72	49	55	6659	3	2	At4g10450	4,00E-75	68417.m01717 60S ribosomal protein L9 (RPL90D) ribosomal protein L9, cytosolic - garden pea, PIR2:S19978
359411	1	72	49	55	6659	3	2	At4g10450	1,00E-08	68417.m01717 60S ribosomal protein L9 (RPL90D) ribosomal protein L9, cytosolic - garden pea, PIR2:S19978
353626	2	74	47	52	6672	1	3	At3g43810	1,00E-75	68416.m04682 calmodulin-7 (CAM7) almost identical to calmodulin GI:16227 from [Arabidopsis thaliana], SP|P59220 Calmodulin-7 {Arabidopsis thaliana}
353894	3	74	47	52	6672	1	3	At3g43810	2,00E-81	68416.m04682 calmodulin-7 (CAM7) almost identical to calmodulin GI:16227 from [Arabidopsis thaliana], SP|P59220 Calmodulin-7 {Arabidopsis thaliana}

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354416	7	74	47	52	6672	1	3	At3g43810	3,00E-81	68416.m04682 calmodulin-7 (CAM7) almost identical to calmodulin GI:16227 from [Arabidopsis thaliana], SP|P59220 Calmodulin-7 {Arabidopsis thaliana}
355596	1	74	47	52	6672	1	3	At3g43810	2,00E-81	68416.m04682 calmodulin-7 (CAM7) almost identical to calmodulin GI:16227 from [Arabidopsis thaliana], SP|P59220 Calmodulin-7 {Arabidopsis thaliana}
356663	1	74	47	52	8234	2	2	At2g43290	2,00E-16	68415.m05382 calmodulin-like protein (MSS3) identical to calmodulin-like MSS3 from GI:9965747 [Arabidopsis thaliana]
353821	2	75	32	65	6625	3	4	At4g00150	6,00E-51	68417.m00015 scarecrow-like transcription factor 6 (SCL6)
355941	1	75	32	65	6625	3	4	At2g45160	1,00E-10	68415.m05622 scarecrow transcription factor family protein
357635	1	75	32	65				At3g03450	1,00E-19	68416.m00343 gibberellin response modulator, putative / gibberellin-responsive modulator, putative similar to GAI (GI:2569938), RGA1 (GB:AAC67333) and RGA2 (GI:2339980) [Arabidopsis thaliana]; possible involvement in nitrogen metabolism
358767	1	76	43	52	168	1	1	At4g03430	4,00E-62	68417.m00470 pre-mRNA splicing factor-related similar to pre-mRNA splicing factor pre-mRNA splicing factor prp1 (SP:Q12381) [Fission yeast]
359571	1	76	43	52	3122	2	1	At3g17430	3,00E-72	68416.m02226 phosphate translocator-related low similarity to phosphoenolpyruvate/phosphate translocator precursor [Mesembryanthemum crystallinum] GI:9295275, SP|P52178 Triose phosphate/phosphate translocator, non-green plastid, chloroplast precursor (CTPT) {Brassica oleracea}
353645	2	76	43	52	3170	1	1	At1g61800	2,00E-43	68414.m06969 glucose-6-phosphate/phosphate translocator, putative similar to glucose-6-phosphate/phosphate-translocator precursor GI:2997591 from [Pisum sativum]
356904	1	76	43	52	3170	1	1	At1g61800	4,00E-42	68414.m06969 glucose-6-phosphate/phosphate translocator, putative similar to glucose-6-phosphate/phosphate-translocator precursor GI:2997591 from [Pisum sativum]
357552	1	76	43	52	3170	1	1	At1g61800	5,00E-26	68414.m06969 glucose-6-phosphate/phosphate translocator, putative similar to glucose-6-phosphate/phosphate-translocator precursor GI:2997591 from [Pisum sativum]

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
353857	3	76	43	52	3562	3	2	At4g09810	4,00E-108	68417.m01610 transporter-related low similarity to UDP-sugar transporter [Drosophila melanogaster] GI:14971008, UDP-glucuronic acid transporter [Homo sapiens] GI:11463949
358118	1	76	43	52	3562	3	2	At1g34020	2,00E-33	68414.m04218 transporter-related low similarity to UDP-sugar transporter [Drosophila melanogaster] GI:14971008, UDP-glucuronic acid transporter [Homo sapiens] GI:11463949
353099	2	76	43	52	3876	1	1	At5g33320	2,00E-58	68418.m03955 triose phosphate/phosphate translocator, putative similar to SWISS-PROT:P52178 triose phosphate/phosphate translocator [Cauliflower] {Brassica oleracea}
357071	1	76	43	52	3876	1	1	At5g33320	2,00E-62	68418.m03955 triose phosphate/phosphate translocator, putative similar to SWISS-PROT:P52178 triose phosphate/phosphate translocator [Cauliflower] {Brassica oleracea}
356650	1	77	37	56	5960	1	1	At5g62990	3,00E-22	68418.m07903 hypothetical protein
359471	1	77	37	56	6581	1	1	At2g39120	1,00E-51	68415.m04806 expressed protein
356147	1	77	37	56	7238	1	1	At3g58520	1,00E-18	68416.m06523 expressed protein
358522	1	78	88	5	2985	1	1	At1g67370	2,00E-09	68414.m07669 meiotic asynaptic mutant 1 (ASY1) identical to meiotic asynaptic mutant 1 [Arabidopsis thaliana] GI:7939627; contains Pfam profiles PF02301: DNA-binding HORMA domain, PF04433: SWIRM domain
354619	1	78	88	5				At2g07320	4,00E-11	68415.m00839 SWIM zinc finger family protein contains Pfam profile PF04434: SWIM zinc finger
354226	2	79	35	58				At2g24210	9,00E-23	68415.m02892 myrcene/ocimene synthase (TPS10) nearly identical to GI:9957293; contains Pfam profile: PF01397 terpene synthase family
356055	1	79	35	58				At4g16740	7,00E-22	68417.m02528 terpene synthase/cyclase family protein similar to myrcene/ocimene synthase [GI:9957293]; contains Pfam profile PF01397: Terpene synthase, N-terminal domain; contains Pfam profile PF03936: Terpene synthase family, metal binding domain; identical to cDNA (partial mRNA) E-beta-ocimene synthase GI:30349137
357201	1	79	35	58				At3g25830	3,00E-40	68416.m03218 myrcene/ocimene synthase, putative similar to myrcene/ocimene synthase [Arabidopsis thaliana] GI:9957293; contains Pfam profiles PF03936: Terpene synthase family, metal binding domain, PF01397: Terpene synthase, N-terminal domain

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
355813	1	80	37	55	9404	1	1	At1g64640	1,00E-32	68414.m07328 plastocyanin-like domain-containing protein contains InterPro:IPR003245 plastocyanin-like domain
353164	6	80	37	55				At4g30590	8,00E-09	68417.m04340 plastocyanin-like domain-containing protein
356731	1	80	37	55				At5g25090	5,00E-28	68418.m02973 plastocyanin-like domain-containing protein
354806	1	81	50	41	853	3	1	At2g29190	2,00E-84	68415.m03548 pumilio/Puf RNA-binding domain-containing protein
357666	1	81	50	41	853	3	1	At2g29200	9,00E-104	68415.m03549 pumilio/Puf RNA-binding domain-containing protein similar to BPM [Hordeum vulgare] GI:20513851
356539	1	81	50	41	1707	2	1	At3g60320	2,00E-18	68416.m06742 expressed protein contains Pfam profiles: PF04782: protein of unknown function (DUF632), PF04783: protein of unknown function (DUF630)
353265	2	81	50	41	2094	1	1	At5g25590	4,00E-41	68418.m03045 expressed protein contains Pfam profile PF04783: Protein of unknown function (DUF630)
354168	2	81	50	41	2094	1	1	At5g25590	6,00E-99	68418.m03045 expressed protein contains Pfam profile PF04783: Protein of unknown function (DUF630)
359607	1	81	50	41	2160	1	2	At3g20250	1,00E-30	68416.m02565 pumilio/Puf RNA-binding domain-containing protein contains Pfam profile: PF00806 Pumilio-family RNA binding domains (aka PUM-HD, Pumilio homology domain) (8 copies at C-terminus)
354487	1	81	50	41	3335	1	1	At3g51290	8,00E-31	68416.m05614 proline-rich family protein
356560	1	81	50	41	3335	1	1	At3g51290	2,00E-18	68416.m05614 proline-rich family protein
358377	1	81	50	41	3564	2	2	At4g35240	2,00E-22	68417.m05009 expressed protein contains Pfam domains, PF04782: Protein of unknown function (DUF632) and PF04783: Protein of unknown function (DUF630)
359659	1	81	50	41	5647	2	2	At1g78160	7,00E-49	68414.m09108 pumilio/Puf RNA-binding domain-containing protein contains Pfam profile: PF00806 Pumilio-family RNA binding domains (aka PUM-HD, Pumilio homology domain) (8 copies at C-terminal half of protein)
358183	1	81	50	41	6005	1	1	At2g34670	2,00E-42	68415.m04259 proline-rich family protein contains proline-rich region, INTERPRO:IPR000694
359689	1	81	50	41				At1g52320	4,00E-33	68414.m05905 expressed protein contains Pfam profile: PF04782 protein of unknown function (DUF632)
352968	3	82	50	40	2277	3	3	At1g55360	1,00E-36	68414.m06327 expressed protein contains Pfam profile PF03080: Arabidopsis proteins of unknown function

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356422	1	82	50	40	2277	3	3	At3g13510	2,00E-34	68416.m01699 expressed protein Pfam profile PF03080: Arabidopsis proteins of unknown function
358851	1	82	50	40	2277	3	3	At3g13510	5,00E-34	68416.m01699 expressed protein Pfam profile PF03080: Arabidopsis proteins of unknown function
352958	2	83	34	55	2368	2	1	At1g47128	2,00E-41	68414.m05222 cysteine proteinase (RD21A) / thiol protease identical to SP|P43297 Cysteine proteinase RD21A precursor (EC 3.4.22.-) {Arabidopsis thaliana}, thiol protease RD21A SP:P43297 from [Arabidopsis thaliana]
355303	1	83	34	55	3195	1	1	At1g09850	1,00E-64	68414.m01109 cysteine protease, papain-like (XBCP3) identical to papain-like cysteine peptidase XBCP3 GI:14600257 from [Arabidopsis thaliana]; contains Pfam profiles PF00112: Papain family cysteine protease and PF00396: Granulin
359556	1	83	34	55	3693	2	2	At4g39090	3,00E-63	68417.m05535 cysteine proteinase RD19a (RD19A) / thiol protease identical to cysteine proteinase RD19a, thiol protease SP:P43296, GI:435618 from [Arabidopsis thaliana]
353969	3	83	34	55	3714	3	1	At4g01610	1,00E-39	68417.m00211 cathepsin B-like cysteine protease, putative similar to cathepsin B-like cysteine proteinase GI:609175 from [Nicotiana rustica]; contains an unusually short, 5nt exon
353613	2	84	44	45	90	2	2	At3g06400	3,00E-61	68416.m00738 DNA-dependent ATPase, putative similar to DNA-dependent ATPase SNF2H [Mus musculus] GI:14028669; contains Pfam profiles PF00271: Helicase conserved C-terminal domain, PF00176: SNF2 family N-terminal domain, PF00249: Myb-like DNA-binding domain
358426	1	84	44	45	155	1	1	At3g57300	3,00E-51	68416.m06378 transcriptional activator, putative similar to transcriptional activator SRCAP [Homo sapiens] GI:5106572; contains Pfam profiles PF00271: Helicase conserved C-terminal domain, PF00176: SNF2 family N-terminal domain
353934	2	84	44	45	173	1	1	At5g44800	5,00E-08	68418.m05492 chromodomain-helicase-DNA-binding family protein / CHD family protein similar to chromatin remodeling factor CHD3 (PICKLE) [Arabidopsis thaliana] GI:6478518; contains Pfam profiles PF00271: Helicase conserved C-terminal domain, PF00176: SNF2 family N-terminal domain, PF00628: PHD-finger, PF00385: 'chromo' (CHRromatin Organization MOdifier)
355288	1	84	44	45	272	1	1	At2g25170	2,00E-59	68415.m03010 chromatin remodeling factor CHD3 (PICKLE) identical to chromatin remodeling factor CHD3 [Arabidopsis thaliana] GI:6478518

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358616	1	84	44	45	448	1	1	At5g22750	1,00E-75	68418.m02657 SNF2 domain-containing protein / helicase domain-containing protein / RING finger domain-containing protein similar to SP|P36607 DNA repair protein rad8 {Schizosaccharomyces pombe}; contains Pfam profiles PF00271: Helicase conserved C-terminal domain, PF00176: SNF2 family N-terminal domain, PF00097: Zinc finger, C3HC4 type (RING finger)
353432	2	84	44	45	707	1	1	At1g03750	2,00E-86	68414.m00355 helicase, putative similar to SP|Q03468 Excision repair protein ERCC-6 (Cockayne syndrome protein CSB) {Homo sapiens}; contains Pfam profiles PF00271: Helicase conserved C-terminal domain, PF00176: SNF2 family N-terminal domain, PF02810: SEC-C motif
354517	1	84	44	45	826	1	2	At5g66750	6,00E-54	68418.m08414 SNF2 domain-containing protein / helicase domain-containing protein similar to proliferation-associated SNF2-like protein [Homo sapiens] GI:8980660; contains Pfam profiles PF00271: Helicase conserved C-terminal domain, PF00176: SNF2 family N-terminal domain
359150	1	84	44	45	1049	2	1	At1g50410	8,00E-13	68414.m05650 SNF2 domain-containing protein / helicase domain-containing protein / RING finger domain-containing protein similar to transcription factor RUSH-1alpha [Oryctolagus cuniculus] GI:1655930; contains Pfam profiles PF00271: Helicase conserved C-terminal domain, PF00176: SNF2 family N-terminal domain, PF00097: Zinc finger, C3HC4 type (RING finger)
356193	1	84	44	45	1275	1	1	At2g02090	6,00E-49	68415.m00145 SNF2 domain-containing protein / helicase domain-containing protein similar to transcriptional activator SRCAP [Homo sapiens] GI:5106572; contains Pfam profiles PF00271: Helicase conserved C-terminal domain, PF00176: SNF2 family N-terminal domain
353954	2	84	44	45				At1g05480	5,00E-09	68414.m00557 SNF2 domain-containing protein / helicase domain-containing protein low similarity to SP|Q9U7E0 Transcriptional regulator ATRX homolog {Caenorhabditis elegans}; contains PFam profiles PF00271: Helicase conserved C-terminal domain, PF00176: SNF2 family N-terminal domain

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357942	1	85	78	11	73	2	2	At3g11910	7,00E-62	68416.m01460 ubiquitin-specific protease, putative strong similarity to ubiquitin-specific protease 12 (UBP12) [Arabidopsis thaliana] GI:11993471; contains Pfam profiles PF00443: Ubiquitin carboxyl-terminal hydrolase, PF00917: MATH domain
352930	3	85	78	11	7945	2	1	At1g51600	1,00E-53	68414.m05811 zinc finger (GATA type) family protein contains similarity to zinc-finger protein ZIM [Arabidopsis thaliana] gi|8918533|dbj|BAA97679; contains Pfam PF00320: GATA zinc finger
355428	1	86	28	61	2505	1	1	At1g43190	1,00E-64	68414.m04977 polypyrimidine tract-binding protein, putative / heterogeneous nuclear ribonucleoprotein, putative similar to Polypyrimidine tract-binding protein 1 (PTB) (Heterogeneous nuclear ribonucleoprotein I) (hnRNP I) from {Rattus norvegicus} SP|Q00438, {Homo sapiens} SP|P26599, [Homo sapiens] GI:35770; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)
357309	1	86	28	61	2505	1	1	At1g43190	2,00E-39	68414.m04977 polypyrimidine tract-binding protein, putative / heterogeneous nuclear ribonucleoprotein, putative similar to Polypyrimidine tract-binding protein 1 (PTB) (Heterogeneous nuclear ribonucleoprotein I) (hnRNP I) from {Rattus norvegicus} SP|Q00438, {Homo sapiens} SP|P26599, [Homo sapiens] GI:35770; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)
357181	1	86	28	61				At5g53180	9,00E-98	68418.m06611 polypyrimidine tract-binding protein, putative / heterogeneous nuclear ribonucleoprotein, putative similar to Polypyrimidine tract-binding protein 1 (PTB) (Heterogeneous nuclear ribonucleoprotein I) (hnRNP I) from {Rattus norvegicus} SP|Q00438, {Homo sapiens} SP|P26599; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)
355901	1	87	46	42	1999	2	1	At3g18080	1,00E-48	68416.m02299 glycosyl hydrolase family 1 protein contains Pfam PF00232 : Glycosyl hydrolase family 1 domain; TIGRFAM TIGR01233: 6-phospho-beta-galactosidase; similar to beta-glucosidase BGQ60 precursor GB:A57512 [Hordeum vulgare]; similar to beta-mannosidase enzyme (GI:17226270) [Lycopersicon esculentum]

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358782	1	87	46	42	1999	2	1	At3g18080	4,00E-90	68416.m02299 glycosyl hydrolase family 1 protein contains Pfam PF00232 : Glycosyl hydrolase family 1 domain; TIGRFAM TIGR01233: 6-phospho-beta-galactosidase; similar to beta-glucosidase BGQ60 precursor GB:A57512 [Hordeum vulgare]; similar to beta-mannosidase enzyme (GI:17226270) [Lycopersicon esculentum]
359384	1	87	46	42	2098	1	1	At5g36890	7,00E-31	68418.m04419 glycosyl hydrolase family 1 protein pcontains Pfam PF00232 : Glycosyl hydrolase family 1 domain; similar to amygdalin hydrolase isoform AH I precursor (GI:16757966) [Prunus serotina]; prunasin hydrolase isoform PHA precursor, Prunus serotina, EMBL:AF221526
357247	1	87	46	42	2770	5	4	At2g25630	2,00E-64	68415.m03072 glycosyl hydrolase family 1 protein contains Pfam PF00232 : Glycosyl hydrolase family 1 domain; TIGRFAM TIGR01233: 6-phospho-beta-galactosidase; similar to amygdalin hydrolase isoform AH I precursor (GI:16757966) [Prunus serotina]
356751	1	88	43	45	855	1	1	At2g16920	9,00E-31	68415.m01949 ubiquitin-conjugating enzyme family protein low similarity to ubiquitin-conjugating BIR-domain enzyme APOLLON [Homo sapiens] GI:8489831, ubiquitin-conjugating enzyme [Mus musculus] GI:3319990; contains Pfam profile PF00179: Ubiquitin-conjugating enzyme
353551	2	88	43	45	5996	1	1	At5g05080	8,00E-55	68418.m00539 ubiquitin-conjugating enzyme, putative similar to SP|Q16763 Ubiquitin-conjugating enzyme E2-24 kDa (EC 6.3.2.19) (Ubiquitin- protein ligase) (Ubiquitin carrier protein) {Homo sapiens}; contains Pfam profile PF00179: Ubiquitin-conjugating enzyme
354071	2	88	43	45	6441	2	2	At2g02760	2,00E-86	68415.m00219 ubiquitin-conjugating enzyme 2 (UBC2) E2; identical to gi:2689242, SP:P42745
357439	1	88	43	45	6441	2	2	At1g14400	2,00E-21	68414.m01708 ubiquitin-conjugating enzyme 1 (UBC1) E2; identical to gi:431259, SP:P25865
357675	1	88	43	45	6478	2	1	At1g17280	2,00E-21	68414.m02105 ubiquitin-conjugating enzyme, putative similar to ubiquitin conjugating enzyme 6 from [Homo sapiens] GI:14029267, [Mus musculus] GI:14029263; contains Pfam profile PF00179: Ubiquitin-conjugating enzyme

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359262	1	88	43	45	6478	2	1	At1g17280	4,00E-82	68414.m02105 ubiquitin-conjugating enzyme, putative similar to ubiquitin conjugating enzyme 6 from [Homo sapiens] GI:14029267, [Mus musculus] GI:14029263; contains Pfam profile PF00179: Ubiquitin-conjugating enzyme
353899	5	88	43	45	6511	1	1	At1g64230	6,00E-84	68414.m07276 ubiquitin-conjugating enzyme, putative identical or nearly so to Ubiquitin-conjugating enzymes SP|P35132, SP|P35131, SP|P35133 from {Arabidopsis thaliana}; contains Pfam profile PF00179: Ubiquitin-conjugating enzyme
354210	2	88	43	45	6511	1	1	At1g64230	1,00E-83	68414.m07276 ubiquitin-conjugating enzyme, putative identical or nearly so to Ubiquitin-conjugating enzymes SP|P35132, SP|P35131, SP|P35133 from {Arabidopsis thaliana}; contains Pfam profile PF00179: Ubiquitin-conjugating enzyme
353786	2	88	43	45	6565	1	1	At3g46460	3,00E-77	68416.m05037 ubiquitin-conjugating enzyme 13 (UBC13) E2; identical to gi:992706
358187	1	88	43	45	6565	1	1	At3g46460	2,00E-66	68416.m05037 ubiquitin-conjugating enzyme 13 (UBC13) E2; identical to gi:992706
359525	1	88	43	45	6613	1	2	At3g08690	9,00E-19	68416.m01010 ubiquitin-conjugating enzyme 11 (UBC11) E2; identical to gi:12643427, SP:P35134
353312	3	88	43	45	6796	1	2	At2g18600	5,00E-72	68415.m02166 RUB1-conjugating enzyme, putative strong similarity to gi:6635457 RUB1 conjugating enzyme [Arabidopsis thaliana]; contains Pfam profile PF00179: Ubiquitin-conjugating enzyme
353831	4	88	43	45	6796	1	2	At2g18600	5,00E-82	68415.m02166 RUB1-conjugating enzyme, putative strong similarity to gi:6635457 RUB1 conjugating enzyme [Arabidopsis thaliana]; contains Pfam profile PF00179: Ubiquitin-conjugating enzyme
353544	2	88	43	45	6982	1	1	At5g50870	9,00E-34	68418.m06304 ubiquitin-conjugating enzyme, putative strong similarity to ubiquitin conjugating enzyme [Lycopersicon esculentum] GI:886679; contains Pfam profile PF00179: Ubiquitin-conjugating enzyme
358692	1	88	43	45	7008	3	1	At1g63800	3,00E-79	68414.m07220 ubiquitin-conjugating enzyme 5 (UBC5) E2; identical to gi:431269, SP:P42749
353372	2	88	43	45	7466	2	1	At1g50490	2,00E-71	68414.m05662 ubiquitin-conjugating enzyme 20 (UBC20) nearly identical to ubiquitin-conjugating enzyme UBC20 [Arabidopsis thaliana] GI:22530867; contains Pfam profile PF00179: Ubiquitin-conjugating enzyme

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
357488	1	88	43	45	7592	2	1	At1g78870	1,00E-35	68414.m09194 ubiquitin-conjugating enzyme, putative nearly identical to ubiquitin-conjugating enzyme E2 [Catharanthus roseus] GI:5381319; contains Pfam profile PF00179: Ubiquitin-conjugating enzyme
352921	3	88	43	45				At4g27960	3,00E-71	68417.m04012 ubiquitin-conjugating enzyme E2-17 kDa 9 (UBC9) E2; identical to gi:297883, SP:P35132; identical to cDNA UBC9 for ubiquitin conjugating enzyme homolog GI:297883
353288	5	88	43	45				At1g75440	2,00E-70	68414.m08763 ubiquitin-conjugating enzyme 16 (UBC16) E2; identical to gi:2801444, GB:AAC39325 from [Arabidopsis thaliana] (Plant Mol. Biol. 23 (2), 387-396 (1993))
355582	1	88	43	45				At1g75440	1,00E-20	68414.m08763 ubiquitin-conjugating enzyme 16 (UBC16) E2; identical to gi:2801444, GB:AAC39325 from [Arabidopsis thaliana] (Plant Mol. Biol. 23 (2), 387-396 (1993))
356680	1	88	43	45				At5g53300	4,00E-59	68418.m06625 ubiquitin-conjugating enzyme 10 (UBC10) E2; identical to gi:297877, SP:P35133
360035	1	89	20	68	4328	3	1	At3g63010	8,00E-06	68416.m07078 expressed protein similar to PrMC3 [Pinus radiata] GI:5487873
356649	1	89	20	68	6298	1	1	At5g16080	5,00E-06	68418.m01879 expressed protein similar to PrMC3 [Pinus radiata] GI:5487873
352950	2	90	44	43	375	1	1	At5g36880	9,00E-112	68418.m04418 acetyl-CoA synthetase, putative / acetate-CoA ligase, putative similar to SP|P27550 (Escherichia coli) and gi:8439651 (Homo sapiens); contains Pfam AMP-binding enzyme domain PF00501
356052	1	90	44	43	375	1	1	At5g36880	1,00E-19	68418.m04418 acetyl-CoA synthetase, putative / acetate-CoA ligase, putative similar to SP|P27550 (Escherichia coli) and gi:8439651 (Homo sapiens); contains Pfam AMP-binding enzyme domain PF00501
356367	1	90	44	43	738	3	2	At1g64400	1,00E-24	68414.m07299 long-chain-fatty-acid--CoA ligase, putative / long-chain acyl-CoA synthetase, putative similar to GI:1617270 (MF7P) from [Brassica napus]
355714	1	90	44	43	849	1	1	At2g04350	9,00E-53	68415.m00434 long-chain-fatty-acid--CoA ligase family protein / long-chain acyl-CoA synthetase family protein (LACS8) similar to LACS 4 [SP|O35547] from Rattus norvegicus, LACS 4 [SP|O60488] from Homo sapiens; contains Pfam HMM hit: AMP-binding enzymes PF00501

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
352945	2	90	44	43	1039	1	1	At2g47240	7,00E-65	68415.m05899 long-chain-fatty-acid--CoA ligase family protein / long-chain acyl-CoA synthetase family protein similar to GI:1617270 (MF7P) and gi:1617628 (MF45P) from [Brassica napus] ; contains Pfam AMP-binding enzyme domain PF00501
352983	2	90	44	43	1039	1	1	At2g47240	1,00E-59	68415.m05899 long-chain-fatty-acid--CoA ligase family protein / long-chain acyl-CoA synthetase family protein similar to GI:1617270 (MF7P) and gi:1617628 (MF45P) from [Brassica napus] ; contains Pfam AMP-binding enzyme domain PF00501
355468	1	90	44	43	1039	1	1	At2g47240	5,00E-64	68415.m05899 long-chain-fatty-acid--CoA ligase family protein / long-chain acyl-CoA synthetase family protein similar to GI:1617270 (MF7P) and gi:1617628 (MF45P) from [Brassica napus] ; contains Pfam AMP-binding enzyme domain PF00501
356242	1	90	44	43	1039	1	1	At2g47240	8,00E-58	68415.m05899 long-chain-fatty-acid--CoA ligase family protein / long-chain acyl-CoA synthetase family protein similar to GI:1617270 (MF7P) and gi:1617628 (MF45P) from [Brassica napus] ; contains Pfam AMP-binding enzyme domain PF00501
360014	1	90	44	43	1844	3	1	At5g16370	6,00E-20	68418.m01913 AMP-binding protein, putative similar to AMP-binding protein GI:1903034 from [Brassica napus]; contains Pfam AMP-binding domain PF00501; identical to cDNA adenosine monophosphate binding protein 5 AMPBP5 (AMPBP5) GI:20799718
357142	1	90	44	43	1921	1	2	At1g20560	1,00E-14	68414.m02563 AMP-dependent synthetase and ligase family protein similar to AMP-binding protein GI:1903034 from [Brassica napus]; contains Pfam AMP-binding domain PF00501; identical to adenosine monophosphate binding protein 1 AMPBP1 (AMPBP1) GI:20799710
359276	1	90	44	43	1950	1	1	At1g62940	5,00E-09	68414.m07107 4-coumarate--CoA ligase family protein / 4-coumaroyl-CoA synthase family protein similar to gi:112801 from Petroselinum crispum, GB:AAD40664 from [Solanum tuberosum] (J. Biol. Chem. 266 (13), 8551-8559 (1991)); contains Pfam AMP-binding enzyme domain PF00501

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
358185	1	90	44	43	2654	1	1	At4g05160	2,00E-99	68417.m00775 4-coumarate--CoA ligase, putative / 4-coumaroyl-CoA synthase, putative similar to 4CL2 [gi:12229665] from Arabidopsis thaliana, 4CL1 [gi:12229631] from Nicotiana tabacum; contains Pfam AMP-binding enzyme domain PF00501; acyl-activating enzyme superfamily; identical to cDNA 4-coumarate-CoA ligase-like protein (At4g05160) GI:29893226
353491	2	90	44	43	5098	1	1	At3g16170	4,00E-67	68416.m02041 acyl-activating enzyme 13 (AAE13) similar to malonyl CoA synthetase GB:AAF28840 from [Bradyrhizobium japonicum]; contains Pfam AMP-binding enzyme domain PF00501; identical to cDNA acyl-activating enzyme 13 (At3g16170) GI:29893232, acyl-activating enzyme 13 [Arabidopsis thaliana] GI:29893233
355285	1	91	8	78	3240	1	1	At1g01880	1,00E-09	68414.m00106 DNA repair protein, putative similar to Swiss-Prot:P28706 DNA repair protein rad13 [Schizosaccharomyces pombe]; similar to UV hypersensitive protein [Arabidopsis thaliana] gi|13649704|gb|AAK37472
355452	1	91	8	78	4048	1	1	At5g26680	2,00E-20	68418.m03171 endonuclease, putative similar to Swiss-Prot:P39748 FLAP endonuclease-1 (Maturation factor 1) (MF1) [Homo sapiens]
355930	1	91	8	78	4048	1	1	At5g26680	1,00E-55	68418.m03171 endonuclease, putative similar to Swiss-Prot:P39748 FLAP endonuclease-1 (Maturation factor 1) (MF1) [Homo sapiens]
359161	1	92	39	45	1186	1	1	At4g12420	3,00E-63	68417.m01964 multi-copper oxidase, putative (SKU5) identical to multi-copper oxidase-related protein (SKU5)(GI:18158154) [Arabidopsis thaliana]; similar to pollen-specific protein precursor - common tobacco, PIR2:S22495; contains Pfam profile: PF00394 Multicopper oxidase
352911	2	92	39	45				At1g76160	3,00E-103	68414.m08844 multi-copper oxidase type I family protein similar to pollen-specific BP10 protein [SP|Q00624][Brassica napus]; contains Pfam profile: PF00394 Multicopper oxidase
354253	2	92	39	45				At5g09360	2,00E-50	68418.m01084 laccase family protein / diphenol oxidase family protein similar to laccase [Pinus taeda][GI:13661201]
356208	1	92	39	45				At5g48450	2,00E-27	68418.m05991 multi-copper oxidase type I family protein contains Pfam profile: PF00394 Multicopper oxidase; also similar to l-ascorbate oxidase and pollen-specific protein

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357766	1	92	39	45				At5g09360	2,00E-54	68418.m01084 laccase family protein / diphenol oxidase family protein similar to laccase [Pinus taeda][GI:13661201]
358476	1	92	39	45				At5g09360	8,00E-56	68418.m01084 laccase family protein / diphenol oxidase family protein similar to laccase [Pinus taeda][GI:13661201]
358644	1	92	39	45				At1g76160	8,00E-23	68414.m08844 multi-copper oxidase type I family protein similar to pollen-specific BP10 protein [SP|Q00624][Brassica napus]; contains Pfam profile: PF00394 Multicopper oxidase
357392	1	93	44	39	866	1	1	At2g23380	3,00E-122	68415.m02792 curly leaf protein (CURLY LEAF) / polycomb-group protein identical to polycomb group [Arabidopsis thaliana] GI:1903019 (curly leaf); contains Pfam profile PF00856: SET domain
354662	1	93	44	39	1435	2	1	At1g05830	1,00E-44	68414.m00610 trithorax protein, putative / PHD finger family protein / SET domain-containing protein similar to trithorax-like protein 1 [Arabidopsis thaliana] GI:12659210; contains Pfam domain, PF00628: PHD-finger and PF00856: SET domain
355989	1	93	44	39	1435	2	1	At2g31650	4,00E-29	68415.m03864 trithorax 1 (ATX-1) (TRX1) identical to trithorax-like protein 1 GI:12659210 from [Arabidopsis thaliana]; characterized in Alvarez-Venegas R,et al, ATX-1, an Arabidopsis Homolog of Trithorax, Activates Flower Homeotic Genes.(Curr Biol. 2003 Apr 15;13(8):627-37 PMID: 12699618); contains Pfam profiles PF00856: SET domain, PF00855: PWWP domain, PF00628, PHD-finger; identical to cDNA trithorax-like protein 1 (TRX1) GI:12659209
359703	1	93	44	39	1531	1	2	At1g77800	8,00E-11	68414.m09059 PHD finger family protein contains Pfam domain, PF00628: PHD-finger
358287	1	93	44	39	2645	1	1	At5g13960	1,00E-53	68418.m01632 SET domain-containing protein (SUVH4) identical to SUVH4 [Arabidopsis thaliana] GI:13517749; contains Pfam profiles PF00856: SET domain, PF05033: Pre-SET motif, PF02182: YDG/SRA domain; identical to cDNA SUVH4 (SUVH4) GI:13517748
353549	2	93	44	39	2696	2	3	At5g04940	7,00E-16	68418.m00523 SET domain-containing protein (SUVH1) contains Pfam profiles PF00856: SET domain, PF05033: Pre-SET motif, PF02182: YDG/SRA domain; identical to cDNA SUVH1 (SUVH1) GI:13517742

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356277	1	93	44	39	2696	2	3	At5g04940	6,00E-31	68418.m00523 SET domain-containing protein (SUVH1) contains Pfam profiles PF00856: SET domain, PF05033: Pre-SET motif, PF02182: YDG/SRA domain; identical to cDNA SUVH1 (SUVH1) GI:13517742
359212	1	93	44	39	2696	2	3	At5g04940	5,00E-50	68418.m00523 SET domain-containing protein (SUVH1) contains Pfam profiles PF00856: SET domain, PF05033: Pre-SET motif, PF02182: YDG/SRA domain; identical to cDNA SUVH1 (SUVH1) GI:13517742
353204	2	93	44	39	3228	1	1	At1g76710	1,00E-49	68414.m08928 SET domain-containing protein (ASHH1) low similarity to huntingtin interacting protein 1 [Homo sapiens] GI:12697196; contains Pfam profile PF00856: SET domain; identical to cDNA ASH1-like protein 1 (ASHH1) partial cds GI:15488417
356955	1	93	44	39	9791	1	1	At5g50810	2,00E-22	68418.m06295 mitochondrial import inner membrane translocase (TIM8) identical to mitochondrial import inner membrane translocase subunit Tim8 [Arabidopsis thaliana] Swiss-Prot:Q9XGY4; contains Pfam domain, PF02953: Tim10/DDP family zinc finger
354112	3	94	30	53	3831	2	1	At5g19440	1,00E-92	68418.m02316 cinnamyl-alcohol dehydrogenase, putative (CAD) similar to cinnamyl-alcohol dehydrogenase, Eucalyptus gunnii [GI:1143445], apple tree, PIR:T16995
356763	1	94	30	53	3831	2	1	At5g19440	2,00E-33	68418.m02316 cinnamyl-alcohol dehydrogenase, putative (CAD) similar to cinnamyl-alcohol dehydrogenase, Eucalyptus gunnii [GI:1143445], apple tree, PIR:T16995
355822	1	94	30	53	4127	1	1	At4g33360	1,00E-62	68417.m04743 terpene cyclase/mutase-related low similarity to squalene-hopene cyclase from Zymomonas mobilis [SP|P33990]
353722	4	94	30	53	4606	2	1	At2g21270	7,00E-53	68415.m02532 ubiquitin fusion degradation UFD1 family protein similar to SP|P70362 Ubiquitin fusion degradation protein 1 homolog (UB fusion protein 1) {Mus musculus}; contains Pfam profile PF03152: Ubiquitin fusion degradation protein UFD1
355038	1	94	30	53	4606	2	1	At2g21270	2,00E-14	68415.m02532 ubiquitin fusion degradation UFD1 family protein similar to SP|P70362 Ubiquitin fusion degradation protein 1 homolog (UB fusion protein 1) {Mus musculus}; contains Pfam profile PF03152: Ubiquitin fusion degradation protein UFD1

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359994	1	94	30	53	5033	2	1	At1g68540	2,00E-60	68414.m07830 oxidoreductase family protein similar to cinnamoyl CoA reductase [Eucalyptus gunnii, gi:2058311], cinnamyl-alcohol dehydrogenase, E. gunnii [gi:1143445], CPRD14 protein, Vigna unguiculata [gi:1854445]
357725	1	94	30	53	6323	1	1	At5g42800	3,00E-66	68418.m05213 dihydroflavonol 4-reductase (dihydrokaempferol 4-reductase) (DFR) nearly identical to GI:166686
352903	2	94	30	53	6572	1	5	At1g61720	5,00E-43	68414.m06961 dihydroflavonol 4-reductase (dihydrokaempferol 4-reductase) family (BAN) similar to dihydroflavonol 4-reductase GI:1332411 from [Rosa hybrida]
356909	1	94	30	53	6649	1	2	At5g14700	3,00E-18	68418.m01723 cinnamoyl-CoA reductase-related similar to cinnamoyl-CoA reductase from Pinus taeda [GI:17978649], Saccharum officinarum [GI:3341511]
359137	1	94	30	53	7638	2	1	At4g30470	3,00E-41	68417.m04326 cinnamoyl-CoA reductase-related similar to cinnamoyl-CoA reductase from Pinus taeda [GI:17978649], Saccharum officinarum [GI:3341511]
355794	1	95	56	26	9778	5	2	At1g75580	3,00E-33	68414.m08782 auxin-responsive protein, putative similar to auxin-induced protein TGSAUR22 (GI:10185820) [Tulipa gesneriana]
359407	1	95	56	26	10190	20	2	At4g38840	8,00E-16	68417.m05499 auxin-responsive protein, putative auxin-inducible SAUR gene, Raphanus sativus,AB000708
356190	1	97	35	46	97	2	2	At3g47950	1,00E-14	68416.m05228 ATPase, plasma membrane-type, putative / proton pump, putative strong similarity to P-type H(+)-transporting ATPase from Nicotiana plumbaginifolia [SP|Q08435, SP|Q08436], Lycopersicon esculentum [GI:5901757, SP|P22180], Solanum tuberosum [GI:435003]; contains InterPro accession IPR001757: ATPase, E1-E2 type
352935	2	97	35	46	133	1	2	At1g07810	9,00E-69	68414.m00846 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
353695	2	97	35	46	133	1	2	At1g07810	6,00E-21	68414.m00846 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

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360004	1	97	35	46	220	2	1	At5g57110	2,00E-54	68418.m07131 calcium-transporting ATPase 8, plasma membrane-type / Ca(2+)-ATPase isoform 8 (ACA8) identical to calcium-transporting ATPase 8, plasma membrane-type SP:Q9LF79 from [Arabidopsis thaliana]
357437	1	97	35	46	322	1	1	At5g44790	4,00E-72	68418.m05491 copper-exporting ATPase / responsive-to-antagonist 1 / copper-transporting ATPase (RAN1) identical to SP|Q9S7J8
354037	2	97	35	46	562	1	1	At1g63440	6,00E-88	68414.m07174 copper-exporting ATPase, putative / responsive-to-antagonist 1, putative / copper-transporting ATPase, putative similar to ATP dependent copper transporter SP|Q9S7J8 [Arabidopsis thaliana]
352920	2	97	35	46				At3g21180	1,00E-159	68416.m02677 calcium-transporting ATPase, plasma membrane-type, putative / Ca2+-ATPase, putative (ACA9) identical to SP|Q9LU41 Potential calcium-transporting ATPase 9, plasma membrane-type (EC 3.6.3.8) (Ca(2+)-ATPase isoform 9) {Arabidopsis thaliana}
355117	1	99	39	40	8084	2	2	At2g31380	4,00E-09	68415.m03835 zinc finger (B-box type) family protein / salt tolerance-like protein (STH) contains Pfam profile PF00643: B-box zinc finger; identical to cDNA B-box zinc finger protein STH GI:12698721, SP|Q9SID1 Salt tolerance-like protein (Arabidopsis thaliana)
357027	1	100	33	45	2905	1	1	At2g20360	2,00E-29	68415.m02377 expressed protein
359261	1	100	33	45	2905	1	1	At2g20360	3,00E-63	68415.m02377 expressed protein
359420	1	100	33	45	3926	1	2	At1g44110	1,00E-10	68414.m05095 cyclin, putative similar to mitotic cyclin a2-type [Glycine max] GI:857397, cyclin A-like protein [Nicotiana tabacum] GI:1064927; contains Pfam profiles PF00134: Cyclin, N-terminal domain, PF02984: Cyclin, C-terminal domain
358415	1	100	33	45	5337	4	2	At5g43080	8,00E-67	68418.m05259 cyclin, putative similar to A-type cyclins from [Nicotiana tabacum] GI:1064931, [Catharanthus roseus] GI:2190259; contains Pfam profiles PF00134: Cyclin, N-terminal domain, PF02984: Cyclin, C-terminal domain
353220	3	100	33	45	5642	4	2	At5g06150	9,00E-94	68418.m00684 cyclin 1b (CYC1b) identical to cyclin [Arabidopsis thaliana] GI:1360646
358082	1	100	33	45	5642	4	2	At5g06150	3,00E-75	68418.m00684 cyclin 1b (CYC1b) identical to cyclin [Arabidopsis thaliana] GI:1360646
356167	1	100	33	45	7531	1	1	At1g70210	2,00E-41	68414.m08079 cyclin delta-1 (CYCD1) nearly identical to SP|P42751 Cyclin delta-1 {Arabidopsis thaliana}

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354350	4	100	33	45				At5g67260	1,00E-69	68418.m08478 cyclin family protein similar to cyclin D3.1 protein [Nicotiana tabacum] GI:4160300; contains Pfam profiles PF00134: Cyclin, N-terminal domain, PF02984: Cyclin, C-terminal domain
354519	1	100	33	45				At4g34160	2,00E-18	68417.m04847 cyclin delta-3 (CYCD3) identical to SP|P42753 Cyclin delta-3 {Arabidopsis thaliana}
358993	1	100	33	45				At1g16330	2,00E-40	68414.m01954 cyclin family protein similar to SP|P25011 G2/mitotic-specific cyclin S13-6 (B-like cyclin) {Glycine max}; contains Pfam profiles PF00134: Cyclin, N-terminal domain, PF02984: Cyclin, C-terminal domain
354379	2	102	45	31	3595	1	1	At4g19670	2,00E-15	68417.m02889 zinc finger (C3HC4-type RING finger) family protein contains a Prosite:PS00518 Zinc finger, C3HC4 type (RING finger), signature and Pfam domain PF01485: IBR domain
358108	1	102	45	31	3595	1	1	At4g19670	2,00E-34	68417.m02889 zinc finger (C3HC4-type RING finger) family protein contains a Prosite:PS00518 Zinc finger, C3HC4 type (RING finger), signature and Pfam domain PF01485: IBR domain
352927	2	104	29	44	1726	1	1	At5g20620	3,00E-98	68418.m02449 polyubiquitin (UBQ4) identical to GI:17677
353297	4	104	29	44	1726	1	1	At5g20620	7,00E-106	68418.m02449 polyubiquitin (UBQ4) identical to GI:17677
353345	2	104	29	44	1726	1	1	At5g20620	8,00E-44	68418.m02449 polyubiquitin (UBQ4) identical to GI:17677
353826	5	104	29	44	1726	1	1	At5g20620	5,00E-82	68418.m02449 polyubiquitin (UBQ4) identical to GI:17677
354020	2	104	29	44	1726	1	1	At5g20620	2,00E-85	68418.m02449 polyubiquitin (UBQ4) identical to GI:17677
354075	2	104	29	44	1726	1	1	At5g20620	5,00E-76	68418.m02449 polyubiquitin (UBQ4) identical to GI:17677
355191	1	104	29	44	1726	1	1	At5g20620	3,00E-29	68418.m02449 polyubiquitin (UBQ4) identical to GI:17677
357000	1	104	29	44	1726	1	1	At5g20620	5,00E-33	68418.m02449 polyubiquitin (UBQ4) identical to GI:17677
354388	3	104	29	44	6753	3	2	At2g47110	2,00E-63	68415.m05883 ubiquitin extension protein 6 (UBQ6) / 40S ribosomal protein S27A (RPS27aB) identical to GI:166936
353350	7	104	29	44	7341	2	1	At3g52590	1,00E-68	68416.m05792 ubiquitin extension protein 1 (UBQ1) / 60S ribosomal protein L40 (RPL40B) identical to GI:166929, GI:166930

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
353532	3	104	29	44	7341	2	1	At3g52590	9,00E-25	68416.m05792 ubiquitin extension protein 1 (UBQ1) / 60S ribosomal protein L40 (RPL40B) identical to GI:166929, GI:166930
360048	1	104	29	44				At2g35635	3,00E-44	68415.m04370 ubiquitin family protein contains INTERPRO:IPR000626 ubiquitin domain
353438	4	105	34	36	3791	4	1	At1g01620	3,00E-68	68414.m00079 plasma membrane intrinsic protein 1C (PIP1C) / aquaporin PIP1.3 (PIP1.3) / transmembrane protein B (TMPB) identical to plasma membrane intrinsic protein 1c SP:Q08733 from [Arabidopsis thaliana]
354203	6	105	34	36	3791	4	1	At4g23400	1,00E-90	68417.m03373 major intrinsic family protein / MIP family protein contains Pfam profile: MIP PF00230
354242	4	105	34	36	3791	4	1	At4g23400	3,00E-85	68417.m03373 major intrinsic family protein / MIP family protein contains Pfam profile: MIP PF00230
354355	2	105	34	36	3791	4	1	At1g01620	1,00E-11	68414.m00079 plasma membrane intrinsic protein 1C (PIP1C) / aquaporin PIP1.3 (PIP1.3) / transmembrane protein B (TMPB) identical to plasma membrane intrinsic protein 1c SP:Q08733 from [Arabidopsis thaliana]
353338	4	105	34	36	4122	2	1	At2g16850	2,00E-56	68415.m01937 plasma membrane intrinsic protein, putative very strong similarity to plasma membrane intrinsic protein (SIMIP) [Arabidopsis thaliana] GI:2306917
354913	1	105	34	36	4122	2	1	At2g16850	1,00E-60	68415.m01937 plasma membrane intrinsic protein, putative very strong similarity to plasma membrane intrinsic protein (SIMIP) [Arabidopsis thaliana] GI:2306917
356051	1	105	34	36	4979	2	1	At2g36830	7,00E-07	68415.m04516 major intrinsic family protein / MIP family protein contains Pfam profile: MIP PF00230
356408	1	105	34	36				At3g16240	6,00E-10	68416.m02049 delta tonoplast integral protein (delta-TIP) identical to delta tonoplast integral protein (delta-TIP) (GI:9279707)(GB:U39485) [Arabidopsis thaliana] (Plant Cell 8 (4), 587-599 (1996))
354803	1	106	21	49	63	1	2	At4g33200	1,00E-27	68417.m04727 myosin, putative similar to myosin (GI:433663) [Arabidopsis thaliana]
355779	1	106	21	49	211	2	1	At3g19960	2,00E-33	68416.m02526 myosin (ATM) nearly identical to myosin [Arabidopsis thaliana] GI:6491702; similar to myosin GI:6491702 from [Arabidopsis thaliana] ;contains Pfam profiles: PF00063: myosin head (motor domain), PF00612: IQ calmodulin-binding motif; identical to cDNA myosin (ATM) GI:297068
358093	1	106	21	49	211	2	1	At1g50360	7,00E-34	68414.m05645 myosin family protein contains Pfam profiles: PF00063 myosin head (motor domain), PF00612 IQ calmodulin-binding motif

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
353258	3	107	32	37	1390	1	2	At1g30440	5,00E-86	68414.m03719 phototropic-responsive NPH3 family protein contains NPH3 family domain, Pfam:PF03000
358846	1	107	32	37	1390	1	2	At1g30440	5,00E-19	68414.m03719 phototropic-responsive NPH3 family protein contains NPH3 family domain, Pfam:PF03000
356793	1	107	32	37	2660	2	2	At3g08570	2,00E-45	68416.m00994 phototropic-responsive protein, putative similar to root phototropism RPT2 [Arabidopsis thaliana] gi|6959488|gb|AAF33112, a signal transducer of phototropic response PMID:10662859
357820	1	107	32	37	2881	1	2	At4g31820	2,00E-26	68417.m04522 phototropic-responsive NPH3 family protein contains NPH3 family domain, Pfam:PF03000
356816	1	109	35	33	3267	1	1	At1g11000	9,00E-24	68414.m01263 seven transmembrane MLO family protein / MLO-like protein 4 (MLO4) identical to membrane protein Mlo4 [Arabidopsis thaliana] gi|14091578|gb|AAK53797; similar to MLO protein SWISS-PROT:P93766, NCBI_gi:1877221 [Hordeum vulgare][Barley]
357135	1	109	35	33	3900	1	1	At4g09750	2,00E-59	68417.m01601 short-chain dehydrogenase/reductase (SDR) family protein similar to androgen-regulated short-chain dehydrogenase/reductase 1 GI:9622124 from [Homo sapiens]
356112	1	109	35	33	4546	2	1	At5g02540	1,00E-18	68418.m00188 short-chain dehydrogenase/reductase (SDR) family protein contains INTERPRO family IPR002198 Short-chain dehydrogenase/reductase (SDR) superfamily
359672	1	109	35	33	4546	2	1	At2g37540	4,00E-67	68415.m04604 short-chain dehydrogenase/reductase (SDR) family protein contains INTERPRO family IPR002198 Short-chain dehydrogenase/reductase (SDR) superfamily
353190	2	109	35	33	4823	3	1	At4g23430	3,00E-90	68417.m03378 short-chain dehydrogenase/reductase (SDR) family protein contains INTERPRO family IPR002198 Short-chain dehydrogenase/reductase (SDR) superfamily; contains Pfam PF00106: oxidoreductase, short chain dehydrogenase/reductase family
354291	2	109	35	33	4823	3	1	At4g23430	4,00E-56	68417.m03378 short-chain dehydrogenase/reductase (SDR) family protein contains INTERPRO family IPR002198 Short-chain dehydrogenase/reductase (SDR) superfamily; contains Pfam PF00106: oxidoreductase, short chain dehydrogenase/reductase family

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357608	1	112	29	37	2787	2	1	At1g19250	1,00E-11	68414.m02395 flavin-containing monooxygenase family protein / FMO family protein low similarity to SP|P97501 Dimethylaniline monooxygenase [N-oxide forming] 3 (EC 1.14.13.8) (Hepatic flavin-containing monooxygenase 3) (FMO 3) {Mus musculus}; contains Pfam profile PF00743: Flavin-binding monooxygenase-like
357927	1	112	29	37	3802	1	1	At4g32540	7,00E-34	68417.m04632 flavin-containing monooxygenase / FMO (YUCCA) identical to gi:16555352
353290	2	113	36	30	6956	1	3	At5g39660	1,00E-24	68418.m04803 Dof-type zinc finger domain-containing protein similar to H-protein promoter binding factor-2a GI:3386546 from [Arabidopsis thaliana]
357007	1	113	36	30	6956	1	3	At5g39660	3,00E-26	68418.m04803 Dof-type zinc finger domain-containing protein similar to H-protein promoter binding factor-2a GI:3386546 from [Arabidopsis thaliana]
358537	1	113	36	30	6956	1	3	At5g39660	2,00E-21	68418.m04803 Dof-type zinc finger domain-containing protein similar to H-protein promoter binding factor-2a GI:3386546 from [Arabidopsis thaliana]
355906	1	113	36	30				At5g62940	3,00E-34	68418.m07897 Dof-type zinc finger domain-containing protein Dof zinc finger protein, Oryza sativa, EMBL:AB028129
353394	2	114	36	29	8450	1	1	At1g31320	2,00E-55	68414.m03832 LOB domain protein 4 / lateral organ boundaries domain protein 4 (LBD4) identical to SP|Q9SHE9 LOB domain protein 4 {Arabidopsis thaliana}
355534	1	115	24	41				At1g68040	3,00E-14	68414.m07773 S-adenosyl-L-methionine:carboxyl methyltransferase family protein similar to defense-related protein cjs1 [Brassica carinata][GI:14009292], S-adenosyl-L-methionine:salicylic acid carboxyl methyltransferase [Clarkia breweri][GI:6002712]
358156	1	116	26	39	6859	1	1	At3g16350	4,00E-43	68416.m02068 myb family transcription factor ; contains Pfam profile: PF00249 Myb-like DNA-binding domain
359021	1	116	26	39				At1g74840	4,00E-32	68414.m08672 myb family transcription factor similar to myb-related transcription activator GI:9279717 from [Arabidopsis thaliana]
353013	2	117	36	28	3504	1	1	At5g53150	6,00E-13	68418.m06607 DNAJ heat shock N-terminal domain-containing protein low similarity to AHM1 [Triticum aestivum] GI:6691467; contains Pfam profile PF00226: DnaJ domain
354576	1	117	36	28	3504	1	1	At5g53150	1,00E-26	68418.m06607 DNAJ heat shock N-terminal domain-containing protein low similarity to AHM1 [Triticum aestivum] GI:6691467; contains Pfam profile PF00226: DnaJ domain

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356662	1	117	36	28	8371	1	2	At2g01710	2,00E-11	68415.m00099 DNAJ heat shock N-terminal domain-containing protein simlar to AHM1 [Triticum aestivum] GI:6691467; contains Pfam profile PF00226: DnaJ domain
353318	7	117	36	28				At2g05250	1,00E-42	68415.m00553 DNAJ heat shock N-terminal domain-containing protein contains Pfam profile PF00226 DnaJ domain
358614	1	117	36	28				At2g05250	6,00E-07	68415.m00553 DNAJ heat shock N-terminal domain-containing protein contains Pfam profile PF00226 DnaJ domain
355451	1	118	31	33	17	1	1	At2g13680	2,00E-32	68415.m01508 glycosyl transferase family 48 protein contains Pfam profile: PF02364 1,3-beta-glucan synthase
355773	1	118	31	33	33	1	1	At3g07160	6,00E-25	68416.m00853 glycosyl transferase family 48 protein similar to glucan synthase GB:AAD11794 [Filobasidiella neoformans var. neoformans]
359462	1	118	31	33	33	1	1	At3g07160	1,00E-06	68416.m00853 glycosyl transferase family 48 protein similar to glucan synthase GB:AAD11794 [Filobasidiella neoformans var. neoformans]
353251	2	118	31	33	2978	1	1	At5g15270	1,00E-34	68418.m01789 KH domain-containing protein various predicted proteins, Arabidopsis thaliana and Oryza sativa
353543	2	118	31	33	2978	1	1	At5g15270	6,00E-21	68418.m01789 KH domain-containing protein various predicted proteins, Arabidopsis thaliana and Oryza sativa
355050	1	118	31	33	2978	1	1	At5g15270	2,00E-23	68418.m01789 KH domain-containing protein various predicted proteins, Arabidopsis thaliana and Oryza sativa
358860	1	118	31	33	3599	1	1	At2g25970	1,00E-10	68415.m03117 KH domain-containing protein
356558	1	118	31	33	4215	1	2	At3g04610	1,00E-40	68416.m00493 KH domain-containing protein similar putative nucleic acid binding protein GB:CAB39665 [Arabidopsis thaliana]; Pfam HMM hit: KH domain family of RNA binding proteins
359106	1	118	31	33	4215	1	2	At3g04610	6,00E-37	68416.m00493 KH domain-containing protein similar putative nucleic acid binding protein GB:CAB39665 [Arabidopsis thaliana]; Pfam HMM hit: KH domain family of RNA binding proteins
354917	1	118	31	33	5347	1	1	At5g04430	2,00E-24	68418.m00438 KH domain-containing protein NOVA, putative astrocytic NOVA-like RNA-binding protein, Homo sapiens, U70477

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356783	1	118	31	33	5347	1	1	At5g04430	2,00E-25	68418.m00438 KH domain-containing protein NOVA, putative astrocytic NOVA-like RNA-binding protein, Homo sapiens, U70477
357398	1	118	31	33	5347	1	1	At5g04430	2,00E-06	68418.m00438 KH domain-containing protein NOVA, putative astrocytic NOVA-like RNA-binding protein, Homo sapiens, U70477
354353	3	118	31	33	5370	2	1	At4g10070	3,00E-18	68417.m01647 KH domain-containing protein DNA-directed RNA polymerase (EC 2.7.7.6) II largestchain - mouse, PIR2:A28490
354349	2	118	31	33	5378	1	1	At4g26000	3,00E-53	68417.m03745 KH domain-containing protein single-stranded nucleic acid-binding protein CBP - mouse, PIR2:S78515
355036	1	118	31	33	5378	1	1	At4g26000	5,00E-21	68417.m03745 KH domain-containing protein single-stranded nucleic acid-binding protein CBP - mouse, PIR2:S78515
357169	1	118	31	33	5378	1	1	At4g26000	3,00E-27	68417.m03745 KH domain-containing protein single-stranded nucleic acid-binding protein CBP - mouse, PIR2:S78515
353344	13	118	31	33	5494	2	1	At5g46190	3,00E-64	68418.m05681 KH domain-containing protein strong similarity to unknown protein (pir||T04533)
358117	1	118	31	33	5494	2	1	At5g46190	3,00E-19	68418.m05681 KH domain-containing protein strong similarity to unknown protein (pir||T04533)
354959	1	118	31	33	6844	1	1	At1g51580	2,00E-21	68414.m05806 KH domain-containing protein
354390	2	118	31	33				At1g06490	8,00E-24	68414.m00688 glycosyl transferase family 48 protein contains Pfam profile: PF02364 1,3-beta-glucan synthase
354720	1	118	31	33				At2g36850	4,00E-45	68415.m04519 glycosyl transferase family 48 protein contains Pfam profile: PF02364 1,3-beta-glucan synthase
356518	1	118	31	33				At1g06490	1,00E-61	68414.m00688 glycosyl transferase family 48 protein contains Pfam profile: PF02364 1,3-beta-glucan synthase
357296	1	118	31	33				At3g59100	5,00E-17	68416.m06589 glycosyl transferase family 48 protein contains Pfam profile: PF02364 1,3-beta-glucan synthase
358112	1	118	31	33				At5g13000	2,00E-72	68418.m01490 glycosyl transferase family 48 protein contains Pfam profile: PF02364 1,3-beta-glucan synthase

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
354208	2	119	17	47	4442	1	1	At5g54160	5,00E-52	68418.m06744 quercetin 3-O-methyltransferase 1 / flavonol 3-O-methyltransferase 1 / caffeic acid/5-hydroxyferulic acid O-methyltransferase (OMT1) identical to O-methyltransferase 1 [Arabidopsis thaliana][GI:2781394], SP|Q9FK25 Quercetin 3-O-methyltransferase 1 (EC 2.1.1.76) (AtOMT1) (Flavonol 3-O-methyltransferase 1) (Caffeic acid/5-hydroxyferulic acid O-methyltransferase) {Arabidopsis thaliana}
354456	2	120	34	29	1904	2	1	At2g21520	2,00E-60	68415.m02561 SEC14 cytosolic factor, putative / phosphoglyceride transfer protein, putative contains Pfam PF00650 : CRAL/TRIO domain; contains Pfam PF03765 : CRAL/TRIO, N-terminus; similar to phosphatidylinositol transfer-like protein IV (GI:14486707) [Lotus japonicus]
356844	1	120	34	29	1904	2	1	At2g21520	2,00E-18	68415.m02561 SEC14 cytosolic factor, putative / phosphoglyceride transfer protein, putative contains Pfam PF00650 : CRAL/TRIO domain; contains Pfam PF03765 : CRAL/TRIO, N-terminus; similar to phosphatidylinositol transfer-like protein IV (GI:14486707) [Lotus japonicus]
356144	1	120	34	29	2827	2	1	At2g18180	4,00E-48	68415.m02115 SEC14 cytosolic factor, putative / phosphoglyceride transfer protein, putative contains Pfam PF00650 : CRAL/TRIO domain; contains Pfam PF03765 : CRAL/TRIO, N-terminussimilar to phosphatidylinositol transfer-like protein IV (GI:14486707) [Lotus japonicus];
359937	1	120	34	29	2877	1	3	At1g55690	1,00E-18	68414.m06377 SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein similar to similar to phosphatidylinositol transfer-like protein IV (GI:14486707) [Lotus japonicus] and Phosphatidylinositol Transfer Protein GB:2780955 GI:2780955 [Saccharomyces cerevisiae]
358796	1	120	34	29	3475	1	1	At3g51670	1,00E-42	68416.m05666 SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein similar to polyphosphoinositide binding protein Ssh2p (GI:2739046) {Glycine max};; contains Pfam PF00650 : CRAL/TRIO domain; contains Pfam PF03765 : CRAL/TRIO, N-terminus

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
359336	1	120	34	29	3475	1	1	At3g51670	5,00E-19	68416.m05666 SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein similar to polyphosphoinositide binding protein Ssh2p (GI:2739046) {Glycine max};; contains Pfam PF00650 : CRAL/TRIO domain; contains Pfam PF03765 : CRAL/TRIO, N-terminus
355392	1	120	34	29	3912	1	1	At1g30690	2,00E-25	68414.m03752 SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein contains Pfam PF00650 : CRAL/TRIO domain; contains Pfam PF03765 : CRAL/TRIO, N-terminus; similar to cytosolic factor (Phosphatidylinositol/phosphatidylcholine transfer protein) (PI/PCTP) (SP:P24280) [Saccharomyces cerevisiae]; ESTs gb|T76582, gb|N06574 and gb|Z25700 come from this gene
359862	1	120	34	29	3912	1	1	At1g30690	9,00E-31	68414.m03752 SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein contains Pfam PF00650 : CRAL/TRIO domain; contains Pfam PF03765 : CRAL/TRIO, N-terminus; similar to cytosolic factor (Phosphatidylinositol/phosphatidylcholine transfer protein) (PI/PCTP) (SP:P24280) [Saccharomyces cerevisiae]; ESTs gb|T76582, gb|N06574 and gb|Z25700 come from this gene
354173	3	120	34	29	6018	2	1	At1g75170	5,00E-97	68414.m08731 SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein similar to polyphosphoinositide binding protein Ssh1p (GI:2739044) {Glycine max}; similar to SEC14 cytosolic factor (Phosphatidylinositol/phosphatidylcholine transfer protein) (PI/PCTP) (SP:P24859) [Kluyveromyces lactis] and to SEC14 cytosolic factor (SP:P53989) [Candida glabrata]
353487	4	120	34	29				At5g47730	5,00E-88	68418.m05897 SEC14 cytosolic factor, putative / polyphosphoinositide-binding protein, putative similar to polyphosphoinositide binding protein SEC14 homolog Ssh1p (GI:2739044) {Glycine max}
359499	1	120	34	29				At5g47730	2,00E-11	68418.m05897 SEC14 cytosolic factor, putative / polyphosphoinositide-binding protein, putative similar to polyphosphoinositide binding protein SEC14 homolog Ssh1p (GI:2739044) {Glycine max}
358282	1	121	27	36				At1g02040	1,00E-10	68414.m00124 zinc finger (C2H2 type) family protein contains Pfam profile: PF00096 zinc finger, C2H2 type
353488	2	122	22	41	558	1	1	At2g40930	2,00E-40	68415.m05052 ubiquitin-specific protease 5, putative (UBP5) similar to GI:6648604

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
359228	1	122	22	41	558	1	1	At2g40930	3,00E-38	68415.m05052 ubiquitin-specific protease 5, putative (UBP5) similar to GI:6648604
357574	1	122	22	41	2487	2	1	At2g22310	1,00E-96	68415.m02647 ubiquitin-specific protease 4 (UBP4) identical to GI:2347100
358270	1	122	22	41	2487	2	1	At4g39910	2,00E-39	68417.m05653 ubiquitin-specific protease 3 (UBP3) identical to GI:2347098
359977	1	122	22	41	4261	1	1	At3g49600	3,00E-17	68416.m05421 ubiquitin-specific protease 26 (UBP26) similar to GI:11993492; RNA binding protein - Homo sapiens, EMBL:AB016089 (N-terminus), several ubiquitin carboxyl-terminal hydrolases from aa pos. 712
354704	1	122	22	41	4357	1	1	At4g30890	7,00E-42	68417.m04387 ubiquitin-specific protease 24, putative (UBP24) identical to ubiquitin-specific protease 24 [Arabidopsis thaliana] GI:11993488
357167	1	122	22	41	4357	1	1	At4g30890	2,00E-18	68417.m04387 ubiquitin-specific protease 24, putative (UBP24) identical to ubiquitin-specific protease 24 [Arabidopsis thaliana] GI:11993488
358798	1	122	22	41	4357	1	1	At4g30890	3,00E-77	68417.m04387 ubiquitin-specific protease 24, putative (UBP24) identical to ubiquitin-specific protease 24 [Arabidopsis thaliana] GI:11993488
358967	1	122	22	41	4805	2	1	At2g32780	3,00E-17	68415.m04013 ubiquitin-specific protease 1, putative (UBP1) similar to GI:11993461
358575	1	125	33	29	5177	4	1	At5g48070	1,00E-61	68418.m05939 xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative similar to xyloglucan endotransglycosylase TCH4 GI:886116 from [Arabidopsis thaliana]
358312	1	125	33	29	5179	2	2	At2g36870	2,00E-32	68415.m04520 xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative similar to cellulase (xyloglucan endo-transglycosylase) GI:311835 from [Tropaeolum majus]
353985	2	125	33	29				At3g23730	1,00E-64	68416.m02984 xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative similar to xyloglucan endotransglycosylase-related protein GI:1244760 from [Arabidopsis thaliana]
355832	1	125	33	29				At3g23730	1,00E-75	68416.m02984 xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative similar to xyloglucan endotransglycosylase-related protein GI:1244760 from [Arabidopsis thaliana]

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
353354	3	127	36	25	3431	1	1	At4g22670	1,00E-55	68417.m03272 tetratricopeptide repeat (TPR)-containing protein similar to Hsc70-interacting protein (Hip) from {Homo sapiens} SP|P50502, {Rattus norvegicus} SP|P50503; contains Pfam profile PF00515: tetratricopeptide repeat (TPR) domain
358206	1	127	36	25				At4g03520	4,00E-07	68417.m00480 thioredoxin M-type 2, chloroplast (TRX-M2) nearly identical to SP|Q9SEU8 Thioredoxin M-type 2, chloroplast precursor (TRX-M2) {Arabidopsis thaliana}
357254	1	128	11	50	153	2	1	At1g06220	4,00E-96	68414.m00656 elongation factor Tu family protein similar to Cryptosporidium parvum elongation factor-2 GB:U21667 GI:706974 from [Cryptosporidium parvum]
358092	1	128	11	50	153	2	1	At5g25230	3,00E-45	68418.m02991 elongation factor Tu family protein translation Elongation Factor 2, Schizosaccharomyces pombe, PIR:T39902
354005	2	128	11	50	159	1	2	At1g56070	8,00E-97	68414.m06438 elongation factor 2, putative / EF-2, putative similar to ELONGATION FACTOR 2 GB:O14460 from [Schizosaccharomyces pombe]
354765	1	128	11	50	159	1	2	At1g56070	6,00E-44	68414.m06438 elongation factor 2, putative / EF-2, putative similar to ELONGATION FACTOR 2 GB:O14460 from [Schizosaccharomyces pombe]
359754	1	128	11	50	159	1	2	At1g56070	2,00E-11	68414.m06438 elongation factor 2, putative / EF-2, putative similar to ELONGATION FACTOR 2 GB:O14460 from [Schizosaccharomyces pombe]
356195	1	128	11	50	388	2	1	At2g45030	1,00E-66	68415.m05606 mitochondrial elongation factor, putative similar to SP|P25039 Elongation factor G 1, mitochondrial precursor (mEF-G-1) {Saccharomyces cerevisiae}; contains Pfam profiles PF00009: Elongation factor Tu GTP binding domain, PF03764: Elongation factor G domain IV, PF00679: Elongation factor G C-terminus
359563	1	129	26	35	1168	1	1	At4g33210	1,00E-66	68417.m04728 F-box family protein (FBL15) contains similarity to F-box protein FBL2 GI:6063090 from [Homo sapiens]
357898	1	129	26	35	1720	1	1	At1g15740	2,00E-59	68414.m01888 leucine-rich repeat family protein
353984	2	129	26	35	2775	1	1	At2g17020	1,00E-33	68415.m01962 F-box family protein (FBL10) contains similarity to F-box protein Partner of Paired GI:10441427 from [Drosophila melanogaster]
358704	1	129	26	35	3916	1	1	At5g27920	1,00E-25	68418.m03354 F-box family protein contains similarity to leucine-rich repeats containing F-box protein FBL3 GI:5919219 from [Homo sapiens]
358596	1	129	26	35	4132	1	1	At4g23840	7,00E-22	68417.m03428 leucine-rich repeat family protein

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359373	1	129	26	35	5489	3	1	At5g51380	7,00E-29	68418.m06370 F-box family protein contains Pfam PF00646: F-box domain; similar to F-box protein FBL2 (GI:6063090) [Homo sapiens]
359487	1	129	26	35	7277	1	1	At5g67140	4,00E-54	68418.m08464 F-box family protein similar to unknown protein (dbj|BAA78736.1) ; similar to SKP1 interacting partner 2 (SKIP2) TIGR_Ath1:At5g67250
359998	1	130	21	40	6162	2	1	At1g18250	7,00E-68	68414.m02276 thaumatin, putative identical to SP|P50699 Thaumatin-like protein precursor {Arabidopsis thaliana}; strong similarity to pathogenesis-related group 5 protein GI:2749943 from [Brassica rapa]
358965	1	130	21	40	7084	1	1	At5g40020	1,00E-70	68418.m04853 pathogenesis-related thaumatin family protein similar to SP|P50699 Thaumatin-like protein precursor {Arabidopsis thaliana}, pathogenesis-related group 5 protein [Brassica rapa] GI:2749943; contains Pfam profile PF00314: Thaumatin family
359367	1	131	29	32	2760	1	1	At4g02990	1,00E-29	68417.m00406 mitochondrial transcription termination factor family protein / mTERF family protein weak similarity to mtDBP protein [Paracentrotus lividus] GI:4584695; contains Pfam profile PF02536: mTERF
357610	1	131	29	32	3711	1	1	At5g55580	1,00E-15	68418.m06929 mitochondrial transcription termination factor family protein / mTERF family protein weak similarity to mtDBP protein [Paracentrotus lividus] GI:4584695; contains Pfam profile PF02536: mTERF
354171	2	131	29	32	8564	2	1	At1g21150	3,00E-20	68414.m02645 mitochondrial transcription termination factor family protein / mTERF family protein weak similarity to mtDBP protein [Paracentrotus lividus] GI:4584695; contains Pfam profile PF02536: mTERF
360043	1	131	29	32	8564	2	1	At1g21150	1,00E-12	68414.m02645 mitochondrial transcription termination factor family protein / mTERF family protein weak similarity to mtDBP protein [Paracentrotus lividus] GI:4584695; contains Pfam profile PF02536: mTERF
353207	2	133	29	30	903	1	1	At4g22200	6,00E-92	68417.m03209 potassium channel protein 2 (AKT2) (AKT3) identical to potassium channel [Arabidopsis thaliana] gi|1100898|gb|AAA97865; Note: also identical to AKT3 [Arabidopsis thaliana] gi|1172218|gb|AAA96153, which is a truncated version of AKT2, PMID:10852932; member of the 1 pore, 6 transmembrane (1P/6TM- Shaker-type) K+ channel family, PMID:11500563; identical to cDNA inward-rectifying K+ channel (AKT3) GI:1172219

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355065	1	134	31	28	440	3	1	At1g78570	3,00E-53	68414.m09157 NAD-dependent epimerase/dehydratase family protein similar to dTDP-glucose 4,6-dehydratase from Aneurinibacillus thermoaerophilus GI:16357461, RmlB from Leptospira borgpetersenii GI:4234803; contains Pfam profile PF01370 NAD dependent epimerase/dehydratase family
355947	1	134	31	28	440	3	1	At1g78570	5,00E-39	68414.m09157 NAD-dependent epimerase/dehydratase family protein similar to dTDP-glucose 4,6-dehydratase from Aneurinibacillus thermoaerophilus GI:16357461, RmlB from Leptospira borgpetersenii GI:4234803; contains Pfam profile PF01370 NAD dependent epimerase/dehydratase family
353978	2	134	31	28	2110	2	1	At1g08200	2,00E-145	68414.m00906 expressed protein
353166	2	134	31	28	2292	2	1	At3g62830	2,00E-06	68416.m07059 NAD-dependent epimerase/dehydratase family protein similar to UDP-glucuronic acid decarboxylase Uxs1p from Filobasidiella neoformans GI:14318327; contains Pfam profile PF01370 NAD dependent epimerase/dehydratase family; contains non-consensus CA donor splice site at exon 1 and TA acceptor splice site at exon 2
359105	1	134	31	28	2308	2	2	At1g30620	1,00E-46	68414.m03745 UDP-D-xylose 4-epimerase, putative (MUR4) similar to SP|P55180 UDP-glucose 4-epimerase (EC 5.1.3.2) from Bacillus subtilis, GI:3021357 UDP-galactose 4-epimerase from Cyamopsis tetragonoloba; contains Pfam profile PF01370 NAD dependent epimerase/dehydratase family; contains TIGRfam profile TIGR01179: UDP-glucose 4-epimerase
358739	1	134	31	28	2458	1	1	At5g28840	9,00E-28	68418.m03547 NAD-dependent epimerase/dehydratase family protein similar to sugar epimerase BlmG from Streptomyces verticillus GI:9937230; contains Pfam profile PF01370 NAD dependent epimerase/dehydratase family
356427	1	134	31	28	3338	3	2	At4g10960	8,00E-46	68417.m01781 UDP-glucose 4-epimerase, putative / UDP-galactose 4-epimerase, putative / Galactowaldenase, putative similar to UDP-galactose 4-epimerase from Arabidopsis thaliana SP|Q42605, Cyamopsis tetragonoloba GI:3021357 [AJ005082]
354623	1	134	31	28	3584	2	1	At1g73250	9,00E-50	68414.m08477 GDP-4-keto-6-deoxy-D-mannose-3,5-epimerase-4-reductase (GER1) identical to GDP-4-keto-6-deoxy-D-mannose-3,5-epimerase-4-reductase (GER1)GI:6016479 from [Arabidopsis thaliana]
354436	2	134	31	28	3800	1	1	At1g63000	2,00E-100	68414.m07114 expressed protein

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359925	1	135	28	31	8788	2	1	At1g04550	5,00E-16	68414.m00448 auxin-responsive protein / indoleacetic acid-induced protein 12 (IAA12) identical to SP|Q38830 Auxin-responsive protein IAA12 (Indoleacetic acid-induced protein 12) {Arabidopsis thaliana}
356486	1	135	28	31				At4g28640	2,00E-37	68417.m04094 auxin-responsive protein / indoleacetic acid-induced protein 11 (IAA11) identical to SP|Q38829 Auxin-responsive protein IAA11 (Indoleacetic acid-induced protein 11) {Arabidopsis thaliana}
352893	3	136	30	29	850	3	1	At4g14360	1,00E-138	68417.m02212 dehydration-responsive protein-related similar to early-responsive to dehydration stress ERD3 protein [Arabidopsis thaliana] GI:15320410; contains Pfam profile PF03141: Putative methyltransferase
354394	2	136	30	29	850	3	1	At4g14360	8,00E-102	68417.m02212 dehydration-responsive protein-related similar to early-responsive to dehydration stress ERD3 protein [Arabidopsis thaliana] GI:15320410; contains Pfam profile PF03141: Putative methyltransferase
357948	1	136	30	29	873	2	1	At1g33170	1,00E-64	68414.m04096 dehydration-responsive family protein similar to early-responsive to dehydration stress ERD3 protein [Arabidopsis thaliana] GI:15320410; contains Pfam profile PF03141: Putative methyltransferase
358932	1	136	30	29	873	2	1	At1g33170	8,00E-91	68414.m04096 dehydration-responsive family protein similar to early-responsive to dehydration stress ERD3 protein [Arabidopsis thaliana] GI:15320410; contains Pfam profile PF03141: Putative methyltransferase
355463	1	136	30	29	886	2	1	At2g39750	2,00E-50	68415.m04881 dehydration-responsive family protein similar to early-responsive to dehydration stress ERD3 protein [Arabidopsis thaliana] GI:15320410; contains Pfam profile PF03141: Putative methyltransferase
354102	2	136	30	29	1019	1	3	At4g18030	9,00E-78	68417.m02684 dehydration-responsive family protein similar to early-responsive to dehydration stress ERD3 protein [Arabidopsis thaliana] GI:15320410; contains Pfam profile PF03141: Putative methyltransferase
358422	1	136	30	29	1019	1	3	At4g18030	8,00E-49	68417.m02684 dehydration-responsive family protein similar to early-responsive to dehydration stress ERD3 protein [Arabidopsis thaliana] GI:15320410; contains Pfam profile PF03141: Putative methyltransferase
353843	2	136	30	29	1170	2	1	At5g04060	3,00E-49	68418.m00387 dehydration-responsive protein-related similar to early-responsive to dehydration stress ERD3 protein [Arabidopsis thaliana] GI:15320410; contains Pfam profile PF03141: Putative methyltransferase

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353208	2	136	30	29	1307	1	1	At5g14430	2,00E-52	68418.m01689 dehydration-responsive protein-related similar to early-responsive to dehydration stress ERD3 protein [Arabidopsis thaliana] GI:15320410; contains Pfam profile PF03141: Putative methyltransferase
354616	1	136	30	29				At3g51070	1,00E-32	68416.m05592 dehydration-responsive protein-related similar to early-responsive to dehydration stress ERD3 protein [Arabidopsis thaliana] GI:15320410; contains Pfam profile PF03141: Putative methyltransferase
354741	1	136	30	29				At1g13860	2,00E-39	68414.m01627 dehydration-responsive protein-related similar to early-responsive to dehydration stress ERD3 protein [Arabidopsis thaliana] GI:15320410; contains Pfam profile PF03141: Putative methyltransferase
356801	1	136	30	29				At1g31850	4,00E-69	68414.m03915 dehydration-responsive protein, putative strong similarity to early-responsive to dehydration stress ERD3 protein [Arabidopsis thaliana] GI:15320410; contains Pfam profile PF03141: Putative methyltransferase
353692	2	137	26	32	69	2	1	At4g32410	1,00E-83	68417.m04614 cellulose synthase, catalytic subunit, putative similar to cellulose synthase-1 [gi:9622874] and -2 [gi:9622876] from Zea mays
353953	3	137	26	32	84	1	1	At5g17420	1,00E-57	68418.m02044 cellulose synthase, catalytic subunit (IRX3) identical to gi:5230423
353494	2	137	26	32	87	1	2	At5g05170	5,00E-121	68418.m00550 cellulose synthase, catalytic subunit (Ath-B) nearly identical to gi:2827143, cellulose synthase, catalytic subunit (Ath-B)
359260	1	137	26	32	87	1	2	At5g05170	2,00E-38	68418.m00550 cellulose synthase, catalytic subunit (Ath-B) nearly identical to gi:2827143, cellulose synthase, catalytic subunit (Ath-B)
353989	2	137	26	32	129	1	1	At1g02730	2,00E-77	68414.m00226 cellulose synthase family protein similar to cellulose synthase catalytic subunit [gi:13925881] from Nicotiana alata, cellulose synthase-4 [gi:9622880] from Zea mays
359751	1	138	31	27	118	1	1	At5g13010	1,00E-95	68418.m01491 RNA helicase, putative similar to DEAH-box RNA helicase [Chlamydomonas reinhardtii] GI:12044832; contains Pfam profiles PF04408: Helicase associated domain (HA2), PF00271: Helicase conserved C-terminal domain
356505	1	138	31	27	169	2	1	At1g32490	1,00E-43	68414.m04009 RNA helicase, putative similar to ATP-dependent RNA helicase #3 [Homo sapiens] GI:3107913; contains Pfam profiles PF04408: Helicase associated domain (HA2), PF00271: Helicase conserved C-terminal domain

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359404	1	138	31	27	169	2	1	At1g32490	6,00E-30	68414.m04009 RNA helicase, putative similar to ATP-dependent RNA helicase #3 [Homo sapiens] GI:3107913; contains Pfam profiles PF04408: Helicase associated domain (HA2), PF00271: Helicase conserved C-terminal domain
357146	1	138	31	27	654	1	1	At4g18465	2,00E-109	68417.m02740 RNA helicase, putative similar to SP|Q14562 ATP-dependent helicase DDX8 (RNA helicase HRH1) (DEAH-box protein 8) {Homo sapiens}; contains Pfam profiles PF04408: Helicase associated domain (HA2), PF00271: Helicase conserved C-terminal domain
353688	2	138	31	27	888	1	1	At1g26370	5,00E-81	68414.m03217 RNA helicase, putative similar to SP|Q14562 ATP-dependent helicase DDX8 (RNA helicase HRH1) (DEAH-box protein 8) {Homo sapiens}; contains Pfam profiles PF04408: Helicase associated domain (HA2), PF00271: Helicase conserved C-terminal domain
359511	1	138	31	27				At2g47250	4,00E-43	68415.m05900 RNA helicase, putative similar to SP|P53131 Pre-mRNA splicing factor RNA helicase PRP43 (Helicase JA1) {Saccharomyces cerevisiae}; contains Pfam profiles PF04408: Helicase associated domain (HA2), PF00271: Helicase conserved C-terminal domain
359577	1	138	31	27				At2g01140	3,00E-75	68415.m00023 fructose-bisphosphate aldolase, putative similar to plastidic aldolase NPALDP1 from Nicotiana paniculata [GI:4827251]; contains Pfam profile PF00274 Fructose-bisphosphate aldolase class-I
353732	3	139	28	30	629	1	1	At3g57630	9,00E-125	68416.m06421 exostosin family protein contains Pfam profile: PF03016 exostosin family
359744	1	139	28	30	2289	1	1	At5g03800	5,00E-55	68418.m00347 exostosin family protein / pentatricopeptide (PPR) repeat-containing protein contains Pfam profiles: PF03016 exostosin family, PF01535 PPR repeat
355825	1	139	28	30				At5g19670	1,00E-63	68418.m02340 exostosin family protein contains Pfam domain, PF03016: Exostosin family
357494	1	139	28	30				At4g32790	3,00E-41	68417.m04665 exostosin family protein contains Pfam domain, PF03016: Exostosin family
355664	1	141	25	32	5611	1	1	At3g26744	2,00E-57	68416.m03344 basix helix-loop-helix (bHLH) family protein contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain

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355048	1	141	25	32	6140	2	3	At1g63650	6,00E-09	68414.m07202 basic helix-loop-helix (bHLH) family protein similar to bHLH transcription factor (JAF13) GB:AAC39455 [Petunia x hybrida]; contains Pfam profile: PF00010 Helix-loop-helix DNA-binding domain
356627	1	141	25	32	6140	2	3	At1g63650	6,00E-35	68414.m07202 basic helix-loop-helix (bHLH) family protein similar to bHLH transcription factor (JAF13) GB:AAC39455 [Petunia x hybrida]; contains Pfam profile: PF00010 Helix-loop-helix DNA-binding domain
359913	1	141	25	32	6140	2	3	At1g63650	3,00E-10	68414.m07202 basic helix-loop-helix (bHLH) family protein similar to bHLH transcription factor (JAF13) GB:AAC39455 [Petunia x hybrida]; contains Pfam profile: PF00010 Helix-loop-helix DNA-binding domain
354953	1	141	25	32	6327	1	1	At4g09820	3,00E-20	68417.m01611 basic helix-loop-helix (bHLH) family protein contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain
359341	1	141	25	32				At4g00480	2,00E-09	68417.m00066 myc-related transcription factor (MYC1) identical to ATMYC1 GI:1853965 from [Arabidopsis thaliana]
354431	2	147	29	27	7502	2	2	At1g69780	2,00E-69	68414.m08029 homeobox-leucine zipper protein 13 (HB-13) / HD-ZIP transcription factor 13 identical to homeobox gene 13 protein (GP:12325190) [Arabidopsis thaliana]
359708	1	147	29	27	7728	2	1	At2g22800	2,00E-25	68415.m02706 homeobox-leucine zipper protein 9 (HAT9) / HD-ZIP protein 9 identical to GB:U09341
356305	1	147	29	27	10366	1	2	At1g27050	5,00E-22	68414.m03298 homeobox-leucine zipper family protein contains Pfam profile:PF00046 Homeobox domain and Pfam profile:PF00076 RNA recognition motif
354521	1	150	21	34	3139	1	1	At5g53580	1,00E-13	68418.m06657 aldo/keto reductase family protein contains Pfam profile PF00248: oxidoreductase, aldo/keto reductase family
353048	2	150	21	34	3302	3	2	At1g60710	1,00E-112	68414.m06834 aldo/keto reductase family protein contains Pfam profile PF00248: oxidoreductase, aldo/keto reductase family
353266	3	150	21	34	3302	3	2	At1g60710	1,00E-38	68414.m06834 aldo/keto reductase family protein contains Pfam profile PF00248: oxidoreductase, aldo/keto reductase family
358999	1	150	21	34	4110	1	1	At4g33670	1,00E-64	68417.m04783 L-galactose dehydrogenase (L-GalDH) identical to L-galactose dehydrogenase [Arabidopsis thaliana] GI:16555790; similar to L-fucose dehydrogenase [Pseudomonas sp.] GI:829054; contains Pfam profile PF00248: oxidoreductase, aldo/keto reductase family

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355656	1	150	21	34				At2g37770	3,00E-50	68415.m04637 aldo/keto reductase family protein similar to chalcone reductase [Sesbania rostrata][GI:2792155] and aldose reductase [GI:202852][Rattus norvegicus]
357910	1	150	21	34				At2g37770	2,00E-07	68415.m04637 aldo/keto reductase family protein similar to chalcone reductase [Sesbania rostrata][GI:2792155] and aldose reductase [GI:202852][Rattus norvegicus]
353592	2	151	24	31	8929	4	1	At4g12470	3,00E-13	68417.m01972 protease inhibitor/seed storage/lipid transfer protein (LTP) family protein similar to pEARLI 1 (Accession No. L43080): an Arabidopsis member of a conserved gene family (PGF95-099), Plant Physiol. 109 (4), 1497 (1995); contains Pfam protease inhibitor/seed storage/LTP family domain PF00234
353039	19	151	24	31				At2g45180	4,00E-12	68415.m05625 protease inhibitor/seed storage/lipid transfer protein (LTP) family protein similar to 14 kDa polypeptide [Catharanthus roseus] GI:407410; contains Pfam protease inhibitor/seed storage/LTP family domain PF00234
353972	18	151	24	31				At2g10940	3,00E-17	68415.m01168 protease inhibitor/seed storage/lipid transfer protein (LTP) family protein similar to proline-rich cell wall protein [Medicago sativa] GI:3818416; contains Pfam profile PF00234 Protease inhibitor/seed storage/LTP family
354029	24	151	24	31				At2g10940	5,00E-23	68415.m01168 protease inhibitor/seed storage/lipid transfer protein (LTP) family protein similar to proline-rich cell wall protein [Medicago sativa] GI:3818416; contains Pfam profile PF00234 Protease inhibitor/seed storage/LTP family
354621	1	151	24	31				At2g10940	7,00E-07	68415.m01168 protease inhibitor/seed storage/lipid transfer protein (LTP) family protein similar to proline-rich cell wall protein [Medicago sativa] GI:3818416; contains Pfam profile PF00234 Protease inhibitor/seed storage/LTP family
353927	2	152	31	24	6386	1	1	At2g33620	1,00E-37	68415.m04122 DNA-binding family protein / AT-hook protein 1 (AHP1) identical to AT-hook protein 1 [Arabidopsis thaliana] gi|2598227|emb|CAA10857
354231	3	152	31	24	6386	1	1	At2g33620	2,00E-38	68415.m04122 DNA-binding family protein / AT-hook protein 1 (AHP1) identical to AT-hook protein 1 [Arabidopsis thaliana] gi|2598227|emb|CAA10857
354566	1	152	31	24	6386	1	1	At2g33620	9,00E-09	68415.m04122 DNA-binding family protein / AT-hook protein 1 (AHP1) identical to AT-hook protein 1 [Arabidopsis thaliana] gi|2598227|emb|CAA10857

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354366	2	152	31	24	7065	2	2	At4g12080	1,00E-31	68417.m01920 DNA-binding family protein contains a AT hook motif (DNA binding motifs with a preference for A/T rich regions), Pfam:PF02178
357111	1	154	25	29	564	1	2	At1g30330	7,00E-84	68414.m03709 auxin-responsive factor (ARF6) identical to ARF6 [Arabidopsis thaliana] GI:4102600 (Science 276 (5320), 1865-1868 (1997))
355692	1	154	25	29	919	1	1	At5g37020	1,00E-38	68418.m04440 auxin-responsive factor (ARF8) identical to auxin response factor 8 GI:4104931 from [Arabidopsis thaliana]
353965	2	154	25	29	1349	1	1	At5g62000	1,00E-36	68418.m07784 transcriptional factor B3 family protein / auxin-responsive factor, putative (ARF1) contains Pfam profile: PF02362 B3 DNA binding domain; identical to cDNA ARF1 (auxin response factor) binding protein GI:2245393
354123	4	154	25	29	1349	1	1	At5g62000	9,00E-48	68418.m07784 transcriptional factor B3 family protein / auxin-responsive factor, putative (ARF1) contains Pfam profile: PF02362 B3 DNA binding domain; identical to cDNA ARF1 (auxin response factor) binding protein GI:2245393
354304	3	154	25	29	1349	1	1	At5g62000	5,00E-15	68418.m07784 transcriptional factor B3 family protein / auxin-responsive factor, putative (ARF1) contains Pfam profile: PF02362 B3 DNA binding domain; identical to cDNA ARF1 (auxin response factor) binding protein GI:2245393
354879	1	154	25	29	1349	1	1	At5g62000	4,00E-45	68418.m07784 transcriptional factor B3 family protein / auxin-responsive factor, putative (ARF1) contains Pfam profile: PF02362 B3 DNA binding domain; identical to cDNA ARF1 (auxin response factor) binding protein GI:2245393
359536	1	154	25	29				At5g60450	3,00E-35	68418.m07582 auxin-responsive factor (ARF4) contains Pfam profile: PF02362 B3 DNA binding domain; identical to cDNA auxin response factor 4 (ARF4) GI:4102597
358843	1	156	25	28	750	1	2	At5g49720	3,00E-57	68418.m06157 endo-1,4-beta-glucanase KORRIGAN (KOR) / cellulase (OR16pep) identical to endo-1,4-beta-D-glucanase KORRIGAN [Arabidopsis thaliana] GI:3978258; similar to endo-1,4-beta-D-glucanase; cellulase GI:5689613 from [Brassica napus]; identical to cDNA cellulase (OR16pep) GI:1022806
353851	2	156	25	28	1667	2	1	At4g02290	2,00E-75	68417.m00310 glycosyl hydrolase family 9 protein similar to endo-1,4-beta glucanase; ATCEL2 GI:3132891 from [Arabidopsis thaliana]

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
354383	2	156	25	28	1667	2	1	At4g02290	2,00E-25	68417.m00310 glycosyl hydrolase family 9 protein similar to endo-1,4-beta glucanase; ATCEL2 GI:3132891 from [Arabidopsis thaliana]
358260	1	156	25	28	1667	2	1	At1g02800	2,00E-51	68414.m00237 endo-1,4-beta-glucanase / cellulase (CEL2) identical to endo-1,4-beta glucanase; ATCEL2 GI:3132891 from [Arabidopsis thaliana]
352892	3	157	23	30	319	2	2	At2g34710	7,00E-64	68415.m04263 homeobox-leucine zipper transcription factor (HB-14) identical to homeodomain transcription factor (ATHB-14)GP:3132474 GB:Y11122 [Arabidopsis thaliana];
358207	1	157	23	30	951	2	2	At3g61150	6,00E-13	68416.m06843 homeobox-leucine zipper family protein / homeodomain GLABRA2 like protein 1 (HD-GL2-1) similar to Anthocyaninless2 (ANL2) (GP:5702094) Arabidopsis thaliana, EMBL:AF077335
359936	1	157	23	30	2271	2	1	At1g73360	9,00E-39	68414.m08491 homeobox-leucine zipper family protein / lipid-binding START domain-containing protein protodermal factor2 (GI:14276060) [Arabidopsis thaliana]; similar to homeobox protein GI:1173621 from [Phalaenopsis sp.]
355167	1	157	23	30				At1g05230	3,00E-12	68414.m00529 homeobox-leucine zipper family protein / lipid-binding START domain-containing protein similar to homeobox 1 (GP:12002853) {Picea abies}; Strong similarity to Phalaenopsis homeobox protein (gb|U34743)
355237	1	157	23	30				At1g52150	3,00E-87	68414.m05885 homeobox-leucine zipper family protein / lipid-binding START domain-containing protein similar to to HD-zip transcription factor (athb-8) (GI:7270235) [Arabidopsis thaliana]; contains Pfam profiles PF01852: START domain, PF00046: Homeobox domain
359664	1	158	25	28				At2g28660	3,00E-23	68415.m03484 copper-binding family protein similar to copper homeostasis factor gi:3168840 from Arabidopsis thaliana; contains Pfam profile PF00403: Heavy-metal-associated domain
354613	1	160	24	28	5220	1	1	At4g13980	3,00E-14	68417.m02162 heat shock transcription factor family protein contains Pfam profile: PF00447 HSF-type DNA-binding domain
353646	2	160	24	28				At5g16820	1,00E-30	68418.m01971 heat shock factor protein 3 (HSF3) / heat shock transcription factor 3 (HSTF3) identical to heat shock transcription factor 3 (HSF3) SP:O81821 from [Arabidopsis thaliana]

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355806	1	160	24	28				At4g17750	4,00E-11	68417.m02650 heat shock factor protein 1 (HSF1) / heat shock transcription factor 1 (HSTF1) identical to heat shock transcription factor 1 (HSF1) SP:P41151 from [Arabidopsis thaliana] ;contains Pfam profile: PF00447 HSF-type DNA-binding domain
358562	1	161	25	27	1788	1	2	At5g38640	2,00E-52	68418.m04673 eukaryotic translation initiation factor 2B family protein / eIF-2B family protein similar to SP|P41111 Translation initiation factor eIF-2B delta subunit (eIF-2B GDP-GTP exchange factor) {Oryctolagus cuniculus}; contains Pfam profile PF01008: Initiation factor 2 subunit family
355824	1	161	25	27	3563	3	1	At1g72340	1,00E-50	68414.m08368 eukaryotic translation initiation factor 2B family protein / eIF-2B family protein similar to SP|Q64270 Translation initiation factor eIF-2B alpha subunit {Rattus norvegicus}; contains Pfam profile PF01008: Initiation factor 2 subunit family
356130	1	161	25	27	4556	1	1	At2g05830	7,00E-63	68415.m00631 eukaryotic translation initiation factor 2B family protein / eIF-2B family protein similar to CIG2 [Nicotiana tabacum] GI:15216226, IDI2 [Hordeum vulgare subsp. vulgare] GI:12407304; weak similarity to SP|Q64270 Translation initiation factor eIF-2B alpha subunit {Rattus norvegicus}; contains Pfam profile PF01008: Initiation factor 2 subunit family
358437	1	165	22	29	1933	1	1	At3g61050	1,00E-12	68416.m06832 calcium-dependent lipid-binding protein, putative strong similarity to CLB1 [Lycopersicon esculentum] GI:2789434; contains Pfam profile PF00168: C2 domain
359073	1	165	22	29	6656	1	1	At3g21480	8,00E-21	68416.m02710 transcription activation domain-interacting protein-related contains weak similarity to Pax transcription activation domain interacting protein PTIP (GI:4336734) [Mus musculus]
357716	1	165	22	29				At1g05500	9,00E-10	68414.m00561 C2 domain-containing protein similar to Ca2+-dependent lipid-binding protein (CLB1) GI:2789434 from [Lycopersicon esculentum]
358864	1	166	25	26	3227	1	1	At1g52510	5,00E-38	68414.m05928 hydrolase, alpha/beta fold family protein low similarity to SP|P22643 Haloalkane dehalogenase (EC 3.8.1.5) {Xanthobacter autotrophicus}; contains Pfam profile PF00561: hydrolase, alpha/beta fold family

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358563	1	166	25	26	8048	1	1	At4g13870	2,00E-44	68417.m02149 Werner Syndrome-like exonuclease (WEX) contains Pfam profile PF01612: 3'-5' exonuclease; identical to Werner Syndrome-like exonuclease [Arabidopsis thaliana] GP:28195109 gb:AAO33765
356380	1	167	27	23	1213	2	1	At1g23310	2,00E-08	68414.m02915 glutamate:glyoxylate aminotransferase 1 (GGT1) identical to glutamate:glyoxylate aminotransferase 1 [Arabidopsis thaliana] GI:24461827; similar to alanine aminotransferase GI:4730884 from [Oryza sativa]; contains Pfam profile PF00155: aminotransferase, classes I and II
356046	1	167	27	23	2216	1	1	At1g77670	3,00E-23	68414.m09043 aminotransferase class I and II family protein similar to kynurenine aminotransferase /glutamine transaminase K GI:1030066 [Rattus norvegicus]
357202	1	167	27	23	2216	1	1	At1g77670	5,00E-55	68414.m09043 aminotransferase class I and II family protein similar to kynurenine aminotransferase /glutamine transaminase K GI:1030066 [Rattus norvegicus]
354583	1	167	27	23	2859	1	1	At2g22250	6,00E-72	68415.m02642 aminotransferase class I and II family protein similar to aspartate aminotransferase from Bacillus stearothermophilus SP|Q59228, Thermus aquaticus SP|O33822; contains Pfam profile PF00155 aminotransferase, classes I and II
358591	1	167	27	23	2931	1	1	At1g80360	2,00E-34	68414.m09407 aminotransferase class I and II family protein low similarity to GI:14278621 Aromatic Aminotransferase from Pyrococcus horikoshii
357869	1	167	27	23	2963	1	1	At5g51690	4,00E-26	68418.m06409 1-aminocyclopropane-1-carboxylate synthase, putative / ACC synthase, putative similar to ACC synthases from Solanum tuberosum [GI:520958], Triticum aestivum [GI:1173638]
355542	1	168	28	22	3865	2	1	At5g46750	2,00E-13	68418.m05759 human Rev interacting-like family protein / hRIP family protein contains Pfam profile PF01412: Putative GTP-ase activating protein for Arf
356538	1	168	28	22	3865	2	1	At5g46750	4,00E-39	68418.m05759 human Rev interacting-like family protein / hRIP family protein contains Pfam profile PF01412: Putative GTP-ase activating protein for Arf
354470	2	168	28	22	5410	1	1	At1g08680	8,00E-08	68414.m00965 ARF GAP-like zinc finger-containing protein ZiGA4 (ZIGA4) nearly identical to ARF GAP-like zinc finger-containing protein ZiGA4 GI:10441354 from [Arabidopsis thaliana]; contains InterPro accession IPR001164: Human Rev interacting-like protein (hRIP)

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354578	1	168	28	22	5410	1	1	At1g08680	1,00E-08	68414.m00965 ARF GAP-like zinc finger-containing protein ZiGA4 (ZIGA4) nearly identical to ARF GAP-like zinc finger-containing protein ZiGA4 GI:10441354 from [Arabidopsis thaliana]; contains InterPro accession IPR001164: Human Rev interacting-like protein (hRIP)
355123	1	168	28	22				At5g13300	6,00E-25	68418.m01528 ARF GTPase-activating domain-containing protein similar to GCN4-complementing protein (GCP1) GI:6465806 from [Arabidopsis thaliana]
358888	1	168	28	22				At5g13300	7,00E-08	68418.m01528 ARF GTPase-activating domain-containing protein similar to GCN4-complementing protein (GCP1) GI:6465806 from [Arabidopsis thaliana]
353658	2	170	21	28	1245	1	1	At1g19440	3,00E-20	68414.m02422 very-long-chain fatty acid condensing enzyme, putative similar to GB:AAD37122 from [Arabidopsis thaliana]
353233	2	170	21	28				At5g43760	5,00E-78	68418.m05352 beta-ketoacyl-CoA synthase, putative similar to beta-ketoacyl-CoA synthase [Simmondsia chinensis][GI:1045614]
358752	1	170	21	28				At2g26250	2,00E-26	68415.m03151 beta-ketoacyl-CoA synthase family (FIDDLEHEAD) (FDH) identical to GB:AJ010713 (fiddlehead protein)
353442	2	171	18	31	363	1	2	At1g79930	1,00E-64	68414.m09340 heat shock protein, putative contains Pfam profile: PF00012 Heat shock hsp70 proteins; similar to heat-shock proteins GB:CAA94389, GB:AAD55461 [Arabidopsis thaliana]
353526	2	171	18	31	492	1	1	At4g16660	4,00E-35	68417.m02517 heat shock protein 70, putative / HSP70, putative
357875	1	171	18	31	532	1	2	At5g09590	6,00E-93	68418.m01110 heat shock protein 70 / HSP70 (HSC70-5) identical to heat shock protein 70 [Arabidopsis thaliana] GI:6746590
359746	1	171	18	31	532	1	2	At5g09590	1,00E-43	68418.m01110 heat shock protein 70 / HSP70 (HSC70-5) identical to heat shock protein 70 [Arabidopsis thaliana] GI:6746590
354097	2	171	18	31				At4g37910	7,00E-69	68417.m05361 heat shock protein 70, mitochondrial, putative / HSP70, mitochondrial, putative strong similarity to SP|Q01899 Heat shock 70 kDa protein, mitochondrial precursor {Phaseolus vulgaris}
359760	1	171	18	31				At5g02500	5,00E-23	68418.m00183 heat shock cognate 70 kDa protein 1 (HSC70-1) (HSP70-1) identical to SP|P22953 Heat shock cognate 70 kDa protein 1 (Hsc70.1) {Arabidopsis thaliana}

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353193	6	172	21	28				At1g75950	4,00E-55	68414.m08821 E3 ubiquitin ligase SCF complex subunit SKP1/ASK1 (At1) E3 ubiquitin ligase; skp1a; identical to Skp1a GI:3068807, Skp1p GI:1432083 and UIP1 GI:3719209 from [Arabidopsis thaliana]; contains Pfam profiles PF01466: Skp1 family, dimerisation domain and PF03931: Skp1 family, tetramerisation domain;
354718	1	173	28	21	4723	2	2	At4g31340	1,00E-22	68417.m04445 myosin heavy chain-related contains weak similarity to Myosin heavy chain, nonmuscle type A (Cellular myosin heavy chain, type A) (Nonmuscle myosin heavy chain-A) (NMMHC-A) (Swiss-Prot:P35579) [Homo sapiens]
355034	1	173	28	21	4723	2	2	At2g24420	2,00E-29	68415.m02918 DNA repair ATPase-related contains 2 transmembrane domains; similar to DNA double-strand break repair rad50 ATPase. (Swiss-Prot:O33600) [Sulfolobus acidocaldarius]
355669	1	173	28	21	4723	2	2	At4g31340	6,00E-15	68417.m04445 myosin heavy chain-related contains weak similarity to Myosin heavy chain, nonmuscle type A (Cellular myosin heavy chain, type A) (Nonmuscle myosin heavy chain-A) (NMMHC-A) (Swiss-Prot:P35579) [Homo sapiens]
355224	1	174	19	30	1624	1	1	At5g62530	3,00E-66	68418.m07848 delta-1-pyrroline-5-carboxylate dehydrogenase (P5CDH) identical to delta-1-pyrroline-5-carboxylate dehydrogenase precursor [Arabidopsis thaliana] gi|15383744|gb|AAK73756; identical to cDNA delta-1-pyrroline-5-carboxylate dehydrogenase precursor (P5CDH) nuclear gene for mitochondrial product GI:15383743; contains Pfam profile PF00171:aldehyde dehydrogenase (NAD) family protein
358935	1	174	19	30	4777	1	2	At4g37750	2,00E-94	68417.m05344 ovule development protein aintegumenta (ANT) identical to ovule development protein aintegumenta (ANT) (GI:1244708)) [Arabidopsis thaliana]
358366	1	174	19	30	5131	1	1	At4g36920	4,00E-17	68417.m05233 floral homeotic protein APETALA2 (AP2) Identical to (SP:P47927) Floral homeotic protein APETALA2. [Mouse-ear cress] {Arabidopsis thaliana}
356131	1	174	19	30	5811	1	1	At2g41710	7,00E-24	68415.m05155 ovule development protein, putative similar to ovule development protein AINTEGUMENTA (GI:1209099) [Arabidopsis thaliana];Pfam domain (PF00847)

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357630	1	175	19	30	2607	1	1	At2g41190	2,00E-52	68415.m05087 amino acid transporter family protein low similarity to vesicular GABA transporter [Rattus norvegicus] GI:2587061; belongs to INTERPRO:IPR002422 amino acid/polyamine transporter, family II
354407	2	175	19	30	3248	2	1	At2g39130	1,00E-98	68415.m04807 amino acid transporter family protein belongs to INTERPRO:IPR002422 amino acid/polyamine transporter, family II
353380	3	176	26	22	622	1	1	At3g44600	2,00E-111	68416.m04794 peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein similar to SP|P87051 Peptidyl-prolyl cis-trans isomerase cyp2 (EC 5.2.1.8) (Cyclophilin cyp2) {Schizosaccharomyces pombe}; contains Pfam profiles PF00160: peptidyl-prolyl cis-trans isomerase cyclophilin-type, PF00400: WD domain G-beta repeat
356042	1	176	26	22	622	1	1	At3g44600	2,00E-42	68416.m04794 peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein similar to SP|P87051 Peptidyl-prolyl cis-trans isomerase cyp2 (EC 5.2.1.8) (Cyclophilin cyp2) {Schizosaccharomyces pombe}; contains Pfam profiles PF00160: peptidyl-prolyl cis-trans isomerase cyclophilin-type, PF00400: WD domain G-beta repeat
353991	2	176	26	22	3188	1	2	At2g15790	9,00E-65	68415.m01810 peptidyl-prolyl cis-trans isomerase / cyclophilin-40 (CYP40) / rotamase identical to cyclophilin-40 [Arabidopsis thaliana] GI:13442983; supporting cDNA gi|13442982|gb|AY026065.1|
354543	1	176	26	22	6779	3	1	At4g38740	7,00E-21	68417.m05487 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}
353037	2	176	26	22	6803	1	1	At2g36130	9,00E-61	68415.m04436 peptidyl-prolyl cis-trans isomerase, putative / cyclophilin, putative / rotamase, putative contains Pfam domain, PF00160: peptidyl-prolyl cis-trans isomerase, cyclophilin-type
353550	2	176	26	22	6955	3	1	At5g58710	9,00E-65	68418.m07355 peptidyl-prolyl cis-trans isomerase, putative / cyclophilin, putative / rotamase, putative (ROC7) similar to cyclophilin [Arabidopsis thaliana] gi|2443755|gb|AAB71401

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356155	1	176	26	22	7348	1	1	At4g34960	2,00E-07	68417.m04955 peptidyl-prolyl cis-trans isomerase, putative / cyclophilin, putative / rotamase, putative similar to cyclophilin [Arabidopsis thaliana] gi|2443755|gb|AAB71401
354204	3	177	24	24	5428	2	2	At4g02080	6,00E-86	68417.m00279 GTP-binding protein (SAR1A) identical to SP:O04834 GTP-binding protein SAR1A. [Arabidopsis thaliana]
355846	1	177	24	24	5428	2	2	At4g02080	2,00E-62	68417.m00279 GTP-binding protein (SAR1A) identical to SP:O04834 GTP-binding protein SAR1A. [Arabidopsis thaliana]
353591	5	177	24	24	5665	5	2	At1g10630	2,00E-99	68414.m01205 ADP-ribosylation factor, putative similar to ADP-ribosylation factor GI:166586 from [Arabidopsis thaliana]
353791	3	177	24	24	5665	5	2	At5g14670	7,00E-74	68418.m01719 ADP-ribosylation factor, putative similar to ADP-ribosylation factor DcARF1 (GI:965483) [Daucus carota].
354398	4	177	24	24	5665	5	2	At5g14670	3,00E-100	68418.m01719 ADP-ribosylation factor, putative similar to ADP-ribosylation factor DcARF1 (GI:965483) [Daucus carota].
359895	1	177	24	24	5914	1	1	At5g37680	1,00E-91	68418.m04538 ADP-ribosylation factor, putative ADP-ribosylation factor, Leishmania major, EMBL:LMFP1421 and ADP-ribosylation factor-like protein 1 (ARL1) (SP:P40616) Homo sapiens; contains PF00025: ADP-ribosylation factor family
354855	1	177	24	24	5953	2	2	At5g17060	8,00E-81	68418.m01999 ADP-ribosylation factor, putative similar to ADP-ribosylation factor 1; ARF 1 (GP:385340) {Drosophila melanogaster)
357744	1	177	24	24	5953	2	2	At5g17060	2,00E-84	68418.m01999 ADP-ribosylation factor, putative similar to ADP-ribosylation factor 1; ARF 1 (GP:385340) {Drosophila melanogaster)
358383	1	177	24	24	5953	2	2	At5g17060	7,00E-09	68418.m01999 ADP-ribosylation factor, putative similar to ADP-ribosylation factor 1; ARF 1 (GP:385340) {Drosophila melanogaster)
355353	1	177	24	24	6374	1	1	At2g24765	2,00E-32	68415.m02959 ADP-ribosylation factor 3 (ARF3) identical to GP:453191 ADP-ribosylation factor 3 {Arabidopsis thaliana}; contains domain PF00025: ADP-ribosylation factor family
360066	1	177	24	24	6374	1	1	At2g24765	7,00E-50	68415.m02959 ADP-ribosylation factor 3 (ARF3) identical to GP:453191 ADP-ribosylation factor 3 {Arabidopsis thaliana}; contains domain PF00025: ADP-ribosylation factor family

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353131	4	179	27	20	5398	1	1	At2g26180	2,00E-58	68415.m03144 calmodulin-binding family protein low similarity to SF16 protein [Helianthus annuus] GI:560150; contains Pfam profile PF00612: IQ calmodulin-binding motif
358503	1	179	27	20	6180	1	2	At3g52290	7,00E-14	68416.m05747 calmodulin-binding family protein similar to SF16 protein [Helianthus annuus] GI:560150; contains Pfam profile PF00612: IQ calmodulin-binding motif
359860	1	179	27	20	6180	1	2	At3g52290	6,00E-36	68416.m05747 calmodulin-binding family protein similar to SF16 protein [Helianthus annuus] GI:560150; contains Pfam profile PF00612: IQ calmodulin-binding motif
356665	1	179	27	20	6442	2	2	At1g74690	2,00E-14	68414.m08650 calmodulin-binding family protein low similarity to SF16 protein [Helianthus annuus] GI:560150; contains Pfam profile PF00612: IQ calmodulin-binding motif
359291	1	179	27	20	6442	2	2	At1g74690	2,00E-09	68414.m08650 calmodulin-binding family protein low similarity to SF16 protein [Helianthus annuus] GI:560150; contains Pfam profile PF00612: IQ calmodulin-binding motif
358546	1	179	27	20	7201	1	1	At1g19870	1,00E-14	68414.m02492 calmodulin-binding family protein contains Pfam profile: PF00612 IQ calmodulin-binding motif
354693	1	179	27	20				At2g02790	4,00E-10	68415.m00222 calmodulin-binding family protein very low similarity to SP|P12036 Neurofilament triplet H protein {Homo sapiens}; contains Pfam profile PF00612: IQ calmodulin-binding motif
358755	1	180	21	26	619	1	1	At2g25050	8,00E-97	68415.m02996 formin homology 2 domain-containing protein / FH2 domain-containing protein contains formin homology 2 domain, Pfam:PF02128
353603	2	180	21	26	3472	1	1	At3g05470	4,00E-78	68416.m00599 formin homology 2 domain-containing protein / FH2 domain-containing protein contains formin homology 2 domain, Pfam:PF02181
359637	1	181	21	25	98	1	1	At3g14270	6,00E-33	68416.m01806 phosphatidylinositol-4-phosphate 5-kinase family protein similar to SP|Q9Z1T6 FYVE finger-containing phosphoinositide kinase (EC 2.7.1.68) (1-phosphatidylinositol-4-phosphate kinase) (PIP5K) (PtdIns(4)P-5-kinase) {Mus musculus}; contains Pfam profiles PF01504: Phosphatidylinositol-4-phosphate 5-Kinase, PF01363: FYVE zinc finger, PF00118: TCP-1/cpn60 chaperonin family

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358580	1	181	21	25	266	1	2	At1g71010	4,00E-11	68414.m08192 phosphatidylinositol-4-phosphate 5-kinase family protein low similarity to phosphatidylinositol 3,5-kinase [Candida albicans] GI:14571648; contains Pfam profile PF01504: Phosphatidylinositol-4-phosphate 5-Kinase
359157	1	182	21	25	961	1	3	At1g13750	1,00E-29	68414.m01614 calcineurin-like phosphoesterase family protein contains Pfam profile: PF00149 calcineurin-like phosphoesterase
359058	1	182	21	25	1463	2	1	At1g13900	5,00E-06	68414.m01631 calcineurin-like phosphoesterase family protein contains Pfam profile: PF00149 calcineurin-like phosphoesterase
354969	1	182	21	25	2410	1	1	At3g20500	2,00E-64	68416.m02596 calcineurin-like phosphoesterase family protein contains Pfam profile: PF00149 calcineurin-like phosphoesterase
357829	1	182	21	25				At5g50400	1,00E-72	68418.m06242 calcineurin-like phosphoesterase family protein contains Pfam profile: PF00149 calcineurin-like phosphoesterase
359671	1	182	21	25				At4g24890	1,00E-43	68417.m03562 calcineurin-like phosphoesterase family protein contains Pfam profile: PF00149 calcineurin-like phosphoesterase
354629	1	183	18	28	1037	1	1	At3g25230	4,00E-20	68416.m03152 peptidyl-prolyl cis-trans isomerase / FK506-binding protein (ROF1) identical to rotamase FKBP (ROF1) GB:U49453 [Arabidopsis thaliana] (Mol. Gen. Genet. 252 (5), 510-517 (1996))
357743	1	183	18	28	6372	1	1	At4g25340	1,00E-29	68417.m03647 immunophilin-related / FKBP-type peptidyl-prolyl cis-trans isomerase-related immunophilin FKBP46 - Spodoptera frugiperda (fall armyworm),PIR2:A55320
353579	3	183	18	28	7685	2	3	At4g18100	2,00E-51	68417.m02692 60S ribosomal protein L32 (RPL32A) ribosomal protein L32, human, PIR1:R5HU32
355457	1	183	18	28	7685	2	3	At4g18100	3,00E-49	68417.m02692 60S ribosomal protein L32 (RPL32A) ribosomal protein L32, human, PIR1:R5HU32
357514	1	183	18	28	7934	1	1	At3g25220	4,00E-48	68416.m03150 FK506-binding protein 2-1 (FKBP15-1) / immunophilin / peptidyl-prolyl cis-trans isomerase / rotamase identical to SP|Q38935 FK506-binding protein 2-1 precursor (EC 5.2.1.8) (Peptidyl-prolyl cis- trans isomerase) (PPiase) (Rotamase) (15 kDa FKBP) (FKBP-15-1) {Arabidopsis thaliana}, immunophilin (FKBP15-1) GB:U52046 [Arabidopsis thaliana] (Proc. Natl. Acad. Sci. U.S.A. 93 (14), 6964-6969 (1996))

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
359839	1	184	21	24	3435	1	1	At1g22040	1,00E-78	68414.m02757 kelch repeat-containing F-box family protein contains Pfam profiles PF01344: Kelch motif, PF00646: F-box domain
359405	1	184	21	24	4056	3	1	At1g14330	2,00E-33	68414.m01698 kelch repeat-containing F-box family protein contains Pfam profile PF01344: Kelch motif; contains weak Pfam PF00646: F-box domain; weak similarity to Kelch-like protein 1 (Swiss-Prot:Q9NR64) [Homo sapiens]
354653	1	184	21	24	4834	1	1	At3g63220	6,00E-52	68416.m07103 kelch repeat-containing F-box family protein contains Pfam profiles PF01344: Kelch motif, PF00646: F-box domain
355219	1	185	20	25	2093	1	1	At5g43940	8,00E-25	68418.m05376 alcohol dehydrogenase class III / glutathione-dependent formaldehyde dehydrogenase / GSH-FDH (ADHIII) identical to gi:1143388
355261	1	185	20	25	2093	1	1	At5g43940	4,00E-13	68418.m05376 alcohol dehydrogenase class III / glutathione-dependent formaldehyde dehydrogenase / GSH-FDH (ADHIII) identical to gi:1143388
355681	1	185	20	25	2243	1	2	At1g77120	5,00E-45	68414.m08982 alcohol dehydrogenase (ADH) identical to alcohol dehydrogenase GI:469467 from (Arabidopsis thaliana)
357515	1	185	20	25	2243	1	2	At1g77120	8,00E-55	68414.m08982 alcohol dehydrogenase (ADH) identical to alcohol dehydrogenase GI:469467 from (Arabidopsis thaliana)
357751	1	185	20	25	2243	1	2	At1g77120	5,00E-25	68414.m08982 alcohol dehydrogenase (ADH) identical to alcohol dehydrogenase GI:469467 from (Arabidopsis thaliana)
356732	1	185	20	25	2792	1	1	At5g63620	2,00E-21	68418.m07988 oxidoreductase, zinc-binding dehydrogenase family protein contains PFAM zinc-binding dehydrogenase domain PF00107
359623	1	185	20	25	3757	1	1	At1g72680	2,00E-23	68414.m08405 cinnamyl-alcohol dehydrogenase, putative similar to cinnamyl-alcohol dehydrogenase GB:AAC35846 [Medicago sativa], SP|Q08350 [Picea abies]
354047	2	186	6	39	140	1	1	At5g45140	5,00E-75	68418.m05542 DNA-directed RNA polymerase, putative similar to SP|P22276 DNA-directed RNA polymerase III 130 kDa polypeptide (EC 2.7.7.6) (RNA polymerase III subunit 2) {Saccharomyces cerevisiae}; contains Pfam profiles PF04560: RNA polymerase Rpb2 domain 7, PF04561: RNA polymerase Rpb2 domain 2, PF04565: RNA polymerase Rpb2 domain 3, PF04566: RNA polymerase Rpb2 domain 4, PF04567: RNA polymerase Rpb2 domain 5

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
353730	5	186	6	39	5962	1	1	At5g11770	2,00E-79	68418.m01374 NADH-ubiquinone oxidoreductase 20 kDa subunit, mitochondrial identical to NADH-ubiquinone oxidoreductase 20 kDa subunit mitochondrial [precursor] SP:Q42577 from [Arabidopsis thaliana]; contains Pfam profile: PF01058 NADH ubiquinone oxidoreductase, 20 Kd subunit
359681	1	186	6	39	5962	1	1	At5g11770	1,00E-27	68418.m01374 NADH-ubiquinone oxidoreductase 20 kDa subunit, mitochondrial identical to NADH-ubiquinone oxidoreductase 20 kDa subunit mitochondrial [precursor] SP:Q42577 from [Arabidopsis thaliana]; contains Pfam profile: PF01058 NADH ubiquinone oxidoreductase, 20 Kd subunit
355590	1	187	17	28	3337	3	2	At1g34470	4,00E-23	68414.m04283 permease-related low similarity to purine permease [Arabidopsis thaliana] GI:7620007
356546	1	187	17	28	3337	3	2	At1g34470	3,00E-69	68414.m04283 permease-related low similarity to purine permease [Arabidopsis thaliana] GI:7620007
358235	1	187	17	28	3490	1	1	At3g26670	1,00E-37	68416.m03334 expressed protein
357190	1	190	2	42	5900	1	1	At4g20330	1,00E-22	68417.m02968 transcription initiation factor-related contains weak similarity to Transcription initiation factor IIE, beta subunit (TFIIE-beta) (Swiss-Prot:P29084) [Homo sapiens]
358665	1	192	18	25	1495	2	1	At5g49730	2,00E-09	68418.m06158 ferric reductase-like transmembrane component family protein similar to ferric-chelate reductase (FRO1) [Pisum sativum] GI:15341529; contains Pfam profile PF01794: Ferric reductase like transmembrane componenent
356253	1	192	18	25				At5g07390	2,00E-41	68418.m00846 respiratory burst oxidase protein A (RbohA) / NADPH oxidase identical to respiratory burst oxidase protein A from Arabidopsis thaliana [gi:3242781]
358149	1	193	18	25	38	1	1	At2g38770	1,00E-14	68415.m04760 expressed protein
356562	1	193	18	25	206	2	1	At4g30100	2,00E-35	68417.m04280 tRNA-splicing endonuclease positive effector-related contains similarity to SEN1, a positive effector of tRNA-splicing endonuclease [Saccharomyces cerevisiae] gi|172574|gb|AAB63976
354174	3	193	18	25	216	1	1	At5g47010	5,00E-24	68418.m05794 RNA helicase, putative similar to type 1 RNA helicase pNORF1 [Homo sapiens] GI:1885356
353268	2	193	18	25	625	1	2	At5g35970	2,00E-57	68418.m04332 DNA-binding protein, putative similar to SWISS-PROT:Q60560 DNA-binding protein SMUBP-2 (Immunoglobulin MU binding protein 2, SMUBP-2) [Mesocricetus auratus]

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
359311	1	194	17	26	7800	3	7	At5g59720	2,00E-36	68418.m07486 18.1 kDa class I heat shock protein (HSP18.1-CI) identical to 18.2 kDa class I heat shock protein (HSP 18.2) (SP:P19037)[Arabidopsis thaliana]; contains Pfam profile: PF00011 Hsp20/alpha crystallin family
358356	1	194	17	26				At2g29500	3,00E-15	68415.m03583 17.6 kDa class I small heat shock protein (HSP17.6B-CI) contains Pfam PF00011: Hsp20/alpha crystallin family; identified in Scharf, K-D., et al, Cell Stress & Chaperones (2001) 6: 225-237.
357951	1	196	20	23	769	1	1	At3g11830	1,00E-43	68416.m01450 chaperonin, putative similar to SWISS-PROT:P80313 T-complex protein 1, eta subunit (TCP-1-eta) [Mus musculus]; contains Pfam:PF00118 domain, TCP-1/cpn60 chaperonin family
358504	1	196	20	23	775	1	2	At3g23990	4,00E-61	68416.m03013 chaperonin (CPN60) (HSP60) identical to SWISS-PROT:P29197- chaperonin CPN60, mitochondrial precursor (HSP60) [Arabidopsis thaliana]
355217	1	196	20	23	778	3	1	At3g13470	1,00E-39	68416.m01695 chaperonin, putative similar SWISS-PROT:P21240- RuBisCO subunit binding-protein beta subunit, chloroplast precursor (60 kDa chaperonin beta subunit, CPN-60 beta) [Arabidopsis thaliana]; contains Pfam:PF00118 domain, TCP-1/cpn60 chaperonin family
358389	1	196	20	23	778	3	1	At3g13470	2,00E-08	68416.m01695 chaperonin, putative similar SWISS-PROT:P21240- RuBisCO subunit binding-protein beta subunit, chloroplast precursor (60 kDa chaperonin beta subunit, CPN-60 beta) [Arabidopsis thaliana]; contains Pfam:PF00118 domain, TCP-1/cpn60 chaperonin family
360041	1	196	20	23	778	3	1	At3g13470	2,00E-70	68416.m01695 chaperonin, putative similar SWISS-PROT:P21240- RuBisCO subunit binding-protein beta subunit, chloroplast precursor (60 kDa chaperonin beta subunit, CPN-60 beta) [Arabidopsis thaliana]; contains Pfam:PF00118 domain, TCP-1/cpn60 chaperonin family
359059	1	196	20	23	799	1	1	At5g26360	3,00E-71	68418.m03151 chaperonin, putative similar to SWISS-PROT:P50143- T-complex protein 1, gamma subunit (TCP-1-gamma) [Xenopus laevis]; contains Pfam:PF00118 domain, TCP-1/cpn60 chaperonin family
359848	1	196	20	23	799	1	1	At5g26360	1,00E-88	68418.m03151 chaperonin, putative similar to SWISS-PROT:P50143- T-complex protein 1, gamma subunit (TCP-1-gamma) [Xenopus laevis]; contains Pfam:PF00118 domain, TCP-1/cpn60 chaperonin family

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
354585	1	196	20	23	817	2	1	At3g02530	1,00E-87	68416.m00241 chaperonin, putative similar to SWISS-PROT:P80317- T-complex protein 1, zeta subunit (TCP-1-zeta) [Mus musculus]; contains Pfam:PF00118 domain, TCP-1/cpn60 chaperonin family
357890	1	196	20	23	817	2	1	At3g02530	2,00E-53	68416.m00241 chaperonin, putative similar to SWISS-PROT:P80317- T-complex protein 1, zeta subunit (TCP-1-zeta) [Mus musculus]; contains Pfam:PF00118 domain, TCP-1/cpn60 chaperonin family
358347	1	196	20	23	817	2	1	At3g02530	5,00E-07	68416.m00241 chaperonin, putative similar to SWISS-PROT:P80317- T-complex protein 1, zeta subunit (TCP-1-zeta) [Mus musculus]; contains Pfam:PF00118 domain, TCP-1/cpn60 chaperonin family
354287	2	196	20	23	879	1	1	At3g20050	1,00E-67	68416.m02536 T-complex protein 1 alpha subunit / TCP-1-alpha / chaperonin (CCT1) identical to SWISS-PROT:P28769-T-complex protein 1, alpha subunit (TCP-1-alpha) [Arabidopsis thaliana]
358730	1	196	20	23	879	1	1	At3g20050	4,00E-74	68416.m02536 T-complex protein 1 alpha subunit / TCP-1-alpha / chaperonin (CCT1) identical to SWISS-PROT:P28769-T-complex protein 1, alpha subunit (TCP-1-alpha) [Arabidopsis thaliana]
359600	1	196	20	23	879	1	1	At3g20050	2,00E-89	68416.m02536 T-complex protein 1 alpha subunit / TCP-1-alpha / chaperonin (CCT1) identical to SWISS-PROT:P28769-T-complex protein 1, alpha subunit (TCP-1-alpha) [Arabidopsis thaliana]
358211	1	196	20	23	927	1	2	At5g20890	3,00E-35	68418.m02481 chaperonin, putative similar to SWISS-PROT:P78371- T-complex protein 1, beta subunit (TCP-1-beta) [Homo sapiens]; contains Pfam:PF00118 domain, TCP-1/cpn60 chaperonin family
359181	1	196	20	23	976	1	1	At3g03960	5,00E-73	68416.m00415 chaperonin, putative similar to SWISS-PROT:P42932- T-complex protein 1, theta subunit (TCP-1-theta) [Mus musculus]; contains Pfam:PF00118 domain, TCP-1/cpn60 chaperonin family
352990	4	196	20	23	977	1	1	At2g28000	4,00E-95	68415.m03393 RuBisCO subunit binding-protein alpha subunit, chloroplast / 60 kDa chaperonin alpha subunit / CPN-60 alpha identical to SWISS-PROT:P21238- RuBisCO subunit binding-protein alpha subunit, chloroplast precursor (60 kDa chaperonin alpha subunit, CPN-60 alpha) [Arabidopsis thaliana]

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
356388	1	196	20	23	1287	1	1	At1g24510	4,00E-53	68414.m03085 T-complex protein 1 epsilon subunit, putative / TCP-1-epsilon, putative / chaperonin, putative identical to SWISS-PROT:O04450- T-complex protein 1, epsilon subunit (TCP-1-epsilon) [Arabidopsis thaliana]; strong similarity to SP|P54411 T-complex protein 1, epsilon subunit (TCP-1-epsilon) (CCT-epsilon) (TCP-K36) {Avena sativa}; contains Pfam:PF00118 domain, TCP-1/cpn60 chaperonin family
358384	1	196	20	23	1287	1	1	At1g24510	1,00E-96	68414.m03085 T-complex protein 1 epsilon subunit, putative / TCP-1-epsilon, putative / chaperonin, putative identical to SWISS-PROT:O04450- T-complex protein 1, epsilon subunit (TCP-1-epsilon) [Arabidopsis thaliana]; strong similarity to SP|P54411 T-complex protein 1, epsilon subunit (TCP-1-epsilon) (CCT-epsilon) (TCP-K36) {Avena sativa}; contains Pfam:PF00118 domain, TCP-1/cpn60 chaperonin family
353762	9	197	24	18	9473	1	1	At1g27950	5,00E-23	68414.m03424 lipid transfer protein-related low similarity to lipid transfer protein Picea abies GI:2627141; contains Pfam profile: PF00234: Protease inhibitor/seed storage/LTP family
356770	1	197	24	18	9473	1	1	At1g27950	7,00E-24	68414.m03424 lipid transfer protein-related low similarity to lipid transfer protein Picea abies GI:2627141; contains Pfam profile: PF00234: Protease inhibitor/seed storage/LTP family
353062	5	197	24	18				At5g64140	6,00E-17	68418.m08054 40S ribosomal protein S28 (RPS28C)
356265	1	198	20	22	3841	3	2	At5g06950	1,00E-35	68418.m00786 bZIP transcription factor HBP-1b homolog identical to transcription factor HBP-1b homolog SP:P43273 from [Arabidopsis thaliana]
359372	1	199	24	18	8027	9	3	At5g24560	8,00E-33	68418.m02900 F-box family protein / SKP1 interacting partner 3-related contains similarity to SKP1 interacting partner 3 GI:10716951 from [Arabidopsis thaliana]
356970	1	201	13	29	481	2	1	At4g33530	5,00E-09	68417.m04765 potassium transporter family protein similar to K+ transporter HAK5 [Arabidopsis thaliana] GI:7108597; KUP/HAK/KT Transporter family member, PMID:11500563; contains Pfam profile PF02705: K+ potassium transporter
359112	1	201	13	29	536	2	1	At5g14880	5,00E-71	68418.m01745 potassium transporter, putative similar to potassium transporter HAK2p [Mesembryanthemum crystallinum] gi|14091471|gb|AAK53759; KUP/HAK/KT Transporter family member, PMID:11500563; contains Pfam profile PF02705: K+ potassium transporter

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358475	1	201	13	29				At2g30070	3,00E-24	68415.m03658 potassium transporter (KUP1) identical to potassium transporter [Arabidopsis thaliana] gi|2654088|gb|AAB87687; KUP/HAK/KT Transporter family member, PMID:11500563
357778	1	202	18	24	3279	1	3	At3g61790	1,00E-36	68416.m06933 seven in absentia (SINA) family protein similar to siah-1A protein [Mus musculus] GI:297035; contains Pfam profile PF03145: Seven in absentia protein family
356387	1	202	18	24				At3g54480	1,00E-12	68416.m06028 SKP1 interacting partner 5 (SKIP5) identical to GP:14348816 SKP1-interacting partner 5 {Arabidopsis thaliana}
355618	1	203	16	25	6934	2	1	At5g14680	6,00E-36	68418.m01720 universal stress protein (USP) family protein similar to ER6 protein [Lycopersicon esculentum] GI:5669654; contains Pfam profile PF00582: universal stress protein family
359517	1	203	16	25	6977	1	3	At1g11360	1,00E-27	68414.m01305 universal stress protein (USP) family protein contains Pfam PF00582: universal stress protein family domain; similar to ethylene-responsive ER6 protein (GI:5669654) [Lycopersicon esculentum]
356785	1	203	16	25	8203	1	1	At3g17020	1,00E-35	68416.m02173 universal stress protein (USP) family protein similar to early nodulin ENOD18 [Vicia faba] GI:11602747; contains Pfam profile PF00582: universal stress protein family
352965	2	203	16	25	8240	1	1	At3g03270	4,00E-38	68416.m00324 universal stress protein (USP) family protein / early nodulin ENOD18 family protein contains Pfam profile PF00582: universal stress protein family; similar to early nodulin ENOD18 (GI:11602747) [Vicia faba]
357487	1	203	16	25	9269	2	1	At3g58450	4,00E-29	68416.m06515 universal stress protein (USP) family protein contains Pfam PF00582: universal stress protein family
354105	4	203	16	25	9359	1	1	At1g68300	5,00E-37	68414.m07802 universal stress protein (USP) family protein similar to ER6 protein [Lycopersicon esculentum] GI:5669654; contains Pfam profile PF00582: universal stress protein family
358955	1	206	1	39	5957	1	1	At2g02500	2,00E-56	68415.m00189 expressed protein contains Pfam profile: PF01128 uncharacterized protein family UPF0007; identical to GP:12697583 2-C-methyl-D-erythritol 4-phosphate cytidyltransferase {Arabidopsis thaliana}; identical to cDNA 4-Diphosphocytidyl-2C-methyl-D-erythritol synthase (ISPD) GI:7385140

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353359	3	207	1	39	5081	1	1	At2g37990	4,00E-82	68415.m04663 ribosome biogenesis regulatory protein (RRS1) family protein contains Pfam profile PF04939: Ribosome biogenesis regulatory protein (RRS1); similar to Ribosome biogenesis regulatory protein homolog (Swiss-Prot:Q15050) [Homo sapiens]
358564	1	209	14	25	7836	1	1	At2g04780	2,00E-52	68415.m00489 fasciclin-like arabinogalactan-protein (FLA7) identical to gi_13377782_gb_AAK20860
354582	1	209	14	25				At5g60490	3,00E-15	68418.m07586 fasciclin-like arabinogalactan-protein (FLA12)
355525	1	209	14	25				At5g44130	2,00E-18	68418.m05401 fasciclin-like arabinogalactan-protein, putative similar to gi_13377784_gb_AAK20861
357052	1	213	20	19	4676	1	1	At3g29770	5,00E-34	68416.m03774 hydrolase, alpha/beta fold family protein similar to SP|Q40708 PIR7A protein {Oryza sativa}, polyneuridine aldehyde esterase [Rauvolfia serpentina] GI:6651393; contains Pfam profile: PF00561 alpha/beta hydrolase fold
356858	1	213	20	19	7199	1	2	At3g10870	1,00E-45	68416.m01309 hydrolase, alpha/beta fold family protein similar to ethylene-induced esterase [Citrus sinensis] GI:14279437, SP|Q43360 PIR7B protein {Oryza sativa}; contains Pfam profile PF00561: hydrolase, alpha/beta fold family
352939	3	214	18	20	7147	3	2	At5g10980	1,00E-71	68418.m01277 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
353276	5	214	18	20	7147	3	2	At5g10980	7,00E-72	68418.m01277 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
353901	23	214	18	20	7147	3	2	At5g10980	8,00E-72	68418.m01277 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
354038	7	214	18	20	7147	3	2	At5g10980	1,00E-70	68418.m01277 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

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
356832	1	214	18	20	7147	3	2	At5g10980	9,00E-59	68418.m01277 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
359001	1	214	18	20	7147	3	2	At5g10980	1,00E-23	68418.m01277 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
353097	2	214	18	20	7196	5	6	At5g65360	1,00E-41	68418.m08221 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
353214	11	214	18	20	7196	5	6	At5g65360	2,00E-70	68418.m08221 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
353256	8	214	18	20	7196	5	6	At5g65360	2,00E-70	68418.m08221 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
353339	5	214	18	20	7196	5	6	At5g65360	2,00E-70	68418.m08221 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
353956	25	214	18	20	7196	5	6	At5g65360	3,00E-61	68418.m08221 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
354146	13	214	18	20	7196	5	6	At5g65360	1,00E-68	68418.m08221 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

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355137	1	214	18	20	7196	5	6	At5g65360	8,00E-22	68418.m08221 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
359043	1	214	18	20	7196	5	6	At5g65360	7,00E-58	68418.m08221 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
359265	1	214	18	20	7196	5	6	At5g65360	2,00E-15	68418.m08221 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
358867	1	214	18	20				At1g75600	1,00E-16	68414.m08784 histone H3.2, putative strong similarity to histone H3.2 SP|P11105 GI:417103 from Lolium temulentum, histone H3.2 from Mus pahari GI:515005; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4
353177	2	215	15	23	2172	2	2	At1g57720	4,00E-69	68414.m06549 elongation factor 1B-gamma, putative / eEF-1B gamma, putative similar to elongation factor 1B gamma GI:3868758 from [Oryza sativa]
353731	6	215	15	23	2172	2	2	At1g57720	4,00E-81	68414.m06549 elongation factor 1B-gamma, putative / eEF-1B gamma, putative similar to elongation factor 1B gamma GI:3868758 from [Oryza sativa]
354920	1	215	15	23	2172	2	2	At1g09640	4,00E-58	68414.m01081 elongation factor 1B-gamma, putative / eEF-1B gamma, putative Similar to elongation factor 1-gamma (gb|EF1G_XENLA). ESTs gb|T20564,gb|T45940,gb|T04527 come from this gene
359561	1	215	15	23	8148	1	10	At3g62760	4,00E-29	68416.m07050 glutathione S-transferase, putative Glutathione transferase III(b) - Zea mays, EMBL:AJ010296
356954	1	216	22	16	8624	2	1	At4g28730	4,00E-40	68417.m04109 glutaredoxin family protein contains glutaredoxin domain, Pfam:PF00462
355674	1	217	26	12				At1g67750	1,00E-12	68414.m07731 pectate lyase family protein similar to pectate lyase GI:14289169 from [Salix gilgiana]
357279	1	217	26	12				At5g48900	1,00E-46	68418.m06049 pectate lyase family protein similar to pectate lyase GP:14531296 from [Fragaria x ananassa]; non-consensus AG donor splice site at exon 2

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
359794	1	218	21	17	2820	2	1	At5g54780	2,00E-31	68418.m06824 RabGAP/TBC domain-containing protein contains similarity to SP|P09379 GTPase-activating protein GYP7 (Fragment) {Yarrowia lipolytica}; contains Pfam profile PF00566: TBC domain
357301	1	218	21	17	3360	2	1	At3g02460	1,00E-22	68416.m00234 plant adhesion molecule, putative strong similarity to plant adhesion molecule 1 [Arabidopsis thaliana] GI:3511223; contains Pfam profile PF00566: TBC domain
359745	1	218	21	17	4040	2	1	At4g13730	1,00E-18	68417.m02131 RabGAP/TBC domain-containing protein low similarity to SP|Q08484 GTPase-activating protein GYP1 {Saccharomyces cerevisiae}; contains Pfam profile PF00566: TBC domain
353723	3	219	12	26	6036	3	3	At2g34480	9,00E-91	68415.m04233 60S ribosomal protein L18A (RPL18aB)
354284	3	219	12	26	6036	3	3	At2g34480	3,00E-91	68415.m04233 60S ribosomal protein L18A (RPL18aB)
356357	1	219	12	26	6036	3	3	At2g34480	4,00E-18	68415.m04233 60S ribosomal protein L18A (RPL18aB)
355020	1	219	12	26	10075	2	2	At4g17670	2,00E-09	68417.m02640 senescence-associated protein-related similar to senescence-associated protein SAG102 (GI:22331931) [Arabidopsis thaliana];
356789	1	219	12	26	10075	2	2	At4g17670	4,00E-20	68417.m02640 senescence-associated protein-related similar to senescence-associated protein SAG102 (GI:22331931) [Arabidopsis thaliana];
355524	1	219	12	26	10339	3	1	At1g22160	2,00E-13	68414.m02770 senescence-associated protein-related similar to senescence-associated protein SAG102 (GI:22331931) [Arabidopsis thaliana]
354213	2	220	21	17	313	1	1	At4g36360	5,00E-53	68417.m05164 beta-galactosidase, putative / lactase, putative similar to beta-galactosidase precursor SP:P48980 from [Lycopersicon esculentum]
356586	1	220	21	17				At2g32810	5,00E-36	68415.m04016 beta-galactosidase, putative / lactase, putative similar to beta-galactosidase GI:7939617 from [Lycopersicon esculentum]
360063	1	222	14	23	646	3	2	At5g25100	4,00E-31	68418.m02974 endomembrane protein 70, putative TM4 family;
355244	1	222	14	23	696	1	3	At1g10950	3,00E-56	68414.m01257 endomembrane protein 70, putative
356117	1	222	14	23	696	1	3	At1g10950	1,00E-32	68414.m01257 endomembrane protein 70, putative
357372	1	222	14	23	696	1	3	At1g10950	6,00E-20	68414.m01257 endomembrane protein 70, putative
355415	1	222	14	23	774	2	1	At2g01970	4,00E-61	68415.m00132 endomembrane protein 70, putative
358790	1	222	14	23	774	2	1	At2g01970	6,00E-37	68415.m00132 endomembrane protein 70, putative
357992	1	222	14	23	946	1	3	At4g12650	1,00E-124	68417.m01990 endomembrane protein 70, putative TM4 family;

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
356613	1	222	14	23				At5g37310	1,00E-36	68418.m04481 endomembrane protein 70, putative multispanning membrane protein, Homo sapiens, EMBL:HSU94831
353668	2	223	19	18	1631	1	1	At5g09810	9,00E-91	68418.m01135 actin 7 (ACT7) / actin 2 identical to SP|P53492 Actin 7 (Actin-2) {Arabidopsis thaliana}
353803	2	223	19	18	1631	1	1	At5g09810	4,00E-101	68418.m01135 actin 7 (ACT7) / actin 2 identical to SP|P53492 Actin 7 (Actin-2) {Arabidopsis thaliana}
354215	12	223	19	18	1631	1	1	At5g09810	0	68418.m01135 actin 7 (ACT7) / actin 2 identical to SP|P53492 Actin 7 (Actin-2) {Arabidopsis thaliana}
354369	6	223	19	18	1631	1	1	At5g09810	4,00E-162	68418.m01135 actin 7 (ACT7) / actin 2 identical to SP|P53492 Actin 7 (Actin-2) {Arabidopsis thaliana}
353773	3	223	19	18	1660	1	1	At1g13180	6,00E-79	68414.m01528 actin-related protein 3 (ARP3) identical to actin-related protein 3 (ARP3) [Arabidopsis thaliana] GI:21427461; contains Pfam profile PF00022: Actin
356966	1	223	19	18	1660	1	1	At1g13180	2,00E-50	68414.m01528 actin-related protein 3 (ARP3) identical to actin-related protein 3 (ARP3) [Arabidopsis thaliana] GI:21427461; contains Pfam profile PF00022: Actin
356757	1	224	16	21	765	1	2	At4g07960	1,00E-26	68417.m01276 glycosyl transferase family 2 protein similar to cellulose synthase from Agrobacterium tumeficiens [gi:710492] and Agrobacterium radiobacter [gi:710493]; contains Pfam glycosyl transferase, group 2 family protein domain PF00535
357588	1	224	16	21	765	1	2	At4g07960	3,00E-14	68417.m01276 glycosyl transferase family 2 protein similar to cellulose synthase from Agrobacterium tumeficiens [gi:710492] and Agrobacterium radiobacter [gi:710493]; contains Pfam glycosyl transferase, group 2 family protein domain PF00535
355828	1	224	16	21	785	2	1	At4g31590	1,00E-48	68417.m04487 glycosyl transferase family 2 protein similar to cellulose synthase from Agrobacterium tumeficiens [gi:710492] and Agrobacterium radiobacter [gi:710493]; contains Pfam glycosyl transferase, group 2 family protein domain PF00535
357698	1	224	16	21	785	2	1	At4g31590	3,00E-13	68417.m04487 glycosyl transferase family 2 protein similar to cellulose synthase from Agrobacterium tumeficiens [gi:710492] and Agrobacterium radiobacter [gi:710493]; contains Pfam glycosyl transferase, group 2 family protein domain PF00535

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355300	1	224	16	21	1434	2	2	At5g03760	2,00E-106	68418.m00339 glycosyl transferase family 2 protein similar to beta-(1-3)-glucosyl transferase GB:AAC62210 GI:3687658 from [Bradyrhizobium japonicum], cellulose synthase from Agrobacterium tumeficiens [gi:710492] and Agrobacterium radiobacter [gi:710493]; contains Pfam glycosyl transferase, group 2 family protein domain PF00535
359402	1	225	22	15	4111	5	3	At2g34430	1,00E-41	68415.m04223 chlorophyll A-B binding protein / LHCII type I (LHB1B1) identical to photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] GI:16366
356389	1	225	22	15	5488	1	1	At3g47470	8,00E-63	68416.m05162 chlorophyll A-B binding protein 4, chloroplast / LHCI type III CAB-4 (CAB4) identical to SP|P27521 Chlorophyll A-B binding protein 4, chloroplast precursor (LHCI type III CAB-4) (LHCP) {Arabidopsis thaliana}
356032	1	226	12	24	4983	1	2	At4g18550	2,00E-16	68417.m02748 lipase class 3 family protein similar to lipase [Dianthus caryophyllus] GI:4103627; contains Pfam profile PF01764: Lipase
353606	2	226	12	24				At1g51440	3,00E-69	68414.m05790 lipase class 3 family protein similar to DEFECTIVE IN ANTHER DEHISCENCE1 [Arabidopsis thaliana] GI:16215706, lipase [Dianthus caryophyllus] GI:4103627; contains Pfam profile PF01764: Lipase
355026	1	226	12	24				At1g06250	3,00E-12	68414.m00661 lipase class 3 family protein similar to lipase GB:AAD01804 GI:4103627 from [Dianthus caryophyllus]; contains Pfam profile PF01764: Lipase
354132	3	227	15	21	713	2	1	At1g76550	4,00E-128	68414.m08908 pyrophosphate--fructose-6-phosphate 1-phosphotransferase alpha subunit, putative / pyrophosphate-dependent 6-phosphofructose-1-kinase, putative strong similarity to SP|Q41140 Pyrophosphate--fructose 6-phosphate 1-phosphotransferase alpha subunit (EC 2.7.1.90) (PFP) (PPI-PFK) {Ricinus communis}; contains Pfam profile PF00365: Phosphofructokinase
353475	2	227	15	21	1555	2	1	At1g12000	3,00E-110	68414.m01386 pyrophosphate--fructose-6-phosphate 1-phosphotransferase beta subunit, putative / pyrophosphate-dependent 6-phosphofructose-1-kinase, putative strong similarity to SP|Q41141 Pyrophosphate--fructose 6-phosphate 1-phosphotransferase beta subunit (EC 2.7.1.90) (PFP) ((PPI-PFK) {Ricinus communis}; contains Pfam profile PF00365: Phosphofructokinase

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
354482	1	227	15	21	1936	1	1	At2g22480	3,00E-74	68415.m02667 phosphofructokinase family protein similar to phosphofructokinase [Amycolatopsis methanolica] GI:17432243; contains Pfam profile PF00365: Phosphofructokinase
359488	1	227	15	21	1992	1	1	At3g02090	2,00E-59	68416.m00175 mitochondrial processing peptidase beta subunit, putative similar to mitochondrial processing peptidase beta subunit, mitochondrial precursor, Beta-MPP [Human] SWISS-PROT:O75439
358006	1	227	15	21	2359	2	2	At1g51980	5,00E-77	68414.m05863 mitochondrial processing peptidase alpha subunit, putative similar to mitochondrial processing peptidase alpha subunit, mitochondrial precursor, Alpha-MPP (Ubiquinol-cytochrome C reductase subunit II) [Potato] SWISS-PROT:P29677
359697	1	227	15	21	2359	2	2	At3g16480	1,00E-27	68416.m02103 mitochondrial processing peptidase alpha subunit, putative similar to mitochondrial processing peptidase alpha subunit, mitochondrial precursor, Alpha-MPP (Ubiquinol-cytochrome C reductase subunit II) [Potato] SWISS-PROT:P29677
356575	1	227	15	21				At5g61580	7,00E-47	68418.m07727 phosphofructokinase family protein similar to phosphofructokinase [Amycolatopsis methanolica] GI:17432243; contains Pfam profile PF00365: Phosphofructokinase
353296	4	228	18	18	7167	2	2	At5g24870	2,00E-51	68418.m02943 zinc finger (C3HC4-type RING finger) family protein similar to Pfam domain, PF00097: Zinc finger, C3HC4 type (RING finger)
354713	1	228	18	18	7167	2	2	At5g10650	2,00E-26	68418.m01233 zinc finger (C3HC4-type RING finger) family protein similar to Pfam domain, PF00097: Zinc finger, C3HC4 type (RING finger)
354154	2	228	18	18	7491	1	1	At3g63530	2,00E-08	68416.m07156 zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)
356749	1	228	18	18	7491	1	1	At3g63530	7,00E-07	68416.m07156 zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)
357955	1	229	10	26	164	1	2	At1g48410	2,00E-72	68414.m05409 argonaute protein (AGO1) identical to SP|O04379 Argonaute protein (AGO1) {Arabidopsis thaliana}; contains Pfam profiles PF02171: Piwi domain, PF02170: PAZ domain

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353590	2	229	10	26	193	1	1	At5g43810	1,00E-76	68418.m05357 pinhead protein (PINHEAD) / zwille protein (ZWILLE) identical to SP|Q9XGW1 PINHEAD protein (ZWILLE protein) {Arabidopsis thaliana}; contains Pfam profiles PF02171: Piwi domain, PF02170: PAZ domain
357288	1	229	10	26	193	1	1	At5g43810	2,00E-17	68418.m05357 pinhead protein (PINHEAD) / zwille protein (ZWILLE) identical to SP|Q9XGW1 PINHEAD protein (ZWILLE protein) {Arabidopsis thaliana}; contains Pfam profiles PF02171: Piwi domain, PF02170: PAZ domain
359560	1	229	10	26	1973	2	2	At1g31280	5,00E-62	68414.m03828 PAZ domain-containing protein / piwi domain-containing protein similar to SP|O04379 Argonaute protein (AGO1) {Arabidopsis thaliana}, SP|Q9XGW1 PINHEAD protein (ZWILLE protein) {Arabidopsis thaliana}; contains Pfam profiles PF02171: Piwi domain, PF02170: PAZ domain
355273	1	229	10	26				At2g27880	1,00E-31	68415.m03380 argonaute protein, putative / AGO, putative similar to SP|O04379 Argonaute protein (AGO1) {Arabidopsis thaliana}; contains Pfam profiles PF02170: PAZ domain, PF02171: Piwi domain
357455	1	229	10	26				At5g21150	1,00E-09	68418.m02526 PAZ domain-containing protein / piwi domain-containing protein similar to SP|O04379 Argonaute protein (AGO1) {Arabidopsis thaliana}; contains Pfam profile: PF02170 PAZ (Piwi Argonaut and Zwille), PF02171 Piwi domain
353427	6	230	10	26	1470	1	3	At3g22200	1,00E-102	68416.m02801 4-aminobutyrate aminotransferase / gamma-amino-N-butyrate transaminase / GABA transaminase / beta-alanine--oxoglutarate aminotransferase identical to gamma-aminobutyrate transaminase subunit precursor [Arabidopsis thaliana] (EC 2.6.1.19) GI:14030435; contains Pfam profile PF00202: aminotransferase, class III; identical to cDNA gamma-aminobutyrate transaminase subunit precursor, nuclear gene for mitochondrial product GI:14030434

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354945	1	230	10	26	1470	1	3	At3g22200	2,00E-99	68416.m02801 4-aminobutyrate aminotransferase / gamma-amino-N-butyrate transaminase / GABA transaminase / beta-alanine--oxoglutarate aminotransferase identical to gamma-aminobutyrate transaminase subunit precursor [Arabidopsis thaliana] (EC 2.6.1.19) GI:14030435; contains Pfam profile PF00202: aminotransferase, class III; identical to cDNA gamma-aminobutyrate transaminase subunit precursor, nuclear gene for mitochondrial product GI:14030434
356934	1	230	10	26	1636	1	1	At4g39660	4,00E-11	68417.m05608 alanine--glyoxylate aminotransferase, putative / beta-alanine-pyruvate aminotransferase, putative / AGT, putative similar to SP|Q64565 Alanine--glyoxylate aminotransferase 2, mitochondrial precursor (EC 2.6.1.44) (AGT 2) (Beta-alanine-pyruvate aminotransferase) {Rattus norvegicus}; contains Pfam profile PF00202: aminotransferase, class III
357529	1	233	17	18	1967	2	1	At3g60030	1,00E-21	68416.m06704 squamosa promoter-binding protein-like 12 (SPL12) identical to squamosa promoter binding protein-like 12 [Arabidopsis thaliana] GI:6006395; contains Pfam profiles PF03110: SBP domain, PF00023: Ankyrin repeat
356830	1	233	17	18	3785	1	1	At5g18830	6,00E-11	68418.m02238 squamosa promoter-binding protein-like 7 (SPL7) identical to squamosa promoter binding protein-like 7 [Arabidopsis thaliana] GI:5931635; contains Pfam profile PF03110: SBP domain
355001	1	233	17	18	8007	2	2	At1g27370	4,00E-09	68414.m03335 squamosa promoter-binding protein-like 10 (SPL10) identical to squamosa promoter binding protein-like 10 [Arabidopsis thaliana] GI:5931669; contains Pfam profile PF03110: SBP domain
353035	3	233	17	18	8388	2	1	At3g57920	1,00E-18	68416.m06456 squamosa promoter-binding protein, putative similar to squamosa promoter binding protein-like 9 [Arabidopsis thaliana] GI:5931677; contains Pfam profile PF03110: SBP domain
354453	2	233	17	18	8388	2	1	At3g57920	2,00E-08	68416.m06456 squamosa promoter-binding protein, putative similar to squamosa promoter binding protein-like 9 [Arabidopsis thaliana] GI:5931677; contains Pfam profile PF03110: SBP domain
354797	1	233	17	18	8388	2	1	At2g42200	2,00E-11	68415.m05223 squamosa promoter-binding protein-like 9 (SPL9) identical to squamosa promoter binding protein-like 9 [Arabidopsis thaliana] GI:5931673; contains Pfam profile PF03110: SBP domain

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358481	1	233	17	18	8388	2	1	At3g57920	1,00E-10	68416.m06456 squamosa promoter-binding protein, putative similar to squamosa promoter binding protein-like 9 [Arabidopsis thaliana] GI:5931677; contains Pfam profile PF03110: SBP domain
354009	5	233	17	18	8852	2	2	At5g50670	2,00E-09	68418.m06279 squamosa promoter-binding protein, putative similar to squamosa promoter binding protein-like 9 [Arabidopsis thaliana] GI:5931673; contains Pfam profile PF03110: SBP domain
356085	1	233	17	18	8852	2	2	At5g50670	2,00E-17	68418.m06279 squamosa promoter-binding protein, putative similar to squamosa promoter binding protein-like 9 [Arabidopsis thaliana] GI:5931673; contains Pfam profile PF03110: SBP domain
356607	1	233	17	18	8852	2	2	At5g50670	6,00E-10	68418.m06279 squamosa promoter-binding protein, putative similar to squamosa promoter binding protein-like 9 [Arabidopsis thaliana] GI:5931673; contains Pfam profile PF03110: SBP domain
356293	1	233	17	18	9396	3	1	At3g15270	4,00E-37	68416.m01929 squamosa promoter-binding protein-like 5 (SPL5) identical to squamosa promoter binding protein-like 5 [Arabidopsis thaliana] GI:5931629; contains Pfam profile PF03110: SBP domain
358441	1	233	17	18				At1g27360	7,00E-31	68414.m03333 squamosa promoter-binding protein-like 11 (SPL11) identical to squamosa promoter binding protein-like 11 [Arabidopsis thaliana] GI:5931665; contains Pfam profile PF03110: SBP domain
353119	3	234	17	18	1966	2	2	At1g14910	2,00E-110	68414.m01782 epsin N-terminal homology (ENTH) domain-containing protein contains Pfam PF01417: ENTH domain. ENTH (Epsin N-terminal homology) domain; similar to Chain A, Calm-N N-Terminal Domain Of Clathrin Assembly Lymphoid Myeloid Leukaemia Protein, Pi(4,5)p2 Complex (GP:13399999) {Homo sapiens}
357597	1	234	17	18	1966	2	2	At2g01600	5,00E-27	68415.m00084 epsin N-terminal homology (ENTH) domain-containing protein contains Pfam PF01417: ENTH domain. ENTH (Epsin N-terminal homology) domain; similar to clathrin assembly protein AP180 (GI:6492344) [Xenopus laevis]
358468	1	234	17	18	1966	2	2	At2g01600	3,00E-26	68415.m00084 epsin N-terminal homology (ENTH) domain-containing protein contains Pfam PF01417: ENTH domain. ENTH (Epsin N-terminal homology) domain; similar to clathrin assembly protein AP180 (GI:6492344) [Xenopus laevis]
356654	1	235	20	15	480	2	1	At3g03940	2,00E-48	68416.m00412 protein kinase family protein contains Pfam domains, PF00069: Protein kinase domain

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356813	1	235	20	15	480	2	1	At3g03940	2,00E-18	68416.m00412 protein kinase family protein contains Pfam domains, PF00069: Protein kinase domain
353558	2	235	20	15	657	1	1	At2g25760	4,00E-178	68415.m03092 protein kinase family protein contains protein kinase domain, Pfam:PF00069
353729	2	235	20	15	1934	1	3	At1g72710	1,00E-19	68414.m08408 casein kinase, putative similar to casein kinase I, delta isoform [Arabidopsis thaliana] SWISS-PROT:P42158
358590	1	235	20	15	2127	1	1	At3g04480	1,00E-48	68416.m00475 endoribonuclease L-PSP family protein contains Pfam domain PF01902: Domain of unknown function
353041	2	235	20	15				At4g28540	9,00E-48	68417.m04083 casein kinase, putative similar to casein kinase I [Arabidopsis thaliana] gi|1103318|emb|CAA55395; contains protein kinase domain, Pfam:PF00069
354048	2	235	20	15				At3g13670	1,00E-121	68416.m01722 protein kinase family protein contains Pfam domains, PF00069: Protein kinase domain
359846	1	235	20	15				At3g23340	6,00E-92	68416.m02944 casein kinase, putative similar to casein kinase I [Arabidopsis thaliana] gi|1197461|emb|CAA55396
359797	1	236	15	20	2136	1	2	At3g63240	1,00E-51	68416.m07105 endonuclease/exonuclease/phosphatase family protein similar to inositol polyphosphate 5-phosphatase I (GI:10444261) and II (GI:10444263) [Arabidopsis thaliana]; contains Pfam profile PF03372: Endonuclease/Exonuclease/phosphatase family
359611	1	236	15	20				At1g65580	5,00E-27	68414.m07439 endonuclease/exonuclease/phosphatase family protein similar to inositol polyphosphate 5-phosphatase II isoform (GI:15418718) [Mus musculus]; contains 6 (5 weak) Pfam: Pf00400 WD domain, G-beta repeats and Pfam PF03372: Endonuclease/Exonuclease/phosphatase family
353286	2	239	18	17	339	1	1	At4g24190	1,00E-104	68417.m03473 shepherd protein (SHD) / clavata formation protein, putative nearly identical to SHEPHERD [Arabidopsis thaliana] GI:19570872; contains Pfam profiles PF02518: ATPase, histidine kinase-, DNA gyrase B-, and HSP90-like domain protein, PF00183: Hsp90 protein

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358836	1	239	18	17	339	1	1	At4g24190	2,00E-26	68417.m03473 shepherd protein (SHD) / clavata formation protein, putative nearly identical to SHEPHERD [Arabidopsis thaliana] GI:19570872; contains Pfam profiles PF02518: ATPase, histidine kinase-, DNA gyrase B-, and HSP90-like domain protein, PF00183: Hsp90 protein
358747	1	239	18	17	392	1	1	At2g04030	1,00E-85	68415.m00372 heat shock protein, putative strong similarity to heat shock protein [Arabidopsis thaliana] GI:1906830; contains Pfam profiles PF02518: ATPase, histidine kinase-, DNA gyrase B-, and HSP90-like domain protein, PF00183: Hsp90 protein
353700	2	239	18	17	548	1	1	At3g07770	5,00E-128	68416.m00947 heat shock protein-related strong similarity to heat-shock protein [Secale cereale] GI:556673; contains Pfam profiles PF02518: ATPase, histidine kinase-, DNA gyrase B-, and HSP90-like domain protein, PF00183: Hsp90 protein
353998	2	239	18	17	548	1	1	At3g07770	2,00E-85	68416.m00947 heat shock protein-related strong similarity to heat-shock protein [Secale cereale] GI:556673; contains Pfam profiles PF02518: ATPase, histidine kinase-, DNA gyrase B-, and HSP90-like domain protein, PF00183: Hsp90 protein
355721	1	239	18	17	3971	3	1	At4g24760	1,00E-72	68417.m03545 expressed protein
353033	2	239	18	17				At5g52640	1,00E-57	68418.m06535 heat shock protein 81-1 (HSP81-1) / heat shock protein 83 (HSP83) nearly identical to SP|P27323 Heat shock protein 81-1 (HSP81-1) (Heat shock protein 83) {Arabidopsis thaliana}; contains Pfam profiles PF02518: ATPase, histidine kinase-, DNA gyrase B-, and HSP90-like domain protein, PF00183: Hsp90 protein
354192	2	239	18	17				At5g52640	3,00E-96	68418.m06535 heat shock protein 81-1 (HSP81-1) / heat shock protein 83 (HSP83) nearly identical to SP|P27323 Heat shock protein 81-1 (HSP81-1) (Heat shock protein 83) {Arabidopsis thaliana}; contains Pfam profiles PF02518: ATPase, histidine kinase-, DNA gyrase B-, and HSP90-like domain protein, PF00183: Hsp90 protein

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
355523	1	239	18	17				At5g52640	1,00E-51	68418.m06535 heat shock protein 81-1 (HSP81-1) / heat shock protein 83 (HSP83) nearly identical to SP|P27323 Heat shock protein 81-1 (HSP81-1) (Heat shock protein 83) {Arabidopsis thaliana}; contains Pfam profiles PF02518: ATPase, histidine kinase-, DNA gyrase B-, and HSP90-like domain protein, PF00183: Hsp90 protein
355772	1	239	18	17				At5g52640	6,00E-49	68418.m06535 heat shock protein 81-1 (HSP81-1) / heat shock protein 83 (HSP83) nearly identical to SP|P27323 Heat shock protein 81-1 (HSP81-1) (Heat shock protein 83) {Arabidopsis thaliana}; contains Pfam profiles PF02518: ATPase, histidine kinase-, DNA gyrase B-, and HSP90-like domain protein, PF00183: Hsp90 protein
356880	1	241	20	15	1181	2	2	At5g54510	1,00E-91	68418.m06787 auxin-responsive GH3 protein, putative (DFL-1) identical to auxin-responsive GH3 homologue [Arabidopsis thaliana] GI:11041726; similar to auxin-responsive GH3 product [Glycine max] GI:18591; contains Pfam profile PF03321: GH3 auxin-responsive promoter
356565	1	241	20	15	1675	1	1	At2g46370	6,00E-39	68415.m05771 auxin-responsive GH3 family protein similar to auxin-responsive GH3 product [Glycine max] GI:18591; contains Pfam profile PF03321: GH3 auxin-responsive promoter
353209	2	242	7	28	9995	4	1	At1g61070	1,00E-17	68414.m06876 plant defensin-fusion protein, putative (PDF2.4) plant defensin protein family member, personal communication, Bart Thomma (Bart.Thomma@agr.kuleuven.ac.be); contains gamma-thionin domain
353336	10	242	7	28	9995	4	1	At2g02100	4,00E-18	68415.m00146 plant defensin-fusion protein, putative (PDF2.2) plant defensin protein family member, personal communication, Bart Thomma (Bart.Thomma@agr.kuleuven.ac.be); similar to SWISS-PROT:O65740
354660	1	242	7	28	9995	4	1	At2g02120	2,00E-16	68415.m00148 plant defensin-fusion protein, putative (PDF2.1) plant defensin protein family member, personal communication, Bart Thomma (Bart.Thomma@agr.kuleuven.ac.be); contains a gamma-thionin family signature (PDOC00725)

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357575	1	242	7	28	9995	4	1	At2g02120	4,00E-15	68415.m00148 plant defensin-fusion protein, putative (PDF2.1) plant defensin protein family member, personal communication, Bart Thomma (Bart.Thomma@agr.kuleuven.ac.be); contains a gamma-thionin family signature (PDOC00725)
353090	2	246	9	25	3230	1	1	At1g03780	4,00E-57	68414.m00358 targeting protein-related similar to microtubule-associated protein / targeting protein for Xklp2 ((TPX2) GI:8926138) {Homo sapiens}; similar to Restricted expression proliferation associated protein 100 (p100) (Differentially expressed in lung cells 2) (DIL-2) (Targeting protein for Xklp2) (C20orf1 protein) (C20orf2 protein) (Protein FLS353)(SP:Q9ULW0) {Homo sapiens}
353003	3	247	18	16	1949	2	1	At3g20560	2,00E-52	68416.m02603 thioredoxin family protein contains Pfam profile PF00085: Thioredoxin
355544	1	247	18	16	2131	2	1	At1g04980	2,00E-44	68414.m00497 thioredoxin family protein similar to SP|Q63081 Protein disulfide isomerase A6 precursor (EC 5.3.4.1) {Rattus norvegicus}; contains Pfam profile PF00085: Thioredoxin
356917	1	247	18	16	2570	1	1	At3g54960	1,00E-29	68416.m06094 thioredoxin family protein similar to protein disulfide isomerase GI:5902592 from [Volvox carteri f. nagariensis], GI:2708314 from Chlamydomonas reinhardtii; contains Pfam profile: PF00085 Thioredoxin
357034	1	247	18	16	2570	1	1	At3g54960	5,00E-76	68416.m06094 thioredoxin family protein similar to protein disulfide isomerase GI:5902592 from [Volvox carteri f. nagariensis], GI:2708314 from Chlamydomonas reinhardtii; contains Pfam profile: PF00085 Thioredoxin
354163	8	247	18	16	2742	2	1	At1g21750	1,00E-130	68414.m02723 protein disulfide isomerase, putative similar to SP|P29828 Protein disulfide isomerase precursor (PDI) (EC 5.3.4.1) {Medicago sativa}; isoform contains non-consensus GA donor splice site at intron 9
358157	1	247	18	16	2742	2	1	At1g77510	1,00E-31	68414.m09026 protein disulfide isomerase, putative similar to protein disulfide isomerase precursor GB:P29828 GI:4704766 [Medicago sativa]; Pfam HMM hit: PF00085 Thioredoxins
353553	2	247	18	16	3100	2	1	At1g36050	2,00E-102	68414.m04479 expressed protein
355905	1	247	18	16	3100	2	1	At1g36050	3,00E-42	68414.m04479 expressed protein
357620	1	247	18	16	3100	2	1	At1g36050	1,00E-16	68414.m04479 expressed protein

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
359524	1	247	18	16	3100	2	1	At1g36050	1,00E-14	68414.m04479 expressed protein
357865	1	247	18	16	3740	2	1	At3g16110	3,00E-29	68416.m02035 thioredoxin family protein similar to protein disulfide isomerase GI:5902592 from [Volvox carteri f. nagariensis], GI:2708314 from Chlamydomonas reinhardtii; contains Pfam profile: PF00085 Thioredoxin
359635	1	247	18	16	8239	1	1	At1g07960	3,00E-37	68414.m00867 thioredoxin family protein low similarity to protein disulfide isomerase 4 [Giardia intestinalis] GI:13489047; contains Pfam profile PF00085: Thioredoxin
354252	2	247	18	16				At5g60640	1,00E-82	68418.m07611 thioredoxin family protein similar to protein disulfide isomerase GI:5902592 from [Volvox carteri f. nagariensis], GI:2708314 from Chlamydomonas reinhardtii; contains Pfam profile: PF00085 Thioredoxin
359964	1	248	11	23	2965	2	2	At1g08250	5,00E-42	68414.m00910 prephenate dehydratase family protein contains similarity to prephenate dehydratase GI:1008717 from [Amycolatopsis methanolica]
359602	1	248	11	23	4714	1	2	At3g07630	4,00E-15	68416.m00914 prephenate dehydratase family protein similar to P-protein: chorismate mutase, prephenate dehydratase GB:P43900 [Haemophilus influenzae]
358015	1	249	16	18	4236	1	1	At5g16120	3,00E-57	68418.m01883 hydrolase, alpha/beta fold family protein similar to monoglyceride lipase from [Homo sapiens] GI:14594904, [Mus musculus] GI:2632162; contains Pfam profile PF00561: hydrolase, alpha/beta fold family
360070	1	249	16	18	4396	1	1	At5g11650	2,00E-73	68418.m01362 hydrolase, alpha/beta fold family protein contains Pfam profile PF00561: hydrolase, alpha/beta fold family; low similarity to monoglyceride lipase from [Homo sapiens] GI:14594904, [Mus musculus] GI:2632162
359650	1	249	16	18	5159	1	1	At1g77420	4,00E-15	68414.m09016 hydrolase, alpha/beta fold family protein similar to monoglyceride lipase from [Homo sapiens] GI:14594904, [Mus musculus] GI:2632162; contains Pfam profile PF00561: hydrolase, alpha/beta fold family
355144	1	250	17	17	568	1	1	At5g64940	4,00E-78	68418.m08169 ABC1 family protein contains Pfam domain, PF03109: ABC1 family
356692	1	250	17	17	568	1	1	At5g64940	9,00E-19	68418.m08169 ABC1 family protein contains Pfam domain, PF03109: ABC1 family
355515	1	250	17	17	1496	1	1	At1g11390	5,00E-13	68414.m01308 ABC1 family protein contains Pfam domain, PF03109: ABC1 family
356119	1	250	17	17	1513	1	1	At1g79600	8,00E-41	68414.m09281 ABC1 family protein contains Pfam domain, PF03109: ABC1 family

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
359793	1	250	17	17	1597	1	1	At5g05200	5,00E-58	68418.m00554 ABC1 family protein contains Pfam domain, PF03109: ABC1 family
358727	1	251	26	8	10063	4	2	At4g00390	2,00E-07	68417.m00053 expressed protein contains Pfam profile: PF04504 protein of unknown function, DUF573
353832	2	252	17	17	3238	1	1	At5g06140	1,00E-57	68418.m00683 phox (PX) domain-containing protein similar to SP|O60749 Sorting nexin 2 {Homo sapiens}; contains Pfam profile PF00787: PX domain
357483	1	252	17	17	4029	1	2	At5g12470	2,00E-33	68418.m01465 expressed protein
354212	5	252	17	17	8417	3	1	At4g39200	3,00E-29	68417.m05550 40S ribosomal protein S25 (RPS25E) ribosomal protein S25, Lycopersicon esculentum, PIR2:S40089
354352	3	252	17	17	8417	3	1	At4g39200	3,00E-30	68417.m05550 40S ribosomal protein S25 (RPS25E) ribosomal protein S25, Lycopersicon esculentum, PIR2:S40089
355984	1	252	17	17	8417	3	1	At4g39200	2,00E-08	68417.m05550 40S ribosomal protein S25 (RPS25E) ribosomal protein S25, Lycopersicon esculentum, PIR2:S40089
356612	1	254	14	19	4430	2	2	At1g05850	4,00E-08	68414.m00612 chitinase-like protein 1 (CTL1) similar to class I chitinase GI:7798656 from [Halimolobos perplexa var. perplexa]; contains Pfam profile PF00182: Chitinase class I; identical to cDNA chitinase-like protein 1 (CTL1) CTL1-ELP1 allele GI:17226328
357376	1	254	14	19				At2g43590	2,00E-15	68415.m05417 chitinase, putative similar to basic endochitinase CHB4 precursor SP:Q06209 from [Brassica napus]
355090	1	255	9	24	1475	1	1	At5g07360	4,00E-51	68418.m00840 amidase family protein low similarity to enantiomerase-selective amidase [Rhodococcus sp.] GI:152052; contains Pfam profile PF01425: Amidase
354151	2	255	9	24	1860	1	1	At3g17970	3,00E-11	68416.m02286 chloroplast outer membrane translocon subunit, putative similar to Toc64 [Pisum sativum] GI:7453538; contains Pfam profile PF00515 TPR Domain
358048	1	255	9	24	2276	1	1	At5g09420	1,00E-34	68418.m01091 chloroplast outer membrane translocon subunit, putative similar to component of chloroplast outer membrane translocon Toc64 [Pisum sativum] GI:7453538; contains Pfam profiles PF01425: Amidase, PF00515: TPR Domain
355433	1	255	9	24	2349	1	1	At3g25660	3,00E-47	68416.m03194 glutamyl-tRNA(Gln) amidotransferase, putative similar to SP|O06491 Glutamyl-tRNA(Gln) amidotransferase subunit A (EC 6.3.5.-) {Bacillus subtilis}; contains Pfam profile PF01425: Amidase

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
357318	1	255	9	24	2349	1	1	At3g25660	1,00E-37	68416.m03194 glutamyl-tRNA(Gln) amidotransferase, putative similar to SP|O06491 Glutamyl-tRNA(Gln) amidotransferase subunit A (EC 6.3.5.-) {Bacillus subtilis}; contains Pfam profile PF01425: Amidase
354474	4	257	18	15	7117	3	1	At1g28230	1,00E-28	68414.m03465 purine permease (PUP1) identical to purine permease GI:7620007 from [Arabidopsis thaliana]
352898	2	258	12	21	1723	2	1	At3g12860	9,00E-64	68416.m01603 nucleolar protein Nop56, putative similar to XNop56 protein [Xenopus laevis] GI:14799394; contains Pfam profile PF01798: Putative snoRNA binding domain
356234	1	258	12	21	1723	2	1	At3g12860	4,00E-56	68416.m01603 nucleolar protein Nop56, putative similar to XNop56 protein [Xenopus laevis] GI:14799394; contains Pfam profile PF01798: Putative snoRNA binding domain
359175	1	258	12	21	1723	2	1	At3g12860	4,00E-78	68416.m01603 nucleolar protein Nop56, putative similar to XNop56 protein [Xenopus laevis] GI:14799394; contains Pfam profile PF01798: Putative snoRNA binding domain
356591	1	258	12	21	1948	1	2	At1g60170	4,00E-42	68414.m06778 pre-mRNA processing ribonucleoprotein binding region-containing protein similar to U4/U6 snRNP-associated 61 kDa protein [Homo sapiens] GI:18249847; contains Pfam profile PF01798: Putative snoRNA binding domain
356833	1	258	12	21	1948	1	2	At1g60170	2,00E-29	68414.m06778 pre-mRNA processing ribonucleoprotein binding region-containing protein similar to U4/U6 snRNP-associated 61 kDa protein [Homo sapiens] GI:18249847; contains Pfam profile PF01798: Putative snoRNA binding domain
353178	2	258	12	21	3938	2	1	At5g56280	2,00E-45	68418.m07024 COP9 signalosome subunit 6 / CSN subunit 6 (CSN6A) identical to CSN complex subunit 6A [Arabidopsis thaliana] GI:18056665, COP9 complex subunit 6 [Arabidopsis thaliana] GI:15809663; contains Pfam profile PF01398: Mov34/MPN/PAD-1 family; identical to cDNA CSN complex subunit 6A (CSN6A) GI:18056664

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354957	1	258	12	21	3938	2	1	At4g26430	3,00E-32	68417.m03803 COP9 signalosome subunit 6 / CSN subunit 6 (CSN6B) identical to COP9 signalosome subunit 6 [Arabidopsis thaliana] GI:17940314, CSN complex subunit 6B [Arabidopsis thaliana] GI:18056667; contains Pfam profile PF01398: Mov34/MPN/PAD-1 family; supporting cDNA gi|17940313|gb|AF434762.1|AF434762; identical to cDNA CSN complex subunit 6B (CSN6B) GI:18056666
358781	1	258	12	21	4913	1	1	At2g39990	2,00E-36	68415.m04914 eukaryotic translation initiation factor 3 subunit 5 / eIF-3 epsilon / eIF3f (TIF3F1) identical to SP|O04202 Eukaryotic translation initiation factor 3 subunit 5 (eIF-3 epsilon) (eIF3 p32 subunit) (eIF3f) {Arabidopsis thaliana}; contains Pfam profile PF01398: Mov34/MPN/PAD-1 family
359720	1	258	12	21	4913	1	1	At2g39990	2,00E-06	68415.m04914 eukaryotic translation initiation factor 3 subunit 5 / eIF-3 epsilon / eIF3f (TIF3F1) identical to SP|O04202 Eukaryotic translation initiation factor 3 subunit 5 (eIF-3 epsilon) (eIF3 p32 subunit) (eIF3f) {Arabidopsis thaliana}; contains Pfam profile PF01398: Mov34/MPN/PAD-1 family
353561	3	258	12	21	5009	2	1	At5g05780	1,00E-141	68418.m00636 26S proteasome non-ATPase regulatory subunit 7, putative / 26S proteasome regulatory subunit S12, putative / MOV34 protein, putative contains similarity to 26s proteasome regulatory subunit s12 (proteasome subunit p40) (mov34 protein) SP:P26516 from [Mus musculus]; contains Pfam profile PF01398: Mov34/MPN/PAD-1 family
357373	1	258	12	21	5009	2	1	At5g05780	4,00E-71	68418.m00636 26S proteasome non-ATPase regulatory subunit 7, putative / 26S proteasome regulatory subunit S12, putative / MOV34 protein, putative contains similarity to 26s proteasome regulatory subunit s12 (proteasome subunit p40) (mov34 protein) SP:P26516 from [Mus musculus]; contains Pfam profile PF01398: Mov34/MPN/PAD-1 family
355492	1	259	1	32	5153	1	2	At5g24090	4,00E-49	68418.m02829 acidic endochitinase (CHIB1) identical to SP|P19172 Acidic endochitinase precursor (EC 3.2.1.14) {Arabidopsis thaliana}
359647	1	261	25	7	4891	1	1	At3g62200	2,00E-28	68416.m06988 expressed protein contains Pfam profile PF04396: Protein of unknown function, DUF537
356135	1	262	16	16	820	2	1	At5g20950	6,00E-47	68418.m02490 glycosyl hydrolase family 3 protein beta-D-glucan exohydrolase, Nicotiana tabacum, EMBL:AB017502

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
358920	1	262	16	16	820	2	1	At5g20950	5,00E-47	68418.m02490 glycosyl hydrolase family 3 protein beta-D-glucan exohydrolase, Nicotiana tabacum, EMBL:AB017502
353810	5	262	16	16	833	2	1	At5g64570	3,00E-111	68418.m08115 glycosyl hydrolase family 3 protein
358881	1	262	16	16	833	2	1	At5g64570	4,00E-70	68418.m08115 glycosyl hydrolase family 3 protein
354902	1	262	16	16	863	1	3	At1g78060	3,00E-47	68414.m09096 glycosyl hydrolase family 3 protein similar to xylosidase GI:2102655 from [Aspergillus niger]
355106	1	262	16	16	863	1	3	At1g78060	1,00E-33	68414.m09096 glycosyl hydrolase family 3 protein similar to xylosidase GI:2102655 from [Aspergillus niger]
359453	1	262	16	16				At5g04885	1,00E-58	68418.m00512 glycosyl hydrolase family 3 protein contains Pfam profiles PF00933: Glycosyl hydrolase family 3 N terminal domain, PF01915: Glycosyl hydrolase family 3 C terminal domain
353352	2	263	17	15	260	2	1	At3g57880	2,00E-109	68416.m06452 C2 domain-containing protein contains INTERPRO:IPR000008 C2 domain
357267	1	263	17	15	260	2	1	At3g57880	2,00E-35	68416.m06452 C2 domain-containing protein contains INTERPRO:IPR000008 C2 domain
353397	3	264	10	22	499	1	2	At1g78900	1,00E-125	68414.m09198 vacuolar ATP synthase catalytic subunit A / V-ATPase A subunit / vacuolar proton pump alpha subunit / V-ATPase 69 kDa subunit identical to SP|O23654 Vacuolar ATP synthase catalytic subunit A (EC 3.6.3.14) (V-ATPase A subunit) (Vacuolar proton pump alpha subunit) (V-ATPase 69 kDa subunit) {Arabidopsis thaliana}
355179	1	264	10	22	878	1	1	At4g38510	1,00E-29	68417.m05447 vacuolar ATP synthase subunit B, putative / V-ATPase B subunit, putative / vacuolar proton pump B subunit, putative / V-ATPase 57 kDa subunit, putative very strong similarity to SP|P11574 Vacuolar ATP synthase subunit B (EC 3.6.3.14) (V-ATPase B subunit) (Vacuolar proton pump B subunit) (V-ATPase 57 kDa subunit) {Arabidopsis thaliana}; contains Pfam profiles PF00006: ATP synthase alpha/beta family nucleotide-binding domain, PF00306: ATP synthase ab C terminal, PF02874: ATP synthase alpha/beta family beta-barrel domain

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
357315	1	264	10	22	878	1	1	At4g38510	2,00E-31	68417.m05447 vacuolar ATP synthase subunit B, putative / V-ATPase B subunit, putative / vacuolar proton pump B subunit, putative / V-ATPase 57 kDa subunit, putative very strong similarity to SP|P11574 Vacuolar ATP synthase subunit B (EC 3.6.3.14) (V-ATPase B subunit) (Vacuolar proton pump B subunit) (V-ATPase 57 kDa subunit) {Arabidopsis thaliana}; contains Pfam profiles PF00006: ATP synthase alpha/beta family nucleotide-binding domain, PF00306: ATP synthase ab C terminal, PF02874: ATP synthase alpha/beta family beta-barrel domain
360059	1	264	10	22	878	1	1	At4g38510	2,00E-19	68417.m05447 vacuolar ATP synthase subunit B, putative / V-ATPase B subunit, putative / vacuolar proton pump B subunit, putative / V-ATPase 57 kDa subunit, putative very strong similarity to SP|P11574 Vacuolar ATP synthase subunit B (EC 3.6.3.14) (V-ATPase B subunit) (Vacuolar proton pump B subunit) (V-ATPase 57 kDa subunit) {Arabidopsis thaliana}; contains Pfam profiles PF00006: ATP synthase alpha/beta family nucleotide-binding domain, PF00306: ATP synthase ab C terminal, PF02874: ATP synthase alpha/beta family beta-barrel domain
357443	1	264	10	22	954	3	2	At5g08690	1,00E-99	68418.m01034 ATP synthase beta chain 2, mitochondrial identical to SP|P83484 ATP synthase beta chain 2, mitochondrial precursor (EC 3.6.3.14) {Arabidopsis thaliana}; strong similarity to SP|P17614 ATP synthase beta chain, mitochondrial precursor (EC 3.6.3.14) {Nicotiana plumbaginifolia}; contains Pfam profiles PF00006: ATP synthase alpha/beta family nucleotide-binding domain, PF00306: ATP synthase ab C terminal, PF02874: ATP synthase alpha/beta family beta-barrel domain; supporting cDNA gi|26452187|dbj|AK118582.1|

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357848	1	264	10	22	954	3	2	At5g08690	2,00E-32	68418.m01034 ATP synthase beta chain 2, mitochondrial identical to SP|P83484 ATP synthase beta chain 2, mitochondrial precursor (EC 3.6.3.14) {Arabidopsis thaliana}; strong similarity to SP|P17614 ATP synthase beta chain, mitochondrial precursor (EC 3.6.3.14) {Nicotiana plumbaginifolia}; contains Pfam profiles PF00006: ATP synthase alpha/beta family nucleotide-binding domain, PF00306: ATP synthase ab C terminal, PF02874: ATP synthase alpha/beta family beta-barrel domain; supporting cDNA gi|26452187|dbj|AK118582.1|
357114	1	264	10	22	996	1	1	At2g07698	5,00E-06	68415.m00949 ATP synthase alpha chain, mitochondrial, putative very strong similarity to SP|P23413 ATP synthase alpha chain, mitochondrial (EC 3.6.3.14) {Brassica campestris}; contains Pfam profiles PF00006: ATP synthase alpha/beta family nucleotide-binding domain, PF00306: ATP synthase ab C terminal, PF02874: ATP synthase alpha/beta family beta-barrel domain
358091	1	264	10	22	996	1	1	At2g07698	2,00E-102	68415.m00949 ATP synthase alpha chain, mitochondrial, putative very strong similarity to SP|P23413 ATP synthase alpha chain, mitochondrial (EC 3.6.3.14) {Brassica campestris}; contains Pfam profiles PF00006: ATP synthase alpha/beta family nucleotide-binding domain, PF00306: ATP synthase ab C terminal, PF02874: ATP synthase alpha/beta family beta-barrel domain
358423	1	264	10	22	996	1	1	At2g07698	2,00E-73	68415.m00949 ATP synthase alpha chain, mitochondrial, putative very strong similarity to SP|P23413 ATP synthase alpha chain, mitochondrial (EC 3.6.3.14) {Brassica campestris}; contains Pfam profiles PF00006: ATP synthase alpha/beta family nucleotide-binding domain, PF00306: ATP synthase ab C terminal, PF02874: ATP synthase alpha/beta family beta-barrel domain

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
359809	1	264	10	22	996	1	1	At2g07698	2,00E-85	68415.m00949 ATP synthase alpha chain, mitochondrial, putative very strong similarity to SP|P23413 ATP synthase alpha chain, mitochondrial (EC 3.6.3.14) {Brassica campestris}; contains Pfam profiles PF00006: ATP synthase alpha/beta family nucleotide-binding domain, PF00306: ATP synthase ab C terminal, PF02874: ATP synthase alpha/beta family beta-barrel domain
353804	2	265	13	19	995	1	1	At2g24270	9,00E-64	68415.m02900 NADP-dependent glyceraldehyde-3-phosphate dehydrogenase, putative similar to NADP-dependent glyceraldehyde-3-phosphate dehydrogenase (NON-phosphorylating glyceraldehyde 3-phosphate; glyceraldehyde-3-phosphate dehydrogenase [NADP+]) [Nicotiana plumbaginifolia] SWISS-PROT:P93338
358849	1	265	13	19	1165	1	1	At1g23800	2,00E-94	68414.m03002 aldehyde dehydrogenase, mitochondrial (ALDH3) nearly identical to mitochondrial aldehyde dehydrogenase ALDH3 [Arabidopsis thaliana] gi|19850249|gb|AAL99612; contains Pfam profile PF00171: aldehyde dehydrogenase (NAD) family protein
353093	5	265	13	19	1202	2	1	At3g48170	3,00E-174	68416.m05254 betaine-aldehyde dehydrogenase, putative similar to betaine-aldehyde dehydrogenase, chloroplast precursor (BADH) [Arabidopsis thaliana] SWISS-PROT:Q9S795
359482	1	265	13	19	1202	2	1	At1g74920	2,00E-75	68414.m08691 betaine-aldehyde dehydrogenase, putative identical to betaine-aldehyde dehydrogenase, chloroplast precursor (BADH) [Arabidopsis thaliana] SWISS-PROT:Q9S795; strong similarity to betaine aldehyde dehydrogenase [Amaranthus hypochondriacus] GI:2388710
353903	2	265	13	19	1297	1	1	At2g14170	4,00E-64	68415.m01578 methylmalonate-semialdehyde dehydrogenase, putative similar to methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial precursor (MMSDH) [Rattus norvegicus] SWISS-PROT:Q02253

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
355092	1	265	13	19	1331	1	1	At1g79440	3,00E-39	68414.m09258 succinate-semialdehyde dehydrogenase (SSADH1) similar to succinate-semialdehyde dehydrogenase [NADP+] (SSDH) [Escherichia coli] SWISS-PROT:P25526; identical to succinic semialdehyde dehydrogenase mRNA, nuclear gene encoding mitochondrial protein GI:6684441; contains TIGRfam profile TIGR01780:succinic semialdehyde dehydrogenase; contains Pfam profile PF00171: aldehyde dehydrogenase (NAD) family protein
359072	1	265	13	19	1447	1	1	At1g54100	5,00E-30	68414.m06167 aldehyde dehydrogenase, putative / antiquitin, putative strong similarity to SP|Q41247 Aldehyde dehydrogenase family 7 member A1 (EC 1.2.1.3) (Antiquitin 1) (Brassica turgor-responsive/drought-induced gene 26 protein) (Btg-26) {Brassica napus}; similar to turgor-responsive protein 26G (aldehyde dehydrogenase family 7 member A1) [Pisum sativum] SWISS-PROT:P25795
353098	2	265	13	19	2613	1	2	At1g44170	5,00E-89	68414.m05102 aldehyde dehydrogenase, putative (ALDH) similar to aldehyde dehydrogenase ALDH [Craterostigma plantagineum] gi|17065918|emb|CAC84900
359761	1	265	13	19	2613	1	2	At1g44170	5,00E-63	68414.m05102 aldehyde dehydrogenase, putative (ALDH) similar to aldehyde dehydrogenase ALDH [Craterostigma plantagineum] gi|17065918|emb|CAC84900
356391	1	266	14	18	358	1	1	At2g07050	4,00E-33	68415.m00806 cycloartenol synthase (CAS1) / 2,3-epoxysqualene--cycloartenol cyclase / (S)-2,3-epoxysqualene mutase identical to cycloartenol synthase [SP:P38605 | GI:452446] [PMID:7505443]
353546	2	269	17	14	957	2	1	At5g19780	7,00E-108	68418.m02351 tubulin alpha-3/alpha-5 chain (TUA5) nearly identical to SP|P20363 Tubulin alpha-3/alpha-5 chain {Arabidopsis thaliana}
353891	2	269	17	14	957	2	1	At5g19780	7,00E-52	68418.m02351 tubulin alpha-3/alpha-5 chain (TUA5) nearly identical to SP|P20363 Tubulin alpha-3/alpha-5 chain {Arabidopsis thaliana}
354222	5	269	17	14	957	2	1	At5g19780	4,00E-97	68418.m02351 tubulin alpha-3/alpha-5 chain (TUA5) nearly identical to SP|P20363 Tubulin alpha-3/alpha-5 chain {Arabidopsis thaliana}
353184	5	269	17	14	978	3	1	At5g23860	4,00E-164	68418.m02801 tubulin beta-8 chain (TUB8) (TUBB8) identical to SP|P29516 Tubulin beta-8 chain {Arabidopsis thaliana}; supporting cDNA gi|15451225|gb|AY054693.1|

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
353428	17	269	17	14	978	3	1	At5g23860	0	68418.m02801 tubulin beta-8 chain (TUB8) (TUBB8) identical to SP|P29516 Tubulin beta-8 chain {Arabidopsis thaliana}; supporting cDNA gi|15451225|gb|AY054693.1|
354446	3	269	17	14	978	3	1	At5g23860	1,00E-142	68418.m02801 tubulin beta-8 chain (TUB8) (TUBB8) identical to SP|P29516 Tubulin beta-8 chain {Arabidopsis thaliana}; supporting cDNA gi|15451225|gb|AY054693.1|
357684	1	269	17	14	978	3	1	At5g23860	2,00E-59	68418.m02801 tubulin beta-8 chain (TUB8) (TUBB8) identical to SP|P29516 Tubulin beta-8 chain {Arabidopsis thaliana}; supporting cDNA gi|15451225|gb|AY054693.1|
358138	1	269	17	14	978	3	1	At5g23860	6,00E-65	68418.m02801 tubulin beta-8 chain (TUB8) (TUBB8) identical to SP|P29516 Tubulin beta-8 chain {Arabidopsis thaliana}; supporting cDNA gi|15451225|gb|AY054693.1|
359564	1	269	17	14	978	3	1	At5g23860	1,00E-75	68418.m02801 tubulin beta-8 chain (TUB8) (TUBB8) identical to SP|P29516 Tubulin beta-8 chain {Arabidopsis thaliana}; supporting cDNA gi|15451225|gb|AY054693.1|
359668	1	269	17	14	978	3	1	At5g62700	5,00E-130	68418.m07868 tubulin beta-2/beta-3 chain (TUB3) nearly identical to SP|P29512 Tubulin beta-2/beta-3 chain {Arabidopsis thaliana}
352907	3	269	17	14	1015	3	1	At4g14960	4,00E-26	68417.m02299 tubulin alpha-6 chain (TUA6) nearly identical to SP|P29511 Tubulin alpha-6 chain {Arabidopsis thaliana}
354281	9	269	17	14	1015	3	1	At4g14960	1,00E-170	68417.m02299 tubulin alpha-6 chain (TUA6) nearly identical to SP|P29511 Tubulin alpha-6 chain {Arabidopsis thaliana}
355964	1	269	17	14	1015	3	1	At4g14960	5,00E-24	68417.m02299 tubulin alpha-6 chain (TUA6) nearly identical to SP|P29511 Tubulin alpha-6 chain {Arabidopsis thaliana}
352952	3	269	17	14				At1g75780	2,00E-73	68414.m08801 tubulin beta-1 chain (TUB1) nearly identical to SP|P12411 Tubulin beta-1 chain {Arabidopsis thaliana}
353520	2	270	17	14	795	1	1	At3g60240	3,00E-25	68416.m06732 MIF4G domain-containing protein / MA3 domain-containing protein similar to eukaryotic protein synthesis initiation factor [Homo sapiens] GI:3941724; contains Pfam profiles PF02854: MIF4G domain, PF02847: MA3 domain
356799	1	270	17	14	795	1	1	At3g60240	7,00E-24	68416.m06732 MIF4G domain-containing protein / MA3 domain-containing protein similar to eukaryotic protein synthesis initiation factor [Homo sapiens] GI:3941724; contains Pfam profiles PF02854: MIF4G domain, PF02847: MA3 domain

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
357998	1	270	17	14	795	1	1	At3g60240	1,00E-23	68416.m06732 MIF4G domain-containing protein / MA3 domain-containing protein similar to eukaryotic protein synthesis initiation factor [Homo sapiens] GI:3941724; contains Pfam profiles PF02854: MIF4G domain, PF02847: MA3 domain
359956	1	270	17	14	4694	1	1	At3g12680	5,00E-16	68416.m01582 floral homeotic protein (HUA1) identical to floral homeotic protein HUA1 [Arabidopsis thaliana] gi|16797661|gb|AAK01470
359295	1	270	17	14	8921	1	1	At5g10810	4,00E-41	68418.m01256 enhancer of rudimentary protein, putative identical to enhancer of rudimentary homolog SP:Q96319 from [Arabidopsis thaliana]; contains Pfam profile: PF01133 enhancer of rudimentary
353864	3	272	16	15	8124	2	3	At3g14230	4,00E-34	68416.m01802 AP2 domain-containing protein RAP2.2 (RAP2.2) identical to AP2 domain containing protein RAP2.2 GI:2281629 from [Arabidopsis thaliana]
354023	2	272	16	15	8124	2	3	At3g14230	1,00E-45	68416.m01802 AP2 domain-containing protein RAP2.2 (RAP2.2) identical to AP2 domain containing protein RAP2.2 GI:2281629 from [Arabidopsis thaliana]
353429	3	272	16	15	8774	1	1	At1g50640	2,00E-16	68414.m05692 ethylene-responsive element-binding factor 3 (ERF3) identical to SP|O80339 Ethylene responsive element binding factor 3 (AtERF3) [Arabidopsis thaliana]
359530	1	274	16	15	7842	2	2	At4g24660	6,00E-24	68417.m03530 zinc finger homeobox family protein / ZF-HD homeobox family protein hypothetical protein T8K22.16, Arabidopsis thalianachromosome II BAC T8K22, PATX:G3184285
355022	1	275	14	17	6781	1	2	At2g45010	1,00E-51	68415.m05605 expressed protein weak similarity to PGPS/D12 [Petunia x hybrida] GI:4105794; contains Pfam profile PF04749: Protein of unknown function, DUF614
353662	3	277	13	18	1498	2	2	At3g27190	5,00E-119	68416.m03400 uracil phosphoribosyltransferase, putative / UMP pyrophosphorylase, putative / UPRTase, putative similar to SP|O65583 Uracil phosphoribosyltransferase (EC 2.4.2.9) (UMP pyrophosphorylase) (UPRTase) {Arabidopsis thaliana}; contains Pfam profile PF00485: Phosphoribulokinase / Uridine kinase family
359098	1	277	13	18	7755	2	1	At5g05140	1,00E-07	68418.m00545 transcription elongation factor-related low similarity to transcription elongation factor TFIIS.h [Mus musculus] GI:3288547, elongin A [Mus musculus] GI:6009624

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
353968	2	277	13	18	7874	1	1	At5g09850	5,00E-14	68418.m01139 transcription elongation factor-related low similarity to SP|P10712 Transcription elongation factor S-II (Transcription elongation factor A) {Mus musculus}
356023	1	277	13	18	7874	1	1	At5g09850	2,00E-12	68418.m01139 transcription elongation factor-related low similarity to SP|P10712 Transcription elongation factor S-II (Transcription elongation factor A) {Mus musculus}
357407	1	278	10	21	4004	3	2	At5g11420	3,00E-21	68418.m01333 expressed protein contains Pfam profile PF04862: Protein of unknown function, DUF642
353419	10	278	10	21	5591	3	2	At3g08030	3,00E-111	68416.m00981 expressed protein contains Pfam profile PF04862: Protein of unknown function, DUF642
357446	1	278	10	21	5591	3	2	At3g08030	2,00E-35	68416.m00981 expressed protein contains Pfam profile PF04862: Protein of unknown function, DUF642
359383	1	279	18	13	7350	6	1	At1g50830	4,00E-07	68414.m05716 hypothetical protein
353015	3	280	9	22	1679	3	3	At5g57580	2,00E-24	68418.m07194 calmodulin-binding protein similar to calmodulin-binding protein TCB60 GI:1698548 from [Nicotiana tabacum]
353173	2	282	6	24	3623	2	2	At2g28680	1,00E-53	68415.m03486 cupin family protein similar to legumin (11S-globulin) from Ginkgo biloba [GI:949869], 11S globulin from Avena sativa [GI:472867]; contains a 11-S plant seed storage protein signature (PS00305)
357294	1	287	8	22	213	1	1	At4g10710	3,00E-48	68417.m01751 transcriptional regulator-related similar to chromatin-specific transcription elongation factor FACT 140 kDa subunit (GI:5499741) [Homo sapiens]
357727	1	287	8	22	213	1	1	At4g10710	3,00E-82	68417.m01751 transcriptional regulator-related similar to chromatin-specific transcription elongation factor FACT 140 kDa subunit (GI:5499741) [Homo sapiens]
358875	1	288	13	17	2382	1	1	At3g01910	2,00E-31	68416.m00139 sulfite oxidase, putative similar to sulfite oxidase GB:3212610 SP|P07850 [Gallus gallus], Moco containing protein [Oryza sativa (japonica cultivar-group)] GI:22759584; contains Pfam profiles: PF00174: Oxidoreductase molybdopterin binding domain and PF03404: Mo-co oxidoreductase dimerisation domain
354149	2	288	13	17	2940	2	1	At3g61580	7,00E-18	68416.m06897 delta-8 sphingolipid desaturase (SLD1) identical to delta-8 sphingolipid desaturase GI:3819710 from [Arabidopsis thaliana]; contains Pfam profile PF00487: Fatty acid desaturase; contains Pfam profile PF00173: Heme/Steroid binding domain

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360011	1	288	13	17	2940	2	1	At3g61580	3,00E-19	68416.m06897 delta-8 sphingolipid desaturase (SLD1) identical to delta-8 sphingolipid desaturase GI:3819710 from [Arabidopsis thaliana]; contains Pfam profile PF00487: Fatty acid desaturase; contains Pfam profile PF00173: Heme/Steroid binding domain
357457	1	288	13	17	4334	1	2	At5g17770	3,00E-80	68418.m02084 NADH-cytochrome b5 reductase identical to NADH-cytochrome b5 reductase [Arabidopsis thaliana] GI:4240116
353650	2	288	13	17	7844	1	2	At2g32720	7,00E-23	68415.m04004 cytochrome b5, putative similar to Cytochrome B5 SP:P49098 from [Nicotiana tabacum]
353249	7	288	13	17				At5g53560	9,00E-53	68418.m06655 cytochrome b5 isoform 1 identical to SP|Q42342 Cytochrome b5 isoform 1 [Arabidopsis thaliana]
354892	1	288	13	17				At1g26340	2,00E-35	68414.m03212 cytochrome b5, putative similar to cytochrome b5 GB:BAA74839 GI:4240120 from [Arabidopsis thaliana]
359247	1	288	13	17				At5g53560	1,00E-40	68418.m06655 cytochrome b5 isoform 1 identical to SP|Q42342 Cytochrome b5 isoform 1 [Arabidopsis thaliana]
356377	1	289	24	6	10168	11	4	At4g31640	5,00E-09	68417.m04494 transcriptional factor B3 family protein low similarity to reproductive meristem gene 1 [Brassica oleracea var. botrytis] GI:3170424; contains Pfam profile PF02362: B3 DNA binding domain
354266	2	292	15	15	5921	3	2	At4g23630	4,00E-49	68417.m03403 reticulon family protein (RTNLB1) weak similarity to Nogo-C protein [Rattus norvegicus] GI:6822251; contains Pfam profile PF02453: Reticulon
352971	9	292	15	15	7023	1	2	At3g10260	5,00E-71	68416.m01230 reticulon family protein weak similarity to Nogo-C protein [Rattus norvegicus] GI:6822251; contains Pfam profile PF02453: Reticulon; identical to cDNA GI:32331854
353828	3	292	15	15				At1g64090	1,00E-73	68414.m07260 reticulon family protein (RTNLB3) weak similarity to SP|O95197 Reticulon protein 3 (Neuroendocrine-specific protein-like) {Homo sapiens}; contains Pfam profile PF02453: Reticulon
359368	1	292	15	15				At2g46170	5,00E-34	68415.m05741 reticulon family protein (RTNLB5) weak similarity to Nogo-C protein [Rattus norvegicus] GI:6822251; contains Pfam profile PF02453: Reticulon
353000	7	293	11	19	9623	7	11	At5g59320	5,00E-21	68418.m07433 lipid transfer protein 3 (LTP3) identical to lipid transfer protein 3 from Arabidopsis thaliana [gi:8571921]; contains Pfam protease inhibitor/seed storage/LTP family domain PF00234

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353728	3	293	11	19	9623	7	11	At5g59320	2,00E-21	68418.m07433 lipid transfer protein 3 (LTP3) identical to lipid transfer protein 3 from Arabidopsis thaliana [gi:8571921]; contains Pfam protease inhibitor/seed storage/LTP family domain PF00234
355101	1	294	9	21	6630	1	2	At4g08980	3,00E-37	68417.m01481 F-box family protein (FBW2) contains similarity to N7 protein GI:3273101 from [Medicago truncatula]
353091	2	297	9	20	1790	1	1	At2g38110	5,00E-72	68415.m04678 phospholipid/glycerol acyltransferase family protein low similarity to SP|O87707 CicA protein {Caulobacter crescentus}; contains Pfam profile PF01553: Acyltransferase
353665	3	298	14	15	943	1	1	At1g66340	4,00E-43	68414.m07534 ethylene receptor 1 (ETR1) identical to GB:P49333 from [Arabidopsis thaliana] (Science 262 (5133), 539-544 (1993))
359357	1	298	14	15	2089	1	2	At3g04580	9,00E-34	68416.m00487 ethylene receptor, putative (EIN4) similar to ethylene receptor GB:AAC31123 [Malus domestica], identical to putative ethylene receptor GB:AAD02485 [Arabidopsis thaliana]; Pfam HMM hit: response regulator receiver domain, signal C terminal domain
358145	1	298	14	15				At5g35750	5,00E-51	68418.m04281 histidine kinase (AHK2) identical to histidine kinase AHK2 [Arabidopsis thaliana] gi|13537196|dbj|BAB40774
359473	1	298	14	15				At5g35750	2,00E-10	68418.m04281 histidine kinase (AHK2) identical to histidine kinase AHK2 [Arabidopsis thaliana] gi|13537196|dbj|BAB40774
356964	1	300	28	1	9037	3	1	At4g04780	1,00E-40	68417.m00700 expressed protein very low similarity to SP|Q13503 RNA polymerase II holoenzyme component SRB7 (RNAPII complex component SRB7) {Homo sapiens}
357528	1	300	28	1	9037	3	1	At4g04780	1,00E-16	68417.m00700 expressed protein very low similarity to SP|Q13503 RNA polymerase II holoenzyme component SRB7 (RNAPII complex component SRB7) {Homo sapiens}
358466	1	300	28	1	9037	3	1	At4g04780	4,00E-34	68417.m00700 expressed protein very low similarity to SP|Q13503 RNA polymerase II holoenzyme component SRB7 (RNAPII complex component SRB7) {Homo sapiens}
355168	1	301	20	9	9375	6	3	At5g62360	8,00E-08	68418.m07827 invertase/pectin methylesterase inhibitor family protein similar to pectinesterase from Arabidosis thaliana SP|Q42534, Lycopersicon esculentum SP|Q43143; contains Pfam profile PF04043: Plant invertase/pectin methylesterase inhibitor

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358401	1	301	20	9	9375	6	3	At5g62360	2,00E-32	68418.m07827 invertase/pectin methylesterase inhibitor family protein similar to pectinesterase from Arabidosis thaliana SP|Q42534, Lycopersicon esculentum SP|Q43143; contains Pfam profile PF04043: Plant invertase/pectin methylesterase inhibitor
355830	1	301	20	9				At5g20740	8,00E-14	68418.m02465 invertase/pectin methylesterase inhibitor family protein low similarity to pectinesterase from Arabidopsis thaliana SP|Q42534, Lycopersicon esculentum SP|Q43143; contains Pfam profile PF04043: Plant invertase/pectin methylesterase inhibitor
355602	1	305	9	20	591	2	1	At3g27020	7,00E-57	68416.m03380 oligopeptide transporter OPT family protein similar to iron-phytosiderophore transporter protein yellow stripe 1 [Zea mays] GI:10770865; contains Pfam profile PF03169: OPT oligopeptide transporter protein
354743	1	306	12	17	250	1	1	At3g16785	1,00E-21	68416.m02143 phospholipase D zeta1 / PLDzeta1 (PLDP1) identical to phospholipase D zeta1 [Arabidopsis thaliana] GI:15723315, SP|Q9LRZ5 Phospholipase D p1 (EC 3.1.4.4) (AtPLDp1) (Phospholipase D1 PHOX and PX containing domain) (Phospholipase D zeta 1) (PLDzeta1) {Arabidopsis thaliana}; supported by cDNA gi:15723314; non-consensus splice site (GC) at the beginning of first intron.
353409	3	306	12	17	268	2	2	At3g15730	3,00E-153	68416.m01993 phospholipase D alpha 1 / PLD alpha 1 (PLDALPHA1) (PLD1) / choline phosphatase 1 identical to SP:Q38882 Phospholipase D alpha 1 (EC 3.1.4.4) (AtPLDalpha1) (PLD alpha 1) (Choline phosphatase 1) (Phosphatidylcholine-hydrolyzing phospholipase D 1) (PLDalpha) [Arabidopsis thaliana]
359335	1	306	12	17	268	2	2	At1g52570	2,00E-83	68414.m05935 phospholipase D alpha 2 / PLD alpha 2 (PLDALPHA2) (PLD2) / choline phosphatase 2 identical to phospholipase D alpha 2 (PLD alpha 2) SP:Q9SSQ9 from [Arabidopsis thaliana]
352959	8	310	14	14	1030	4	3	At5g60390	1,00E-122	68418.m07574 elongation factor 1-alpha / EF-1-alpha identical to SWISS-PROT:P13905 elongation factor 1-alpha (EF-1-alpha) [Arabidopsis thaliana]
353245	4	310	14	14	1030	4	3	At5g60390	1,00E-125	68418.m07574 elongation factor 1-alpha / EF-1-alpha identical to SWISS-PROT:P13905 elongation factor 1-alpha (EF-1-alpha) [Arabidopsis thaliana]
354249	2	310	14	14	1030	4	3	At5g60390	2,00E-18	68418.m07574 elongation factor 1-alpha / EF-1-alpha identical to SWISS-PROT:P13905 elongation factor 1-alpha (EF-1-alpha) [Arabidopsis thaliana]

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354393	2	310	14	14	1030	4	3	At5g60390	5,00E-103	68418.m07574 elongation factor 1-alpha / EF-1-alpha identical to SWISS-PROT:P13905 elongation factor 1-alpha (EF-1-alpha) [Arabidopsis thaliana]
356807	1	310	14	14	1030	4	3	At5g60390	7,00E-53	68418.m07574 elongation factor 1-alpha / EF-1-alpha identical to SWISS-PROT:P13905 elongation factor 1-alpha (EF-1-alpha) [Arabidopsis thaliana]
356878	1	310	14	14	1030	4	3	At5g60390	2,00E-91	68418.m07574 elongation factor 1-alpha / EF-1-alpha identical to SWISS-PROT:P13905 elongation factor 1-alpha (EF-1-alpha) [Arabidopsis thaliana]
359397	1	310	14	14	1030	4	3	At5g60390	2,00E-68	68418.m07574 elongation factor 1-alpha / EF-1-alpha identical to SWISS-PROT:P13905 elongation factor 1-alpha (EF-1-alpha) [Arabidopsis thaliana]
356851	1	310	14	14	1804	1	1	At4g20360	3,00E-50	68417.m02971 elongation factor Tu / EF-Tu (TUFA) identical to SWISS-PROT:P17745 elongation factor Tu, chloroplast precursor (EF-Tu) [Arabidopsis thaliana]
353910	2	310	14	14	1869	1	1	At1g18070	1,00E-13	68414.m02236 EF-1-alpha-related GTP-binding protein, putative similar to EF-1-alpha-related GTP-binding protein gi|1009232|gb|AAA79032
359467	1	310	14	14	1869	1	1	At1g18070	9,00E-65	68414.m02236 EF-1-alpha-related GTP-binding protein, putative similar to EF-1-alpha-related GTP-binding protein gi|1009232|gb|AAA79032
353222	4	310	14	14	1906	1	1	At4g02930	2,00E-104	68417.m00399 elongation factor Tu, putative / EF-Tu, putative similar to mitochondrial elongation factor Tu [Arabidopsis thaliana] gi|1149571|emb|CAA61511
352936	2	310	14	14	2082	1	2	At5g10630	8,00E-60	68418.m01231 elongation factor 1-alpha, putative / EF-1-alpha, putative contains similarity to SWISS-PROT:Q9YAV0 elongation factor 1-alpha (EF-1-alpha) [Aeropyrum pernix]
353031	3	310	14	14				At1g68310	1,00E-46	68414.m07803 expressed protein contains Pfam profile PF01883: Domain of unknown function
358042	1	310	14	14				At1g68310	7,00E-16	68414.m07803 expressed protein contains Pfam profile PF01883: Domain of unknown function
355412	1	312	14	14	2567	2	1	At1g05170	1,00E-58	68414.m00520 galactosyltransferase family protein
356639	1	312	14	14	2567	2	1	At1g05170	7,00E-79	68414.m00520 galactosyltransferase family protein
354432	2	312	14	14	3215	2	2	At1g77810	5,00E-131	68414.m09061 galactosyltransferase family protein contains Pfam profile PF01762: Galactosyltransferase
355521	1	312	14	14	4163	2	2	At2g25300	8,00E-43	68415.m03026 galactosyltransferase family protein contains Pfam profile: PF01762 galactosyltransferase
355633	1	312	14	14	4247	2	1	At1g53290	2,00E-21	68414.m06040 galactosyltransferase family protein contains Pfam profile: PF01762 galactosyltransferase ;contains similarity to Avr9 elicitor response protein GI:4138265 from [Nicotiana tabacum]

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
357316	1	312	14	14				At4g26940	8,00E-63	68417.m03877 galactosyltransferase family protein contains Pfam profile: PF01762 galactosyltransferase
353148	2	313	11	17	7659	6	9	At5g59910	7,00E-45	68418.m07513 histone H2B nearly identical to histone H2B Arabidopsis thaliana GI:2407802; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4
353313	2	313	11	17	7659	6	9	At2g28720	8,00E-45	68415.m03491 histone H2B, putative strong similarity to histone H2B Arabidopsis thaliana GI:2407802, Gossypium hirsutum SP|O22582; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4
353581	7	313	11	17	7659	6	9	At5g59910	2,00E-44	68418.m07513 histone H2B nearly identical to histone H2B Arabidopsis thaliana GI:2407802; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4
353724	2	313	11	17	7659	6	9	At2g28720	6,00E-40	68415.m03491 histone H2B, putative strong similarity to histone H2B Arabidopsis thaliana GI:2407802, Gossypium hirsutum SP|O22582; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4
353758	3	313	11	17	7659	6	9	At5g59910	3,00E-45	68418.m07513 histone H2B nearly identical to histone H2B Arabidopsis thaliana GI:2407802; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4
353929	6	313	11	17	7659	6	9	At2g28720	8,00E-47	68415.m03491 histone H2B, putative strong similarity to histone H2B Arabidopsis thaliana GI:2407802, Gossypium hirsutum SP|O22582; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4
354062	15	313	11	17	7659	6	9	At2g28720	1,00E-44	68415.m03491 histone H2B, putative strong similarity to histone H2B Arabidopsis thaliana GI:2407802, Gossypium hirsutum SP|O22582; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4
354419	2	313	11	17	7659	6	9	At2g28720	3,00E-40	68415.m03491 histone H2B, putative strong similarity to histone H2B Arabidopsis thaliana GI:2407802, Gossypium hirsutum SP|O22582; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4
356276	1	313	11	17	7659	6	9	At5g59910	3,00E-22	68418.m07513 histone H2B nearly identical to histone H2B Arabidopsis thaliana GI:2407802; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4
356713	1	313	11	17	7659	6	9	At2g28720	1,00E-14	68415.m03491 histone H2B, putative strong similarity to histone H2B Arabidopsis thaliana GI:2407802, Gossypium hirsutum SP|O22582; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
353321	4	314	14	14	4661	5	3	At2g36290	8,00E-100	68415.m04453 hydrolase, alpha/beta fold family protein low similarity to 2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoate hydrolase [Rhodococcus sp. RHA1] GI:8978311; contains Pfam profile PF00561: hydrolase, alpha/beta fold family
354371	5	314	14	14	4661	5	3	At1g74300	2,00E-73	68414.m08604 esterase/lipase/thioesterase family protein low similarity to 2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoate hydrolase [Rhodococcus sp. RHA1] GI:8978311; contains Interpro entry IPR000379
355043	1	314	14	14	4661	5	3	At3g48410	6,00E-21	68416.m05284 hydrolase, alpha/beta fold family protein low simiilarity to 2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoate hydrolase [Rhodococcus sp. RHA1] GI:8978311, SP|Q59695|ACOC_PSEPU Dihydrolipoamide acetyltransferase component of acetoin cleaving system (EC 2.3.1.12) (Acetoin dehydrogenase E2 component) {Pseudomonas putida}; contains Pfam profile PF00561: hydrolase, alpha/beta fold family
358560	1	314	14	14	4661	5	3	At3g48410	6,00E-10	68416.m05284 hydrolase, alpha/beta fold family protein low simiilarity to 2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoate hydrolase [Rhodococcus sp. RHA1] GI:8978311, SP|Q59695|ACOC_PSEPU Dihydrolipoamide acetyltransferase component of acetoin cleaving system (EC 2.3.1.12) (Acetoin dehydrogenase E2 component) {Pseudomonas putida}; contains Pfam profile PF00561: hydrolase, alpha/beta fold family
352913	6	315	13	15	7447	1	1	At5g02560	2,00E-39	68418.m00190 histone H2A, putative similar to histone H2A from Pisum sativum SP|P25470, Zea mays SP|P40280, Petroselinum crispum SP|P19177; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4
353510	5	315	13	15	7447	1	1	At5g02560	2,00E-37	68418.m00190 histone H2A, putative similar to histone H2A from Pisum sativum SP|P25470, Zea mays SP|P40280, Petroselinum crispum SP|P19177; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4
353868	2	315	13	15	7447	1	1	At5g02560	1,00E-37	68418.m00190 histone H2A, putative similar to histone H2A from Pisum sativum SP|P25470, Zea mays SP|P40280, Petroselinum crispum SP|P19177; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4
354220	6	315	13	15	7447	1	1	At5g02560	3,00E-38	68418.m00190 histone H2A, putative similar to histone H2A from Pisum sativum SP|P25470, Zea mays SP|P40280, Petroselinum crispum SP|P19177; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
357847	1	315	13	15	7447	1	1	At5g02560	1,00E-14	68418.m00190 histone H2A, putative similar to histone H2A from Pisum sativum SP|P25470, Zea mays SP|P40280, Petroselinum crispum SP|P19177; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4
358963	1	315	13	15	7447	1	1	At5g02560	8,00E-16	68418.m00190 histone H2A, putative similar to histone H2A from Pisum sativum SP|P25470, Zea mays SP|P40280, Petroselinum crispum SP|P19177; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4
357095	1	315	13	15	7689	2	2	At1g54690	9,00E-45	68414.m06235 histone H2A, putative strong similarity to histone H2A GI:3204129 SP|O65759 from Cicer arietinum, Picea abies SP|P35063; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4
357505	1	315	13	15	7689	2	2	At1g54690	4,00E-41	68414.m06235 histone H2A, putative strong similarity to histone H2A GI:3204129 SP|O65759 from Cicer arietinum, Picea abies SP|P35063; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4
354238	2	315	13	15	7719	4	2	At5g54640	8,00E-39	68418.m06803 histone H2A identical to histone H2A Arabidopsis thaliana GI:7595337
357121	1	315	13	15	7719	4	2	At1g51060	4,00E-14	68414.m05740 histone H2A, putative similar to histone H2A GI:7595337 from Arabidopsis thaliana, Triticum aestivum GI:536892, Picea abies SP|P35063; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4
353622	10	315	13	15				At5g59870	2,00E-33	68418.m07507 histone H2A, putative similar to histone H2A Petroselinum crispum SP|P19177, Lycopersicon esculentum SP|P25469, Zea mays SP|P40280; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4
353848	4	315	13	15				At1g52740	1,00E-61	68414.m05962 histone H2A, putative similar to histone H2A.F/Z Arabidopsis thaliana GI:2407800; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4
357195	1	316	7	21	8903	2	2	At1g56580	1,00E-30	68414.m06507 expressed protein contains Pfam profile PF04398: Protein of unknown function, DUF538
359240	1	316	7	21	8903	2	2	At1g09310	6,00E-35	68414.m01042 expressed protein contains Pfam profile PF04398: Protein of unknown function, DUF538
358114	1	318	14	14	581	1	1	At1g53140	2,00E-23	68414.m06017 dynamin family protein low similarity to dynamin-like protein E [Arabidopsis thaliana] GI:19423872; contains Pfam profile PF00350: Dynamin family

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
359234	1	318	14	14	693	1	2	At3g61760	3,00E-68	68416.m06927 dynamin-like protein B (DL1B) identical to dynamin-like protein B [Arabidopsis thaliana] GI:27543504; strong similarity to GTP-binding protein [Arabidopsis thaliana] GI:807577, phragmoplastin SDL5A [Glycine max] GI:1218004; contains Pfam profiles PF01031: Dynamin central region, PF00350: Dynamin family, PF02212: Dynamin GTPase effector domain
353439	2	318	14	14	704	1	1	At3g60190	8,00E-140	68416.m06724 dynamin-like protein E (DL1E) nearly identical to dynamin-like protein E [Arabidopsis thaliana] GI:19423872; contains Pfam profiles PF01031: Dynamin central region, PF00350: Dynamin family, PF02212: Dynamin GTPase effector domain
359692	1	318	14	14	704	1	1	At3g60190	6,00E-10	68416.m06724 dynamin-like protein E (DL1E) nearly identical to dynamin-like protein E [Arabidopsis thaliana] GI:19423872; contains Pfam profiles PF01031: Dynamin central region, PF00350: Dynamin family, PF02212: Dynamin GTPase effector domain
355770	1	319	13	15	5479	2	3	At4g34610	1,00E-39	68417.m04916 homeodomain-containing protein similaritry to homeotic protein BEL1, Arabidopsis thaliana, PIR2:A57632
354698	1	325	14	13	6800	1	1	At5g53160	4,00E-55	68418.m06609 expressed protein similar to unknown protein (pir||T02893)
354727	1	325	14	13	7890	2	3	At2g38310	1,00E-08	68415.m04707 expressed protein low similarity to early flowering protein 1 [Asparagus officinalis] GI:1572683, SP|P80889 Ribonuclease 1 (EC 3.1.-.-) {Panax ginseng}
355417	1	328	5	22	6945	3	3	At3g04400	7,00E-76	68416.m00466 60S ribosomal protein L23 (RPL23C) similar to ribosomal protein L17 GB:AAA34113.1 from [Nicotiana tabacum]
358073	1	328	5	22	6945	3	3	At3g04400	2,00E-38	68416.m00466 60S ribosomal protein L23 (RPL23C) similar to ribosomal protein L17 GB:AAA34113.1 from [Nicotiana tabacum]
353447	2	330	16	11	2834	1	2	At5g03300	2,00E-72	68418.m00281 adenosine kinase 2 (ADK2) contains Pfam profile: PF00294 pfkB family carbohydrate kinase; identical to cDNA adenosine kinase 2 (ADK2) GI:12017763
359446	1	330	16	11	2834	1	2	At5g03300	3,00E-44	68418.m00281 adenosine kinase 2 (ADK2) contains Pfam profile: PF00294 pfkB family carbohydrate kinase; identical to cDNA adenosine kinase 2 (ADK2) GI:12017763

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
359091	1	330	16	11	3320	1	1	At4g27600	2,00E-60	68417.m03966 pfkB-type carbohydrate kinase family protein contains Pfam profile: PF00294 pfkB family carbohydrate kinase
353095	2	330	16	11	3914	1	1	At4g10260	4,00E-58	68417.m01684 pfkB-type carbohydrate kinase family protein contains Pfam profile: PF00294 pfkB family carbohydrate kinase
356548	1	330	16	11	4055	4	1	At1g06030	9,00E-37	68414.m00631 pfkB-type carbohydrate kinase family protein contains Pfam profile: PF00294 pfkB family carbohydrate kinase
359442	1	331	10	17	980	1	1	At4g34200	8,00E-63	68417.m04854 D-3-phosphoglycerate dehydrogenase, putative / 3-PGDH, putative similar to phosphoglycerate dehydrogenase, Arabidopsis thaliana, SP:O04130
353462	2	331	10	17	2673	1	2	At5g14780	6,00E-98	68418.m01734 formate dehydrogenase (FDH) identical to GI:7677266
358891	1	331	10	17	5095	1	1	At1g79870	9,00E-54	68414.m09330 oxidoreductase family protein contains Pfam profile: PF02826 D-isomer specific 2-hydroxyacid dehydrogenase, NAD binding domain; similar to glyoxylate reductase from Thermococcus litoralis [gi:13515409]
353043	2	337	10	17	5093	2	1	At5g55990	6,00E-110	68418.m06986 calcineurin B-like protein 2 (CBL2) identical to calcineurin B-like protein 2 GI:3309084 from [Arabidopsis thaliana]
356653	1	337	10	17	7169	2	1	At4g17615	9,00E-54	68417.m02635 calcineurin B-like protein 1 (CBL1) identical to calcineurin B-like protein 1 (GI:3309082) [Arabidopsis thaliana]
353895	2	340	14	12	2826	1	2	At5g02010	2,00E-69	68418.m00120 expressed protein contains Pfam profile PF03759: Domain of unknown function (DUF315)
356768	1	340	14	12	2826	1	2	At5g02010	9,00E-62	68418.m00120 expressed protein contains Pfam profile PF03759: Domain of unknown function (DUF315)
352901	2	340	14	12	5735	1	1	At1g31650	7,00E-81	68414.m03886 expressed protein contains Pfam profile PF03759: Domain of unknown function (DUF315)
355240	1	340	14	12	5735	1	1	At1g31650	3,00E-19	68414.m03886 expressed protein contains Pfam profile PF03759: Domain of unknown function (DUF315)
359616	1	340	14	12	5735	1	1	At1g31650	5,00E-06	68414.m03886 expressed protein contains Pfam profile PF03759: Domain of unknown function (DUF315)
357881	1	341	13	13	5906	2	1	At5g52040	2,00E-63	68418.m06459 arginine/serine-rich splicing factor RSP41 (RSP41) nearly identical to SP|P92966 Arginine/serine-rich splicing factor RSP41 {Arabidopsis thaliana}
354152	3	341	13	13	6533	1	1	At3g61860	9,00E-78	68416.m06947 arginine/serine-rich splicing factor RSP31 (RSP31) identical to SP|P92964 Arginine/serine-rich splicing factor RSP31 {Arabidopsis thaliana}

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
357081	1	341	13	13	7403	2	2	At2g24590	6,00E-10	68415.m02936 splicing factor, putative similar to to RSZp22 protein [Arabidopsis thaliana] gi|2582645|emb|CAA05352
356456	1	341	13	13				At3g49430	2,00E-54	68416.m05403 pre-mRNA splicing factor, putative strong similarity to SP|O22315 Pre-mRNA splicing factor SF2 (SR1 protein) {Arabidopsis thaliana}
352970	2	342	13	13	535	1	1	At5g22010	5,00E-87	68418.m02561 AAA-type ATPase family protein / BRCT domain-containing protein contains Pfam profiles: PF00533 BRCA1 C Terminus (BRCT) domain, PF00004 ATPase family associated with various cellular activities (AAA)
355679	1	342	13	13	1548	2	2	At2g02480	7,00E-22	68415.m00187 DNA polymerase-related weak similarity to DNA polymerase III holoenzyme tau subunit [Thermus thermophilus] GI:2583049
355661	1	342	13	13	1653	2	2	At4g18820	8,00E-69	68417.m02778 expressed protein
358041	1	342	13	13	1653	2	2	At4g18820	8,00E-14	68417.m02778 expressed protein
358709	1	342	13	13	1653	2	2	At4g18820	1,00E-12	68417.m02778 expressed protein
355245	1	342	13	13	2309	1	1	At1g04730	2,00E-11	68414.m00469 AAA-type ATPase family protein contains Pfam domain, PF00004: ATPase, AAA family ('A'TPases 'A'ssociated with diverse cellular 'A'ctivities)
357428	1	342	13	13	2309	1	1	At1g04730	5,00E-25	68414.m00469 AAA-type ATPase family protein contains Pfam domain, PF00004: ATPase, AAA family ('A'TPases 'A'ssociated with diverse cellular 'A'ctivities)
358620	1	342	13	13	2822	1	1	At5g27740	3,00E-86	68418.m03327 expressed protein
355084	1	342	13	13	2956	1	1	At1g63160	7,00E-15	68414.m07138 replication factor C 40 kDa, putative similar to SWISS-PROT:Q9WUK4 activator 1 40 kDa subunit (Replication factor C 40 kDa subunit, A1 40 kDa subunit, RF-C 40 kDa subunit, RFC40) [Mus musculus]
357995	1	342	13	13	2956	1	1	At1g63160	6,00E-73	68414.m07138 replication factor C 40 kDa, putative similar to SWISS-PROT:Q9WUK4 activator 1 40 kDa subunit (Replication factor C 40 kDa subunit, A1 40 kDa subunit, RF-C 40 kDa subunit, RFC40) [Mus musculus]
355012	1	342	13	13	3559	1	1	At1g21690	3,00E-10	68414.m02715 replication factor C 37 kDa, putative Similar to SWISS-PROT:P35249 activator 1 37 kDa subunit (Replication factor C 37 kDa subunit, A1 37 kDa subunit, RF-C 37 kDa subunit, RFC37) [Homo sapiens]; contains Pfam domain, PF00004: ATPase, AAA family
356236	1	344	16	10	1424	1	2	At3g18660	8,00E-62	68416.m02370 glycogenin glucosyltransferase (glycogenin)-related low similarity to glycogenin-1 from Homo sapiens [SP|P46976], Oryctolagus cuniculus [SP|P13280]

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
359481	1	345	12	14	214	1	1	At5g04930	1,00E-44	68418.m00521 phospholipid-transporting ATPase 1 / aminophospholipid flippase 1 / magnesium-ATPase 1 (ALA1) nearly identical to SP|P98204 Phospholipid-transporting ATPase 1 (EC 3.6.3.1) (Aminophospholipid flippase 1) {Arabidopsis thaliana}; contains InterPro accession IPR005834: Haloacid dehalogenase-like hydrolase
356602	1	346	25	1	10364	7	1	At1g24020	2,00E-18	68414.m03032 Bet v I allergen family protein similar to major pollen allergen Bet v 1 GB:CAA96544 GI:1321726 from [Betula pendula]; contains Pfam profile PF00407: Pathogenesis-related protein Bet v I family
360032	1	347	12	14	4380	1	2	At2g27020	7,00E-99	68415.m03244 20S proteasome alpha subunit G (PAG1) (PRC8) identical to proteasome subunit alpha type 3 SP:O23715, GI:12644056 from [Arabidopsis thaliana]; identical to cDNA proteasome subunit prc8 GI:2511591
353949	4	347	12	14	4649	2	1	At2g05840	4,00E-125	68415.m00632 20S proteasome alpha subunit A2 (PAA2) identical to GB:AF043519
353106	5	347	12	14	4786	2	2	At1g16470	5,00E-112	68414.m01970 20S proteasome alpha subunit B (PAB1) (PRC3) identical to proteasome subunit alpha type 2 SP:O23708, GI:6093778; identical to cDNA proteasome subunit prc3 GI:2511573
353128	2	347	12	14	4864	1	3	At3g22110	9,00E-66	68416.m02791 20S proteasome alpha subunit C (PAC1) (PRC9) identical to GB:AAC32057 from [Arabidopsis thaliana] (Genetics (1998) 149 (2), 677-692); identical to cDNA proteasome subunit prc9 GI:2511583
353747	2	347	12	14	4864	1	3	At3g22110	2,00E-95	68416.m02791 20S proteasome alpha subunit C (PAC1) (PRC9) identical to GB:AAC32057 from [Arabidopsis thaliana] (Genetics (1998) 149 (2), 677-692); identical to cDNA proteasome subunit prc9 GI:2511583
354751	1	347	12	14	4864	1	3	At3g22110	2,00E-55	68416.m02791 20S proteasome alpha subunit C (PAC1) (PRC9) identical to GB:AAC32057 from [Arabidopsis thaliana] (Genetics (1998) 149 (2), 677-692); identical to cDNA proteasome subunit prc9 GI:2511583
352974	2	347	12	14	5368	2	1	At5g42790	5,00E-114	68418.m05212 20S proteasome alpha subunit F1 (PAF1) (gb|AAC32062.1)
354185	2	347	12	14	7454	2	1	At3g14290	1,00E-59	68416.m01808 20S proteasome alpha subunit E2 (PAE2) identical to 20S proteasome subunit PAE2 GB:AAC32061 from [Arabidopsis thaliana]
354230	3	347	12	14	7454	2	1	At3g14290	3,00E-66	68416.m01808 20S proteasome alpha subunit E2 (PAE2) identical to 20S proteasome subunit PAE2 GB:AAC32061 from [Arabidopsis thaliana]

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
355924	1	347	12	14	7454	2	1	At1g53850	2,00E-21	68414.m06129 20S proteasome alpha subunit E1 (PAE1) identical to 20S proteasome subunit PAE1 GI:3421087 from [Arabidopsis thaliana]
355380	1	348	11	15				At5g66980	2,00E-06	68418.m08444 transcriptional factor B3 family protein contains Pfam profile PF02362: B3 DNA binding domain
359226	1	348	11	15				At5g66980	1,00E-13	68418.m08444 transcriptional factor B3 family protein contains Pfam profile PF02362: B3 DNA binding domain
355996	1	349	14	12	4170	9	1	At3g03080	2,00E-37	68416.m00304 NADP-dependent oxidoreductase, putative similar to probable NADP-dependent oxidoreductase (zeta-crystallin homolog) P2 [SP|Q39173][gi:886430], Arabidopsis thaliana; similar to allyl alcohol dehydrogenase [Nicotiana tabacum] GI:6692816
353666	3	350	13	13	9955	2	2	At1g48750	2,00E-14	68414.m05455 protease inhibitor/seed storage/lipid transfer protein (LTP) family protein similar to TED4 [Zinnia elegans] GI:493721; contains Pfam protease inhibitor/seed storage/LTP family domain PF00234
354081	2	350	13	13	10062	3	6	At5g38170	3,00E-11	68418.m04600 protease inhibitor/seed storage/lipid transfer protein (LTP) family protein contains Pfam profile: PF00234 protease inhibitor/seed storage/LTP family
357253	1	350	13	13				At1g73780	1,00E-10	68414.m08542 protease inhibitor/seed storage/lipid transfer protein (LTP) family protein contains Pfam profile: PF00234 protease inhibitor/seed storage/LTP family
353807	3	355	10	15				At4g02280	6,00E-66	68417.m00309 sucrose synthase, putative / sucrose-UDP glucosyltransferase, putative strong similarity to sucrose synthase GI:6682841 from [Citrus unshiu]
353878	2	355	10	15				At4g02280	7,00E-36	68417.m00309 sucrose synthase, putative / sucrose-UDP glucosyltransferase, putative strong similarity to sucrose synthase GI:6682841 from [Citrus unshiu]
354361	2	355	10	15				At5g49190	1,00E-89	68418.m06088 sucrose synthase / sucrose-UDP glucosyltransferase (SUS2) nearly identical to SP|Q00917 Sucrose synthase (EC 2.4.1.13) (Sucrose-UDP glucosyltransferase) {Arabidopsis thaliana} (SUS2); contains Pfam profile: PF00862 sucrose synthase
354439	5	355	10	15				At4g02280	0	68417.m00309 sucrose synthase, putative / sucrose-UDP glucosyltransferase, putative strong similarity to sucrose synthase GI:6682841 from [Citrus unshiu]

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
354641	1	355	10	15				At4g02280	1,00E-41	68417.m00309 sucrose synthase, putative / sucrose-UDP glucosyltransferase, putative strong similarity to sucrose synthase GI:6682841 from [Citrus unshiu]
359143	1	355	10	15				At4g02280	5,00E-17	68417.m00309 sucrose synthase, putative / sucrose-UDP glucosyltransferase, putative strong similarity to sucrose synthase GI:6682841 from [Citrus unshiu]
355276	1	356	11	14	312	1	1	At1g68020	5,00E-45	68414.m07771 glycosyl transferase family 20 protein / trehalose-phosphatase family protein similar to SP|Q00764 Alpha,alpha-trehalose-phosphate synthase [UDP-forming] 56 kDa subunit (EC 2.4.1.15) (Trehalose-6-phosphate synthase) {Saccharomyces cerevisiae}; contains Pfam profile: PF02358 trehalose-phosphatase
357738	1	356	11	14	312	1	1	At1g68020	6,00E-51	68414.m07771 glycosyl transferase family 20 protein / trehalose-phosphatase family protein similar to SP|Q00764 Alpha,alpha-trehalose-phosphate synthase [UDP-forming] 56 kDa subunit (EC 2.4.1.15) (Trehalose-6-phosphate synthase) {Saccharomyces cerevisiae}; contains Pfam profile: PF02358 trehalose-phosphatase
359231	1	356	11	14	312	1	1	At1g68020	2,00E-43	68414.m07771 glycosyl transferase family 20 protein / trehalose-phosphatase family protein similar to SP|Q00764 Alpha,alpha-trehalose-phosphate synthase [UDP-forming] 56 kDa subunit (EC 2.4.1.15) (Trehalose-6-phosphate synthase) {Saccharomyces cerevisiae}; contains Pfam profile: PF02358 trehalose-phosphatase
354804	1	356	11	14	476	3	2	At1g23870	6,00E-76	68414.m03011 glycosyl transferase family 20 protein / trehalose-phosphatase family protein contains Pfam profile: PF02358 trehalose-phosphatase
357053	1	356	11	14				At4g17770	6,00E-31	68417.m02652 glycosyl transferase family 20 protein / trehalose-phosphatase family protein contains Pfam profile: PF02358 trehalose-phosphatase
353216	2	358	12	13	6724	2	1	At2g45140	1,00E-13	68415.m05618 vesicle-associated membrane protein, putative / VAMP, putative similar to VAP27 GI:6688926 [Nicotiana plumbaginifolia]
354772	1	358	12	13	6724	2	1	At2g45140	2,00E-58	68415.m05618 vesicle-associated membrane protein, putative / VAMP, putative similar to VAP27 GI:6688926 [Nicotiana plumbaginifolia]
356269	1	358	12	13	6724	2	1	At3g60600	1,00E-38	68416.m06781 vesicle-associated membrane protein, putative / VAMP, putative similar to VAP27 GI:6688926 [Nicotiana plumbaginifolia]

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
355302	1	359	7	18	999	2	1	At5g13110	5,00E-72	68418.m01502 glucose-6-phosphate 1-dehydrogenase, putative / G6PD, putative similar to SP|Q43839 Glucose-6-phosphate 1-dehydrogenase, chloroplast precursor (EC 1.1.1.49) (G6PD) {Solanum tuberosum}; contains Pfam profiles PF02781: Glucose-6-phosphate dehydrogenase C-terminal, PF00479: Glucose-6-phosphate dehydrogenase NAD binding domain
356847	1	359	7	18	1398	2	1	At5g40760	3,00E-68	68418.m04946 glucose-6-phosphate 1-dehydrogenase / G6PD (ACG12) idential to glucose-6-phosphate 1-dehydrogenase (acg12) [Arabidopsis thaliana] GI:5732197
357023	1	359	7	18	1398	2	1	At3g27300	1,00E-42	68416.m03412 glucose-6-phosphate 1-dehydrogenase / G6PD (ACG9) identical to glucose-6-phosphate 1-dehydrogenase (acg9) [Arabidopsis thaliana] GI:5732195
359205	1	359	7	18	1398	2	1	At5g40760	5,00E-56	68418.m04946 glucose-6-phosphate 1-dehydrogenase / G6PD (ACG12) idential to glucose-6-phosphate 1-dehydrogenase (acg12) [Arabidopsis thaliana] GI:5732197
354478	1	359	7	18	2069	1	1	At1g09420	5,00E-97	68414.m01054 glucose-6-phosphate 1-dehydrogenase, putative / G6PD, putative similar to SP|Q43839 Glucose-6-phosphate 1-dehydrogenase, chloroplast precursor (EC 1.1.1.49) (G6PD) {Solanum tuberosum}; contains Pfam profiles PF02781: Glucose-6-phosphate dehydrogenase C-terminal, PF00479: Glucose-6-phosphate dehydrogenase NAD binding domain; gc exon splice site at 20574 is based on protein alignment, and is not confirmed experimentally
357840	1	359	7	18				At5g35790	1,00E-21	68418.m04292 glucose-6-phosphate 1-dehydrogenase / G6PD (APG1) identical to SP|Q43727 Glucose-6-phosphate 1-dehydrogenase, cytoplasmic isoform (EC 1.1.1.49) (G6PD) {Arabidopsis thaliana}
353455	3	360	13	12	3622	2	2	At3g13460	7,00E-85	68416.m01694 expressed protein contains Pfam profile PF04146: YT521-B-like family
354279	2	360	13	12	3622	2	2	At1g55500	1,00E-35	68414.m06349 expressed protein contains Pfam profile PF04146: YT521-B-like family
355030	1	360	13	12	3622	2	2	At3g13460	2,00E-46	68416.m01694 expressed protein contains Pfam profile PF04146: YT521-B-like family
356275	1	360	13	12	3622	2	2	At3g13460	4,00E-13	68416.m01694 expressed protein contains Pfam profile PF04146: YT521-B-like family
358343	1	360	13	12	5567	2	1	At3g17330	6,00E-55	68416.m02215 expressed protein contains Pfam profile PF04146: YT521-B-like family

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
353540	2	360	13	12	6121	1	1	At1g79270	3,00E-53	68414.m09241 expressed protein contains Pfam profile PF04146: YT521-B-like family
353053	2	361	10	15	8224	1	2	At1g51200	3,00E-21	68414.m05759 zinc finger (AN1-like) family protein contains Pfam domains, PF01428: AN1-like Zinc finger and PF01754: A20-like zinc finger
353607	8	361	10	15	8224	1	2	At1g51200	1,00E-47	68414.m05759 zinc finger (AN1-like) family protein contains Pfam domains, PF01428: AN1-like Zinc finger and PF01754: A20-like zinc finger
357282	1	361	10	15	8224	1	2	At1g51200	1,00E-25	68414.m05759 zinc finger (AN1-like) family protein contains Pfam domains, PF01428: AN1-like Zinc finger and PF01754: A20-like zinc finger
353010	2	361	10	15				At4g12040	7,00E-11	68417.m01916 zinc finger (AN1-like) family protein contains Pfam domains, PF01428: AN1-like Zinc finger and PF01754: A20-like zinc finger
355079	1	362	13	12	5575	1	1	At4g33910	2,00E-55	68417.m04812 oxidoreductase, 2OG-Fe(II) oxygenase family protein similar to prolyl 4-hydroxylase, alpha subunit, from Gallus gallus [GI:212530], Rattus norvegicus [GI:474940], Drosophila melanogaster [GI:4336512]; contains PF03171 2OG-Fe(II) oxygenase superfamily domain
358820	1	362	13	12	5575	1	1	At4g33910	3,00E-65	68417.m04812 oxidoreductase, 2OG-Fe(II) oxygenase family protein similar to prolyl 4-hydroxylase, alpha subunit, from Gallus gallus [GI:212530], Rattus norvegicus [GI:474940], Drosophila melanogaster [GI:4336512]; contains PF03171 2OG-Fe(II) oxygenase superfamily domain
352987	2	364	9	16	641	1	1	At5g45380	3,00E-50	68418.m05577 sodium:solute symporter family protein contains Pfam profile: PF00474 sodium:solute symporter family
353349	2	364	9	16				At1g62990	2,00E-77	68414.m07113 homeodomain transcription factor (KNAT7) contains Pfam profiles: PF03789 ELK domain, PF03790 KNOX1 domain, PF03791 KNOX2 domain; similar to homeobox protein HD1 SP:P46606 from [Brassica napus]; identical to cDNA homeodomain transcription factor KNAT7 (KNAT7) GI:11878229
354722	1	364	9	16				At1g62990	2,00E-59	68414.m07113 homeodomain transcription factor (KNAT7) contains Pfam profiles: PF03789 ELK domain, PF03790 KNOX1 domain, PF03791 KNOX2 domain; similar to homeobox protein HD1 SP:P46606 from [Brassica napus]; identical to cDNA homeodomain transcription factor KNAT7 (KNAT7) GI:11878229

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
358055	1	366	14	11	3899	1	1	At3g44160	7,00E-89	68416.m04734 chloroplast outer membrane protein-related low similarity to chloroplastic outer envelope membrane protein (OEP75) [Pisum sativum] GI:633607
354012	3	367	14	11	877	2	1	At3g52990	3,00E-92	68416.m05841 pyruvate kinase, putative similar to pyruvate kinase, cytosolic isozyme [Glycine max] SWISS-PROT:Q42806
357915	1	367	14	11	877	2	1	At3g52990	1,00E-67	68416.m05841 pyruvate kinase, putative similar to pyruvate kinase, cytosolic isozyme [Glycine max] SWISS-PROT:Q42806
358008	1	367	14	11	877	2	1	At3g52990	3,00E-70	68416.m05841 pyruvate kinase, putative similar to pyruvate kinase, cytosolic isozyme [Glycine max] SWISS-PROT:Q42806
359764	1	367	14	11	877	2	1	At3g52990	3,00E-70	68416.m05841 pyruvate kinase, putative similar to pyruvate kinase, cytosolic isozyme [Glycine max] SWISS-PROT:Q42806
353907	2	367	14	11	1052	1	1	At5g52920	1,00E-88	68418.m06567 pyruvate kinase, putative similar to pyruvate kinase isozyme G, chloroplast precursor [Nicotiana tabacum] SWISS-PROT:Q40546
358374	1	368	13	12	9225	2	2	At5g08330	2,00E-08	68418.m00980 TCP family transcription factor, putative similar to PCF1 (GI:2580438) and PCF2 [(GI:2580440) Oryza sativa] ; auxin-induced basic helix-loop-helix transcription factor, Gossypium hirsutum, EMBL:AF165924
358718	1	369	8	17	9429	1	1	At1g79770	1,00E-18	68414.m09308 expressed protein
353999	4	370	9	16	7088	2	1	At2g22840	5,00E-19	68415.m02712 expressed protein identical to transcription activator GRL1 [Arabidopsis thaliana] GI:21539880 (unpublished); supporting cDNA gi|21539879|gb|AY102634.1|
353764	2	370	9	16	7860	1	2	At3g13960	6,00E-47	68416.m01762 expressed protein identical to transcription activator GRL5 [Arabidopsis thaliana] GI:21539888 (unpublished); supporting cDNA gi|21539887|gb|AY102638.1|
355747	1	370	9	16	8647	2	3	At3g52910	6,00E-23	68416.m05831 expressed protein nearly identical to transcription activator GRL4 [Arabidopsis thaliana] GI:21539886 (unpublished)
356657	1	374	11	13	23	1	1	At1g01040	1,00E-84	68414.m00004 DEAD/DEAH box helicase carpel factory / CAF identical to RNA helicase/RNaseIII CAF protein GB:AAF03534 GI:6102610 from [Arabidopsis thaliana]
358009	1	375	15	9				At4g25040	1,00E-15	68417.m03592 integral membrane family protein contains TIGRFAM TIGR01569 : plant integral membrane protein TIGR01569; contains Pfam PF04535 : Domain of unknown function (DUF588)

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
358047	1	379	14	10	8169	1	1	At4g28910	6,00E-10	68417.m04132 expressed protein
356941	1	380	16	8	4240	1	1	At2g34630	4,00E-65	68415.m04254 geranyl diphosphate synthase, putative / GPPS, putative / dimethylallyltransferase, putative / prenyl transferase, putative identical to GI:11322965 A. thaliana geranyl diphosphate synthase
354356	2	381	6	18	846	1	1	At3g45140	3,00E-116	68416.m04872 lipoxygenase (LOX2) identical to SP|P38418
359528	1	381	6	18				At1g67560	1,00E-63	68414.m07697 lipoxygenase family protein similar to 13-lipoxygenase GB:CAA65269 [Solanum tuberosum], gi:1654140 [Lycopersicon esculentum]
359468	1	383	12	12	10	2	2	At1g20960	2,00E-68	68414.m02624 U5 small nuclear ribonucleoprotein helicase, putative similar to SP|O75643 U5 small nuclear ribonucleoprotein 200 kDa helicase {Homo sapiens}; contains Pfam profiles PF00270: DEAD/DEAH box helicase, PF00271: Helicase conserved C-terminal domain, PF02889: Sec63 domain
356248	1	383	12	12	20	1	1	At5g61140	4,00E-45	68418.m07670 DEAD box RNA helicase, putative similar to ASC-1 complex subunit P200 [Homo sapiens] GI:12061185; contains Pfam profiles PF00270: DEAD/DEAH box helicase, PF00271: Helicase conserved C-terminal domain, PF02889: Sec63 domain
356696	1	383	12	12	20	1	1	At5g61140	6,00E-15	68418.m07670 DEAD box RNA helicase, putative similar to ASC-1 complex subunit P200 [Homo sapiens] GI:12061185; contains Pfam profiles PF00270: DEAD/DEAH box helicase, PF00271: Helicase conserved C-terminal domain, PF02889: Sec63 domain
358307	1	383	12	12	136	1	1	At3g46960	3,00E-60	68416.m05099 DEAD/DEAH box helicase, putative similar to SP|P35207 Antiviral protein SKI2 {Saccharomyces cerevisiae}; contains Pfam profiles PF00270: DEAD/DEAH box helicase, PF00271: Helicase conserved C-terminal domain
357974	1	383	12	12	746	1	1	At1g79940	1,00E-44	68414.m09342 DNAJ heat shock N-terminal domain-containing protein / sec63 domain-containing protein similar to SP|Q9UGP8 Translocation protein SEC63 homolog {Homo sapiens}; contains Pfam profiles PF00226 DnaJ domain, PF02889 Sec63 domain
359519	1	383	12	12	746	1	1	At1g79940	5,00E-81	68414.m09342 DNAJ heat shock N-terminal domain-containing protein / sec63 domain-containing protein similar to SP|Q9UGP8 Translocation protein SEC63 homolog {Homo sapiens}; contains Pfam profiles PF00226 DnaJ domain, PF02889 Sec63 domain
353611	2	385	15	9	8069	1	1	At2g35880	2,00E-42	68415.m04405 expressed protein

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
353719	3	385	15	9	10209	2	2	At1g24160	1,00E-17	68414.m03048 expressed protein Location of EST gb|H36355
356141	1	386	10	14	2988	1	2	At2g47900	3,00E-29	68415.m05985 F-box family protein / tubby family protein similar to Chain A, C-Terminal Domain Of Mouse Brain Tubby Protein Length(GI:6730158) [Mus musculus]; similar to phosphodiesterase (GI:467578) [Mus musculus]; similar to Tubby protein homolog (Swiss-Prot:O88808) [Rattus norvegicus]; contains Pfam PF00646: F-box domain and Pfam PF01167: Tub family
358329	1	386	10	14	4309	1	2	At1g53320	1,00E-56	68414.m06043 F-box family protein / tubby family protein (TULP7) similar to Tubby related protein 2 (Tubby-like protein 2) (P4-6 protein) (Fragment) (SP:P46686) [Mus musculus]; similar to phosphodiesterase (GI:467578) [Mus musculus]; similar to Tubby protein homolog 1. (Swiss-Prot:Q09306) [Caenorhabditis elegans] contains Pfam profile: PF01167: Tub family; contains Pfam PF00646: F-box domain
358440	1	387	9	15	1169	1	1	At3g63520	2,00E-15	68416.m07155 9-cis-epoxycarotenoid dioxygenase / neoxanthin cleavage enzyme / NCED1 / carotenoid cleavage dioxygenase 1 (CCD1) identical to putative 9-cis-epoxy-carotenoid dioxygenase [GI:3096910]; contains Pfam profile PF03055: Retinal pigment epithelial membrane protein
354141	2	390	12	12	348	1	1	At2g42490	2,00E-84	68415.m05256 copper amine oxidase, putative similar to copper methylamine oxidase precursor (MAOXII) [Arthrobacter sp.] SWISS-PROT:Q07123
354140	2	393	10	14	3128	2	1	At3g59760	3,00E-15	68416.m06669 cysteine synthase, mitochondrial, putative / O-acetylserine (thiol)-lyase, putative / O-acetylserine sulfhydrylase, putative similar to SP|Q43725 Cysteine synthase, mitochondrial precursor (EC 4.2.99.8) (O-acetylserine sulfhydrylase) (O-acetylserine (Thiol)-lyase) {Arabidopsis thaliana}
355516	1	393	10	14	3128	2	1	At3g59760	4,00E-48	68416.m06669 cysteine synthase, mitochondrial, putative / O-acetylserine (thiol)-lyase, putative / O-acetylserine sulfhydrylase, putative similar to SP|Q43725 Cysteine synthase, mitochondrial precursor (EC 4.2.99.8) (O-acetylserine sulfhydrylase) (O-acetylserine (Thiol)-lyase) {Arabidopsis thaliana}

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
353244	2	395	3	21	4049	1	1	At1g63990	1,00E-49	68414.m07248 DNA topoisomerase VIA, putative (SPO11-2) similar to topoisomerase 6 subunit A (spo11) [Arabidopsis thaliana] GI:12331186; contains Pfam profile PF04406: Type IIB DNA topoisomerase; identical to cDNA putative topoisomerase VIA (SPO11 gene 2) GI:7270976
352914	3	398	12	11	7667	2	1	At3g46010	3,00E-64	68416.m04978 actin-depolymerizing factor 1 (ADF1) identical to SP|Q39250 Actin-depolymerizing factor 1 (ADF-1) (AtADF1) {Arabidopsis thaliana}
353414	3	398	12	11	7667	2	1	At3g46010	2,00E-63	68416.m04978 actin-depolymerizing factor 1 (ADF1) identical to SP|Q39250 Actin-depolymerizing factor 1 (ADF-1) (AtADF1) {Arabidopsis thaliana}
356381	1	398	12	11	7929	1	2	At2g31200	1,00E-54	68415.m03810 actin-depolymerizing factor 6 (ADF6) identical to SP|Q9ZSK2 Actin-depolymerizing factor 6 (ADF-6) (AtADF6) {Arabidopsis thaliana}
359680	1	399	9	14	5682	1	1	At5g45390	3,00E-83	68418.m05578 ATP-dependent Clp protease proteolytic subunit (ClpP4) identical to nClpP4 GI:5360593 from [Arabidopsis thaliana]
353161	3	399	9	14	6060	1	1	At1g12410	2,00E-57	68414.m01434 ATP-dependent Clp protease proteolytic subunit (ClpP2) identical to nClpP2 GI:5360589 from [Arabidopsis thaliana]
353877	2	399	9	14	6962	1	1	At1g02560	2,00E-51	68414.m00207 ATP-dependent Clp protease proteolytic subunit (ClpP1) identical to nClpP1 GB:BAA82065 GI:5360579 from [Arabidopsis thaliana]; contains Pfam profile PF00574: Clp protease; contains TIGRfam profile TIGR00493: ATP-dependent Clp protease, proteolytic subunit ClpP
357382	1	399	9	14	6962	1	1	At1g02560	1,00E-09	68414.m00207 ATP-dependent Clp protease proteolytic subunit (ClpP1) identical to nClpP1 GB:BAA82065 GI:5360579 from [Arabidopsis thaliana]; contains Pfam profile PF00574: Clp protease; contains TIGRfam profile TIGR00493: ATP-dependent Clp protease, proteolytic subunit ClpP
359414	1	399	9	14	8196	1	1	At1g09130	7,00E-29	68414.m01017 ATP-dependent Clp protease proteolytic subunit, putative similar to nClpP5 GI:5360595 from [Arabidopsis thaliana]
353528	2	400	10	13	9730	3	2	At4g15800	2,00E-25	68417.m02404 rapid alkalinization factor (RALF) family protein similar to RALF precursor [Nicotiana tabacum] GI:16566316
358033	1	400	10	13				At5g67070	6,00E-26	68418.m08457 rapid alkalinization factor (RALF) family protein similar to RALF precursor [Nicotiana tabacum] GI:16566316

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
353474	3	401	12	11	6673	2	2	At1g15030	2,00E-47	68414.m01796 expressed protein
354448	5	401	12	11	6673	2	2	At1g15030	7,00E-15	68414.m01796 expressed protein
355081	1	401	12	11	6673	2	2	At2g01260	5,00E-27	68415.m00039 expressed protein
358259	1	401	12	11	6673	2	2	At1g15030	6,00E-52	68414.m01796 expressed protein
354534	1	404	11	12	2715	2	1	At5g43330	1,00E-102	68418.m05296 malate dehydrogenase, cytosolic, putative strong similarity to cytosolic malate dehydrogenase (EC 1.1.1.37) SP|O24047 {Mesembryanthemum crystallinum}, SP|O48905 {Medicago sativa}, [Prunus persica] GI:15982948; contains InterPro entry IPR001236: Lactate/malate dehydrogenase
359538	1	404	11	12	3131	2	1	At2g22780	8,00E-75	68415.m02702 malate dehydrogenase, glyoxysomal, putative strong similarity to glyoxysomal malate dehydrogenase (EC 1.1.1.37) SP|P19446 {Citrullus lanatus}, SP|P46488 {Cucumis sativus}, [Medicago sativa] GI:2827078, SP|Q42972 {Oryza sativa}, SP|Q9ZP05 {Arabidopsis thaliana}, SP|P37228 {Glycine max}; contains InterPro entry IPR001236: Lactate/malate dehydrogenase
359255	1	404	11	12	3205	1	1	At3g47520	3,00E-119	68416.m05168 malate dehydrogenase [NAD], chloroplast (MDH) identical to chloroplast NAD-malate dehydrogenase [Arabidopsis thaliana] GI:3256066; contains InterPro entry IPR001236: Lactate/malate dehydrogenase; contains Pfam profiles PF00056: lactate/malate dehydrogenase, NAD binding domain and PF02866: lactate/malate dehydrogenase, alpha/beta C-terminal domain
353774	3	404	11	12	3245	2	2	At3g15020	4,00E-135	68416.m01900 malate dehydrogenase [NAD], mitochondrial, putative similar to mitochondrial NAD-dependent malate dehydrogenase GB:CAA10320 SP|Q9ZP06 [Arabidopsis thaliana]; contains InterPro entry IPR001236: Lactate/malate dehydrogenase
359334	1	405	7	16	1953	1	1	At4g16070	8,00E-27	68417.m02437 lipase class 3 family protein low similarity to calmodulin-binding heat-shock protein CaMBP [Nicotiana tabacum] GI:1087073; contains Pfam profile PF01764: Lipase, PF03893: Lipase 3 N-terminal region
353032	4	406	12	11	4909	2	1	At3g08620	1,00E-76	68416.m01001 KH domain-containing protein
354391	2	406	12	11	5072	2	1	At4g26480	7,00E-39	68417.m03810 KH domain-containing protein qkI-7, Mus musculus

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
355703	1	406	12	11	5072	2	1	At4g26480	1,00E-38	68417.m03810 KH domain-containing protein qkI-7, Mus musculus
359540	1	406	12	11				At1g09660	1,00E-10	68414.m01085 KH domain-containing quaking protein, putative similar to GB:AAC67357
354197	5	407	12	11	1017	2	3	At5g62890	2,00E-165	68418.m07892 permease, putative similar to permease 1 [Zea mays] GI:7844006; contains Pfam profile: PF00860 Xanthine/uracil permeases family; identical to cDNA putative permease 1 (MQB2.21) GI:21326024
356623	1	407	12	11	1859	1	1	At2g27810	6,00E-49	68415.m03372 xanthine/uracil permease family protein contains Pfam profile: PF00860 permease family
358375	1	410	9	14	134	1	1	At3g59770	2,00E-24	68416.m06670 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
353753	4	411	9	14	4962	1	1	At4g39230	7,00E-106	68417.m05553 isoflavone reductase, putative similar to allergenic isoflavone reductase-like protein Bet v 6.0102 [Betula pendula][GI:10764491]; contains Pfam profile PF02716: Isoflavone reductase
353226	3	411	9	14				At1g75290	1,00E-49	68414.m08746 isoflavone reductase, putative similar to SP|P52577 Isoflavone reductase homolog P3 (EC 1.3.1.-) {Arabidopsis thaliana}; contains Pfam profile PF02716: Isoflavone reductase
358510	1	411	9	14				At1g75280	7,00E-08	68414.m08745 isoflavone reductase, putative identical to SP|P52577 Isoflavone reductase homolog P3 (EC 1.3.1.-) {Arabidopsis thaliana}; contains Pfam profile PF02716: isoflavone reductase
359089	1	412	18	5	4219	1	1	At2g30320	8,00E-37	68415.m03690 tRNA pseudouridine synthase family protein similar to pseudouridine synthase [Schizosaccharomyces pombe] GI:6469502; contains Pfam profile PF01416: tRNA pseudouridine synthase
353850	2	413	15	8	4446	2	2	At3g02520	4,00E-62	68416.m00240 14-3-3 protein GF14 nu (GRF7) identical to 14-3-3 protein GF14 nu GI:1531631 from [Arabidopsis thaliana]
353911	2	413	15	8	4446	2	2	At5g16050	4,00E-50	68418.m01876 14-3-3 protein GF14 upsilon (GRF5) identical to 14-3-3 protein GF14 upsilon GI:2232148 from [Arabidopsis thaliana]
353697	3	413	15	8				At1g78300	8,00E-66	68414.m09125 14-3-3 protein GF14 omega (GRF2) identical to GF14omega isoform GI:487791 from [Arabidopsis thaliana]

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
355351	1	413	15	8				At5g10450	2,00E-56	68418.m01211 14-3-3 protein GF14 lambda (GRF6) (AFT1) identical to 14-3-3 GF14lambda GI:1345595 from [Arabidopsis thaliana]
355355	1	413	15	8				At2g42590	1,00E-44	68415.m05270 14-3-3 protein GF14 mu (GRF9) identical to GF14 mu GI:3551052, SP:Q96299 from [Arabidopsis thaliana]
358380	1	413	15	8				At4g09000	9,00E-54	68417.m01487 14-3-3-like protein GF14 chi / general regulatory factor 1 (GRF1) identical to 14-3-3 protein GF14 chi chain GI:1702986, SP:P42643 from [Arabidopsis thaliana]
359546	1	413	15	8				At1g26480	2,00E-96	68414.m03229 14-3-3 protein GF14 iota (GRF12) identical to 14-3-3 protein GF14iota GI:12963453 from [Arabidopsis thaliana]
355189	1	414	5	18	2432	3	2	At1g23760	2,00E-63	68414.m02998 BURP domain-containing protein / polygalacturonase, putative similar to polygalacturonase isoenzyme 1 beta subunit [Lycopersicon esculentum] GI:170480; contains Pfam profile PF03181: BURP domain
359441	1	414	5	18	5601	1	1	At5g25610	2,00E-40	68418.m03047 dehydration-responsive protein (RD22) identical to SP|Q08298 Dehydration-responsive protein RD22 precursor {Arabidopsis thaliana}
359537	1	416	9	14	3637	1	1	At4g38380	2,00E-53	68417.m05426 MATE efflux protein-related T19C21.18 Arabidopsis thaliana chromosome II BAC T19C21 genomic sequence, PID:g3395439
356101	1	416	9	14	6088	2	1	At2g21340	1,00E-06	68415.m02540 enhanced disease susceptibility protein, putative / salicylic acid induction deficient protein, putative similar to enhanced disease susceptibility 5 [Arabidopsis thaliana] GI:16589070
358531	1	416	9	14	9052	1	1	At5g57170	9,00E-06	68418.m07141 macrophage migration inhibitory factor family protein / MIF family protein contains Pfam profile: PF01187 Macrophage migration inhibitory factor(MIF)
353772	2	416	9	14				At5g01650	2,00E-50	68418.m00081 macrophage migration inhibitory factor family protein / MIF family protein contains pfam profile: PF001187 Macrophage migration inhibitory factor
359010	1	416	9	14				At5g01650	5,00E-49	68418.m00081 macrophage migration inhibitory factor family protein / MIF family protein contains pfam profile: PF001187 Macrophage migration inhibitory factor
359910	1	417	2	21				At4g31240	2,00E-25	68417.m04435 expressed protein
358072	1	419	10	13	4627	1	1	At5g19680	2,00E-30	68418.m02341 leucine-rich repeat family protein contains leucine rich repeat (LRR) domains, Pfam:PF00560

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
355591	1	419	10	13	5403	3	1	At4g26050	4,00E-06	68417.m03750 leucine-rich repeat family protein contains Pfam PF00560: Leucine Rich Repeat domains;
359996	1	419	10	13	6031	1	1	At5g22320	2,00E-36	68418.m02604 leucine-rich repeat family protein contains leucine rich repeat (LRR) domains, Pfam:PF00560
360039	1	422	9	13	374	1	2	At4g02570	5,00E-77	68417.m00351 cullin family protein similar to cullin 3 [Homo sapiens] GI:3639052; contains Pfam profile PF00888: Cullin family
355407	1	422	9	13	423	2	1	At1g26830	3,00E-73	68414.m03270 cullin, putative similar to Cullin homolog 3 (CUL-3) SP:Q13618, GI:3639052 from [Homo sapiens]; contains Pfam profile PF00888: Cullin family
353088	2	422	9	13	436	1	1	At5g46210	5,00E-126	68418.m05686 cullin, putative similar to SP|Q13619 Cullin homolog 4A (CUL-4A) {Homo sapiens}; contains Pfam profile PF00888: Cullin family
356795	1	423	11	11	2970	2	1	At5g39990	2,00E-14	68418.m04849 glycosyltransferase family 14 protein / core-2/I-branching enzyme family protein contains Pfam profile: PF02485 Core-2/I-Branching enzyme
355510	1	423	11	11	3132	2	1	At1g03520	1,00E-48	68414.m00333 glycosyltransferase family 14 protein / core-2/I-branching enzyme family protein contains Pfam profile PF02485: Core-2/I-Branching enzyme
356910	1	423	11	11	3132	2	1	At1g03520	2,00E-57	68414.m00333 glycosyltransferase family 14 protein / core-2/I-branching enzyme family protein contains Pfam profile PF02485: Core-2/I-Branching enzyme
354251	2	425	13	9	7049	1	1	At5g58610	2,00E-10	68418.m07345 PHD finger transcription factor, putative
358399	1	425	13	9				At4g14920	3,00E-09	68417.m02292 PHD finger transcription factor, putative
355176	1	426	11	11				At1g13000	1,00E-18	68414.m01509 expressed protein contains Pfam profile PF05212: Protein of unknown function (DUF707)
355498	1	426	11	11				At1g08040	2,00E-59	68414.m00878 expressed protein contains Pfam profile PF05212: Protein of unknown function (DUF707)
356963	1	427	10	12	7504	1	2	At1g56170	2,00E-48	68414.m06454 transcription factor, putative similar to Transcription factor GB:CAA74053 GI:2398533 from [Arabidopsis thaliana] similarity to transcription factor Hap5a similar to transcription factor Hap5a [Arabidopsis thaliana](GI:6523090)
353034	2	427	10	12				At1g08970	3,00E-57	68414.m01000 CCAAT-box binding transcription factor Hap5a, putative
353679	4	428	11	11	1537	2	1	At3g20580	9,00E-60	68416.m02605 phytochelatin synthetase-related contains Pfam PF04833: Phytochelatin synthetase-like conserved region; supporting cDNA gi|26452232|dbj|AK118605.1|

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
358084	1	428	11	11	1982	3	2	At4g16120	4,00E-32	68417.m02443 phytochelatin synthetase-related contains Pfam PF04833: Phytochelatin synthetase-like conserved region; supporting cDNA gi|26449620|dbj|AK117261.1|
354984	1	428	11	11				At3g29810	3,00E-25	68416.m03794 phytochelatin synthetase family protein / COBRA cell expansion protein COBL2 similar to phytochelatin synthetase [Hordeum vulgare subsp. vulgare] GI:29570314; identified in Roudier, et al, Plant Phys. (2002) 130:538-548 (PMID:12376623); contains Pfam profile PF04833: Phytochelatin synthetase-like conserved region
355453	1	428	11	11				At3g29810	6,00E-26	68416.m03794 phytochelatin synthetase family protein / COBRA cell expansion protein COBL2 similar to phytochelatin synthetase [Hordeum vulgare subsp. vulgare] GI:29570314; identified in Roudier, et al, Plant Phys. (2002) 130:538-548 (PMID:12376623); contains Pfam profile PF04833: Phytochelatin synthetase-like conserved region
355155	1	429	12	10				At1g76890	1,00E-11	68414.m08948 trihelix DNA-binding protein / GT-2 factor (GT2) identical to GT2 factor [Arabidopsis thaliana] GI:416490, GI:2664202 (DNA binding factor GT-2 from Arabidopsis)
357691	1	429	12	10				At1g76880	8,00E-43	68414.m08946 trihelix DNA-binding protein, putative similar to DNA-binding protein DF1 [Pisum sativum] GI:13646986
354320	2	431	12	10	4304	1	1	At3g25530	4,00E-123	68416.m03174 6-phosphogluconate dehydrogenase NAD-binding domain-containing protein low similarity to SP|P23523 2-hydroxy-3-oxopropionate reductase (EC 1.1.1.60) (Tartronate semialdehyde reductase) {Escherichia coli}; contains Pfam profile PF03446: NAD binding domain of 6-phosphogluconate dehydrogenase; supporting cDNA gi|15375067|gb|AY044183.1|
356812	1	431	12	10				At5g60580	4,00E-54	68418.m07597 zinc finger (C3HC4-type RING finger) family protein contains Pfam profile PF00097: Zinc finger, C3HC4 type (RING finger)
357771	1	433	10	12	7335	2	4	At1g22490	1,00E-39	68414.m02810 basic helix-loop-helix (bHLH) family protein contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain
358793	1	433	10	12	7335	2	4	At1g22490	2,00E-34	68414.m02810 basic helix-loop-helix (bHLH) family protein contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain

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356435	1	433	10	12				At4g01460	1,00E-20	68417.m00189 basic helix-loop-helix (bHLH) family protein contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain
352963	2	434	13	9	9462	2	1	At5g15230	2,00E-38	68418.m01784 gibberellin-regulated protein 4 (GASA4) / gibberellin-responsive protein 4 identical to SP|P46690 Gibberellin-regulated protein 4 precursor {Arabidopsis thaliana}
353766	3	434	13	9	10032	1	1	At5g14920	8,00E-18	68418.m01750 gibberellin-regulated family protein similar to SP|P46689 Gibberellin-regulated protein 1 precursor {Arabidopsis thaliana}; contains Pfam profile PF02704: Gibberellin regulated protein
353431	2	434	13	9				At2g14900	2,00E-22	68415.m01694 gibberellin-regulated family protein similar to SP|P46690 Gibberellin-regulated protein 4 precursor {Arabidopsis thaliana} GASA4; contains Pfam profile PF02704: Gibberellin regulated protein
356788	1	436	14	8	1061	1	2	At5g40200	6,00E-74	68418.m04878 DegP protease, putative contains similarity to DegP2 protease GI:13172275 from [Arabidopsis thaliana]
359398	1	436	14	8	1061	1	2	At5g40200	2,00E-54	68418.m04878 DegP protease, putative contains similarity to DegP2 protease GI:13172275 from [Arabidopsis thaliana]
358337	1	436	14	8	1328	1	1	At2g47940	7,00E-18	68415.m05995 DegP2 protease (DEGP2) identical to DegP2 protease GI:13172275 from [Arabidopsis thaliana]; identical to cDNA DegP2 protease (DEGP2) nuclear gene for chloroplast product GI:13172274
355636	1	436	14	8	2551	1	1	At3g27925	1,00E-41	68416.m03484 DegP protease, putative SP:022609; almost identical to DegP protease precursor GB:AF028842 from [Arabidopsis thaliana] (J. Biol. Chem. 273 (12), 7094-7098 (1998))
358883	1	436	14	8	5837	1	1	At5g27660	7,00E-25	68418.m03315 DegP protease, putative similar to Serine protease HTRA2, mitochondrial precursor (High temperature requirement protein A2) (HtrA2) (Omi stress-regulated endoprotease) (Serine proteinase OMI) (SP:O43464) {Homo sapiens}
359905	1	437	9	13	3251	1	2	At4g21470	1,00E-48	68417.m03105 riboflavin kinase/FAD synthetase family protein contains Pfam profiles PF01687: Riboflavin kinase / FAD synthetase, PF00702: haloacid dehalogenase-like hydrolase
359707	1	437	9	13	6301	1	1	At3g07060	2,00E-13	68416.m00838 expressed protein ; expression supported by MPSS

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
353701	2	438	10	12	174	1	2	At5g50920	4,00E-76	68418.m06315 ATP-dependent Clp protease ATP-binding subunit / ClpC almost identical to ClpC GI:2921158 from [Arabidopsis thaliana]; contains Pfam profile PF02861: Clp amino terminal domain; contains Pfam profile PF00004: ATPase, AAA family; contains Pfam profile PF02151: UvrB/uvrC motif
353152	2	438	10	12	181	1	1	At5g15450	3,00E-156	68418.m01808 heat shock protein 100, putative / HSP100, putative / heat shock protein clpB, putative / HSP100/ClpB, putative similar to HSP100/ClpB GI:9651530 [Phaseolus lunatus]
359811	1	438	10	12	278	1	1	At2g25140	8,00E-46	68415.m03007 heat shock protein 100, putative / HSP100, putative / heat shock protein clpB, putative / HSP100/ClpB, putative similar to HSP100/ClpB GI:9651530 [Phaseolus lunatus]
358224	1	438	10	12	8177	1	1	At4g25370	3,00E-48	68417.m03650 Clp amino terminal domain-containing protein contains Pfam profile: PF02861 Clp amino terminal domain
355423	1	440	10	12	1779	1	1	At5g35170	4,00E-32	68418.m04168 adenylate kinase family protein contains Pfam profile: PF00406 adenylate kinase
354406	2	440	10	12	4787	2	2	At5g50370	7,00E-98	68418.m06238 adenylate kinase, putative similar to adenylate kinase (ATP-AMP transphosphorylase) [Arabidopsis thaliana] SWISS-PROT:O82514
353083	3	440	10	12	5449	1	1	At2g37250	5,00E-53	68415.m04570 adenylate kinase family protein contains Pfam profile: PF00406 adenylate kinase
357112	1	440	10	12	5449	1	1	At2g37250	3,00E-24	68415.m04570 adenylate kinase family protein contains Pfam profile: PF00406 adenylate kinase
359222	1	440	10	12	5449	1	1	At2g37250	2,00E-67	68415.m04570 adenylate kinase family protein contains Pfam profile: PF00406 adenylate kinase
353926	2	440	10	12	6213	1	1	At5g47840	2,00E-64	68418.m05911 adenylate kinase, chloroplast, putative / ATP-AMP transphosphorylase, putative similar to SP|P43188 Adenylate kinase, chloroplast (EC 2.7.4.3) (ATP-AMP transphosphorylase) {Zea mays}; contains Pfam profile PF00406: Adenylate kinase
357345	1	440	10	12	7475	1	1	At4g25280	6,00E-23	68417.m03636 adenylate kinase family protein contains Pfam profile: PF00406 adenylate kinase
356421	1	441	7	14	376	2	1	At2g36390	1,00E-69	68415.m04466 1,4-alpha-glucan branching enzyme / starch branching enzyme class II (SBE2-1) nearly identical to starch branching enzyme class II [Arabidopsis thaliana] GI:619939

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
354843	1	441	7	14	495	1	1	At5g04360	7,00E-88	68418.m00428 pullulanase, putative / starch debranching enzyme, putative similar to pullulanase [Spinacia oleracea] GI:634093 (EC 3.2.1.41); contains Pfam profiles PF00128: Alpha amylase catalytic domain, PF02922: Isoamylase N-terminal domain
357032	1	441	7	14	500	1	1	At2g39930	2,00E-62	68415.m04907 isoamylase, putative / starch debranching enzyme, putative similar to isoamylase from [Solanum tuberosum] GI:27728145, [Triticum aestivum] GI:17932898, [Hordeum vulgare] GI:21314275, [Oryza sativa] GI:3252794; contains Pfam profiles PF00128: Alpha amylase catalytic domain, PF02922: Isoamylase N-terminal domain
356360	1	441	7	14	545	1	1	At4g09020	2,00E-65	68417.m01489 isoamylase, putative / starch debranching enzyme, putative similar to isoamylase isoform 3 [Solanum tuberosum] GI:27728149, isoamylase [Oryza sativa] GI:3252794; contains Pfam profiles PF00128: Alpha amylase catalytic domain, PF02922: Isoamylase N-terminal domain
353020	2	442	11	10	2471	1	1	At5g19180	7,00E-53	68418.m02284 ubiquitin activating enzyme, putative (ECR1) identical to putative ubiquitin activating enzyme E1 [Arabidopsis thaliana] GI:2952433; similar to NEDD8 activating enzyme [Mus musculus] GI:17061821
357511	1	442	11	10	5016	3	1	At4g24940	1,00E-50	68417.m03572 SUMO activating enzyme 1a (SAE1a) identical to SUMO activating enzyme 1a [Arabidopsis thaliana] GI:22652850; contains Pfam profile PF00899: ThiF family
357128	1	443	9	12	1268	1	1	At2g34960	4,00E-17	68415.m04290 amino acid permease family protein similar to cationic amino acid transporter 3 [Rattus norvegicus] GI:2116552; contains Pfam profile PF00324: Amino acid permease
353116	2	443	9	12	1639	1	1	At1g05940	1,00E-54	68414.m00623 amino acid permease family protein low similarity to SP|P30823 High-affinity cationic amino acid transporter-1 (CAT-1) {Rattus norvegicus}; contains Pfam profile PF00324: Amino acid permease
356603	1	444	8	13	6719	1	5	At1g08080	1,00E-28	68414.m00884 carbonic anhydrase family protein similar to storage protein (dioscorin) [Dioscorea cayenensis] GI:433463; contains Pfam profile PF00194: Eukaryotic-type carbonic anhydrase
360002	1	445	9	12	991	1	1	At3g48430	4,00E-59	68416.m05287 zinc finger (C2H2 type) family protein / transcription factor jumonji (jmj) family protein contains Pfam domains PF02375: jmjN domain, PF02373: jmjC domain and PF00096: Zinc finger, C2H2 type

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354303	2	446	11	10				At4g19420	3,00E-22	68417.m02858 pectinacetylesterase family protein contains Pfam profile: PF03283 pectinacetylesterase
354331	4	446	11	10				At3g62060	4,00E-26	68416.m06973 pectinacetylesterase family protein similar to pectinacetylesterase precursor GI:1431629 from [Vigna radiata]; contains Pfam profile: PF03283 pectinacetylesterase
354347	2	446	11	10				At5g23870	2,00E-63	68418.m02803 pectinacetylesterase family protein contains Pfam profile: PF03283 pectinacetylesterase
352967	2	447	12	9	6207	1	1	At3g22845	9,00E-91	68416.m02879 emp24/gp25L/p24 protein-related contains weak similarity to transmembrane protein (GI:1212965) [Homo sapiens]
353461	2	447	12	9	6412	1	1	At3g07680	2,00E-83	68416.m00921 emp24/gp25L/p24 family protein similar to SP|Q15363 Cop-coated vesicle membrane protein p24 precursor (p24A) {Homo sapiens}; contains Pfam profile PF01105: emp24/gp25L/p24 family
354073	2	447	12	9	7004	3	2	At1g26690	1,00E-64	68414.m03251 emp24/gp25L/p24 family protein similar to SP|P49755 Transmembrane protein Tmp21 precursor (21 kDa Transmembrane trafficking protein) {Homo sapiens}; contains Pfam profile PF01105: emp24/gp25L/p24 family
356163	1	447	12	9	7007	2	2	At1g57620	2,00E-22	68414.m06539 emp24/gp25L/p24 family protein similar to SP|P49755 Transmembrane protein Tmp21 precursor (21 kDa Transmembrane trafficking protein) {Homo sapiens}; contains Pfam profile PF01105: emp24/gp25L/p24 family
359886	1	447	12	9	7007	2	2	At1g57620	3,00E-11	68414.m06539 emp24/gp25L/p24 family protein similar to SP|P49755 Transmembrane protein Tmp21 precursor (21 kDa Transmembrane trafficking protein) {Homo sapiens}; contains Pfam profile PF01105: emp24/gp25L/p24 family
354677	1	449	8	13	3304	2	1	At1g69040	1,00E-54	68414.m07899 ACT domain containing protein (ACR4) low similarity to uridylyltransferase [Gluconacetobacter diazotrophicus] GI:17226253; contains Pfam profile PF01842: ACT domain
356179	1	449	8	13	3304	2	1	At1g69040	2,00E-35	68414.m07899 ACT domain containing protein (ACR4) low similarity to uridylyltransferase [Gluconacetobacter diazotrophicus] GI:17226253; contains Pfam profile PF01842: ACT domain
356859	1	449	8	13				At3g01990	2,00E-15	68416.m00158 ACT domain-containing protein (ACR6) contains Pfam ACT domain PF01842; similar to uridylyl transferase-like proteins GB:AAD20075, GB:AAC00631 [Arabidopsis thaliana]

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
354837	1	450	8	13	2044	1	2	At1g72970	9,00E-40	68414.m08439 glucose-methanol-choline (GMC) oxidoreductase family protein similar to mandelonitrile lyase from Prunus serotina [SP|P52706, SP|P52707]; contains Pfam profile PF00732 GMC oxidoreductase
359217	1	450	8	13	2044	1	2	At1g72970	9,00E-64	68414.m08439 glucose-methanol-choline (GMC) oxidoreductase family protein similar to mandelonitrile lyase from Prunus serotina [SP|P52706, SP|P52707]; contains Pfam profile PF00732 GMC oxidoreductase
353580	8	451	9	12	1601	2	1	At5g55230	0	68418.m06884 microtubule associated protein (MAP65/ASE1) family protein low similarity to protein regulating cytokinesis 1 (PRC1) [Homo sapiens] GI:2865521; contains Pfam profile PF03999: Microtubule associated protein (MAP65/ASE1 family)
354357	2	451	9	12	1601	2	1	At5g55230	4,00E-78	68418.m06884 microtubule associated protein (MAP65/ASE1) family protein low similarity to protein regulating cytokinesis 1 (PRC1) [Homo sapiens] GI:2865521; contains Pfam profile PF03999: Microtubule associated protein (MAP65/ASE1 family)
355994	1	451	9	12	1601	2	1	At5g55230	8,00E-26	68418.m06884 microtubule associated protein (MAP65/ASE1) family protein low similarity to protein regulating cytokinesis 1 (PRC1) [Homo sapiens] GI:2865521; contains Pfam profile PF03999: Microtubule associated protein (MAP65/ASE1 family)
353545	2	451	9	12	2462	1	2	At2g01910	8,00E-53	68415.m00125 microtubule associated protein (MAP65/ASE1) family protein low similarity to protein regulating cytokinesis 1 (PRC1) [Homo sapiens] GI:2865521; contains Pfam profile PF03999: Microtubule associated protein (MAP65/ASE1 family)
358677	1	451	9	12	2462	1	2	At2g01910	7,00E-55	68415.m00125 microtubule associated protein (MAP65/ASE1) family protein low similarity to protein regulating cytokinesis 1 (PRC1) [Homo sapiens] GI:2865521; contains Pfam profile PF03999: Microtubule associated protein (MAP65/ASE1 family)
358643	1	452	15	6	1218	1	1	At2g33540	5,00E-51	68415.m04111 CTD phosphatase-like protein 3 (CPL3) identical to CTD phosphatase-like 3 (CPL3) [Arabidopsis thaliana] GI:22212705; contains Pfam profile PF03031: NLI interacting factor
356601	1	452	15	6	4497	1	1	At5g58000	4,00E-16	68418.m07256 phosphatase-related weak similarity to CTD phosphatase-like 3 [Arabidopsis thaliana] GI:22212705; contains Pfam profiles PF02453: Reticulon, PF00533: BRCA1 C Terminus (BRCT) domain, PF03031: NLI interacting factor

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
359220	1	452	15	6	8583	2	1	At4g28430	2,00E-23	68417.m04069 reticulon family protein contains Pfam profile PF02453: Reticulon
358539	1	453	8	13	1197	1	2	At1g73590	1,00E-51	68414.m08519 auxin efflux carrier protein, putative (PIN1) identical to putative auxin efflux carrier protein; AtPIN1 [Arabidopsis thaliana] GI:4151319; contains Pfam profile PF03547: Auxin Efflux Carrier
354162	3	453	8	13	1598	3	1	At1g70940	4,00E-28	68414.m08184 auxin transport protein, putative (PIN3) similar to auxin transport protein [Arabidopsis thaliana] gi|5817301|gb|AAD52695
353181	2	456	8	13	4525	1	1	At5g51550	4,00E-41	68418.m06392 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
353858	3	456	8	13	5650	2	1	At4g08950	9,00E-48	68417.m01473 phosphate-responsive protein, putative (EXO) similar to phi-1 (phosphate-induced gene) [Nicotiana tabacum] GI:3759184; contains Pfam profile PF04674: Phosphate-induced protein 1 conserved region
354259	2	456	8	13	5650	2	1	At4g08950	3,00E-61	68417.m01473 phosphate-responsive protein, putative (EXO) similar to phi-1 (phosphate-induced gene) [Nicotiana tabacum] GI:3759184; contains Pfam profile PF04674: Phosphate-induced protein 1 conserved region
356212	1	456	8	13	5650	2	1	At4g08950	1,00E-43	68417.m01473 phosphate-responsive protein, putative (EXO) similar to phi-1 (phosphate-induced gene) [Nicotiana tabacum] GI:3759184; contains Pfam profile PF04674: Phosphate-induced protein 1 conserved region
359591	1	457	10	11	3738	2	2	At5g53500	6,00E-35	68418.m06649 WD-40 repeat family protein contains Pfam PF00400: WD domain, G-beta repeat; similar to WD-repeat protein 5 (WD repeat protein BIG-3) (SP: Q9UGP9) [Homo sapiens]
359814	1	458	12	9	823	1	1	At2g32950	6,00E-11	68415.m04039 COP1 regulatory protein photomorphogenesis repressor; identical to COP1 regulatory protein/FUSCA protein FUS1 GI:402685 SP:P43254
355049	1	458	12	9	1188	2	1	At3g15354	2,00E-53	68416.m01939 WD-40 repeat family protein / phytochrome A-related contains 7 WD-40 repeats (PF00400); phytochrome A supressor spa1 (GI:4809171) [Arabidopsis thaliana]

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
359816	1	458	12	9	3706	2	1	At4g18905	3,00E-64	68417.m02787 transducin family protein / WD-40 repeat family protein contains 5 (4 significant) WD-40 repeats; similar to periodic tryptophan protein 1 homolog (Keratinocyte protein IEF SSP 9502) (PWP1)(SP:Q13610) (PIR2:I39360) [Homo sapiens]
355478	1	458	12	9				At4g11110	6,00E-07	68417.m01803 WD-40 repeat family protein / phytochrome A-related contains 7 WD-40 repeats (PF00400); similar to phytochrome A supressor spa1 (GI:4809171) [Arabidopsis thaliana]; contains non-consensus (GC) donor splice sites at introns 4 and 6
355987	1	459	11	10	9796	2	2	At5g63500	2,00E-23	68418.m07971 expressed protein
359959	1	465	11	9	6619	1	2	At5g52660	7,00E-27	68418.m06538 myb family transcription factor contains PFAM profile: PF00249 myb-like DNA-binding domain
355119	1	465	11	9	7510	1	1	At1g01060	1,00E-09	68414.m00007 myb family transcription factor contains Pfam profile: PF00249 myb-like DNA-binding domain; identical to cDNA LATE ELONGATED HYPOCOTYL MYB transcription factor GI:3281845
356074	1	465	11	9				At3g09600	7,00E-24	68416.m01140 myb family transcription factor contains Pfam profile: PF00249 myb-like DNA-binding domain
354676	1	466	9	11	30	2	1	At3g60860	1,00E-10	68416.m06808 guanine nucleotide exchange family protein similar to guanine nucleotide exchange factor, Homo sapiens, GI:5456754; contains Pfam profile PF01369: Sec7 domain
358898	1	466	9	11	39	1	1	At3g43300	9,00E-52	68416.m04570 guanine nucleotide exchange family protein similar to SP|Q9Y6D5 Brefeldin A-inhibited guanine nucleotide-exchange protein 2 {Homo sapiens}; contains Pfam profile PF01369: Sec7 domain
358470	1	466	9	11	66	2	2	At4g38200	3,00E-43	68417.m05392 guanine nucleotide exchange family protein similar to Brefeldin A-inhibited guanine nucleotide-exchange protein 2 [Homo sapiens] SP|Q9Y6D5; contains Pfam profile PF01369: Sec7 domain
357471	1	466	9	11	88	1	1	At1g13980	4,00E-37	68414.m01647 pattern formation protein (EMB30) (GNOM) identical to SP|Q42510; contains Pfam profile PF01369: Sec7 domain
356876	1	466	9	11	203	1	1	At5g27970	2,00E-24	68418.m03369 expressed protein
358284	1	466	9	11	203	1	1	At5g27970	1,00E-39	68418.m03369 expressed protein
355823	1	467	12	8	4872	1	1	At5g27460	1,00E-14	68418.m03279 pentatricopeptide (PPR) repeat-containing protein low similarity to DNA-binding protein [Triticum aestivum] GI:6958202; contains Pfam profile PF01535: PPR repeat

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
356836	1	467	12	8	5476	1	1	At5g09450	3,00E-39	68418.m01094 pentatricopeptide (PPR) repeat-containing protein low similiarity to DNA-binding protein [Triticum aestivum] GI:6958202; contains Pfam profile: PF01535 PPR repeat
352934	2	469	9	11	635	2	1	At4g16760	2,00E-92	68417.m02531 acyl-CoA oxidase (ACX1) identical to acyl-CoA oxidase [Arabidopsis thaliana] GI:3044214
359712	1	469	9	11	635	2	1	At4g16760	7,00E-21	68417.m02531 acyl-CoA oxidase (ACX1) identical to acyl-CoA oxidase [Arabidopsis thaliana] GI:3044214
358085	1	469	9	11	930	2	1	At1g06310	9,00E-26	68414.m00667 acyl-CoA oxidase, putative strong similarity to acyl-CoA oxidase ACX3 GI:8163758 from [Arabidopsis thaliana]
354339	2	469	9	11	2088	1	2	At3g51840	2,00E-88	68416.m05685 short-chain acyl-CoA oxidase identical to Short-chain acyl CoA oxidase [Arabidopsis thaliana] GI:5478795; contains InterPro entry IPR006089: Acyl-CoA dehydrogenase
356039	1	470	8	12	1980	1	1	At1g30580	2,00E-86	68414.m03741 expressed protein
356171	1	470	8	12	1980	1	1	At1g30580	9,00E-29	68414.m03741 expressed protein
354860	1	470	8	12	2107	1	1	At4g39520	9,00E-85	68417.m05588 GTP-binding protein, putative similar to SP|Q9Y295 Developmentally regulated GTP-binding protein 1 (DRG 1) {Homo sapiens}; contains Pfam profiles PF02824: TGS domain, PF01018: GTP1/OBG family
353322	3	471	10	10	6379	1	2	At2g33430	2,00E-58	68415.m04097 plastid developmental protein DAG, putative similar to DAG protein, chloroplast precursor [Garden snapdragon] SWISS-PROT:Q38732
357772	1	471	10	10	6731	1	1	At1g11430	2,00E-48	68414.m01313 plastid developmental protein DAG, putative similar to DAG protein, chloroplast precursor [Garden snapdragon] SWISS-PROT:Q38732
355186	1	472	8	12				At3g13790	7,00E-16	68416.m01742 beta-fructosidase (BFRUCT1) / beta-fructofuranosidase / cell wall invertase identical to beta-fructofuranosidase GI:402740 from [Arabidopsis thaliana]
358387	1	473	8	12	9915	1	1	At5g20900	3,00E-08	68418.m02482 expressed protein
353242	2	473	8	12	10076	2	2	At3g17860	4,00E-09	68416.m02277 expressed protein
358628	1	475	6	14	4601	1	1	At4g21580	2,00E-47	68417.m03122 oxidoreductase, zinc-binding dehydrogenase family protein Pig3 Homo sapiens, PID:G2754812; contains Pfam zinc-binding dehydrogenase domain PF00107
358551	1	476	8	12	1490	1	1	At4g21060	4,00E-70	68417.m03045 galactosyltransferase family protein contains Pfam profile: PF01762 galactosyltransferase

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
355047	1	477	4	16	3512	2	1	At4g36890	5,00E-22	68417.m05230 glycosyl transferase family 43 protein low similarity to Galactosylgalactosylxylosylprotein 3-beta-glucuronosyltransferase 1, Homo sapiens [SP|Q9P2W7], Rattus norvegicus [SP|O35789]; contains Pfam domain Glycosyltransferase family 43 [PF03360]
355384	1	477	4	16	6411	1	1	At1g27600	6,00E-38	68414.m03368 glycosyl transferase family 43 protein similar to Galactosylgalactosylxylosylprotein 3-beta-glucuronosyltransferase 1, Rattus norvegicus [SP|O35789], Homo sapiens [SP|Q9P2W7]; contains Pfam domain Glycosyltransferase family 43 [PF03360]
357168	1	478	9	11	2523	2	2	At3g19540	9,00E-33	68416.m02477 expressed protein contains Pfam profile PF04788: Protein of unknown function (DUF620)
358544	1	479	9	11	6170	1	1	At1g28200	3,00E-60	68414.m03461 GRAM domain-containing protein / ABA-responsive protein-related similar to ABA-responsive protein [Hordeum vulgare] GI:4103635; contains Pfam profile PF02893: GRAM domain
359251	1	480	10	10	5945	1	1	At5g63530	3,00E-35	68418.m07974 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
354733	1	481	8	12	5097	1	1	At2g02170	5,00E-26	68415.m00153 remorin family protein contains Pfam domain, PF03763: Remorin, C-terminal region
357300	1	481	8	12	5097	1	1	At2g02170	3,00E-25	68415.m00153 remorin family protein contains Pfam domain, PF03763: Remorin, C-terminal region
353360	2	482	12	8	6425	1	1	At1g75560	2,00E-49	68414.m08781 zinc knuckle (CCHC-type) family protein contains Pfam domain, PF00098: Zinc knuckle
359642	1	482	12	8	6425	1	1	At1g75560	3,00E-72	68414.m08781 zinc knuckle (CCHC-type) family protein contains Pfam domain, PF00098: Zinc knuckle
355698	1	483	11	9	1069	1	1	At3g11710	5,00E-80	68416.m01435 lysyl-tRNA synthetase, putative / lysine--tRNA ligase, putative similar to SP|Q43776 Lysyl-tRNA synthetase (EC 6.1.1.6) (Lysine--tRNA ligase) {Lycopersicon esculentum}; contains Pfam profile PF00152: tRNA synthetases class II (D, K and N)
353182	2	483	11	9	1422	2	1	At1g70980	5,00E-127	68414.m08188 asparaginyl-tRNA synthetase, cytoplasmic, putative / asparagine-tRNA ligase, putative similar to SYNC1 protein GI:5670315 [SP|Q9SW96] from [Arabidopsis thaliana]
356473	1	483	11	9	1422	2	1	At1g70980	6,00E-60	68414.m08188 asparaginyl-tRNA synthetase, cytoplasmic, putative / asparagine-tRNA ligase, putative similar to SYNC1 protein GI:5670315 [SP|Q9SW96] from [Arabidopsis thaliana]

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
353575	3	483	11	9	1917	2	1	At4g26870	5,00E-53	68417.m03867 aspartyl-tRNA synthetase, putative / aspartate--tRNA ligase, putative simialr to aspartate-tRNA ligase (EC 6.1.1.12) from Drosophila melanogaster GI:4512034, Homo sapiens SP|P14868, Rattus norvegicus SP|P15178; contains Pfam profile PF00152 tRNA synthetases class II (D, K and N)
357866	1	484	7	13	3722	1	1	At3g63270	9,00E-49	68416.m07110 expressed protein
358266	1	488	9	10	3326	1	2	At4g18570	8,00E-71	68417.m02749 proline-rich family protein common family members: At3g25690, At4g04980, At5g61090 [Arabidopsis thaliana]
355051	1	488	9	10				At1g48280	4,00E-44	68414.m05393 hydroxyproline-rich glycoprotein family protein
355753	1	489	9	10	4323	1	2	At5g19980	4,00E-11	68418.m02378 integral membrane family protein contains Pfam profile: PF00892 Integral membrane protein; similar to LPG2 protein (GI:9998817) [Leishmania mexicana]
359097	1	489	9	10	9556	1	1	At3g07860	7,00E-30	68416.m00961 expressed protein
358900	1	490	9	10	4545	2	1	At3g02580	2,00E-98	68416.m00249 delta 7-sterol-C5-desaturase (STE1) identical to sterol-C5-desaturase GB:AAD12944 GI:4234768 from [Arabidopsis thaliana]
356164	1	490	9	10	4547	1	2	At2g29390	4,00E-33	68415.m03570 sterol 4-alpha-methyl-oxidase 1 (SMO1) nearly identical to sterol 4-alpha-methyl-oxidase GI:16973469 from [Arabidopsis thaliana]; identical to cDNA sterol 4-alpha-methyl-oxidase (SMO) partial cds, GI:16973431
354882	1	490	9	10	5178	2	2	At1g69640	2,00E-14	68414.m08012 acid phosphatase, putative similar to GI:5360721 from [Lupinus albus]
352943	3	491	8	11	8147	8	9	At5g59970	7,00E-46	68418.m07521 histone H4 identical to histone H4 from Lycopersicon esculentum GI:297150, Lolium temulentum SP|P02308, Acropora formosa GI:455652, Citrus jambhiri GI:16797797
353608	2	491	8	11	8147	8	9	At5g59970	2,00E-43	68418.m07521 histone H4 identical to histone H4 from Lycopersicon esculentum GI:297150, Lolium temulentum SP|P02308, Acropora formosa GI:455652, Citrus jambhiri GI:16797797
353785	2	491	8	11	8147	8	9	At5g59970	5,00E-46	68418.m07521 histone H4 identical to histone H4 from Lycopersicon esculentum GI:297150, Lolium temulentum SP|P02308, Acropora formosa GI:455652, Citrus jambhiri GI:16797797

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
354150	2	491	8	11	8147	8	9	At5g59970	1,00E-36	68418.m07521 histone H4 identical to histone H4 from Lycopersicon esculentum GI:297150, Lolium temulentum SP|P02308, Acropora formosa GI:455652, Citrus jambhiri GI:16797797
354278	3	491	8	11	8147	8	9	At5g59970	8,00E-38	68418.m07521 histone H4 identical to histone H4 from Lycopersicon esculentum GI:297150, Lolium temulentum SP|P02308, Acropora formosa GI:455652, Citrus jambhiri GI:16797797
354358	4	491	8	11	8147	8	9	At5g59970	1,00E-40	68418.m07521 histone H4 identical to histone H4 from Lycopersicon esculentum GI:297150, Lolium temulentum SP|P02308, Acropora formosa GI:455652, Citrus jambhiri GI:16797797
356761	1	491	8	11	8147	8	9	At5g59970	5,00E-26	68418.m07521 histone H4 identical to histone H4 from Lycopersicon esculentum GI:297150, Lolium temulentum SP|P02308, Acropora formosa GI:455652, Citrus jambhiri GI:16797797
358921	1	491	8	11	8147	8	9	At5g59970	1,00E-25	68418.m07521 histone H4 identical to histone H4 from Lycopersicon esculentum GI:297150, Lolium temulentum SP|P02308, Acropora formosa GI:455652, Citrus jambhiri GI:16797797
356872	1	493	10	9	5975	2	1	At4g15880	3,00E-52	68417.m02413 Ulp1 protease family protein contains Pfam profile PF02902: Ulp1 protease family, C-terminal catalytic domain; low similarity to sentrin/SUMO-specific protease [Homo sapiens] GI:6906859; identical to cDNA hypothetical protein, partial (1189 bp) GI:2326349
357762	1	493	10	9	5975	2	1	At4g15880	6,00E-15	68417.m02413 Ulp1 protease family protein contains Pfam profile PF02902: Ulp1 protease family, C-terminal catalytic domain; low similarity to sentrin/SUMO-specific protease [Homo sapiens] GI:6906859; identical to cDNA hypothetical protein, partial (1189 bp) GI:2326349
354609	1	493	10	9	8154	2	1	At1g60220	8,00E-07	68414.m06782 Ulp1 protease family protein contains Pfam profile PF02902: Ulp1 protease family, C-terminal catalytic domain
356545	1	493	10	9	8154	2	1	At1g60220	7,00E-07	68414.m06782 Ulp1 protease family protein contains Pfam profile PF02902: Ulp1 protease family, C-terminal catalytic domain
359124	1	494	9	10	475	1	1	At5g64410	2,00E-37	68418.m08091 oligopeptide transporter OPT family protein similar to SP|P40900 Sexual differentiation process protein isp4 {Schizosaccharomyces pombe}; contains Pfam profile PF03169: OPT oligopeptide transporter protein

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357672	1	494	9	10	743	2	1	At4g26590	3,00E-66	68417.m03833 oligopeptide transporter OPT family protein similar to SP|P40900 Sexual differentiation process protein isp4 {Schizosaccharomyces pombe}; contains Pfam profile PF03169: OPT oligopeptide transporter protein
355962	1	495	10	9	3244	2	3	At5g65780	6,00E-60	68418.m08277 branched-chain amino acid aminotransferase 5 / branched-chain amino acid transaminase 5 (BCAT5) nearly identical to SP|Q9FYA6 Branched-chain amino acid aminotransferase 5, chloroplast precursor (EC 2.6.1.42) (Atbcat-5) {Arabidopsis thaliana}; contains Pfam profile: PF01063 aminotransferase class IV
353957	3	496	11	8	8126	2	1	At1g10650	4,00E-38	68414.m01207 expressed protein
359645	1	497	9	10	4308	2	1	At1g50660	7,00E-20	68414.m05696 expressed protein similar to liver stage antigen-1 (GI:510184) [Plasmodium falciparum]; similar to Myosin II heavy chain, non muscle (Swiss-Prot:P08799) [Dictyostelium discoideum]; similar to liver stage antigen (GI:9916) [Plasmodium falciparum]; similar to Kinesin-like protein KLPA (Swiss-Prot:P28739) [Emericella nidulans]
355522	1	498	10	9				At1g63120	1,00E-20	68414.m07133 rhomboid family protein contains PFAM domain PF01694, Rhomboid family
358578	1	499	9	10	2006	4	4	At4g15415	1,00E-59	68417.m02357 serine/threonine protein phosphatase 2A (PP2A) regulatory subunit B' (B'gamma) identical to B' regulatory subunit of PP2A [Arabidopsis thaliana] GI:2160694; similar to SWISS-PROT:Q28653 serine/threonine protein phosphatase 2A, 56 kDa regulatory subunit, delta isoform (PP2A, B subunit, B' delta isoform, PP2A, B subunit, B56 delta isoform, PP2A, B subunit, PR61 delta isoform, PP2A, B subunit, R5 delta isoform, PP2A, B subunit, B'-gamma) [Oryctolagus cuniculus]; contains Pfam domain, PF01603: Protein phosphatase 2A regulatory B subunit (B56 family)

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354832	1	499	9	10	2116	2	1	At3g09880	1,00E-16	68416.m01178 serine/threonine protein phosphatase 2A (PP2A) regulatory subunit B' (B'beta) identical to B' regulatory subunit of PP2A [Arabidopsis thaliana] GI:2160692; similar to SWISS-PROT:Q28653 serine/threonine protein phosphatase 2A, 56 kDa regulatory subunit, delta isoform (PP2A, B subunit, B' delta isoform, PP2A, B subunit, B56 delta isoform, PP2A, B subunit, PR61 delta isoform, PP2A, B subunit, R5 delta isoform, PP2A, B subunit, B'-gamma) [Oryctolagus cuniculus]; contains Pfam domain, PF01603: Protein phosphatase 2A regulatory B subunit (B56 family)
355018	1	500	7	12	1899	1	1	At4g19180	5,00E-23	68417.m02830 nucleoside phosphatase family protein / GDA1/CD39 family protein low similarity to SP|O18956 Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5) (Ecto-apyrase) {Bos taurus}; contains Pfam profile PF01150: GDA1/CD39 (nucleoside phosphatase) family
356822	1	501	10	9	5970	1	1	At3g24740	9,00E-24	68416.m03106 expressed protein
357248	1	501	10	9	7265	1	1	At1g68140	3,00E-12	68414.m07783 expressed protein
354805	1	502	11	8	6754	2	2	At4g32610	4,00E-56	68417.m04643 mitochondrial glycoprotein family protein / MAM33 family protein low similarity to SP|P40513 Mitochondrial acidic protein MAM33, mitochondrial precursor {Saccharomyces cerevisiae}; contains Pfam profile PF02330: Mitochondrial glycoprotein
357141	1	502	11	8	6754	2	2	At4g32610	2,00E-10	68417.m04643 mitochondrial glycoprotein family protein / MAM33 family protein low similarity to SP|P40513 Mitochondrial acidic protein MAM33, mitochondrial precursor {Saccharomyces cerevisiae}; contains Pfam profile PF02330: Mitochondrial glycoprotein
353110	3	503	10	9	8960	2	1	At1g30500	7,00E-34	68414.m03729 CCAAT-binding transcription factor (CBF-B/NF-YA) family protein contains Pfam profile: PF02045 CCAAT-binding transcription factor (CBF-B/NF-YA)
359942	1	504	13	6	6528	1	2	At3g62580	1,00E-45	68416.m07030 expressed protein
353519	2	509	7	12	1923	2	1	At1g31830	3,00E-83	68414.m03909 amino acid permease family protein weak similarity to y+LAT1a (amino acid transporter) [Mus musculus] GI:3970791; contains Pfam profile PF00324: Amino acid permease
353370	2	512	9	10	390	1	1	At3g18524	7,00E-147	68416.m02355 DNA mismatch repair protein MSH2 (MSH2) identical to SP|O24617 DNA mismatch repair protein MSH2 (AtMsh2) {Arabidopsis thaliana}

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356476	1	512	9	10	390	1	1	At3g18524	1,00E-21	68416.m02355 DNA mismatch repair protein MSH2 (MSH2) identical to SP|O24617 DNA mismatch repair protein MSH2 (AtMsh2) {Arabidopsis thaliana}
359756	1	512	9	10	1332	1	1	At3g24320	6,00E-26	68416.m03054 DNA mismatch repair MutS family (MSH1) low similarity to SP|Q56239 DNA mismatch repair protein mutS {Thermus aquaticus}; contains Pfam profiles PF05190: MutS family domain IV, PF01624: MutS domain I, PF01541: Endo/excinuclease amino terminal domain
354232	2	512	9	10	2583	1	1	At5g54090	3,00E-58	68418.m06734 DNA mismatch repair MutS family protein low similarity to SP|Q56239 DNA mismatch repair protein mutS {Thermus aquaticus; contains Pfam profile PF00488: MutS domain V
353960	5	515	10	9	5053	2	2	At2g17390	4,00E-61	68415.m02008 ankyrin repeat family protein contains ankyrin repeats, Pfam:PF00023
356860	1	515	10	9	5053	2	2	At4g35450	3,00E-16	68417.m05039 ankyrin repeat family protein / AFT protein (AFT) contains ankyrin repeats, Pfam:PF00023; identical to cDNA AFT protein (AFT) GI:3478699
357535	1	515	10	9	5053	2	2	At4g35450	1,00E-52	68417.m05039 ankyrin repeat family protein / AFT protein (AFT) contains ankyrin repeats, Pfam:PF00023; identical to cDNA AFT protein (AFT) GI:3478699
355912	1	515	10	9	8645	1	1	At5g12320	1,00E-24	68418.m01448 ankyrin repeat family protein contains ankyrin repeats, Pfam:PF00023
355213	1	515	10	9	9074	2	1	At4g27780	1,00E-48	68417.m03990 acyl-CoA binding protein 2 (ACBP2) identical to acyl-CoA binding protein 2 [Arabidopsis thaliana] gi|12039034|gb|AAG46057
356263	1	515	10	9	9074	2	1	At5g53470	5,00E-24	68418.m06645 acyl-CoA binding protein, putative / ACBP, putative similar to acyl-CoA binding protein 2 [Arabidopsis thaliana] gi|12039034|gb|AAG46057
358243	1	515	10	9	9074	2	1	At5g53470	2,00E-10	68418.m06645 acyl-CoA binding protein, putative / ACBP, putative similar to acyl-CoA binding protein 2 [Arabidopsis thaliana] gi|12039034|gb|AAG46057
356892	1	516	10	9	1538	2	1	At4g14510	2,00E-19	68417.m02236 expressed protein contains Pfam domain, PF04581: Protein of unknown function (DUF578)
355783	1	516	10	9	5345	1	1	At2g28480	2,00E-27	68415.m03461 expressed protein contains Pfam profile PF01985: Uncharacterised protein family; expression supported by MPSS

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
354091	2	518	9	9	4034	3	2	At1g79330	4,00E-51	68414.m09245 latex-abundant protein, putative (AMC6) / caspase family protein similar to latex-abundant protein [Hevea brasiliensis] gb:AAD13216; contains Pfam domain, PF00656: ICE-like protease (caspase) p20 domain
355722	1	519	8	10	4008	2	1	At5g66460	3,00E-53	68418.m08381 (1-4)-beta-mannan endohydrolase, putative similar to (1-4)-beta-mannan endohydrolase [Coffea arabica] GI:10178872; contains Pfam profile PF00150: Cellulase (glycosyl hydrolase family 5)
358354	1	519	8	10	4008	2	1	At5g66460	4,00E-40	68418.m08381 (1-4)-beta-mannan endohydrolase, putative similar to (1-4)-beta-mannan endohydrolase [Coffea arabica] GI:10178872; contains Pfam profile PF00150: Cellulase (glycosyl hydrolase family 5)
354409	2	521	8	10	5510	2	2	At2g29670	2,00E-44	68415.m03606 expressed protein
359327	1	522	9	9	4505	2	1	At2g33280	4,00E-22	68415.m04079 integral membrane transporter family protein contains 9 transmembrane domains; contains Pfam PF03092: BT1 family; contains TIGRFAMS TIGR00788: folate/biopterin transporter
354124	2	523	10	8	842	1	1	At2g28320	3,00E-54	68415.m03442 pleckstrin homology (PH) domain-containing protein / lipid-binding START domain-containing protein contains Pfam profiles PF01852: START domain, PF00169: PH domain
358770	1	523	10	8	842	1	1	At2g28320	1,00E-20	68415.m03442 pleckstrin homology (PH) domain-containing protein / lipid-binding START domain-containing protein contains Pfam profiles PF01852: START domain, PF00169: PH domain
353784	2	525	9	9	5846	1	1	At1g08560	3,00E-20	68414.m00949 syntaxin-related protein KNOLLE (KN) / syntaxin 111 (SYP111) identical to SP|Q42374 Syntaxin-related protein KNOLLE (Syntaxin 111) (AtSYP111) {Arabidopsis thaliana}; BAC F22O13 has a deletion of a cytosine at position 7887
357774	1	526	8	10	1984	2	1	At5g61900	3,00E-65	68418.m07767 copine BONZAI1 (BON1) nearly identical to BONZAI1 [Arabidopsis thaliana] GI:15487382; contains Pfam profile PF00168: C2 domain
353691	2	526	8	10	3392	2	1	At5g14420	6,00E-103	68418.m01687 copine-related low similarity to SP|Q99829 Copine I {Homo sapiens}
358308	1	526	8	10	3392	2	1	At5g14420	1,00E-29	68418.m01687 copine-related low similarity to SP|Q99829 Copine I {Homo sapiens}
355269	1	526	8	10	4672	1	1	At5g63970	7,00E-35	68418.m08032 copine-related low similarity to SP|Q99829 Copine I {Homo sapiens}
353371	2	526	8	10				At1g67800	2,00E-17	68414.m07738 copine-related low similarity to SP|Q99829 Copine I {Homo sapiens}

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
356580	1	527	6	12	306	1	2	At1g11720	2,00E-51	68414.m01345 starch synthase, putative strong similarity to soluble-starch-synthase [Solanum tuberosum] GI:1911166
357880	1	527	6	12	1381	1	1	At1g32900	3,00E-38	68414.m04053 starch synthase, putative similar to starch synthase SP:Q42857 from [Ipomoea batatas]
359629	1	527	6	12	5026	1	1	At5g65685	6,00E-18	68418.m08268 soluble glycogen synthase-related contains weak similarity to Soluble glycogen synthase, chloroplast precursor (EC 2.4.1.11) (SS III) (Swiss-Prot:Q43846) [Solanum tuberosum]
353373	3	529	10	8	95	1	1	At3g23890	2,00E-35	68416.m03002 DNA topoisomerase, ATP-hydrolyzing / DNA topoisomerase II / DNA gyrase (TOP2) identical to SP|P30182 DNA topoisomerase II (EC 5.99.1.3) {Arabidopsis thaliana}
356038	1	530	7	11	1742	2	1	At2g23150	2,00E-16	68415.m02765 NRAMP metal ion transporter 3 (NRAMP3) identical to metal transporter Nramp3 [Arabidopsis thaliana] gi|6468012|gb|AAF13278; member of the natural resistance-associated macrophage protein (NRAMP) metal transporter family, PMID:11500563
353351	2	534	8	10	2307	2	2	At3g13930	7,00E-136	68416.m01759 dihydrolipoamide S-acetyltransferase, putative similar to dihydrolipoamide S-acetyltransferase [Zea mays] GI:5669871; contains Pfam profiles PF00198: 2-oxo acid dehydrogenases acyltransferase (catalytic domain), PF00364: Biotin-requiring enzyme, PF02817: e3 binding domain
359876	1	534	8	10	2844	1	1	At1g34430	1,00E-49	68414.m04277 dihydrolipoamide S-acetyltransferase, putative similar to dihydrolipoamide S-acetyltransferase (LTA2) [Arabidopsis thaliana] GI:5881963; contains Pfam profiles PF00198: 2-oxo acid dehydrogenases acyltransferase (catalytic domain), PF00364: Biotin-requiring enzyme, PF02817: e3 binding domain
359947	1	534	8	10	2869	2	1	At4g26910	1,00E-63	68417.m03871 2-oxoacid dehydrogenase family protein similar to SP|P36957 Dihydrolipoamide succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial precursor (EC 2.3.1.61) {Homo sapiens}; contains Pfam profiles PF00198: 2-oxo acid dehydrogenases acyltransferase (catalytic domain), PF00364: Biotin-requiring enzyme

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
356574	1	534	8	10	4014	1	1	At3g52200	3,00E-29	68416.m05733 dihydrolipoamide S-acetyltransferase, putative similar to dihydrolipoamide acetyltransferase (E2) subunit of PDC [Arabidopsis thaliana] GI:559395; contains Pfam profiles PF00198: 2-oxo acid dehydrogenases acyltransferase (catalytic domain), PF00364: Biotin-requiring enzyme, PF02817: e3 binding domain; supporting cDNA gi|5881964|gb|AF066080.1|AF066080
353405	2	535	8	10	5225	4	2	At1g35720	8,00E-90	68414.m04440 annexin 1 (ANN1) identical to annexin (AnnAt1) [Arabidopsis thaliana] GI:4959106
356882	1	535	8	10	6577	1	2	At1g68090	6,00E-53	68414.m07778 annexin 5 (ANN5) identical to calcium-binding protein annexin 5 [Arabidopsis thaliana] GI:12667520
352984	22	535	8	10				At5g12380	8,00E-98	68418.m01456 annexin, putative similar to annexin [Fragaria x ananassa] GI:6010777, annexin p33 [Zea mays] GI:6272285; contains Pfam profile PF00191: Annexin
353605	6	537	8	10	263	1	1	At1g44900	0	68414.m05144 DNA replication licensing factor, putative similar to DNA replication licensing factor MCM2 from {Xenopus laevis} SP|P55861, SP|P49736 {Homo sapiens}; contains Pfam profile PF00493: MCM2/3/5 family
352946	2	537	8	10	449	1	1	At5g44635	4,00E-125	68418.m05469 minichromosome maintenance family protein / MCM family protein similar to SP|P97311 DNA replication licensing factor MCM6 {Mus musculus}; contains Pfam profile PF00493: MCM2/3/5 family
354918	1	537	8	10	463	1	1	At4g02060	9,00E-93	68417.m00276 prolifera protein (PRL) / DNA replication licensing factor Mcm7 (MCM7) identical to DNA replication licensing factor Mcm7 SP|P43299 PROLIFERA protein {Arabidopsis thaliana}; contains Pfam profile PF00493: MCM2/3/5 family
358497	1	537	8	10	540	1	1	At2g16440	2,00E-99	68415.m01883 DNA replication licensing factor, putative similar to SP|P49717 DNA replication licensing factor MCM4 (CDC21 homolog) {Mus musculus}, SP|P29458 Cdc21 protein {Schizosaccharomyces pombe}; contains Pfam profile PF00493: MCM2/3/5 family
359474	1	537	8	10	540	1	1	At2g16440	6,00E-53	68415.m01883 DNA replication licensing factor, putative similar to SP|P49717 DNA replication licensing factor MCM4 (CDC21 homolog) {Mus musculus}, SP|P29458 Cdc21 protein {Schizosaccharomyces pombe}; contains Pfam profile PF00493: MCM2/3/5 family

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353651	2	537	8	10	599	1	1	At2g07690	7,00E-153	68415.m00993 minichromosome maintenance family protein / MCM family protein similar to SP|P55862 DNA replication licensing factor MCM5 (CDC46 homolog) {Xenopus laevis}; contains Pfam profile PF00493: MCM2/3/5 family
359819	1	537	8	10	682	1	1	At5g46280	4,00E-07	68418.m05697 DNA replication licensing factor, putative similar to SP|Q43704 DNA replication licensing factor MCM3 homolog (Replication origin activator) (ROA protein) {Zea mays}; contains Pfam profile PF00493: MCM2/3/5 family
354651	1	537	8	10	1857	1	1	At3g09660	7,00E-50	68416.m01145 minichromosome maintenance family protein / MCM family protein similar to SP|P49717 DNA replication licensing factor MCM4 (CDC21 homolog) {Mus musculus}; contains Pfam profile PF00493: MCM2/3/5 family
355557	1	540	6	12	9685	1	1	At2g39440	9,00E-24	68415.m04841 expressed protein
354541	1	544	7	11	5556	1	1	At3g27090	3,00E-52	68416.m03388 expressed protein similar to gda-1 [Pisum sativum] GI:2765418
356697	1	544	7	11	5556	1	1	At3g27090	7,00E-16	68416.m03388 expressed protein similar to gda-1 [Pisum sativum] GI:2765418
359236	1	544	7	11	5556	1	1	At3g27090	5,00E-31	68416.m03388 expressed protein similar to gda-1 [Pisum sativum] GI:2765418
353788	6	544	7	11	8477	1	2	At2g32910	3,00E-37	68415.m04035 expressed protein
353966	3	544	7	11	8477	1	2	At2g32910	2,00E-09	68415.m04035 expressed protein
355262	1	544	7	11	8477	1	2	At2g32910	1,00E-07	68415.m04035 expressed protein
354691	1	549	7	10	409	1	1	At1g03370	2,00E-24	68414.m00316 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(GI:6980525); similar to Synaptotagmin III (SytIII) (Swiss-Prot:P40748) [Rattus norvegicus]
353518	12	553	6	11	3538	2	5	At1g76690	1,00E-158	68414.m08924 12-oxophytodienoate reductase (OPR2) identical to 12-oxophytodienoate reductase OPR2 GB:AAC78441 [Arabidopsis thaliana]
354610	1	553	6	11	3538	2	5	At1g76690	3,00E-70	68414.m08924 12-oxophytodienoate reductase (OPR2) identical to 12-oxophytodienoate reductase OPR2 GB:AAC78441 [Arabidopsis thaliana]
356019	1	553	6	11	3538	2	5	At1g76690	6,00E-45	68414.m08924 12-oxophytodienoate reductase (OPR2) identical to 12-oxophytodienoate reductase OPR2 GB:AAC78441 [Arabidopsis thaliana]

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
358176	1	555	13	4				At2g32295	1,00E-24	68415.m03948 EXS family protein / ERD1/XPR1/SYG1 family protein low similarity to xenotropic and polytropic murine leukemia virus receptor [Mustela vison] GI:6093316; contains Pfam profile PF03124: EXS family
355260	1	556	7	10	5194	1	1	At5g26210	1,00E-46	68418.m03119 PHD finger family protein contains Pfam domain, PF00628: PHD-finger
359154	1	556	7	10	5194	1	1	At5g26210	7,00E-36	68418.m03119 PHD finger family protein contains Pfam domain, PF00628: PHD-finger
359406	1	556	7	10	5194	1	1	At5g26210	5,00E-51	68418.m03119 PHD finger family protein contains Pfam domain, PF00628: PHD-finger
353687	2	556	7	10	6040	2	2	At5g05610	3,00E-47	68418.m00611 PHD finger family protein contains Pfam domain, PF00628: PHD-finger
358285	1	556	7	10				At5g20510	4,00E-16	68418.m02437 PHD finger family protein contains Pfam domain, PF00628: PHD-finger
354074	2	557	5	12	8127	2	1	At5g15120	5,00E-07	68418.m01771 expressed protein
355782	1	558	10	7	461	2	1	At3g63460	5,00E-36	68416.m07146 WD-40 repeat family protein hypothetical protein contains similarity to ec31p [Oryza sativa] gi|13928450|dbj|BAB47154; contains Pfam profile PF00400: WD domain, G-beta repeat
356272	1	558	10	7	461	2	1	At3g63460	9,00E-52	68416.m07146 WD-40 repeat family protein hypothetical protein contains similarity to ec31p [Oryza sativa] gi|13928450|dbj|BAB47154; contains Pfam profile PF00400: WD domain, G-beta repeat
357039	1	558	10	7	1794	2	1	At2g19520	7,00E-53	68415.m02281 WD-40 repeat protein (MSI4) contains 6 (4 significant) WD-40 repeats (PF0400); identical to WD-40 repeat protein MSI4 (SP:O22607) [Arabidopsis thaliana]
359054	1	558	10	7	1794	2	1	At2g19520	7,00E-77	68415.m02281 WD-40 repeat protein (MSI4) contains 6 (4 significant) WD-40 repeats (PF0400); identical to WD-40 repeat protein MSI4 (SP:O22607) [Arabidopsis thaliana]
358533	1	558	10	7	2320	1	2	At2g19540	2,00E-57	68415.m02283 transducin family protein / WD-40 repeat family protein contains WD-40 repeats (PF00400); similar to Glutamate-rich WD repeat protein (GRWD) (SP:Q9BQ67)[Homo sapiens]
354043	3	558	10	7	2519	1	1	At5g58230	8,00E-122	68418.m07290 WD-40 repeat protein (MSI1) contains 6 WD-40 repeats (PF0400); identical to WD-40 repeat protein (SP:O22467) [Arabidopsis thaliana]
359804	1	558	10	7	2519	1	1	At5g58230	2,00E-44	68418.m07290 WD-40 repeat protein (MSI1) contains 6 WD-40 repeats (PF0400); identical to WD-40 repeat protein (SP:O22467) [Arabidopsis thaliana]

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
359102	1	558	10	7	4637	2	1	At1g20540	4,00E-72	68414.m02559 transducin family protein / WD-40 repeat family protein contains 6 WD-40 repeats (PF00400); similar to Rbap46 polypeptide (GI:9454362) [Gallus gallus]
356911	1	559	9	8	7309	1	3	At1g19310	1,00E-24	68414.m02401 zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)
358974	1	559	9	8	9211	2	2	At3g58030	4,00E-17	68416.m06469 zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)
353115	3	561	10	7	4174	2	1	At4g23800	1,00E-85	68417.m03422 high mobility group (HMG1/2) family protein similar to HMG2B [Homo sapiens] GI:32335; contains Pfam profile PF00505: HMG (high mobility group) box
357718	1	561	10	7	8708	1	1	At5g23420	5,00E-30	68418.m02747 high mobility group (HMG1/2) family protein similar to high mobility group protein 2 HMG2 [Ipomoea nil] GI:1052956; contains Pfam profile PF00505: HMG (high mobility group) box
353390	2	561	10	7	8729	2	1	At1g20693	6,00E-28	68414.m02592 high mobility group protein beta1 (HMGbeta1) / HMG protein beta1 nearly identical to HMG protein (HMGbeta1) [Arabidopsis thaliana] GI:2832359
353726	14	561	10	7	8729	2	1	At1g20693	9,00E-35	68414.m02592 high mobility group protein beta1 (HMGbeta1) / HMG protein beta1 nearly identical to HMG protein (HMGbeta1) [Arabidopsis thaliana] GI:2832359
353983	2	561	10	7	8729	2	1	At1g20693	8,00E-24	68414.m02592 high mobility group protein beta1 (HMGbeta1) / HMG protein beta1 nearly identical to HMG protein (HMGbeta1) [Arabidopsis thaliana] GI:2832359
354099	9	561	10	7	8729	2	1	At1g20693	2,00E-24	68414.m02592 high mobility group protein beta1 (HMGbeta1) / HMG protein beta1 nearly identical to HMG protein (HMGbeta1) [Arabidopsis thaliana] GI:2832359
354267	49	561	10	7	8729	2	1	At1g20693	3,00E-26	68414.m02592 high mobility group protein beta1 (HMGbeta1) / HMG protein beta1 nearly identical to HMG protein (HMGbeta1) [Arabidopsis thaliana] GI:2832359
357647	1	561	10	7	9403	1	1	At2g34450	4,00E-06	68415.m04227 high mobility group (HMG1/2) family protein similar to HMG protein [Arabidopsis thaliana] GI:2832361; contains Pfam profile PF00505: HMG (high mobility group) box
353736	3	561	10	7				At3g51880	1,00E-25	68416.m05690 high mobility group protein alpha (HMGalpha) / HMG protein alpha nearly identical to HMG protein (HMGalpha) [Arabidopsis thaliana] GI:2832357; contains Pfam profile PF00505: HMG (high mobility group) box

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
355697	1	562	9	8	1060	1	2	At5g22510	7,00E-80	68418.m02627 beta-fructofuranosidase, putative / invertase, putative / saccharase, putative / beta-fructosidase, putative similar to neutral invertase [Daucus carota] GI:4200165; contains Pfam profile PF04853: Plant neutral invertase
356945	1	562	9	8	1592	1	1	At4g09510	2,00E-136	68417.m01564 beta-fructofuranosidase, putative / invertase, putative / saccharase, putative / beta-fructosidase, putative similar to neutral invertase [Daucus carota] GI:4200165; contains Pfam profile PF04853: Plant neutral invertase
353203	2	563	11	6	2705	1	1	At3g27740	7,00E-37	68416.m03463 carbamoyl-phosphate synthase [glutamine-hydrolyzing] (CARA) / glutamine-dependent carbamoyl-phosphate synthase small subunit identical to carbamoyl phosphate synthetase small subunit GI:2462781 [Arabidopsis thaliana]
357578	1	563	11	6	2705	1	1	At3g27740	7,00E-43	68416.m03463 carbamoyl-phosphate synthase [glutamine-hydrolyzing] (CARA) / glutamine-dependent carbamoyl-phosphate synthase small subunit identical to carbamoyl phosphate synthetase small subunit GI:2462781 [Arabidopsis thaliana]
353285	2	564	8	9	4958	1	1	At1g25580	6,00E-18	68414.m03176 no apical meristem (NAM) family protein contains Pfam PF02365: No apical meristem (NAM) domain; similar to putative NAM protein (GP:21554371) (Arabidopsis thaliana)
359491	1	564	8	9				At5g16610	9,00E-45	68418.m01945 expressed protein
354672	1	566	9	8	9609	2	2	At5g48630	2,00E-58	68418.m06014 cyclin family protein similar to SP|P55168 Cyclin C {Gallus gallus}; contains Pfam profile PF00134: Cyclin, N-terminal domain
356805	1	569	7	10	2953	2	1	At1g51760	9,00E-48	68414.m05833 IAA-amino acid hydrolase 3 / IAA-Ala hydrolase 3 (IAR3) identical to IAA-Ala hydrolase (IAR3) [Arabidopsis thaliana] GI:3421384
358079	1	570	9	8	7153	1	2	At5g19750	2,00E-59	68418.m02348 peroxisomal membrane 22 kDa family protein similar to SP|P42925 22 kDa peroxisomal membrane protein {Mus musculus}; contains Pfam profile PF04117: Mpv17 / PMP22 family
353162	5	573	6	11	6718	1	1	At5g64200	2,00E-43	68418.m08063 arginine/serine-rich splicing factor SC35 contains similarity to splicing factor; contains Pfam profile PF00076: RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
356402	1	573	6	11	6718	1	1	At5g64200	1,00E-24	68418.m08063 arginine/serine-rich splicing factor SC35 contains similarity to splicing factor; contains Pfam profile PF00076: RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
356850	1	574	6	11	624	1	1	At1g55740	7,00E-13	68414.m06382 alkaline alpha galactosidase, putative similar to alkaline alpha galactosidase I [Cucumis melo] GI:29838629; contains Pfam profile PF05691: Raffinose synthase or seed imbibition protein Sip1
359966	1	574	6	11	723	1	1	At5g20250	1,00E-11	68418.m02411 raffinose synthase family protein / seed imbibition protein, putative (din10) similar to seed imbibition protein GB:AAA32975 GI:167100 from [Hordeum vulgare]; contains nonconsensus AT donor splice site at intron 1; contains Pfam profile PF05691: Raffinose synthase or seed imbibition protein Sip1; identical to cDNA seed imbibition protein (din10) partial cds GI:10834551
354592	1	576	6	11	3101	1	2	At3g50780	3,00E-15	68416.m05561 expressed protein
357983	1	576	6	11	3101	1	2	At3g50780	5,00E-77	68416.m05561 expressed protein
353446	3	576	6	11	4880	1	2	At2g13690	7,00E-63	68415.m01510 PRLI-interacting factor, putative similar to PRLI-interacting factor G [Arabidopsis thaliana] GI:11139264 (PMID:9765207); supporting cDNA gi|26450291|dbj|AK117606.1|
353019	2	577	9	8	1692	4	3	At5g55480	3,00E-40	68418.m06910 glycerophosphoryl diester phosphodiesterase family protein contains Pfam PF03009 : Glycerophosphoryl diester phosphodiesterase family; similar to Glycerophosphoryl diester phosphodiesterase precursor (Glycerophosphodiester phosphodiesterase) (Surface-exposed lipoprotein D) (Protein D) (ImmunoglobulinD-binding protein) (IGD-binding protein) (SP:Q06282) {Haemophilus influenzae}
355156	1	578	6	11	3747	1	1	At5g62740	1,00E-25	68418.m07876 band 7 family protein strong similarity to hypersensitive-induced response protein [Zea mays] GI:7716470; contains Pfam profile PF01145: SPFH domain / Band 7 family; supporting cDNA gi|17065547|gb|AY062850.1|
354368	3	578	6	11	4228	1	1	At5g51570	5,00E-112	68418.m06394 band 7 family protein similar to hypersensitive-induced response protein [Zea mays] GI:7716468; contains Pfam profile PF01145: SPFH domain / Band 7 family
359580	1	581	5	12	9445	1	2	At2g46150	6,00E-23	68415.m05739 expressed protein and genefinder

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
355266	1	589	6	10	7148	3	2	At2g24190	4,00E-26	68415.m02890 short-chain dehydrogenase/reductase (SDR) family protein contains INTERPRO family IPR002198 short-chain dehydrogenase/reductase (SDR) superfamily
355529	1	590	9	7	4	2	1	At1g03060	5,00E-62	68414.m00280 WD-40 repeat family protein / beige-related similar to BEIGE (GI:3928547) [Rattus norvegicus]; Similar to gb|U70015 lysosomal trafficking regulator from Mus musculus and contains 2 Pfam PF00400 WD-40, G-beta repeats. ESTs gb|T43386 and gb|AA395236 come from this gene
355709	1	590	9	7	15	1	1	At2g45540	2,00E-26	68415.m05663 WD-40 repeat family protein / beige-related contains Pfam PF02138: Beige/BEACH domain; contains Pfam PF00400: WD domain, G-beta repeat (3 copies)
355869	1	592	10	6	8621	3	2	At1g05870	1,00E-22	68414.m00615 expressed protein
356542	1	594	7	9	3907	1	2	At4g13370	8,00E-26	68417.m02090 expressed protein
357987	1	594	7	9	3907	1	2	At4g13370	2,00E-19	68417.m02090 expressed protein
352964	2	594	7	9	5685	2	1	At1g23790	4,00E-34	68414.m03001 expressed protein
355948	1	595	8	8	3728	2	1	At5g54630	6,00E-15	68418.m06802 zinc finger protein-related contains Prosite:PS00028 Zinc finger, C2H2 type, domain
355035	1	596	7	9	2228	2	1	At5g49980	4,00E-41	68418.m06189 transport inhibitor response protein, putative E3 ubiquitin ligase SCF complex F-box subunit; similar to F-box containing protein TIR1 GI:13249030 from [Populus tremula x Populus tremuloides]
357904	1	597	8	8	4280	2	1	At5g40580	6,00E-78	68418.m04925 20S proteasome beta subunit B (PBB2) (PRCFC) identical to 20S proteasome beta subunit PBB2 [Arabidopsis thaliana] GI:3421104, cDNA proteasome subunit prcfc GI:2511575
355153	1	597	8	8	5369	1	2	At4g31300	3,00E-113	68417.m04441 20S proteasome beta subunit A (PBA1) (PRCD) identical to cDNA proteasome subunit prcd GI:2511593
359365	1	597	8	8	5522	2	2	At1g21720	5,00E-96	68414.m02719 20S proteasome beta subunit C1 (PBC1) (PRCT) almost identical to GB:AAC32069 from [Arabidopsis thaliana], EST gb|T76747 comes from this gene; identical to cDNA proteasome subunit prct GI:2511567
354524	1	597	8	8	5877	1	2	At3g60820	5,00E-67	68416.m06804 20S proteasome beta subunit F1 (PBF1)
354639	1	597	8	8	5877	1	2	At3g60820	1,00E-35	68416.m06804 20S proteasome beta subunit F1 (PBF1)
359472	1	597	8	8	5877	1	2	At3g60820	1,00E-12	68416.m06804 20S proteasome beta subunit F1 (PBF1)

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
359896	1	598	11	5	1341	2	2	At4g22540	2,00E-29	68417.m03252 oxysterol-binding family protein similar to SP|P16258 Oxysterol-binding protein 1 {Oryctolagus cuniculus}; contains Pfam profiles PF00169: PH domain, PF01237: Oxysterol-binding protein
355532	1	598	11	5	1620	3	1	At5g02100	2,00E-08	68418.m00131 oxysterol-binding family protein similar to SWH1 [Saccharomyces cerevisiae] GI:402658; contains Pfam profile PF01237: Oxysterol-binding protein
358052	1	598	11	5	1620	3	1	At3g09300	3,00E-21	68416.m01104 oxysterol-binding family protein similar to SP|P22059 Oxysterol-binding protein 1 {Homo sapiens}; contains Pfam profile PF01237: Oxysterol-binding protein
359915	1	600	6	10	138	1	1	At4g10320	3,00E-43	68417.m01697 isoleucyl-tRNA synthetase, putative / isoleucine--tRNA ligase, putative similar to SP|P41252 Isoleucyl-tRNA synthetase, cytoplasmic (EC 6.1.1.5) (Isoleucine--tRNA ligase) (IleRS) (IRS) {Homo sapiens}; contains Pfam profile PF00133: tRNA synthetases class I (I, L, M and V)
356463	1	600	6	10	251	1	1	At4g04350	3,00E-54	68417.m00622 leucyl-tRNA synthetase, putative / leucine--tRNA ligase, putative similar to SP|P36430 Leucyl-tRNA synthetase (EC 6.1.1.4) (Leucine--tRNA ligase) (LeuRS) {Bacillus subtilis}; contains Pfam profile PF00133: tRNA synthetases class I (I, L, M and V)
353937	2	601	8	8	1344	2	1	At3g05030	4,00E-33	68416.m00546 sodium proton exchanger, putative (NHX2) similar to sodium proton exchanger Nhx1 GB:AAD16946 [Arabidopsis thaliana]; Member of The Monovalent Cation:Proton Antiporter (CPA1) Family, PMID:11500563
353374	2	602	6	10	9884	1	2	At2g04240	4,00E-20	68415.m00413 zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)
356000	1	602	6	10	9884	1	2	At2g04240	1,00E-25	68415.m00413 zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)
357468	1	603	9	7	170	1	1	At3g18290	1,00E-95	68416.m02326 zinc finger protein-related weak alignment to Pfam profiles: PF00097 Zinc finger, C3HC4 type (RING finger) (2 copies)
358160	1	603	9	7	170	1	1	At3g18290	3,00E-37	68416.m02326 zinc finger protein-related weak alignment to Pfam profiles: PF00097 Zinc finger, C3HC4 type (RING finger) (2 copies)
354752	1	603	9	7	4566	1	1	At5g25560	6,00E-96	68418.m03041 zinc finger (C3HC4-type RING finger) family protein contains Pfam domain PF00097: Zinc finger, C3HC4 type (RING finger)

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
357671	1	603	9	7				At5g18650	4,00E-52	68418.m02214 zinc finger (C3HC4-type RING finger) family protein contains Pfam domain PF00097: Zinc finger, C3HC4 type (RING finger)
357979	1	603	9	7				At5g18650	1,00E-50	68418.m02214 zinc finger (C3HC4-type RING finger) family protein contains Pfam domain PF00097: Zinc finger, C3HC4 type (RING finger)
353931	2	604	8	8	803	1	1	At4g30210	9,00E-10	68417.m04297 NADPH-cytochrome p450 reductase, putative / NADPH-ferrihemoprotein reductase, putative similar to NADPH-cytochrome P450 oxydoreductase from [Populus balsamifera subsp. trichocarpa x Populus deltoides] GI:13183564, GI:13183566
355150	1	604	8	8	803	1	1	At4g30210	6,00E-82	68417.m04297 NADPH-cytochrome p450 reductase, putative / NADPH-ferrihemoprotein reductase, putative similar to NADPH-cytochrome P450 oxydoreductase from [Populus balsamifera subsp. trichocarpa x Populus deltoides] GI:13183564, GI:13183566
353054	4	604	8	8				At4g24520	2,00E-88	68417.m03515 NADPH-cytochrome p450 reductase, putative / NADPH-ferrihemoprotein reductase, putative similar to NADPH-ferrihemoprotein reductase NADPH-cytochrome P450 oxydoreductase isoform 1 [Populus balsamifera subsp. trichocarpa x Populus deltoides] GI:13183562, SP|P37116 NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) [Vigna radiata] {Phaseolus aureus}
353155	2	605	8	8	2323	1	1	At4g38500	2,00E-79	68417.m05444 expressed protein contains Pfam profile: PF04765 protein of unknown function (DUF616)
355741	1	605	8	8	2811	2	1	At4g09630	1,00E-68	68417.m01583 expressed protein contains Pfam profile: PF04765 protein of unknown function (DUF616)
354941	1	606	9	7	1852	2	1	At5g07290	5,00E-28	68418.m00832 RNA recognition motif (RRM)-containing protein Mei2-like protein - Arabidopsis thaliana, EMBL:D86122
356169	1	607	10	6	6521	1	1	At4g22360	2,00E-13	68417.m03232 SWIB complex BAF60b domain-containing protein contains Pfam profile PF02201: BAF60b domain of the SWIB complex
359000	1	607	10	6	6521	1	1	At4g22360	2,00E-25	68417.m03232 SWIB complex BAF60b domain-containing protein contains Pfam profile PF02201: BAF60b domain of the SWIB complex
356097	1	607	10	6	9354	2	1	At4g34290	1,00E-12	68417.m04874 SWIB complex BAF60b domain-containing protein contains Pfam profile PF02201: BAF60b domain of the SWIB complex

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
359477	1	609	8	8	2593	1	1	At1g56350	1,00E-48	68414.m06479 peptide chain release factor, putative similar to SP|P28353 Peptide chain release factor 2 (RF-2). {Salmonella typhi}; contains Pfam profiles PF00472: Peptidyl-tRNA hydrolase domain, PF03462: PCRF domain
355727	1	609	8	8	9536	2	2	At3g59540	5,00E-32	68416.m06645 60S ribosomal protein L38 (RPL38B) 60S RIBOSOMAL PROTEIN L38 - Lycopersicon esculentum, EMBL:X69979
358043	1	609	8	8	9536	2	2	At3g59540	4,00E-11	68416.m06645 60S ribosomal protein L38 (RPL38B) 60S RIBOSOMAL PROTEIN L38 - Lycopersicon esculentum, EMBL:X69979
353472	2	610	6	10	1957	2	1	At4g29130	5,00E-67	68417.m04169 hexokinase 1 (HXK1) identical to hexokinase 1 [Arabidopsis thaliana] Swiss-Prot:Q42525
354089	2	610	6	10	1957	2	1	At2g19860	4,00E-74	68415.m02322 hexokinase 2 (HXK2) identical to hexokinase 2 [Arabidopsis thaliana] Swiss-Prot:P93834
358785	1	613	6	10	9080	1	2	At4g18593	8,00E-09	68417.m02753 dual specificity protein phosphatase-related contains weak similarity to Dual specificity protein phosphatase 12 (EC 3.1.3.48) (EC 3.1.3.16) (Dual-specificity tyrosine phosphatase YVH1) (Swiss-Prot:Q9UNI6) [Homo sapiens]
358167	1	614	6	10	1612	1	1	At3g59410	4,00E-07	68416.m06626 protein kinase family protein low similarity to GCN2 eIF2alpha kinase [Mus musculus] GI:6066585; contains Pfam profiles PF03129: Anticodon binding domain, PF00069: Protein kinase domain
359782	1	614	6	10	2716	1	1	At3g46100	1,00E-50	68416.m04988 histidyl-tRNA synthetase / histidine--tRNA ligase identical to histidyl-tRNA synthetase [Arabidopsis thaliana] GI:3659909
356231	1	616	8	8	7076	1	1	At5g04250	1,00E-45	68418.m00415 OTU-like cysteine protease family protein contains Pfam profile PF02338: OTU-like cysteine protease
353065	2	618	2	14	6988	1	2	At5g02960	2,00E-74	68418.m00239 40S ribosomal protein S23 (RPS23B) ribosomal protein S23, Fragaria x ananassa, PIR:S56673
353516	4	618	2	14	6988	1	2	At5g02960	2,00E-74	68418.m00239 40S ribosomal protein S23 (RPS23B) ribosomal protein S23, Fragaria x ananassa, PIR:S56673
353595	3	623	6	9	5406	1	2	At3g53620	2,00E-101	68416.m05923 inorganic pyrophosphatase, putative [soluble] / pyrophosphate phospho-hydrolase, putative / PPase, putative similar to magnesium dependent soluble inorganic pyrophosphatase [Solanum tuberosum] GI:2706450; contains Pfam profile PF00719: inorganic pyrophosphatase

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353121	2	624	10	5	1154	1	1	At3g06720	3,00E-105	68416.m00797 importin alpha-1 subunit, putative (IMPA1) similar to importin alpha-1 subunit (Karyopherin alpha-1 subunit, KAP alpha) [Arabidopsis thaliana] SWISS-PROT:Q96321
355635	1	624	10	5				At4g16143	5,00E-09	68417.m02447 importin alpha-2, putative (IMPA-2) similar to importin alpha 2 [Capsicum annuum] GI:13752562; contains Pfam profiles PF01749: Importin beta binding domain, PF00514: Armadillo/beta-catenin-like repeat; non-consensus GG donor splice site at exon 1 and 6; CT acceptor splice site at exon 2
356281	1	627	8	7	3888	1	1	At1g06550	3,00E-41	68414.m00694 enoyl-CoA hydratase/isomerase family protein similar to CHY1 [gi:8572760]; contains Pfam profile PF00388 enoyl-CoA hydratase/isomerase family protein
353675	3	627	8	7	4054	1	1	At4g31810	3,00E-69	68417.m04521 enoyl-CoA hydratase/isomerase family protein similar to CHY1 [gi:8572760]; contains Pfam profile PF00388 enoyl-CoA hydratase/isomerase family protein
360051	1	627	8	7	5876	3	1	At5g65940	3,00E-45	68418.m08301 3-hydroxyisobutyryl-coenzyme A hydrolase / CoA-thioester hydrolase (CHY1) identical to gi:8572760; contains Pfam profile PF00388 enoyl-CoA hydratase/isomerase family protein
357043	1	627	8	7				At3g60510	4,00E-63	68416.m06768 enoyl-CoA hydratase/isomerase family protein similar to enoyl-CoA-hydratase, Avicennia marina, EMBL:AF190450 [GI:6014701], CoA-thioester hydrolase CHY1 from Arabidopsis thaliana [GI:8572760]; contains Pfam profile PF00378 enoyl-CoA hydratase/isomerase family protein
352909	2	629	7	8	3424	2	2	At5g26740	1,00E-91	68418.m03164 expressed protein contains Pfam profile PF03619: Domain of unknown function
354067	2	629	7	8	4275	1	1	At4g21570	7,00E-65	68417.m03120 expressed protein contains Pfam profile PF03619: Domain of unknown function
355063	1	629	7	8				At1g11200	1,00E-37	68414.m01283 expressed protein contains Pfam profile PF03619: Domain of unknown function
353421	2	630	8	7	3731	2	1	At4g36130	3,00E-87	68417.m05142 60S ribosomal protein L8 (RPL8C) ribosomal protein L8, cytosolic, tomato, PIR1:R5TOL8
354461	3	630	8	7				At2g44065	1,00E-22	68415.m05480 ribosomal protein L2 family protein similar to ribosomal protein L2 [Gossypium arboreum] GI:17644114; contains Pfam profile PF03947: Ribosomal Proteins L2, C-terminal domain

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354111	2	633	8	7	1851	2	1	At3g62720	2,00E-73	68416.m07045 galactosyl transferase GMA12/MNN10 family protein low similarity to alpha-1,2-galactosyltransferase, Schizosaccharomyces pombe [SP|Q09174]
355013	1	636	6	9	3513	1	1	At1g27340	6,00E-70	68414.m03330 F-box family protein contains Pfam PF00646: F-box domain; similar to fim protein; similar to ESTs gb|T42445, gb|T76780, gb|AA650733, and emb|Z17748
357954	1	636	6	9	4028	1	2	At3g61590	2,00E-06	68416.m06898 F-box family protein contains weak hit to Pfam PF00646: F-box domain; stamina pistilloidia (Stp) - Pisum sativum, EMBL:AF004843
357229	1	637	7	8	3377	1	1	At2g40070	3,00E-50	68415.m04923 expressed protein
353885	5	638	8	7	5195	2	3	At1g29370	2,00E-56	68414.m03591 kinase-related similar to putative protein kinase (GI:11125348) [Homo sapiens]; similar to Paired box protein Pax-8 (Swiss-Prot:P47240) [Canis familiaris]
358341	1	639	6	9	325	2	1	At4g19710	8,00E-77	68417.m02895 bifunctional aspartate kinase/homoserine dehydrogenase, putative / AK-HSDH, putative similar to gb|X71364 [PIR|S46497] aspartate kinase / homoserine dehydrogenase from Arabidopsis thaliana
353942	2	639	6	9	1546	1	1	At5g13280	2,00E-116	68418.m01525 aspartate kinase identical to aspartate kinase [Arabidopsis thaliana] GI:4376158
353693	5	640	6	9	3864	1	2	At5g48385	1,00E-73	68418.m05980 expressed protein
355500	1	640	6	9	3864	1	2	At5g48385	7,00E-08	68418.m05980 expressed protein
357971	1	642	7	8	2436	1	1	At2g43710	2,00E-27	68415.m05434 acyl-[acyl-carrier-protein] desaturase / stearoyl-ACP desaturase (SSI2) identical to gi:15149310; contains Pfam profile PF03405: Fatty acid desaturase; identical to cDNA stearoyl ACP desaturase (SSI2), SSI2-FAB2 allele, GI:15149309
359101	1	642	7	8	2436	1	1	At2g43710	4,00E-58	68415.m05434 acyl-[acyl-carrier-protein] desaturase / stearoyl-ACP desaturase (SSI2) identical to gi:15149310; contains Pfam profile PF03405: Fatty acid desaturase; identical to cDNA stearoyl ACP desaturase (SSI2), SSI2-FAB2 allele, GI:15149309
355980	1	644	8	7	9969	1	1	At2g38905	6,00E-18	68415.m04782 hydrophobic protein, putative / low temperature and salt responsive protein, putative strong similarity to SP|Q9ZNQ7 Hydrophobic protein RCI2A (Low temperature and salt responsive protein LTI6A) {Arabidopsis thaliana}; contains Pfam profile PF01679: Uncharacterized protein family

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356838	1	644	8	7	10022	2	3	At3g05880	1,00E-19	68416.m00661 hydrophobic protein (RCI2A) / low temperature and salt responsive protein (LTI6A) identical to SP|Q9ZNQ7 Hydrophobic protein RCI2A (Low temperature and salt responsive protein LTI6A) {Arabidopsis thaliana}
353492	2	646	5	10	4176	2	1	At3g19770	4,00E-16	68416.m02502 vacuolar sorting protein 9 domain-containing protein / VPS9 domain-containing protein contains Pfam domain PF02204: Vacuolar sorting protein 9 (VPS9) domain
354668	1	647	3	12	2409	1	1	At1g76130	1,00E-18	68414.m08841 alpha-amylase, putative / 1,4-alpha-D-glucan glucanohydrolase, putative strong similarity to alpha-amylase GI:7532799 from [Malus x domestica];contains Pfam profile PF00128: Alpha amylase, catalytic domain
356566	1	647	3	12	2846	1	1	At1g69830	3,00E-57	68414.m08034 alpha-amylase, putative / 1,4-alpha-D-glucan glucanohydrolase, putative similar to SP|P17859 Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase) {Vigna mungo}, alpha-amylase [Malus x domestica] GI:7532799; contains Pfam profile PF00128: Alpha amylase, catalytic domain
352954	2	647	3	12	3404	1	8	At4g25000	7,00E-57	68417.m03587 alpha-amylase, putative / 1,4-alpha-D-glucan glucanohydrolase, putative similar to alpha-amylase from Vigna mungo SP|P17859, Ipomoea nil GI:21670851; contains Pfam profile PF00128: Alpha amylase, catalytic domain
358825	1	649	7	8	2629	3	1	At5g57690	1,00E-94	68418.m07211 diacylglycerol kinase, putative contains INTERPRO domain, IPR001206, DAG-kinase catalytic domain
353887	2	650	8	7	5454	1	1	At5g12040	4,00E-69	68418.m01407 carbon-nitrogen hydrolase family protein similar to Nit protein 2 [Homo sapiens] GI:9367116; contains Pfam profile PF00795: hydrolase, carbon-nitrogen family
359418	1	650	8	7	5640	1	1	At4g08790	2,00E-46	68417.m01448 nitrilase, putative similar to nitrilase 1 [Mus musculus] GI:3228668; contains Pfam profile PF00795: hydrolase, carbon-nitrogen family
358170	1	651	5	10	2340	2	1	At3g11170	9,00E-40	68416.m01355 omega-3 fatty acid desaturase, chloroplast (FAD7) (FADD) identical to omega-3 fatty acid desaturase, chloroplast precursor SP:P46310 [Arabidopsis thaliana (Mouse-ear cress)]; identical to Pfam profile PF00487: Fatty acid desaturase; identical to cDNA plastid fatty acid desaturase GI:809491

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354362	3	651	5	10	4053	1	1	At4g30950	1,00E-96	68417.m04394 omega-6 fatty acid desaturase, chloroplast (FAD6) (FADC) identical to GI:493068
353484	3	652	6	9	8753	2	2	At5g55160	6,00E-44	68418.m06877 small ubiquitin-like modifier 2 (SUMO) similar to ubiquitin-like protein SMT3 SP:P55852 from [Arabidopsis thaliana]; identical to cDNA small ubiquitin-like modifier 2 (SUMO) GI:22652843; contains Pfam profile PF00240: Ubiquitin family
353311	2	654	9	6	4196	3	1	At3g22810	3,00E-08	68416.m02875 expressed protein ; expression supported by MPSS
355550	1	655	6	9				At5g62100	2,00E-24	68418.m07795 BAG domain-containing protein similar to BAG domain containing proteins (At5g07220, At5g52060)
353938	3	664	7	7	3108	1	2	At2g03120	1,00E-130	68415.m00265 signal peptide peptidase family protein contains Pfam domain PF04258: Membrane protein of unknown function (DUF435)
358130	1	664	7	7	3157	1	1	At4g33410	7,00E-32	68417.m04748 signal peptide peptidase family protein contains Pfam domain PF04258: Membrane protein of unknown function (DUF435)
354365	3	665	4	10	1415	1	1	At1g02205	1,00E-59	68414.m00154 CER1 protein identical to maize gl1 homolog (glossy1 locus) GI:1209703 and CER1 GI:1199467 from [Arabidopsis thaliana]
354443	3	665	4	10	1415	1	1	At1g02205	5,00E-60	68414.m00154 CER1 protein identical to maize gl1 homolog (glossy1 locus) GI:1209703 and CER1 GI:1199467 from [Arabidopsis thaliana]
359683	1	666	8	6	543	1	1	At4g02510	3,00E-20	68417.m00343 chloroplast outer membrane protein, putative similar to chloroplast protein import component Toc159 [Pisum sativum] GI:8489806, chloroplast outer envelope protein 86 [Pisum sativum] GI:599958, GTP-binding protein [Pisum sativum] GI:576509
356201	1	666	8	6	660	2	1	At3g16620	1,00E-32	68416.m02124 chloroplast outer membrane protein, putative similar to chloroplast protein import component Toc159 [Pisum sativum] GI:8489806, chloroplast outer envelope protein 86 [Pisum sativum] GI:599958, GTP-binding protein [Pisum sativum] GI:576509
354455	4	666	8	6	2305	1	1	At5g20300	3,00E-09	68418.m02416 chloroplast outer membrane protein, putative similar to chloroplast protein import component Toc159 [Pisum sativum] GI:8489806, chloroplast outer envelope protein 86 [Pisum sativum] GI:599958, GTP-binding protein [Pisum sativum] GI:576509

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
357825	1	666	8	6	2305	1	1	At5g20300	2,00E-35	68418.m02416 chloroplast outer membrane protein, putative similar to chloroplast protein import component Toc159 [Pisum sativum] GI:8489806, chloroplast outer envelope protein 86 [Pisum sativum] GI:599958, GTP-binding protein [Pisum sativum] GI:576509
353250	2	666	8	6	6854	2	1	At5g05000	4,00E-72	68418.m00531 translocate of chloroplast 34 (TOC34) / GTP-binding protein (OEP34) contains Pfam PF04548: AIG1 family;contains TIGRFAM TIGR00991: GTP-binding protein and TIGR00231: small GTP-binding protein domain; 99.7% identical to atToc34 protein (GI:11557975) [Arabidopsis thaliana]; similar to Chain A, Pea Toc34 - A Novel Gtpase Of The Chloroplast Protein Translocon (GI:1865556) [Pisum sativum]; almost identical to SP:Q38906 Translocase of chloroplast 34; identical to cDNA GTP-binding protein (OEP34) GI:1151243
353597	4	666	8	6	6854	2	1	At5g05000	3,00E-112	68418.m00531 translocate of chloroplast 34 (TOC34) / GTP-binding protein (OEP34) contains Pfam PF04548: AIG1 family;contains TIGRFAM TIGR00991: GTP-binding protein and TIGR00231: small GTP-binding protein domain; 99.7% identical to atToc34 protein (GI:11557975) [Arabidopsis thaliana]; similar to Chain A, Pea Toc34 - A Novel Gtpase Of The Chloroplast Protein Translocon (GI:1865556) [Pisum sativum]; almost identical to SP:Q38906 Translocase of chloroplast 34; identical to cDNA GTP-binding protein (OEP34) GI:1151243
354859	1	667	8	6	7336	3	1	At1g65980	1,00E-69	68414.m07486 peroxiredoxin type 2, putative strong similarity to type 2 peroxiredoxin [Brassica rapa subsp. pekinensis] GI:4928472; contains Pfam profile: PF00578 AhpC/TSA (alkyl hydroperoxide reductase and thiol-specific antioxidant) family
359156	1	668	7	7	5758	1	1	At2g06530	1,00E-67	68415.m00724 SNF7 family protein contains Pfam domain, PF03357: SNF7 family
353797	4	668	7	7	6020	2	1	At1g73030	1,00E-82	68414.m08445 SNF7 family protein contains Pfam domain, PF03357: SNF7 family
359646	1	668	7	7	6043	1	2	At5g22950	8,00E-65	68418.m02683 SNF7 family protein contains Pfam domain, PF03357: SNF7 family
355164	1	668	7	7	6080	1	1	At5g44560	6,00E-28	68418.m05458 SNF7 family protein contains Pfam domain, PF03357: SNF7 family
353775	2	668	7	7	6286	1	1	At1g03950	1,00E-28	68414.m00380 SNF7 family protein contains Pfam domain, PF03357: SNF7 family

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357753	1	669	6	8	403	1	2	At2g25800	6,00E-84	68415.m03096 expressed protein
352902	2	670	7	7				At4g14950	9,00E-15	68417.m02297 expressed protein
359949	1	671	7	7	1478	1	1	At1g52980	2,00E-24	68414.m05995 GTP-binding family protein contains Pfam domain, PF01926: GTPase of unknown function
358022	1	671	7	7	2130	2	2	At2g27200	6,00E-28	68415.m03269 GTP-binding family protein contains Pfam domain, PF01926: GTPase of unknown function
353255	2	671	7	7	4193	1	1	At2g41670	2,00E-32	68415.m05148 GTP-binding family protein contains Pfam domain, PF01926: GTPase of unknown function
355609	1	671	7	7	4193	1	1	At2g41670	5,00E-18	68415.m05148 GTP-binding family protein contains Pfam domain, PF01926: GTPase of unknown function
358832	1	674	7	7	1830	1	1	At5g27680	3,00E-06	68418.m03319 DEAD/DEAH box helicase, putative similar to WRN (Werner syndrome) protein - Mus musculus, EMBL:AF241636; contains Pfam profiles PF00270: DEAD/DEAH box helicase, PF00271: Helicase conserved C-terminal domain, PF00627: UBA/TS-N domain
356994	1	675	7	7	8269	2	2	At3g26690	2,00E-20	68416.m03338 MutT/nudix family protein similar to SP|Q09790 Diadenosine 5',5'''-P1,P6-hexaphosphate hydrolase (EC 3.6.1.-) (Ap6A hydrolase) {Schizosaccharomyces pombe}; contains Pfam profile PF00293: NUDIX domain
353815	2	676	7	7	2438	2	2	At1g16300	5,00E-49	68414.m01951 glyceraldehyde 3-phosphate dehydrogenase, cytosolic, putative / NAD-dependent glyceraldehyde-3-phosphate dehydrogenase, putative similar to glyceraldehyde-3-phosphate dehydrogenase [Pinus sylvestris] GI:1100223; contains Pfam profiles PF02800: Glyceraldehyde 3-phosphate dehydrogenase C-terminal domain, PF00044: Glyceraldehyde 3-phosphate dehydrogenase NAD binding domain
354177	2	676	7	7	2438	2	2	At1g79530	1,00E-105	68414.m09271 glyceraldehyde 3-phosphate dehydrogenase, cytosolic, putative / NAD-dependent glyceraldehyde-3-phosphate dehydrogenase, putative similar to glyceraldehyde-3-phosphate dehydrogenase [Pinus sylvestris] GI:1100223; contains Pfam profiles PF02800: Glyceraldehyde 3-phosphate dehydrogenase C-terminal domain, PF00044: Glyceraldehyde 3-phosphate dehydrogenase NAD binding domain

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352896	3	676	7	7	2783	2	1	At3g04120	2,00E-53	68416.m00436 glyceraldehyde-3-phosphate dehydrogenase, cytosolic (GAPC) / NAD-dependent glyceraldehyde-3-phosphate dehydrogenase identical to SP|P25858 Glyceraldehyde 3-phosphate dehydrogenase, cytosolic (EC 1.2.1.12) {Arabidopsis thaliana}
353147	2	676	7	7	2783	2	1	At3g04120	2,00E-80	68416.m00436 glyceraldehyde-3-phosphate dehydrogenase, cytosolic (GAPC) / NAD-dependent glyceraldehyde-3-phosphate dehydrogenase identical to SP|P25858 Glyceraldehyde 3-phosphate dehydrogenase, cytosolic (EC 1.2.1.12) {Arabidopsis thaliana}
353206	2	676	7	7	2783	2	1	At3g04120	3,00E-74	68416.m00436 glyceraldehyde-3-phosphate dehydrogenase, cytosolic (GAPC) / NAD-dependent glyceraldehyde-3-phosphate dehydrogenase identical to SP|P25858 Glyceraldehyde 3-phosphate dehydrogenase, cytosolic (EC 1.2.1.12) {Arabidopsis thaliana}
355606	1	676	7	7	2783	2	1	At3g04120	2,00E-94	68416.m00436 glyceraldehyde-3-phosphate dehydrogenase, cytosolic (GAPC) / NAD-dependent glyceraldehyde-3-phosphate dehydrogenase identical to SP|P25858 Glyceraldehyde 3-phosphate dehydrogenase, cytosolic (EC 1.2.1.12) {Arabidopsis thaliana}
359729	1	676	7	7	2783	2	1	At1g13440	5,00E-24	68414.m01570 glyceraldehyde 3-phosphate dehydrogenase, cytosolic, putative / NAD-dependent glyceraldehyde-3-phosphate dehydrogenase, putative very strong similarity to SP|P25858 Glyceraldehyde 3-phosphate dehydrogenase, cytosolic (EC 1.2.1.12) {Arabidopsis thaliana}; contains Pfam profiles PF02800: Glyceraldehyde 3-phosphate dehydrogenase C-terminal domain, PF00044: Glyceraldehyde 3-phosphate dehydrogenase NAD binding domain
353171	2	677	8	6				At3g12710	2,00E-33	68416.m01588 methyladenine glycosylase family protein similar to SP|P05100 DNA-3-methyladenine glycosylase I (EC 3.2.2.20) (3-methyladenine-DNA glycosylase I, constitutive) {Escherichia coli}; contains Pfam profile PF03352: Methyladenine glycosylase
354549	1	678	7	7	6193	2	1	At4g17720	9,00E-55	68417.m02646 RNA recognition motif (RRM)-containing protein
353366	2	679	6	8	6537	1	1	At4g15545	7,00E-22	68417.m02375 expressed protein

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
353523	2	680	8	6	304	2	1	At1g76810	7,00E-107	68414.m08938 eukaryotic translation initiation factor 2 family protein / eIF-2 family protein similar to IF2 protein [Drosophila melanogaster] GI:7108770; contains Pfam profile PF03144: Elongation factor Tu domain 2
358597	1	680	8	6	304	2	1	At1g76810	4,00E-84	68414.m08938 eukaryotic translation initiation factor 2 family protein / eIF-2 family protein similar to IF2 protein [Drosophila melanogaster] GI:7108770; contains Pfam profile PF03144: Elongation factor Tu domain 2
353401	2	681	7	7	2880	3	1	At4g36280	7,00E-40	68417.m05159 ATP-binding region, ATPase-like domain-containing protein low similarity to microrchidia [Mus musculus] GI:5410255; contains Pfam profile PF02518: ATPase, histidine kinase-, DNA gyrase B-, and HSP90-like domain protein
353300	2	682	7	7	2996	1	1	At5g13710	2,00E-107	68418.m01596 sterol 24-C-methyltransferase, putative similar to SP:P25087 Sterol 24-C-methyltransferase, Delta(24)-sterol C- methyltransferase, Saccharomyces cerevisiae
354451	2	682	7	7	2996	1	1	At5g13710	3,00E-107	68418.m01596 sterol 24-C-methyltransferase, putative similar to SP:P25087 Sterol 24-C-methyltransferase, Delta(24)-sterol C- methyltransferase, Saccharomyces cerevisiae
355631	1	682	7	7	3268	2	1	At1g20330	4,00E-16	68414.m02537 S-adenosyl-methionine-sterol-C-methyltransferase identical to sterol-C-methyltransferase GI:1061040 from [Arabidopsis thaliana]
353557	2	683	7	7	2218	2	2	At4g12780	5,00E-87	68417.m02005 auxilin-related low similarity to SP|Q27974 Auxilin {Bos taurus}
357969	1	683	7	7	5358	1	2	At4g36520	2,00E-38	68417.m05185 trichohyalin-related low similarity to SP|Q07283 Trichohyalin {Homo sapiens}
354979	1	684	6	8	3147	1	1	At4g34430	9,00E-16	68417.m04893 DNA-binding family protein contains Pfam domains PF04433: SWIRM domain, PF00249: Myb-like DNA-binding domain and PF00569: Zinc finger, ZZ type
357102	1	684	6	8	5603	1	1	At2g47620	8,00E-11	68415.m05941 SWIRM domain-containing protein / DNA-binding family protein contains similarity to SWI/SNF complex 170 KDa subunit [Homo sapiens] gi|1549241|gb|AAC50694; contains Pfam domains PF04433: SWIRM domain, PF00249: Myb-like DNA-binding domain

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354375	2	685	4	10	1220	1	2	At1g22410	3,00E-58	68414.m02802 2-dehydro-3-deoxyphosphoheptonate aldolase, putative / 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase, putative / DAHP synthetase, putative similar to 3-deoxy-D-arabino-heptulosonate 7-phosphate GI:170224 from [Nicotiana tabacum], SP|P21357 from Solanum tuberosum; contains Pfam Class-II DAHP synthetase family domain PF01474
355894	1	685	4	10				At4g33510	2,00E-64	68417.m04759 2-dehydro-3-deoxyphosphoheptonate aldolase 2 / 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase 2 / DAHP synthetase 2 (DHS2) nearly identical to SP|Q00218
357340	1	687	8	6	4653	1	1	At3g14860	3,00E-11	68416.m01879 NHL repeat-containing protein contains Pfam profile PF01436: NHL repeat
352994	4	689	3	11	1036	2	3	At2g34250	1,00E-149	68415.m04190 protein transport protein sec61, putative similar to PfSec61 [Plasmodium falciparum] GI:3057044; contains Pfam profile PF00344: eubacterial secY protein
358964	1	690	7	7				At4g36730	2,00E-22	68417.m05212 G-box binding factor 1 (GBF1) identical to G-box binding factor 1 SP:P42774 from [Arabidopsis thaliana]; contains Pfam profile: PF00170 bZIP transcription factor
358873	1	692	8	6	8776	1	1	At1g49405	1,00E-14	68414.m05538 integral membrane protein, putative contains 4 transmembrane domains; contains Pfam PF04535 : Domain of unknown function (DUF588)
353069	2	693	5	9	1368	1	1	At1g50200	4,00E-34	68414.m05629 aminoacyl-tRNA synthetase family protein contains Pfam profiles: PF01411 tRNA synthetases class II (A), PF02272 DHHA1 domain
359158	1	694	7	7				At3g23210	5,00E-20	68416.m02926 basic helix-loop-helix (bHLH) family protein similar to hypothetical protein GB:CAB10220 from [Arabidopsis thaliana]
359434	1	694	7	7				At3g23210	4,00E-32	68416.m02926 basic helix-loop-helix (bHLH) family protein similar to hypothetical protein GB:CAB10220 from [Arabidopsis thaliana]
357386	1	695	4	10	8888	1	2	At4g01150	8,00E-17	68417.m00153 expressed protein
356068	1	696	7	7	766	1	2	At1g80930	5,00E-55	68414.m09495 MIF4G domain-containing protein / MA3 domain-containing protein similar to SP|Q9P6R9 Cell cycle control protein cwf22 {Schizosaccharomyces pombe}; contains Pfam profiles PF02854: MIF4G domain, PF02847: MA3 domain
354421	4	697	6	8	4829	1	2	At2g27230	9,00E-55	68415.m03272 transcription factor-related contains weak similarity to anthocyanin 1 (GI:10998404) [Petunia x hybrida]; identical to cDNA bHLH transcription factor (bHLH delta gene) gi:32563001

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357352	1	697	6	8	4829	1	2	At2g27230	1,00E-20	68415.m03272 transcription factor-related contains weak similarity to anthocyanin 1 (GI:10998404) [Petunia x hybrida]; identical to cDNA bHLH transcription factor (bHLH delta gene) gi:32563001
358127	1	700	6	8	1117	3	4	At5g64220	1,00E-33	68418.m08067 calmodulin-binding protein similar to anther ethylene-upregulated calmodulin-binding protein ER1 GI:11612392 from[Nicotiana tabacum]
356382	1	702	4	10	2534	2	2	At1g78130	4,00E-54	68414.m09105 transporter-related low similarity to spinster type III [Drosophila melanogaster] GI:12003974; contains Pfam profile: PF00083 major facilitator superfamily protein
359142	1	703	7	7	6192	1	2	At4g39870	2,00E-53	68417.m05649 expressed protein hypothetical protein, Schizosaccharomyces cerevisae, Z99168
359815	1	703	7	7	6192	1	2	At4g39870	9,00E-09	68417.m05649 expressed protein hypothetical protein, Schizosaccharomyces cerevisae, Z99168
359808	1	703	7	7	7710	1	2	At4g22740	3,00E-16	68417.m03281 glycine-rich protein
354389	2	704	6	8	6350	1	1	At2g19830	1,00E-62	68415.m02319 SNF7 family protein contains Pfam domain, PF03357: SNF7 family
354848	1	704	6	8	6350	1	1	At2g19830	5,00E-08	68415.m02319 SNF7 family protein contains Pfam domain, PF03357: SNF7 family
356451	1	705	2	12	8495	2	5	At2g22170	4,00E-24	68415.m02633 lipid-associated family protein contains PLAT/LH2 (Polycystin-1, Lipoxygenase, Alpha-Toxin/Lipoxygenase homology) domain Pfam:PF01477
358197	1	706	6	8	8781	1	1	At2g34460	5,00E-59	68415.m04229 flavin reductase-related low similarity to SP|P30043 Flavin reductase {Homo sapiens}
354190	7	706	6	8				At5g02240	6,00E-58	68418.m00146 expressed protein
354300	4	706	6	8				At5g02240	1,00E-94	68418.m00146 expressed protein
358759	1	710	9	5	2531	1	1	At5g25800	8,00E-35	68418.m03062 exonuclease family protein contains exonuclease domain, Pfam:PF00929
355442	1	711	7	7	3807	1	1	At5g57330	5,00E-15	68418.m07161 aldose 1-epimerase family protein contains Pfam profile PF01263 Aldose 1-epimerase
357748	1	711	7	7	3807	1	1	At5g57330	6,00E-12	68418.m07161 aldose 1-epimerase family protein contains Pfam profile PF01263 Aldose 1-epimerase
358180	1	711	7	7	3807	1	1	At5g57330	2,00E-36	68418.m07161 aldose 1-epimerase family protein contains Pfam profile PF01263 Aldose 1-epimerase
358621	1	711	7	7	3807	1	1	At5g57330	6,00E-34	68418.m07161 aldose 1-epimerase family protein contains Pfam profile PF01263 Aldose 1-epimerase
356399	1	711	7	7				At5g14500	5,00E-43	68418.m01698 aldose 1-epimerase family protein similar to apospory-associated protein C, Chlamydomonas reinhardtii, EMBL:AF195243 Pfam profile PF01263: Aldose 1-epimerase

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352955	2	712	8	6	6129	1	1	At5g22000	7,00E-77	68418.m02560 zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)
359184	1	712	8	6	8496	3	2	At5g15790	1,00E-34	68418.m01847 zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)
357106	1	714	4	10	7644	1	1	At4g23060	9,00E-19	68417.m03325 calmodulin-binding family protein contains Pfam profile PF00612: IQ calmodulin-binding motif
356927	1	714	4	10	8031	1	2	At4g14750	2,00E-14	68417.m02270 calmodulin-binding family protein contains Pfam profile PF00612: IQ calmodulin-binding motif
359003	1	714	4	10	8031	1	2	At4g14750	8,00E-28	68417.m02270 calmodulin-binding family protein contains Pfam profile PF00612: IQ calmodulin-binding motif
357057	1	715	5	9	1210	2	2	At5g23670	2,00E-68	68418.m02775 serine C-palmitoyltransferase (LCB2) identical to serine palmitoyltransferase [Arabidopsis thaliana] GI:9309380; similar to serine palmitoyltransferase from Solanum tuberosum [GI:4995890], Homo sapiens [SP|O15270], Mus musculus [SP|P97363]; contains Pfam profile PF00155: aminotransferase, classes I and II
356766	1	715	5	9	2187	1	3	At4g36480	9,00E-21	68417.m05180 aminotransferase class I and II family protein similar to Serine palmitoyltransferase 1 (EC 2.3.1.50) from Homo sapiens [SP|O15269], Mus musculus [SP|O35704], Cricetulus griseus [SP|O54695]
358438	1	716	4	10	763	4	1	At5g01320	1,00E-106	68418.m00044 pyruvate decarboxylase, putative strong similarity to pyruvate decarboxylase 1 [Vitis vinifera] GI:10732644; contains InterPro entry IPR000399: Pyruvate decarboxylase
358772	1	716	4	10	763	4	1	At5g54960	2,00E-73	68418.m06845 pyruvate decarboxylase, putative strong similarity to pyruvate decarboxylase 1 [Vitis vinifera] GI:10732644; contains InterPro entry IPR000399: Pyruvate decarboxylase
359877	1	716	4	10	763	4	1	At5g01320	1,00E-94	68418.m00044 pyruvate decarboxylase, putative strong similarity to pyruvate decarboxylase 1 [Vitis vinifera] GI:10732644; contains InterPro entry IPR000399: Pyruvate decarboxylase
353199	2	722	7	6	9681	2	2	At5g49230	4,00E-22	68418.m06094 drought-responsive family protein similar to drought-induced mRNA, Di19 [Arabidopsis thaliana] gi|469110|emb|CAA55321

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356897	1	722	7	6	9681	2	2	At3g06760	1,00E-17	68416.m00801 drought-responsive family protein similar to drought-induced mRNA, Di19 [Arabidopsis thaliana] gi|469110|emb|CAA55321
359333	1	723	9	4				At1g03270	2,00E-19	68414.m00305 expressed protein contains Pfam profile PF01595: Domain of unknown function
356351	1	724	5	8	5538	1	2	At1g32050	5,00E-61	68414.m03943 secretory carrier membrane protein (SCAMP) family protein contains Pfam domain, PF04144: SCAMP family
358673	1	725	6	7	4956	2	1	At2g44770	8,00E-19	68415.m05572 phagocytosis and cell motility protein ELMO1-related contains weak similarity to ELMO1 [Mus musculus] gi|16118551|gb|AAL14464
353677	2	726	7	6	4543	3	2	At4g28510	3,00E-69	68417.m04078 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
355235	1	727	7	6	2122	2	1	At3g06930	1,00E-57	68416.m00823 protein arginine N-methyltransferase family protein similar to protein arginine methyltransferase [Mus musculus] GI:5257221
358232	1	727	7	6	2725	2	1	At4g29510	3,00E-16	68417.m04210 protein arginine N-methyltransferase, putative similar to protein arginine N-methyltransferase 1-variant 2 [Homo sapiens] GI:7453575
354160	2	727	7	6	3053	1	1	At3g12270	4,00E-70	68416.m01532 protein arginine N-methyltransferase family protein similar to protein arginine N-methyltransferase 3 from {Rattus norvegicus} SP|O70467, {Homo sapiens} SP|O60678
356142	1	729	6	7	4564	1	2	At5g22400	2,00E-56	68418.m02613 rac GTPase activating protein, putative similar to rac GTPase activating protein 1 [Lotus japonicus] GI:3695059; contains Pfam profile PF00620: RhoGAP domain
353151	2	730	5	8	1241	2	1	At5g61790	2,00E-12	68418.m07754 calnexin 1 (CNX1) identical to calnexin homolog 1, Arabidopsis thaliana, EMBL:AT08315 [SP|P29402]
353652	4	730	5	8	1241	2	1	At5g07340	3,00E-45	68418.m00838 calnexin, putative identical to calnexin homolog 2 from Arabidopsis thaliana [SP|Q38798], strong similarity to calnexin homolog 1, Arabidopsis thaliana, EMBL:AT08315 [SP|P29402]; contains Pfam profile PF00262 calreticulin family
354681	1	730	5	8	1241	2	1	At5g61790	6,00E-52	68418.m07754 calnexin 1 (CNX1) identical to calnexin homolog 1, Arabidopsis thaliana, EMBL:AT08315 [SP|P29402]
354332	10	730	5	8	2226	2	2	At1g56340	7,00E-109	68414.m06476 calreticulin 1 (CRT1) identical to calreticulin (crt1) GI:2052379 [Arabidopsis thaliana]

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355715	1	730	5	8	2226	2	2	At1g09210	2,00E-40	68414.m01028 calreticulin 2 (CRT2) identical to SP|Q38858 Calreticulin 2 precursor {Arabidopsis thaliana}
355915	1	730	5	8	2226	2	2	At1g56340	1,00E-30	68414.m06476 calreticulin 1 (CRT1) identical to calreticulin (crt1) GI:2052379 [Arabidopsis thaliana]
359658	1	730	5	8	2226	2	2	At1g09210	1,00E-101	68414.m01028 calreticulin 2 (CRT2) identical to SP|Q38858 Calreticulin 2 precursor {Arabidopsis thaliana}
355343	1	730	5	8				At1g08450	6,00E-47	68414.m00935 calreticulin 3 (CRT3) identical to similar to SP|O04153 Calreticulin 3 precursor {Arabidopsis thaliana}
355956	1	732	6	7	6947	1	2	At3g07565	3,00E-21	68416.m00904 expressed protein
357458	1	733	6	7	8757	2	1	At1g60950	4,00E-20	68414.m06861 ferredoxin, chloroplast (PETF) identical to FERREDOXIN PRECURSOR GB:P16972 [SP|P16972] from [Arabidopsis thaliana]
357862	1	733	6	7	8843	1	2	At2g27510	5,00E-44	68415.m03327 ferredoxin, putative similar to non-photosynthetic ferredoxin from Citrus sinensis [GI:1360725], Ferredoxin, root R-B2 from Raphanus sativus [SP|P14937]; contains Pfam profile PF00111 2Fe-2S iron-sulfur cluster binding domain
353896	2	734	7	6	2439	1	3	At2g25737	1,00E-42	68415.m03087 expressed protein contains Pfam profile: PF01925 domain of unknown function DUF81
354707	1	734	7	6	2439	1	3	At2g25737	5,00E-21	68415.m03087 expressed protein contains Pfam profile: PF01925 domain of unknown function DUF81
356434	1	734	7	6	2439	1	3	At2g25737	8,00E-06	68415.m03087 expressed protein contains Pfam profile: PF01925 domain of unknown function DUF81
356879	1	734	7	6	2439	1	3	At2g25737	2,00E-08	68415.m03087 expressed protein contains Pfam profile: PF01925 domain of unknown function DUF81
358177	1	734	7	6	2439	1	3	At2g25737	3,00E-06	68415.m03087 expressed protein contains Pfam profile: PF01925 domain of unknown function DUF81
355875	1	734	7	6	2923	1	1	At2g36630	3,00E-28	68415.m04492 expressed protein contains Pfam profile: PF01925 domain of unknown function DUF81
354392	2	735	5	8	1760	2	2	At1g11910	2,00E-82	68414.m01374 aspartyl protease family protein contains Pfam profiles: PF00026 eukaryotic aspartyl protease, PF03489 surfactant protein B, PF05184 saposin-like type B, region 1
354044	2	736	3	10	6810	1	4	At1g13950	7,00E-71	68414.m01639 eukaryotic translation initiation factor 5A-1 / eIF-5A 1 identical to SP|Q9XI91 Eukaryotic translation initiation factor 5A-1 (eIF-5A 1) {Arabidopsis thaliana}
354051	2	736	3	10	6810	1	4	At1g13950	2,00E-24	68414.m01639 eukaryotic translation initiation factor 5A-1 / eIF-5A 1 identical to SP|Q9XI91 Eukaryotic translation initiation factor 5A-1 (eIF-5A 1) {Arabidopsis thaliana}

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
354011	4	739	7	6	6489	5	2	At4g38920	2,00E-57	68417.m05515 vacuolar ATP synthase 16 kDa proteolipid subunit 3 / V-ATPase 16 kDa proteolipid subunit 3 (AVAP3) (AVA-P3) identical to SP|P59227 Vacuolar ATP synthase 16 kDa proteolipid subunit 1/3/5 (EC 3.6.3.14) (V-ATPase 16 kDa proteolipid subunit 1/3/5) {Arabidopsis thaliana}; contains Pfam profile PF00137: ATP synthase subunit C
358927	1	739	7	6	6676	2	1	At4g32530	1,00E-55	68417.m04631 vacuolar ATP synthase, putative / V-ATPase, putative SP|P23968 Vacuolar ATP synthase 22 kDa proteolipid subunit (EC 3.6.3.14) {Saccharomyces cerevisiae}; contains Pfam profile PF00137: ATP synthase subunit C
358500	1	740	7	6	4205	2	1	At4g38790	6,00E-97	68417.m05492 ER lumen protein retaining receptor family protein similar to SP|P35402 ER lumen protein retaining receptor (HDEL receptor) {Arabidopsis thaliana}; contains Pfam profile PF00810: ER lumen protein retaining receptor
357726	1	740	7	6	5405	1	2	At3g25040	3,00E-50	68416.m03129 ER lumen protein retaining receptor, putative / HDEL receptor, putative similar to SP|P35402 ER lumen protein retaining receptor (HDEL receptor) {Arabidopsis thaliana}; contains Pfam profile PF00810: ER lumen protein retaining receptor
359565	1	741	6	7	9197	1	1	At4g15930	8,00E-10	68417.m02419 dynein light chain, putative similar to dynein light chain 2 [Mus musculus] GI:15545995; contains Pfam profile PF01221: Dynein light chain type 1
355683	1	741	6	7				At4g27360	1,00E-16	68417.m03927 dynein light chain, putative similar to SP|O02414 Dynein light chain LC6, flagellar outer arm {Anthocidaris crassispina}; contains Pfam profile PF01221: Dynein light chain type 1
355551	1	742	7	6	6970	1	1	At4g26220	5,00E-14	68417.m03775 caffeoyl-CoA 3-O-methyltransferase, putative similar to caffeoyl-CoA O-methyltransferase [GI:1622926][Nicotiana tabacum], GI:2960356 [Populus balsamifera subsp. trichocarpa], AF036095 [Pinus taeda]
358311	1	743	7	6	6855	2	1	At1g69430	2,00E-18	68414.m07978 hypothetical protein
355496	1	744	7	6				At3g17760	3,00E-57	68416.m02266 glutamate decarboxylase, putative similar to glutamate decarboxylase GB:Q07346 [Petunia x hybrida] (J. Biol. Chem. 268 (26), 19610-19617 (1993))

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
358346	1	745	9	4	2664	2	1	At5g03290	2,00E-93	68418.m00279 isocitrate dehydrogenase, putative / NAD+ isocitrate dehydrogenase, putative strong similarity to isocitrate dehydrogenase (NAD+) [Nicotiana tabacum] GI:3021506
357245	1	745	9	4	2683	3	1	At1g80560	8,00E-15	68414.m09445 3-isopropylmalate dehydrogenase, chloroplast, putative strong similarity to 3-ISOPROPYLMALATE DEHYDROGENASE PRECURSOR GB:P29102 SP|P29102 from [Brassica napus]
354480	1	746	4	9	3948	2	1	At3g01120	2,00E-66	68416.m00016 cystathionine gamma-synthase, chloroplast / O-succinylhomoserine (Thiol)-lyase (CGS) identical to SP|P55217 Cystathionine gamma-synthase, chloroplast precursor (EC 4.2.99.9) (CGS) (O-succinylhomoserine (Thiol)-lyase) {Arabidopsis thaliana}
354819	1	746	4	9	3948	2	1	At3g01120	1,00E-47	68416.m00016 cystathionine gamma-synthase, chloroplast / O-succinylhomoserine (Thiol)-lyase (CGS) identical to SP|P55217 Cystathionine gamma-synthase, chloroplast precursor (EC 4.2.99.9) (CGS) (O-succinylhomoserine (Thiol)-lyase) {Arabidopsis thaliana}
356503	1	746	4	9	3948	2	1	At3g01120	3,00E-55	68416.m00016 cystathionine gamma-synthase, chloroplast / O-succinylhomoserine (Thiol)-lyase (CGS) identical to SP|P55217 Cystathionine gamma-synthase, chloroplast precursor (EC 4.2.99.9) (CGS) (O-succinylhomoserine (Thiol)-lyase) {Arabidopsis thaliana}
359429	1	746	4	9	3948	2	1	At3g01120	7,00E-65	68416.m00016 cystathionine gamma-synthase, chloroplast / O-succinylhomoserine (Thiol)-lyase (CGS) identical to SP|P55217 Cystathionine gamma-synthase, chloroplast precursor (EC 4.2.99.9) (CGS) (O-succinylhomoserine (Thiol)-lyase) {Arabidopsis thaliana}
355969	1	747	7	6				At2g22125	3,00E-78	68415.m02628 C2 domain-containing protein contains Pfam profile PF00168: C2 domain
358012	1	747	7	6				At1g44120	7,00E-23	68414.m05096 C2 domain-containing protein / armadillo/beta-catenin repeat family protein similar to CCLS 65 [Silene latifolia] GI:2570102; contains Pfam profiles PF00514: Armadillo/beta-catenin-like repeat, PF00168: C2 domain

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
355129	1	750	6	7	1040	2	2	At4g16155	1,00E-84	68417.m02451 dihydrolipoamide dehydrogenase 2, plastidic / lipoamide dehydrogenase 2 (PTLPD2) identical to plastidic lipoamide dehydrogenase from Arabidopsis thaliana [gi:7159284]
358431	1	750	6	7	1337	1	2	At3g54660	2,00E-127	68416.m06048 gluthatione reductase, chloroplast nearly identical to SP|P42770 Glutathione reductase, chloroplast precursor (EC 1.8.1.7) (GR) (GRASE) {Arabidopsis thaliana}; identical to cDNA glutathione reductase GI:451197
354620	1	751	7	6	8467	1	1	At5g42700	8,00E-28	68418.m05201 transcriptional factor B3 family protein contains Pfam profile PF02362: B3 DNA binding domain
354218	2	751	7	6	8766	1	1	At5g58280	3,00E-43	68418.m07296 transcriptional factor B3 family protein contains Pfam profile PF02362: B3 DNA binding domain
354175	4	751	7	6	9794	2	3	At3g18990	8,00E-19	68416.m02410 transcriptional factor B3 family protein contains Pfam profile PF02362: B3 DNA binding domain
356099	1	752	5	8				At2g42600	9,00E-57	68415.m05272 phosphoenolpyruvate carboxylase, putative / PEP carboxylase, putative (PPC2) strong similarity to phosphoenolpyruvate carboxylase [Brassica napus] GI:507808; contains Pfam profile PF00311: phosphoenolpyruvate carboxylase
359950	1	753	6	7	3517	2	2	At3g51860	3,00E-19	68416.m05687 cation exchanger, putative (CAX3) similar to high affinity calcium antiporter CAX1 [Arabidopsis thaliana] gi|9256741|gb|AAB05913; Ca2+:Cation Antiporter (CaCA) Family member PMID:11500563; non-consensus AT-acceptor splice site at intron 1
354095	2	754	8	5	4362	6	2	At1g59359	2,00E-52	68414.m06677 40S ribosomal protein S2 (RPS2B) similar to ribosomal protein S2 GI:430711 from [Drosophila melanogaster]
355535	1	754	8	5	6904	1	1	At2g33800	2,00E-15	68415.m04147 ribosomal protein S5 family protein contains Pfam profiles PF03719: Ribosomal protein S5, C-terminal domain, PF00333: Ribosomal protein S5, N-terminal domain
358795	1	754	8	5	6904	1	1	At2g33800	4,00E-56	68415.m04147 ribosomal protein S5 family protein contains Pfam profiles PF03719: Ribosomal protein S5, C-terminal domain, PF00333: Ribosomal protein S5, N-terminal domain
353514	2	755	8	5	6647	1	2	At4g11600	1,00E-73	68417.m01858 glutathione peroxidase, putative
353501	2	756	6	7	3397	2	2	At5g45110	3,00E-69	68418.m05536 ankyrin repeat family protein / BTB/POZ domain-containing protein contains Pfam domain, PF00023: Ankyrin repeat and Pfam domain, PF00651: BTB/POZ domain

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
359015	1	756	6	7	3397	2	2	At5g45110	5,00E-33	68418.m05536 ankyrin repeat family protein / BTB/POZ domain-containing protein contains Pfam domain, PF00023: Ankyrin repeat and Pfam domain, PF00651: BTB/POZ domain
358151	1	757	4	9	6400	1	1	At3g10210	3,00E-38	68416.m01222 expressed protein similar to putative protein GB:CAA20045 [Arabidopsis thaliana]
358141	1	757	4	9	7410	1	1	At2g40600	1,00E-55	68415.m05008 appr-1-p processing enzyme family protein contains Pfam domain PF01661: Appr-1-p processing enzyme family
354714	1	758	6	7	739	1	1	At2g13560	1,00E-59	68415.m01495 malate oxidoreductase, putative similar to NAD-dependent malic enzyme 62 kDa isoform, mitochondrial precursor (EC 1.1.1.39) (NAD-ME) (SP:P37221) {Solanum tuberosum}
353179	2	758	6	7	891	1	1	At4g00570	2,00E-89	68417.m00080 malate oxidoreductase, putative similar to NAD-dependent malic enzyme 59 kDa isoform, mitochondrial precursor (EC 1.1.1.39) (NAD-ME) (SP:P37225) {Solanum tuberosum}
354134	4	759	5	8	5312	1	2	At4g32720	4,00E-79	68417.m04657 RNA recognition motif (RRM)-containing protein RNA-binding protein LAH1, Saccharomyces cerevisiae, PIR2:B48600; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)
353018	2	759	5	8	6688	1	1	At2g43970	2,00E-51	68415.m05468 La domain-containing protein contains Pfam profile PF05383: La domain
359108	1	759	5	8	8063	1	1	At5g46250	4,00E-06	68418.m05694 RNA recognition motif (RRM)-containing protein contains similarity to RNA-binding protein; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)
358743	1	761	6	7	127	1	1	At5g48600	1,00E-54	68418.m06011 structural maintenance of chromosomes (SMC) family protein similar to SP|P50532 Chromosome assembly protein XCAP-C {Xenopus laevis}; contains Pfam profiles PF02483: SMC family C-terminal domain, PF02463: RecF/RecN/SMC N terminal domain
354229	5	761	6	7	154	2	1	At5g62410	2,00E-108	68418.m07832 SMC2-like condensin, putative (SMC2) (TITAN3) very strong similarity to SMC2-like condensin (TITAN3) [Arabidopsis thaliana] GI:14279543; contains Pfam profiles PF02483: SMC family C-terminal domain, PF02463: RecF/RecN/SMC N terminal domain

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
357180	1	761	6	7	154	2	1	At5g62410	1,00E-25	68418.m07832 SMC2-like condensin, putative (SMC2) (TITAN3) very strong similarity to SMC2-like condensin (TITAN3) [Arabidopsis thaliana] GI:14279543; contains Pfam profiles PF02483: SMC family C-terminal domain, PF02463: RecF/RecN/SMC N terminal domain
358451	1	761	6	7	258	1	1	At3g54670	1,00E-28	68416.m06049 structural maintenance of chromosomes (SMC) family protein similar to SMC1 protein [Bos taurus] GI:4235253, 14S cohesin SMC1 subunit (SMC protein) [Xenopus laevis] GI:3328231; contains Pfam profiles PF02483: SMC family C-terminal domain, PF02463: RecF/RecN/SMC N terminal domain
359086	1	765	6	7				At3g14420	2,00E-63	68416.m01828 (S)-2-hydroxy-acid oxidase, peroxisomal, putative / glycolate oxidase, putative / short chain alpha-hydroxy acid oxidase, putative similar to (S)-2-hydroxy-acid oxidase, peroxisomal (Glycolate oxidase, GOX) (Short chain alpha-hydroxy acid oxidase) [Spinacia oleracea] SWISS-PROT:P05414
357957	1	766	7	6	6395	2	1	At5g27650	2,00E-20	68418.m03313 PWWP domain-containing protein hypothetical protein F22F7.12 - Arabidopsis thaliana, EMBL:AC009606
353795	2	766	7	6	7996	2	2	At5g02950	3,00E-18	68418.m00238 PWWP domain-containing protein predicted protein, Arabidopsis thaliana
355087	1	767	6	7	223	2	1	At3g55220	3,00E-80	68416.m06133 splicing factor, putative contains CPSF A subunit region (PF03178); contains weak WD-40 repeat (PF00400); similar to Splicing factor 3B subunit 3 (SF3b130)/spliceosomal protein/Splicing factor 3B subunit 3 (SAP 130)(KIAA0017)(SP:Q15393) Homo sapiens, EMBL:HSAJ1443_1
356667	1	767	6	7	223	2	1	At3g55220	4,00E-55	68416.m06133 splicing factor, putative contains CPSF A subunit region (PF03178); contains weak WD-40 repeat (PF00400); similar to Splicing factor 3B subunit 3 (SF3b130)/spliceosomal protein/Splicing factor 3B subunit 3 (SAP 130)(KIAA0017)(SP:Q15393) Homo sapiens, EMBL:HSAJ1443_1
354273	2	769	2	11	8028	2	9	At4g14320	7,00E-56	68417.m02206 60S ribosomal protein L36a/L44 (RPL36aB)
354364	2	769	2	11	8028	2	9	At4g14320	9,00E-56	68417.m02206 60S ribosomal protein L36a/L44 (RPL36aB)
359392	1	770	6	7	8077	1	1	At5g35330	1,00E-43	68418.m04188 methyl-CpG-binding domain-containing protein similar to methyl-CpG binding protein MBD4 [Mus musculus] GI:3800807; contains Pfam profile PF01429: Methyl-CpG binding domain

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
354612	1	770	6	7	10296	1	1	At5g35320	8,00E-06	68418.m04186 expressed protein
357266	1	772	7	6	101	2	2	At4g32920	7,00E-11	68417.m04685 glycine-rich protein
353963	2	773	1	12	2034	1	4	At5g05010	6,00E-41	68418.m00532 clathrin adaptor complexes medium subunit-related contains pfam profile: PF00928 adaptor complexes medium subunit family
354646	1	773	1	12	2034	1	4	At5g05010	2,00E-61	68418.m00532 clathrin adaptor complexes medium subunit-related contains pfam profile: PF00928 adaptor complexes medium subunit family
356687	1	773	1	12	2034	1	4	At5g05010	6,00E-62	68418.m00532 clathrin adaptor complexes medium subunit-related contains pfam profile: PF00928 adaptor complexes medium subunit family
356870	1	773	1	12	2034	1	4	At5g05010	2,00E-22	68418.m00532 clathrin adaptor complexes medium subunit-related contains pfam profile: PF00928 adaptor complexes medium subunit family
359701	1	778	9	3	6667	1	1	At4g08455	1,00E-12	68417.m01394 BTB/POZ domain-containing protein Interpro IPR000210/ PS50097: BTBB/POZ domain; similar to POZ 56 protein (GI:17483747) [Mus musculus]
357038	1	780	5	7	5654	3	1	At1g03070	3,00E-32	68414.m00281 expressed protein low similarity to N-methyl-D-aspartate receptor-associated protein [Drosophila melanogaster] GI:567104; contains Pfam profile PF01027: Uncharacterized protein family UPF0005
354255	2	780	5	7				At4g15470	2,00E-76	68417.m02364 expressed protein low similarity to N-methyl-D-aspartate receptor-associated protein [Drosophila melanogaster] GI:567104; contains Pfam profile PF01027: Uncharacterized protein family UPF0005
355263	1	780	5	7				At4g15470	9,00E-33	68417.m02364 expressed protein low similarity to N-methyl-D-aspartate receptor-associated protein [Drosophila melanogaster] GI:567104; contains Pfam profile PF01027: Uncharacterized protein family UPF0005
354589	1	785	6	6	1737	1	1	At1g04780	2,00E-57	68414.m00474 ankyrin repeat family protein contains Pfam PF00023: Ankyrin repeat
359026	1	785	6	6	1737	1	1	At1g04780	2,00E-49	68414.m00474 ankyrin repeat family protein contains Pfam PF00023: Ankyrin repeat
353317	2	785	6	6				At3g04470	5,00E-25	68416.m00474 expressed protein
358930	1	785	6	6				At3g24210	6,00E-12	68416.m03038 ankyrin repeat family protein contains ankyrin repeats, Pfam domain PF00023
360006	1	786	6	6	569	1	1	At4g01810	1,00E-57	68417.m00238 protein transport protein-related related to Sec23 protein [Homo sapiens] gi|1296664|emb|CAA65774

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
356728	1	786	6	6	936	1	1	At2g21630	2,00E-75	68415.m02573 transport protein, putative similar to Swiss-Prot:Q15436 protein transport protein Sec23A [Homo sapiens]
355437	1	789	6	6	1111	1	1	At5g48300	7,00E-56	68418.m05966 glucose-1-phosphate adenylyltransferase small subunit 1 (APS1) / ADP-glucose pyrophosphorylase (ADG1) identical to SP|P55228
358501	1	789	6	6	1111	1	1	At5g48300	4,00E-122	68418.m05966 glucose-1-phosphate adenylyltransferase small subunit 1 (APS1) / ADP-glucose pyrophosphorylase (ADG1) identical to SP|P55228
353710	2	789	6	6				At1g27680	1,00E-38	68414.m03383 glucose-1-phosphate adenylyltransferase large subunit 2 (APL2) / ADP-glucose pyrophosphorylase identical to SP|P55230
358159	1	790	6	6	1968	1	1	At2g26870	6,00E-27	68415.m03224 phosphoesterase family protein low similarity to SP|Q9RGS8 Non-hemolytic phospholipase C precursor (EC 3.1.4.3) (Phosphatidylcholine cholinephosphohydrolase) {Burkholderia pseudomallei}; contains Pfam profile PF04185: Phosphoesterase family
358430	1	791	6	6	4689	1	2	At1g08540	5,00E-52	68414.m00946 RNA polymerase sigma subunit SigB (sigB) / sigma factor 2 (SIG2) identical to sigma factor SigB [Arabidopsis thaliana] GI:5478446, plastid RNA polymerase sigma-subunit [Arabidopsis thaliana] GI:2879922, sigma factor [Arabidopsis thaliana] GI:2597831, sigma factor 2 (SIG2) [Arabidopsis thaliana] GI:2353173; contains Pfam profiles PF04545: Sigma-70, region 4, PF04539: Sigma-70 region 3, PF04542: Sigma-70 region 2
358936	1	791	6	6	4748	1	1	At1g64860	3,00E-57	68414.m07353 RNA polymerase sigma subunit SigA (sigA) / sigma factor 1 (SIG1) identical to sigma factor SigA [Arabidopsis thaliana] GI:5478439, sigma factor 1 [Arabidopsis thaliana] GI:2353171, plastid RNA polymerase sigma-subunit [Arabidopsis thaliana] GI:2398851; contains Pfam profiles PF04545: Sigma-70, region 4, PF04539: Sigma-70 region 3, PF04542: Sigma-70 region 2
358994	1	793	6	6	1695	1	1	At1g09060	1,00E-52	68414.m01011 transcription factor jumonji (jmjC) domain-containing protein contains Pfam domain, PF02373: jmjC domain
355259	1	793	6	6				At4g00990	6,00E-22	68417.m00133 transcription factor jumonji (jmjC) domain-containing protein contains Pfam domain, PF02373: jmjC domain

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
356417	1	793	6	6				At4g21430	2,00E-07	68417.m03097 transcription factor jumonji (jmjC) domain-containing protein contains Pfam domain, PF02373: jmjC domain
358007	1	794	6	6	3436	1	1	At1g09340	2,00E-52	68414.m01045 expressed protein
356550	1	795	6	6	7136	2	3	At1g09575	2,00E-46	68414.m01074 expressed protein contains Pfam domain, PF04678: Protein of unknown function, DUF607
358299	1	798	8	4	6520	1	1	At5g42520	9,00E-19	68418.m05176 expressed protein
357479	1	798	8	4	7995	3	3	At2g01930	1,00E-19	68415.m00128 expressed protein
358606	1	798	8	4				At2g35550	2,00E-43	68415.m04355 expressed protein
352998	2	801	7	5	510	2	1	At2g47160	3,00E-58	68415.m05889 anion exchange family protein contains some similarity to SWISS-PROT:P04919 anion transport protein (anion exchange protein 1) [Mouse] {Mus musculus}
353264	2	801	7	5	510	2	1	At2g47160	1,00E-63	68415.m05889 anion exchange family protein contains some similarity to SWISS-PROT:P04919 anion transport protein (anion exchange protein 1) [Mouse] {Mus musculus}
353633	3	802	5	7	4146	1	1	At5g38470	3,00E-59	68418.m04650 DNA repair protein RAD23, putative similar to DNA repair by nucleotide excision (NER) RAD23 protein, isoform I GI:1914683 from [Daucus carota]
354702	1	802	5	7	4146	1	1	At5g38470	2,00E-09	68418.m04650 DNA repair protein RAD23, putative similar to DNA repair by nucleotide excision (NER) RAD23 protein, isoform I GI:1914683 from [Daucus carota]
356211	1	802	5	7	4146	1	1	At5g38470	7,00E-39	68418.m04650 DNA repair protein RAD23, putative similar to DNA repair by nucleotide excision (NER) RAD23 protein, isoform I GI:1914683 from [Daucus carota]
356122	1	802	5	7	4481	2	1	At1g16190	5,00E-40	68414.m01939 DNA repair protein RAD23, putative similar to DNA repair by nucleotide excision (NER) RAD23 protein, isoform II GI:1914685 from [Daucus carota]
357176	1	802	5	7	4481	2	1	At1g79650	1,00E-08	68414.m09289 DNA repair protein RAD23, putative similar to DNA repair by nucleotide excision (NER) RAD23 protein, isoform II GI:1914685 from [Daucus carota]; contains Pfam profiles PF00240: Ubiquitin family, PF00627: UBA/TS-N domain
355834	1	805	7	5				At1g20925	2,00E-49	68414.m02620 auxin efflux carrier family protein contains auxin efflux carrier domain, Pfam:PF03547

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
359967	1	806	7	5	1514	2	2	At1g36370	4,00E-110	68414.m04518 glycine hydroxymethyltransferase, putative / serine hydroxymethyltransferase, putative / serine/threonine aldolase, putative similar to serine hydroxymethyltransferase [Chlamydomonas reinhardtii] GI:17066746; contains Pfam profile PF00464: serine hydroxymethyltransferase
357913	1	806	7	5				At4g32520	2,00E-12	68417.m04629 glycine hydroxymethyltransferase, putative / serine hydroxymethyltransferase, putative / serine/threonine aldolase, putative similar to serine hydroxymethyltransferase [Chlamydomonas reinhardtii] GI:17066746; contains Pfam profile PF00464: serine hydroxymethyltransferase
360057	1	806	7	5				At4g32520	1,00E-12	68417.m04629 glycine hydroxymethyltransferase, putative / serine hydroxymethyltransferase, putative / serine/threonine aldolase, putative similar to serine hydroxymethyltransferase [Chlamydomonas reinhardtii] GI:17066746; contains Pfam profile PF00464: serine hydroxymethyltransferase
352904	2	807	5	7	7720	2	3	At2g45190	4,00E-53	68415.m05627 axial regulator YABBY1 (YABBY1) / abnormal floral organs protein (AFO) / filamentous flower protein (FIL) identical to YABBY1 [Arabidopsis thaliana] GI:4928749, abnormal floral organs protein (AFO) [Arabidopsis thaliana] GI:4322477; supporting cDNA gi|4322476|gb|AF087015.1|AF087015
353882	6	807	5	7	7720	2	3	At2g45190	3,00E-57	68415.m05627 axial regulator YABBY1 (YABBY1) / abnormal floral organs protein (AFO) / filamentous flower protein (FIL) identical to YABBY1 [Arabidopsis thaliana] GI:4928749, abnormal floral organs protein (AFO) [Arabidopsis thaliana] GI:4322477; supporting cDNA gi|4322476|gb|AF087015.1|AF087015
353063	4	807	5	7	8500	1	2	At2g26580	2,00E-40	68415.m03189 plant-specific transcription factor YABBY family protein contains Pfam profile: PF04690 YABBY protein
356441	1	808	7	5	232	2	1	At5g22780	1,00E-78	68418.m02663 adaptin family protein similar to SP|P18484 adaptor-related protein complex 2 alpha 2 subunit (Alpha-adaptin C) (Clathrin assembly protein complex 2 alpha-C large chain) {Rattus norvegicus}; contains Pfam profiles PF01602 Adaptin N terminal region, PF02883 Adaptin C-terminal domain
357379	1	809	2	10	5429	1	2	At1g67730	2,00E-63	68414.m07729 b-keto acyl reductase, putative (GLOSSY8) similar to b-keto acyl reductase GI:2586127 from [Hordeum vulgare]

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
357650	1	810	8	4				At5g01710	8,00E-40	68418.m00088 expressed protein
353430	2	812	7	5	942	1	2	At3g58560	3,00E-115	68416.m06527 endonuclease/exonuclease/phosphatase family protein similar to SP|P31384 Glucose-repressible alcohol dehydrogenase transcriptional effector (Carbon catabolite repressor protein 4) {Saccharomyces cerevisiae}; contains Pfam profile PF03372: Endonuclease/Exonuclease/phosphatase family
354599	1	813	3	9	7880	1	2	At4g20380	3,00E-48	68417.m02976 zinc finger protein (LSD1) identical to zinc-finger protein Lsd1 [Arabidopsis thaliana] gi|1872521|gb|AAC49660
356521	1	814	6	6	5666	3	2	At4g10610	9,00E-08	68417.m01735 RNA-binding protein, putative
358784	1	814	6	6	5666	3	2	At1g32790	1,00E-37	68414.m04042 RNA-binding protein, putative similar to RNA-binding protein GB:CAB40027 GI:4539439 from [Arabidopsis thaliana]
358805	1	814	6	6	5666	3	2	At1g32790	4,00E-32	68414.m04042 RNA-binding protein, putative similar to RNA-binding protein GB:CAB40027 GI:4539439 from [Arabidopsis thaliana]
359329	1	814	6	6	5666	3	2	At1g32790	2,00E-83	68414.m04042 RNA-binding protein, putative similar to RNA-binding protein GB:CAB40027 GI:4539439 from [Arabidopsis thaliana]
359914	1	817	5	7	6661	2	1	At4g35410	7,00E-81	68417.m05030 clathrin adaptor complex small chain family protein contains Pfam profile: PF01217 clathrin adaptor complex small chain
354866	1	819	7	5	8997	1	1	At3g57280	5,00E-20	68416.m06376 expressed protein contains Pfam profile PF03647: Uncharacterised protein family (UPF0136)
353908	4	819	7	5				At4g02840	6,00E-48	68417.m00384 small nuclear ribonucleoprotein D1, putative / snRNP core protein D1, putative / Sm protein D1, putative similar to small nuclear ribonucleoprotein Sm D1 (snRNP core protein D1, Sm-D1, Sm-D autoantigen) [Mouse] SWISS-PROT:P13641
358467	1	819	7	5				At3g43520	2,00E-15	68416.m04614 expressed protein contains Pfam profile PF03647: Uncharacterised protein family (UPF0136)
356862	1	822	4	8	923	1	1	At4g02260	3,00E-09	68417.m00305 RelA/SpoT protein, putative (RSH1) identical to RSH1 (RelA/SpoT homolog) [Arabidopsis thaliana] GI:7141304; contains Pfam profiles PF02824: TGS domain, PF01966: HD domain, PF04607: Region found in RelA / SpoT proteins

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
359314	1	822	4	8	1300	2	2	At3g14050	1,00E-57	68416.m01773 RelA/SpoT protein, putative (RSH2) nearly identical to RelA/SpoT homolog RSH2 [Arabidopsis thaliana] GI:7141306; contains Pfam profiles PF01966: HD domain, PF04607: Region found in RelA / SpoT proteins
356670	1	822	4	8	2402	1	2	At3g17470	1,00E-45	68416.m02232 RelA/SpoT domain-containing protein / calcium-binding EF-hand family protein contains INTERPRO:IPR002048 calcium-binding EF-hand domain, Pfam profile PF04607: Region found in RelA / SpoT proteins
356950	1	823	6	6	1699	1	1	At1g62390	1,00E-24	68414.m07039 octicosapeptide/Phox/Bem1p (PB1) domain-containing protein / tetratricopeptide repeat (TPR)-containing protein contains Pfam profiles PF00564: PB1 domain, PF00515: TPR Domain
356345	1	823	6	6	7241	1	1	At4g30480	1,00E-66	68417.m04328 tetratricopeptide repeat (TPR)-containing protein similar to SP|Q99614 Tetratricopeptide repeat protein 1 {Homo sapiens}; contains Pfam profile PF00515: TPR Domain
356956	1	825	5	7	700	1	2	At5g60790	5,00E-49	68418.m07627 ABC transporter family protein similar to ABC transporter homolog PnATH GI:7573600 from [Populus nigra]
354748	1	825	5	7	758	2	1	At5g64840	1,00E-30	68418.m08157 ABC transporter family protein
352915	2	828	7	5	1499	1	2	At1g69770	1,00E-71	68414.m08028 chromomethylase 3 (CMT3) nearly identical to chromomethylase CMT3 [Arabidopsis thaliana] GI:14583092, GI:14647157
353794	2	828	7	5				At4g19020	1,00E-81	68417.m02803 chromomethylase 2 (CMT2) nearly identical to chromomethylase CMT2 [Arabidopsis thaliana] GI:14583094
358600	1	828	7	5				At4g19020	1,00E-22	68417.m02803 chromomethylase 2 (CMT2) nearly identical to chromomethylase CMT2 [Arabidopsis thaliana] GI:14583094
358457	1	829	6	6	3502	1	1	At3g55360	6,00E-72	68416.m06148 3-oxo-5-alpha-steroid 4-dehydrogenase family protein / steroid 5-alpha-reductase family protein similar to synaptic glycoprotein SC2 spliced variant from Homo sapiens [EMBL:AF038958], SC2 from Rattus sp. [gi:256994]; contains Pfam 3-oxo-5-alpha-steroid 4-dehydrogenase domain PF02544

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359196	1	829	6	6	3502	1	1	At3g55360	3,00E-82	68416.m06148 3-oxo-5-alpha-steroid 4-dehydrogenase family protein / steroid 5-alpha-reductase family protein similar to synaptic glycoprotein SC2 spliced variant from Homo sapiens [EMBL:AF038958], SC2 from Rattus sp. [gi:256994]; contains Pfam 3-oxo-5-alpha-steroid 4-dehydrogenase domain PF02544
354109	2	830	7	5	3406	2	2	At3g45630	1,00E-20	68416.m04928 RNA recognition motif (RRM)-containing protein similar to SP|P34909 General negative regulator of transcription subunit 4 {Saccharomyces cerevisiae}; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)
354427	2	832	5	7	9298	1	1	At3g22550	3,00E-25	68416.m02849 senescence-associated protein-related similar to senescence-associated protein SAG102 (GI:22331931) [Arabidopsis thaliana]
353637	7	832	5	7	9816	2	1	At5g11460	4,00E-22	68418.m01338 senescence-associated protein-related similar to senescence-associated protein SAG102 (GI:22331931) [Arabidopsis thaliana]
354423	2	832	5	7	9816	2	1	At5g11460	8,00E-15	68418.m01338 senescence-associated protein-related similar to senescence-associated protein SAG102 (GI:22331931) [Arabidopsis thaliana]
353107	2	833	5	7	328	1	1	At2g16950	3,00E-49	68415.m01953 importin beta-2 subunit family protein similar to SP|Q92973 Importin beta-2 subunit (Transportin) {Homo sapiens}; contains Pfam profile PF03810: Importin-beta N-terminal domain
358984	1	833	5	7	496	1	1	At5g53480	7,00E-07	68418.m06646 importin beta-2, putative similar to importin-beta2 [Oryza sativa (japonica cultivar-group)] GI:3983665; contains Pfam profile PF03810: Importin-beta N-terminal domain
359721	1	834	9	3	7041	1	2	At2g17570	4,00E-11	68415.m02033 undecaprenyl pyrophosphate synthetase family protein / UPP synthetase family protein contains putative undecaprenyl diphosphate synthase domain [PF01255]; similar to dehydrodolichyl diphosphate synthetase (DEDOL-PP synthase) [GI:796076] and S. cerevisiae Rer2 [SP|P35196]
354758	1	836	6	6	1082	2	2	At2g22400	2,00E-29	68415.m02656 NOL1/NOP2/sun family protein contains Pfam profile PF01189: NOL1/NOP2/sun family
356485	1	837	5	7	1430	2	2	At3g59920	5,00E-22	68416.m06687 Rab GDP dissociation inhibitor (GDI2) identical to Rab GDP dissociation inhibitor AtGDI2 [Arabidopsis thaliana] GI:2446981
358392	1	837	5	7	1430	2	2	At2g44100	5,00E-27	68415.m05484 Rab GDP dissociation inhibitor (GDI1) identical to GDP dissociation inhibitor [Arabidopsis thaliana] GI:1655424

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359350	1	837	5	7	1430	2	2	At2g44100	1,00E-09	68415.m05484 Rab GDP dissociation inhibitor (GDI1) identical to GDP dissociation inhibitor [Arabidopsis thaliana] GI:1655424
357320	1	837	5	7				At5g09550	1,00E-57	68418.m01106 Rab GDP dissociation inhibitor, putative strong similarity to GDP dissociation inhibitor protein OsGDI1 [Oryza sativa] GI:2384758; contains Pfam profile PF00996: GDP dissociation inhibitor
353139	2	838	5	7	6872	1	1	At3g12490	2,00E-36	68416.m01555 cysteine protease inhibitor, putative / cystatin, putative similar to PRLI-interacting factor M [Arabidopsis thaliana] GI:11139270, cysteine proteinase inhibitor [Brassica rapa] GI:762785; contains Pfam profile PF00031: Cystatin domain
358916	1	839	5	7	829	1	1	At5g04560	2,00E-15	68418.m00456 DEMETER protein (DME) identical to DEMETER protein [Arabidopsis thaliana] GI:21743571; contains Pfam profile PF00730: HhH-GPD superfamily base excision DNA repair protein
353483	2	839	5	7				At2g36490	7,00E-71	68415.m04479 HhH-GPD base excision DNA repair family protein (ROS1) similar to DEMETER protein [Arabidopsis thaliana] GI:21743571; contains Pfam profile PF00730: HhH-GPD superfamily base excision DNA repair protein
359221	1	839	5	7				At2g36490	1,00E-68	68415.m04479 HhH-GPD base excision DNA repair family protein (ROS1) similar to DEMETER protein [Arabidopsis thaliana] GI:21743571; contains Pfam profile PF00730: HhH-GPD superfamily base excision DNA repair protein
354897	1	840	6	6				At5g53940	1,00E-11	68418.m06711 yippee family protein similar to mdgl-1 [Mus musculus] GI:10441648, Yippee protein [Drosophila melanogaster] GI:5713279; contains Pfam profile PF03226: Yippee putative zinc-binding protein
356843	1	841	6	6	3277	1	1	At3g10330	5,00E-95	68416.m01239 transcription initiation factor IIB-2 / general transcription factor TFIIB-2 (TFIIB2) identical to SP|Q9SS44 Transcription initiation factor IIB-2 (General transcription factor TFIIB-2) (AtTFIIB2) {Arabidopsis thaliana}
353234	2	842	6	6	5923	2	2	At3g01280	2,00E-76	68416.m00035 porin, putative similar to SP|P42055 34 kDa outer mitochondrial membrane protein porin (Voltage-dependent anion-selective channel protein) (VDAC) {Solanum tuberosum}; contains Pfam profile PF01459: Eukaryotic porin

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353644	2	842	6	6	5923	2	2	At3g01280	1,00E-68	68416.m00035 porin, putative similar to SP|P42055 34 kDa outer mitochondrial membrane protein porin (Voltage-dependent anion-selective channel protein) (VDAC) {Solanum tuberosum}; contains Pfam profile PF01459: Eukaryotic porin
353932	10	842	6	6	5923	2	2	At3g01280	3,00E-99	68416.m00035 porin, putative similar to SP|P42055 34 kDa outer mitochondrial membrane protein porin (Voltage-dependent anion-selective channel protein) (VDAC) {Solanum tuberosum}; contains Pfam profile PF01459: Eukaryotic porin
354019	2	842	6	6	6024	1	1	At5g67500	4,00E-59	68418.m08512 porin, putative similar to SP|P42055 34 kDa outer mitochondrial membrane protein porin (Voltage-dependent anion-selective channel protein) (VDAC) {Solanum tuberosum}; contains Pfam profile PF01459: Eukaryotic porin
359168	1	842	6	6	6024	1	1	At5g67500	1,00E-69	68418.m08512 porin, putative similar to SP|P42055 34 kDa outer mitochondrial membrane protein porin (Voltage-dependent anion-selective channel protein) (VDAC) {Solanum tuberosum}; contains Pfam profile PF01459: Eukaryotic porin
354372	2	851	6	5	6863	1	1	At3g02700	4,00E-77	68416.m00261 NC domain-containing protein contains Pfam domain, PF04970: NC domain
355545	1	851	6	5	6863	1	1	At3g02700	6,00E-11	68416.m00261 NC domain-containing protein contains Pfam domain, PF04970: NC domain
356742	1	852	7	4	1370	2	1	At5g11800	1,00E-58	68418.m01377 K+ efflux antiporter, putative (KEA6) Monovalent cation:proton antiporter family 2 (CPA2 family) member, PMID:11500563; similar to glutathione-regulated potassium-efflux system protein KEFB, Escherichia coli, SWISSPROT:P45522
356842	1	853	6	5	3036	1	1	At5g12430	1,00E-14	68418.m01461 DNAJ heat shock N-terminal domain-containing protein similarity to TETRATRICOPEPTIDE REPEAT PROTEIN 2 , human, SWISSPROT:TTC2_HUMAN; contains Pfam profiles PF00226: DnaJ domain, PF00515: TPR Domain
358863	1	854	7	4	921	1	1	At1g79950	3,00E-20	68414.m09344 helicase-related similar to BRCA1-binding helicase-like protein BACH1 (GI:13661819) Homo sapiens].; contains similarity to helicase-like protein NHL GI:6969265 from (Homo sapiens)
355771	1	854	7	4	1348	1	1	At1g79890	2,00E-26	68414.m09334 helicase-related similar to CHL1 potential helicase protein (GI:2632247) [Homo sapiens]; similar to helicase GB:AAB06962 [Homo sapiens]

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353077	2	854	7	4	1360	2	1	At1g20720	1,00E-17	68414.m02596 helicase-related similar to BRCA1-binding helicase-like protein BACH1 (GI:13661819) Homo sapiens].;
353101	4	857	5	6	4781	1	1	At2g47590	2,00E-71	68415.m05938 photolyase/blue light photoreceptor (PHR2) identical to photolyase/blue light photoreceptor PHR2 [Arabidopsis thaliana] GI:3319288; contains Pfam domain, PF00875: deoxyribodipyrimidine photolyase
358786	1	857	5	6				At1g04400	3,00E-57	68414.m00431 cryptochrome 2 apoprotein (CRY2) / blue light photoreceptor (PHH1) 97% identical to photolysase (PHH1) (SP:Q96524) and cryptochrome 2 apoprotein (CRY2) (SP:U43397). ESTs gb|W43661 and gb|Z25638 come from this gene; contains Pfam profiles PF03441: FAD binding domain of DNA photolyase and PF00875: deoxyribodipyrimidine photolyase; identical to cDNA Cvi cryptochrome 2 (CRY2) GI:18026275
357802	1	858	8	3				At5g01030	5,00E-14	68418.m00006 expressed protein
354059	6	861	4	7	1010	1	2	At2g41830	7,00E-35	68415.m05169 cyclin-related contains Pfam profile PF02984: Cyclin, C-terminal domain
359399	1	861	4	7	1497	1	1	At5g26850	4,00E-29	68418.m03203 expressed protein
358178	1	861	4	7				At5g21080	2,00E-17	68418.m02510 expressed protein predicted proteins - Arabidopsis thaliana; expression supported by MPSS
359866	1	862	9	2	3819	2	1	At4g09340	4,00E-09	68417.m01543 SPla/RYanodine receptor (SPRY) domain-containing protein low similarity to RanBPM [Homo sapiens] GI:15080674; contains Pfam profile PF00622: SPRY domain
358350	1	862	9	2	6996	1	1	At1g61150	8,00E-12	68414.m06891 expressed protein similar to Protein C20orf11 (Swiss-Prot:Q9NWU2) [Homo sapiens]
357924	1	864	6	5	4940	1	1	At5g11710	2,00E-32	68418.m01368 epsin N-terminal homology (ENTH) domain-containing protein / clathrin assembly protein-related contains Pfam PF01417: ENTH domain. ENTH (Epsin N-terminal homology) domain; similar to Af10-protein (GI:1724114) [Avena fatua]; similar to clathrin assembly protein AP180 (GI:6492344) [Xenopus laevis]; Af10-protein, Avena fatua, EMBL:U80041
358059	1	865	5	6	1956	2	1	At4g32940	1,00E-101	68417.m04687 vacuolar processing enzyme gamma / gamma-VPE nearly identical to SP|Q39119 Vacuolar processing enzyme, gamma-isozyme precursor (EC 3.4.22.-) (Gamma-VPE) {Arabidopsis thaliana}

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355000	1	866	7	4	2703	5	3	At5g14480	1,00E-45	68418.m01694 glycosyl transferase family 17 protein low similarity to beta-1,4-mannosyl-glycoprotein beta-1,4-N-acetylglucosaminyltransferase (EC 2.4.1.144) from Mus musculus [SP|Q10470], Rattus norvegicus [SP|Q02527], Homo sapiens [SP|Q09327] ; contains Pfam profile PF04724 :Glycosyltransferase family 17
356543	1	866	7	4	2703	5	3	At3g27540	1,00E-79	68416.m03442 glycosyl transferase family 17 protein low similarity to beta-1,4-mannosyl-glycoprotein beta-1,4-N-acetylglucosaminyltransferase (EC 2.4.1.144) from Mus musculus [SP|Q10470], Rattus norvegicus [SP|Q02527], Homo sapiens [SP|Q09327] ; contains Pfam profile PF04724 :Glycosyltransferase family 17
357054	1	866	7	4	2703	5	3	At3g01620	9,00E-26	68416.m00093 glycosyl transferase family 17 protein low similarity to beta-1,4-mannosyl-glycoprotein beta-1,4-N-acetylglucosaminyltransferase (EC 2.4.1.144) from Mus musculus [SP|Q10470], Rattus norvegicus [SP|Q02527], Homo sapiens [SP|Q09327] ; contains Pfam profile PF04724 :Glycosyltransferase family 17
356228	1	869	5	6	5302	1	1	At5g01510	5,00E-42	68418.m00065 expressed protein contains Pfam domain, PF04884: Protein of unknown function, DUF647
355342	1	870	6	5	3150	1	1	At1g14030	1,00E-53	68414.m01658 ribulose-1,5 bisphosphate carboxylase oxygenase large subunit N-methyltransferase, putative strong similarity to SP|P94026 Ribulose-1,5 bisphosphate carboxylase/oxygenase large subunit N- methyltransferase, chloroplast precursor (EC 2.1.1.127) ([Ribulose-bisphosphate-carboxylase]-lysine N-methyltransferase) {Nicotiana tabacum}; contains Pfam profile PF00856: SET domain; Rare GC intron splice site at 49572 is inferred from protein alignment and is not confirmed experimentally
359566	1	870	6	5	6348	1	1	At2g18850	7,00E-12	68415.m02196 SET domain-containing protein low similarity to ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit N-methyltransferase I [Spinacia oleracea] GI:3403236; contains Pfam profile PF00856: SET domain
355764	1	870	6	5	8524	1	1	At3g55080	2,00E-42	68416.m06117 SET domain-containing protein low similarity to ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit N-methyltransferase I [Spinacia oleracea] GI:3403236; contains Pfam profile PF00856: SET domain
354674	1	871	4	7	6708	1	3	At4g25570	1,00E-11	68417.m03685 cytochrome B561 family protein contains Pfam domain, PF03188: Cytochrome b561

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357415	1	871	4	7	6708	1	3	At4g25570	2,00E-49	68417.m03685 cytochrome B561 family protein contains Pfam domain, PF03188: Cytochrome b561
354370	4	873	7	4	1945	1	1	At4g30600	1,00E-62	68417.m04341 signal recognition particle receptor alpha subunit family protein similar to Signal recognition particle receptor alpha subunit (SR-alpha) (Docking protein alpha) (DP-alpha) (SP:P08240) [Homo sapiens}; similar to Signal recognition particle receptor alpha subunit (SR-alpha) (Docking protein alpha) (DP-alpha) (SP:P06625) [Canis familiaris}; contains Pfam PF04086: Signal recognition particle, alpha subunit, N-terminal; contains Pfam PF00448: SRP54-type protein, GTPase domain
354148	2	875	5	6	2737	1	1	At1g80670	2,00E-67	68414.m09466 transducin family protein / WD-40 repeat family protein contains 5 WD-40 repeats (PF00400) (1 weak); similar to Hypothetical RAE1-like protein.(SP:Q38942) [Arabidopsis thaliana]; similar to mRNA-associated protein mrnp 41 ((mRNA export protein) (GB:AAC28126) (GI:1903456)(RAE1) (MRNP41) (SP:P78406) [Homo sapiens]
356183	1	876	6	5	8325	1	1	At1g17200	9,00E-16	68414.m02096 integral membrane family protein Location of est 136A23T7 (gb|T45563); contains TIGRFAM TIGR01569 : plant integral membrane protein TIGR01569; contains Pfam PF04535 : Domain of unknown function (DUF588)
357661	1	876	6	5	8325	1	1	At1g17200	3,00E-16	68414.m02096 integral membrane family protein Location of est 136A23T7 (gb|T45563); contains TIGRFAM TIGR01569 : plant integral membrane protein TIGR01569; contains Pfam PF04535 : Domain of unknown function (DUF588)
357996	1	876	6	5	8679	2	1	At2g35760	1,00E-09	68415.m04388 integral membrane family protein contains TIGRFAM TIGR01569 : plant integral membrane protein TIGR01569; contains Pfam PF04535 : Domain of unknown function (DUF588)
359093	1	876	6	5	8679	2	1	At2g35760	8,00E-27	68415.m04388 integral membrane family protein contains TIGRFAM TIGR01569 : plant integral membrane protein TIGR01569; contains Pfam PF04535 : Domain of unknown function (DUF588)
353337	6	879	6	5	8014	1	1	At1g47420	7,00E-69	68414.m05252 expressed protein identical to hypothetical protein GB:AAD46040 GI:5668814 from [Arabidopsis thaliana]

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358978	1	879	6	5				At1g19580	7,00E-53	68414.m02439 bacterial transferase hexapeptide repeat-containing protein contains Pfam profile PF00132: Bacterial transferase hexapeptide (four repeats)
353760	2	881	5	6	509	2	1	At1g76140	2,00E-27	68414.m08842 prolyl oligopeptidase, putative / prolyl endopeptidase, putative / post-proline cleaving enzyme, putative similar to SP|Q9QUR6 Prolyl endopeptidase (EC 3.4.21.26) (Post-proline cleaving enzyme) {Mus musculus}; contains Pfam profiles PF00326: prolyl oligopeptidase family, PF02897: Prolyl oligopeptidase, N-terminal beta-propeller domain
355166	1	881	5	6	509	2	1	At1g76140	5,00E-82	68414.m08842 prolyl oligopeptidase, putative / prolyl endopeptidase, putative / post-proline cleaving enzyme, putative similar to SP|Q9QUR6 Prolyl endopeptidase (EC 3.4.21.26) (Post-proline cleaving enzyme) {Mus musculus}; contains Pfam profiles PF00326: prolyl oligopeptidase family, PF02897: Prolyl oligopeptidase, N-terminal beta-propeller domain
355337	1	881	5	6	586	1	1	At1g50380	9,00E-43	68414.m05647 prolyl oligopeptidase family protein similar to oligopeptidase B [Leishmania major] GI:4581757; contains Pfam profiles PF00326: prolyl oligopeptidase family, PF02897: Prolyl oligopeptidase, N-terminal beta-propeller domain
357838	1	882	6	5	867	1	1	At5g17410	4,00E-30	68418.m02043 tubulin family protein similar to spindle pole body protein [Homo sapiens][GI:2801701][PMID:9566967], gamma-tubulin ring protein Dgrip84 [Drosophila melanogaster][GI:4689225][PMID: 10037793]
357295	1	882	6	5	1271	2	2	At1g20570	4,00E-09	68414.m02565 tubulin family protein
353146	2	883	6	5	8135	2	4	At2g35510	2,00E-08	68415.m04349 WWE domain-containing protein contains Pfam domain, PF02825: WWE domain
353505	2	883	6	5	8135	2	4	At1g32230	2,00E-28	68414.m03965 WWE domain-containing protein / ceo protein, putative (CEO) contains Pfam domain, PF02825: WWE domain; identical to cDNA for ceo protein (ceo gene) GI:11044956
355152	1	883	6	5	8135	2	4	At1g32230	1,00E-28	68414.m03965 WWE domain-containing protein / ceo protein, putative (CEO) contains Pfam domain, PF02825: WWE domain; identical to cDNA for ceo protein (ceo gene) GI:11044956

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
356364	1	883	6	5	8135	2	4	At1g32230	8,00E-09	68414.m03965 WWE domain-containing protein / ceo protein, putative (CEO) contains Pfam domain, PF02825: WWE domain; identical to cDNA for ceo protein (ceo gene) GI:11044956
355597	1	883	6	5				At1g23550	1,00E-25	68414.m02962 expressed protein
356082	1	884	5	6	5952	3	2	At1g70170	4,00E-32	68414.m08074 matrixin family protein similar to SP|P29136 Metalloendoproteinase 1 precursor (EC 3.4.24.-) (SMEP1) {Glycine max}; contains InterPro accession IPR001818: Matrixin
353827	2	887	5	6	6846	1	1	At1g27450	2,00E-42	68414.m03347 adenine phosphoribosyltransferase 1 (APT1) nearly identical to SP|P31166 Adenine phosphoribosyltransferase 1 (EC 2.4.2.7) (APRT) {Arabidopsis thaliana}
353112	2	888	5	6	800	1	1	At3g12670	6,00E-67	68416.m01579 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
355520	1	889	5	6	3221	2	1	At1g55680	3,00E-64	68414.m06374 WD-40 repeat family protein contains 2 (1 significant) WD-40 repeats (PF0400); similar to Trp-Asp repeat protein (PIR:T40094) [Schizosaccharomyces]
353118	5	891	6	5	7944	1	2	At1g44760	4,00E-55	68414.m05128 universal stress protein (USP) family protein contains Pfam profile PF00582: universal stress protein family
356924	1	891	6	5	7944	1	2	At1g44760	1,00E-19	68414.m05128 universal stress protein (USP) family protein contains Pfam profile PF00582: universal stress protein family
353138	2	896	6	5				At3g13700	2,00E-51	68416.m01731 RNA-binding protein, putative similar to mec-8 [Caenorhabditis elegans] GI:1370048; contains Pfam profile:PF00076 rrm:RNA recognition motif
360071	1	897	6	5	2661	1	2	At1g54570	3,00E-49	68414.m06223 esterase/lipase/thioesterase family protein contains Interpro entry IPR000379
353079	2	899	5	6	8492	1	1	At3g14750	4,00E-41	68416.m01865 expressed protein weak similarity to Septation ring formation regulator (Swiss-Prot:O34894) [Bacillus subtilis]
353319	3	899	5	6	8492	1	1	At3g14750	1,00E-51	68416.m01865 expressed protein weak similarity to Septation ring formation regulator (Swiss-Prot:O34894) [Bacillus subtilis]
359799	1	899	5	6	8492	1	1	At3g14750	2,00E-11	68416.m01865 expressed protein weak similarity to Septation ring formation regulator (Swiss-Prot:O34894) [Bacillus subtilis]

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
356244	1	899	5	6	8568	1	1	At1g67170	7,00E-07	68414.m07641 expressed protein similar to enterophilin-2L (GI:12718845) [Cavia porcellus]; similar to Hyaluronan mediated motility receptor (Intracellular hyaluronic acid binding protein) (Receptor for hyaluronan-mediated motility) (CD168 antigen) (Swiss-Prot:O75330) [Homo sapiens]
358647	1	899	5	6	8568	1	1	At1g67170	2,00E-09	68414.m07641 expressed protein similar to enterophilin-2L (GI:12718845) [Cavia porcellus]; similar to Hyaluronan mediated motility receptor (Intracellular hyaluronic acid binding protein) (Receptor for hyaluronan-mediated motility) (CD168 antigen) (Swiss-Prot:O75330) [Homo sapiens]
357059	1	900	5	6	4837	2	1	At4g35640	3,00E-46	68417.m05061 serine O-acetyltransferase, putative similar to serine acetyltransferase, Arabidopsis thaliana, GI:905391; contains Pfam profile PF00132: Bacterial transferase hexapeptide (four repeats)
354944	1	900	5	6				At1g55920	5,00E-11	68414.m06414 serine O-acetyltransferase, putative identical to GI:608677 from [Arabidopsis thaliana]
355459	1	903	6	5	4298	1	1	At1g72390	7,00E-08	68414.m08373 expressed protein
358087	1	903	6	5	8221	4	2	At5g02610	9,00E-55	68418.m00197 60S ribosomal protein L35 (RPL35D) ribosomal protein L35- cytosolic, Arabidopsis thaliana, PIR:T00549
354083	2	904	5	6	2229	2	1	At4g12700	6,00E-49	68417.m01994 expressed protein
355212	1	904	5	6	2229	2	1	At2g04280	4,00E-22	68415.m00420 expressed protein
353103	3	906	6	5	189	2	1	At4g23460	1,00E-88	68417.m03381 beta-adaptin, putative strong similarity to SP|Q10567 Adapter-related protein complex 1 beta 1 subunit (Beta-adaptin 1) [Homo sapiens], beta-adaptin [Drosophila melanogaster] GI:434902; contains Pfam profile: PF01602 Adaptin N terminal region
355383	1	906	6	5	189	2	1	At4g23460	1,00E-33	68417.m03381 beta-adaptin, putative strong similarity to SP|Q10567 Adapter-related protein complex 1 beta 1 subunit (Beta-adaptin 1) [Homo sapiens], beta-adaptin [Drosophila melanogaster] GI:434902; contains Pfam profile: PF01602 Adaptin N terminal region
356977	1	906	6	5	238	1	2	At4g34450	1,00E-50	68417.m04896 coatomer gamma-2 subunit, putative / gamma-2 coat protein, putative / gamma-2 COP, putative similar to SP|Q9UBF2 Coatomer gamma-2 subunit (Gamma-2 coat protein) (Gamma-2 COP) {Homo sapiens}; contains Pfam profile: PF01602 Adaptin N terminal region

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357747	1	906	6	5	1133	1	1	At3g55480	1,00E-42	68416.m06162 adaptin family protein similar to AP-3 complex beta3A subunit, Homo sapiens, SP|O00203; contains Pfam profile: PF01602 Adaptin N terminal region
359716	1	908	2	9	6033	1	1	At2g18950	8,00E-23	68415.m02212 homogentisate phytylprenyltransferase family protein (HPT1) / tocopherol phytyltransferase family protein (TPT1) identical to gi:17104828; contains Pfam profile PF01040: UbiA prenyltransferase family; identical to cDNA tocopherol polyprenyltransferase (TPT1) GI:17104827
356432	1	910	5	6	6646	2	2	At5g65260	5,00E-38	68418.m08209 polyadenylate-binding protein family protein / PABP family protein low similarity to poly(A)-binding protein II [Drosophila melanogaster] GI:6007612; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM) domain
359574	1	910	5	6	6646	2	2	At5g65260	2,00E-17	68418.m08209 polyadenylate-binding protein family protein / PABP family protein low similarity to poly(A)-binding protein II [Drosophila melanogaster] GI:6007612; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM) domain
356088	1	911	7	4	779	2	2	At3g48050	3,00E-17	68416.m05239 bromo-adjacent homology (BAH) domain-containing protein contains Pfam profile PF01426: BAH domain
355272	1	911	7	4	4074	1	1	At4g11560	2,00E-28	68417.m01853 bromo-adjacent homology (BAH) domain-containing protein contains Pfam profile PF01426: BAH domain
353450	2	912	5	6	9013	2	3	At2g27710	5,00E-19	68415.m03359 60S acidic ribosomal protein P2 (RPP2B)
353823	2	912	5	6	9013	2	3	At2g27720	3,00E-20	68415.m03360 60S acidic ribosomal protein P2 (RPP2A)
355218	1	912	5	6	9013	2	3	At2g27710	1,00E-18	68415.m03359 60S acidic ribosomal protein P2 (RPP2B)
358996	1	914	7	4	8540	1	2	At5g05830	2,00E-29	68418.m00641 zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 Zinc finger, C3HC4 type (RING finger); contains PROSITE PS00190: Cytochrome c family heme-binding site signature
358483	1	916	1	10	8767	1	1	At2g38695	2,00E-39	68415.m04752 hypothetical protein
353044	2	917	4	7	4394	1	1	At2g45620	2,00E-102	68415.m05672 nucleotidyltransferase family protein low similarity to SP|O13833| Caffeine-induced death protein 1 {Schizosaccharomyces pombe}; contains Pfam profiles PF03828: PAP/25A associated domain, PF01909: Nucleotidyltransferase domain

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
353358	3	918	7	4	6584	4	2	At2g40300	1,00E-50	68415.m04964 ferritin, putative similar to ferritin subunit cowpea2 precursor [Vigna unguiculata] GI:2970654; contains Pfam profile PF00210: Ferritin-like domain
353709	3	918	7	4	6584	4	2	At2g40300	6,00E-71	68415.m04964 ferritin, putative similar to ferritin subunit cowpea2 precursor [Vigna unguiculata] GI:2970654; contains Pfam profile PF00210: Ferritin-like domain
353367	2	925	1	10	8119	1	1	At4g31130	7,00E-30	68417.m04419 expressed protein
356162	1	935	6	4	2365	2	2	At1g24180	9,00E-72	68414.m03050 pyruvate dehydrogenase E1 component alpha subunit, mitochondrial, putative similar to SP|P52901 Pyruvate dehydrogenase E1 component alpha subunit, mitochondrial precursor (EC 1.2.4.1) (PDHE1-A) {Arabidopsis thaliana}; contains Pfam profile PF00676: Dehydrogenase E1 component
358710	1	936	3	7	7695	1	1	At1g01860	2,00E-34	68414.m00104 dimethyladenosine transferase (PFC1) identical to dimethyladenosine transferase GB:AAC09322 GI:3005590 from [Arabidopsis thaliana]
353423	3	936	3	7				At2g47420	5,00E-107	68415.m05919 dimethyladenosine transferase, putative similar to SP|P41819 Dimethyladenosine transferase (EC 2.1.1.-) (S-adenosylmethionine-6-N', N'-adenosyl(rRNA) dimethyltransferase) {Saccharomyces cerevisiae}; contains Pfam profile PF00398: ribosomal RNA adenine dimethylase family protein
354655	1	936	3	7				At2g47420	4,00E-14	68415.m05919 dimethyladenosine transferase, putative similar to SP|P41819 Dimethyladenosine transferase (EC 2.1.1.-) (S-adenosylmethionine-6-N', N'-adenosyl(rRNA) dimethyltransferase) {Saccharomyces cerevisiae}; contains Pfam profile PF00398: ribosomal RNA adenine dimethylase family protein
353310	4	938	5	5	8382	2	1	At1g23750	1,00E-54	68414.m02997 DNA-binding protein-related contains weak similarity to G-quartet DNA binding protein 3 [Tetrahymena thermophila] gi|4583503|gb|AAD25098
355872	1	938	5	5	8382	2	1	At1g23750	1,00E-11	68414.m02997 DNA-binding protein-related contains weak similarity to G-quartet DNA binding protein 3 [Tetrahymena thermophila] gi|4583503|gb|AAD25098
356127	1	938	5	5	8382	2	1	At1g23750	7,00E-35	68414.m02997 DNA-binding protein-related contains weak similarity to G-quartet DNA binding protein 3 [Tetrahymena thermophila] gi|4583503|gb|AAD25098
357754	1	938	5	5	8382	2	1	At1g23750	3,00E-40	68414.m02997 DNA-binding protein-related contains weak similarity to G-quartet DNA binding protein 3 [Tetrahymena thermophila] gi|4583503|gb|AAD25098

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
353641	4	940	7	3	7034	2	2	At5g09510	4,00E-23	68418.m01100 40S ribosomal protein S15 (RPS15D) ribosomal protein S15 - Arabidopsis thaliana, EMBL:Z23161
354481	1	940	7	3	7034	2	2	At5g09510	7,00E-46	68418.m01100 40S ribosomal protein S15 (RPS15D) ribosomal protein S15 - Arabidopsis thaliana, EMBL:Z23161
356161	1	940	7	3	7034	2	2	At5g09510	2,00E-14	68418.m01100 40S ribosomal protein S15 (RPS15D) ribosomal protein S15 - Arabidopsis thaliana, EMBL:Z23161
360064	1	940	7	3	7034	2	2	At5g09510	1,00E-07	68418.m01100 40S ribosomal protein S15 (RPS15D) ribosomal protein S15 - Arabidopsis thaliana, EMBL:Z23161
354063	2	942	5	5	236	1	1	At3g04240	3,00E-69	68416.m00448 O-linked N-acetyl glucosamine transferase, putative similar to O-GlcNAc transferase, Homo sapiens [SP|O15294], Rattus norvegicus [SP|P56558]; contains Pfam profile PF00515: TPR Domain; identical to cDNA GI:18139886
356630	1	942	5	5	1116	1	1	At3g11540	1,00E-108	68416.m01408 gibberellin signal transduction protein (SPINDLY) identical to spindly GB:AAC49446 (GI:1589778) [Arabidopsis thaliana]; contains Pfam profile PF00515 TPR Domain
354397	2	944	4	6	7179	1	1	At1g08845	3,00E-62	68414.m00986 expressed protein
359165	1	944	4	6	8756	1	2	At5g27820	2,00E-40	68418.m03335 ribosomal protein L18 family protein similar to SP|P52863 50S ribosomal protein L18 [Aeromonas proteolytica] {Vibrio proteolyticus}
358776	1	946	5	5	4784	1	1	At2g28380	2,00E-12	68415.m03449 double-stranded RNA-binding domain (DsRBD)-containing protein contains Pfam profile PF00035: Double-stranded RNA binding motif
358598	1	947	4	6	5110	1	1	At5g51180	3,00E-35	68418.m06346 expressed protein
353594	2	948	7	3	2144	1	1	At5g19320	9,00E-92	68418.m02302 RAN GTPase activating protein 2 (RanGAP2) identical to RAN GTPase activating protein 2 GI:6708468 from [Arabidopsis thaliana]
354156	4	948	7	3				At3g63130	2,00E-113	68416.m07090 RAN GTPase activating protein 1 (RanGAP1) contains Pfam PF00560: Leucine Rich Repeat domains; identical to RAN GTPase activating protein 1 (GI:6708466)[Arabidopsis thaliana]
359438	1	948	7	3				At3g63130	1,00E-12	68416.m07090 RAN GTPase activating protein 1 (RanGAP1) contains Pfam PF00560: Leucine Rich Repeat domains; identical to RAN GTPase activating protein 1 (GI:6708466)[Arabidopsis thaliana]

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
357287	1	949	5	5	4620	1	2	At1g48790	4,00E-31	68414.m05460 mov34 family protein similar to AMSH [Homo sapiens] GI:4098124; contains Pfam profile PF01398: Mov34/MPN/PAD-1 family
358593	1	949	5	5	6072	2	1	At2g25355	1,00E-53	68415.m03033 exonuclease-related similar to Exosome complex exonuclease RRP40 (EC 3.1.13.-) (Ribosomal RNA processing protein 40) (p10) (CGI-102) (Swiss-Prot:Q9NQT5) [Homo sapiens]
356338	1	950	5	5	1444	1	1	At5g46630	5,00E-39	68418.m05740 clathrin adaptor complexes medium subunit family protein contains Pfam profile: PF00928 adaptor complexes medium subunit family
355865	1	950	5	5	1455	2	2	At1g60780	6,00E-63	68414.m06842 clathrin adaptor complexes medium subunit family protein contains Pfam profile: PF00928 adaptor complexes medium subunit family
358787	1	950	5	5	1455	2	2	At1g60780	3,00E-68	68414.m06842 clathrin adaptor complexes medium subunit family protein contains Pfam profile: PF00928 adaptor complexes medium subunit family
358126	1	950	5	5	1690	1	1	At4g24550	2,00E-37	68417.m03519 clathrin adaptor complexes medium subunit family protein contains Pfam profile: PF00928 adaptor complexes medium subunit family
358768	1	953	4	6	2186	1	1	At2g45240	1,00E-98	68415.m05632 methionyl aminopeptidase, putative / methionine aminopeptidase, putative / peptidase M, putative similar to SP|Q01662 Methionine aminopeptidase 1 precursor (EC 3.4.11.18) {Saccharomyces cerevisiae}; contains Pfam profile PF00557: metallopeptidase family M24
357761	1	954	4	6	4164	2	1	At3g19310	1,00E-12	68416.m02449 expressed protein similar to GB:CAB16796 from [Arabidopsis thaliana]
359257	1	954	4	6				At5g67130	4,00E-98	68418.m08463 expressed protein
359478	1	958	5	5	1919	1	1	At1g16180	1,00E-35	68414.m01938 TMS membrane family protein / tumour differentially expressed (TDE) family protein contains Pfam domain, PF03348: TMS membrane protein/tumour differentially expressed protein (TDE)
358527	1	959	5	5	6610	2	2	At1g79590	2,00E-62	68414.m09280 syntaxin 52 (SYP52) identical to Swiss-Prot:Q94KK7 syntaxin 52 (AtSYP52) [Arabidopsis thaliana]
356018	1	959	5	5	6713	1	1	At1g28490	6,00E-35	68414.m03503 syntaxin 61 (SYP61) / osmotic stess-sensitive mutant 1 (OSM1) identical to SP|Q946Y7 Syntaxin 61 (AtSYP61) (Osmotic stess-sensitive mutant 1) {Arabidopsis thaliana}; identical to cDNA syntaxin of plants 61 (SYP61) GI:16041649

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353628	2	960	6	4	1799	2	1	At4g22350	1,00E-83	68417.m03231 ubiquitin carboxyl-terminal hydrolase family protein similar to U4/U6.U5 tri-snRNP-associated 65 kDa protein [Homo sapiens] GI:13926071; contains Pfam profile PF00443: Ubiquitin carboxyl-terminal hydrolase
356588	1	960	6	4	2010	2	2	At1g16860	4,00E-55	68414.m02035 merozoite surface protein-related contains weak similarity to merozoite surface protein [Plasmodium falciparum] gi|12043655|gb|AAG47601
358290	1	960	6	4	2010	2	2	At1g78880	9,00E-61	68414.m09195 balbiani ring 1-related / BR1-related contains weak similarity to BR1 [Chironomus tentans] gi|7042|emb|CAA45607
354689	1	960	6	4				At4g22410	1,00E-36	68417.m03238 ubiquitin carboxyl-terminal hydrolase family protein similar to U4/U6.U5 tri-snRNP-associated 65 kDa protein [Homo sapiens] GI:13926071; contains Pfam profile PF00443: Ubiquitin carboxyl-terminal hydrolase
353361	3	961	5	5	7183	1	1	At5g63310	9,00E-58	68418.m07945 nucleotide diphosphate kinase II, chloroplast (NDPK2) identical to SP|O64903 Nucleoside diphosphate kinase II, chloroplast precursor (NDK II) (NDP kinase II) (NDPK II) (NDPK Ia) [Arabidopsis thaliana]; contains Pfam PF00334 : Nucleoside diphosphate kinase domain; contains Pfam profile PF00334: Nucleoside diphosphate kinase
353573	3	961	5	5	7330	1	1	At4g09320	2,00E-62	68417.m01542 nucleoside diphosphate kinase 1 (NDK1) identical to identical to Nucleoside diphosphate kinase I (NDK I) (NDP kinase I) (NDPK I) (SP:P39207) [Arabidopsis thaliana]; contains Pfam PF00334 : Nucleoside diphosphate kinase domain;
354309	2	961	5	5	7330	1	1	At4g09320	2,00E-68	68417.m01542 nucleoside diphosphate kinase 1 (NDK1) identical to identical to Nucleoside diphosphate kinase I (NDK I) (NDP kinase I) (NDPK I) (SP:P39207) [Arabidopsis thaliana]; contains Pfam PF00334 : Nucleoside diphosphate kinase domain;
353417	2	962	6	4	6895	1	2	At1g49950	1,00E-59	68414.m05604 DNA-binding protein, putative contains similarity to DNA-binding protein PcMYB1 [Petroselinum crispum] gi|2224899|gb|AAB61699
353702	2	962	6	4	6895	1	2	At1g49950	5,00E-39	68414.m05604 DNA-binding protein, putative contains similarity to DNA-binding protein PcMYB1 [Petroselinum crispum] gi|2224899|gb|AAB61699
358003	1	962	6	4				At1g17520	8,00E-12	68414.m02153 DNA-binding protein, putative contains similarity to DNA-binding protein PcMYB1 [Petroselinum crispum] gi|2224899|gb|AAB61699

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353356	2	964	4	6	3440	2	1	At1g73920	8,00E-77	68414.m08561 lipase family protein similar to lipase GB:CAA74737 [SP|O46108] from [Drosophila melanogaster]
355086	1	964	4	6	5028	1	1	At2g15230	5,00E-43	68415.m01737 lipase family protein similar to SP|P07098 Triacylglycerol lipase, gastric precursor (EC 3.1.1.3) {Homo sapiens}; contains Pfam profile PF04083: ab-hydrolase associated lipase region
359737	1	965	6	4	5935	3	2	At1g74450	3,00E-52	68414.m08625 expressed protein
358568	1	968	3	7	5326	2	1	At1g21880	4,00E-34	68414.m02739 peptidoglycan-binding LysM domain-containing protein contains Pfam profile PF01476: LysM domain
358532	1	972	6	4	3617	1	1	At2g07170	9,00E-08	68415.m00821 expressed protein
353754	3	972	6	4	6167	1	2	At5g62580	1,00E-31	68418.m07855 expressed protein
356342	1	975	6	4	6388	4	2	At3g47590	2,00E-37	68416.m05181 esterase/lipase/thioesterase family protein low similarity to cinnamoyl ester hydrolase CinI [Butyrivibrio fibrisolvens] GI:1622732; contains Interpro entry IPR000379
355809	1	975	6	4				At3g13120	6,00E-44	68416.m01642 30S ribosomal protein S10, chloroplast, putative similar to 30S ribosomal protein S10 GB:P02364 [Escherichia coli] (est matches suggest the N-terminal extension)
353671	2	976	5	5	2666	2	1	At2g34590	3,00E-47	68415.m04250 transketolase family protein similar to SP|O66113 Pyruvate dehydrogenase E1 component, beta subunit (EC 1.2.4.1). {Zymomonas mobilis}; contains Pfam profiles PF02779: Transketolase, pyridine binding domain, PF02780: Transketolase, C-terminal domain
357988	1	976	5	5	2666	2	1	At2g34590	2,00E-117	68415.m04250 transketolase family protein similar to SP|O66113 Pyruvate dehydrogenase E1 component, beta subunit (EC 1.2.4.1). {Zymomonas mobilis}; contains Pfam profiles PF02779: Transketolase, pyridine binding domain, PF02780: Transketolase, C-terminal domain
355427	1	977	4	6	541	1	2	At1g31930	6,00E-46	68414.m03924 extra-large guanine nucleotide binding protein, putative / G-protein, putative similar to extra-large G-protein (XLG) [Arabidopsis thaliana] GI:3201680; contains Pfam profile PF00503: G-protein alpha subunit

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
360076	1	977	4	6	541	1	2	At1g31930	3,00E-18	68414.m03924 extra-large guanine nucleotide binding protein, putative / G-protein, putative similar to extra-large G-protein (XLG) [Arabidopsis thaliana] GI:3201680; contains Pfam profile PF00503: G-protein alpha subunit
354492	1	977	4	6	1334	1	1	At2g23460	3,00E-66	68415.m02801 extra-large guanine nucleotide binding protein / G-protein (XLG) identical to extra-large G-protein (XLG) [Arabidopsis thaliana] GI:3201680
353263	2	978	5	5	6833	1	2	At3g12390	7,00E-60	68416.m01544 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
353631	2	978	5	5	6833	1	2	At3g12390	2,00E-44	68416.m01544 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
355192	1	978	5	5	6833	1	2	At3g12390	7,00E-37	68416.m01544 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
354977	1	978	5	5				At5g13850	2,00E-13	68418.m01619 nascent polypeptide-associated complex (NAC) domain-containing protein similar to alpha-NAC, non-muscle form [Mus musculus] GI:1666690; contains Pfam profile PF01849: NAC domain
359321	1	981	6	4	2153	3	1	At1g66200	8,00E-25	68414.m07514 glutamine synthetase, putative similar to glutamine synthetase, cytosolic isozyme (Glutamate--ammonia ligase, GS1) [Lotus japonicus] SWISS-PROT:Q42899
359726	1	981	6	4	2153	3	1	At5g37600	1,00E-88	68418.m04529 glutamine synthetase, putative similar to glutamine synthetase, cytosolic isozyme (Glutamate--ammonia ligase, GS1) [Lotus japonicus] SWISS-PROT:Q42899
357916	1	982	5	5	19	1	1	At5g40820	8,00E-19	68418.m04956 FAT domain-containing protein / phosphatidylinositol 3- and 4-kinase family protein similar to Atr protein [Xenopus laevis] GI:11385422; contains Pfam profiles PF00454 Phosphatidylinositol 3- and 4-kinase, PF02259 FAT domain, PF02260 FAT C domain

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
358910	1	985	5	5	9545	4	2	At3g05020	7,00E-18	68416.m00545 acyl carrier protein 1, chloroplast (ACP-1) identical to SP|P11829 Acyl carrier protein 1, chloroplast precursor (ACP) {Arabidopsis thaliana}
354234	3	985	5	5	9636	1	2	At4g25050	3,00E-20	68417.m03594 acyl carrier family protein / ACP family protein similar to Acyl carrier protein, chloroplast precursor from {Spinacia oleracea} SP|P23235, {Casuarina glauca} SP|P93092; contains InterPro accession IPR003881: Isochorismatase
359953	1	986	3	7	8889	1	2	At4g20300	5,00E-24	68417.m02965 expressed protein
354187	2	987	4	6	7083	1	1	At4g26500	7,00E-30	68417.m03813 BolA-like family protein / Fe-S metabolism associated domain-containing protein similar to SufE protein [Erwinia chrysanthemi] GI:11342550; contains Pfam profiles PF02657: Fe-S metabolism associated domain, PF01722: BolA-like protein
353437	6	989	4	6	1741	2	1	At3g12780	2,00E-163	68416.m01596 phosphoglycerate kinase, putative similar to SP|P41758 Phosphoglycerate kinase, chloroplast precursor (EC 2.7.2.3) {Chlamydomonas reinhardtii}; contains Pfam profile PF00162: phosphoglycerate kinase
356011	1	989	4	6	1741	2	1	At3g12780	4,00E-65	68416.m01596 phosphoglycerate kinase, putative similar to SP|P41758 Phosphoglycerate kinase, chloroplast precursor (EC 2.7.2.3) {Chlamydomonas reinhardtii}; contains Pfam profile PF00162: phosphoglycerate kinase
354901	1	989	4	6	2090	1	2	At1g79550	1,00E-53	68414.m09274 phosphoglycerate kinase, putative similar to SP|P41758 Phosphoglycerate kinase, chloroplast precursor (EC 2.7.2.3) {Chlamydomonas reinhardtii}; contains Pfam profile PF00162: phosphoglycerate kinase
359535	1	989	4	6	2090	1	2	At1g79550	5,00E-13	68414.m09274 phosphoglycerate kinase, putative similar to SP|P41758 Phosphoglycerate kinase, chloroplast precursor (EC 2.7.2.3) {Chlamydomonas reinhardtii}; contains Pfam profile PF00162: phosphoglycerate kinase
353213	9	990	3	7	275	1	1	At1g63770	0	68414.m07216 peptidase M1 family protein similar to SP|P04825 Aminopeptidase N (EC 3.4.11.2) (Alpha-aminoacylpeptide hydrolase) {Escherichia coli}; contains Pfam profile PF01433: Peptidase family M1
355281	1	991	5	5	2079	1	1	At3g52880	2,00E-42	68416.m05827 monodehydroascorbate reductase, putative monodehydroascorbate reductase (NADH), Lycoperison esculentum, PIR:T06407

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
353479	2	991	5	5	2224	1	1	At5g03630	1,00E-66	68418.m00322 monodehydroascorbate reductase, putative monodehydroascorbate reductase (NADH), cucumber, PIR:JU0182
358557	1	991	5	5	2224	1	1	At5g03630	4,00E-26	68418.m00322 monodehydroascorbate reductase, putative monodehydroascorbate reductase (NADH), cucumber, PIR:JU0182
353962	2	993	4	6	7614	3	4	At5g38410	1,00E-55	68418.m04643 ribulose bisphosphate carboxylase small chain 3B / RuBisCO small subunit 3B (RBCS-3B) (ATS3B) identical to SP|P10798 Ribulose bisphosphate carboxylase small chain 3B, chloroplast precursor (EC 4.1.1.39) (RuBisCO small subunit 3B) {Arabidopsis thaliana}
358065	1	993	4	6	7614	3	4	At5g38430	3,00E-24	68418.m04645 ribulose bisphosphate carboxylase small chain 1B / RuBisCO small subunit 1B (RBCS-1B) (ATS1B) identical to SP|P10796 Ribulose bisphosphate carboxylase small chain 1B, chloroplast precursor (EC 4.1.1.39) (RuBisCO small subunit 1B) {Arabidopsis thaliana}
359144	1	993	4	6	7614	3	4	At5g38430	1,00E-21	68418.m04645 ribulose bisphosphate carboxylase small chain 1B / RuBisCO small subunit 1B (RBCS-1B) (ATS1B) identical to SP|P10796 Ribulose bisphosphate carboxylase small chain 1B, chloroplast precursor (EC 4.1.1.39) (RuBisCO small subunit 1B) {Arabidopsis thaliana}
353185	6	994	5	5	6645	3	1	At5g38690	2,00E-36	68418.m04678 expressed protein
356285	1	994	5	5	6645	3	1	At5g38690	1,00E-17	68418.m04678 expressed protein
357853	1	994	5	5	6645	3	1	At5g38690	1,00E-13	68418.m04678 expressed protein
359732	1	994	5	5	6645	3	1	At1g67780	1,00E-38	68414.m07734 hypothetical protein
359983	1	994	5	5	6645	3	1	At1g67780	1,00E-30	68414.m07734 hypothetical protein
353884	2	996	5	5	947	1	1	At2g46520	2,00E-56	68415.m05798 cellular apoptosis susceptibility protein, putative / importin-alpha re-exporter, putative similar to cellular apoptosis susceptibility protein [Homo sapiens] GI:3598795, SP|Q9ERK4 Importin-alpha re-exporter (Chromosome segregation 1-like protein) (Cellular apoptosis susceptibility protein) {Mus musculus}; contains Pfam profiles PF03810: Importin-beta N-terminal domain, PF03378: CAS/CSE protein C-terminus
358106	1	997	5	5	2743	1	1	At2g26900	8,00E-51	68415.m03227 bile acid:sodium symporter family protein low similarity to SP|Q12908 Ileal sodium/bile acid cotransporter {Homo sapiens}; contains Pfam profile PF01758: Sodium Bile acid symporter family

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
357364	1	1003	4	6	7017	1	1	At3g48890	1,00E-12	68416.m05341 cytochrome b5 domain-containing protein similar to SP|O00264 Membrane associated progesterone receptor component (mPR) {Homo sapiens}; contains Pfam profile PF00173: Heme/Steroid binding domain
355071	1	1006	5	5	277	1	1	At4g30160	8,00E-12	68417.m04289 villin, putative similar to villin 2 (VLN2) [Arabidopsis thaliana] GI:3415115, villin 3 (VLN3) [Arabidopsis thaliana] GI:3415117; contains Pfam profiles PF00626: Gelsolin repeat, PF02209: Villin headpiece domain
357173	1	1006	5	5	277	1	1	At4g30160	4,00E-70	68417.m04289 villin, putative similar to villin 2 (VLN2) [Arabidopsis thaliana] GI:3415115, villin 3 (VLN3) [Arabidopsis thaliana] GI:3415117; contains Pfam profiles PF00626: Gelsolin repeat, PF02209: Villin headpiece domain
355394	1	1006	5	5	341	2	1	At2g41740	5,00E-34	68415.m05159 villin 2 (VLN2) nearly identical to villin 2 (VLN2) [Arabidopsis thaliana] GI:3415115
356105	1	1006	5	5	341	2	1	At2g41740	9,00E-07	68415.m05159 villin 2 (VLN2) nearly identical to villin 2 (VLN2) [Arabidopsis thaliana] GI:3415115
353341	7	1009	3	7	3427	1	2	At2g38670	1,00E-15	68415.m04749 ethanolamine-phosphate cytidylyltransferase, putative / phosphorylethanolamine transferase, putative / CTP:phosphoethanolamine cytidylyltransferase, putative similar to SP|Q99447 Ethanolamine-phosphate cytidylyltransferase (EC 2.7.7.14) {Homo sapiens}; contains Pfam profile PF01467: Cytidylyltransferase
358837	1	1009	3	7	3427	1	2	At2g38670	2,00E-72	68415.m04749 ethanolamine-phosphate cytidylyltransferase, putative / phosphorylethanolamine transferase, putative / CTP:phosphoethanolamine cytidylyltransferase, putative similar to SP|Q99447 Ethanolamine-phosphate cytidylyltransferase (EC 2.7.7.14) {Homo sapiens}; contains Pfam profile PF01467: Cytidylyltransferase
355440	1	1011	5	5	1946	3	1	At5g50640	4,00E-31	68418.m06274 CBS domain-containing protein / octicosapeptide/Phox/Bemp1 (PB1) domain-containing protein contains Pfam profiles: PF00571 CBS domain, PF00564: PB1 domain
356113	1	1011	5	5	2367	2	2	At3g52950	8,00E-35	68416.m05837 CBS domain-containing protein / octicosapeptide/Phox/Bemp1 (PB1) domain-containing protein contains Pfam profiles: PF00571 CBS domain, PF00564: PB1 domain

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352989	2	1013	4	6	5439	1	1	At3g11210	1,00E-62	68416.m01362 GDSL-motif lipase/hydrolase family protein contains Pfam profile PF00657: Lipase/Acylhydrolase with GDSL-like motif
356125	1	1016	5	5	3026	2	1	At2g40810	2,00E-57	68415.m05035 WD-40 repeat protein family similar to Gsa12p(GI:18307769)[Pichia pastoris]; contains 3 Pfam PF00400: WD domain, G-beta repeats
358352	1	1017	6	4	6742	1	1	At3g22320	2,00E-37	68416.m02819 DNA-directed RNA polymerase, putative similar to SP|P19388 DNA-directed RNA polymerase II 23 kDa polypeptide (EC 2.7.7.6) {Homo sapiens}; contains Pfam profiles PF03871: RNA polymerase Rpb5 N-terminal domain, PF01191: RNA polymerase Rpb5 C-terminal domain
357504	1	1017	6	4	8189	2	2	At2g41340	2,00E-28	68415.m05103 eukaryotic rpb5 RNA polymerase subunit family protein similar to SP|Q09191 DNA-directed RNA polymerases II 24 kDa polypeptide (EC 2.7.7.6) {Schizosaccharomyces pombe}; contains Pfam profiles PF03871: RNA polymerase Rpb5 N-terminal domain, PF01191: RNA polymerase Rpb5 C-terminal domain
354058	9	1018	4	6	5951	3	3	At5g45775	3,00E-87	68418.m05629 60S ribosomal protein L11 (RPL11D)
356146	1	1019	5	5	1256	2	1	At2g42790	2,00E-79	68415.m05298 citrate synthase, glyoxysomal, putative strong similarity to SP|P49299 Citrate synthase, glyoxysomal precursor {Cucurbita maxima}; contains Pfam profile PF00285: Citrate synthase
353262	2	1020	4	6	4105	1	1	At4g08170	4,00E-55	68417.m01350 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]
353670	3	1020	4	6	4105	1	1	At4g08170	2,00E-51	68417.m01350 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]
357683	1	1020	4	6	4105	1	1	At4g08170	3,00E-56	68417.m01350 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]

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
359795	1	1021	5	5				At3g61260	1,00E-41	68416.m06856 DNA-binding family protein / remorin family protein similar to DNA-binding protein gi|601843 [Arabidopsis thaliana], remorin [Solanum tuberosum] GI:1881585; contains Pfam profiles PF03763: Remorin C-terminal region, PF03766: Remorin N-terminal region
353619	3	1024	4	6	2360	1	2	At3g06350	7,00E-81	68416.m00733 dehydroquinate dehydratase, putative / shikimate dehydrogenase, putative similar to dehydroquinate dehydratase/shikimate dehydrogenase [Nicotiana tabacum][GI:535771], dehydroquinate dehydratase/shikimate:NADP oxidoreductase [Lycopersicon esculentum][GI:3169883]
354801	1	1024	4	6	2360	1	2	At3g06350	7,00E-52	68416.m00733 dehydroquinate dehydratase, putative / shikimate dehydrogenase, putative similar to dehydroquinate dehydratase/shikimate dehydrogenase [Nicotiana tabacum][GI:535771], dehydroquinate dehydratase/shikimate:NADP oxidoreductase [Lycopersicon esculentum][GI:3169883]
359103	1	1024	4	6	2360	1	2	At3g06350	5,00E-38	68416.m00733 dehydroquinate dehydratase, putative / shikimate dehydrogenase, putative similar to dehydroquinate dehydratase/shikimate dehydrogenase [Nicotiana tabacum][GI:535771], dehydroquinate dehydratase/shikimate:NADP oxidoreductase [Lycopersicon esculentum][GI:3169883]
358304	1	1024	4	6				At4g03115	4,00E-12	68417.m00424 mitochondrial substrate carrier family protein contains Pfam profile: PF00153 mitochondrial carrier protein
355675	1	1025	3	7	9656	1	1	At3g25070	2,00E-18	68416.m03132 RPM1-interacting protein 4 (RIN4) identical to SP|Q8GYN5 RPM1-interacting protein 4 {Arabidopsis thaliana}
354402	2	1025	3	7	10053	2	1	At5g48655	2,00E-26	68418.m06019 zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)
352962	3	1027	5	5	6440	2	2	At3g22850	1,00E-71	68416.m02881 expressed protein similar to auxin down-regulated protein ARG10 [Vigna radiata] GI:2970051, wali7 (aluminum-induced protein) [Triticum aestivum] GI:451193
356500	1	1027	5	5	6440	2	2	At3g22850	2,00E-11	68416.m02881 expressed protein similar to auxin down-regulated protein ARG10 [Vigna radiata] GI:2970051, wali7 (aluminum-induced protein) [Triticum aestivum] GI:451193

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354794	1	1027	5	5				At4g27450	1,00E-43	68417.m03945 expressed protein similar to auxin down-regulated protein ARG10 [Vigna radiata] GI:2970051, wali7 (aluminum-induced protein) [Triticum aestivum] GI:451193
355369	1	1029	4	6				At5g28770	3,00E-22	68418.m03535 bZIP transcription factor family protein similar to seed storage protein opaque-2(bZIP family)GI:168428 from Zea mays; contains Pfam profile PF00170: bZIP transcription factor; identical to cDNA bZIP protein BZO2H3 GI:10954098
354445	9	1032	2	8	3886	2	1	At5g53530	4,00E-124	68418.m06652 vacuolar protein sorting-associated protein 26, putative / VPS26, putative similar to vacuolar sorting protein 26 [Homo sapiens] GI:9622852; contains Pfam profile PF03643: Vacuolar protein sorting-associated protein 26
355197	1	1050	4	5	1606	2	2	At4g01850	6,00E-112	68417.m00242 S-adenosylmethionine synthetase 2 (SAM2) identical to S-adenosylmethionine synthetase 2 (Methionine adenosyltransferase 2, AdoMet synthetase 2) [Arabidopsis thaliana] SWISS-PROT:P17562
359180	1	1050	4	5	1606	2	2	At4g01850	9,00E-06	68417.m00242 S-adenosylmethionine synthetase 2 (SAM2) identical to S-adenosylmethionine synthetase 2 (Methionine adenosyltransferase 2, AdoMet synthetase 2) [Arabidopsis thaliana] SWISS-PROT:P17562
355054	1	1050	4	5				At2g36880	3,00E-100	68415.m04521 S-adenosylmethionine synthetase, putative similar to S-adenosylmethionine synthetase 3 (Methionine adenosyltransferase 3, AdoMet synthetase 3) [Lycopersicon esculentum] SWISS-PROT:P43282
353587	3	1054	5	4	1824	2	1	At2g33150	2,00E-132	68415.m04062 acetyl-CoA C-acyltransferase, putative / 3-ketoacyl-CoA thiolase, putative similar to 3-ketoacyl-CoA thiolase (E.C. 2.3.1.16) from [Arabidopsis thaliana] GI:2981616, [Cucumis sativus] GI:393707, [Cucurbita cv. Kurokawa Amakuri] GI:1694621; contains InterPro accession IPR002155: Thiolase
354007	2	1054	5	4	1824	2	1	At2g33150	1,00E-73	68415.m04062 acetyl-CoA C-acyltransferase, putative / 3-ketoacyl-CoA thiolase, putative similar to 3-ketoacyl-CoA thiolase (E.C. 2.3.1.16) from [Arabidopsis thaliana] GI:2981616, [Cucumis sativus] GI:393707, [Cucurbita cv. Kurokawa Amakuri] GI:1694621; contains InterPro accession IPR002155: Thiolase

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
355765	1	1054	5	4	2343	1	1	At5g48230	3,00E-42	68418.m05959 acetyl-CoA C-acyltransferase, putative / 3-ketoacyl-CoA thiolase, putative strong similarity to Acetoacetyl-coenzyme A thiolase (E.C. 2.3.1.9) [Raphanus sativus] GI:1542941; contains InterPro accession IPR002155: Thiolase
356021	1	1054	5	4	2343	1	1	At5g48230	1,00E-26	68418.m05959 acetyl-CoA C-acyltransferase, putative / 3-ketoacyl-CoA thiolase, putative strong similarity to Acetoacetyl-coenzyme A thiolase (E.C. 2.3.1.9) [Raphanus sativus] GI:1542941; contains InterPro accession IPR002155: Thiolase
357236	1	1054	5	4				At5g47720	4,00E-100	68418.m05895 acetyl-CoA C-acyltransferase, putative / 3-ketoacyl-CoA thiolase, putative strong similarity to Acetoacetyl-coenzyme A thiolase (E.C. 2.3.1.9) [Raphanus sativus] GI:1542941; contains InterPro accession IPR002155: Thiolase
358637	1	1054	5	4				At5g47720	6,00E-75	68418.m05895 acetyl-CoA C-acyltransferase, putative / 3-ketoacyl-CoA thiolase, putative strong similarity to Acetoacetyl-coenzyme A thiolase (E.C. 2.3.1.9) [Raphanus sativus] GI:1542941; contains InterPro accession IPR002155: Thiolase
353504	2	1056	4	5	7589	2	2	At5g01430	7,00E-24	68418.m00056 Got1-like family protein contains Pfam profile: PF04178 Got1-like family
358179	1	1059	6	3	7354	3	1	At5g59850	8,00E-55	68418.m07505 40S ribosomal protein S15A (RPS15aF) cytoplasmic ribosomal protein S15a, Arabidopsis thaliana, EMBL:ATAF1412
354695	1	1062	5	4	231	1	1	At4g13750	5,00E-12	68417.m02134 expressed protein
357713	1	1064	5	4	6864	1	1	At1g08570	2,00E-22	68414.m00950 thioredoxin family protein contains Pfam profile: PF00085 Thioredoxin; similar to ESTs gb|T46281, gb|R83933, gb|N65879, emb|F14466, gb|N96726, gb|AA042340, and emb|Z18150
353027	3	1066	5	4	642	1	1	At1g80680	4,00E-27	68414.m09467 nucleoporin family protein contains Pfam profile: PF04096 nucleoporin autopeptidase
354791	1	1067	5	4	4876	3	1	At2g44530	2,00E-13	68415.m05539 ribose-phosphate pyrophosphokinase, putative / phosphoribosyl diphosphate synthetase, putative very strong similarity to phosphoribosyl pyrophosphate synthase [Spinacia oleracea] GI:4902849; contains Pfam profile PF00156: Phosphoribosyl transferase domain
358952	1	1069	6	3	3652	2	1	At1g14360	1,00E-71	68414.m01702 UDP-galactose/UDP-glucose transporter, putative very similar to UDP-galactose/UDP-glucose transporter (GI:22651763) {Arabidopsis thaliana}

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356496	1	1070	4	5	3492	1	1	At5g30510	1,00E-77	68418.m03752 30S ribosomal protein S1, putative similar to Swiss-Prot:P29344 30S ribosomal protein S1, chloroplast precursor (CS1) [Spinacia oleracea]
353860	2	1071	5	4	5781	1	2	At5g24400	8,00E-32	68418.m02876 glucosamine/galactosamine-6-phosphate isomerase family protein low similarity to SP|O95336 6-phosphogluconolactonase (EC 3.1.1.31) (6PGL) {Homo sapiens}; contains Pfam profile PF01182: Glucosamine-6-phosphate isomerase/6-phosphogluconolactonase
359771	1	1072	3	6	9246	1	1	At5g48720	1,00E-10	68418.m06030 expressed protein
353941	3	1074	5	4	1243	3	2	At1g68060	2,00E-33	68414.m07775 expressed protein
357795	1	1075	3	6	5927	1	2	At5g20720	1,00E-67	68418.m02461 20 kDa chaperonin, chloroplast (CPN21) (CHCPN10) (CPN20) identical to chloroplast 20 kDa chaperonin, chloroplast precursor (Protein Cpn21), chloroplast protein Cpn10, chloroplast chaperonin 10 (Ch-CPN10), SP|O65282 from [Arabidopsis thaliana]; identical to cDNA chaperonin 20 GI:14587372
359878	1	1075	3	6	5927	1	2	At5g20720	9,00E-35	68418.m02461 20 kDa chaperonin, chloroplast (CPN21) (CHCPN10) (CPN20) identical to chloroplast 20 kDa chaperonin, chloroplast precursor (Protein Cpn21), chloroplast protein Cpn10, chloroplast chaperonin 10 (Ch-CPN10), SP|O65282 from [Arabidopsis thaliana]; identical to cDNA chaperonin 20 GI:14587372
354248	2	1075	3	6	9263	2	2	At1g14980	2,00E-40	68414.m01790 10 kDa chaperonin (CPN10) identical to SP:P34893 from [Arabidopsis thaliana]
357796	1	1075	3	6	9263	2	2	At1g14980	4,00E-39	68414.m01790 10 kDa chaperonin (CPN10) identical to SP:P34893 from [Arabidopsis thaliana]
358573	1	1075	3	6	9263	2	2	At1g14980	3,00E-41	68414.m01790 10 kDa chaperonin (CPN10) identical to SP:P34893 from [Arabidopsis thaliana]
358686	1	1078	6	3	75	2	1	At1g80490	5,00E-56	68414.m09430 WD-40 repeat family protein contains 9 WD-40 repeats domain (PF00400) (6 weak)
353353	2	1078	6	3	145	1	1	At3g16830	4,00E-38	68416.m02149 WD-40 repeat family protein contains 10 WD-40 repeats (PF00400) (1 weak)
355650	1	1080	5	4	9582	2	1	At1g78430	6,00E-11	68414.m09139 tropomyosin-related similar to Tropomyosin 1 [Baker's yeast](SP:P17536) {Saccharomyces cerevisiae}; similar to enterophilin-2L (GI:12718845) [Cavia porcellus]; similar to latent nuclear antigen (GI:5669894) [Human herpesvirus 8]; similar to multiple ligand-binding protein 1 (GI:1403575) [Streptococcus sp.]

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
358854	1	1081	5	4	2754	1	2	At5g43310	4,00E-14	68418.m05293 COP1-interacting protein-related contains similarity to COP1-Interacting Protein 7 (CIP7) [Arabidopsis thaliana] GI:3327868
355372	1	1081	5	4	4099	2	1	At1g72410	3,00E-09	68414.m08374 COP1-interacting protein-related similar to COP1-Interacting ProteinI 7 (CIP7) [Arabidopsis thaliana] GI:3327870
356077	1	1081	5	4	4099	2	1	At1g72410	3,00E-13	68414.m08374 COP1-interacting protein-related similar to COP1-Interacting ProteinI 7 (CIP7) [Arabidopsis thaliana] GI:3327870
354898	1	1087	4	5	896	1	2	At3g20290	9,00E-103	68416.m02571 calcium-binding EF hand family protein similar to EH-domain containing protein 1 from {Mus musculus} SP|Q9WVK4 and {Homo sapiens} SP|Q9H4M9, receptor-mediated endocytosis 1 from [Caenorhabditis elegans] GI:13487775, GI:13487777, GI:13487779; contains INTERPRO:IPR002048 calcium-binding EF-hand domain
355848	1	1087	4	5	896	1	2	At3g20290	7,00E-43	68416.m02571 calcium-binding EF hand family protein similar to EH-domain containing protein 1 from {Mus musculus} SP|Q9WVK4 and {Homo sapiens} SP|Q9H4M9, receptor-mediated endocytosis 1 from [Caenorhabditis elegans] GI:13487775, GI:13487777, GI:13487779; contains INTERPRO:IPR002048 calcium-binding EF-hand domain
354013	2	1089	3	6	2981	1	2	At5g23540	5,00E-106	68418.m02763 26S proteasome regulatory subunit, putative similar to 26S proteasome-associated pad1 homolog [Homo sapiens] GI:1923256, 26S proteasome, non-ATPase subunit [Mus musculus] GI:2505940; contains Pfam profile PF01398: Mov34/MPN/PAD-1 family
354967	1	1089	3	6	3087	2	1	At1g71230	1,00E-37	68414.m08220 COP9 signalosome subunit 5A / CSN subunit 5A (CSN5A) / c-JUN coactivator protein AJH2, putative (AJH2) COP9 complex subunit CSN5-2; identical to c-Jun coactivator protein AJH2 GI:3641312 from [Arabidopsis thaliana]; identical to cDNA CSN complex subunit 5A (CSN5A) GI:18056660; contains Pfam profile PF01398: Mov34/MPN/PAD-1 family
359627	1	1090	5	4	4955	1	2	At4g24670	1,00E-66	68417.m03532 alliinase family protein contains Pfam profiles: PF04864 allinase C-terminal domain, PF04863 alliinase EGF-like domain
359779	1	1094	1	8	5275	1	1	At1g28120	2,00E-39	68414.m03445 expressed protein

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
352953	3	1095	2	7	3171	2	2	At2g33840	9,00E-101	68415.m04153 tRNA synthetase class I (W and Y) family protein similar to SP|P54577 Tyrosyl-tRNA synthetase (EC 6.1.1.1) (Tyrosyl--tRNA ligase) (TyrRS) {Homo sapiens}; contains Pfam profile PF00579: tRNA synthetases class I (W and Y)
358498	1	1095	2	7	3171	2	2	At2g33840	4,00E-44	68415.m04153 tRNA synthetase class I (W and Y) family protein similar to SP|P54577 Tyrosyl-tRNA synthetase (EC 6.1.1.1) (Tyrosyl--tRNA ligase) (TyrRS) {Homo sapiens}; contains Pfam profile PF00579: tRNA synthetases class I (W and Y)
358223	1	1096	5	4	4924	1	1	At2g38440	9,00E-13	68415.m04721 expressed protein
354086	2	1098	8	1	7895	2	1	At3g11470	1,00E-11	68416.m01398 4'-phosphopantetheinyl transferase family protein contains Pfam profile PF01648: 4'-phosphopantetheinyl transferase superfamily
356057	1	1102	4	5	7046	1	1	At1g32400	1,00E-10	68414.m03998 senescence-associated family protein contains Pfam profile PF00335: Tetraspanin family
353768	2	1102	4	5	8771	2	1	At4g28770	2,00E-49	68417.m04114 expressed protein
357160	1	1106	4	5	5152	2	1	At2g20120	1,00E-27	68415.m02351 expressed protein contains Pfam domain, PF04367: Protein of unknown function (DUF502); identical to cDNA putative membrane protein COV (COV) GI:30059123
354244	2	1107	4	5	2852	1	2	At1g43670	8,00E-68	68414.m05016 fructose-1,6-bisphosphatase, putative / D-fructose-1,6-bisphosphate 1-phosphohydrolase, putative / FBPase, putative very strong similarity to SP|P46267 Fructose-1,6-bisphosphatase, cytosolic (EC 3.1.3.11) (D-fructose-1,6- bisphosphate 1-phosphohydrolase) (FBPase) {Brassica napus}; contains Pfam profile PF00316: fructose-1,6-bisphosphatase
353854	3	1110	4	5	5264	2	1	At5g06290	1,00E-103	68418.m00705 2-cys peroxiredoxin, chloroplast, putative very strong similarity to SP|Q96291 2-cys peroxiredoxin BAS1, chloroplast precursor {Arabidopsis thaliana}; contains Pfam profile: PF00578 AhpC/TSA (alkyl hydroperoxide reductase and thiol-specific antioxidant) family
357559	1	1110	4	5	6263	1	2	At1g48130	6,00E-35	68414.m05371 peroxiredoxin (PER1) / rehydrin, putative identical to peroxiredoxin (Rehydrin homolog) [Arabidopsis thaliana] SWISS-PROT:O04005; contains Pfam profile: PF00578 AhpC/TSA (alkyl hydroperoxide reductase and thiol-specific antioxidant) family
358903	1	1111	5	4	293	2	1	At5g09350	4,00E-41	68418.m01083 phosphatidylinositol 4-kinase, putative strong similarity to gi:4467359

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
359316	1	1114	6	3	3601	1	1	At1g70630	2,00E-47	68414.m08141 expressed protein
353982	2	1114	6	3	5080	1	1	At2g35610	5,00E-60	68415.m04365 expressed protein
357138	1	1115	7	2	1423	1	2	At1g58440	4,00E-31	68414.m06648 squalene monooxygenase, putative / squalene epoxidase, putative similar to SP|O65404 (SE 1,1), SP|O65402 (SE 1,2) 6566341 dbj AB008021.1 AB008021
357907	1	1115	7	2				At4g37760	3,00E-42	68417.m05345 squalene monooxygenase, putative / squalene epoxidase, putative similar to SP|O65404 (SE 1,1), SP|O65402 (SE 1,2), SP|O65403 (SE 2)
359868	1	1115	7	2				At4g37760	2,00E-23	68417.m05345 squalene monooxygenase, putative / squalene epoxidase, putative similar to SP|O65404 (SE 1,1), SP|O65402 (SE 1,2), SP|O65403 (SE 2)
359739	1	1116	4	5	2017	1	1	At1g60900	6,00E-17	68414.m06856 U2 snRNP auxiliary factor large subunit, putative similar to U2 snRNP auxiliary factor, large subunit GB:CAA77136 from [Nicotiana plumbaginifolia]
358186	1	1116	4	5	8303	1	1	At2g33440	6,00E-06	68415.m04099 splicing factor family protein similar to Splicing factor U2AF 65 kDa subunit (U2 snRNP auxiliary factor large subunit) {Homo sapiens} SP|P26368, {Mus musculus} SP|P26369; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)
355127	1	1116	4	5				At4g36690	2,00E-30	68417.m05206 U2 snRNP auxiliary factor large subunit, putative similar to U2 snRNP auxiliary factor, large subunit [Nicotiana plumbaginifolia] GI:3850823
356394	1	1118	5	4	1854	1	2	At2g30970	5,00E-37	68415.m03777 aspartate aminotransferase, mitochondrial / transaminase A (ASP1) identical to SP|P46643 Aspartate aminotransferase, mitochondrial precursor (EC 2.6.1.1) (Transaminase A) {Arabidopsis thaliana}
359444	1	1118	5	4	1854	1	2	At2g30970	1,00E-87	68415.m03777 aspartate aminotransferase, mitochondrial / transaminase A (ASP1) identical to SP|P46643 Aspartate aminotransferase, mitochondrial precursor (EC 2.6.1.1) (Transaminase A) {Arabidopsis thaliana}
354283	4	1118	5	4	1994	1	1	At5g11520	3,00E-97	68418.m01344 aspartate aminotransferase, chloroplast / transaminase A (ASP3) (YLS4) identical to SP|P46644 Aspartate aminotransferase, chloroplast precursor (EC 2.6.1.1) (Transaminase A) {Arabidopsis thaliana}; identical to cDNA YLS4 mRNA for aspartate aminotransferase (ASP3), partial cds GI:13122285

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
359822	1	1119	3	6	7989	1	1	At4g34150	4,00E-31	68417.m04846 C2 domain-containing protein similar to calcium-dependent protein kinase [Dunaliella tertiolecta] GI:6644464; contains Pfam profile PF00168: C2 domain
356750	1	1121	5	4	5550	2	1	At4g25230	3,00E-26	68417.m03631 zinc finger (C3HC4-type RING finger) family protein similar to autocrine motility factor receptor [Mus musculus] GI:5931953; contains Pfam profiles PF00097: Zinc finger, C3HC4 type (RING finger), PF02845: CUE domain
358381	1	1122	5	4	5588	1	1	At3g09740	4,00E-45	68416.m01154 syntaxin 71 (SYP71) identified as syntaxin of plants 71 (SYP71) in Sanderfoot, A.A., et al, Plant Physiology 124:1558-69(2000); identical to SP|Q9SF29 Syntaxin 71 (AtSYP71) {Arabidopsis thaliana}
354468	2	1122	5	4	6896	2	1	At5g38110	2,00E-80	68418.m04591 ASF1-like anti-silencing family protein similar to SP|P32447 Anti-silencing protein 1 {Saccharomyces cerevisiae}; contains Pfam profile PF04729: Anti-silencing protein, ASF1-like
353143	2	1123	3	6	9530	1	1	At5g64130	6,00E-29	68418.m08053 expressed protein
357768	1	1124	2	7	3838	1	1	At3g48530	1,00E-28	68416.m05299 CBS domain-containing protein low similarity to SP|Q9UGI9 5'-AMP-activated protein kinase, gamma-3 subunit (AMPK gamma-3 chain) (AMPK gamma3) {Homo sapiens}; contains Pfam profile PF00571: CBS domain
360040	1	1125	5	4	2423	1	1	At1g74910	1,00E-60	68414.m08687 ADP-glucose pyrophosphorylase family protein contains Pfam profile PF00483: Nucleotidyl transferase; low similarity to mannose-1-phosphate guanylyltransferase [Hypocrea jecorina] GI:3323397
355965	1	1131	5	4	119	1	1	At2g05710	1,00E-82	68415.m00611 aconitate hydratase, cytoplasmic, putative / citrate hydro-lyase/aconitase, putative nearly identical to SP|P49608 Aconitate hydratase, cytoplasmic (EC 4.2.1.3) (Citrate hydro-lyase) (Aconitase) {Cucurbita maxima}; contains Pfam profiles PF00330: Aconitase family (aconitate hydratase), PF00694: Aconitase C-terminal domain
356592	1	1137	5	4	4285	1	2	At3g24440	7,00E-27	68416.m03067 fibronectin type III domain-containing protein contains Pfam profile PF00041: Fibronectin type III domain
353618	2	1137	5	4	4384	1	1	At4g30200	6,00E-13	68417.m04295 expressed protein contains weak similarities to Pfam profiles: PF00041 Fibronectin type III domain, PF00628 PHD-finger; supporting cDNA gi|11177136|dbj|AB050977.1|

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
354077	2	1137	5	4	4384	1	1	At4g30200	1,00E-22	68417.m04295 expressed protein contains weak similarities to Pfam profiles: PF00041 Fibronectin type III domain, PF00628 PHD-finger; supporting cDNA gi|11177136|dbj|AB050977.1|
353435	4	1138	8	1	9917	2	3	At4g02210	4,00E-07	68417.m00298 expressed protein
358615	1	1138	8	1	9917	2	3	At4g02210	2,00E-24	68417.m00298 expressed protein
359130	1	1138	8	1	9917	2	3	At2g24960	4,00E-25	68415.m02985 expressed protein ; expression supported by MPSS
360065	1	1143	4	5	524	1	1	At3g01720	2,00E-52	68416.m00107 expressed protein
357667	1	1143	4	5	3797	2	1	At5g25265	3,00E-110	68418.m02995 expressed protein
358719	1	1144	3	6	6861	1	1	At2g26280	1,00E-21	68415.m03154 smr (Small MutS Related) domain-containing protein weak similarity to PRLI-interacting factor N [Arabidopsis thaliana] GI:11139276; contains Pfam profile PF01713: Smr domain
355308	1	1144	3	6				At3g52210	5,00E-54	68416.m05735 mRNA capping enzyme family protein contains Pfam profile PF03291: mRNA capping enzyme, large subunit
353556	2	1146	4	5	400	1	1	At3g07100	6,00E-45	68416.m00845 protein transport protein Sec24, putative similar to protein transport protein Sec24A (SEC24-related protein) [Homo sapiens] SWISS-PROT:O95486
358748	1	1146	4	5	666	1	1	At2g27460	4,00E-50	68415.m03319 sec23/sec24 transport family protein weak similarity to SP|P53992 Protein transport protein Sec24C (SEC24-related protein C) {Homo sapiens}; contains Pfam domains PF04811: Sec23/Sec24 trunk domain, PF04815: Sec23/Sec24 helical domain and PF04810: Sec23/Sec24 zinc finger
356410	1	1147	4	5	4884	1	1	At3g14890	4,00E-17	68416.m01883 phosphoesterase identical to phosphoesterase [Arabidopsis thaliana] GI:21630064; contains Pfam profile PF00645: Poly(ADP-ribose) polymerase and DNA-Ligase Zn-finger region
357056	1	1150	4	5	511	1	1	At4g13780	2,00E-32	68417.m02137 methionine--tRNA ligase, putative / methionyl-tRNA synthetase, putative / MetRS, putative similar to methionyl-tRNA synthetase [Oryza sativa] GI:4091008; contains Pfam profiles PF00133: tRNA synthetases class I (I, L, M and V), PF01588: Putative tRNA binding domain

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
357532	1	1150	4	5	511	1	1	At4g13780	2,00E-23	68417.m02137 methionine--tRNA ligase, putative / methionyl-tRNA synthetase, putative / MetRS, putative similar to methionyl-tRNA synthetase [Oryza sativa] GI:4091008; contains Pfam profiles PF00133: tRNA synthetases class I (I, L, M and V), PF01588: Putative tRNA binding domain
355559	1	1150	4	5	1443	1	1	At3g55400	4,00E-18	68416.m06153 methionyl-tRNA synthetase / methionine--tRNA ligase / MetRS (cpMetRS) identical to methionyl-tRNA synthetase MEtRS [Arabidopsis thaliana] GI:2266985
355769	1	1152	6	3	2515	2	2	At3g57780	8,00E-25	68416.m06436 expressed protein
356323	1	1155	4	5	7319	1	1	At2g46225	2,00E-63	68415.m05748 expressed protein
356647	1	1155	4	5	7634	2	1	At5g24310	5,00E-36	68418.m02860 expressed protein strong similarity to unknown protein (emb|CAB66408.1)
354526	1	1157	5	4				At3g53410	6,00E-43	68416.m05894 zinc finger (C3HC4-type RING finger) family protein contains Pfam domain: PF00097: Zinc finger, C3HC4 type (RING finger)
359548	1	1160	4	5	2850	1	1	At3g56310	7,00E-13	68416.m06260 alpha-galactosidase, putative / melibiase, putative / alpha-D-galactoside galactohydrolase, putative similar to alpha-galactosidase SP:Q42656 from [Coffea arabica]
354628	1	1160	4	5	3348	1	1	At5g08370	4,00E-31	68418.m00986 alpha-galactosidase, putative / melibiase, putative / alpha-D-galactoside galactohydrolase, putative similar to alpha-galactosidase SP:Q42656 from [Coffea arabica]
356400	1	1161	4	5	255	1	1	At5g13980	9,00E-58	68418.m01635 glycosyl hydrolase family 38 protein similar to alpha-mannosidase GI:1419374 from [Homo sapiens]
356123	1	1161	4	5				At3g26720	3,00E-45	68416.m03341 glycosyl hydrolase family 38 protein similar to lysosomal alpha-mannosidase GI:3522867 from [Homo sapiens]
354740	1	1163	3	6	6571	1	1	At5g22620	1,00E-12	68418.m02643 phosphoglycerate/bisphosphoglycerate mutase family protein weak similarity to SP|P15259 Phosphoglycerate mutase, muscle form (EC 5.4.2.1 {Homo sapiens}; contains Pfam profile PF00300: phosphoglycerate mutase family
358754	1	1164	5	4	4011	1	1	At5g16270	3,00E-27	68418.m01900 Rad21/Rec8-like family protein weak similarity to cohesion family protein SYN2 [Arabidopsis thaliana] GI:12006360; contains Pfam profiles PF04824: Conserved region of Rad21 / Rec8 like protein, PF04825: N terminus of Rad21 / Rec8 like protein; supporting cDNA gi|18157648|gb|AF400129.1|AF400129

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
352924	2	1165	7	2	4736	1	1	At3g60340	9,00E-08	68416.m06746 palmitoyl protein thioesterase family protein palmitoyl-protein thioesterase precursor, Mus musculus, EMBL:AF071025
358705	1	1166	4	5	3107	1	1	At4g10790	5,00E-30	68417.m01759 UBX domain-containing protein low similarity to SP|Q9UNN5 FAS-associated factor 1 (FAF1 protein) {Homo sapiens}; contains Pfam profile PF00789: UBX domain
354297	3	1166	4	5	4069	2	2	At4g11740	2,00E-45	68417.m01872 ara4-interacting protein, putative (SAY1) similar to Ara4-interacting protein [Arabidopsis thaliana] GI:13160609; contains Pfam profiles PF00789: UBX domain, PF02809: Ubiquitin interaction motif
356590	1	1167	4	5	8418	1	2	At5g20090	5,00E-08	68418.m02392 expressed protein contains Pfam domain, PF03650: Uncharacterized protein family (UPF0041)
355780	1	1168	3	6	4822	2	2	At5g18640	1,00E-43	68418.m02213 lipase class 3 family protein low similarity to Triacylglycerol Acylhydrolase (E.C.3.1.1.3) [Rhizomucor miehei] GI:230348; contains Pfam profile PF01764: Lipase
353294	2	1169	3	6	1279	1	2	At5g23450	1,00E-51	68418.m02752 diacylglycerol kinase family protein contains INTERPRO domain, IPR001206, DAG-kinase catalytic domain
359430	1	1169	3	6	1279	1	2	At5g23450	3,00E-28	68418.m02752 diacylglycerol kinase family protein contains INTERPRO domain, IPR001206, DAG-kinase catalytic domain
353289	3	1182	4	4	5645	2	2	At3g61670	6,00E-15	68416.m06911 expressed protein weak similarity to extra-large G-protein [Arabidopsis thaliana] GI:3201682
353849	2	1183	3	5	4239	1	2	At2g44060	9,00E-32	68415.m05478 late embryogenesis abundant family protein / LEA family protein similar to ethylene-responsive late embryogenesis-like protein [Lycopersicon esculentum] GI:1684830; contains Pfam profile PF03168: Late embryogenesis abundant protein
352931	3	1186	5	3				At1g04340	4,00E-34	68414.m00424 lesion inducing protein-related similar to ORF, able to induce HR-like lesions [Nicotiana tabacum]
358662	1	1190	3	5	3671	1	1	At1g67280	8,00E-28	68414.m07657 lactoylglutathione lyase, putative / glyoxalase I, putative similar to putative lactoylglutathione lyase SP:Q39366, GI:2494843 from [Brassica oleracea]
356782	1	1190	3	5	6382	1	1	At1g08110	4,00E-42	68414.m00889 lactoylglutathione lyase, putative / glyoxalase I, putative similar to lactoylglutathione lyase SP:O04885 from [Brassica juncea]

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
356475	1	1190	3	5				At1g11840	4,00E-27	68414.m01360 lactoylglutathione lyase, putative / glyoxalase I, putative highly similar to putative lactoylglutathione lyase SP:Q39366 from [Brassica oleracea]
360069	1	1191	3	5	7186	1	2	At1g08830	5,00E-26	68414.m00983 superoxide dismutase [Cu-Zn] (SODCC) / copper/zinc superoxide dismutase (CSD1) identical to SWISS-PROT: P24704
354307	3	1192	5	3	207	1	1	At1g09570	1,00E-100	68414.m01073 phytochrome A (PHYA) identical to SP|P14712 Phytochrome A {Arabidopsis thaliana}
356971	1	1192	5	3	207	1	1	At1g09570	2,00E-21	68414.m01073 phytochrome A (PHYA) identical to SP|P14712 Phytochrome A {Arabidopsis thaliana}
356998	1	1192	5	3	207	1	1	At1g09570	2,00E-69	68414.m01073 phytochrome A (PHYA) identical to SP|P14712 Phytochrome A {Arabidopsis thaliana}
360079	1	1192	5	3	207	1	1	At1g09570	1,00E-41	68414.m01073 phytochrome A (PHYA) identical to SP|P14712 Phytochrome A {Arabidopsis thaliana}
357520	1	1193	5	3	4027	2	2	At3g29180	3,00E-45	68416.m03657 expressed protein
360036	1	1196	4	4	2207	1	1	At1g61670	2,00E-85	68414.m06956 expressed protein similar to membrane protein PTM1 precursor isolog GI:1931644 from [Arabidopsis thaliana]
355205	1	1198	3	5	3970	2	2	At2g02180	2,00E-09	68415.m00154 tobamovirus multiplication protein 3 (TOM3) identical to tobamovirus multiplication protein (TOM3) GI:15425641 from [Arabidopsis thaliana]
356583	1	1198	3	5	4607	1	2	At4g21790	1,00E-19	68417.m03152 transmembrane protein-related (TOM1) contains some similarity to transmembrane protein TOM3 GI:15425641 from [Arabidopsis thaliana]; identical to cDNA TOM1 GI:9967414
353669	2	1199	4	4	2279	2	1	At5g48160	5,00E-34	68418.m05949 tropomyosin-related contains weak similarity to Tropomyosin, muscle (Allergen Ani s 3). (Swiss-Prot:Q9NAS5) [Anisakis simplex]
358244	1	1199	4	4	4116	1	1	At3g63500	1,00E-32	68416.m07153 expressed protein
354739	1	1200	5	3	8201	1	1	At5g25360	2,00E-24	68418.m03008 expressed protein
355177	1	1200	5	3	8201	1	1	At5g25360	7,00E-33	68418.m03008 expressed protein
353715	2	1201	3	5	2662	2	1	At1g80480	5,00E-89	68414.m09427 PRLI-interacting factor L, putative similar to PRLI-interacting factor L [Arabidopsis thaliana] GI:11139268; contains Pfam profile PF02492: Cobalamin synthesis protein/P47K
354418	2	1202	5	3	4791	1	1	At1g25682	8,00E-91	68414.m03178 cell cycle control protein-related contains similarity to Swiss-Prot:Q9P7C5 cell cycle control protein cwf16 [Schizosaccharomyces pombe]

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
356929	1	1205	4	4	8296	1	2	At1g22450	1,00E-43	68414.m02806 cytochrome c oxidase subunit 6b, putative (COX6b) nearly identical to subunit 6b of cytochrome c oxidase [Arabidopsis thaliana] GI:6518353
359393	1	1205	4	4				At5g57815	2,00E-21	68418.m07230 cytochrome c oxidase subunit 6b, putative similar to subunit 6b of cytochrome c oxidase [Arabidopsis thaliana] gi|6518353|dbj|BAA87883
357500	1	1207	6	2	4383	1	1	At3g18210	3,00E-33	68416.m02316 oxidoreductase, 2OG-Fe(II) oxygenase family protein contains Pfam domain PF03171 2OG-Fe(II) oxygenase superfamily
357828	1	1208	6	2	8654	2	1	At4g33580	2,00E-22	68417.m04771 carbonic anhydrase family protein / carbonate dehydratase family protein similar to SP|P46512 Carbonic anhydrase 1 (EC 4.2.1.1) (Carbonate dehydratase 1) {Flaveria linearis}; contains Pfam profile PF00484: Carbonic anhydrase
355662	1	1209	4	4	3350	1	2	At5g53120	4,00E-07	68418.m06603 spermidine synthase, putative / putrescine aminopropyltransferase, putative similar to SP|O82147 Spermidine synthase (EC 2.5.1.16) (Putrescine aminopropyltransferase) (SPDSY) {Coffea arabica}; contains Pfam profile PF01564: Spermine/spermidine synthase
355928	1	1209	4	4	3350	1	2	At5g53120	3,00E-52	68418.m06603 spermidine synthase, putative / putrescine aminopropyltransferase, putative similar to SP|O82147 Spermidine synthase (EC 2.5.1.16) (Putrescine aminopropyltransferase) (SPDSY) {Coffea arabica}; contains Pfam profile PF01564: Spermine/spermidine synthase
355673	1	1209	4	4	3656	1	1	At1g70310	8,00E-64	68414.m08089 spermidine synthase 2 (SPDSYN2) / putrescine aminopropyltransferase 2 identical to SP|O48661 Spermidine synthase 2 (EC 2.5.1.16) (Putrescine aminopropyltransferase 2) (SPDSY 2) {Arabidopsis thaliana}
360001	1	1209	4	4	4126	1	1	At5g19530	3,00E-107	68418.m02326 spermine/spermidine synthase family protein similar to SP|P09158 Spermidine synthase (EC 2.5.1.16) (Putrescine aminopropyltransferase) {Escherichia coli}; contains Pfam profile PF01564: Spermine/spermidine synthase
357349	1	1209	4	4				At1g23820	1,00E-22	68414.m03004 spermidine synthase 1 (SPDSYN1) / putrescine aminopropyltransferase 1 identical to SP|Q9ZUB3 Spermidine synthase 1 (EC 2.5.1.16) (Putrescine aminopropyltransferase 1) (SPDSY 1) {Arabidopsis thaliana}

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
354080	2	1213	3	5	1708	1	2	At4g28600	6,00E-50	68417.m04090 calmodulin-binding protein similar to pollen-specific calmodulin-binding protein MPCBP GI:10086260 from [Zea mays]
359948	1	1213	3	5	1708	1	2	At4g28600	9,00E-24	68417.m04090 calmodulin-binding protein similar to pollen-specific calmodulin-binding protein MPCBP GI:10086260 from [Zea mays]
359541	1	1213	3	5	2507	1	1	At1g27460	9,00E-29	68414.m03348 calmodulin-binding protein similar to calmodulin-binding protein MPCBP [Zea mays] GI:10086260; contains Pfam profile PF00515: TPR Domain
358096	1	1214	4	4	1504	1	1	At3g27960	1,00E-13	68416.m03489 kinesin light chain-related low similarity to kinesin light chain [Plectonema boryanum] GI:2645229; contains Pfam profile PF00515: TPR Domain
358333	1	1214	4	4	2554	1	2	At4g10840	1,00E-39	68417.m01764 kinesin light chain-related low similarity to kinesin light chain [Plectonema boryanum] GI:2645229; contains Pfam profile PF00515 TPR Domain
354246	2	1215	6	2	7202	1	1	At3g50830	3,00E-61	68416.m05566 stress-responsive protein, putative similar to cold acclimation WCOR413-like protein gamma form [Hordeum vulgare] gi|18449100|gb|AAL69988; similar to stress-regulated protein SAP1 [Xerophyta viscosa] gi|21360378|gb|AAM47505; identical to cDNA cold acclimation protein WCOR413-like protein beta form GI:10121842
354425	2	1216	5	3	6345	1	1	At4g18040	3,00E-71	68417.m02685 eukaryotic translation initiation factor 4E 1 / eIF-4E1 / mRNA cap-binding protein 1 (EIF4E1) identical to SP|O23252 Eukaryotic translation initiation factor 4E (eIF-4E) (eIF4E) (mRNA cap-binding protein) (eIF-4F 25 kDa subunit) (eIF-4F P26 subunit) {Arabidopsis thaliana}
355507	1	1216	5	3	6345	1	1	At4g18040	2,00E-54	68417.m02685 eukaryotic translation initiation factor 4E 1 / eIF-4E1 / mRNA cap-binding protein 1 (EIF4E1) identical to SP|O23252 Eukaryotic translation initiation factor 4E (eIF-4E) (eIF4E) (mRNA cap-binding protein) (eIF-4F 25 kDa subunit) (eIF-4F P26 subunit) {Arabidopsis thaliana}
355963	1	1218	5	3	884	1	1	At5g46920	4,00E-90	68418.m05785 intron maturase, type II family protein similar to SP|Q57005 Group II intron-encoded protein ltrA {Lactococcus lactis subsp}; contains Pfam profiles PF00078: Reverse transcriptase (RNA-dependent DNA polymerase), PF01348: Type II intron maturase

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353195	3	1219	4	4	4933	3	1	At4g16700	6,00E-27	68417.m02523 phosphatidylserine decarboxylase similar to SP|P27465 Phosphatidylserine decarboxylase proenzyme (EC 4.1.1.65 {Cricetulus griseus}; contains Pfam profile PF02666: phosphatidylserine decarboxylase
357330	1	1219	4	4	6264	1	2	At1g31220	3,00E-57	68414.m03821 phosphoribosylglycinamide formyltransferase similar to phosphoribosylglycinamide formyltransferase, chloroplast precursor [Arabidopsis thaliana] SWISS-PROT:P52422
358618	1	1221	4	4	3594	1	1	At4g34660	1,00E-06	68417.m04921 SH3 domain-containing protein 2 (SH3P2) nearly identical to SH3 domain-containing protein 2 [Arabidopsis thaliana] GI:16974678; contains Pfam profile PF00018: SH3 domain
357982	1	1222	5	3	4763	2	1	At1g48450	2,00E-14	68414.m05416 expressed protein
355600	1	1223	3	5	7690	1	2	At2g35120	3,00E-48	68415.m04308 glycine cleavage system H protein, mitochondrial, putative similar to SP|Q39732 Glycine cleavage system H protein, mitochondrial precursor {Flaveria anomala}; contains Pfam profile PF01597: Glycine cleavage H-protein
356734	1	1223	3	5	7690	1	2	At2g35120	2,00E-14	68415.m04308 glycine cleavage system H protein, mitochondrial, putative similar to SP|Q39732 Glycine cleavage system H protein, mitochondrial precursor {Flaveria anomala}; contains Pfam profile PF01597: Glycine cleavage H-protein
357693	1	1226	4	4	661	1	1	At2g03140	6,00E-06	68415.m00267 CAAX amino terminal protease family protein very low similarity to SP|Q40863 Late embryogenesis abundant protein EMB8 from Picea glauca; contains Pfam profile PF02517 CAAX amino terminal protease family protein
353912	2	1226	4	4				At5g49950	8,00E-06	68418.m06185 embryogenesis-associated protein-related contains weak similarity to Embryogenesis-associated protein EMB8 (Swiss-Prot:Q40863) [Picea glauca]
357159	1	1227	4	4	7979	2	1	At1g34780	3,00E-12	68414.m04329 protein disulfide isomerase-related contains weak similarity to Pfam:P08003 protein disulfide isomerase A4 precursor (Protein ERp-72, ERp72) [Mus musculus]
358605	1	1227	4	4	7999	2	1	At3g03860	2,00E-08	68416.m00398 expressed protein
359317	1	1227	4	4	7999	2	1	At5g18120	2,00E-41	68418.m02127 expressed protein
358649	1	1228	4	4	5856	1	2	At4g39860	2,00E-35	68417.m05648 expressed protein
357506	1	1228	4	4	6628	2	2	At1g78150	1,00E-06	68414.m09107 expressed protein

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
359396	1	1229	4	4	6443	2	2	At4g26780	7,00E-09	68417.m03857 co-chaperone grpE family protein similar to chaperone GrpE type 2 [Nicotiana tabacum] GI:3851640; contains Pfam profile PF01025: co-chaperone GrpE
353987	2	1231	4	4	5130	1	1	At1g68720	4,00E-09	68414.m07851 cytidine/deoxycytidylate deaminase family protein contains Pfam profile PF00383: Cytidine and deoxycytidylate deaminase zinc-binding region
356428	1	1231	4	4	5130	1	1	At1g68720	2,00E-57	68414.m07851 cytidine/deoxycytidylate deaminase family protein contains Pfam profile PF00383: Cytidine and deoxycytidylate deaminase zinc-binding region
355321	1	1232	3	5	6131	1	1	At1g67325	2,00E-25	68414.m07663 zinc finger (Ran-binding) family protein similar to ZIS2 [Homo sapiens] GI:4191329; contains Pfam profile PF00641: Zn-finger in Ran binding protein and others
356706	1	1235	4	4	1105	1	1	At1g51720	2,00E-75	68414.m05828 glutamate dehydrogenase, putative similar to NADP-specific glutatamate dehydrogenase (NADP-GDH) SP:P28724 [Giardia lamblia (Giardia intestinalis)]
358278	1	1237	4	4	3921	1	1	At1g56180	1,00E-29	68414.m06456 expressed protein
356794	1	1239	4	4	5983	1	1	At3g07750	9,00E-25	68416.m00940 3' exoribonuclease family domain 1-containing protein similar to SP|Q15024 Exosome complex exonuclease RRP42 (EC 3.1.13.-) (Ribosomal RNA processing protein 42) {Homo sapiens}; contains Pfam profile PF01138: 3' exoribonuclease family, domain 1
358097	1	1239	4	4	5983	1	1	At3g07750	7,00E-13	68416.m00940 3' exoribonuclease family domain 1-containing protein similar to SP|Q15024 Exosome complex exonuclease RRP42 (EC 3.1.13.-) (Ribosomal RNA processing protein 42) {Homo sapiens}; contains Pfam profile PF01138: 3' exoribonuclease family, domain 1
354505	1	1240	5	3	471	1	1	At4g32180	3,00E-66	68417.m04580 eukaryotic pantothenate kinase family protein similar to pantothenate kinase [Emericella nidulans] GI:4191500; contains Pfam profiles PF03630: Fumble, PF01937: Protein of unknown function
359065	1	1240	5	3	471	1	1	At4g32180	3,00E-60	68417.m04580 eukaryotic pantothenate kinase family protein similar to pantothenate kinase [Emericella nidulans] GI:4191500; contains Pfam profiles PF03630: Fumble, PF01937: Protein of unknown function

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
359653	1	1240	5	3	4152	3	1	At4g35360	7,00E-107	68417.m05024 pantothenate kinase family protein contains Pfam domain, PF01937: Protein of unknown function; similar to SP|Q9NVE7 Pantothenate kinase 4 (EC 2.7.1.33) (Pantothenic acid kinase 4) (hPanK4) {Homo sapiens}
355861	1	1241	4	4	5978	2	1	At2g15430	1,00E-08	68415.m01765 DNA-directed RNA polymerase II 36 kDa polypeptide A / RNA polymerase II subunit 3 (RPB36A) identical to SP|Q39211 DNA-directed RNA polymerase II 36 kDa polypeptide A (EC 2.7.7.6) (RNA polymerase II subunit 3) {Arabidopsis thaliana}
359847	1	1242	5	3	2529	1	1	At4g19900	5,00E-77	68417.m02916 glycosyl transferase-related contains Pfam profiles PF01535: PPR repeat, PF04572: Alpha 1,4-glycosyltransferase conserved region, PF04488: Glycosyltransferase sugar-binding region containing DXD motif; several hypothetical proteins - Arabidopsis thaliana
360020	1	1243	4	4	8947	1	1	At1g65290	1,00E-22	68414.m07403 acyl carrier family protein / ACP family protein similar to SP|P53665 Acyl carrier protein, mitochondrial precursor (ACP) (NADH-ubiquinone oxidoreductase 9.6 kDa subunit) (MtACP-1) {Arabidopsis thaliana}; contains InterPro accession IPR003881: Isochorismatase
356378	1	1244	3	5	4764	1	1	At1g65320	1,00E-24	68414.m07407 CBS domain-containing protein contains Pfam profile PF00571: CBS domain
354399	2	1245	3	5	3576	1	1	At1g65650	4,00E-80	68414.m07448 ubiquitin carboxyl-terminal hydrolase family 1 protein similar to 26S proteasome regulatory complex subunit p37A [Drosophila melanogaster] GI:6434962; contains Pfam profile PF01088: Ubiquitin carboxyl-terminal hydrolase, family 1
358603	1	1245	3	5	3576	1	1	At1g65650	2,00E-51	68414.m07448 ubiquitin carboxyl-terminal hydrolase family 1 protein similar to 26S proteasome regulatory complex subunit p37A [Drosophila melanogaster] GI:6434962; contains Pfam profile PF01088: Ubiquitin carboxyl-terminal hydrolase, family 1
357375	1	1246	4	4				At2g01340	1,00E-07	68415.m00051 expressed protein
354138	3	1247	5	3	9337	1	2	At1g69230	6,00E-17	68414.m07930 expressed protein
354410	2	1247	5	3	9337	1	2	At1g69230	1,00E-14	68414.m07930 expressed protein
353303	2	1248	5	3	5590	1	1	At3g20260	7,00E-30	68416.m02566 expressed protein

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
354270	9	1249	3	5	1545	1	1	At2g36530	0	68415.m04481 enolase identical to SWISS-PROT:P25696 enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase)(2-phospho-D- glycerate hydro-lyase) [Arabidopsis thaliana]
354996	1	1249	3	5	1545	1	1	At2g36530	2,00E-63	68415.m04481 enolase identical to SWISS-PROT:P25696 enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase)(2-phospho-D- glycerate hydro-lyase) [Arabidopsis thaliana]
358069	1	1249	3	5	2861	1	1	At2g29560	2,00E-55	68415.m03590 enolase, putative similar to enolase [Spinacia oleracea] gi|8919731|emb|CAB96173
359386	1	1252	3	5	281	1	1	At2g17510	1,00E-92	68415.m02025 ribonuclease II family protein similar to SP|P37202 Mitotic control protein dis3 {Schizosaccharomyces pombe}; contains Pfam profile PF00773: RNB-like protein
357929	1	1253	3	5	7486	1	2	At5g32440	4,00E-12	68418.m03825 expressed protein
353073	2	1254	4	4	5112	3	2	At2g01250	4,00E-96	68415.m00037 60S ribosomal protein L7 (RPL7B)
353680	5	1254	4	4	5112	3	2	At2g01250	4,00E-106	68415.m00037 60S ribosomal protein L7 (RPL7B)
353971	3	1254	4	4	5112	3	2	At2g01250	6,00E-80	68415.m00037 60S ribosomal protein L7 (RPL7B)
354649	1	1254	4	4	5112	3	2	At2g01250	3,00E-15	68415.m00037 60S ribosomal protein L7 (RPL7B)
357149	1	1254	4	4	5112	3	2	At2g01250	8,00E-19	68415.m00037 60S ribosomal protein L7 (RPL7B)
357363	1	1255	4	4	798	1	1	At3g02060	2,00E-66	68416.m00169 DEAD/DEAH box helicase, putative similar to C-terminal half of transcription-repair coupling factor (TRCF) GB:Q55750 [Synechocystis PCC6803]; contains Pfam profile: helicases conserved C-terminal domain
355402	1	1256	4	4	7166	3	1	At5g37070	8,00E-40	68418.m04450 expressed protein contains Pfam profile PF04398: Protein of unknown function, DUF538
353006	3	1257	4	4	3587	2	1	At5g47540	2,00E-142	68418.m05869 Mo25 family protein similar to MO25 protein (early mouse development protein family) [Mouse] SWISS-PROT:Q06138
357939	1	1258	5	3				At5g48460	6,00E-82	68418.m05992 fimbrin-like protein, putative strong similarity to fimbrin-like protein AtFim2 [Arabidopsis thaliana] GI:2737926; contains Pfam profile PF00307: Calponin homology (CH) domain
358344	1	1258	5	3				At5g48460	2,00E-56	68418.m05992 fimbrin-like protein, putative strong similarity to fimbrin-like protein AtFim2 [Arabidopsis thaliana] GI:2737926; contains Pfam profile PF00307: Calponin homology (CH) domain
356947	1	1262	4	4	5241	2	1	At4g34420	7,00E-62	68417.m04889 expressed protein ; expression supported by MPSS

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
355476	1	1263	4	4	8035	1	1	At3g15680	7,00E-15	68416.m01987 zinc finger (Ran-binding) family protein contains Pfam domain, PF00641: Zn-finger in Ran binding protein and others
360077	1	1263	4	4	8035	1	1	At3g15680	1,00E-11	68416.m01987 zinc finger (Ran-binding) family protein contains Pfam domain, PF00641: Zn-finger in Ran binding protein and others
357564	1	1265	4	4	5595	2	2	At3g50960	2,00E-30	68416.m05580 expressed protein
355077	1	1265	4	4	8990	2	1	At2g18990	3,00E-22	68415.m02216 expressed protein
358376	1	1265	4	4	8990	2	1	At2g18990	8,00E-12	68415.m02216 expressed protein
359649	1	1265	4	4	8990	2	1	At3g25580	1,00E-49	68416.m03181 thioredoxin-related contains weak similarity to thioredoxin (Swiss-Prot:O17486) [Echinococcus granulosus]
353465	2	1266	5	3	7721	2	3	At4g29340	4,00E-57	68417.m04192 profilin 3 (PRO3) (PFN3) identical to profilin 3 SP:Q38904 GI:1353765 from [Arabidopsis thaliana]
355797	1	1266	5	3				At5g56600	1,00E-15	68418.m07065 profilin 5 (PRO5) (PRF3) identical to SP|Q9FE63 Profilin 5 {Arabidopsis thaliana}
355055	1	1267	4	4	1350	1	1	At2g20000	2,00E-91	68415.m02338 cell division cycle family protein / CDC family protein low similarity to SP|P30260|CC27_HUMAN Protein CDC27Hs (Cell division cycle protein 27 homolog) Homo sapiens; contains Pfam profile PF00515: TPR Domain
357126	1	1267	4	4	1438	1	1	At3g48150	2,00E-65	68416.m05251 cell division cycle family protein / CDC family protein similar to cell division cycle protein 23 [Homo sapiens] GI:3283051, anaphase-promoting complex subunit 8 [Homo sapiens] GI:6180017; contains Pfam profile PF00515: TPR Domain
357047	1	1268	4	4				At3g26900	2,00E-43	68416.m03366 shikimate kinase family protein similar to shikimate kinase precursor GB:CAA45121 [Lycopersicon esculentum]; contains Pfam shikimate kinase domain PF01202
354567	1	1269	5	3	1582	2	1	At5g06220	2,00E-18	68418.m00694 expressed protein
354725	1	1269	5	3	2498	1	1	At5g64300	5,00E-86	68418.m08077 riboflavin biosynthesis protein, putative (RIBA) similar to SP|P47924 {Arabidopsis thaliana}, SP|P51695 Riboflavin biosynthesis protein ribA [Includes: GTP cyclohydrolase II (EC 3.5.4.25); 3,4-dihydroxy-2-butanone 4-phosphate synthase (DHBP synthase)] {Bacillus amyloliquefaciens}; contains Pfam profiles PF00925: GTP cyclohydrolase II, PF00926: 3,4-dihydroxy-2-butanone 4-phosphate synthase

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354847	1	1269	5	3				At2g22450	2,00E-24	68415.m02662 riboflavin biosynthesis protein, putative similar to SP|P50855 Riboflavin biosynthesis protein ribA [Includes: GTP cyclohydrolase II (EC 3.5.4.25); 3,4-dihydroxy-2-butanone 4-phosphate synthase (DHBP synthase)] {Actinobacillus pleuropneumoniae}; contains Pfam profiles PF00925: GTP cyclohydrolase II, PF00926: 3,4-dihydroxy-2-butanone 4-phosphate synthase
355226	1	1271	4	4	4678	1	1	At5g47790	2,00E-27	68418.m05903 forkhead-associated domain-containing protein / FHA domain-containing protein
358696	1	1271	4	4	4678	1	1	At5g47790	6,00E-58	68418.m05903 forkhead-associated domain-containing protein / FHA domain-containing protein
357130	1	1275	4	4	5987	3	2	At4g14710	2,00E-28	68417.m02260 iron-deficiency-responsive protein, putative strong similarity to iron-deficiency induced gene [Hordeum vulgare] GI:14522834; contains Pfam profile PF03079: ARD/ARD' family
353902	3	1276	5	3	6816	2	1	At5g53400	1,00E-73	68418.m06635 nuclear movement family protein contains Pfam profile: PF03593 nuclear movement protein
358107	1	1276	5	3	6816	2	1	At5g53400	6,00E-15	68418.m06635 nuclear movement family protein contains Pfam profile: PF03593 nuclear movement protein
353604	9	1281	3	5	7116	2	3	At2g36620	2,00E-56	68415.m04490 60S ribosomal protein L24 (RPL24A)
358829	1	1281	3	5	7116	2	3	At2g36620	6,00E-49	68415.m04490 60S ribosomal protein L24 (RPL24A)
359884	1	1281	3	5	7848	1	2	At2g44860	2,00E-62	68415.m05585 60S ribosomal protein L24, putative
353876	2	1283	5	3				At5g58930	2,00E-17	68418.m07382 expressed protein contains Pfam PF05340: Protein of unknown function (DUF740)
359792	1	1284	4	4	9381	2	1	At5g01450	2,00E-36	68418.m00058 expressed protein
356567	1	1284	4	4	9392	1	1	At5g48870	3,00E-41	68418.m06045 small nuclear ribonucleoprotein, putative / snRNP, putative / Sm protein, putative similar to U6 snRNA-associated Sm-like protein LSm5 [Homo sapiens] SWISS-PROT:Q9Y4Y9
359213	1	1285	4	4	7096	1	1	At2g39550	4,00E-81	68415.m04852 geranylgeranyl transferase type I beta subunit (GGT-IB) nearly identical to GI:11878247
354298	2	1286	4	4	4591	2	1	At3g05290	2,00E-68	68416.m00577 mitochondrial substrate carrier family protein contains Pfam profile: PF00153 mitochondrial carrier protein
356225	1	1286	4	4	4591	2	1	At3g05290	2,00E-25	68416.m00577 mitochondrial substrate carrier family protein contains Pfam profile: PF00153 mitochondrial carrier protein

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
358412	1	1289	4	4	5011	1	2	At5g13020	2,00E-11	68418.m01492 emsy N terminus domain-containing protein / ENT domain-containing protein contains Pfam profile PF03735: ENT domain
359752	1	1289	4	4	5011	1	2	At5g13020	8,00E-28	68418.m01492 emsy N terminus domain-containing protein / ENT domain-containing protein contains Pfam profile PF03735: ENT domain
359881	1	1292	4	4	5974	2	3	At5g14790	1,00E-31	68418.m01735 expressed protein
353328	4	1292	4	4	6840	1	1	At4g15830	5,00E-72	68417.m02408 expressed protein
358125	1	1293	3	5	5644	2	2	At3g01560	1,00E-21	68416.m00086 proline-rich family protein contains proline rich extensin domains, INTERPRO:IPR002965
353460	2	1294	5	3				At3g08900	3,00E-90	68416.m01036 reversibly glycosylated polypeptide-3 (RGP3) nearly identical to reversibly glycosylated polypeptide-3 [Arabidopsis thaliana] GI:11863238; contains non-consensus GA-donor splice site at intron 2
358732	1	1296	4	4	3204	1	1	At3g04680	6,00E-40	68416.m00502 pre-mRNA cleavage complex family protein similar to Pre-mRNA cleavage complex II protein Clp1 (Swiss-Prot:Q92989) [Homo sapiens]
358909	1	1297	4	4	4528	2	2	At3g04840	1,00E-80	68416.m00525 40S ribosomal protein S3A (RPS3aA) similar to 40S ribosomal protein S3A (S phase specific protein GBIS289) GB:P49396 [Brassica rapa]
359121	1	1297	4	4	4528	2	2	At4g34670	5,00E-66	68417.m04922 40S ribosomal protein S3A (RPS3aB)
357277	1	1299	5	3	6366	2	1	At3g10920	5,00E-100	68416.m01317 superoxide dismutase [Mn], mitochondrial (SODA) / manganese superoxide dismutase (MSD1) identical to manganese superoxide dismutase [Arabidopsis thaliana] gi|3273751|gb|AAC24832
353441	26	1299	5	3	7792	2	1	At5g51100	2,00E-81	68418.m06335 superoxide dismutase [Fe], putative / iron superoxide dismutase, putative similar to Fe-superoxide dismutase precursor [Medicago sativa] gi|16974682|gb|AAL32441
354880	1	1299	5	3	7792	2	1	At5g51100	4,00E-08	68418.m06335 superoxide dismutase [Fe], putative / iron superoxide dismutase, putative similar to Fe-superoxide dismutase precursor [Medicago sativa] gi|16974682|gb|AAL32441
356232	1	1299	5	3	7792	2	1	At4g25100	6,00E-80	68417.m03608 superoxide dismutase [Fe], chloroplast (SODB) / iron superoxide dismutase (FSD1) identical to Fe-superoxide dismutase [Arabidopsis thaliana] gi|166700|gb|AAA32791; supported by cDNA, Ceres:32935

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
358806	1	1299	5	3	7792	2	1	At4g25100	4,00E-67	68417.m03608 superoxide dismutase [Fe], chloroplast (SODB) / iron superoxide dismutase (FSD1) identical to Fe-superoxide dismutase [Arabidopsis thaliana] gi|166700|gb|AAA32791; supported by cDNA, Ceres:32935
360075	1	1305	4	4	3730	2	1	At4g35140	1,00E-46	68417.m04996 transducin family protein / WD-40 repeat family protein contains 6 (3 significant) WD-40 repeats; similar to PC326 protein (GI:200241) (PIR2:S37694) [Mus musculus]; Human (H326) mRNA, Homo sapiens, gb:U06631
358865	1	1309	3	5	1365	1	1	At4g38890	2,00E-12	68417.m05508 dihydrouridine synthase family protein contains Pfam domain, PF01207: Dihydrouridine synthase (Dus)
354338	2	1309	3	5	3805	1	1	At3g49640	5,00E-114	68416.m05425 nitrogen regulation family protein similar to NITROGEN REGULATION PROTEIN NIFR3 (SP:Q08111) [Rhodobacter capsulatus]; contains Pfam domain PF01207: Dihydrouridine synthase (Dus)
354812	1	1309	3	5	3805	1	1	At3g49640	5,00E-10	68416.m05425 nitrogen regulation family protein similar to NITROGEN REGULATION PROTEIN NIFR3 (SP:Q08111) [Rhodobacter capsulatus]; contains Pfam domain PF01207: Dihydrouridine synthase (Dus)
356846	1	1313	4	4	7771	3	1	At4g12600	1,00E-51	68417.m01986 ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein Similar to NHP2/L7Ae family proteins, see SWISSPROT:P32495 and PMID:2063628.
357501	1	1313	4	4	7771	3	1	At4g22380	6,00E-30	68417.m03234 ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein Similar to NHP2/L7Ae family proteins, see SWISSPROT:P32495 and PMID:2063628.
358070	1	1313	4	4	7771	3	1	At5g20160	3,00E-23	68418.m02400 ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein Similar to NHP2/L7Ae family proteins, see SWISSPROT:P32495 and PMID:2063628.
359601	1	1314	3	5	4656	1	1	At4g12790	4,00E-46	68417.m02007 ATP-binding family protein contains Pfam domain, PF03029: Conserved hypothetical ATP binding protein
359415	1	1315	3	5	6218	1	2	At4g16830	4,00E-29	68417.m02540 nuclear RNA-binding protein (RGGA) identical to nuclear RNA binding protein GI:6492264 from [Arabidopsis thaliana]
356772	1	1315	3	5	6228	2	1	At4g17520	5,00E-11	68417.m02621 nuclear RNA-binding protein, putative similar to nuclear RNA binding protein GI:6492264 from [Arabidopsis thaliana]

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
354441	2	1316	2	6	6415	1	1	At5g13720	7,00E-78	68418.m01597 expressed protein
354314	2	1319	3	5	1990	2	1	At5g07830	2,00E-50	68418.m00898 glycosyl hydrolase family 79 N-terminal domain-containing protein similar to beta-glucuronidase GI:8918740 from [Scutellaria baicalensis]
353856	2	1320	2	6	2830	1	1	At5g12260	2,00E-16	68418.m01441 expressed protein
359342	1	1321	2	6	2333	1	1	At5g27730	2,00E-24	68418.m03326 expressed protein
353705	2	1352	2	5	9563	2	3	At1g01170	3,00E-27	68414.m00028 ozone-responsive stress-related protein, putative similar to stress-related ozone-induced protein AtOZI1 (GI:790583) [Arabidopsis thaliana]; contains 1 predicted transmembrane domain;
356322	1	1353	5	2	10251	5	2	At5g53200	8,00E-17	68418.m06613 myb family transcription factor (TRIPTYCHON) contains Pfam profile: PF00249 myb-like DNA-binding domain
355923	1	1354	2	5	9954	2	2	At3g60520	5,00E-10	68416.m06769 expressed protein
358230	1	1355	4	3	5841	2	2	At4g02230	6,00E-20	68417.m00302 60S ribosomal protein L19 (RPL19C) similar to L19 from several species
357940	1	1357	4	3				At5g35360	9,00E-38	68418.m04203 acetyl-CoA carboxylase, biotin carboxylase subunit (CAC2) identical to acetyl-CoA carboxylase, biotin carboxylase subunit (CAC2) [Arabidopsis thaliana] GI:1905876
354211	2	1358	3	4	494	1	2	At5g46070	3,00E-28	68418.m05665 guanylate-binding family protein contains Pfam domains PF02263: Guanylate-binding protein, N-terminal domain and PF02841: Guanylate-binding protein, C-terminal domain
359426	1	1361	5	2	7693	2	1	At4g30996	2,00E-28	68417.m04401 expressed protein
354178	3	1362	3	4	8187	2	2	At1g06760	2,00E-08	68414.m00718 histone H1, putative similar to histone H1-1 GB:CAA44312 GI:16314 from [Arabidopsis thaliana]; identical to cDNA H1-1C mRNA for histone H1-1 (partial) GI:732560
359907	1	1362	3	4	8187	2	2	At1g06760	1,00E-08	68414.m00718 histone H1, putative similar to histone H1-1 GB:CAA44312 GI:16314 from [Arabidopsis thaliana]; identical to cDNA H1-1C mRNA for histone H1-1 (partial) GI:732560
353167	2	1362	3	4				At2g18050	8,00E-17	68415.m02099 histone H1-3 (HIS1-3) similar to histone H1 [Lycopersicon pennellii] SWISS-PROT:P40267; identical to cDNA histone H1-3 (His1-3) GI:1809314, histone H1-3 [Arabidopsis thaliana] GI:1809305
356758	1	1362	3	4				At2g18050	2,00E-17	68415.m02099 histone H1-3 (HIS1-3) similar to histone H1 [Lycopersicon pennellii] SWISS-PROT:P40267; identical to cDNA histone H1-3 (His1-3) GI:1809314, histone H1-3 [Arabidopsis thaliana] GI:1809305

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
359391	1	1363	3	4	6248	2	2	At2g30580	2,00E-35	68415.m03726 zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)
359634	1	1363	3	4	6248	2	2	At2g30580	4,00E-54	68415.m03726 zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)
353761	4	1364	4	3	8292	4	2	At1g07070	5,00E-54	68414.m00753 60S ribosomal protein L35a (RPL35aA) similar to ribosomal protein L35a GI:57118 from [Rattus norvegicus]
354040	5	1365	3	4	5293	3	3	At1g08360	2,00E-95	68414.m00925 60S ribosomal protein L10A (RPL10aA) similar to 60S ribosomal protein L10A GB:AAC73045 GI:3860277 from [Arabidopsis thaliana]
354324	4	1365	3	4	5293	3	3	At2g27530	8,00E-57	68415.m03331 60S ribosomal protein L10A (RPL10aB)
356890	1	1369	4	3	4274	1	1	At1g80770	2,00E-85	68414.m09476 expressed protein
353813	2	1370	4	3	4828	2	1	At1g27650	1,00E-50	68414.m03379 U2 snRNP auxiliary factor small subunit, putative Strong similarity to gb|Y18349 U2 snRNP auxiliary factor, small subunit from Oryza sativa. ESTs gb|AA586295 and gb|AA597332 come from this gene
354661	1	1371	3	4	6144	2	1	At3g10810	9,00E-19	68416.m01301 zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 Zinc finger, C3HC4 type (RING finger)
357803	1	1371	3	4	6144	2	1	At3g10810	3,00E-07	68416.m01301 zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 Zinc finger, C3HC4 type (RING finger)
358104	1	1371	3	4	6144	2	1	At3g10810	1,00E-06	68416.m01301 zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 Zinc finger, C3HC4 type (RING finger)
358771	1	1371	3	4	6144	2	1	At3g56590	8,00E-19	68416.m06293 hydroxyproline-rich glycoprotein family protein
358783	1	1371	3	4	6144	2	1	At3g10810	5,00E-06	68416.m01301 zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 Zinc finger, C3HC4 type (RING finger)
356895	1	1385	5	2	6542	3	1	At5g36270	6,00E-11	68418.m04375 dehydroascorbate reductase, putative similar to dehydroascorbate reductase {Spinacia oleracea} gi:10952511 gb:AF195783, PMID:11148269
358155	1	1388	4	3				At3g07730	1,00E-13	68416.m00933 expressed protein
353659	2	1391	4	3	824	1	1	At5g63190	2,00E-92	68418.m07934 MA3 domain-containing protein low similarity to programmed cell death 4 protein [Gallus gallus] GI:12958564; contains Pfam profile PF02847: MA3 domain
352981	5	1392	3	4	6917	3	3	At4g09800	4,00E-69	68417.m01609 40S ribosomal protein S18 (RPS18C)

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
353721	2	1392	3	4	6917	3	3	At4g09800	4,00E-70	68417.m01609 40S ribosomal protein S18 (RPS18C)
353052	2	1394	3	4	416	1	2	At1g25350	2,00E-57	68414.m03145 glutamine-tRNA ligase, putative / glutaminyl-tRNA synthetase, putative / GlnRS, putative similar to tRNA-glutamine synthetase GI:2995454 from [Lupinus luteus]
358446	1	1394	3	4	694	1	2	At5g26710	5,00E-130	68418.m03168 glutamate-tRNA ligase, putative / glutamyl-tRNA synthetase, putatuve / GluRS, putative identical to gi:3435196
353696	3	1395	4	3	7022	2	1	At5g39510	7,00E-80	68418.m04784 vesicle transport v-SNARE 11 (VTI11) / vesicle soluble NSF attachment protein receptor VTI1a (VTI1A) identical to SP|Q9SEL6 Vesicle transport v-SNARE 11 (AtVTI11) (Vesicle transport v-SNARE protein VTI1a) (Vesicle soluble NSF attachment protein receptor VTI1a) (AtVTI1a) {Arabidopsis thaliana}
354762	1	1397	5	2	1008	1	1	At5g01400	1,00E-13	68418.m00053 expressed protein contains low similarity to symplekin SP:Q92797 from [Homo sapiens]
358642	1	1397	5	2	1733	1	1	At1g27595	3,00E-51	68414.m03365 expressed protein similar to Symplekin (SP:Q92797) {Homo sapiens}
358815	1	1398	3	4	9194	2	1	At4g30240	4,00E-06	68417.m04300 expressed protein predicted protein, Arabidopsis thaliana
359085	1	1399	1	6	6116	1	2	At1g27760	6,00E-21	68414.m03393 interferon-related developmental regulator family protein / IFRD protein family contains Pfam PF05004: Interferon-related developmental regulator (IFRD); similar to IFR1 protein GI:16580630 [Gallus gallus]; similar to Interferon-related developmental regulator 1 (TPA induced sequence 7) (TIS7 protein) (SP:P19182) {Mus musculus}
353124	2	1403	3	4	8283	2	2	At1g29250	1,00E-41	68414.m03577 expressed protein contains TIGRFAM TIGR00285: conserved hypothetical protein TIGR00285
355821	1	1403	3	4	8283	2	2	At1g29250	5,00E-42	68414.m03577 expressed protein contains TIGRFAM TIGR00285: conserved hypothetical protein TIGR00285
353369	4	1404	4	3	6070	2	2	At1g30230	4,00E-70	68414.m03698 elongation factor 1-beta / EF-1-beta identical to SP|P48006 Elongation factor 1-beta (EF-1-beta) {Arabidopsis thaliana}
353624	3	1404	4	3	6296	2	1	At5g19510	1,00E-64	68418.m02324 elongation factor 1B alpha-subunit 2 (eEF1Balpha2) identical to elongation factor 1B alpha-subunit [Arabidopsis thaliana] GI:6686821
356056	1	1404	4	3	6296	2	1	At5g12110	1,00E-32	68418.m01422 elongation factor 1B alpha-subunit 1 (eEF1Balpha1) identical to elongation factor 1B alpha-subunit [Arabidopsis thaliana] GI:6686819
353923	2	1406	4	3	8193	1	2	At4g34340	3,00E-53	68417.m04880 expressed protein

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
357854	1	1407	3	4	2143	1	1	At5g53350	7,00E-77	68418.m06630 ATP-dependent Clp protease ATP-binding subunit ClpX1 (CLPX) identical to CLP protease regulatory subunit CLPX GI:2674203 from [Arabidopsis thaliana]
359831	1	1412	4	3	4336	2	1	At5g62090	8,00E-76	68418.m07793 expressed protein
354429	2	1414	3	4	5251	1	2	At2g36010	7,00E-44	68415.m04422 E2F transcription factor-3 (E2F3) identical to E2F transcription factor-3 E2F3 [Arabidopsis thaliana] gi|10443853|gb|AAG17610
353280	10	1415	3	4	6541	1	3	At1g48830	3,00E-86	68414.m05465 40S ribosomal protein S7 (RPS7A) similar to 40S ribosomal protein S7 homolog GI:5532505 from [Brassica oleracea]
353506	7	1415	3	4				At3g02560	5,00E-84	68416.m00247 40S ribosomal protein S7 (RPS7B) similar to ribosomal protein S7 GB:AAD26256 from [Secale cereale]
354001	2	1417	3	4	2387	1	1	At5g44740	2,00E-26	68418.m05484 UMUC-like DNA repair family protein low similarity to DNA polymerase eta [Homo sapiens] GI:11463971; contains Pfam profile PF00817: ImpB/MucB/SamB family
354064	3	1418	4	3	5744	2	1	At5g55530	7,00E-64	68418.m06918 C2 domain-containing protein low similarity to cold-regulated gene SRC2 [Glycine max] GI:2055230; contains Pfam profile PF00168: C2 domain
359233	1	1419	4	3	4981	2	1	At2g43120	4,00E-42	68415.m05355 pirin, putative similar to SP|O00625 Pirin {Homo sapiens}; contains Pfam profile PF02678: Pirin
357507	1	1421	4	3	4726	2	1	At3g57650	6,00E-55	68416.m06423 acyl-CoA:1-acylglycerol-3-phosphate acyltransferase, putative similar to acyl-CoA:1-acylglycerol-3-phosphate acyltransferase GI:4583544 from [Brassica napus]
359122	1	1424	3	4	3585	2	1	At1g53280	1,00E-52	68414.m06038 DJ-1 family protein similar to DJ-1 protein [Homo sapiens] GI:1780755; similar to DJ-1 beta (GI:18642508) [Drosophila melanogaster]; contains Pfam profile: PF01965 ThiJ/PfpI family; TIGRFAM TIGR01383: DJ-1 family protein
359266	1	1425	4	3	9113	1	1	At1g53520	5,00E-70	68414.m06070 chalcone-flavanone isomerase-related low similarity to GI:499036 (Vitis vinifera)
359064	1	1425	4	3				At3g55120	2,00E-33	68416.m06121 chalcone-flavanone isomerase / chalcone isomerase (CHI) identical to SP|P41088
358622	1	1426	4	3	5363	2	2	At4g30780	3,00E-07	68417.m04361 expressed protein hypothetical protein F27D4.1 - Arabidopsis thaliana,PID:g4115371
353385	2	1427	3	4	1632	1	2	At1g65930	9,00E-89	68414.m07481 isocitrate dehydrogenase, putative / NADP+ isocitrate dehydrogenase, putative strong similarity to isocitrate dehydrogenase SP|Q40345 from [Medicago sativa]

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
357896	1	1427	3	4	1632	1	2	At1g65930	5,00E-27	68414.m07481 isocitrate dehydrogenase, putative / NADP+ isocitrate dehydrogenase, putative strong similarity to isocitrate dehydrogenase SP|Q40345 from [Medicago sativa]
355617	1	1427	3	4	1728	1	1	At5g14590	1,00E-56	68418.m01711 isocitrate dehydrogenase, putative / NADP+ isocitrate dehydrogenase, putative strong similarity to isocitrate dehydrogenase (NADP+) [Nicotiana tabacum] GI:3021512; contains Pfam domain PF00180: dehydrogenase, isocitrate/isopropylmalate family
356103	1	1427	3	4	1728	1	1	At5g14590	3,00E-85	68418.m01711 isocitrate dehydrogenase, putative / NADP+ isocitrate dehydrogenase, putative strong similarity to isocitrate dehydrogenase (NADP+) [Nicotiana tabacum] GI:3021512; contains Pfam domain PF00180: dehydrogenase, isocitrate/isopropylmalate family
359901	1	1427	3	4				At1g54340	9,00E-78	68414.m06195 isocitrate dehydrogenase, putative / NADP+ isocitrate dehydrogenase, putative strong similarity to NADP-isocitrate dehydrogenase GI:5764653 from [Citrus limon]; Nicotiana tabacum SP|P50218
353202	3	1433	4	3	5778	1	2	At1g76660	2,00E-33	68414.m08920 expressed protein
353129	2	1434	3	4	3540	2	1	At2g30050	6,00E-28	68415.m03654 transducin family protein / WD-40 repeat family protein similar to SEC13-related protein (SP:P55735) [Homo sapiens]
353362	2	1434	3	4	3540	2	1	At2g30050	7,00E-43	68415.m03654 transducin family protein / WD-40 repeat family protein similar to SEC13-related protein (SP:P55735) [Homo sapiens]
357076	1	1435	4	3	1515	2	1	At4g27720	5,00E-52	68417.m03984 expressed protein contains Pfam PF05631: Protein of unknown function (DUF791)
358078	1	1435	4	3	1515	2	1	At1g64650	3,00E-56	68414.m07329 expressed protein
358191	1	1435	4	3	1515	2	1	At1g64650	5,00E-56	68414.m07329 expressed protein
353108	3	1436	5	2	6146	1	2	At2g46470	8,00E-71	68415.m05783 OXA1 protein, putative similar to Oxa1 protein [Arabidopsis thaliana] GI:10176922
354159	3	1437	5	2	3702	1	1	At4g04885	4,00E-53	68417.m00711 pre-mRNA cleavage complex-related contains weak similarity to Pre-mRNA cleavage complex II protein Pcf11 (Fragment) (Swiss-Prot:O94913) [Homo sapiens]
359957	1	1437	5	2	3702	1	1	At4g04885	7,00E-08	68417.m00711 pre-mRNA cleavage complex-related contains weak similarity to Pre-mRNA cleavage complex II protein Pcf11 (Fragment) (Swiss-Prot:O94913) [Homo sapiens]

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
353980	2	1438	4	3	6693	3	1	At3g58650	4,00E-13	68416.m06537 expressed protein
355072	1	1439	3	4	131	1	1	At5g63960	2,00E-24	68418.m08031 DNA-directed DNA polymerase delta catalytic subunit, putative (POLD1) similar to DNA polymerase delta [Glycine max] GI:2895198, OsPol delta large subunit [Oryza sativa (japonica cultivar-group) GI:9188570; contains Pfam profiles: PF03175 DNA polymerase type B, organellar and viral, PF00136 DNA polymerase family B, PF03104 DNA polymerase family B, exonuclease domain
353698	2	1441	3	4	5551	1	1	At1g69370	3,00E-72	68414.m07962 chorismate mutase, putative similar to gi:5732016 and SP|P42738; contains Pfam profile: PF01817: Chorismate mutase
358635	1	1442	4	3	1657	2	1	At4g39650	7,00E-59	68417.m05606 gamma-glutamyltranspeptidase family protein SP|P07314 Gamma-glutamyltranspeptidase precursor (EC 2.3.2.2) (Gamma- glutamyltransferase) (GGT) {Rattus norvegicus}; contains Pfam profilePF01019: Gamma-glutamyltranspeptidase
359766	1	1443	3	4	1160	1	2	At1g70160	1,00E-74	68414.m08073 expressed protein similar to hypothetical protein GI:4455225 from [Arabidopsis thaliana]
358934	1	1444	2	5	6654	1	1	At3g47120	8,00E-38	68416.m05116 RNA recognition motif (RRM)-containing protein contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)
357646	1	1446	3	4	1048	1	2	At1g74790	2,00E-103	68414.m08665 expressed protein contains similarity to hedgehog-interacting protein GI:4868122 from [Mus musculus]
356058	1	1447	3	4	1621	1	2	At5g46290	1,00E-75	68418.m05698 3-oxoacyl-[acyl-carrier-protein] synthase I identical to Swiss-Prot:P52410 3-oxoacyl-[acyl-carrier-protein] synthase I, chloroplast precursor (EC 2.3.1.41) (Beta-ketoacyl-ACP synthase I) (KAS I) [Arabidopsis thaliana]
359888	1	1447	3	4	1621	1	2	At5g46290	2,00E-20	68418.m05698 3-oxoacyl-[acyl-carrier-protein] synthase I identical to Swiss-Prot:P52410 3-oxoacyl-[acyl-carrier-protein] synthase I, chloroplast precursor (EC 2.3.1.41) (Beta-ketoacyl-ACP synthase I) (KAS I) [Arabidopsis thaliana]
357405	1	1447	3	4	1751	1	1	At1g74960	1,00E-15	68414.m08700 3-ketoacyl-ACP synthase, putative similar to 3-ketoacyl-ACP synthase [Cuphea pulcherrima] gi|3800747|gb|AAC68860; identical to cDNA beta-ketoacyl-ACP synthetase 2 nuclear gene for plastid product GI:14582700

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
359147	1	1447	3	4	1751	1	1	At1g74960	6,00E-94	68414.m08700 3-ketoacyl-ACP synthase, putative similar to 3-ketoacyl-ACP synthase [Cuphea pulcherrima] gi|3800747|gb|AAC68860; identical to cDNA beta-ketoacyl-ACP synthetase 2 nuclear gene for plastid product GI:14582700
354631	1	1447	3	4	2839	1	1	At2g04540	2,00E-64	68415.m00460 3-oxoacyl-[acyl-carrier-protein] synthase II, putative similar to Swiss-Prot:P56902 3-oxoacyl-[acyl-carrier-protein] synthase II (EC 2.3.1.41) (Beta- ketoacyl-ACP synthase II) (KAS II) [Rhizobium meliloti]
354237	2	1450	3	4	2337	2	2	At3g22270	1,00E-09	68416.m02815 expressed protein
355937	1	1451	3	4	1329	1	1	At5g04500	1,00E-30	68418.m00449 glycosyltransferase family protein 47 low similarity to Exostosin-like 2, Homo sapiens [SP|Q9UBQ6], EXTL2, Mus musculus [GI:10443633]
354142	2	1456	4	3				At5g04860	4,00E-35	68418.m00509 expressed protein
359614	1	1458	4	3	6046	1	1	At3g03900	1,00E-14	68416.m00404 adenylylsulfate kinase, putative similar to adenylylsulfate kinase 1, chloroplast precursor (APS kinase, Adenosine-5'phosphosulfate kinase, ATP adenosine-5'-phosphosulfate 3'-phosphotransferase) [Arabidopsis thaliana] SWISS-PROT:Q43295
357732	1	1458	4	3				At2g14750	4,00E-83	68415.m01666 adenylylsulfate kinase 1 (AKN1) identical to adenylylsulfate kinase 1, chloroplast precursor (APS kinase, Adenosine-5'phosphosulfate kinase, ATP adenosine-5'-phosphosulfate 3'-phosphotransferase) [Arabidopsis thaliana] SWISS-PROT:Q43295
357905	1	1459	2	5	889	1	1	At5g04590	1,00E-48	68418.m00458 sulfite reductase / ferredoxin (SIR) identical to sulfite reductase [Arabidopsis thaliana] GI:804953, GI:2584721
358799	1	1459	2	5	889	1	1	At5g04590	2,00E-34	68418.m00458 sulfite reductase / ferredoxin (SIR) identical to sulfite reductase [Arabidopsis thaliana] GI:804953, GI:2584721
353837	4	1460	4	3	6383	1	1	At3g44150	7,00E-90	68416.m04733 expressed protein hypothetical proteins - Arabidopsis thaliana
357431	1	1464	3	4	1644	1	1	At2g41680	3,00E-101	68415.m05149 thioredoxin reductase, putative / NADPH-dependent thioredoxin reductase, putative The last 2 exons encode thioredoxin. There is an EST match to exons 5-7, and the distance between exon 7 and exon 8 is only 90bp. It is unlikely this is two separate genes, but more likely a hybrid protein.
359758	1	1465	4	3	6694	2	2	At2g21600	8,00E-13	68415.m02569 RER1B protein identical to SP|O48671 RER1B protein (AtRER1B) {Arabidopsis thaliana}

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
357442	1	1466	3	4				At5g11790	6,00E-60	68418.m01376 Ndr family protein similar to SP|O23969 Pollen specific protein SF21 {Helianthus annuus}; contains Pfam profile PF03096: Ndr family
353011	2	1467	3	4	4511	1	1	At5g58370	4,00E-30	68418.m07309 expressed protein
356462	1	1470	3	4	7505	1	2	At5g66550	6,00E-08	68418.m08390 Maf family protein contains Pfam domain PF02545: Maf-like protein
359315	1	1473	3	4	6276	1	2	At5g21170	1,00E-67	68418.m02530 5'-AMP-activated protein kinase beta-2 subunit, putative similar to Swiss-Prot:Q9QZH4 5'-AMP-activated protein kinase, beta-2 subunit (AMPK beta-2 chain) [Rattus norvegicus]
354503	1	1473	3	4				At4g16360	2,00E-22	68417.m02478 5'-AMP-activated protein kinase beta-2 subunit, putative similar to Swiss-Prot:Q9QZH4 5'-AMP-activated protein kinase, beta-2 subunit (AMPK beta-2 chain) [Rattus norvegicus]
358031	1	1473	3	4				At4g16360	2,00E-13	68417.m02478 5'-AMP-activated protein kinase beta-2 subunit, putative similar to Swiss-Prot:Q9QZH4 5'-AMP-activated protein kinase, beta-2 subunit (AMPK beta-2 chain) [Rattus norvegicus]
355032	1	1477	4	3	2749	1	1	At5g51230	8,00E-17	68418.m06353 embryonic flower 2 (EMF2) identical to embryonic flower 2 [Arabidopsis thaliana] GI:14276050; supporting cDNA gi|14276049|dbj|AB053171.1|
353046	8	1478	3	4	6883	3	3	At3g52580	3,00E-67	68416.m05790 40S ribosomal protein S14 (RPS14C) ribosomal protein S14 -Zea mays,PIR2:A30097
354318	2	1478	3	4	6883	3	3	At3g52580	2,00E-50	68416.m05790 40S ribosomal protein S14 (RPS14C) ribosomal protein S14 -Zea mays,PIR2:A30097
358418	1	1480	6	1				At3g18420	4,00E-35	68416.m02342 tetratricopeptide repeat (TPR)-containing protein contains Pfam profile: PF00515 tetratricopeptide repeat domain (TPR domain)
354052	2	1484	2	5	1711	2	2	At2g38630	2,00E-35	68415.m04745 expressed protein
355414	1	1485	4	3	4290	1	1	At3g12290	7,00E-65	68416.m01534 tetrahydrofolate dehydrogenase/cyclohydrolase, putative similar to SP|P07245 C-1-tetrahydrofolate synthase, cytoplasmic (C1-THF synthase) [Includes: Methylenetetrahydrofolate dehydrogenase (EC 1.5.1.5); Methenyltetrahydrofolate cyclohydrolase (EC 3.5.4.9); Formyltetrahydrofolate synthetase (EC 6.3.4.3)] {Saccharomyces cerevisiae}; contains Pfam profiles PF02882: Tetrahydrofolate dehydrogenase/cyclohydrolase, NAD(P)-binding domain, PF00763: Tetrahydrofolate dehydrogenase/cyclohydrolase, catalytic domain

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358209	1	1488	3	4				At5g23240	1,00E-08	68418.m02719 DNAJ heat shock N-terminal domain-containing protein low similarity to SP|O34136 Chaperone protein dnaJ (40 kDa heat shock chaperone protein) (HSP40) {Deinococcus proteolyticus}; contains Pfam profile PF00226: DnaJ domain
355330	1	1490	4	3	4361	1	1	At5g63140	4,00E-66	68418.m07928 calcineurin-like phosphoesterase family protein contains Pfam profile: PF00149 calcineurin-like phosphoesterase
357365	1	1493	3	4	5630	1	2	At3g10940	2,00E-22	68416.m01319 protein phosphatase-related similar to protein phosphatase PTPKIS1 protein (GI:11595504) [Arabidopsis thaliana]
356888	1	1495	4	3	8988	2	2	At5g36800	4,00E-19	68418.m04409 expressed protein
356973	1	1498	4	3	7954	1	1	At5g20570	1,00E-18	68418.m02442 ring-box protein-related similar to ring-box protein 1 GI:4769004 from [Homo sapiens]
353830	2	1499	4	3	5623	4	2	At3g24830	9,00E-72	68416.m03115 60S ribosomal protein L13A (RPL13aB) similar to 60S RIBOSOMAL PROTEIN L13A GB:P35427 from [Rattus norvegicus]
353038	2	1501	4	3	4558	3	1	At3g09350	2,00E-99	68416.m01109 armadillo/beta-catenin repeat family protein contains Pfam profile: PF00514 armadillo/beta-catenin-like repeat
353022	2	1501	4	3	5757	1	1	At3g51980	1,00E-96	68416.m05702 expressed protein
359377	1	1503	4	3	7207	1	1	At5g41480	2,00E-44	68418.m05037 dihydrofolate synthetase/folylpolyglutamate synthetase (DHFS/FPGS1) nearly identical to GI:17976703; identical to cDNA dihydrofolate synthetase/folylpolyglutamate synthetase (dhfs/fpgs1 gene) GI:17976702
354606	1	1503	4	3				At3g10160	1,00E-32	68416.m01218 dihydrofolate synthetase/folylpolyglutamate synthetase (DHFS/FPGS3) nearly identical to gi:17976757
354747	1	1503	4	3				At3g10160	3,00E-40	68416.m01218 dihydrofolate synthetase/folylpolyglutamate synthetase (DHFS/FPGS3) nearly identical to gi:17976757
354792	1	1503	4	3				At3g10160	1,00E-47	68416.m01218 dihydrofolate synthetase/folylpolyglutamate synthetase (DHFS/FPGS3) nearly identical to gi:17976757
354428	2	1504	2	5	1867	1	3	At3g11670	9,00E-108	68416.m01431 digalactosyldiacylglycerol synthase 1 (DGD1) / MGDG:MGDG galactosyltransferase / galactolipid galactosyltransferase identical to digalactosyldiacylglycerol synthase (DGD1) GI:5354158 [Arabidopsis thaliana]

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358328	1	1504	2	5	2426	1	1	At4g00550	2,00E-54	68417.m00076 UDP-galactose:MGDG galactosyltransferase 2 / digalactosyldiacylglycerol synthase 2 (DGD2) identical to digalactosyldiacylglycerol synthase (DGD2) GI:18141112 [Arabidopsis thaliana]
356640	1	1505	3	4	2440	1	2	At4g24820	2,00E-98	68417.m03556 26S proteasome regulatory subunit, putative (RPN7) contains similarity to ubiquitin activating enzyme GI:3647283 from [Lycopersicon esculentum]
359018	1	1506	2	5	5464	2	1	At5g11880	6,00E-44	68418.m01390 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
358248	1	1507	1	6	7306	1	1	At3g15140	8,00E-76	68416.m01915 exonuclease family protein contains exonuclease domain, Pfam:PF00929
354182	2	1509	3	4	3351	1	2	At5g23570	2,00E-26	68418.m02765 XS domain-containing protein / XS zinc finger domain-containing protein-related contains Pfam profiles PF03468: XS domain, weak hit to PF03470: XS zinc finger domain
357302	1	1509	3	4	3351	1	2	At5g23570	4,00E-40	68418.m02765 XS domain-containing protein / XS zinc finger domain-containing protein-related contains Pfam profiles PF03468: XS domain, weak hit to PF03470: XS zinc finger domain
356916	1	1509	3	4	8322	1	2	At3g22435	6,00E-53	68416.m02835 XS domain-containing protein contains Pfam profile PF03468: XS domain
354036	2	1510	3	4	4669	1	2	At3g22740	4,00E-74	68416.m02868 homocysteine S-methyltransferase 3 (HMT-3) identical to homocysteine S-methyltransferase HMT-3 [Arabidopsis thaliana] GI:9966515; similar to homocysteine S-methyltransferase AtHMT-2 (GI:6685163) [Arabidopsis thaliana]; similar to selenocysteine methyltransferase GB:P56707 from [Astragalus bisulcatus]
358175	1	1510	3	4				At3g63250	1,00E-37	68416.m07106 homocysteine S-methyltransferase 2 (HMT-2) 99.7% identical to homocysteine S-methyltransferase AtHMT-2 (GI:6685163) [Arabidopsis thaliana]
354604	1	1512	2	5	8101	2	1	At4g14100	7,00E-82	68417.m02174 expressed protein
356027	1	1514	3	4				At5g65180	4,00E-27	68418.m08199 expressed protein contains Pfam domain, PF04818: Protein of unknown function, DUF618

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353559	2	1517	2	5	9193	2	1	At3g44750	3,00E-12	68416.m04817 histone deacetylase, putative (HD2A) contains Pfam domain, PF00096: Zinc finger, C2H2 type; identical to cDNA putative histone deacetylase (HD2A) GI:11066134
359509	1	1517	2	5	9193	2	1	At3g44750	2,00E-27	68416.m04817 histone deacetylase, putative (HD2A) contains Pfam domain, PF00096: Zinc finger, C2H2 type; identical to cDNA putative histone deacetylase (HD2A) GI:11066134
353609	2	1518	3	4	1476	1	2	At5g22330	2,00E-141	68418.m02605 TATA box-binding protein-interacting protein-related similar to TATA box-binding protein-interacting protein SP:O35753 from [Mus musculus]
358839	1	1519	3	4	410	1	1	At4g02680	2,00E-123	68417.m00363 tetratricopeptide repeat (TPR)-containing protein contains Pfam profile PF00515 TPR Domain
355121	1	1520	3	4	7400	1	1	At5g26610	2,00E-18	68418.m03181 D111/G-patch domain-containing protein contains Pfam PF01585: G-patch domain
353377	8	1521	2	5				At4g02610	6,00E-77	68417.m00355 tryptophan synthase, alpha subunit, putative similar to A. thaliana tryptophan synthase alpha chain (EC 4.2.1.20), GenBank accession number U18993 (gi:619753)
353900	2	1527	2	5	9914	1	1	At5g47550	3,00E-15	68418.m05870 cysteine protease inhibitor, putative / cystatin, putative similar to SP|P09229 Cysteine proteinase inhibitor-I (Oryzacystatin-I) {Oryza sativa}; contains Pfam profile PF00031: Cystatin domain
358979	1	1528	2	5	3408	1	2	At5g47770	6,00E-80	68418.m05901 farnesyl pyrophosphate synthetase 1, mitochondrial (FPS1) / FPP synthetase 1 / farnesyl diphosphate synthase 1 identical to SP|Q09152 Farnesyl pyrophosphate synthetase 1, mitochondrial precursor (FPP synthetase 1) (FPS 1) (Farnesyl diphosphate synthetase 1) [Includes: Dimethylallyltransferase (EC 2.5.1.1); Geranyltranstransferase (EC 2.5.1.10)] {Arabidopsis thaliana}
359197	1	1533	3	4	825	2	2	At5g12150	3,00E-11	68418.m01426 pleckstrin homology (PH) domain-containing protein / RhoGAP domain-containing protein weak similarity to glucocorticoid receptor DNA binding factor 1 [Canis familiaris] GI:23266717; contains Pfam profiles PF00169: PH domain, PF00620: RhoGAP domain
353384	2	1535	3	4	353	1	1	At5g15920	3,00E-30	68418.m01862 structural maintenance of chromosomes (SMC) family protein (MSS2) similar to SMC-related protein MSS2 [Arabidopsis thaliana] GI:9965743; contains Pfam profiles PF02483: SMC family C-terminal domain, PF02463: RecF/RecN/SMC N terminal domain

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353050	2	1536	2	5	780	2	2	At5g12950	1,00E-23	68418.m01485 expressed protein putative secreted protein SCF41.30c, Streptomyces coelicolor, EMBL:SCF41_30
353560	10	1537	5	2	10052	2	2	At5g48485	9,00E-06	68418.m05995 protease inhibitor/seed storage/lipid transfer protein (LTP) family protein contains Pfam protease inhibitor/seed storage/LTP family domain PF00234
354315	5	1537	5	2	10052	2	2	At5g48485	7,00E-07	68418.m05995 protease inhibitor/seed storage/lipid transfer protein (LTP) family protein contains Pfam protease inhibitor/seed storage/LTP family domain PF00234
359494	1	1559	3	3	8715	1	1	At5g28640	3,00E-16	68418.m03503 SSXT protein-related / glycine-rich protein contains weak hit to Pfam profile PF05030: SSXT protein (N-terminal region)
353306	2	1559	3	3	9226	2	2	At4g00850	1,00E-08	68417.m00116 SSXT family protein low similarity to synovial sarcoma associated SS18-delta [Mus musculus] GI:17978535; contains Pfam profile PF05030: SSXT protein (N-terminal region)
353243	3	1565	3	3	1744	1	1	At1g04080	1,00E-45	68414.m00396 hydroxyproline-rich glycoprotein family protein Contains similarity to pre-mRNA processing protein PRP39 gb L29224 from S. cerevisiae. ESTs gb|R64908 and gb|T88158, gb|N38703 and gb|AA651043 come from this gene
354373	3	1565	3	3	1744	1	1	At1g04080	4,00E-50	68414.m00396 hydroxyproline-rich glycoprotein family protein Contains similarity to pre-mRNA processing protein PRP39 gb L29224 from S. cerevisiae. ESTs gb|R64908 and gb|T88158, gb|N38703 and gb|AA651043 come from this gene
359893	1	1568	2	4	4515	2	1	At1g05140	3,00E-10	68414.m00517 membrane-associated zinc metalloprotease, putative similar to Hypothetical zinc metalloprotease All3971 (SP:Q8YQ64) [strain PCC 7120] {Anabaena sp.}; Similar to Synechocystis hypothetical protein (gb|D90908);contains Pfam PF00595: PDZ domain (Also known as DHR or GLGF); contains TIGRFAM TIGR00054: membrane-associated zinc metalloprotease, putative
355320	1	1571	4	2	809	2	1	At4g12620	3,00E-57	68417.m01988 replication control protein, putative similar to origin recognition complex subunit 1 (Replication control protein 1)[Homo sapiens] SWISS-PROT:Q13415

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354374	2	1573	4	2	2202	2	2	At2g29580	3,00E-40	68415.m03592 zinc finger (CCCH-type) family protein / RNA recognition motif (RRM)-containing protein similar to SP|O59800 Cell cycle control protein cwf5 {Schizosaccharomyces pombe}; contains Pfam profile: PF00076 RNA recognition motif (aka RRM, RBD, or RNP domain)
358968	1	1574	2	4	2539	1	2	At5g59710	1,00E-62	68418.m07485 transcription regulator NOT2/NOT3/NOT5 family protein contains Pfam domain PF04153: NOT2 / NOT3 / NOT5 family
353273	2	1576	3	3	1600	1	2	At1g09430	2,00E-103	68414.m01055 ATP-citrate synthase (ATP-citrate (pro-S-)-lyase/citrate cleavage enzyme), putative similar to ATP-citrate-lyase (GI:16648642) [Arabidopsis thaliana]; similar to ATP-citrate (pro-S-)-lyase (EC 4.1.3.8) (Citrate cleavage enzyme)(SP:Q91V92) {Mus musculus}; Location of EST gb|Z34587
357660	1	1576	3	3	1600	1	2	At1g09430	7,00E-16	68414.m01055 ATP-citrate synthase (ATP-citrate (pro-S-)-lyase/citrate cleavage enzyme), putative similar to ATP-citrate-lyase (GI:16648642) [Arabidopsis thaliana]; similar to ATP-citrate (pro-S-)-lyase (EC 4.1.3.8) (Citrate cleavage enzyme)(SP:Q91V92) {Mus musculus}; Location of EST gb|Z34587
357873	1	1576	3	3				At1g10670	9,00E-59	68414.m01213 expressed protein
355995	1	1577	4	2				At1g09470	1,00E-06	68414.m01059 expressed protein ; expression supported by MPSS
355395	1	1578	4	2	6387	4	2	At1g57860	2,00E-46	68414.m06565 60S ribosomal protein L21 similar to 60S ribosomal protein L21 GI:3885884 from [Oryza sativa]
354513	1	1579	5	1	6734	3	1	At1g58280	1,00E-41	68414.m06630 expressed protein
353454	2	1584	3	3	2853	1	2	At5g27470	5,00E-130	68418.m03281 seryl-tRNA synthetase / serine--tRNA ligase identical to SP|Q39230 Seryl-tRNA synthetase (EC 6.1.1.11) (Serine--tRNA ligase) (SerRS) {Arabidopsis thaliana}
359191	1	1585	2	4	5213	1	1	At1g11890	3,00E-41	68414.m01371 vesicle transport protein SEC22, putative identified as SEC22 by Raikhel, NV, et al. in Plant Physiol. 124: 1558-69 (2000); similar to vesicle trafficking protein gb|U91538 from Mus musculus; ESTs gb|F15494 and gb|F14097 come from this gene
353567	2	1586	3	3				At1g12070	2,00E-41	68414.m01393 Rho GDP-dissociation inhibitor family protein similar to SP|P52565 Rho GDP-dissociation inhibitor 1 (Rho GDI 1) (Rho-GDI alpha) {Homo sapiens}; contains Pfam profile PF02115: RHO protein GDP dissociation inhibitor

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356806	1	1588	3	3	7450	2	2	At1g23290	6,00E-44	68414.m02913 60S ribosomal protein L27A (RPL27aB) similar to 60S RIBOSOMAL PROTEIN L27A GB:P49637 GI:1710530 from [Arabidopsis thaliana]
357496	1	1588	3	3	7450	2	2	At1g23290	4,00E-56	68414.m02913 60S ribosomal protein L27A (RPL27aB) similar to 60S RIBOSOMAL PROTEIN L27A GB:P49637 GI:1710530 from [Arabidopsis thaliana]
357625	1	1588	3	3	7450	2	2	At1g70600	1,00E-18	68414.m08133 60S ribosomal protein L27A (RPL27aC) identical to 60S ribosomal protein L27A GB:P49637 [Arabidopsis thaliana]
353482	2	1589	3	3	5052	2	2	At3g26400	7,00E-07	68416.m03292 eukaryotic translation initiation factor 4B, putative/ eIF-4B, putative similar to eukaryotic initiation factor 4B [Arabidopsis thaliana] GI:6739518
356529	1	1589	3	3	5052	2	2	At3g26400	4,00E-10	68416.m03292 eukaryotic translation initiation factor 4B, putative/ eIF-4B, putative similar to eukaryotic initiation factor 4B [Arabidopsis thaliana] GI:6739518
354447	8	1592	3	3	5294	3	2	At1g26910	2,00E-113	68414.m03281 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
358405	1	1592	3	3	5294	3	2	At1g66580	1,00E-17	68414.m07565 60S ribosomal protein L10 (RPL10C) contains Pfam profile: PF00826: Ribosomal L10
353833	4	1593	3	3	8751	3	3	At1g15250	3,00E-41	68414.m01825 60S ribosomal protein L37 (RPL37A) almost identical to GB:Q43292
356629	1	1595	3	3	6732	1	1	At1g15860	3,00E-37	68414.m01903 expressed protein
352978	2	1595	3	3	8168	1	1	At3g12760	5,00E-47	68416.m01593 expressed protein similar to RP42 protein [Homo sapiens] GI:9896486; contains Pfam profile PF00627: UBA/TS-N domain, PF03556: Domain of unknown function (DUF298)
356104	1	1595	3	3	8168	1	1	At3g12760	2,00E-40	68416.m01593 expressed protein similar to RP42 protein [Homo sapiens] GI:9896486; contains Pfam profile PF00627: UBA/TS-N domain, PF03556: Domain of unknown function (DUF298)
356086	1	1595	3	3	8494	1	1	At3g28970	1,00E-37	68416.m03621 expressed protein contains Pfam domain PF03556: Domain of unknown function (DUF298)
353205	2	1596	3	3	3804	1	1	At5g08415	7,00E-46	68418.m00991 lipoic acid synthase family protein similar to lipoic acid synthase from Arabidopsis thaliana [gi:3928758], from Mus musculus [gi:14669826] Pfam profile PF04055: radical SAM domain protein

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357742	1	1596	3	3	3804	1	1	At5g08415	1,00E-42	68418.m00991 lipoic acid synthase family protein similar to lipoic acid synthase from Arabidopsis thaliana [gi:3928758], from Mus musculus [gi:14669826] Pfam profile PF04055: radical SAM domain protein
353742	3	1597	4	2	4345	2	1	At1g79230	4,00E-47	68414.m09237 mercaptopyruvate sulfurtransferase (MST1) (RDH1) identical to mercaptopyruvate sulfurtransferase GI:6009981 and thiosulfate sulfurtransferase GI:5834508 from [Arabidopsis thaliana]
354954	1	1598	3	3	8465	1	1	At1g53400	3,00E-38	68414.m06053 expressed protein
357125	1	1603	3	3	1972	1	1	At5g35220	2,00E-06	68418.m04176 peptidase M50 family protein / sterol-regulatory element binding protein (SREBP) site 2 protease family protein contains PFam PF02163: sterol-regulatory element binding protein (SREBP) site 2 protease
353278	4	1607	4	2	6556	3	1	At1g18540	2,00E-83	68414.m02313 60S ribosomal protein L6 (RPL6A) similar to 60S ribosomal protein L6 GI:7208784 from [Cicer arietinum]
358871	1	1607	4	2	6556	3	1	At1g74060	1,00E-54	68414.m08578 60S ribosomal protein L6 (RPL6B) similar to 60S ribosomal protein L6 (YL 16 like) GB:CAB57309 from [Cyanophora paradoxa]
358162	1	1609	3	3	10226	3	1	At5g20700	3,00E-16	68418.m02458 senescence-associated protein-related similar to senescence-associated protein SAG102 (GI:22331931) [Arabidopsis thaliana];
359363	1	1609	3	3	10226	3	1	At5g20700	6,00E-23	68418.m02458 senescence-associated protein-related similar to senescence-associated protein SAG102 (GI:22331931) [Arabidopsis thaliana];
355927	1	1611	4	2	2145	3	1	At3g22890	1,00E-74	68416.m02885 sulfate adenylyltransferase 1 / ATP-sulfurylase 1 (APS1) nearly identical to ATP sulfurylase (APS1) [Arabidopsis thaliana] GI:6606509
358520	1	1612	3	3	895	2	1	At4g35090	3,00E-102	68417.m04984 catalase 2 identical to catalase 2 SP:P25819, GI:17865693 from [Arabidopsis thaliana]
359254	1	1613	2	4	8498	2	2	At1g76940	6,00E-06	68414.m08957 RNA recognition motif (RRM)-containing protein contains Pfam PF00076: RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain); similar to RNA-binding protein with multiple splicing homolog (RBP-MS) (HEart, RRM Expressed Sequence) (Hermes) (Swiss-Prot:Q9YGI5) [Xenopus laevis]; similar to RNA-binding protein with multiple splicing (RBP-MS) (Swiss-Prot:Q93062) [Homo sapiens]

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
358421	1	1614	3	3				At1g77060	7,00E-63	68414.m08972 mutase family protein similar to carboxyvinyl-carboxyphosphonate phosphorylmutase GB:O49290 from [Arabidopsis thaliana]; similar to carboxyphosphonoenolpyruvate mutase (GI:47149) [Streptomyces hygroscopicus]; contains Prosite PS00161: Isocitrate lyase signature
353585	2	1615	2	4	508	1	1	At1g21640	3,00E-111	68414.m02709 ATP-NAD kinase family protein contains similarity to NAD kinase [Homo sapiens] gi|20070086|gb|AAM01195; contains Pfam domain, PF01513: ATP-NAD kinase
353030	2	1617	3	3	1284	1	1	At1g26170	8,00E-41	68414.m03194 importin beta-2 subunit family protein similar to Importin9 isoform 1 [Mus musculus] GI:15186756; contains Pfam profile PF03810: Importin-beta N-terminal domain
353248	2	1618	3	3	8082	3	3	At1g69620	6,00E-45	68414.m08008 60S ribosomal protein L34 (RPL34B) similar to SP:Q42351 from [Arabidopsis thaliana]
354464	2	1618	3	3	8082	3	3	At1g69620	7,00E-54	68414.m08008 60S ribosomal protein L34 (RPL34B) similar to SP:Q42351 from [Arabidopsis thaliana]
355486	1	1620	3	3	7257	2	2	At1g28960	1,00E-38	68414.m03539 MutT/nudix family protein similar to coenzyme A diphosphatase [Mus musculus] GI:12746410; contains Pfam profile PF00293: NUDIX domain
358819	1	1623	4	2	7970	3	1	At5g44785	3,00E-31	68418.m05490 expressed protein contains Pfam PF05329: Protein of unknown function (DUF731)
359032	1	1624	3	3	1500	2	1	At1g31070	8,00E-50	68414.m03804 UDP-N-acetylglucosamine pyrophosphorylase-related low similarity to SP|P43123 UDP-N-acetylglucosamine pyrophosphorylase (EC 2.7.7.23) {Saccharomyces cerevisiae}
354381	2	1625	3	3	4998	1	1	At1g32220	7,00E-86	68414.m03963 expressed protein
354781	1	1625	3	3	4998	1	1	At1g32220	2,00E-09	68414.m03963 expressed protein
359206	1	1627	5	1	9776	1	1	At5g14140	2,00E-49	68418.m01654 zinc finger (C2H2 type) family protein contains Pfam profile: PF00096 zinc finger, C2H2 type
353508	4	1629	3	3	8580	3	3	At1g77940	2,00E-48	68414.m09083 60S ribosomal protein L30 (RPL30B) similar to ribosomal protein L30 GI:388034 from [Homo sapiens]
354881	1	1637	3	3	4264	2	2	At1g51560	5,00E-98	68414.m05803 expressed protein
357221	1	1641	3	3	2576	1	1	At5g35910	1,00E-07	68418.m04312 3'-5' exonuclease domain-containing protein / helicase and RNase D C-terminal domain-containing protein / HRDC domain-containing protein low similarity to SP|Q01780 Polymyositis/scleroderma autoantigen 2 {Homo sapiens}; contains Pfam profiles PF00570: HRDC domain, PF01612: 3'-5' exonuclease

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357549	1	1641	3	3	2576	1	1	At5g35910	4,00E-14	68418.m04312 3'-5' exonuclease domain-containing protein / helicase and RNase D C-terminal domain-containing protein / HRDC domain-containing protein low similarity to SP|Q01780 Polymyositis/scleroderma autoantigen 2 {Homo sapiens}; contains Pfam profiles PF00570: HRDC domain, PF01612: 3'-5' exonuclease
354932	1	1644	4	2	6021	2	1	At2g26670	5,00E-06	68415.m03199 heme oxygenase 1 (HO1) (HY1) identical to plastid heme oxygenase (HY1) [Arabidopsis thaliana] GI:4877362, heme oxygenase 1 [Arabidopsis thaliana] GI:4530591 GB:AF132475; annotation updated per Seth J. Davis at University of Wisconsin-Madison
354060	2	1645	3	3	3193	1	1	At1g60230	5,00E-19	68414.m06783 radical SAM domain-containing protein contains Pfam profile PF04055: radical SAM domain protein
353809	2	1647	3	3				At3g09800	7,00E-50	68416.m01166 clathrin adaptor complex small chain family protein contains Pfam profile: PF01217 clathrin adaptor complex small chain
359076	1	1650	3	3	5818	2	1	At4g11150	1,00E-50	68417.m01807 vacuolar ATP synthase subunit E / V-ATPase E subunit / vacuolar proton pump E subunit (VATE) identical to SP|Q39258 Vacuolar ATP synthase subunit E (EC 3.6.3.14) (V-ATPase E subunit) (Vacuolar proton pump E subunit) {Arabidopsis thaliana}
354404	2	1656	3	3	8538	2	1	At3g07170	6,00E-27	68416.m00854 sterile alpha motif (SAM) domain-containing protein contains Pfam profile PF00536: SAM domain (Sterile alpha motif)
357870	1	1656	3	3	8538	2	1	At3g07170	4,00E-28	68416.m00854 sterile alpha motif (SAM) domain-containing protein contains Pfam profile PF00536: SAM domain (Sterile alpha motif)
355429	1	1657	4	2	5608	1	1	At3g04790	3,00E-23	68416.m00516 ribose 5-phosphate isomerase-related similar to ribose-5-phosphate isomerase GI:18654317 from [Spinacia oleracea]
353271	2	1658	2	4	5325	1	2	At1g72050	2,00E-67	68414.m08328 zinc finger (C2H2 type) family protein contains multiple zinc finger domains: PF00096: Zinc finger, C2H2 type
359651	1	1660	3	3	697	2	1	At3g13870	1,00E-63	68416.m01752 root hair defective 3 (RHD3) identical to root hair defective 3 (RHD3) GI:1839188 from [Arabidopsis thaliana] (Genes Dev (1997) 11(6), 799-811)
357433	1	1664	3	3	1535	1	1	At3g12080	4,00E-52	68416.m01504 GTP-binding family protein contains Pfam domain, PF01926: GTPase of unknown function
359984	1	1667	2	4	7301	2	1	At2g02380	1,00E-30	68415.m00176 glutathione S-transferase, putative similar to gi:167970 gb:AAA72320 gb:AY052332

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353386	2	1668	4	2	8072	4	2	At5g04800	1,00E-56	68418.m00499 40S ribosomal protein S17 (RPS17D) 40S ribosomal protein S17, Lycopersicon esculentum, EMBL:AF161704
354066	2	1669	3	3	1712	1	1	At4g31780	1,00E-62	68417.m04510 1,2-diacylglycerol 3-beta-galactosyltransferase, putative / monogalactosyldiacylglycerol synthase, putative / MGDG synthase, putative similar to MGD synthase type A from Arabidopsis thaliana [gi:9927297], similar to monogalactosyldiacylglycerol synthase, Cucumis sativus, PID:g1805254
354968	1	1669	3	3	1712	1	1	At4g31780	3,00E-07	68417.m04510 1,2-diacylglycerol 3-beta-galactosyltransferase, putative / monogalactosyldiacylglycerol synthase, putative / MGDG synthase, putative similar to MGD synthase type A from Arabidopsis thaliana [gi:9927297], similar to monogalactosyldiacylglycerol synthase, Cucumis sativus, PID:g1805254
357629	1	1673	4	2	8686	2	2	At3g11780	5,00E-10	68416.m01445 MD-2-related lipid recognition domain-containing protein / ML domain-containing protein weak similarity to phosphatidylglycerol/phosphatidylinositol transfer protein [Aspergillus oryzae] GI:10178615; contains Pfam profile PF02221: ML domain
352961	4	1675	3	3	3905	3	3	At5g58420	1,00E-125	68418.m07315 40S ribosomal protein S4 (RPS4D) ribosomal protein S4, Arabidopsis thaliana, PIR:T48480
353227	2	1675	3	3	3905	3	3	At5g07090	1,00E-50	68418.m00804 40S ribosomal protein S4 (RPS4B)
354027	8	1675	3	3	3905	3	3	At5g58420	2,00E-136	68418.m07315 40S ribosomal protein S4 (RPS4D) ribosomal protein S4, Arabidopsis thaliana, PIR:T48480
359339	1	1678	3	3	4087	2	1	At4g29790	4,00E-06	68417.m04242 expressed protein
353201	2	1679	3	3	8427	3	1	At2g19680	3,00E-53	68415.m02300 mitochondrial ATP synthase g subunit family protein contains Pfam profile: PF04718 mitochondrial ATP synthase g subunit
354157	2	1679	3	3	8427	3	1	At4g26210	6,00E-47	68417.m03774 mitochondrial ATP synthase g subunit family protein contains Pfam profile: PF04718 mitochondrial ATP synthase g subunit
353888	2	1680	3	3	8293	3	3	At5g56710	5,00E-15	68418.m07078 60S ribosomal protein L31 (RPL31C)
359743	1	1680	3	3	8293	3	3	At5g56710	6,00E-08	68418.m07078 60S ribosomal protein L31 (RPL31C)
354137	3	1681	3	3	267	2	3	At2g20580	4,00E-78	68415.m02404 26S proteasome regulatory subunit S2 (RPN1) contains an APC-complex (cyclosome) and proteasome component repeat (PS50248)

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359016	1	1681	3	3	267	2	3	At2g20580	1,00E-69	68415.m02404 26S proteasome regulatory subunit S2 (RPN1) contains an APC-complex (cyclosome) and proteasome component repeat (PS50248)
359412	1	1681	3	3	267	2	3	At2g20580	3,00E-13	68415.m02404 26S proteasome regulatory subunit S2 (RPN1) contains an APC-complex (cyclosome) and proteasome component repeat (PS50248)
359014	1	1682	3	3				At2g40060	4,00E-39	68415.m04922 expressed protein
357324	1	1683	3	3	379	1	1	At2g28520	4,00E-91	68415.m03465 vacuolar proton ATPase, putative similar to Swiss-Prot:Q93050 vacuolar proton translocating ATPase 116 kDa subunit A isoform 1 (Clathrin-coated vesicle/synaptic vesicle proton pump 116 kDa subunit, Vacuolar proton pump subunit 1, Vacuolar adenosine triphosphatase subunit Ac116) [Homo sapiens]
355742	1	1684	3	3	9723	2	2	At4g39235	7,00E-26	68417.m05554 expressed protein
356166	1	1687	3	3	9880	2	3	At4g31985	1,00E-16	68417.m04549 60S ribosomal protein L39 (RPL39C)
358972	1	1687	3	3	9880	2	3	At4g31985	9,00E-18	68417.m04549 60S ribosomal protein L39 (RPL39C)
357852	1	1690	3	3	4934	2	2	At3g10300	3,00E-26	68416.m01236 calcium-binding EF hand family protein low similarity to SP|P12815 Programmed cell death protein 6 (Probable calcium-binding protein ALG-2) {Mus musculus}; contains INTERPRO:IPR002048 calcium-binding EF-hand domain
358567	1	1692	3	3	4204	2	2	At3g54020	1,00E-06	68416.m05973 phosphatidic acid phosphatase-related / PAP2-related
359991	1	1692	3	3	4204	2	2	At3g54020	2,00E-41	68416.m05973 phosphatidic acid phosphatase-related / PAP2-related
354529	1	1694	3	3	1952	1	1	At2g31170	2,00E-86	68415.m03805 tRNA synthetase class I (C) family protein similar to cysteine-tRNA ligase [Escherichia coli] GI:41203; contains Pfam profile PF01406: tRNA synthetases class I (C)
357357	1	1694	3	3	1952	1	1	At2g31170	6,00E-19	68415.m03805 tRNA synthetase class I (C) family protein similar to cysteine-tRNA ligase [Escherichia coli] GI:41203; contains Pfam profile PF01406: tRNA synthetases class I (C)
354254	2	1695	3	3	711	1	2	At4g31210	8,00E-38	68417.m04432 DNA topoisomerase family protein similar to DNA Topoisomerase I (SP:Q9X3X7) {Zymomonas mobilis}
354336	2	1696	2	4	3828	1	1	At5g08160	3,00E-94	68418.m00953 serine/threonine protein kinase, putative identical to serine/threonine protein kinase [Arabidopsis thaliana] gi|2109293|gb|AAB69123

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357192	1	1697	2	4	6318	1	1	At2g33470	2,00E-24	68415.m04103 glycolipid transfer protein-related similar to phosphoinositol 4-phosphate adaptor protein-2 (GI:14165198) [Homo sapiens]; similar to Glycolipid transfer protein (GLTP) (Swiss-Prot:Q9JL62) [Mus musculus]; similar to Glycolipid transfer protein (GLTP) (Swiss-Prot:Q9NZD2) [Homo sapiens]
352938	3	1702	3	3				At5g55280	1,00E-129	68418.m06889 cell division protein FtsZ, chloroplast, putative (FTSZ) identical to SP|Q42545 Cell division protein ftsZ homolog, chloroplast precursor {Arabidopsis thaliana}; similar to FtsZ1 [Tagetes erecta] GI:8896066; contains Pfam profiles PF00091: Tubulin/FtsZ family, GTPase domain, PF03953: Tubulin/FtsZ family, C-terminal domain
358893	1	1706	2	4	7522	1	2	At3g57810	5,00E-11	68416.m06445 OTU-like cysteine protease family protein contains Pfam profile PF02338: OTU-like cysteine protease
359437	1	1708	3	3	4682	2	1	At5g27490	2,00E-06	68418.m03286 integral membrane Yip1 family protein contains Pfam domain, PF04893: Yip1 domain
359597	1	1708	3	3	4682	2	1	At5g27490	8,00E-20	68418.m03286 integral membrane Yip1 family protein contains Pfam domain, PF04893: Yip1 domain
358907	1	1708	3	3	6686	1	1	At2g39805	2,00E-08	68415.m04889 integral membrane Yip1 family protein contains Pfam domain, PF04893: Yip1 domain
359337	1	1708	3	3	6686	1	1	At2g39805	5,00E-33	68415.m04889 integral membrane Yip1 family protein contains Pfam domain, PF04893: Yip1 domain
353426	11	1709	3	3	3810	3	3	At2g40010	7,00E-135	68415.m04916 60S acidic ribosomal protein P0 (RPP0A)
359833	1	1709	3	3	3810	3	3	At2g40010	1,00E-69	68415.m04916 60S acidic ribosomal protein P0 (RPP0A)
360019	1	1709	3	3	3810	3	3	At2g40010	7,00E-32	68415.m04916 60S acidic ribosomal protein P0 (RPP0A)
354308	4	1710	3	3	8267	3	2	At2g40590	2,00E-33	68415.m05007 40S ribosomal protein S26 (RPS26B)
353196	3	1711	4	2	8955	4	1	At3g10770	1,00E-51	68416.m01297 expressed protein
356375	1	1714	3	3	6950	1	1	At2g42220	6,00E-60	68415.m05225 rhodanese-like domain-containing protein contains rhodanese-like domain PF:00581
357283	1	1714	3	3	8242	1	1	At4g24750	2,00E-67	68417.m03542 expressed protein
353225	2	1715	3	3	3004	1	1	At3g51800	3,00E-62	68416.m05681 metallopeptidase M24 family protein similar to SP|P50580 Proliferation-associated protein 2G4 {Mus musculus}; contains Pfam profile PF00557: metallopeptidase family M24
354136	2	1715	3	3	3004	1	1	At3g51800	3,00E-57	68416.m05681 metallopeptidase M24 family protein similar to SP|P50580 Proliferation-associated protein 2G4 {Mus musculus}; contains Pfam profile PF00557: metallopeptidase family M24

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358168	1	1715	3	3	3004	1	1	At3g51800	6,00E-38	68416.m05681 metallopeptidase M24 family protein similar to SP|P50580 Proliferation-associated protein 2G4 {Mus musculus}; contains Pfam profile PF00557: metallopeptidase family M24
353539	2	1716	3	3	8271	2	2	At5g06770	6,00E-42	68418.m00765 KH domain-containing protein / zinc finger (CCCH type) family protein contains Pfam domains PF00013: KH domain and PF00642: Zinc finger C-x8-C-x5-C-x3-H type (and similar)
353642	2	1716	3	3	8271	2	2	At3g12130	3,00E-09	68416.m01509 KH domain-containing protein / zinc finger (CCCH type) family protein
354113	2	1716	3	3	8271	2	2	At5g06770	3,00E-37	68418.m00765 KH domain-containing protein / zinc finger (CCCH type) family protein contains Pfam domains PF00013: KH domain and PF00642: Zinc finger C-x8-C-x5-C-x3-H type (and similar)
354327	4	1717	4	2	4916	1	1	At2g44680	3,00E-90	68415.m05561 casein kinase II beta chain, putative similar to casein kinase II beta-3 chain (CK II) [Arabidopsis thaliana] SWISS-PROT:O81275
353259	2	1717	4	2				At4g17640	3,00E-97	68417.m02637 casein kinase II beta chain, putative similar to casein kinase II beta' chain (CK II) [Arabidopsis thaliana] SWISS-PROT:P40229
356177	1	1722	3	3	6332	2	3	At5g27850	6,00E-33	68418.m03341 60S ribosomal protein L18 (RPL18C) 60S ribosomal protein L18, Arabidopsis thaliana, SWISSPROT:RL18_ARATH
359326	1	1722	3	3	6332	2	3	At3g05590	2,00E-37	68416.m00621 60S ribosomal protein L18 (RPL18B) similar to GB:P42791
356820	1	1723	3	3	8969	1	1	At3g01440	2,00E-11	68416.m00068 oxygen evolving enhancer 3 (PsbQ) family protein photosystem II oxygen-evolving complex protein; contains Pfam profile PF05757: Oxygen evolving enhancer protein 3 (PsbQ)
356206	1	1725	3	3	4930	1	1	At5g51410	1,00E-39	68418.m06374 LUC7 N_terminus domain-containing protein similar to cisplatin resistance-associated overexpressed protein [Homo sapiens] GI:6899846; contains Pfam profile PF03194: LUC7 N_terminus
354532	1	1727	1	5				At3g05040	2,00E-38	68416.m00547 expressed protein weak similarity to exportin 5 [Homo sapiens] GI:10444427
355182	1	1733	4	2	577	2	1	At3g06650	2,00E-93	68416.m00774 ATP-citrate synthase, putative / ATP-citrate (pro-S-)-lyase, putative / citrate cleavage enzyme, putative strong similarity to ATP:citrate lyase [Capsicum annuum] GI:13160653; contains Pfam profiles PF00549: CoA-ligase, PF02629: CoA binding domain

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354974	1	1735	3	3	2676	1	1	At4g34100	2,00E-60	68417.m04838 zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)
357270	1	1736	2	4	4291	1	1	At3g08650	6,00E-76	68416.m01005 metal transporter family protein contains ZIP Zinc transporter domain, Pfam:PF02535
356423	1	1740	2	4	10011	1	2	At3g17210	2,00E-16	68416.m02198 stable protein 1-related similar to stable protein 1 (GI:13445204) [Populus tremula] PMID:12376651; similar to pop3 peptide GB:AAC26526 from [Populus balsamifera subsp. trichocarpa X Populus deltoides]
355592	1	1742	3	3	3923	1	1	At3g58460	2,00E-44	68416.m06516 rhomboid family protein / ubiquitin-associated (UBA)/TS-N domain-containing protein contains Pfam profiles PF01694: Rhomboid family, PF00627: UBA/TS-N domain
359772	1	1743	3	3	458	1	1	At4g15560	1,00E-27	68417.m02377 1-deoxy-D-xylulose 5-phosphate synthase, putative / 1-deoxyxylulose-5-phosphate synthase, putative / DXP-synthase, putative (DEF) (CLA1) identical to SP|Q38854 Probable 1-deoxy-D-xylulose 5-phosphate synthase, chloroplast precursor (EC 4.1.3.37) (1-deoxyxylulose-5-phosphate synthase) (DXP synthase) (DXPS). [Mouse-ear cress] {Arabidopsis thaliana}, DEF (deficient in photosynthesis) protein [Arabidopsis thaliana] GI:1399261
359798	1	1745	4	2	6908	1	1	At5g59180	1,00E-57	68418.m07417 DNA-directed RNA polymerase II identical to Swiss-Prot:P38421 DNA-directed RNA polymerase II 19 kDa polypeptide (EC 2.7.7.6) (RNA polymerase II subunit 5) [Arabidopsis thaliana]
354729	1	1750	2	4	177	1	2	At4g16130	4,00E-58	68417.m02444 GHMP kinase family protein contains GHMP kinases putative ATP-binding protein domain, Pfam:PF00288
354034	3	1753	3	3	9606	3	3	At4g33865	1,00E-25	68417.m04805 40S ribosomal protein S29 (RPS29C)
354333	2	1755	3	3	9838	2	2	At5g22280	2,00E-17	68418.m02597 expressed protein
352972	4	1756	3	3	8268	3	2	At5g62300	1,00E-53	68418.m07821 40S ribosomal protein S20 (RPS20C) ribosomal protein S20, Arabidopsis thaliana, PIR:T12992
357809	1	1757	4	2				At5g14930	5,00E-08	68418.m01752 leaf senescence-associated protein (SAG101) nearly identical to leaf senescence-associated gene SAG101 (putative acyl hydrolase) [Arabidopsis thaliana] GI:8699168; contains Pfam profile PF01764: Lipase
356746	1	1758	2	4	6967	1	1	At4g34215	1,00E-35	68417.m04859 expressed protein

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
357731	1	1759	3	3	7353	2	2	At5g64650	1,00E-16	68418.m08125 ribosomal protein L17 family protein contains Pfam profile: PF01196 ribosomal protein L17
355546	1	1761	2	4	876	1	2	At3g56640	1,00E-17	68416.m06298 exocyst complex subunit Sec15-like family protein contains Pfam profile PF04091: Exocyst complex subunit Sec15-like
353212	2	1764	2	4	7151	2	2	At4g00100	2,00E-74	68417.m00010 40S ribosomal protein S13 (RPS13A) similar to ribosomal protein S13; PF00312 (View Sanger Pfam): ribosomal protein S15; identical to cDNA AtRPS13A mRNA for cytoplasmic ribosomal protein S13 GI:6521011
355776	1	1764	2	4	7151	2	2	At4g00100	2,00E-26	68417.m00010 40S ribosomal protein S13 (RPS13A) similar to ribosomal protein S13; PF00312 (View Sanger Pfam): ribosomal protein S15; identical to cDNA AtRPS13A mRNA for cytoplasmic ribosomal protein S13 GI:6521011
357921	1	1764	2	4	7151	2	2	At4g00100	2,00E-08	68417.m00010 40S ribosomal protein S13 (RPS13A) similar to ribosomal protein S13; PF00312 (View Sanger Pfam): ribosomal protein S15; identical to cDNA AtRPS13A mRNA for cytoplasmic ribosomal protein S13 GI:6521011
353824	3	1766	4	2	9959	2	1	At5g09250	3,00E-18	68418.m01067 transcriptional coactivator p15 (PC4) family protein similar to SP|P11031 Activated RNA polymerase II transcriptional coactivator p15 precursor (PC4) (p14) (Single-stranded DNA binding protein p9) {Mus musculus}; contains Pfam profile PF02229: Transcriptional Coactivator p15 (PC4)
356007	1	1771	2	4	2890	1	3	At4g09980	1,00E-10	68417.m01634 methyltransferase MT-A70 family protein low similarity to SP|P25583 Karyogamy protein KAR4 {Saccharomyces cerevisiae}, (N6-adenosine)-methyltransferase [Mus musculus] GI:10179948; contains Pfam profile PF05063: MT-A70 (S-adenosylmethionine-binding subunit of human mRNA:m6A methyl-transferase (MTase))
357069	1	1773	2	4	7159	1	1	At4g11120	5,00E-47	68417.m01804 translation elongation factor Ts (EF-Ts), putative similar to ethylene-responsive elongation factor EF-Ts precursor [Lycopersicon esculentum] GI:5669636; contains Pfam profile PF00889: Elongation factor TS
359559	1	1776	2	4	830	1	2	At5g36210	3,00E-43	68418.m04365 expressed protein

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
357986	1	1778	1	5	340	1	1	At4g17610	2,00E-08	68417.m02633 tRNA/rRNA methyltransferase (SpoU) family protein similar to TAR RNA loop binding protein [Homo sapiens] GI:1184692; contains Pfam profile PF00588: SpoU rRNA Methylase (RNA methyltransferase, TrmH) family
357606	1	1779	4	2	3269	2	1	At4g19880	2,00E-41	68417.m02914 glutathione S-transferase-related contains weak hit to Pfam profile PF00043: Glutathione S-transferase, C-terminal domain
354665	1	1783	3	3	6733	2	3	At5g52650	4,00E-43	68418.m06536 40S ribosomal protein S10 (RPS10C) contains similarity to 40S ribosomal protein S10
353218	2	1784	4	2	2756	2	1	At4g27070	7,00E-84	68417.m03892 tryptophan synthase, beta subunit 2 (TSB2) identical to SP|25269
355802	1	1793	3	3	858	2	1	At5g22760	1,00E-06	68418.m02658 PHD finger family protein contains Pfam domain, PF00628: PHD-finger
353443	2	1795	2	4	5902	2	3	At5g39850	1,00E-26	68418.m04829 40S ribosomal protein S9 (RPS9C) 40S ribosomal protein S9 - Chlamydomonas sp.,EMBL:AU066528
357098	1	1795	2	4	5902	2	3	At5g39850	1,00E-23	68418.m04829 40S ribosomal protein S9 (RPS9C) 40S ribosomal protein S9 - Chlamydomonas sp.,EMBL:AU066528
354931	1	1798	5	1	5238	4	1	At5g39450	1,00E-25	68418.m04778 F-box family protein contains Pfam:PF00646 F-box domain ; similar to SKP1 interacting partner 2 (SKIP2) TIGR_Ath1:At5g67250
359638	1	1800	1	5	10134	1	2	At5g56550	5,00E-12	68418.m07057 expressed protein
357551	1	1801	1	5	46	1	1	At5g64270	4,00E-114	68418.m08074 splicing factor, putative similar to splicing factor 3B subunit 1 (Spliceosome associated protein 155) (SAP 155) (SF3b155) (Pre-mRNA splicing factor SF3b 155 kDa subunit) (146 kDa nuclear protein) SP:O57683 from [Xenopus laevis]
354444	2	1834	4	1	9237	3	1	At1g01100	1,00E-11	68414.m00013 60S acidic ribosomal protein P1 (RPP1A) similar to 60S ACIDIC RIBOSOMAL PROTEIN P1 GB:O23095 from [Arabidopsis thaliana]
354181	2	1834	4	1				At5g24510	7,00E-22	68418.m02889 60s acidic ribosomal protein P1, putative
357170	1	1834	4	1				At5g24510	1,00E-21	68418.m02889 60s acidic ribosomal protein P1, putative
354561	1	1835	2	3	6792	1	2	At1g01230	6,00E-81	68414.m00038 ORMDL family protein contains Pfam domain PF04061: ORMDL family
355005	1	1836	4	1	7244	2	1	At2g46080	7,00E-15	68415.m05732 expressed protein

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360015	1	1838	3	2	3315	1	1	At1g01910	3,00E-38	68414.m00109 anion-transporting ATPase, putative similar to SP|O43681 Arsenical pump-driving ATPase (EC 3.6.3.16) (Arsenite-translocating ATPase) (Arsenical resistance ATPase) (Arsenite-transporting ATPase) (ARSA) (ASNA-I) {Homo sapiens}; contains Pfam profile PF02374: Anion-transporting ATPase
353392	5	1841	3	2	8085	2	2	At3g05560	4,00E-21	68416.m00614 60S ribosomal protein L22-2 (RPL22B) identical to 60S ribosomal protein L22-2 SP:Q9M9W1 from [Arabidopsis thaliana]
355033	1	1841	3	2	8085	2	2	At3g05560	2,00E-32	68416.m00614 60S ribosomal protein L22-2 (RPL22B) identical to 60S ribosomal protein L22-2 SP:Q9M9W1 from [Arabidopsis thaliana]
355295	1	1841	3	2	8085	2	2	At3g05560	2,00E-33	68416.m00614 60S ribosomal protein L22-2 (RPL22B) identical to 60S ribosomal protein L22-2 SP:Q9M9W1 from [Arabidopsis thaliana]
358411	1	1841	3	2	8085	2	2	At3g05560	1,00E-10	68416.m00614 60S ribosomal protein L22-2 (RPL22B) identical to 60S ribosomal protein L22-2 SP:Q9M9W1 from [Arabidopsis thaliana]
354735	1	1842	2	3	6975	1	1	At5g47030	1,00E-16	68418.m05796 ATP synthase delta' chain, mitochondrial identical to SP|Q96252 ATP synthase delta' chain, mitochondrial precursor (EC 3.6.3.14) {Arabidopsis thaliana}; contains Pfam profile PF02823: ATP synthase, Delta/Epsilon chain, beta-sandwich domain
356327	1	1843	3	2	7211	2	1	At1g03290	3,00E-28	68414.m00307 expressed protein ESTs gb|H36966, gb|R65511, gb|T42324 and gb|T20569 come from this gene
354340	2	1844	3	2				At1g03360	4,00E-60	68414.m00315 exonuclease family protein similar to Exosome complex exonuclease RRP4 (Ribosomal RNA processing protein 4)(SP:P38792) {Saccharomyces cerevisiae}
354964	1	1848	3	2	715	1	1	At5g13640	1,00E-10	68418.m01582 lecithin:cholesterol acyltransferase family protein / LACT family protein similar to SP|P40345 Phospholipid:diacylglycerol acyltransferase (EC 2.3.1.158) (PDAT) {Saccharomyces cerevisiae}; contains Pfam profile PF02450: Lecithin:cholesterol acyltransferase (phosphatidylcholine-sterol acyltransferase)
359551	1	1854	2	3	4326	1	1	At2g36310	6,00E-07	68415.m04457 inosine-uridine preferring nucleoside hydrolase family protein similar to Chain A, Crystal Structure Of Nucleoside Hydrolase From Leishmania MajorGI:8569431; contains Pfam profile PF01156: Inosine-uridine preferring nucleoside hydrolase

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356318	1	1858	1	4	9009	1	1	At1g05970	2,00E-31	68414.m00626 expressed protein
353126	2	1861	3	2	7137	3	2	At5g58590	2,00E-61	68418.m07342 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
355487	1	1861	3	2	7137	3	2	At5g58590	2,00E-44	68418.m07342 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
358433	1	1862	2	3	7515	2	2	At2g30000	1,00E-39	68415.m03650 expressed protein contains Pfam domain PF03660: Uncharacterised protein family (UPF0123)
355622	1	1866	1	4	6651	1	1	At1g08280	1,00E-07	68414.m00914 glycosyl transferase family 29 protein / sialyltransferase family protein contains Pfam profile: PF00777 sialyltransferase (Glycosyltransferase family 29)
360025	1	1870	2	3	2249	1	1	At3g48820	3,00E-31	68416.m05332 glycosyl transferase family 29 protein / sialyltransferase family protein contains Pfam profile: PF00777 sialyltransferase (Glycosyltransferase family 29)
355849	1	1872	3	2				At4g29500	3,00E-14	68417.m04209 prolidase-related contains similarity to prolidase GI:3114966 from [Suberites domuncula]
353881	2	1873	2	3	937	2	1	At1g09780	2,00E-147	68414.m01097 2,3-biphosphoglycerate-independent phosphoglycerate mutase, putative / phosphoglyceromutase, putative strong similarity to SP|Q42908 2,3-bisphosphoglycerate-independent phosphoglycerate mutase (EC 5.4.2.1) (Phosphoglyceromutase) {Mesembryanthemum crystallinum}; contains Pfam profile PF01676: Metalloenzyme superfamily
358813	1	1876	2	3				At1g11440	2,00E-09	68414.m01314 expressed protein
357885	1	1878	1	4	5207	1	1	At1g11800	5,00E-46	68414.m01354 endonuclease/exonuclease/phosphatase family protein contains Pfam profile PF03372: Endonuclease/Exonuclease/phosphatase family
359173	1	1878	1	4	5207	1	1	At1g11800	1,00E-44	68414.m01354 endonuclease/exonuclease/phosphatase family protein contains Pfam profile PF03372: Endonuclease/Exonuclease/phosphatase family

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
357341	1	1879	2	3	3975	1	2	At5g12900	7,00E-57	68418.m01480 expressed protein
353536	6	1882	4	1	7209	4	1	At3g25780	8,00E-54	68416.m03209 allene oxide cyclase, putative / early-responsive to dehydration protein, putative / ERD protein, putative similar to allene oxide cyclase GI:8977961 from [Lycopersicon esculentum]; similar to early-responsive to dehydration (ERD12) protein [GI:15320414]; contains Pfam profile PF06351: Allene oxide cyclase
354272	2	1886	2	3	5277	1	1	At2g41250	7,00E-13	68415.m05094 haloacid dehalogenase-like hydrolase family protein low similarity to SP|Q94915 Rhythmically expressed gene 2 protein (DREG-2) {Drosophila melanogaster}; contains InterPro accession IPR005834: Haloacid dehalogenase-like hydrolase
353718	5	1887	3	2	7952	1	1	At1g71260	8,00E-43	68414.m08224 expressed protein
358507	1	1888	4	1	3890	1	1	At1g14520	1,00E-50	68414.m01721 oxygenase-related similar to myo-inositol oxygenase [Sus scrofa] gi|17432544|gb|AAL39076
357634	1	1891	2	3	6937	1	1	At1g15390	3,00E-73	68414.m01843 peptide deformylase, mitochondrial / polypeptide deformylase 1A (PDF1A) nearly identical to SP|Q9FV53 Peptide deformylase, mitochondrial precursor (EC 3.5.1.88) (PDF) (Polypeptide deformylase) {Arabidopsis thaliana}; contains Pfam profile PF01327: polypeptide deformylase; supporting cDNA gi|11320951|gb|AF250959.1|AF250959
359935	1	1892	2	3	3491	1	1	At5g11240	5,00E-37	68418.m01313 transducin family protein / WD-40 repeat family protein contains 3 WD-40 repeats (PF00400); similar to uncharacterized protein KIAA0007 (GI:1663708) {Homo sapiens} 1.2e-11
354039	2	1893	3	2	4800	1	1	At2g33040	3,00E-111	68415.m04052 ATP synthase gamma chain, mitochondrial (ATPC) identical to SP|Q96250 ATP synthase gamma chain, mitochondrial precursor (EC 3.6.3.14) {Arabidopsis thaliana}; contains Pfam profile: PF00231 ATP synthase
354103	2	1893	3	2	4800	1	1	At2g33040	2,00E-57	68415.m04052 ATP synthase gamma chain, mitochondrial (ATPC) identical to SP|Q96250 ATP synthase gamma chain, mitochondrial precursor (EC 3.6.3.14) {Arabidopsis thaliana}; contains Pfam profile: PF00231 ATP synthase
354119	2	1895	2	3	7481	2	3	At1g80620	3,00E-38	68414.m09461 ribosomal protein S15 family protein similar to ribosomal protein S15 GB:AAD36415 from [Thermotoga maritima]

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355094	1	1896	2	3	6424	1	1	At1g15880	6,00E-17	68414.m01905 Golgi SNARE 11 protein identical to Golgi SNARE 11 protein (GI:13898893) {Arabidopsis thaliana}; similar to putative cis-Golgi SNARE protein GI:2583133 from [Arabidopsis thaliana];similar toSP|O95249| 28 kDa Golgi SNARE protein (28 kDa cis-Golgi SNARE p28) (GOS-28). [Homo sapiens]; similar to Golgi SNARE protein (Golgi SNAP receptor complex member 1) (28 kDa cis-Golgi SNARE p28) (GOS-28) (SP:Q62931) {Rattus norvegicus}
357461	1	1900	2	3	1301	1	2	At1g17210	5,00E-13	68414.m02097 expressed protein distantly related to dentin phosphoryn [Homo sapiens] (GI:4322670)
353068	3	1902	2	3	7426	1	1	At1g73230	2,00E-63	68414.m08475 nascent polypeptide-associated complex (NAC) domain-containing protein similar to SP|P20290 Transcription factor BTF3 (RNA polymerase B transcription factor 3) {Homo sapiens}; contains Pfam profile PF01849: NAC domain
353542	3	1902	2	3	7426	1	1	At1g73230	1,00E-62	68414.m08475 nascent polypeptide-associated complex (NAC) domain-containing protein similar to SP|P20290 Transcription factor BTF3 (RNA polymerase B transcription factor 3) {Homo sapiens}; contains Pfam profile PF01849: NAC domain
353639	5	1902	2	3	7426	1	1	At1g73230	5,00E-66	68414.m08475 nascent polypeptide-associated complex (NAC) domain-containing protein similar to SP|P20290 Transcription factor BTF3 (RNA polymerase B transcription factor 3) {Homo sapiens}; contains Pfam profile PF01849: NAC domain
357157	1	1902	2	3	7426	1	1	At1g73230	1,00E-15	68414.m08475 nascent polypeptide-associated complex (NAC) domain-containing protein similar to SP|P20290 Transcription factor BTF3 (RNA polymerase B transcription factor 3) {Homo sapiens}; contains Pfam profile PF01849: NAC domain
359308	1	1907	2	3	7928	2	1	At1g18720	7,00E-61	68414.m02335 expressed protein similar to YGL010w-like protein GI:2982301 from [Picea mariana]
353467	4	1910	2	3	7123	2	1	At1g19330	5,00E-33	68414.m02403 expressed protein
358691	1	1910	2	3	7123	2	1	At1g19330	5,00E-49	68414.m02403 expressed protein
353191	3	1912	3	2	6309	2	1	At1g19480	3,00E-79	68414.m02426 HhH-GPD base excision DNA repair family protein contains Pfam PF00730: HhH-GPD superfamily base excision DNA repair; similar to DNA-3-methyladenine glycosylase 1 (3-methyladenine DNA glycosidase 1) (3MEA DNA glycosylase 1) (SP:Q92383) {Schizosaccharomyces pombe}

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357622	1	1913	4	1				At3g15940	8,00E-63	68416.m02016 glycosyl transferase family 1 protein contains Pfam profile:PF00534 Glycosyl transferases group 1
357849	1	1918	2	3				At4g09150	1,00E-25	68417.m01515 T-complex protein 11 contains Pfam PF05794: T-complex protein 11
358535	1	1919	3	2	741	2	1	At1g23190	1,00E-110	68414.m02897 phosphoglucomutase, cytoplasmic, putative / glucose phosphomutase, putative strong similarity to SP|P93805 Phosphoglucomutase, cytoplasmic 2 (EC 5.4.2.2) (Glucose phosphomutase 2) (PGM 2) {Zea mays}; contains InterPro accession IPR006352: Phosphoglucosamine mutase
356636	1	1923	3	2	4179	1	1	At1g26110	1,00E-26	68414.m03186 expressed protein
353192	3	1926	4	1	10087	4	1	At3g27080	6,00E-48	68416.m03387 mitochondrial import receptor subunit TOM20-3 / translocase of outer membrane 20 kDa subunit 3 (TOM20-3) identical to mitochondrial import receptor subunit TOM20-3 SP:P82874 from [Arabidopsis thaliana]
354116	2	1926	4	1	10087	4	1	At1g27390	2,00E-12	68414.m03339 mitochondrial import receptor subunit TOM20-2 (TOM20-2) identical to mitochondrial import receptor subunit TOM20-2 SP:P82873 from [Arabidopsis thaliana]
354030	2	1929	3	2	5881	1	1	At1g28760	5,00E-20	68414.m03537 expressed protein ; expression supported by MPSS
355691	1	1930	2	3	1557	1	1	At2g26990	3,00E-36	68415.m03241 COP9 signalosome complex subunit 2 / CSN complex subunit 2 (CSN2) proteasome, COP9-complex and eIF3-domain protein; identical to CSN complex subunit 2 [Arabidopsis thaliana] GI:18056655; identical to cDNA CSN complex subunit 2 (CSN2) GI:18056654
355896	1	1930	2	3	2045	1	1	At1g29150	2,00E-49	68414.m03567 26S proteasome regulatory subunit, putative (RPN6) similar to 19S proteosome subunit 9 GB:AAC34120 GI:3450889 from [Arabidopsis thaliana]
356207	1	1931	3	2	6936	2	1	At1g29760	4,00E-31	68414.m03639 expressed protein
359011	1	1931	3	2	6936	2	1	At1g29760	3,00E-22	68414.m03639 expressed protein
353378	2	1933	3	2	584	1	1	At1g29880	4,00E-138	68414.m03652 glycyl-tRNA synthetase / glycine--tRNA ligase identical to SP|O23627 Glycyl-tRNA synthetase (EC 6.1.1.14) (Glycine--tRNA ligase) (GlyRS) {Arabidopsis thaliana}
359012	1	1938	2	3				At3g56490	2,00E-18	68416.m06282 zinc-binding protein, putative / protein kinase C inhibitor, putative similar to 14 kDa zinc-binding protein (Protein kinase C inhibitor, PKCI) [Zea mays] Swiss-Prot:P42856

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356472	1	1941	3	2	8320	3	1	At4g09670	1,00E-31	68417.m01588 oxidoreductase family protein similar to AX110P [Daucus carota] GI:285739; contains Pfam profiles PF01408: Oxidoreductase family NAD-binding Rossmann fold, PF02894: Oxidoreductase family C-terminal alpha/beta domain
353187	3	1944	1	4	1558	1	1	At1g43710	7,00E-64	68414.m05021 serine decarboxylase identical to serine decarboxylase [Arabidopsis thaliana] GI:15011302; contains Pfam profile PF00282: Pyridoxal-dependent decarboxylase conserved domain
353239	2	1944	1	4	1558	1	1	At1g43710	3,00E-44	68414.m05021 serine decarboxylase identical to serine decarboxylase [Arabidopsis thaliana] GI:15011302; contains Pfam profile PF00282: Pyridoxal-dependent decarboxylase conserved domain
353638	3	1949	3	2	1179	1	1	At1g44910	2,00E-14	68414.m05146 FF domain-containing protein / WW domain-containing protein contains Pfam profiles PF01846: FF domain, PF00397: WW domain
354306	4	1955	2	3	1460	1	1	At1g50430	2,00E-172	68414.m05652 7-dehydrocholesterol reductase / 7-DHC reductase / sterol delta-7-reductase (ST7R) / dwarf5 protein (DWF5) identical to SP|Q9LDU6 7-dehydrocholesterol reductase (EC 1.3.1.21) (7-DHC reductase) (Sterol delta-7-reductase) (Dwarf5 protein) {Arabidopsis thaliana}
357960	1	1960	2	3	6346	1	1	At1g52600	2,00E-71	68414.m05938 signal peptidase, putative similar to SP|P13679 Microsomal signal peptidase 21 kDa subunit (EC 3.4.-.-) {Canis familiaris}; contains Pfam profile PF00461: Signal peptidase I
358850	1	1961	5					At3g56130	2,00E-12	68416.m06239 biotin/lipoyl attachment domain-containing protein low similarity to SP|Q06881 Biotin carboxyl carrier protein of acetyl-CoA carboxylase (BCCP) {Anabaena sp.}; contains Pfam profile PF00364: Biotin-requiring enzyme
359931	1	1962	3	2	9059	2	2	At3g15670	8,00E-11	68416.m01986 late embryogenesis abundant protein, putative / LEA protein, putative similar to SP|P13934 Late embryogenesis abundant protein 76 (LEA 76) {Brassica napus}; contains Pfam profile PF02987: Late embryogenesis abundant protein
352999	3	1963	3	2	8284	2	2	At1g80230	3,00E-33	68414.m09389 cytochrome c oxidase family protein contains Pfam domain, PF01215: Cytochrome c oxidase subunit Vb
359171	1	1967	3	2	1977	1	1	At2g44950	7,00E-55	68415.m05596 zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
356223	1	1967	3	2				At1g55250	1,00E-16	68414.m06310 expressed protein weak similarity to PUMA1 [Parascaris univalens] GI:3068590
358985	1	1971	3	2	2489	2	1	At4g37900	7,00E-30	68417.m05360 glycine-rich protein
354243	2	1972	2	3	6771	1	1	At5g24340	2,00E-58	68418.m02868 3'-5' exonuclease domain-containing protein contains Pfam profile PF01612: 3'-5' exonuclease
355499	1	1974	3	2	40	1	1	At1g58250	3,00E-69	68414.m06624 SABRE, putative similar to SABRE (GI:719291) [Arabidopsis thaliana]
353247	2	1977	3	2				At1g61255	4,00E-06	68414.m06903 expressed protein
353913	2	1980	3	2	4615	1	1	At5g61410	6,00E-74	68418.m07705 ribulose-phosphate 3-epimerase, chloroplast, putative / pentose-5-phosphate 3-epimerase, putative strong similarity to SP|Q43157 Ribulose-phosphate 3-epimerase, chloroplast precursor (EC 5.1.3.1) (Pentose-5-phosphate 3-epimerase) (PPE) (RPE) (R5P3E) {Spinacia oleracea}; contains Pfam profile PF00834: Ribulose-phosphate 3 epimerase family
359522	1	1980	3	2	7313	2	1	At3g01850	1,00E-15	68416.m00129 ribulose-phosphate 3-epimerase, cytosolic, putative / pentose-5-phosphate 3-epimerase, putative strong similarity to D-ribulose-5-phosphate 3-epimerase [Oryza sativa] GI:6007803; contains Pfam profile PF00834: Ribulose-phosphate 3 epimerase family; contains non-consensus splice sites at exon 1 and exon2
354319	2	1982	3	2	1194	1	1	At3g02360	3,00E-110	68416.m00220 6-phosphogluconate dehydrogenase family protein contains Pfam profiles: PF00393 6-phosphogluconate dehydrogenase C-terminal domain, PF03446 NAD binding domain of 6-phosphogluconate ;similar to 6-phosphogluconate dehydrogenase GB:BAA22812 GI:2529229 [Glycine max]
356409	1	1982	3	2	1194	1	1	At3g02360	3,00E-78	68416.m00220 6-phosphogluconate dehydrogenase family protein contains Pfam profiles: PF00393 6-phosphogluconate dehydrogenase C-terminal domain, PF03446 NAD binding domain of 6-phosphogluconate ;similar to 6-phosphogluconate dehydrogenase GB:BAA22812 GI:2529229 [Glycine max]
359941	1	1982	3	2	1194	1	1	At3g02360	3,00E-47	68416.m00220 6-phosphogluconate dehydrogenase family protein contains Pfam profiles: PF00393 6-phosphogluconate dehydrogenase C-terminal domain, PF03446 NAD binding domain of 6-phosphogluconate ;similar to 6-phosphogluconate dehydrogenase GB:BAA22812 GI:2529229 [Glycine max]

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
353275	2	1986	3	2	7530	1	1	At3g05500	8,00E-54	68416.m00602 rubber elongation factor (REF) family protein contains Pfam profile: PF05755 rubber elongation factor protein (REF)
359071	1	1986	3	2	7530	1	1	At3g05500	7,00E-32	68416.m00602 rubber elongation factor (REF) family protein contains Pfam profile: PF05755 rubber elongation factor protein (REF)
356118	1	1986	3	2				At2g47780	3,00E-19	68415.m05964 rubber elongation factor (REF) protein-related similar to Small rubber particle protein (SRPP) (22 kDa rubber particle protein) (22 kDa RPP) (Latex allergen Hev b 3) (27 kDa natural rubber allergen) (Swiss-Prot:O82803) [Hevea brasiliensis]; similar to Stress-related protein (Swiss-Prot:Q9SW70) [Vitis riparia]
355560	1	1987	3	2	472	2	1	At5g15700	1,00E-56	68418.m01836 DNA-directed RNA polymerase (RPOT2) identical to phage-type RNA polymerase rpoT2 [Arabidopsis thaliana] GI:11340683
357556	1	1990	2	3	1691	1	1	At5g17530	2,00E-69	68418.m02057 phosphoglucosamine mutase family protein low similarity to phosphoglucomutase/phosphomannomutase [Sphingomonas paucimobilis] GI:6103619; contains InterPro accession IPR006352: Phosphoglucosamine mutase
355360	1	1991	2	3	9243	1	1	At1g71310	8,00E-39	68414.m08231 expressed protein
356217	1	1991	2	3	9243	1	1	At1g71310	4,00E-37	68414.m08231 expressed protein
356255	1	1996	2	3	1517	1	1	At1g76490	5,00E-60	68414.m08899 3-hydroxy-3-methylglutaryl-CoA reductase 1 / HMG-CoA reductase 1 (HMG1) identical to HMG-CoA reductase 1 [SP|P14891]
353835	3	1996	2	3				At2g17370	2,00E-23	68415.m02006 3-hydroxy-3-methylglutaryl-CoA reductase 2 / HMG-CoA reductase 2 (HMGR2) identical to SP|P43256 3-hydroxy-3-methylglutaryl-coenzyme A reductase 2 (EC 1.1.1.34) (HMG- CoA reductase 2) (HMGR2) {Arabidopsis thaliana}
358655	1	1996	2	3				At2g17370	9,00E-16	68415.m02006 3-hydroxy-3-methylglutaryl-CoA reductase 2 / HMG-CoA reductase 2 (HMGR2) identical to SP|P43256 3-hydroxy-3-methylglutaryl-coenzyme A reductase 2 (EC 1.1.1.34) (HMG- CoA reductase 2) (HMGR2) {Arabidopsis thaliana}
358676	1	2007	3	2	1255	2	2	At4g34570	6,00E-34	68417.m04912 bifunctional dihydrofolate reductase-thymidylate synthase 2 / DHFR-TS (THY-2) identical to SP|Q05763

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353946	2	2011	3	2	459	1	1	At5g66760	3,00E-32	68418.m08415 succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial / flavoprotein subunit of complex II identical to SP|O82663 Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial (EC 1.3.5.1) (FP) (Flavoprotein subunit of complex II) {Arabidopsis thaliana}
357158	1	2011	3	2	1020	1	1	At5g14760	2,00E-39	68418.m01732 L-aspartate oxidase family protein similar to L-aspartate oxidase, Escherichia coli [SP|P10902]; contains Pfam profiles PF00890 FAD binding domain, PF02910 Fumarate reductase/succinate dehydrogenase flavoprotein C-terminal domain
357413	1	2011	3	2				At2g18450	2,00E-12	68415.m02147 succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial, putative / flavoprotein subunit of complex II, putative strong similarity to SP|O82663 Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial (EC 1.3.5.1) (FP) (Flavoprotein subunit of complex II) {Arabidopsis thaliana}
354014	2	2014	2	3	8150	2	2	At4g29410	4,00E-27	68417.m04200 60S ribosomal protein L28 (RPL28C) unknown protein chromosome II BAC F6F22 - Arabidopsis thaliana,PID:g3687251
357806	1	2014	2	3	8150	2	2	At4g29410	4,00E-08	68417.m04200 60S ribosomal protein L28 (RPL28C) unknown protein chromosome II BAC F6F22 - Arabidopsis thaliana,PID:g3687251
356449	1	2017	2	3	4539	1	1	At2g21170	4,00E-65	68415.m02511 triosephosphate isomerase, chloroplast, putative similar to Triosephosphate isomerase, chloroplast precursor: SP|P48496 from Spinacia oleracea, SP|P46225 from Secale cereale
354245	6	2017	2	3	5267	1	1	At3g55440	6,00E-103	68416.m06157 triosephosphate isomerase, cytosolic, putative strong similarity to triosephosphate isomerase, cytosolic from Petunia hybrida [SP|P48495], from Coptis japonica [SP|P21820]
357784	1	2018	2	3	6894	2	2	At2g22230	3,00E-59	68415.m02638 beta-hydroxyacyl-ACP dehydratase, putative similar to beta-hydroxyacyl-ACP dehydratase from Toxoplasma gondii [GI:3850997]; contains Pfam profile PF01377 Thioester dehydratase

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356352	1	2019	3	2	952	2	1	At5g10170	3,00E-20	68418.m01177 inositol-3-phosphate synthase, putative / myo-inositol-1-phosphate synthase, putative / MI-1-P synthase, putative very strong similarity to SP|Q38862 Myo-inositol-1-phosphate synthase isozyme 2 (EC 5.5.1.4) (MI-1-P synthase 2) (IPS 2) {Arabidopsis thaliana}; identical to SP|Q9LX12| Probable inositol-3-phosphate synthase isozyme 3 (EC 5.5.1.4) (Myo- inositol-1-phosphate synthase 3) (MI-1-P synthase 3) (IPS 3) {Arabidopsis thaliana}; contains Pfam profile PF01658: Myo-inositol-1-phosphate synthase
353410	2	2020	3	2	1335	3	1	At2g24200	2,00E-96	68415.m02891 cytosol aminopeptidase identical to cytosol aminopeptidase SP:P30184 from [Arabidopsis thaliana]; contains Pfam profiles: PF00883 cytosol aminopeptidase family catalytic domain, PF02789: cytosol aminopeptidase family N-terminal domain
357645	1	2021	2	3	8561	2	1	At2g24490	4,00E-15	68415.m02926 replication protein, putative similar to replication protein A 30kDa [Oryza sativa (japonica cultivar-group)] GI:13516746; contains InterPro entry IPR004365: OB-fold nucleic acid binding domain
358229	1	2021	2	3	8561	2	1	At3g02920	3,00E-07	68416.m00287 replication protein-related similar to replication protein A 30kDa [Oryza sativa (japonica cultivar-group)] GI:13516746; contains InterPro entry IPR004365: OB-fold nucleic acid binding domain
355789	1	2023	3	2	2578	2	1	At4g30490	1,00E-35	68417.m04329 AFG1-like ATPase family protein contains Pfam profile: PF03969 AFG1-like ATPase
359200	1	2027	2	3	7253	1	1	At3g63170	3,00E-42	68416.m07095 expressed protein
357207	1	2029	1	4	1683	1	1	At2g27100	2,00E-10	68415.m03256 C2H2 zinc-finger protein SERRATE (SE) identical to C2H2 zinc-finger protein SERRATE GI:14486602 from [Arabidopsis thaliana]
359338	1	2032	2	3	6436	1	1	At2g31270	4,00E-11	68415.m03818 hydroxyproline-rich glycoprotein family protein
353515	5	2033	3	2	5197	3	2	At5g35530	2,00E-112	68418.m04226 40S ribosomal protein S3 (RPS3C)
359027	1	2033	3	2	5197	3	2	At2g31610	8,00E-91	68415.m03862 40S ribosomal protein S3 (RPS3A)
353746	2	2034	3	2	7841	3	2	At4g15000	8,00E-54	68417.m02304 60S ribosomal protein L27 (RPL27C)
357262	1	2037	2	3	7235	1	1	At2g34690	6,00E-74	68415.m04261 expressed protein
355053	1	2038	3	2	3725	3	1	At2g34970	5,00E-41	68415.m04291 eIF4-gamma/eIF5/eIF2-epsilon domain-containing protein similar to SP|Q64350 Translation initiation factor eIF-2B epsilon subunit (eIF-2B GDP-GTP exchange factor) {Rattus norvegicus}; contains Pfam profile PF02020: eIF4-gamma/eIF5/eIF2-epsilon
360068	1	2039	1	4	10305	1	2	At2g35290	1,00E-10	68415.m04328 expressed protein

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354093	5	2042	3	2	6585	3	2	At2g37190	1,00E-64	68415.m04562 60S ribosomal protein L12 (RPL12A)
353745	4	2045	3	2	8785	3	2	At3g53740	3,00E-45	68416.m05937 60S ribosomal protein L36 (RPL36B) 60S RIBOSOMAL PROTEIN L36 - Schizosaccharomyces pombe, swissprot:Q92365
354299	2	2045	3	2	8785	3	2	At3g53740	3,00E-46	68416.m05937 60S ribosomal protein L36 (RPL36B) 60S RIBOSOMAL PROTEIN L36 - Schizosaccharomyces pombe, swissprot:Q92365
356579	1	2045	3	2	8785	3	2	At3g53740	5,00E-45	68416.m05937 60S ribosomal protein L36 (RPL36B) 60S RIBOSOMAL PROTEIN L36 - Schizosaccharomyces pombe, swissprot:Q92365
353154	3	2048	3	2	6507	2	1	At2g39290	1,00E-33	68415.m04824 phosphatidylglycerolphosphate synthase (PGS1) identical to phosphatidylglycerolphosphate synthase GI:13365519 from [Arabidopsis thaliana]
356295	1	2049	2	3	7482	2	1	At2g39960	2,00E-60	68415.m04910 microsomal signal peptidase 25 kDa subunit, putative (SPC25) identical to Probable microsomal signal peptidase 25 kDa subunit (EC 3.4.-.-) (SPase 25 kDa subunit) (SPC25) (Swiss-Prot:P58684) [Arabidopsis thaliana]; contains non-consensus AT-AC splice sites; contains 1 transmembrane domain;
354412	2	2051	2	3	2841	1	1	At2g40490	7,00E-70	68415.m04997 uroporphyrinogen decarboxylase, putative / UPD, putative similar to uroporphyrinogen decarboxylase (chloroplast) from Nicotiana tabacum [SP|Q42967], Hordeum vulgare [SP|Q42855], Zea mays [SP|O81220]; contains Pfam domain uroporphyrinogen decarboxylase (URO-D) PF01208
358729	1	2052	3	2	5581	3	1	At2g40950	3,00E-07	68415.m05056 bZIP transcription factor family protein similar to AtbZIP transcription factor GI:17065880 from [Arabidopsis thaliana]; contains Pfam profile: bZIP transcription factor PF00170
354851	1	2055	2	3	1539	1	1	At2g41540	2,00E-119	68415.m05134 NAD-dependent glycerol-3-phosphate dehydrogenase family protein weak similarity to SP|P46919 Glycerol-3-phosphate dehydrogenase [NAD(P)+] (EC 1.1.1.94) {Bacillus subtilis}; contains Pfam profile PF01210: NAD-dependent glycerol-3-phosphate dehydrogenase
357109	1	2055	2	3	1539	1	1	At2g41540	1,00E-41	68415.m05134 NAD-dependent glycerol-3-phosphate dehydrogenase family protein weak similarity to SP|P46919 Glycerol-3-phosphate dehydrogenase [NAD(P)+] (EC 1.1.1.94) {Bacillus subtilis}; contains Pfam profile PF01210: NAD-dependent glycerol-3-phosphate dehydrogenase

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353327	2	2059	3	2	7668	2	1	At2g42680	5,00E-64	68415.m05283 ethylene-responsive transcriptional coactivator, putative similar to ethylene-responsive transcriptional coactivator [Lycopersicon esculentum] gi|5669634|gb|AAD46402
354274	2	2059	3	2	7668	2	1	At3g58680	9,00E-55	68416.m06540 ethylene-responsive transcriptional coactivator, putative similar to ethylene-responsive transcriptional coactivator [Lycopersicon esculentum] gi|5669634|gb|AAD46402
356855	1	2059	3	2	7668	2	1	At3g58680	5,00E-17	68416.m06540 ethylene-responsive transcriptional coactivator, putative similar to ethylene-responsive transcriptional coactivator [Lycopersicon esculentum] gi|5669634|gb|AAD46402
358509	1	2059	3	2	7668	2	1	At3g58680	2,00E-08	68416.m06540 ethylene-responsive transcriptional coactivator, putative similar to ethylene-responsive transcriptional coactivator [Lycopersicon esculentum] gi|5669634|gb|AAD46402
353714	2	2060	1	4	8397	1	2	At2g42840	2,00E-15	68415.m05305 protodermal factor 1 (PDF1) identical to protodermal factor 1 [Arabidopsis thaliana] gi|4929130|gb|AAD33869
359892	1	2060	1	4	8397	1	2	At2g42840	8,00E-24	68415.m05305 protodermal factor 1 (PDF1) identical to protodermal factor 1 [Arabidopsis thaliana] gi|4929130|gb|AAD33869
353916	2	2062	3	2				At2g43810	2,00E-36	68415.m05446 small nuclear ribonucleoprotein F, putative / U6 snRNA-associated Sm-like protein, putative / Sm protein F, putative similar to SWISS-PROT:Q9Y4Y8 U6 snRNA-associated Sm-like protein LSm6 [Mus musculus]
355171	1	2062	3	2				At2g43810	3,00E-15	68415.m05446 small nuclear ribonucleoprotein F, putative / U6 snRNA-associated Sm-like protein, putative / Sm protein F, putative similar to SWISS-PROT:Q9Y4Y8 U6 snRNA-associated Sm-like protein LSm6 [Mus musculus]
356598	1	2067	2	3	2777	1	1	At4g22720	1,00E-49	68417.m03278 glycoprotease M22 family protein similar to sialylglycoprotease [Haemophilus ducreyi] GI:6942294; contains Pfam profile PF00814: Glycoprotease family
355672	1	2067	2	3	4572	1	1	At2g45270	2,00E-65	68415.m05635 glycoprotease M22 family protein similar to SP|P36175 O-sialoglycoprotein endopeptidase (EC 3.4.24.57) (Glycoprotease) {Pasteurella haemolytica}; contains Pfam profile PF00814: Glycoprotease family

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359417	1	2067	2	3	4572	1	1	At2g45270	5,00E-27	68415.m05635 glycoprotease M22 family protein similar to SP|P36175 O-sialoglycoprotein endopeptidase (EC 3.4.24.57) (Glycoprotease) {Pasteurella haemolytica}; contains Pfam profile PF00814: Glycoprotease family
353348	6	2068	3	2	8839	3	2	At3g61110	4,00E-44	68416.m06839 40S ribosomal protein S27 (ARS27A) identical to cDNA ribosomal protein S27 (ARS27A) GI:4193381
356114	1	2069	2	3	4279	2	1	At3g63000	1,00E-44	68416.m07077 NPL4 family protein contains Pfam domain, PF05021: NPL4 family
353231	2	2076	3	2	7801	3	2	At3g02080	1,00E-64	68416.m00173 40S ribosomal protein S19 (RPS19A) similar to 40S ribosomal protein S19 GB:P40978 [Oryza sativa]
354999	1	2076	3	2	7801	3	2	At3g02080	7,00E-61	68416.m00173 40S ribosomal protein S19 (RPS19A) similar to 40S ribosomal protein S19 GB:P40978 [Oryza sativa]
360013	1	2077	3	2	7636	2	1	At5g16800	3,00E-18	68418.m01967 GCN5-related N-acetyltransferase (GNAT) family protein very low similarity to SP|P39909 Spermine/spermidine acetyltransferase (EC 2.3.1.57) {Bacillus subtilis}; contains Pfam profile PF00583: acetyltransferase, GNAT family
353329	2	2080	2	3	1391	2	1	At3g03250	6,00E-114	68416.m00321 UTP--glucose-1-phosphate uridylyltransferase, putative / UDP-glucose pyrophosphorylase, putative / UGPase, putative strong similarity to SP|P19595 UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) (UDP-glucose pyrophosphorylase) (UDPGP) (UGPase) {Solanum tuberosum}; contains Pfam profile PF01704: UTP--glucose-1-phosphate uridylyltransferase
354330	2	2082	3	2	271	2	2	At3g03780	3,00E-63	68416.m00387 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase, putative / vitamin-B12-independent methionine synthase, putative / cobalamin-independent methionine synthase, putative very strong similarity to SP|O50008 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase (EC 2.1.1.14) (Vitamin-B12-independent methionine synthase isozyme) (Cobalamin-independent methionine synthase isozyme) {Arabidopsis thaliana}; contains Pfam profile PF01717: Methionine synthase, vitamin-B12 independent

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357966	1	2082	3	2				At5g20980	4,00E-19	68418.m02494 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase, putative / vitamin-B12-independent methionine synthase, putative / cobalamin-independent methionine synthase, putative strong similarity to SP|O50008 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase (EC 2.1.1.14) (Vitamin-B12-independent methionine synthase isozyme) (Cobalamin-independent methionine synthase isozyme) {Arabidopsis thaliana}; contains Pfam profile PF01717: Methionine synthase, vitamin-B12 independent
357140	1	2083	3	2	7503	2	1	At3g04090	6,00E-25	68416.m00433 major intrinsic family protein / MIP family protein contains Pfam profile: MIP PF00230
355628	1	2083	3	2	7642	1	1	At3g56950	1,00E-13	68416.m06336 small basic membrane integral family protein contains similarity to small basic membrane integral protein ZmSIP2-1 (GI:13447817) [Zea mays]
356519	1	2084	2	3	2072	1	1	At3g04490	6,00E-07	68416.m00476 exportin-related weak similarity to Exportin 4 (Exp4) (Swiss-Prot:Q9ESJ0) [Mus musculus] and (Swiss-Prot:Q9C0E2) [Homo sapiens]
353602	3	2085	2	3	7768	2	3	At3g04920	1,00E-57	68416.m00534 40S ribosomal protein S24 (RPS24A) similar to ribosomal protein S19 GB:445612 [Solanum tuberosum] and similar to ribosomal protein S24 GB:4506703 [Homo sapiens]
356753	1	2085	2	3	7768	2	3	At3g04920	2,00E-54	68416.m00534 40S ribosomal protein S24 (RPS24A) similar to ribosomal protein S19 GB:445612 [Solanum tuberosum] and similar to ribosomal protein S24 GB:4506703 [Homo sapiens]
354161	4	2089	2	3	81	2	1	At3g08850	2,00E-43	68416.m01029 transducin family protein / WD-40 repeat family protein similar to WD-repeat protein mip1 (SP:P87141) [Schizosaccharomyces pombe]; contains Pfam PF00400: WD domain, G-beta repeat (5 copies, 1 weak)
356530	1	2090	3	2	1395	2	2	At3g09100	5,00E-25	68416.m01070 mRNA capping enzyme family protein similar to mRNA capping enzyme [Xenopus laevis] GI:7239232; contains Pfam profiles PF01331: mRNA capping enzyme catalytic domain, PF00782: Dual specificity phosphatase catalytic domain
356735	1	2090	3	2	1395	2	2	At3g09100	5,00E-11	68416.m01070 mRNA capping enzyme family protein similar to mRNA capping enzyme [Xenopus laevis] GI:7239232; contains Pfam profiles PF01331: mRNA capping enzyme catalytic domain, PF00782: Dual specificity phosphatase catalytic domain

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
356777	1	2090	3	2	1395	2	2	At3g09100	4,00E-15	68416.m01070 mRNA capping enzyme family protein similar to mRNA capping enzyme [Xenopus laevis] GI:7239232; contains Pfam profiles PF01331: mRNA capping enzyme catalytic domain, PF00782: Dual specificity phosphatase catalytic domain
356287	1	2093	2	3	6591	2	1	At3g10730	2,00E-30	68416.m01292 sad1/unc-84-like 2 family protein contains 1 transmembrane domain; similar to Sad1 unc-84 domain protein 2 (GI:6538749) [Homo sapiens]; similar to Sad1/unc-84-like protein 2 (Fragment) (Swiss-Prot:Q9UH99) [Homo sapiens]
357989	1	2098	3	2	7753	2	1	At3g11450	6,00E-45	68416.m01396 DNAJ heat shock N-terminal domain-containing protein / cell division protein-related similar to GlsA [Volvox carteri f. nagariensis] GI:4633129; contains Pfam profiles PF00226 DnaJ domain, PF00249 Myb-like DNA-binding domain
352985	2	2100	3	2	516	1	1	At4g19210	4,00E-93	68417.m02834 RNase L inhibitor protein, putative similar to 68 kDa protein HP68 GI:16755057 from [Triticum aestivum]
357453	1	2101	1	4	612	1	2	At3g15380	2,00E-68	68416.m01950 choline transporter-related contains weak similarity to CD92 protein [Homo sapiens] gi|16945323|emb|CAC82175
356233	1	2102	2	3				At3g15560	4,00E-18	68416.m01972 expressed protein
353904	3	2104	2	3	6430	2	1	At4g15940	4,00E-39	68417.m02420 fumarylacetoacetate hydrolase family protein contains Pfam domain, PF01557: fumarylacetoacetate hydrolase family protein
357162	1	2104	2	3	6430	2	1	At4g15940	3,00E-40	68417.m02420 fumarylacetoacetate hydrolase family protein contains Pfam domain, PF01557: fumarylacetoacetate hydrolase family protein
353325	4	2107	2	3	6899	1	2	At5g66010	2,00E-58	68418.m08312 heterogeneous nuclear ribonucleoprotein, putative / hnRNP, putative similar to Heterogeneous nuclear ribonucleoprotein SP|P55795, SP|P31943, SP|P52597 {Homo sapiens}; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM) domain
357156	1	2107	2	3				At3g20890	5,00E-26	68416.m02641 heterogeneous nuclear ribonucleoprotein, putative / hnRNP, putative similar to SP|P52597 Heterogeneous nuclear ribonucleoprotein F (hnRNP F) {Homo sapiens}; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)

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353134	2	2116	3	2	675	2	1	At5g10240	2,00E-83	68418.m01189 asparagine synthetase 3 (ASN3) identical to asparagine synthetase (ASN3) [Arabidopsis thaliana] GI:3859534
358990	1	2116	3	2	675	2	1	At5g10240	1,00E-38	68418.m01189 asparagine synthetase 3 (ASN3) identical to asparagine synthetase (ASN3) [Arabidopsis thaliana] GI:3859534
359245	1	2116	3	2	675	2	1	At5g10240	9,00E-06	68418.m01189 asparagine synthetase 3 (ASN3) identical to asparagine synthetase (ASN3) [Arabidopsis thaliana] GI:3859534
353570	2	2118	3	2	5394	1	1	At5g67270	3,00E-18	68418.m08480 microtubule-associated EB1 family protein similar to SP|Q9UPY8 Microtubule-associated protein RP/EB family member 3 (Protein EB3) {Homo sapiens}; contains Pfam profiles PF00307: Calponin homology (CH) domain, PF03271: EB1 protein
356191	1	2118	3	2	5394	1	1	At5g67270	1,00E-26	68418.m08480 microtubule-associated EB1 family protein similar to SP|Q9UPY8 Microtubule-associated protein RP/EB family member 3 (Protein EB3) {Homo sapiens}; contains Pfam profiles PF00307: Calponin homology (CH) domain, PF03271: EB1 protein
353040	2	2119	3	2	9417	2	1	At5g50460	3,00E-22	68418.m06248 protein transport protein SEC61 gamma subunit, putative similar to Swiss-Prot:Q19967 protein transport protein SEC61 gamma subunit [Caenorhabditis elegans]
353194	10	2120	3	2	5731	2	2	At3g49010	2,00E-84	68416.m05354 60S ribosomal protein L13 (RPL13B) / breast basic conserved protein 1-related (BBC1)
354003	11	2122	2	3	7840	2	3	At5g67510	1,00E-41	68418.m08513 60S ribosomal protein L26 (RPL26B)
358245	1	2125	2	3	10225	2	3	At5g66800	1,00E-14	68418.m08422 expressed protein
353004	2	2132	2	3	7853	1	1	At3g57090	6,00E-49	68416.m06356 expressed protein
355279	1	2133	1	4	10287	1	1	At3g57450	4,00E-12	68416.m06396 expressed protein
353170	2	2134	1	4	837	1	2	At3g58610	4,00E-77	68416.m06532 ketol-acid reductoisomerase identical to ketol-acid reductoisomerase, chloroplast precursor (EC 1.1.1.86) (Acetohydroxy-acid reductoisomerase) (Alpha-keto-beta-hydroxylacil reductoisomerase) (Swiss-Prot:Q05758) [Arabidopsis thaliana]
359485	1	2134	1	4	837	1	2	At3g58610	5,00E-87	68416.m06532 ketol-acid reductoisomerase identical to ketol-acid reductoisomerase, chloroplast precursor (EC 1.1.1.86) (Acetohydroxy-acid reductoisomerase) (Alpha-keto-beta-hydroxylacil reductoisomerase) (Swiss-Prot:Q05758) [Arabidopsis thaliana]

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
356659	1	2135	3	2	3455	2	1	At4g24490	2,00E-10	68417.m03510 geranylgeranyl transferase alpha subunit-related / RAB geranylgeranyltransferase alpha subunit-related low similarity to SP|Q08602 [Rattus norvegicus]
354114	2	2136	2	3	5415	1	1	At5g23060	8,00E-44	68418.m02696 expressed protein
359999	1	2140	3	2	4826	2	1	At4g04860	4,00E-81	68417.m00708 Der1-like family protein / degradation in the ER-like family protein contains Pfam profile: PF04511 Der1-like family
356525	1	2140	3	2	6045	1	1	At4g29330	1,00E-28	68417.m04191 Der1-like family protein / degradation in the ER-like family protein contains Pfam profile: PF04511 Der1-like family
355322	1	2141	3	2	6138	1	1	At5g54110	3,00E-40	68418.m06737 vesicle-associated membrane family protein / VAMP family protein similar to VAP27 GI:6688926 [Nicotiana plumbaginifolia]
356919	1	2143	2	3				At4g23000	2,00E-69	68417.m03318 calcineurin-like phosphoesterase family protein contains Pfam profile: PF00149 calcineurin-like phosphoesterase
353404	5	2144	2	3	5311	2	2	At4g16720	9,00E-94	68417.m02526 60S ribosomal protein L15 (RPL15A)
354056	4	2144	2	3	5311	2	2	At4g17390	1,00E-68	68417.m02606 60S ribosomal protein L15 (RPL15B)
358193	1	2145	2	3	2306	1	1	At5g43600	5,00E-15	68418.m05330 N-carbamyl-L-amino acid hydrolase, putative similar to N-carbamoyl-L-amino acid hydrolase [Bacillus stearothermophilus] SWISS-PROT:Q53389
359202	1	2145	2	3	6486	1	1	At4g20070	2,00E-31	68417.m02936 peptidase M20/M25/M40 family protein contains similarity to hydantoin utilization protein C [Pseudomonas sp.] SWISS-PROT:Q01264; contains Pfam profile PF01546: Peptidase family M20/M25/M40
358417	1	2146	1	4	6735	1	3	At4g21110	6,00E-43	68417.m03053 G10 family protein contains Pfam profile: PF01125 G10 protein
356376	1	2147	2	3	982	1	2	At4g21670	2,00E-09	68417.m03139 double-stranded RNA-binding domain (DsRBD)-containing protein contains Pfam profile PF00035: Double-stranded RNA binding motif
358306	1	2147	2	3	982	1	2	At4g21670	9,00E-10	68417.m03139 double-stranded RNA-binding domain (DsRBD)-containing protein contains Pfam profile PF00035: Double-stranded RNA binding motif
359062	1	2150	3	2				At4g24610	2,00E-39	68417.m03525 expressed protein
354031	5	2152	3	2	3812	2	1	At4g25630	1,00E-118	68417.m03691 fibrillarin 2 (FIB2) identical to fibrillarin 2 GI:9965655 from [Arabidopsis thaliana]
359162	1	2155	2	3	3236	2	1	At5g55120	4,00E-21	68418.m06871 expressed protein strong similarity to unknown protein (pir||T04808)

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
357045	1	2157	4	1	2356	1	1	At4g29680	7,00E-79	68417.m04228 type I phosphodiesterase/nucleotide pyrophosphatase family protein similar to SP|P06802 Ectonucleotide pyrophosphatase/phosphodiesterase 1 (Plasma-cell membrane glycoprotein PC-1) [Includes: Alkaline phosphodiesterase I (EC 3.1.4.1); Nucleotide pyrophosphatase (EC 3.6.1.9) {Mus musculus}; contains Pfam profile PF01663: Type I phosphodiesterase / nucleotide pyrophosphatase
353951	3	2159	2	3	8432	1	2	At5g25450	8,00E-37	68418.m03023 ubiquinol-cytochrome C reductase complex 14 kDa protein, putative similar to SP|P48502 Ubiquinol-cytochrome C reductase complex 14 kDa protein (EC 1.10.2.2) (CR14) {Solanum tuberosum}; contains Pfam profile PF02271: Ubiquinol-cytochrome C reductase complex 14kD subunit
359529	1	2162	2	3	5252	1	2	At5g03415	1,00E-17	68418.m00294 DPB-1 transcription factor, putative (DPB) similar to Swiss-Prot:Q14186 transcription factor DP-1 [Homo sapiens]; contains Pfam profile PF02319: Transcription factor E2F/dimerisation partner (TDP)
354122	2	2167	2	3	8469	1	1	At5g54600	1,00E-46	68418.m06799 50S ribosomal protein L24, chloroplast (CL24) identical to SP|P92959 50S ribosomal protein L24, chloroplast precursor {Arabidopsis thaliana}
356959	1	2170	2	3	332	2	1	At5g41370	4,00E-119	68418.m05027 DNA repair protein, putative / TFIIH basal transcription factor complex helicase XPB subunit, putative (XPB1) contains Pfam profile PF00271:Helicase conserved C-terminal domain; identical to cDNA putative DNA repair protein (XPB1) GI:10314019
354685	1	2172	1	4	8550	1	1	At5g57370	5,00E-24	68418.m07168 expressed protein low similarity to nucleic acid binding protein [Homo sapiens] GI:431953
355981	1	2236	3	1	3311	1	1	At1g01710	7,00E-36	68414.m00089 acyl-CoA thioesterase family protein contains Pfam profiles: PF02551 acyl-CoA thioesterase, PF00027 cyclic nucleotide-binding domain
358526	1	2238	2	2	5706	1	2	At4g37280	8,00E-87	68417.m05276 MRG family protein contains Pfam domain PF05712: MRG
359867	1	2246	2	2	5487	1	1	At1g03900	6,00E-51	68414.m00374 expressed protein
359466	1	2247	2	2	3680	2	1	At5g44070	3,00E-19	68418.m05392 phytochelatin synthase 1 (PCS1) identical to phytochelatin synthase [Arabidopsis thaliana] gi|18254401|gb|AAL66747; identical to cDNA phytochelatin synthase, GI:18254400
357465	1	2252	2	2	212	2	1	At2g32730	7,00E-47	68415.m04005 26S proteasome regulatory subunit, putative contains similarity to 26S proteasome regulatory subunit S1 SP:O88761, GI:3288594 from [Rattus norvegicus]

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
357353	1	2262	3	1	555	1	1	At2g38010	4,00E-105	68415.m04666 ceramidase family protein contains Pfam domain, PF04734: Neutral/alkaline nonlysosomal ceramidase
353838	2	2263	3	1	5819	2	1	At1g07480	2,00E-10	68414.m00801 transcription factor IIA large subunit / TFIIA large subunit (TFIIA-L) identical to transcription factor IIA large subunit GI:2826884 from [Arabidopsis thaliana]
358992	1	2263	3	1	5819	2	1	At1g07480	4,00E-11	68414.m00801 transcription factor IIA large subunit / TFIIA large subunit (TFIIA-L) identical to transcription factor IIA large subunit GI:2826884 from [Arabidopsis thaliana]
355938	1	2266	2	2	2255	1	1	At5g65720	2,00E-13	68418.m08271 cysteine desulfurase, mitochondrial (NIFS) identical to Cysteine desulfurase, mitochondrial precursor (SP:O49543) {Arabidopsis thaliana}; identical to cDNA GI:12656131; contains Pfam profile PF00266: aminotransferase, class V
356075	1	2266	2	2	3276	1	1	At1g08490	8,00E-48	68414.m00940 cysteine desulfurase, putative similar to nitrogen fixation protein (nifS) GB:D64004 GI:1001701 from [Synechocystis sp]; contains TIGRFAM TIGR01364: phosphoserine aminotransferase; contains Pfam PF00266: aminotransferase, class V
358102	1	2271	2	2	1583	1	1	At1g71350	6,00E-47	68414.m08235 eukaryotic translation initiation factor SUI1 family protein weak similarity to SP|P41214 Ligatin (Hepatocellular carcinoma-associated antigen 56) {Homo sapiens}; contains Pfam profile PF01253: Translation initiation factor SUI1
353872	4	2273	1	3	157	1	2	At1g09620	7,00E-92	68414.m01079 tRNA synthetase class I (I, L, M and V) family protein similar to cytosolic leucyl-tRNA synthetase [Candida albicans] GI:9858190; contains Pfam profile PF00133: tRNA synthetases class I (I, L, M and V)
357595	1	2273	1	3	157	1	2	At1g09620	1,00E-33	68414.m01079 tRNA synthetase class I (I, L, M and V) family protein similar to cytosolic leucyl-tRNA synthetase [Candida albicans] GI:9858190; contains Pfam profile PF00133: tRNA synthetases class I (I, L, M and V)
358716	1	2274	2	2	7518	2	1	At1g58080	4,00E-20	68414.m06582 ATP phosphoribosyl transferase 1 (ATP-PRT1) identical to ATP phosphoribosyl transferase GI:6683617 from [Arabidopsis thaliana]
357035	1	2277	2	2				At1g10030	2,00E-49	68414.m01131 integral membrane family protein contains Pfam PF03694: Erg28 like protein

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358674	1	2287	2	2	5703	2	2	At1g12350	2,00E-48	68414.m01427 DNA/panthothenate metabolism flavoprotein family protein contains Pfam domain PF04127: DNA / pantothenate metabolism flavoprotein
359968	1	2289	1	3	9612	1	2	At1g12400	7,00E-18	68414.m01433 expressed protein
356411	1	2291	2	2	3098	2	1	At1g12640	2,00E-72	68414.m01468 membrane bound O-acyl transferase (MBOAT) family protein low similarity to porcupine from [Xenopus laevis] GI:6714514, GI:6714520, GI:6714518, GI:6714516; contains Pfam profile PF03062: MBOAT family
354385	4	2293	3	1	677	2	1	At3g25800	3,00E-96	68416.m03211 serine/threonine protein phosphatase 2A (PP2A) 65 KDa regulatory subunit A identical to protein phosphatase 2A 65 kDa regulatory subunit (pDF1) GI:683502 from [Arabidopsis thaliana]
355314	1	2293	3	1	677	2	1	At3g25800	6,00E-63	68416.m03211 serine/threonine protein phosphatase 2A (PP2A) 65 KDa regulatory subunit A identical to protein phosphatase 2A 65 kDa regulatory subunit (pDF1) GI:683502 from [Arabidopsis thaliana]
355409	1	2293	3	1	677	2	1	At3g25800	5,00E-22	68416.m03211 serine/threonine protein phosphatase 2A (PP2A) 65 KDa regulatory subunit A identical to protein phosphatase 2A 65 kDa regulatory subunit (pDF1) GI:683502 from [Arabidopsis thaliana]
353368	2	2294	4		10336	4	1	At3g02555	1,00E-08	68416.m00245 expressed protein
357261	1	2295	2	2	4623	2	1	At1g13560	7,00E-15	68414.m01589 aminoalcoholphosphotransferase (AAPT1) identical to aminoalcoholphosphotransferase GI:3661593 from [Arabidopsis thaliana]
354500	1	2300	2	2	2480	1	1	At1g15060	9,00E-22	68414.m01800 expressed protein
355207	1	2301	1	3	2133	1	1	At1g15110	7,00E-99	68414.m01804 phosphatidyl serine synthase family protein contains Pfam profile: PF03034 phosphatidyl serine synthase
353776	2	2302	2	2	9490	1	1	At1g15120	8,00E-33	68414.m01805 ubiquinol-cytochrome C reductase complex 7.8 kDa protein, putative / mitochondrial hinge protein, putative similar to SP|P48504 Ubiquinol-cytochrome C reductase complex 7.8 kDa protein (EC 1.10.2.2) (Mitochondrial hinge protein) (CR7) {Solanum tuberosum}; contains Pfam profile PF02320: Ubiquinol-cytochrome C reductase hinge protein
354745	1	2303	2	2	2572	1	1	At2g15900	2,00E-24	68415.m01822 phox (PX) domain-containing protein weak similarity to SP|Q9Y5W8 Sorting nexin 13 {Homo sapiens}; contains Pfam profiles PF00787: PX domain, PF02194: PXA domain

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355752	1	2303	2	2	2572	1	1	At2g15900	3,00E-37	68415.m01822 phox (PX) domain-containing protein weak similarity to SP|Q9Y5W8 Sorting nexin 13 {Homo sapiens}; contains Pfam profiles PF00787: PX domain, PF02194: PXA domain
353889	2	2304	2	2	1323	2	2	At1g80300	1,00E-35	68414.m09401 chloroplast ADP, ATP carrier protein 1 / ADP, ATP translocase 1 / adenine nucleotide translocase 1 (AATP1) identical to SP|Q39002 Chloroplast ADP,ATP carrier protein 1, chloroplast precursor (ADP/ATP translocase 1) (Adenine nucleotide translocase 1) {Arabidopsis thaliana}
353375	6	2306	2	2	8426	2	2	At2g32060	2,00E-50	68415.m03918 40S ribosomal protein S12 (RPS12C)
358660	1	2306	2	2	8426	2	2	At2g32060	1,00E-49	68415.m03918 40S ribosomal protein S12 (RPS12C)
358529	1	2307	3	1				At5g16630	1,00E-21	68418.m01947 DNA repair protein Rad4 family low similarity to SP|Q01831 DNA-repair protein complementing XP-C cells (Xeroderma pigmentosum group C complementing protein) {Homo sapiens}; contains Pfam profile PF03835: DNA repair protein Rad4
354098	2	2310	2	2	1483	1	1	At1g16720	2,00E-39	68414.m02005 expressed protein
357548	1	2315	2	2	6199	1	1	At1g17440	1,00E-23	68414.m02133 transcription initiation factor IID (TFIID) subunit A family protein similar to SP|Q16514 Transcription initiation factor TFIID 20/15 kDa subunits (TAFII-20/TAFII-15) {Homo sapiens}; contains Pfam profile PF03847: Transcription initiation factor TFIID subunit A
355282	1	2316	3	1	7665	2	1	At1g72650	2,00E-09	68414.m08402 myb family transcription factor contains Pfam PF00249: Myb-like DNA-binding domain
359662	1	2316	3	1	7665	2	1	At1g72650	7,00E-28	68414.m08402 myb family transcription factor contains Pfam PF00249: Myb-like DNA-binding domain
356901	1	2321	3	1	2927	3	1	At1g75110	4,00E-37	68414.m08723 expressed protein
359203	1	2323	2	2	4713	2	1	At1g27840	3,00E-81	68414.m03412 transducin family protein / WD-40 repeat family protein contains similarity to cockayne syndrome complementation group A protein GB:U28413 GI:975301 from [Homo sapiens]; confirmed by cDNA gi:1598289
354749	1	2328	4					At1g20870	7,00E-06	68414.m02614 expressed protein
354479	1	2333	2	2	7694	2	1	At1g78110	5,00E-09	68414.m09103 expressed protein
353066	3	2334	3	1	10418	3	3	At1g78170	4,00E-16	68414.m09109 expressed protein
358477	1	2342	3	1	3322	2	1	At1g70770	9,00E-09	68414.m08158 expressed protein
358496	1	2342	3	1	3322	2	1	At1g70770	1,00E-67	68414.m08158 expressed protein
359786	1	2353	2	2	6136	1	1	At1g27090	9,00E-20	68414.m03302 glycine-rich protein

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
354363	18	2354	2	2	6629	2	2	At1g67430	2,00E-82	68414.m07675 60S ribosomal protein L17 (RPL17B) similar to ribosomal protein GI:19101 from [Hordeum vulgare]
359267	1	2354	2	2	6629	2	2	At1g67430	3,00E-09	68414.m07675 60S ribosomal protein L17 (RPL17B) similar to ribosomal protein GI:19101 from [Hordeum vulgare]
353315	2	2359	3	1	9565	2	1	At1g28330	1,00E-18	68414.m03480 dormancy-associated protein, putative (DRM1) identical to dormancy-associated protein [Arabidopsis thaliana] GI:2995990; similar to dormancy-associated protein GI:2605887 from [Pisum sativum]; contains Pfam profile PF05564: Dormancy/auxin associated protein
354408	4	2359	3	1	9565	2	1	At2g33830	3,00E-13	68415.m04151 dormancy/auxin associated family protein contains Pfam profile: PF05564 dormancy/auxin associated protein
355876	1	2360	2	2	8075	1	1	At1g28510	5,00E-26	68414.m03505 expressed protein
358577	1	2362	2	2	9023	2	1	At4g14600	2,00E-11	68417.m02246 expressed protein
355953	1	2363	2	2	8627	1	1	At1g29810	2,00E-30	68414.m03644 dehydratase family similar to Pterin-4-alpha-carbinolamine dehydratase (EC 4.2.1.96) (PHS) (4-alpha-hydroxy-tetrahydropterin dehydratase) (Pterin carbinolamine dehydratase) (PCD). (Swiss-Prot:P43335) [Pseudomonas aeruginosa]; contains Pfam PF01329: pterin-4-alpha-carbinolamine dehydratase
358553	1	2365	1	3	4272	1	1	At1g30240	2,00E-06	68414.m03699 PELP1-related contains weak similarity to PELP1 [Homo sapiens] gi|21426922|gb|AAC17708
358722	1	2365	1	3	4272	1	1	At1g30240	1,00E-08	68414.m03699 PELP1-related contains weak similarity to PELP1 [Homo sapiens] gi|21426922|gb|AAC17708
356642	1	2368	2	2	4175	2	1	At1g30630	3,00E-80	68414.m03746 coatomer protein epsilon subunit family protein / COPE family protein similar to SP|O14579 Coatomer epsilon subunit (Epsilon-coat protein) (Epsilon-COP) from Homo sapiens, SP|Q60445 from Cricetulus griseus; ESTs gb|Z17908, gb|AA728673, gb|N96555, gb|H76335, gb|AA712463, gb|W43247, gb|T45611, gb|T21160, gb|T14119 and AI100483 come from this gene
357329	1	2371	2	2	5034	2	1	At3g59500	5,00E-58	68416.m06640 integral membrane HRF1 family protein contains Pfam domain PF03878: Hrf1 family

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354188	2	2380	2	2	303	1	1	At5g19690	7,00E-13	68418.m02342 oligosaccharyl transferase STT3 subunit family protein similar to SP|P39007 Oligosaccharyl transferase STT3 subunit {Saccharomyces cerevisiae}; contains Pfam profile PF02516: Oligosaccharyl transferase STT3 subunit
358217	1	2380	2	2	344	1	1	At1g34130	7,00E-43	68414.m04234 oligosaccharyl transferase STT3 subunit, putative similar to SP|P39007 Oligosaccharyl transferase STT3 subunit {Saccharomyces cerevisiae}; contains Pfam profile PF02516: Oligosaccharyl transferase STT3 subunit
354680	1	2385	1	3	407	1	1	At1g35220	2,00E-28	68414.m04368 expressed protein
357670	1	2385	1	3	407	1	1	At1g35220	4,00E-63	68414.m04368 expressed protein
355934	1	2387	2	2	7529	1	1	At4g30930	2,00E-21	68417.m04391 50S ribosomal protein L21, mitochondrial (RPL21M) identical to SP|Q8L9A0 50S ribosomal protein L21, mitochondrial precursor {Arabidopsis thaliana}
357091	1	2388	2	2	3083	1	2	At1g36730	1,00E-26	68414.m04569 eukaryotic translation initiation factor 5, putative / eIF-5, putative similar to SP|P55876 Eukaryotic translation initiation factor 5 (eIF-5) {Zea mays}; contains Pfam profiles PF02020: eIF4-gamma/eIF5/eIF2-epsilon, PF01873: Domain found in IF2B/IF5
354280	4	2393	2	2	1955	2	2	At1g61580	0	68414.m06939 60S ribosomal protein L3 (RPL3B) identical to ribosomal protein GI:806279 from [Arabidopsis thaliana]
355614	1	2393	2	2	1955	2	2	At1g61580	1,00E-73	68414.m06939 60S ribosomal protein L3 (RPL3B) identical to ribosomal protein GI:806279 from [Arabidopsis thaliana]
353230	2	2395	2	2	9084	1	1	At1g47310	3,00E-20	68414.m05238 expressed protein
357576	1	2400	2	2	6172	1	1	At1g49350	2,00E-20	68414.m05532 pfkB-type carbohydrate kinase family protein contains Pfam profile: PF00294 pfkB family carbohydrate kinase
356461	1	2400	2	2	8926	1	1	At5g60340	2,00E-19	68418.m07564 maoC-like dehydratase domain-containing protein contains similarity to (R)-specific enoyl-CoA hydratase PhaJ1 [Pseudomonas oleovorans] gi|22506675|gb|AAM97601; contains Pfam domain PF01575: MaoC like domain
354667	1	2410	2	2	7574	1	1	At1g53800	1,00E-10	68414.m06123 expressed protein
359480	1	2411	2	2	6203	1	1	At1g53345	3,00E-39	68414.m06047 expressed protein

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355286	1	2412	2	2	10381	2	1	At5g41010	4,00E-22	68418.m04985 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
357728	1	2416	2	2	5586	1	1	At1g54390	8,00E-40	68414.m06205 PHD finger protein-related contains low similarity to PHD-finger domain proteins
356480	1	2416	2	2	6998	1	1	At3g24010	2,00E-14	68416.m03016 PHD finger family protein contains Pfam profile: PF00628 PHD-finger
356755	1	2416	2	2	6998	1	1	At3g24010	1,00E-29	68416.m03016 PHD finger family protein contains Pfam profile: PF00628 PHD-finger
352905	2	2425	2	2	3894	1	1	At2g30700	3,00E-84	68415.m03745 expressed protein
358298	1	2425	2	2	4496	1	1	At1g61900	6,00E-62	68414.m06984 expressed protein contains similarity to glutamic acid/alanine-rich protein GI:6707830 from [Trypanosoma congolense]
358373	1	2429	2	2	5898	1	1	At4g01560	2,00E-66	68417.m00202 brix domain-containing protein contains Pfam domain, PF04427: Brix domain
353240	2	2435	2	2	992	2	1	At4g26300	7,00E-72	68417.m03783 arginyl-tRNA synthetase, putative / arginine--tRNA ligase, putative similar to SP|P37880 Arginyl-tRNA synthetase (EC 6.1.1.19) (Arginine--tRNA ligase) (ArgRS) {Cricetulus longicaudatus}; contains Pfam profiles PF00750: arginyl-tRNA synthetase, PF03485: arginyl-tRNA synthetase N-terminal domain
359900	1	2435	2	2	992	2	1	At4g26300	1,00E-43	68417.m03783 arginyl-tRNA synthetase, putative / arginine--tRNA ligase, putative similar to SP|P37880 Arginyl-tRNA synthetase (EC 6.1.1.19) (Arginine--tRNA ligase) (ArgRS) {Cricetulus longicaudatus}; contains Pfam profiles PF00750: arginyl-tRNA synthetase, PF03485: arginyl-tRNA synthetase N-terminal domain
357526	1	2439	2	2	2727	1	1	At5g01920	7,00E-53	68418.m00111 protein kinase family protein contains eukaryotic protein kinase domain, INTERPRO:IPR000719
359017	1	2441	2	2	5332	1	1	At1g69380	3,00E-34	68414.m07964 expressed protein predicated by genscan+
358959	1	2446	2	2	1155	1	1	At4g36390	8,00E-20	68417.m05170 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

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
354165	2	2447	2	2	4665	2	2	At1g72370	7,00E-74	68414.m08371 40S ribosomal protein SA (RPSaA) identical to laminin receptor-like protein GB:U01955 [Arabidopsis thaliana]; identical to cDNA laminin receptor homologue GI:16379
357860	1	2447	2	2	4665	2	2	At1g72370	4,00E-63	68414.m08371 40S ribosomal protein SA (RPSaA) identical to laminin receptor-like protein GB:U01955 [Arabidopsis thaliana]; identical to cDNA laminin receptor homologue GI:16379
352976	2	2449	2	2	6705	1	1	At4g14930	4,00E-53	68417.m02293 acid phosphatase survival protein SurE, putative similar to Swiss-Prot:P36664 acid phosphatase surE (EC 3.1.3.2) (Stationary-phase survival protein surE) [Escherichia coli O157:H7]; contains Pfam domain PF01975: Survival protein SurE
353301	2	2452	2	2	9529	1	1	At1g73940	2,00E-29	68414.m08563 expressed protein
359123	1	2456	2	2	7623	1	1	At1g74970	1,00E-46	68414.m08703 ribosomal protein S9 (RPS9) identical to ribosomal protein S9 [Arabidopsis thaliana] GI:5456946
354258	2	2457	2	2	3743	1	1	At1g75330	9,00E-114	68414.m08750 ornithine carbamoyltransferase, chloroplast / ornithine transcarbamylase / OTCase (OTC) identical to SP|O50039 Ornithine carbamoyltransferase, chloroplast precursor (EC 2.1.3.3) (OTCase) (Ornithine transcarbamylase) {Arabidopsis thaliana}
354045	2	2458	2	2	6715	1	1	At1g75510	2,00E-75	68414.m08774 transcription initiation factor IIF beta subunit (TFIIF-beta) family protein contains Pfam profile: PF02270 transcription initiation factor IIF, beta subunit
357592	1	2460	2	2	4256	2	1	At2g44270	6,00E-44	68415.m05509 expressed protein contains Pfam profile PF01171: PP-loop family
353994	2	2470	2	2	5	1	2	At1g80070	4,00E-76	68414.m09373 splicing factor, putative strong similarity to splicing factor Prp8 [Homo sapiens] GI:3661610; contains Pfam profile PF01398: Mov34/MPN/PAD-1 family
354579	1	2472	2	2	4495	1	1	At1g80950	7,00E-51	68414.m09498 phospholipid/glycerol acyltransferase family protein low similarity to SP|Q59601 1-acyl-sn-glycerol-3-phosphate acyltransferase (EC 2.3.1.51) {Neisseria gonorrhoeae}; contains Pfam profile PF01553: Acyltransferase
358367	1	2475	2	2	4854	1	1	At5g62270	3,00E-12	68418.m07818 expressed protein
353452	2	2478	2	2	7448	1	1	At4g28030	4,00E-36	68417.m04021 GCN5-related N-acetyltransferase (GNAT) family protein contains Pfam profile PF00583: acetyltransferase, GNAT family

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
356455	1	2478	2	2	7448	1	1	At4g28030	5,00E-27	68417.m04021 GCN5-related N-acetyltransferase (GNAT) family protein contains Pfam profile PF00583: acetyltransferase, GNAT family
353331	2	2478	2	2	7606	1	1	At2g06025	2,00E-63	68415.m00659 GCN5-related N-acetyltransferase (GNAT) family protein low similarity to streptothricin acetyltransferase homolog [Campylobacter jejuni] GI:6650363; contains Pfam profile PF00583: acetyltransferase, GNAT family
352947	2	2480	2	2	1835	1	1	At4g33680	4,00E-67	68417.m04784 aminotransferase class I and II family protein low similarity to Aromatic Aminotransferase from Pyrococcus horikoshii GP|14278621; contains Pfam profile PF00155 aminotransferase, classes I and II
354687	1	2482	1	3	8871	1	3	At2g14110	3,00E-43	68415.m01571 expressed protein
356414	1	2486	2	2	5253	2	1	At2g16800	1,00E-50	68415.m01926 high-affinity nickel-transport family protein contains Pfam domain, PF03824: High-affinity nickel-transport protein
354865	1	2487	2	2	3175	1	1	At2g16940	7,00E-46	68415.m01952 RNA recognition motif (RRM)-containing protein
357956	1	2487	2	2	3175	1	1	At2g16940	1,00E-32	68415.m01952 RNA recognition motif (RRM)-containing protein
355465	1	2488	2	2	3715	2	2	At2g17200	5,00E-24	68415.m01986 ubiquitin family protein weak similarity to PLIC-2 (ubiquitin-like type II) [Homo sapiens] GI:9937505; contains Pfam profiles PF00240: Ubiquitin family, PF00627: UBA/TS-N domain
356528	1	2493	2	2				At4g36210	3,00E-23	68417.m05152 expressed protein contains Pfam PF05277: Protein of unknown function (DUF726)
353406	2	2494	2	2	2291	1	1	At2g18220	5,00E-08	68415.m02123 expressed protein contains Pfam domain PF03715: Uncharacterised protein family (UPF0120)
359455	1	2494	2	2	4963	1	1	At3g55510	6,00E-32	68416.m06164 expressed protein
356903	1	2495	2	2	5062	1	1	At3g19970	1,00E-31	68416.m02527 expressed protein
356488	1	2498	2	2	8876	2	1	At4g30330	1,00E-22	68417.m04311 small nuclear ribonucleoprotein E, putative / snRNP-E, putative / Sm protein E, putative similar to SWISS-PROT:P08578 small nuclear ribonucleoprotein E (snRNP-E) (Sm protein E, Sm-E, SmE) [Chicken]
353643	3	2499	2	2	6312	2	1	At5g05670	4,00E-67	68418.m00624 expressed protein
353198	2	2502	3	1	9534	3	1	At5g56670	2,00E-22	68418.m07074 40S ribosomal protein S30 (RPS30C)
354117	2	2502	3	1	9534	3	1	At5g56670	9,00E-22	68418.m07074 40S ribosomal protein S30 (RPS30C)
357637	1	2503	1	3	117	1	2	At2g20190	7,00E-59	68415.m02361 CLIP-associating protein (CLASP) -related similar to CLIP-associating protein CLASP2 (GI:13508651) [Rattus norvegicus]

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
358424	1	2503	1	3	117	1	2	At2g20190	3,00E-63	68415.m02361 CLIP-associating protein (CLASP) -related similar to CLIP-associating protein CLASP2 (GI:13508651) [Rattus norvegicus]
353530	4	2505	2	2	7926	2	2	At2g20450	4,00E-49	68415.m02387 60S ribosomal protein L14 (RPL14A)
354082	7	2505	2	2	7926	2	2	At4g27090	1,00E-55	68417.m03894 60S ribosomal protein L14 (RPL14B) ribosomal protein L14 - Human,PIR3:JC5954
353217	2	2512	2	2	9174	2	2	At2g23930	3,00E-24	68415.m02857 small nuclear ribonucleoprotein G, putative / snRNP-G, putative / Sm protein G, putative similar to small nuclear ribonucleoprotein G (snRNP-G, Sm protein G, Sm-G, SmG) [Homo sapiens] SWISS-PROT:Q15357
359776	1	2512	2	2	9174	2	2	At2g23930	2,00E-34	68415.m02857 small nuclear ribonucleoprotein G, putative / snRNP-G, putative / Sm protein G, putative similar to small nuclear ribonucleoprotein G (snRNP-G, Sm protein G, Sm-G, SmG) [Homo sapiens] SWISS-PROT:Q15357
353521	2	2514	2	2	3928	2	1	At4g31420	1,00E-37	68417.m04461 zinc finger (C2H2 type) family protein contains Pfam profile: PF00096 zinc finger, C2H2 type
354542	1	2514	2	2	3928	2	1	At4g31420	9,00E-34	68417.m04461 zinc finger (C2H2 type) family protein contains Pfam profile: PF00096 zinc finger, C2H2 type
356759	1	2514	2	2	3928	2	1	At4g31420	3,00E-26	68417.m04461 zinc finger (C2H2 type) family protein contains Pfam profile: PF00096 zinc finger, C2H2 type
359113	1	2516	3	1	4039	2	1	At4g32160	4,00E-54	68417.m04574 phox (PX) domain-containing protein contains Pfam profile PF00787: PX domain
355449	1	2518	2	2	102	2	2	At2g26080	5,00E-50	68415.m03131 glycine dehydrogenase [decarboxylating], putative / glycine decarboxylase, putative / glycine cleavage system P-protein, putative strong similarity to SP|P26969 Glycine dehydrogenase [decarboxylating], mitochondrial precursor (EC 1.4.4.2) {Pisum sativum}; contains Pfam profile PF02347: Glycine cleavage system P-protein
359179	1	2523	2	2	1736	1	1	At2g30390	5,00E-24	68415.m03698 ferrochelatase II identical to Swiss-Prot:O04921 ferrochelatase II, chloroplast precursor (EC 4.99.1.1) (Protoheme ferro-lyase) (Heme synthetase) [Arabidopsis thaliana]
359908	1	2526	2	2	2876	1	1	At5g16290	1,00E-82	68418.m01904 acetolactate synthase small subunit, putative similar to gi:5931761 from Nicotiana plumbaginifolia
354405	2	2530	2	2	814	1	1	At2g34357	6,00E-37	68415.m04206 expressed protein
357984	1	2533	2	2	5493	2	1	At2g39570	1,00E-44	68415.m04854 ACT domain-containing protein contains Pfam ACT domain PF01842

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
358830	1	2534	2	2	1825	2	1	At2g37160	3,00E-24	68415.m04559 transducin family protein / WD-40 repeat family protein contains 4 WD-40 repeats (PF00400); similar to Dystrophia myotonica-containing WD repeat motif protein DMR-N9 protein (DMWD) (DM9) (SP:Q08274) [Mus musculus]; simlar to DMR protein GI:18028289 [Homo sapiens];
353169	26	2535	2	2	5905	2	2	At2g37270	2,00E-94	68415.m04572 40S ribosomal protein S5 (RPS5A) identical to GP:3043428
356256	1	2541	3	1	4220	1	1	At3g17900	1,00E-27	68416.m02280 expressed protein
354709	1	2544	2	2				At2g39800	3,00E-36	68415.m04887 delta 1-pyrroline-5-carboxylate synthetase A / P5CS A (P5CS1) identical to SP:P54887:P5C1_ARATH
355083	1	2545	2	2	4325	1	1	At3g55620	7,00E-40	68416.m06178 eukaryotic translation initiation factor 6, putative / eIF-6, putative similar to SP|O55135 Eukaryotic translation initiation factor 6 (eIF-6) (B4 integrin interactor) {Mus musculus}; contains Pfam profile PF01912: eIF-6 family
353583	2	2546	2	2	3707	1	2	At5g05470	2,00E-93	68418.m00589 eukaryotic translation initiation factor 2 subunit 1, putative / eIF-2A, putative / eIF-2-alpha, putative similar to SWISS-PROT:P20459 eukaryotic translation initiation factor 2 alpha subunit (eIF-2- alpha) [Saccharomyces cerevisiae]; identical to cDNA cohesin GI:6682280
356175	1	2548	2	2	276	1	1	At2g40840	1,00E-94	68415.m05042 glycoside hydrolase family 77 protein contains Pfam profiles PF02446: 4-alpha-glucanotransferase, PF00686: Starch binding domain; contains a non-consensus AT-AC intron between at intron 5
354793	1	2549	3	1	7941	3	1	At2g41050	8,00E-17	68415.m05069 PQ-loop repeat family protein / transmembrane family protein similar to SP|Q10482 Seven transmembrane protein 1 {Schizosaccharomyces pombe}; contains Pfam profile PF04193: PQ loop repeat
359322	1	2549	3	1	7941	3	1	At2g41050	6,00E-32	68415.m05069 PQ-loop repeat family protein / transmembrane family protein similar to SP|Q10482 Seven transmembrane protein 1 {Schizosaccharomyces pombe}; contains Pfam profile PF04193: PQ loop repeat
353132	2	2550	2	2	5667	2	1	At3g56740	1,00E-83	68416.m06311 ubiquitin-associated (UBA)/TS-N domain-containing protein contains Pfam profile PF00627: UBA/TS-N domain
354980	1	2551	2	2				At4g14270	7,00E-13	68417.m02200 expressed protein

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
357651	1	2554	3	1				At5g18250	2,00E-40	68418.m02145 expressed protein similar to unknown protein (dbj|BAA90342.1)
353653	2	2555	2	2	1261	2	2	At2g41960	2,00E-14	68415.m05191 expressed protein
356823	1	2558	2	2	1997	2	2	At3g57890	3,00E-53	68416.m06453 tubulin-specific chaperone C-related contains weak similarity to Tubulin-specific chaperone C (Tubulin-folding cofactor C) (CFC) (Swiss-Prot:Q15814) [Homo sapiens]
357482	1	2558	2	2	1997	2	2	At3g57890	9,00E-48	68416.m06453 tubulin-specific chaperone C-related contains weak similarity to Tubulin-specific chaperone C (Tubulin-folding cofactor C) (CFC) (Swiss-Prot:Q15814) [Homo sapiens]
356819	1	2559	2	2	10337	2	2	At2g42260	2,00E-09	68415.m05231 expressed protein and genefinder
354262	2	2560	2	2	6081	1	1	At2g42710	6,00E-69	68415.m05289 ribosomal protein L1 family protein
358879	1	2561	2	2	5828	1	1	At2g43030	1,00E-82	68415.m05340 ribosomal protein L3 family protein contains Pfam profile PF00297: ribosomal protein L3
356188	1	2566	2	2	4936	2	1	At3g59890	2,00E-25	68416.m06683 dihydrodipicolinate reductase family protein weak similarity to SP|Q52419 Dihydrodipicolinate reductase (EC 1.3.1.26) (DHPR) {Pseudomonas syringae}; contains Pfam profiles PF01113: Dihydrodipicolinate reductase N-terminus, PF05173: Dihydrodipicolinate reductase C-terminus
354721	1	2567	2	2	1839	2	1	At3g59910	2,00E-79	68416.m06686 expressed protein
359355	1	2568	2	2	3286	1	1	At3g60070	6,00E-72	68416.m06708 lactose permease-related contains weak similarity to Lactose permease (Lactose-proton symport) (Lactose transport protein). (Swiss-Prot:O33814) [Staphylococcus xylosus]
355541	1	2570	2	2	6540	1	1	At5g38460	8,00E-51	68418.m04649 ALG6, ALG8 glycosyltransferase family protein similar to SP|Q9Y672 Dolichyl pyrophosphate Man9GlcNAc2 alpha-1,3-glucosyltransferase (EC 2.4.1.-) (Dolichyl-P-Glc:Man9GlcNAc2-PP-dolichyl glucosyltransferase) {Homo sapiens}; contains Pfam profile PF03155: ALG6, ALG8 glycosyltransferase family
358288	1	2573	2	2	402	2	1	At2g45290	2,00E-27	68415.m05637 transketolase, putative strong similarity to transketolase 1 [Capsicum annuum] GI:3559814; contains Pfam profiles PF02779: Transketolase, pyridine binding domain, PF02780: Transketolase, C-terminal domain, PF00456: Transketolase, thiamine diphosphate binding domain

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358745	1	2574	2	2	3409	2	1	At2g45440	3,00E-105	68415.m05652 dihydrodipicolinate synthase 2 (DHDPS2) identical to dihydrodipicolinate synthase 2 (DHDPS2) [Arabidopsis thaliana] GI:11066382
359699	1	2576	2	2	3372	2	1	At3g61530	3,00E-76	68416.m06892 ketopantoate hydroxymethyltransferase family protein similar to SP|Q9Y7B6 3-methyl-2-oxobutanoate hydroxymethyltransferase (EC 2.1.2.11) (Ketopantoate hydroxymethyltransferase) {Emericella nidulans}; contains Pfam profile PF02548: Ketopantoate hydroxymethyltransferase
353873	2	2578	2	2	4408	2	1	At3g62870	2,00E-73	68416.m07063 60S ribosomal protein L7A (RPL7aB) 60S RIBOSOMAL PROTEIN L7A - Oryza sativa, SWISSPROT:RL7A_ORYSA
354110	12	2578	2	2	4408	2	1	At3g62870	7,00E-89	68416.m07063 60S ribosomal protein L7A (RPL7aB) 60S RIBOSOMAL PROTEIN L7A - Oryza sativa, SWISSPROT:RL7A_ORYSA
355639	1	2578	2	2	4408	2	1	At2g47610	1,00E-06	68415.m05940 60S ribosomal protein L7A (RPL7aA)
359270	1	2578	2	2	4408	2	1	At2g47610	8,00E-58	68415.m05940 60S ribosomal protein L7A (RPL7aA)
354400	2	2587	2	2	6429	2	2	At3g02950	4,00E-35	68416.m00290 expressed protein
357708	1	2589	2	2	2283	1	1	At4g19860	3,00E-55	68417.m02910 lecithin:cholesterol acyltransferase family protein / LACT family protein similar to lysosomal phospholipase A2 [Mus musculus] GI:18699602; contains Pfam profile PF02450: Lecithin:cholesterol acyltransferase (phosphatidylcholine-sterol acyltransferase)
357867	1	2589	2	2	2708	1	1	At3g03310	3,00E-54	68416.m00329 lecithin:cholesterol acyltransferase family protein / LACT family protein weak similarity to LCAT-like lysophospholipase (LLPL) [Homo sapiens] GI:4589720; contains Pfam profile PF02450: Lecithin:cholesterol acyltransferase (phosphatidylcholine-sterol acyltransferase)
356433	1	2593	1	3	91	1	1	At3g04740	3,00E-36	68416.m00510 expressed protein (SWP1)
353780	2	2594	2	2	918	1	1	At4g14210	2,00E-127	68417.m02193 phytoene dehydrogenase, chloroplast / phytoene desaturase (PDS) identical to SP|Q07356 Phytoene dehydrogenase, chloroplast precursor (EC 1.14.99.-) (Phytoene desaturase){Arabidopsis thaliana}; high similarity to phytoene desaturase [Lycopersicon esculentum][GI:19287]
352916	2	2595	2	2	6981	2	1	At5g27430	1,00E-62	68418.m03274 signal peptidase subunit family protein contains Pfam profile: PF04573 signal peptidase subunit

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355124	1	2595	2	2	6981	2	1	At5g27430	5,00E-23	68418.m03274 signal peptidase subunit family protein contains Pfam profile: PF04573 signal peptidase subunit
355238	1	2595	2	2	6981	2	1	At5g27430	6,00E-66	68418.m03274 signal peptidase subunit family protein contains Pfam profile: PF04573 signal peptidase subunit
354344	2	2598	2	2	9837	2	2	At3g06680	2,00E-24	68416.m00788 60S ribosomal protein L29 (RPL29B) similar to 60S ribosomal protein L29 GB:P25886 from (Rattus norvegicus)
354180	2	2601	1	3	5597	1	2	At3g07950	1,00E-62	68416.m00972 rhomboid protein-related contains 6 transmembrane domains; similar to phosphatidyl inositol glycan class T (GI:14456615) [Homo sapiens]
359995	1	2601	1	3	5597	1	2	At3g07950	4,00E-16	68416.m00972 rhomboid protein-related contains 6 transmembrane domains; similar to phosphatidyl inositol glycan class T (GI:14456615) [Homo sapiens]
357648	1	2602	2	2	12	2	2	At3g11130	2,00E-24	68416.m01349 clathrin heavy chain, putative similar to Swiss-Prot:Q00610 clathrin heavy chain 1 (CLH-17) [Homo sapiens]
358581	1	2605	2	2	1380	1	1	At3g10050	8,00E-101	68416.m01205 threonine ammonia-lyase / threonine dehydratase / threonine deaminase (OMR1) identical to SP|Q9ZSS6 Threonine dehydratase biosynthetic, chloroplast precursor (EC 4.3.1.19, formerly EC 4.2.1.16) (Threonine deaminase) (TD) {Arabidopsis thaliana}
358181	1	2606	2	2	2001	1	1	At3g10230	4,00E-65	68416.m01224 lycopene beta cyclase (LYC) identical to lycopene beta cyclase GI:1399183|GB:AAB53337 [Arabidopsis thaliana]
352894	2	2606	2	2	2054	1	1	At5g57030	3,00E-64	68418.m07118 lycopene epsilon cyclase identical to lycopene epsilon cyclase [GI:1399181]
355185	1	2606	2	2	2054	1	1	At5g57030	2,00E-72	68418.m07118 lycopene epsilon cyclase identical to lycopene epsilon cyclase [GI:1399181]
359636	1	2609	2	2	9881	2	2	At5g05370	8,00E-28	68418.m00579 ubiquinol-cytochrome C reductase complex ubiquinone-binding protein, putative / ubiquinol-cytochrome C reductase complex 8.2 kDa protein, putative strong similarity to SP|P46269 Ubiquinol-cytochrome C reductase complex ubiquinone-binding protein QP-C (EC 1.10.2.2) (Ubiquinol-cytochrome C reductase complex 8.2 kDa protein) {Solanum tuberosum}

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359987	1	2609	2	2	9881	2	2	At5g05370	1,00E-24	68418.m00579 ubiquinol-cytochrome C reductase complex ubiquinone-binding protein, putative / ubiquinol-cytochrome C reductase complex 8.2 kDa protein, putative strong similarity to SP|P46269 Ubiquinol-cytochrome C reductase complex ubiquinone-binding protein QP-C (EC 1.10.2.2) (Ubiquinol-cytochrome C reductase complex 8.2 kDa protein) {Solanum tuberosum}
355211	1	2610	2	2				At3g60245	1,00E-44	68416.m06733 60S ribosomal protein L37a (RPL37aC)
358828	1	2610	2	2				At3g60245	3,00E-23	68416.m06733 60S ribosomal protein L37a (RPL37aC)
354557	1	2611	2	2	4948	1	1	At3g11400	1,00E-29	68416.m01390 eukaryotic translation initiation factor 3G / eIF3g nearly identical to eukaryotic translation initiation factor 3g [Arabidopsis thaliana] GI:12407751
355241	1	2613	2	2	617	2	2	At3g13300	1,00E-46	68416.m01675 transducin family protein / WD-40 repeat family protein contains 2 WD-40 repeats (PF00400); autoantigen locus HUMAUTANT (GI:533202) [Homo sapiens] and autoantigen locus HSU17474 (GI:596134) [Homo sapiens]
355100	1	2614	3	1				At5g01780	1,00E-16	68418.m00097 oxidoreductase, 2OG-Fe(II) oxygenase family protein low similarity to alkB protein - Escherichia coli, PIR:BVECKB, alkB [Caulobacter crescentus][GI:2055386]; contains Pfam domain PF03171 2OG-Fe(II) oxygenase superfamily
358056	1	2616	1	3	10198	1	2	At3g15353	9,00E-10	68416.m01944 metallothionein protein, putative
353411	5	2621	2	2	1487	2	2	At3g19240	1,00E-171	68416.m02441 expressed protein
355294	1	2629	2	2	2288	1	1	At3g24530	4,00E-56	68416.m03080 AAA-type ATPase family protein / ankyrin repeat family protein contains Pfam profiles: PF00023 ankyrin repeat, PF00004 ATPase family associated with various cellular activities (AAA)
359145	1	2630	2	2	1411	2	2	At3g24880	2,00E-18	68416.m03120 expressed protein
353657	8	2633	2	2	4036	2	2	At5g39740	7,00E-105	68418.m04813 60S ribosomal protein L5 (RPL5B) ribosomal protein L5, rice
353672	2	2633	2	2	4036	2	2	At5g39740	3,00E-51	68418.m04813 60S ribosomal protein L5 (RPL5B) ribosomal protein L5, rice
354271	3	2633	2	2	4036	2	2	At5g39740	2,00E-56	68418.m04813 60S ribosomal protein L5 (RPL5B) ribosomal protein L5, rice
355950	1	2635	2	2	5761	2	2	At3g26890	1,00E-11	68416.m03365 expressed protein
357423	1	2637	2	2	289	1	1	At3g46970	4,00E-55	68416.m05100 starch phosphorylase, putative similar to alpha-glucan phosphorylase, H isozyme SP:P32811 from [Solanum tuberosum]

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
354438	2	2637	2	2	299	1	1	At3g29320	2,00E-95	68416.m03682 glucan phosphorylase, putative similar to alpha-glucan phosphorylase, L isozyme 1 precursor GB:P04045 from [Solanum tuberosum] (J. Biochem. 106 (4), 691-695 (1989))
355375	1	2637	2	2	299	1	1	At3g29320	4,00E-41	68416.m03682 glucan phosphorylase, putative similar to alpha-glucan phosphorylase, L isozyme 1 precursor GB:P04045 from [Solanum tuberosum] (J. Biochem. 106 (4), 691-695 (1989))
355925	1	2637	2	2	299	1	1	At3g29320	5,00E-74	68416.m03682 glucan phosphorylase, putative similar to alpha-glucan phosphorylase, L isozyme 1 precursor GB:P04045 from [Solanum tuberosum] (J. Biochem. 106 (4), 691-695 (1989))
358254	1	2637	2	2	299	1	1	At3g29320	3,00E-87	68416.m03682 glucan phosphorylase, putative similar to alpha-glucan phosphorylase, L isozyme 1 precursor GB:P04045 from [Solanum tuberosum] (J. Biochem. 106 (4), 691-695 (1989))
356176	1	2638	2	2	5963	1	1	At3g43540	3,00E-30	68416.m04623 expressed protein hypothetical protein slr1699 - Synechocystis sp. (strain PCC 6803), PIR:S75306
354783	1	2645	1	3	6313	1	2	At3g47630	1,00E-42	68416.m05185 expressed protein
357798	1	2645	1	3	6313	1	2	At3g47630	1,00E-13	68416.m05185 expressed protein
353674	3	2651	2	2	8210	2	1	At3g49410	1,00E-51	68416.m05401 transcription factor-related contains weak similarity to transcription factor IIIC63 (GI:5281316) [Homo sapiens]
353801	2	2655	3	1	4483	2	1	At3g50820	2,00E-49	68416.m05565 oxygen-evolving enhancer protein, chloroplast, putative / 33 kDa subunit of oxygen evolving system of photosystem II, putative (PSBO2) identical to SP:Q9S841 Oxygen-evolving enhancer protein 1-2, chloroplast precursor (OEE1) [Arabidopsis thaliana]; strong similarity to SP|P23321 Oxygen-evolving enhancer protein 1-1, chloroplast precursor (OEE1) (33 kDa subunit of oxygen evolving system of photosystem II) (OEC 33 kDa subunit) (33 kDa thylakoid membrane protein) {Arabidopsis thaliana}
354346	3	2656	2	2				At3g51140	2,00E-55	68416.m05600 expressed protein
353612	3	2661	2	2	9236	2	2	At5g27700	6,00E-37	68418.m03322 40S ribosomal protein S21 (RPS21C) ribosomal protein S21, Zea mays, PIR:T03945
358953	1	2661	2	2	9236	2	2	At5g27700	3,00E-37	68418.m03322 40S ribosomal protein S21 (RPS21C) ribosomal protein S21, Zea mays, PIR:T03945
356145	1	2663	2	2	6143	2	2	At3g55000	8,00E-42	68416.m06104 tonneau family protein similar to tonneau 1b (GI:11494367) [Arabidopsis thaliana]

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
353163	4	2664	2	2	103	2	1	At3g55410	8,00E-167	68416.m06154 2-oxoglutarate dehydrogenase E1 component, putative / oxoglutarate decarboxylase, putative / alpha-ketoglutaric dehydrogenase, putative similar to SP|P20967 2-oxoglutarate dehydrogenase E1 component, mitochondrial precursor (EC 1.2.4.2) (Alpha-ketoglutarate dehydrogenase) {Saccharomyces cerevisiae}; contains Pfam profiles PF02779: Transketolase, pyridine binding domain, PF00676: Dehydrogenase E1 component
359821	1	2667	1	3	2366	1	3	At3g57290	4,00E-93	68416.m06377 eukaryotic translation initiation factor 3E / eIF3e (TIF3E1) identical to eukaryotic initiation factor 3E subunit [Arabidopsis thaliana] gi|12407658|gb|AAG53613
355585	1	2668	2	2	8463	1	1	At3g58170	5,00E-48	68416.m06486 Bet1-like SNARE 1-1 / Bet1 / Sft1-like SNARE 14a / BS14a (BET11) identical to SP|Q9M2J9 Bet1-like SNARE 1-1 (AtBET11) (Bet1/Sft1-like SNARE 14a) (AtBS14a) [Mouse-ear cress] {Arabidopsis thaliana}; supporting cDNA gi|14030602|gb|AF368175.1|AF368175
359503	1	2669	2	2	4198	1	1	At5g62030	1,00E-06	68418.m07786 diphthamide synthesis DPH2 family protein contains InterPro accession IPR002728: Diphthamide synthesis DPH2 protein
356504	1	2674	2	2				At3g62130	2,00E-19	68416.m06981 epimerase-related contains weak similarity to isopenicillin N epimerase (Swiss-Prot:P18549) [Streptomyces clavuligerus]
356520	1	2680	2	2	1863	1	1	At4g01210	3,00E-27	68417.m00159 glycosyltransferase family protein 1 contains Pfam profile: PF00534 Glycosyl transferases group 1
359459	1	2681	2	2	3721	1	1	At5g14220	3,00E-23	68418.m01661 protoporphyrinogen oxidase, putative similar to protoporphyrinogen IX oxidase, mitochondrial (PPO II) from Nicotiana tabacum [SP|O24164], Glycine max, AB025102, Spinacia oleracea [GI:14349153]; contains Pfam amine oxidase, flavin-containing domain [PF015930]
357695	1	2683	3	1	4269	2	1	At5g06350	2,00E-30	68418.m00711 expressed protein
358822	1	2684	2	2	1346	1	1	At5g12200	1,00E-11	68418.m01431 dihydropyrimidinase / DHPase / dihydropyrimidine amidohydrolase / hydantoinase (PYD2) identical to dihydropyrimidine amidohydrolase (PYD2) [Arabidopsis thaliana] GI:28194047; similar to SP|Q9EQF5 Dihydropyrimidinase (EC 3.5.2.2) (DHPase) (Hydantoinase) (DHP) {Mus musculus}; contains Pfam profile PF01979: Amidohydrolase family

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
357653	1	2689	2	2	4577	2	1	At4g11260	7,00E-27	68417.m01822 phosphatase-related low similarity to protein phosphatase T [Saccharomyces cerevisiae] GI:897806; contains Pfam profiles PF00515: TPR Domain, PF05002: SGS domain, PF04969: CS domain
353771	2	2690	1	3	1756	1	3	At4g11820	1,00E-80	68417.m01882 hydroxymethylglutaryl-CoA synthase / HMG-CoA synthase / 3-hydroxy-3-methylglutaryl coenzyme A synthase identical to Hydroxymethylglutaryl-CoA synthase (EC 4.1.3.5) (HMG-CoA synthase) (3-hydroxy-3-methylglutaryl coenzyme A synthase) (Swiss-Prot:P54873) [Arabidopsis thaliana]
355754	1	2690	1	3	1756	1	3	At4g11820	2,00E-69	68417.m01882 hydroxymethylglutaryl-CoA synthase / HMG-CoA synthase / 3-hydroxy-3-methylglutaryl coenzyme A synthase identical to Hydroxymethylglutaryl-CoA synthase (EC 4.1.3.5) (HMG-CoA synthase) (3-hydroxy-3-methylglutaryl coenzyme A synthase) (Swiss-Prot:P54873) [Arabidopsis thaliana]
357410	1	2690	1	3	1756	1	3	At4g11820	9,00E-13	68417.m01882 hydroxymethylglutaryl-CoA synthase / HMG-CoA synthase / 3-hydroxy-3-methylglutaryl coenzyme A synthase identical to Hydroxymethylglutaryl-CoA synthase (EC 4.1.3.5) (HMG-CoA synthase) (3-hydroxy-3-methylglutaryl coenzyme A synthase) (Swiss-Prot:P54873) [Arabidopsis thaliana]
357444	1	2690	1	3	1756	1	3	At4g11820	9,00E-29	68417.m01882 hydroxymethylglutaryl-CoA synthase / HMG-CoA synthase / 3-hydroxy-3-methylglutaryl coenzyme A synthase identical to Hydroxymethylglutaryl-CoA synthase (EC 4.1.3.5) (HMG-CoA synthase) (3-hydroxy-3-methylglutaryl coenzyme A synthase) (Swiss-Prot:P54873) [Arabidopsis thaliana]
357260	1	2692	1	3	4917	1	1	At4g12740	2,00E-21	68417.m02001 adenine-DNA glycosylase-related / MYH-related similar to MYH (GI:18845094) [Rattus norvegicus]; similar to adenine-DNA glycosylase (GI:12656850) [Mus musculus]; contains TIGRFAM profile TIGR01084: A/G-specific adenine glycosylase (hits below the trusted cutoff)

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
359193	1	2692	1	3	4917	1	1	At4g12740	9,00E-15	68417.m02001 adenine-DNA glycosylase-related / MYH-related similar to MYH (GI:18845094) [Rattus norvegicus]; similar to adenine-DNA glycosylase (GI:12656850) [Mus musculus]; contains TIGRFAM profile TIGR01084: A/G-specific adenine glycosylase (hits below the trusted cutoff)
353783	2	2695	2	2	1167	1	1	At5g39840	5,00E-58	68418.m04828 ATP-dependent RNA helicase, mitochondrial, putative similar to mitochondrial RNA helicase [Arabidopsis thaliana] GI:5823579; contains Pfam profile PF00271: Helicase conserved C-terminal domain
358870	1	2696	3	1	2542	1	1	At4g15475	2,00E-25	68417.m02365 F-box family protein (FBL4) 99.7% identical to F-box protein family, AtFBL4 (GP:21536497) [Arabidopsis thaliana]; similar to grr1 GI:2407790 from [Glycine max]
353841	2	2697	1	3	256	1	2	At4g15530	1,00E-79	68417.m02373 pyruvate phosphate dikinase family protein contains Pfam profiles: PF01326 pyruvate phosphate dikinase, PEP/pyruvate binding domain, PF02896 PEP-utilizing enzyme, TIM barrel domain
355482	1	2700	3	1	5809	1	1	At5g47120	4,00E-30	68418.m05809 Bax inhibitor-1 putative / BI-1 putative SP:Q9LD45: Bax inhibitor-1 (BI-1) (AtBI-1). [Mouse-ear cress] {Arabidopsis thaliana}
355970	1	2700	3	1	5809	1	1	At5g47120	1,00E-50	68418.m05809 Bax inhibitor-1 putative / BI-1 putative SP:Q9LD45: Bax inhibitor-1 (BI-1) (AtBI-1). [Mouse-ear cress] {Arabidopsis thaliana}
353498	2	2701	2	2	2663	1	2	At4g19006	2,00E-51	68417.m02801 26S proteasome regulatory subunit, putative (RPN9) similar to 26S proteasome subunit p40.5 [Homo sapiens] gi|3618343|dbj|BAA33214
355299	1	2703	3	1	1963	1	1	At4g19610	8,00E-35	68417.m02881 RNA recognition motif (RRM)-containing protein contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)
359579	1	2712	2	2	5607	1	1	At4g25550	2,00E-38	68417.m03683 expressed protein
358090	1	2714	3	1	7681	1	1	At5g56780	7,00E-14	68418.m07086 expressed protein contains similarity to transcription repressor
353150	2	2715	2	2	6831	2	2	At4g27620	1,00E-19	68417.m03970 expressed protein
353471	4	2719	2	2	8350	1	1	At4g31115	7,00E-48	68417.m04416 expressed protein supported by full length cDNA gi:21436034 from [Arabidopsis thaliana]
354153	4	2721	2	2	4468	2	2	At5g10360	3,00E-84	68418.m01202 40S ribosomal protein S6 (RPS6B)
356666	1	2721	2	2	4468	2	2	At5g10360	3,00E-08	68418.m01202 40S ribosomal protein S6 (RPS6B)
357137	1	2721	2	2	4468	2	2	At5g10360	2,00E-31	68418.m01202 40S ribosomal protein S6 (RPS6B)

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
357546	1	2723	2	2	4551	1	1	At4g32620	9,00E-41	68417.m04644 expressed protein predicted protein T10M13.8, Arabidopsis thaliana
355536	1	2730	2	2	1895	1	1	At4g36400	1,00E-73	68417.m05172 FAD linked oxidase family protein low similarity to SP|Q12627 from Kluyveromyces lactis and SP|P32891 from Saccharomyces cerevisiae; contains Pfam FAD linked oxidases, C-terminal domain PF02913, Pfam FAD binding domain PF01565
358194	1	2730	2	2	1944	1	1	At5g06580	3,00E-75	68418.m00743 FAD linked oxidase family protein similar to SP|Q12627 from Kluyveromyces lactis and SP|P32891 from Saccharomyces cerevisiae; contains Pfam FAD linked oxidases, C-terminal domain PF02913, Pfam FAD binding domain PF01565
353473	2	2734	2	2	709	2	1	At5g65690	2,00E-06	68418.m08266 phosphoenolpyruvate carboxykinase [ATP], putative / PEP carboxykinase, putative / PEPCK, putative similar to phosphoenolpyruvate carboxykinase [Lycopersicon esculentum] GI:16950587, SP|Q9SLZ0 Phosphoenolpyruvate carboxykinase [ATP] (EC 4.1.1.49) (PEP carboxykinase) (Phosphoenolpyruvate carboxylase) (PEPCK) {Zea mays}; contains Pfam profile PF01293: phosphoenolpyruvate carboxykinase
359982	1	2734	2	2	709	2	1	At5g65690	2,00E-81	68418.m08266 phosphoenolpyruvate carboxykinase [ATP], putative / PEP carboxykinase, putative / PEPCK, putative similar to phosphoenolpyruvate carboxykinase [Lycopersicon esculentum] GI:16950587, SP|Q9SLZ0 Phosphoenolpyruvate carboxykinase [ATP] (EC 4.1.1.49) (PEP carboxykinase) (Phosphoenolpyruvate carboxylase) (PEPCK) {Zea mays}; contains Pfam profile PF01293: phosphoenolpyruvate carboxykinase
356243	1	2735	2	2	7431	1	1	At4g38370	2,00E-45	68417.m05425 phosphoglycerate/bisphosphoglycerate mutase family protein contains Pfam profile PF00300: phosphoglycerate mutase family
355231	1	2739	2	2	8848	1	1	At5g04260	2,00E-42	68418.m00417 thioredoxin family protein low similarity to SP|P29429 Thioredoxin. [Aspergillus nidulans] {Emericella nidulans}; contains Pfam profile: PF00085 Thioredoxin
355944	1	2740	2	2	1664	1	1	At5g60160	2,00E-13	68418.m07542 aspartyl aminopeptidase, putative similar to SP|Q9ULA0 Aspartyl aminopeptidase (EC 3.4.11.21) {Homo sapiens}; contains Pfam profile PF02127: Aminopeptidase I zinc metalloprotease (M18)

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
359660	1	2740	2	2	1664	1	1	At5g60160	5,00E-87	68418.m07542 aspartyl aminopeptidase, putative similar to SP|Q9ULA0 Aspartyl aminopeptidase (EC 3.4.11.21) {Homo sapiens}; contains Pfam profile PF02127: Aminopeptidase I zinc metalloprotease (M18)
358300	1	2741	2	2	3288	1	1	At5g22350	3,00E-57	68418.m02607 expressed protein
359655	1	2742	3	1	10382	2	1	At5g62080	3,00E-15	68418.m07791 protease inhibitor/seed storage/lipid transfer protein (LTP) family protein similar to tapetum-specific protein a9 precursor {Brassica napus} SP|Q05772; contains Pfam protease inhibitor/seed storage/LTP family domain PF00234; supported by full-length cDNA Ceres:27795
354032	3	2746	2	2	3231	1	1	At5g55760	7,00E-75	68418.m06950 transcriptional regulator Sir2 family protein contains Pfam domain PF02146: transcriptional regulator, Sir2 family
357901	1	2747	2	2	8513	1	1	At5g64400	1,00E-23	68418.m08090 expressed protein contains Pfam domain, PF04933: Protein of unknown function (DUF657)
352992	2	2756	2	2	5209	2	2	At5g13440	3,00E-107	68418.m01547 ubiquinol-cytochrome C reductase iron-sulfur subunit, mitochondrial, putative / Rieske iron-sulfur protein, putative similar to ubiquinol--cytochrome-c reductase from Solanum tuberosum [SP|P37841], Nicotiana tabacum [SP|P51132] [SP|P51133]
354010	4	2765	2	2	5342	1	2	At5g20290	2,00E-58	68418.m02415 40S ribosomal protein S8 (RPS8A) ribosomal protein S8 - Zea mays, PIR:T04088
357016	1	2765	2	2	5342	1	2	At5g20290	3,00E-38	68418.m02415 40S ribosomal protein S8 (RPS8A) ribosomal protein S8 - Zea mays, PIR:T04088
356818	1	2767	2	2	1554	2	2	At5g25757	3,00E-19	68418.m03055 expressed protein
358257	1	2768	1	3	2819	1	2	At5g27380	5,00E-81	68418.m03269 glutathione synthetase (GSH2) non-consensus AT donor splice site at exon 6, AC acceptor splice site at exon 7; identical to Swiss-Prot:P46416 glutathione synthetase, chloroplast precursor (Glutathione synthase) (GSH synthetase) (GSH-S) [Arabidopsis thaliana]
356110	1	2771	1	3	8770	1	2	At5g42890	2,00E-47	68418.m05227 sterol carrier protein 2 (SCP-2) family protein similar to sterol carrier protein-2 [Homo sapiens] GI:432973; contains Pfam profile PF02036: SCP-2 sterol transfer family
353176	2	2772	2	2	9667	2	1	At5g48610	1,00E-14	68418.m06012 expressed protein ; expression supported by MPSS
354106	2	2774	1	3	9047	1	1	At5g46030	1,00E-22	68418.m05661 expressed protein contains Pfam profile PF05129: Putative zinc binding domain (DUF701)
359190	1	2775	2	2	1394	2	2	At5g47490	2,00E-06	68418.m05864 expressed protein

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
353918	2	2782	2	2	6445	2	1	At5g58060	3,00E-17	68418.m07266 SNARE protein-related similar to SNARE protein Ykt6 [Homo sapiens] GI:2507637
357573	1	2782	2	2	6445	2	1	At5g58060	3,00E-69	68418.m07266 SNARE protein-related similar to SNARE protein Ykt6 [Homo sapiens] GI:2507637
359246	1	2782	2	2	6445	2	1	At5g58060	1,00E-39	68418.m07266 SNARE protein-related similar to SNARE protein Ykt6 [Homo sapiens] GI:2507637
354201	2	2783	1	3	7897	1	2	At5g58240	2,00E-07	68418.m07291 bis(5'-adenosyl)-triphosphatase, putative similar to bis(5'-adenosyl)-triphosphatase (Diadenosine 5',5'''-P1,P3-triphosphate hydrolase, Dinucleosidetriphosphatase, AP3A hydrolase, AP3AASE, Fragile histidine triad protein) [Homo sapiens] Swiss-Prot:P49789
359946	1	2783	1	3	7897	1	2	At5g58240	3,00E-46	68418.m07291 bis(5'-adenosyl)-triphosphatase, putative similar to bis(5'-adenosyl)-triphosphatase (Diadenosine 5',5'''-P1,P3-triphosphate hydrolase, Dinucleosidetriphosphatase, AP3A hydrolase, AP3AASE, Fragile histidine triad protein) [Homo sapiens] Swiss-Prot:P49789
355443	1	2899	1	2	1579	1	2	At1g01510	8,00E-55	68414.m00067 C-terminal binding protein (ANGUSTIFOLIA) nearly identical to C-terminal binding protein ANGUSTIFOLIA [Arabidopsis thaliana] GI:15408535; contains Pfam profile PF02826: D-isomer specific 2-hydroxyacid dehydrogenase, NAD binding domain
353507	2	2905	2	1	6856	2	1	At4g02770	8,00E-29	68417.m00377 photosystem I reaction center subunit II, chloroplast, putative / photosystem I 20 kDa subunit, putative / PSI-D, putative (PSAD1) similar to SP|P12353 Photosystem I reaction center subunit II, chloroplast precursor (Photosystem I 20 kDa subunit) (PSI-D) {Spinacia oleracea}; contains Pfam profile PF02531: PsaD
357445	1	2912	2	1	7593	2	1	At2g33220	4,00E-67	68415.m04070 expressed protein
357244	1	2913	2	1	2417	1	1	At1g04950	6,00E-86	68414.m00493 TATA box-binding protein-associated factor (TAF) family protein contains Pfam profile: PF02969 TATA box binding protein associated factor
360052	1	2916	2	1	9861	2	1	At1g05780	6,00E-25	68414.m00602 hypothetical protein
356940	1	2918	1	2	4657	1	1	At1g06110	2,00E-12	68414.m00640 F-box family protein contains similarity to F-box protein FBX3 GI:6103643 from [Homo sapiens] ; similar to SKP1 interacting partner 2 (SKIP2) TIGR_Ath1:At5g67250
358629	1	2919	2	1	7376	2	1	At2g31140	8,00E-35	68415.m03802 expressed protein

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
357858	1	2922	1	2	690	1	1	At1g06950	2,00E-62	68414.m00738 chloroplast inner envelope protein-related similar to chloroplast inner envelope protein GI:1495767 from [Pisum sativum]
354887	1	2925	2	1	4154	2	1	At2g29570	3,00E-76	68415.m03591 proliferating cell nuclear antigen 2 (PCNA2) identical to SP|Q9ZW35 Proliferating cell nuclear antigen 2 (PCNA 2) {Arabidopsis thaliana}; nearly identical to SP|Q43124 Proliferating cell nuclear antigen (PCNA) {Brassica napus}; contains Pfam profiles PF00705: Proliferating cell nuclear antigen N-terminal domain, PF02747: Proliferating cell nuclear antigen C-terminal domain
355580	1	2925	2	1	4154	2	1	At2g29570	3,00E-30	68415.m03591 proliferating cell nuclear antigen 2 (PCNA2) identical to SP|Q9ZW35 Proliferating cell nuclear antigen 2 (PCNA 2) {Arabidopsis thaliana}; nearly identical to SP|Q43124 Proliferating cell nuclear antigen (PCNA) {Brassica napus}; contains Pfam profiles PF00705: Proliferating cell nuclear antigen N-terminal domain, PF02747: Proliferating cell nuclear antigen C-terminal domain
354701	1	2928	2	1	22	2	1	At2g27120	2,00E-21	68415.m03259 DNA-directed DNA polymerase epsilon catalytic subunit, putative similar to SP|Q07864 DNA polymerase epsilon, catalytic subunit A (EC 2.7.7.7) (DNA polymerase II subunit A) {Homo sapiens}; contains Pfam profiles: PF03175 DNA polymerase type B, organellar and viral, PF00136 DNA polymerase family B, PF03104 DNA polymerase family B, exonuclease domain
359218	1	2930	1	2	7198	1	2	At1g08640	3,00E-37	68414.m00959 expressed protein
353387	2	2931	2	1	7359	2	1	At5g41580	3,00E-10	68418.m05052 zinc finger (MIZ type) family protein contains Pfam domain PF02891: MIZ zinc finger
355647	1	2936	1	2	1924	1	2	At1g09830	2,00E-20	68414.m01105 phosphoribosylamine--glycine ligase (PUR2) Identical to phosphoribosylamine--glycine ligase, chloroplast [precursor] SP:P52420 from [Arabidopsis thaliana]
357242	1	2938	2	1	1189	2	1	At1g10490	2,00E-14	68414.m01181 expressed protein contains Pfam profile PF05127: Putative ATPase (DUF699)
354090	2	2945	2	1	2348	1	1	At1g11860	7,00E-105	68414.m01366 aminomethyltransferase, putative similar to aminomethyltransferase, mitochondrial precursor SP:O49849 from [Flaveria anomala]

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
357237	1	2947	2	1	5878	1	1	At1g13120	3,00E-14	68414.m01521 expressed protein contains Prosite PS00012: Phosphopantetheine attachment site; similar to GLE1 (GI:3288817) {Homo sapiens}; EST gb|N37870 comes from this gene
358348	1	2953	2	1	2722	2	1	At2g01270	2,00E-19	68415.m00040 thioredoxin family protein low similarity to quiescin [Homo sapiens] GI:13257405; contains Pfam profiles PF00085: Thioredoxin, PF04777: Erv1 / Alr family
359177	1	2953	2	1	2722	2	1	At2g01270	3,00E-28	68415.m00040 thioredoxin family protein low similarity to quiescin [Homo sapiens] GI:13257405; contains Pfam profiles PF00085: Thioredoxin, PF04777: Erv1 / Alr family
353403	5	2956	2	1	9149	2	1	At3g15790	2,00E-24	68416.m01999 methyl-CpG-binding domain-containing protein contains Pfam profile PF01429: Methyl-CpG binding domain
359944	1	2956	2	1	9149	2	1	At3g15790	7,00E-13	68416.m01999 methyl-CpG-binding domain-containing protein contains Pfam profile PF01429: Methyl-CpG binding domain
358599	1	2957	2	1	9635	2	1	At1g80890	6,00E-11	68414.m09491 expressed protein
359219	1	2958	2	1	10013	2	1	At1g79660	2,00E-06	68414.m09290 expressed protein
359695	1	2963	2	1	5648	2	1	At1g16700	1,00E-16	68414.m02000 NADH-ubiquinone oxidoreductase 23 kDa subunit, mitochondrial, putative very strong similarity to SP|Q42599 NADH-ubiquinone oxidoreductase 23 kDa subunit, mitochondrial precursor (EC 1.6.5.3) (EC 1.6.99.3) (Complex I-23KD) (CI-23KD) (Complex I- 28.5KD) (CI-28.5KD) {Arabidopsis thaliana}; contains Pfam profile PF00037: iron-sulfur cluster-binding protein
359932	1	2968	2	1	5989	2	1	At1g17350	1,00E-67	68414.m02115 auxin-induced-related / indole-3-acetic acid induced-related similar to auxin-induced protein TGSAUR22 (GI:10185820) [Tulipa gesnerian]
358001	1	2970	2	1	2899	2	1	At1g17820	3,00E-46	68414.m02206 expressed protein
356760	1	2980	1	2	10072	1	1	At1g19080	4,00E-33	68414.m02374 expressed protein
354440	2	2983	2	1	8521	1	1	At1g19990	3,00E-23	68414.m02504 expressed protein ; expression supported by MPSS
355640	1	2984	2	1	8162	1	1	At4g20280	1,00E-13	68417.m02962 transcription initiation factor IID (TFIID) 28 kDa subunit (TAFII-28) family protein similar to SP|Q15544 Transcription initiation factor TFIID 28 kDa subunit (TAFII-28) (TAFII28) (TFIID subunit p30-beta) {Homo sapiens}; contains Pfam profile PF04719: hTAFII28-like protein conserved region

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
355804	1	2985	2	1	9989	2	1	At1g76070	6,00E-07	68414.m08834 expressed protein
354697	1	2988	2	1	9177	2	1	At1g20816	3,00E-36	68414.m02607 expressed protein
357336	1	2990	2	1	382	2	1	At1g21170	2,00E-47	68414.m02647 expressed protein
357734	1	2992	1	2	5344	1	2	At1g21600	1,00E-74	68414.m02700 expressed protein similar to hypothetical protein GB:AAD41412 GI:5263310 from [Arabidopsis thaliana]
358247	1	3000	2	1	9025	1	1	At1g24050	8,00E-08	68414.m03036 expressed protein
354286	2	3001	1	2	7715	1	1	At1g24310	1,00E-80	68414.m03067 expressed protein
357589	1	3002	2	1	1104	2	1	At1g67490	5,00E-100	68414.m07686 alpha-glucosidase I (GCS1) / KNOPF (KNF) identical to alpha-glucosidase I (GI:16506680, GI:13398928) [Arabidopsis thaliana]
353036	2	3004	2	1	6300	1	1	At2g46230	9,00E-85	68415.m05749 expressed protein contains Pfam profile: PF04900 protein of unknown function, DUF652
358283	1	3005	2	1	7732	2	1	At1g26665	7,00E-46	68414.m03248 expressed protein
359829	1	3009	2	1	10211	2	1	At2g33510	1,00E-12	68415.m04108 expressed protein
355317	1	3024	2	1	4883	1	1	At1g32130	9,00E-10	68414.m03953 IWS1 C-terminus family protein contains Pfam PF05909: IWS1 C-terminus;
358448	1	3029	3		9676	1	1	At2g35230	2,00E-06	68415.m04322 VQ motif-containing protein contains PF05678: VQ motif
355910	1	3031	2	1	217	2	1	At1g32750	7,00E-07	68414.m04038 HAC13 protein (HAC13) identical to HAC13 [Arabidopsis thaliana] gi|21105767|gb|AAM34782; contains Pfam domains, PF00439: Bromodomain and PF00240: Ubiquitin family
354978	1	3033	2	1	7878	2	1	At1g33490	2,00E-57	68414.m04145 expressed protein
356719	1	3033	2	1	7878	2	1	At1g33490	5,00E-34	68414.m04145 expressed protein
354430	5	3034	2	1	184	1	1	At5g18700	2,00E-72	68418.m02219 protein kinase-related contains protein kinase domain, INTERPRO:IPR000719
353920	2	3036	1	2	8799	1	1	At1g34350	5,00E-41	68414.m04264 expressed protein
352982	2	3037	2	1	5678	1	1	At1g34355	1,00E-20	68414.m04265 forkhead-associated domain-containing protein / FHA domain-containing protein
352949	3	3039	2	1	2298	2	1	At1g36280	4,00E-100	68414.m04509 adenylosuccinate lyase, putative / adenylosuccinase, putative similar to SP|P25739 Adenylosuccinate lyase (EC 4.3.2.2) (Adenylosuccinase) {Escherichia coli}; contains Pfam profile PF00206: Lyase
355257	1	3043	2	1	2619	1	1	At1g69740	8,00E-74	68414.m08025 porphobilinogen synthase, putative / delta-aminolevulinic acid dehydratase, putative similar to delta-aminolevulinic acid dehydratase (Alad) GI:493019 [SP|P43210] from Glycine max, SP|P24493 from Spinacia oleracea, SP|P30124 from Pisum sativum

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
359331	1	3043	2	1	2619	1	1	At1g69740	2,00E-57	68414.m08025 porphobilinogen synthase, putative / delta-aminolevulinic acid dehydratase, putative similar to delta-aminolevulinic acid dehydratase (Alad) GI:493019 [SP|P43210] from Glycine max, SP|P24493 from Spinacia oleracea, SP|P30124 from Pisum sativum
359077	1	3045	2	1	7847	2	1	At5g42960	2,00E-31	68418.m05239 expressed protein
355749	1	3046	2	1	1596	1	1	At5g42920	3,00E-12	68418.m05233 expressed protein
359514	1	3049	2	1	8489	1	1	At1g47640	2,00E-78	68414.m05292 expressed protein similar to seven transmembrane domain protein GI:3550427 from [Homo sapiens]
356370	1	3056	2	1	4086	2	1	At1g48540	3,00E-06	68414.m05428 leucine-rich repeat family protein
355509	1	3059	2	1	1670	2	1	At2g45300	6,00E-43	68415.m05638 3-phosphoshikimate 1-carboxyvinyltransferase / 5-enolpyruvylshikimate-3-phosphate / EPSP synthase nearly identical to SP|P05466
353517	2	3063	2	1	147	2	1	At3g19170	5,00E-164	68416.m02434 peptidase M16 family protein / insulinase family protein contains Pfam domain, PF05193: Peptidase M16 inactive domain
354337	2	3064	1	2	2601	1	2	At1g49820	3,00E-43	68414.m05586 5-methylthioribose kinase family contains TIGRfam TIGR01767: 5-methylthioribose kinase profile
355110	1	3066	1	2	3145	1	2	At1g50450	4,00E-63	68414.m05655 expressed protein
353076	3	3069	1	2	7871	1	1	At1g51510	5,00E-38	68414.m05797 RNA-binding protein, putative similar to RNA-binding protein 8 (Ribonucleoprotein RBM8) SP:Q9Y5S9 from [Homo sapiens], RNA-binding protein Y14 [Xenopus laevis] GI:11034807; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)
355613	1	3070	2	1	2486	2	1	At1g51710	5,00E-44	68414.m05827 ubiquitin-specific protease 6, putative (UBP6) similar to GI:11993465
355798	1	3070	2	1	2486	2	1	At3g21280	3,00E-72	68416.m02689 ubiquitin-specific protease 7, putative (UBP7) similar to GI:11993467
357193	1	3076	2	1	6367	2	1	At1g52380	2,00E-31	68414.m05911 Ran-binding protein 1 domain-containing protein / RanBP1 domain-containing protein weak similarity to SP|Q09717 Ran-specific GTPase-activating protein 1 (Ran binding protein 1) (RANBP1) (Spi1-binding protein) {Schizosaccharomyces pombe}; contains Pfam profile PF00638: RanBP1 domain

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359502	1	3076	2	1	6367	2	1	At1g52380	3,00E-45	68414.m05911 Ran-binding protein 1 domain-containing protein / RanBP1 domain-containing protein weak similarity to SP|Q09717 Ran-specific GTPase-activating protein 1 (Ran binding protein 1) (RANBP1) (Spi1-binding protein) {Schizosaccharomyces pombe}; contains Pfam profile PF00638: RanBP1 domain
354217	2	3081	1	2	8160	1	1	At1g54140	1,00E-55	68414.m06172 transcription initiation factor IID (TFIID) 31 kDa subunit (TAFII-31) family protein contains Pfam profile: PF02291 transcription initiation factor IID, 31kD subunit
353393	2	3082	2	1	5656	2	1	At1g54170	3,00E-20	68414.m06175 ataxin-2-related similar to SCA2 (GI:1770390) [Homo sapiens]; similar to ataxin-2 (GI:3005020) [Mus musculus]
358361	1	3084	3					At4g26060	8,00E-30	68417.m03751 expressed protein
352925	3	3086	2	1	8190	2	1	At5g30495	2,00E-41	68418.m03660 expressed protein
354473	2	3096	1	2	7408	1	1	At1g57680	1,00E-46	68414.m06546 expressed protein
357981	1	3107	2	1	10210	2	1	At5g41685	2,00E-20	68418.m05066 mitochondrial import receptor subunit TOM7 / translocase of outer membrane 7 kDa subunit (TOM7.1) identical to SP|Q9ASY8 Mitochondrial import receptor subunit TOM7 (Translocase of outer membrane 7 kDa subunit) {Arabidopsis thaliana}
353137	3	3108	2	1	6012	1	1	At1g64520	4,00E-110	68414.m07314 26S proteasome regulatory subunit, putative (RPN12) similar to 26S proteasome regulatory complex subunit p30 GB:AAF08395 GI:6434966 from [Drosophila melanogaster]
355216	1	3108	2	1	6012	1	1	At1g64520	3,00E-113	68414.m07314 26S proteasome regulatory subunit, putative (RPN12) similar to 26S proteasome regulatory complex subunit p30 GB:AAF08395 GI:6434966 from [Drosophila melanogaster]
357110	1	3111	1	2	8464	1	1	At1g64850	4,00E-52	68414.m07352 calcium-binding EF hand family protein contains INTERPRO:IPR002048 calcium-binding EF-hand domain
353074	6	3114	2	1	2161	2	1	At5g36230	0	68418.m04371 eIF4-gamma/eIF5/eIF2-epsilon domain-containing protein low similarity to SP|Q13144 Translation initiation factor eIF-2B epsilon subunit (eIF-2B GDP-GTP exchange factor) {Homo sapiens}; contains Pfam profile PF02020: eIF4-gamma/eIF5/eIF2-epsilon
353620	2	3117	1	2	9858	1	2	At1g65720	1,00E-11	68414.m07459 expressed protein

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356312	1	3118	1	2	5968	1	1	At1g66680	6,00E-70	68414.m07579 S locus-linked protein, putative similar to S locus-linked protein SLL2 [Brassica napus] GI:1518113
356638	1	3118	1	2	5968	1	1	At1g66680	2,00E-68	68414.m07579 S locus-linked protein, putative similar to S locus-linked protein SLL2 [Brassica napus] GI:1518113
353867	2	3120	2	1	6339	2	1	At5g38600	3,00E-11	68418.m04669 proline-rich spliceosome-associated (PSP) family protein / zinc knuckle (CCHC-type) family protein contains Pfam domains PF00098: Zinc knuckle, PF04046: PSP
353689	2	3121	2	1	4245	2	1	At1g67440	2,00E-86	68414.m07676 expressed protein contains Pfam domain PF03193: Protein of unknown function, DUF258
358841	1	3121	2	1	4245	2	1	At1g67440	2,00E-41	68414.m07676 expressed protein contains Pfam domain PF03193: Protein of unknown function, DUF258
359632	1	3125	2	1	9045	1	1	At1g68590	8,00E-36	68414.m07838 plastid-specific 30S ribosomal protein 3, putative / PSRP-3, putative similar to SP|P82412 Plastid-specific 30S ribosomal protein 3, chloroplast precursor (PSRP-3) {Spinacia oleracea}; contains Pfam profile PF04839: Plastid and cyanobacterial ribosomal protein (PSRP-3 / Ycf65)
353755	2	3131	2	1	2723	2	1	At5g10330	2,00E-116	68418.m01198 histidinol-phosphate aminotransferase, putative similar to histidinol-phosphate aminotransferase GB:CAA70403 [GI:335562] from [Nicotiana tabacum], Nicotiana plumbaginifolia [GI:12055099]
352929	2	3132	1	2	2624	1	2	At1g72040	6,00E-26	68414.m08327 deoxynucleoside kinase family contains Pfam profile: PF01712 deoxynucleoside kinase
353028	3	3132	1	2	2624	1	2	At1g72040	7,00E-91	68414.m08327 deoxynucleoside kinase family contains Pfam profile: PF01712 deoxynucleoside kinase
359493	1	3135	2	1	1362	1	1	At3g01420	7,00E-34	68416.m00065 pathogen-responsive alpha-dioxygenase, putative similar to pathogen-inducible alpha-dioxygenase [Nicotiana attenuata] GI:12539609; contains Pfam profile PF03098: Animal haem peroxidase
355067	1	3137	1	2	50	1	2	At1g74260	3,00E-41	68414.m08600 AIR synthase-related family protein contains Pfam profiles: PF00586 AIR synthase related protein, N-terminal domain, PF02769 AIR synthase related protein, C-terminal domain
354469	3	3143	2	1	1516	1	1	At1g76400	2,00E-79	68414.m08878 ribophorin I family protein similar to ribophorin I [Sus scrofa] GI:9857227; contains Pfam profile PF04597: Ribophorin I
355569	1	3143	2	1	1516	1	1	At1g76400	1,00E-10	68414.m08878 ribophorin I family protein similar to ribophorin I [Sus scrofa] GI:9857227; contains Pfam profile PF04597: Ribophorin I

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356412	1	3143	2	1	1516	1	1	At1g76400	2,00E-26	68414.m08878 ribophorin I family protein similar to ribophorin I [Sus scrofa] GI:9857227; contains Pfam profile PF04597: Ribophorin I
354490	1	3145	1	2	1543	1	1	At1g78770	8,00E-59	68414.m09180 cell division cycle family protein similar to cell division cycle protein GI:603230 from [Homo sapiens]; contains Pfam profile PF00515 TPR Domain 148977 (apparently not full-length).
355857	1	3151	1	2	528	1	1	At1g80410	4,00E-19	68414.m09413 acetyltransferase-related low similarity to acetyltransferase Tubedown-1 [Mus musculus] GI:8497318, N-TERMINAL ACETYLTRANSFERASE GB:P12945 from (Saccharomyces cerevisiae); contains Pfam profile PF00515 TPR Domain
359880	1	3151	1	2	528	1	1	At1g80410	7,00E-13	68414.m09413 acetyltransferase-related low similarity to acetyltransferase Tubedown-1 [Mus musculus] GI:8497318, N-TERMINAL ACETYLTRANSFERASE GB:P12945 from (Saccharomyces cerevisiae); contains Pfam profile PF00515 TPR Domain
358683	1	3156	2	1	1053	1	1	At3g18060	2,00E-27	68416.m02297 transducin family protein / WD-40 repeat family protein similar to 66 kDa stress protein (SP:P90587) [Physarum polycephalum (Slime mold)]; similar to WDR1 protein GB:AAD05042 [Gallus gallus] (Genomics 56 (1), 59-69 (1999)); contains 11 WD-40 repeats (PF00400)
359838	1	3159	1	2	5832	1	1	At2g01770	1,00E-31	68415.m00107 integral membrane family protein contains integral membrane protein domain, Pfam:PF01988
357356	1	3160	1	2	74	1	1	At2g02560	1,00E-58	68415.m00195 TIP120 protein, putative similar to TBP-interacting protein TIP120 GI:1799570 from [Rattus norvegicus]
355730	1	3162	1	2	5537	1	2	At2g03390	3,00E-40	68415.m00298 uvrB/uvrC motif-containing protein contains Pfam profile PF02151: UvrB/uvrC motif
353340	2	3165	3					At5g06310	7,00E-15	68418.m00707 expressed protein similar to unknown protein (gb|AAD29059.1)
356884	1	3167	1	2	6016	1	2	At2g04940	4,00E-07	68415.m00516 scramblase-related weak similarity to Phospholipid scramblase 1 (PL scramblase 1) (Ca(2)-dependent phospholipid scramblase 1) (Transplantability associated protein 1) (TRA1) (NOR1) (Swiss-Prot:Q9JJ00) [Mus musculus]; weak similarity to Phospholipid scramblase 4 (PL scramblase 4) (Ca(2)-dependent phospholipid scramblase 4) (Swiss-Prot:Q9NRQ2) [Homo sapiens]
353706	3	3179	1	2	6793	1	2	At2g15290	1,00E-57	68415.m01744 expressed protein

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354538	1	3183	2	1	6942	1	1	At2g21160	6,00E-50	68415.m02510 translocon-associated protein alpha (TRAP alpha) family protein contains Pfam profile: PF03896 translocon-associated protein (TRAP), alpha subunit
358679	1	3183	2	1	6942	1	1	At2g21160	2,00E-22	68415.m02510 translocon-associated protein alpha (TRAP alpha) family protein contains Pfam profile: PF03896 translocon-associated protein (TRAP), alpha subunit
356238	1	3189	2	1	6101	1	1	At5g45600	8,00E-67	68418.m05603 YEATS family protein contains Pfam domain PF03366: YEATS family
358342	1	3192	2	1	3495	1	1	At5g57410	6,00E-37	68418.m07172 expressed protein
353648	2	3194	1	2	9936	1	2	At2g18910	3,00E-19	68415.m02206 hydroxyproline-rich glycoprotein family protein
354454	2	3195	2	1	7356	2	1	At4g29870	3,00E-26	68417.m04251 expressed protein predicted protein, Arabidopsis thaliana, PIR2:T01282
357273	1	3196	1	2	2411	1	1	At2g19450	8,00E-88	68415.m02272 diacylglycerol O-acyltransferase / acyl CoA:diacylglycerol acyltransferase (DGAT) identical to gi:5050913, gi:6625553
355868	1	3202	2	1				At2g20940	4,00E-22	68415.m02469 expressed protein
353647	6	3205	1	2	210	1	2	At2g21790	1,00E-127	68415.m02590 ribonucleoside-diphosphate reductase small chain, putative / ribonucleotide reductase, putative similar to ribonucleotide reductase GI:4151068 from [Nicotiana tabacum]
356010	1	3205	1	2	210	1	2	At2g21790	3,00E-43	68415.m02590 ribonucleoside-diphosphate reductase small chain, putative / ribonucleotide reductase, putative similar to ribonucleotide reductase GI:4151068 from [Nicotiana tabacum]
356061	1	3205	1	2	210	1	2	At2g21790	3,00E-63	68415.m02590 ribonucleoside-diphosphate reductase small chain, putative / ribonucleotide reductase, putative similar to ribonucleotide reductase GI:4151068 from [Nicotiana tabacum]
356034	1	3212	2	1	8601	2	1	At2g23370	6,00E-31	68415.m02791 expressed protein
356540	1	3218	1	2	6185	1	1	At2g25110	5,00E-19	68415.m03004 MIR domain-containing protein similar to SP|Q99470 Stromal cell-derived factor 2 precursor (SDF-2) {Homo sapiens}; contains Pfam profile PF02815: MIR domain
356985	1	3221	3		9757	1	1	At2g26110	5,00E-08	68415.m03133 expressed protein
354241	2	3221	3		10219	2	2	At5g56980	9,00E-07	68418.m07112 expressed protein non-consensus CG donor splice site at exon 1, GA donor splice site at exon 3

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359609	1	3231	2	1	8858	1	1	At2g27960	5,00E-41	68415.m03389 cyclin-dependent kinase / CDK (CKS1) identical to Cks1 protein [Arabidopsis thaliana] gi|2274859|emb|CAA03859
353308	2	3238	2	1	7916	1	1	At5g05710	3,00E-55	68418.m00628 pleckstrin homology (PH) domain-containing protein similar to AtPH1 [Arabidopsis thaliana] GI:5926716; contains Pfam profile PF00169: PH domain
354591	1	3255	1	2	21	1	1	At2g35630	2,00E-51	68415.m04369 microtubule organization 1 protein (MOR1) identical to microtubule organization 1 protein GI:14317953 from [Arabidopsis thaliana]
358699	1	3255	1	2	21	1	1	At2g35630	9,00E-14	68415.m04369 microtubule organization 1 protein (MOR1) identical to microtubule organization 1 protein GI:14317953 from [Arabidopsis thaliana]
358332	1	3257	2	1	1991	1	1	At2g36810	4,00E-15	68415.m04514 expressed protein
354359	2	3258	2	1	7168	2	1	At2g36900	2,00E-57	68415.m04526 Golgi SNARE protein membrin 11 (MEMB11) / Golgi SNAP receptor complex member 2-1 identical to SP:Q9SJL6; identical to Probable 27 kDa Golgi SNARE protein (Golgi SNAP receptor complex member 2) (SP:Q9SJL6) [Arabidopsis thaliana]
359464	1	3262	2	1	7946	2	1	At2g38430	4,00E-07	68415.m04720 expressed protein
354311	2	3264	1	2	6912	1	1	At2g39080	7,00E-96	68415.m04802 expressed protein
355638	1	3268	2	1	5443	2	1	At3g55840	2,00E-08	68416.m06204 expressed protein
357562	1	3270	2	1				At2g40630	4,00E-19	68415.m05011 expressed protein
355283	1	3277	1	2	8845	1	2	At2g41750	6,00E-12	68415.m05161 DTW domain-containing protein contains Pfam domain, PF03942: DTW domain
358314	1	3281	2	1	8677	2	1	At3g58110	8,00E-06	68416.m06480 expressed protein
353879	2	3287	2	1	754	2	1	At2g44160	2,00E-102	68415.m05493 methylenetetrahydrofolate reductase 2 (MTHFR2) identical to SP|O80585 Methylenetetrahydrofolate reductase (EC 1.5.1.20) {Arabidopsis thaliana}
354767	1	3287	2	1	754	2	1	At3g59970	7,00E-09	68416.m06695 methylenetetrahydrofolate reductase 1 (MTHFR1) identical to methylenetetrahydrofolate reductase MTHFR1 [Arabidopsis thaliana] GI:5911425
357736	1	3288	2	1	2147	1	1	At5g57020	3,00E-99	68418.m07117 myristoyl-CoA:protein N-myristoyltransferase 1 (NMT1) identical to N-myristoyltransferase 1 (NMT1) [Arabidopsis thaliana] GI:7339834
358657	1	3291	2	1	9112	2	1	At3g60210	1,00E-33	68416.m06728 chloroplast chaperonin 10, putative similar to chloroplast chaperonin 10 GI:14041813 from [Arabidopsis thaliana]

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
357367	1	3303	2	1	1212	2	1	At5g50950	1,00E-42	68418.m06319 fumarate hydratase, putative / fumarase, putative similar to SP|P55250 Fumarate hydratase, mitochondrial precursor (EC 4.2.1.2) (Fumarase) {Rhizopus oryzae}; contains Pfam profile PF00206: Lyase
355571	1	3313	1	2	128	1	2	At3g01780	3,00E-61	68416.m00118 expressed protein est hit,
354903	1	3315	2	1	4213	2	1	At3g02200	4,00E-71	68416.m00199 proteasome family protein contains Pfam domain, PF01399: PCI domain
359290	1	3315	2	1	4213	2	1	At5g15610	5,00E-76	68418.m01827 proteasome family protein contains Pfam domain, PF01399: PCI domain
354305	10	3318	1	2	4137	1	2	At3g02420	3,00E-26	68416.m00229 expressed protein
355630	1	3318	1	2	4137	1	2	At3g02420	5,00E-12	68416.m00229 expressed protein
358962	1	3318	1	2	4137	1	2	At3g02420	9,00E-52	68416.m00229 expressed protein
356247	1	3322	2	1	89	2	1	At5g17020	1,00E-42	68418.m01995 exportin1 (XPO1) nearly identical to Exportin1 (XPO1) protein [Arabidopsis thaliana] GI:7671510
354057	2	3326	1	2	3762	1	1	At3g04600	4,00E-135	68416.m00491 tRNA synthetase class I (W and Y) family protein contains Pfam profile: PF00579 tRNA synthetases class I (W and Y)
358025	1	3327	1	2	2242	1	2	At3g04820	2,00E-62	68416.m00522 expressed protein contains PFam profile PF01142: Uncharacterized protein family UPF0024; expression supported by MPSS
353224	3	3328	2	1	8536	2	1	At5g28220	9,00E-113	68418.m03417 expressed protein predicted proteins, Arabidopsis thaliana, D.melanogaster, C.elegans and S.pombe
353667	2	3329	1	2	7003	1	1	At3g05000	3,00E-70	68416.m00543 transport protein particle (TRAPP) component Bet3 family protein similar to Transport protein particle 33 kDa subunit (TRAPP 33 kDa subunit) (Swiss-Prot:Q99394) [Saccharomyces cerevisiae]; contains Pfam profile PF04051: Transport protein particle (TRAPP) component, Bet3
354155	4	3331	2	1	7102	1	1	At3g16640	7,00E-69	68416.m02127 translationally controlled tumor family protein similar to translationally controlled tumor protein GB:AAD10032 from [Hevea brasiliensis]
353614	2	3336	1	2	6434	1	1	At3g07090	6,00E-72	68416.m00843 expressed protein
358355	1	3337	1	2	4231	1	2	At3g07210	3,00E-32	68416.m00860 expressed protein predicted using genefinder
357310	1	3341	2	1	6785	1	1	At3g07800	6,00E-36	68416.m00953 thymidine kinase, putative similar to thymidine kinase [Oryza sativa] SWISS-PROT:O81263
359275	1	3345	2	1	2535	2	1	At5g01460	1,00E-50	68418.m00059 LMBR1 integral membrane family protein contains Pfam PF04791: LMBR1-like conserved region

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
354958	1	3346	2	1	7718	1	1	At4g39740	7,00E-47	68417.m05626 electron transport SCO1/SenC family protein similar to SP|P23833 SCO1 protein, mitochondrial precursor {Saccharomyces cerevisiae}; contains Pfam profile PF02630: SCO1/SenC
357358	1	3347	3					At5g01090	3,00E-14	68418.m00013 legume lectin family protein contains Pfam domain, PF00139: Legume lectins beta domain
353383	2	3355	2	1	4248	2	1	At5g05700	6,00E-62	68418.m00627 arginine-tRNA-protein transferase 1 / arginyltransferase 1 / arginyl-tRNA-protein transferase 1 (ATE1) identical to SP|Q9ZT48 Arginine-tRNA-protein transferase 1 (EC 2.3.2.8) (R-transferase 1) (Arginyltransferase 1) (Arginyl-tRNA--protein transferase 1) {Arabidopsis thaliana}
353845	2	3359	1	2	456	1	1	At3g12280	9,00E-60	68416.m01533 retinoblastoma-related protein (RBR1) nearly identical to retinoblastoma-related protein [Arabidopsis thaliana] GI:8777927; contains Pfam profiles: PF01858 retinoblastoma-associated protein A domain, PF01857 retinoblastoma-associated protein B domain
354899	1	3359	1	2	456	1	1	At3g12280	4,00E-70	68416.m01533 retinoblastoma-related protein (RBR1) nearly identical to retinoblastoma-related protein [Arabidopsis thaliana] GI:8777927; contains Pfam profiles: PF01858 retinoblastoma-associated protein A domain, PF01857 retinoblastoma-associated protein B domain
356765	1	3360	2	1	8773	1	2	At5g56120	2,00E-37	68418.m07001 expressed protein similar to unknown protein (dbj|BAA81760.1)
356656	1	3362	1	2	6307	1	2	At3g13230	1,00E-76	68416.m01665 expressed protein
356597	1	3365	1	2	6446	1	1	At3g14110	5,00E-17	68416.m01783 tetratricopeptide repeat (TPR)-containing protein contains Pfam profile PF00515: TPR Domain
356392	1	3370	2	1	6699	1	1	At5g11470	6,00E-19	68418.m01339 bromo-adjacent homology (BAH) domain-containing protein contains Pfam profile PF01426: BAH domain
357961	1	3374	1	2	4808	1	2	At3g17340	2,00E-25	68416.m02216 importin-related contains Pfam profile PF03810: Importin-beta N-terminal domain
354574	1	3378	1	2	7304	1	1	At3g18430	1,00E-43	68416.m02343 calcium-binding EF hand family protein similar to Calcineurin B subunit (Protein phosphatase 2B regulatory subunit) (Calcineurin regulatory subunit) SP:P42322 from [Naegleria gruberi]; contains Pfam profile PF00036: EF hand

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357378	1	3379	2	1	2253	1	1	At5g42480	1,00E-48	68418.m05171 DNAJ plastid division protein (ARC6) almost identical to dnaJ plastid division protein ARC6 (GI:33436339) [Arabidopsis thaliana];low similarity to cell division protein Ftn2 [Synechococcus sp. PCC 7942] GI:16226084; contains Pfam profile PF00226: DnaJ domain
357710	1	3379	2	1	2253	1	1	At5g42480	5,00E-17	68418.m05171 DNAJ plastid division protein (ARC6) almost identical to dnaJ plastid division protein ARC6 (GI:33436339) [Arabidopsis thaliana];low similarity to cell division protein Ftn2 [Synechococcus sp. PCC 7942] GI:16226084; contains Pfam profile PF00226: DnaJ domain
352957	2	3381	1	2	9460	1	2	At3g20070	2,00E-15	68416.m02539 expressed protein
355187	1	3384	1	2	3163	1	2	At3g20740	7,00E-07	68416.m02624 fertilization-independent endosperm protein (FIE) contains 6 WD-40 repeats (PF00400); identical to fertilization-independent endosperm protein (GI:4567095) [Arabidopsis thaliana]
355229	1	3387	2	1	5926	2	1	At4g15640	6,00E-18	68417.m02384 expressed protein
359733	1	3388	1	2	7988	1	1	At3g21865	2,00E-29	68416.m02756 expressed protein
354948	1	3391	2	1	5938	2	1	At3g22425	3,00E-45	68416.m02833 imidazoleglycerol-phosphate dehydratase 1 (IGPD1) identical to SP|P34047 Imidazoleglycerol-phosphate dehydratase 1 (EC 4.2.1.19) (IGPD 1) {Arabidopsis thaliana}; supporting cDNA gi|437212|gb|U02689.1|ATU02689
356329	1	3392	1	2	8401	1	2	At3g22480	4,00E-30	68416.m02842 prefoldin-related KE2 family protein similar to Swiss-Prot:Q9UHV9 prefoldin subunit 2 (Protein HSPC231) [Homo sapiens]; contains Pfam domain, PF01920: KE2 family protein
353145	3	3394	2	1	6419	2	1	At3g22630	3,00E-61	68416.m02857 20S proteasome beta subunit D (PBD1) (PRGB) identical to GB:CAA74026 from [Arabidopsis thaliana] (FEBS Lett. (1997) 416 (3), 281-285); identical to cDNA proteasome subunit prgb GI:2511589
354645	1	3395	2	1	8623	2	1	At4g14342	1,00E-45	68417.m02209 pre-mRNA splicing factor 10 kDa subunit, putative similar to Splicing factor 3B subunit 10 (SF3b10) (Pre-mRNA splicing factor SF3b 10 kDa subunit) (Swiss-Prot:Q9BWJ5) [Homo sapiens]; Conserved in Plasmodium, yeast, fly, mouse, human
354719	1	3396	1	2	4945	1	2	At3g23620	5,00E-32	68416.m02971 brix domain-containing protein contains Pfam domain, PF04427: Brix domain
356060	1	3397	2	1				At3g23740	2,00E-10	68416.m02985 expressed protein

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
354724	1	3398	2	1	1096	2	1	At4g13940	2,00E-38	68417.m02157 adenosylhomocysteinase / S-adenosyl-L-homocysteine hydrolase / AdoHcyase (SAHH) identical to SP|O23255 Adenosylhomocysteinase (EC 3.3.1.1) (S-adenosyl-L-homocysteine hydrolase) (AdoHcyase) {Arabidopsis thaliana}; strong similarity to SP|P50248 Adenosylhomocysteinase (EC 3.3.1.1) {Nicotiana sylvestris}
357231	1	3398	2	1	1096	2	1	At4g13940	1,00E-37	68417.m02157 adenosylhomocysteinase / S-adenosyl-L-homocysteine hydrolase / AdoHcyase (SAHH) identical to SP|O23255 Adenosylhomocysteinase (EC 3.3.1.1) (S-adenosyl-L-homocysteine hydrolase) (AdoHcyase) {Arabidopsis thaliana}; strong similarity to SP|P50248 Adenosylhomocysteinase (EC 3.3.1.1) {Nicotiana sylvestris}
358594	1	3398	2	1	1096	2	1	At4g13940	2,00E-41	68417.m02157 adenosylhomocysteinase / S-adenosyl-L-homocysteine hydrolase / AdoHcyase (SAHH) identical to SP|O23255 Adenosylhomocysteinase (EC 3.3.1.1) (S-adenosyl-L-homocysteine hydrolase) (AdoHcyase) {Arabidopsis thaliana}; strong similarity to SP|P50248 Adenosylhomocysteinase (EC 3.3.1.1) {Nicotiana sylvestris}
353935	2	3401	2	1	5409	1	1	At3g24350	5,00E-67	68416.m03057 syntaxin, putative (SYP32) similar to SP|Q9FFK1 Syntaxin 31 (AtSYP31) (AtSED5) {Arabidopsis thaliana}, syntaxin 5A GB:NP_003155 from [Homo sapiens] (J. Mol. Neurosci. (1997) 8 (2), 159-161)
359427	1	3401	2	1				At5g05760	1,00E-56	68418.m00634 syntaxin 31 (SYP31) / SED5 identical to SP|Q9FFK1 Syntaxin 31 (AtSYP31) (AtSED5) {Arabidopsis thaliana}
353727	3	3403	1	2	1392	1	2	At3g25100	2,00E-124	68416.m03135 cell division control protein-related contains weak similarity to cell division control protein 45 homolog (Suppressor of nda4 protein) (Swiss-Prot:O74113) [Schizosaccharomyces pombe]
358740	1	3410	2	1	8486	2	1	At5g40190	2,00E-19	68418.m04877 calmodulin-binding protein
355615	1	3420	1	2	4226	1	1	At3g42050	3,00E-26	68416.m04311 vacuolar ATP synthase subunit H family protein identical to probable vacuolar ATP synthase subunit H (EC 3.6.3.14)(V-ATPase H subunit) (Vacuolar proton pump H subunit) (Vacuolar proton pump subunit SFD) SP:Q9LX65 from [Arabidopsis thaliana]; contains Pfam PF03224: V-ATPase subunit H
354657	1	3422	1	2	1618	1	1	At3g44330	8,00E-49	68416.m04763 expressed protein
359195	1	3422	1	2	1618	1	1	At3g44330	3,00E-66	68416.m04763 expressed protein

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
357621	1	3426	1	2	9054	1	1	At3g46560	6,00E-24	68416.m05054 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
358331	1	3433	2	1	6819	1	1	At3g49250	2,00E-43	68416.m05382 expressed protein
359547	1	3435	2	1	8389	2	1	At5g24610	9,00E-16	68418.m02907 expressed protein similar to unknown protein (emb|CAB62459.1)
360017	1	3435	2	1	8389	2	1	At5g24610	3,00E-48	68418.m02907 expressed protein similar to unknown protein (emb|CAB62459.1)
354256	3	3436	2	1	7052	2	1	At3g49720	4,00E-33	68416.m05436 expressed protein
359323	1	3437	1	2	6184	1	1	At3g49990	5,00E-09	68416.m05466 expressed protein
356553	1	3438	1	2	163	1	1	At3g50380	3,00E-09	68416.m05511 expressed protein
358652	1	3442	1	2	9438	1	1	At3g51100	5,00E-19	68416.m05596 expressed protein
358038	1	3443	2	1	8655	2	1	At5g66230	3,00E-15	68418.m08343 expressed protein
354669	1	3444	1	2	5219	1	2	At3g51520	8,00E-28	68416.m05642 diacylglycerol acyltransferase family contains Pfam PF03982: Diacylglycerol acyltransferase
357374	1	3445	2	1	9597	2	1	At4g18590	3,00E-24	68417.m02752 expressed protein
354024	3	3449	2	1	8735	1	1	At3g54500	2,00E-30	68416.m06031 expressed protein
356986	1	3451	1	2	2437	1	1	At3g54860	3,00E-56	68416.m06078 vacuolar protein sorting protein, putative similar to Swiss-Prot:Q63615 vacuolar protein sorting 33A (r-vps33a) [Rattus norvegicus]; contains Pfam domain, PF00995: Sec1 family
353407	2	3467	1	2	3674	1	1	At3g63410	5,00E-106	68416.m07139 chloroplast inner envelope membrane protein, putative (APG1) similar to SP|P23525 37 kDa inner envelope membrane protein, chloroplast precursor (E37) {Spinacia oleracea}; contains Pfam profile PF01209: methlytransferase, UbiE/COQ5 family
358528	1	3474	1	2	3980	1	1	At4g02220	2,00E-72	68417.m00300 zinc finger (MYND type) family protein / programmed cell death 2 C-terminal domain-containing protein similar to SP|Q16342 Programmed cell death protein 2 (Zinc finger protein Rp-8) {Homo sapiens}; contains Pfam profiles PF01753: MYND finger, PF04194: Programmed cell death protein 2, C-terminal putative domain
358419	1	3481	2	1	7010	2	1	At4g05000	7,00E-40	68417.m00731 vacuolar protein sorting-associated protein 28 family protein / VPS28 family protein contains similarity to Swiss-Prot:Q02767 vacuolar protein sorting-associated protein VPS28 [Saccharomyces cerevisiae]

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355619	1	3486	1	2	7697	1	1	At4g07990	3,00E-19	68417.m01280 DNAJ heat shock N-terminal domain-containing protein similar to SP|Q9QYI5 DnaJ homolog subfamily B member 10 Mus musculus ; contains Pfam profile PF00226 DnaJ domain
353433	2	3487	2	1	2821	1	1	At4g08900	7,00E-56	68417.m01467 arginase identical to Swiss-Prot:P46637 arginase (EC 3.5.3.1) [Arabidopsis thaliana]
354386	2	3487	2	1	2821	1	1	At4g08900	9,00E-89	68417.m01467 arginase identical to Swiss-Prot:P46637 arginase (EC 3.5.3.1) [Arabidopsis thaliana]
357790	1	3489	2	1	10079	2	1	At4g10080	2,00E-23	68417.m01649 expressed protein
356237	1	3492	2	1	10153	2	1	At4g10970	1,00E-08	68417.m01785 expressed protein
357498	1	3492	2	1	10153	2	1	At4g10970	4,00E-07	68417.m01785 expressed protein
357523	1	3496	1	2	9611	1	2	At4g14385	2,00E-18	68417.m02218 expressed protein
353304	4	3499	2	1	3683	1	1	At4g16170	2,00E-142	68417.m02455 expressed protein
353165	2	3507	2	1	8591	1	1	At4g18930	2,00E-41	68417.m02790 cyclic phosphodiesterase identical to cyclic phosphodiesterase [Arabidopsis thaliana] gi|2065013|emb|CAA72363
355068	1	3508	2	1	3815	1	1	At4g20050	2,00E-48	68417.m02934 expressed protein C65DMY30S
354139	2	3510	1	2	8632	1	1	At4g20260	2,00E-23	68417.m02960 DREPP plasma membrane polypeptide family protein contains Pfam profile: PF05558 DREPP plasma membrane polypeptide
353569	2	3513	2	1	1359	2	1	At4g20980	6,00E-127	68417.m03037 eukaryotic translation initiation factor 3 subunit 7, putative / eIF-3 zeta, putative / eIF3d, putative similar to initiation factor 3d [Arabidopsis thaliana] GI:12407755, SP|O15371 Eukaryotic translation initiation factor 3 subunit 7 (eIF-3 zeta) (eIF3 p66) (eIF3d) {Homo sapiens}; contains Pfam profile PF05091: Eukaryotic translation initiation factor 3 subunit 7 (eIF-3)
356186	1	3517	2	1	3586	2	1	At5g49945	1,00E-24	68418.m06184 expressed protein strong similarity to unknown protein (pir||T09896)
353008	2	3518	1	2	8659	1	1	At4g24440	4,00E-49	68417.m03504 transcription initiation factor IIA gamma chain / TFIIA-gamma (TFIIA-S) identical to transcription initiation factor IIA gamma chain SP:Q39236 from [Arabidopsis thaliana];
353564	3	3519	1	2	5437	1	1	At4g24690	8,00E-13	68417.m03534 ubiquitin-associated (UBA)/TS-N domain-containing protein / octicosapeptide/Phox/Bemp1 (PB1) domain-containing protein contains Pfam profiles PF00627: Ubiquitin-associated (UBA)/TS-N domain, PF00569: Zinc finger ZZ type domain, PF00564: PB1 domain

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
352897	3	3520	1	2	1866	1	1	At4g24830	1,00E-137	68417.m03557 arginosuccinate synthase family contains Pfam profile: PF00764 arginosuccinate synthase
355508	1	3522	2	1	9731	2	2	At4g25170	2,00E-17	68417.m03624 expressed protein
357947	1	3525	2	1	9063	2	1	At5g57290	6,00E-17	68418.m07157 60S acidic ribosomal protein P3 (RPP3B)
354200	2	3527	1	2	1113	1	1	At4g26900	2,00E-115	68417.m03870 imidazole glycerol phosphate synthase hisHF, chloroplast / IGP synthase / ImGPP synthase / IGPS identical to SP|Q9SZ30 Imidazole glycerol phosphate synthase hisHF, chloroplast precursor (IGP synthase) {Arabidopsis thaliana}
357572	1	3529	2	1	8855	2	1	At4g26990	2,00E-25	68417.m03883 expressed protein
358338	1	3532	1	2	6259	1	1	At4g27750	1,00E-62	68417.m03987 expressed protein
353756	2	3533	2	1	7746	1	1	At5g52840	4,00E-37	68418.m06559 NADH-ubiquinone oxidoreductase-related contains weak similarity to NADH-ubiquinone oxidoreductase 13 kDa-B subunit (EC 1.6.5.3) (EC 1.6.99.3) (Complex I-13Kd-B) (CI-13Kd-B) (Complex I subunit B13) (Swiss-Prot:Q63362) [Rattus norvegicus]
359882	1	3542	1	2	3779	1	1	At4g32060	6,00E-18	68417.m04563 calcium-binding EF hand family protein contains INTERPRO:IPR002048 calcium-binding EF-hand domain
356291	1	3543	1	2	1507	1	1	At4g33150	4,00E-36	68417.m04723 lysine-ketoglutarate reductase/saccharopine dehydrogenase bifunctional enzyme identical to lysine-ketoglutarate reductase/saccharopine dehydrogenase GI:2052508 from [Arabidopsis thaliana]
358472	1	3544	1	2				At4g33380	3,00E-10	68417.m04745 expressed protein
358515	1	3544	1	2				At4g33380	1,00E-34	68417.m04745 expressed protein
353789	2	3548	1	2	9975	1	1	At4g34190	2,00E-06	68417.m04852 stress enhanced protein 1 (SEP1) identical to stress enhanced protein 1 (SEP1) GI:7384978 from [Arabidopsis thaliana]
353343	2	3550	2	1	5977	2	1	At4g38800	8,00E-76	68417.m05493 phosphorylase family protein contains weak similarity to Swiss-Prot:O51931 nucleosidase [Includes: 5'-methylthioadenosine nucleosidase (EC 3.2.2.16); S-adenosylhomocysteine nucleosidase [Buchnera aphidicola]
354328	2	3553	1	2	9614	1	2	At4g37300	2,00E-19	68417.m05281 expressed protein
358941	1	3562	1	2	9982	1	2	At5g03370	5,00E-17	68418.m00290 acylphosphatase family contains Pfam PF00708: Acylphosphatase
353125	2	3563	1	2	8502	1	2	At5g03455	7,00E-51	68418.m00301 rhodanese-like domain-containing protein contains Rhodanese-like domain PF:00581

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
354107	2	3563	1	2	8502	1	2	At5g03455	2,00E-41	68418.m00301 rhodanese-like domain-containing protein contains Rhodanese-like domain PF:00581
354763	1	3574	2	1	3820	2	1	At5g23200	5,00E-25	68418.m02713 expressed protein
357178	1	3578	2	1	956	2	1	At5g23575	4,00E-39	68418.m02766 transmembrane protein, putative similar to cleft lip and palate transmembrane protein 1 [Homo sapiens] GI:4039014; contains Pfam profile PF05602: Cleft lip and palate transmembrane protein 1 (CLPTM1)
356899	1	3579	2	1	1876	1	1	At5g08550	5,00E-59	68418.m01017 expressed protein
359060	1	3584	2	1	1688	2	1	At5g09740	2,00E-32	68418.m01128 histone acetyltransferase, putative similar to histone acetyltransferase [Homo sapiens] gi|8317213|gb|AAF72665
353424	2	3585	2	1	1853	2	1	At5g09900	6,00E-111	68418.m01145 26S proteasome regulatory subunit, putative (RPN5) p55 protein-like
354867	1	3585	2	1	1853	2	1	At5g09900	8,00E-14	68418.m01145 26S proteasome regulatory subunit, putative (RPN5) p55 protein-like
355169	1	3585	2	1	1853	2	1	At5g09900	4,00E-13	68418.m01145 26S proteasome regulatory subunit, putative (RPN5) p55 protein-like
358459	1	3585	2	1	1853	2	1	At5g09900	7,00E-35	68418.m01145 26S proteasome regulatory subunit, putative (RPN5) p55 protein-like
358111	1	3586	1	2	10056	1	1	At5g09920	2,00E-14	68418.m01147 RNA polymerase II 15.9 kDa subunit (RPB15.9) identical to 15.9 kDa subunit of RNA polymerase II GI:2760362 from [Arabidopsis thaliana]
359784	1	3586	1	2	10056	1	1	At5g09920	2,00E-37	68418.m01147 RNA polymerase II 15.9 kDa subunit (RPB15.9) identical to 15.9 kDa subunit of RNA polymerase II GI:2760362 from [Arabidopsis thaliana]
354292	3	3588	1	2	6534	1	1	At5g10860	9,00E-60	68418.m01261 CBS domain-containing protein contains Pfam profile PF00571: CBS domain
358929	1	3588	1	2	6534	1	1	At5g10860	3,00E-47	68418.m01261 CBS domain-containing protein contains Pfam profile PF00571: CBS domain
352908	2	3589	1	2	5531	1	1	At5g11500	9,00E-76	68418.m01342 expressed protein contains Pfam profile PF05670: Domain of unknown function (DUF814)
357810	1	3596	1	2	32	1	1	At5g13630	2,00E-70	68418.m01580 magnesium-chelatase subunit chlH, chloroplast, putative / Mg-protoporphyrin IX chelatase, putative (CHLH) nearly identical to magnesium chelatase subunit GI:1154627 from [Arabidopsis thaliana]; contains Pfam profile: PF02514 CobN/magnesium chelatase family protein
354857	1	3600	1	2	335	1	1	At5g15400	1,00E-27	68418.m01802 U-box domain-containing protein contains Pfam profile PF04564: U-box domain
358946	1	3609	2	1	4079	1	1	At5g50970	2,00E-08	68418.m06321 WD-40 repeat family protein contains Pfam profile PF00400: WD domain, G-beta repeat

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
359413	1	3609	2	1	4079	1	1	At5g50970	1,00E-23	68418.m06321 WD-40 repeat family protein contains Pfam profile PF00400: WD domain, G-beta repeat
357285	1	3613	1	2	6119	1	2	At5g22110	4,00E-30	68418.m02574 DNA polymerase epsilon subunit B family contains Pfam profile: PF04042 DNA polymerase epsilon subunit B
357539	1	3614	2	1				At5g22480	2,00E-67	68418.m02623 zinc finger (ZPR1-type) family protein contains Pfam doamin, PF03367: ZPR1 zinc-finger domain
358889	1	3616	1	2	111	1	1	At5g23630	2,00E-48	68418.m02771 ATPase E1-E2 type family protein / haloacid dehalogenase-like hydrolase familiy protein similar to SP|O14072 Cation-transporting ATPase 4 (EC 3.6.3.-) {Schizosaccharomyces pombe}; contains InterPro accession IPR001757: ATPase, E1-E2 type; contains Pfam profile PF00702: haloacid dehalogenase-like hydrolase
353254	2	3619	1	2	146	1	1	At5g24710	2,00E-70	68418.m02919 WD-40 repeat family protein contains 3 Pfam PF00400: WD domain, G-beta repeats;
356126	1	3621	2	1	6519	1	1	At5g25752	2,00E-43	68418.m03053 rhomboid family protein contains Pfam profile PF01694: Rhomboid family
355701	1	3628	1	2	5562	1	1	At5g40660	1,00E-28	68418.m04936 ATP12 protein-related weak similarity to SP|P22135 ATP12 protein, mitochondrial precursor {Saccharomyces cerevisiae}
353601	2	3637	1	2	5127	1	2	At5g44730	2,00E-110	68418.m05482 haloacid dehalogenase-like hydrolase family protein low similarity to SP|Q94915 Rhythmically expressed gene 2 protein (DREG-2) {Drosophila melanogaster}; contains InterPro accession IPR005834: Haloacid dehalogenase-like hydrolase
353168	2	3639	1	2	7974	1	2	At5g46020	1,00E-37	68418.m05659 expressed protein
354216	2	3648	2	1	7497	1	1	At5g55940	6,00E-45	68418.m06977 expressed protein contains Pfam PF03665: Uncharacterised protein family (UPF0172)
358757	1	3651	1	2	8950	1	1	At5g52200	8,00E-35	68418.m06479 expressed protein
358413	1	3655	1	2	3524	1	2	At5g53000	7,00E-60	68418.m06583 protein phosphatase 2A-associated 46 kDa protein / PP2A regulatory subunit (TAP46) identical to PP2A regulatory subunit (46 kDa protein phosphatase 2A-associated protein) (TAP46) [Arabidopsis thaliana] GI:5107033; contains Pfam profile PF04177: TAP42-like family
356197	1	3661	1	2	5568	1	2	At5g55000	1,00E-56	68418.m06850 potassium channel tetramerisation domain-containing protein / pentapeptide repeat-containing protein contains Pfam profiles PF02214: K+ channel tetramerisation domain, PF00805: Pentapeptide repeats (8 copies)

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
356790	1	3664	1	2	9436	1	1	At5g55640	2,00E-17	68418.m06938 expressed protein
353453	2	3665	1	2	8374	1	2	At5g55820	1,00E-06	68418.m06956 expressed protein
354594	1	3671	1	2	2689	1	1	At5g60620	3,00E-56	68418.m07608 phospholipid/glycerol acyltransferase family protein contains Pfam PF01553: Acyltransferase
356701	1	3676	1	2	8445	1	2	At5g62390	5,00E-39	68418.m07830 calmodulin-binding family protein contains IQ calmodulin-binding motif, Pfam:PF00612
359239	1	3678	1	2	9358	1	2	At5g63460	2,00E-06	68418.m07967 SAP domain-containing protein contains Pfam domain PF02037: SAP domain
358442	1	3685	1	2	3939	1	2	At5g66540	1,00E-40	68418.m08389 expressed protein ; supported by full-Length cDNA gi:12057175 from [Arabidopsis thaliana]
353060	3	3688	1	2	8171	1	1	At5g67590	4,00E-53	68418.m08523 NADH-ubiquinone oxidoreductase-related contains weak similarity to NADH-ubiquinone oxidoreductase 21 kDa subunit, mitochondrial precursor (EC 1.6.5.3) (EC 1.6.99.3) (Complex I-21KD) (CI-21KD). (Swiss-Prot:P25711) [Neurospora crassa]; contains Pfam PF04800: ETC complex I subunit conserved region
359943	1	3894	1	1	474	1	1	At1g01220	5,00E-37	68414.m00036 GHMP kinase-related contains similarity to L-fucose kinase [Homo sapiens] gi|21212956|emb|CAD29647
359325	1	3900	1	1	7385	1	1	At1g02090	3,00E-40	68414.m00133 COP9 signalosome complex subunit 7ii / CSN complex subunit 7ii (CSN7) (COP15) / FUSCA protein (FUS5) FUSCA5, CSN7, COP15; identical to CSN complex subunit 7ii [Arabidopsis thaliana] GI:18056671, FUS5 protein of the COP9 complex GI:3288823; identical to cDNA CSN complex subunit CSN7, alternatively spliced
354459	2	3903	1	1	6512	1	1	At1g02330	3,00E-51	68414.m00178 expressed protein contains similarity to hepatocellular carcinoma-associated antigen 59 GI:7158847 from [Homo sapiens]
357086	1	3903	1	1	6512	1	1	At1g02330	2,00E-17	68414.m00178 expressed protein contains similarity to hepatocellular carcinoma-associated antigen 59 GI:7158847 from [Homo sapiens]
359934	1	3904	1	1	6432	1	1	At1g02410	5,00E-85	68414.m00188 cytochrome c oxidase assembly protein CtaG / Cox11 family similar to cytochrome c oxidase assembly protein cox11 GI:1244782 from [Saccharomyces cerevisiae]; similar to Cytochrome c oxidase assembly protein COX11, mitochondrial precursor (SP:Q9Y6N1){Homo sapiens}; contains Pfam PF04442: Cytochrome c oxidase assembly protein CtaG / Cox11

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360037	1	3906	1	1	9242	1	1	At1g02680	2,00E-19	68414.m00218 transcription initiation factor IID (TFIID) 18 kDa subunit (TAFII-18) family protein similar to transcription factor TFIID (SP:Q15543) [Homo sapiens]; contains Pfam PF02269: Transcription initiation factor IID, 18kD subunit
359855	1	3919	1	1	5022	1	1	At1g04130	3,00E-53	68414.m00402 tetratricopeptide repeat (TPR)-containing protein contains non-consensus donor splice site AT at exon 4 and acceptor splice site at exon5; Contains similarity to serine/threonine protein phosphatase gb|X83099 from S. cerevisiae, SP|O95801 Tetratricopeptide repeat protein 4 Homo sapiens; contains Pfam profile PF00515: TPR Domain
357871	1	3925	2		10478	2	1	At1g04930	1,00E-21	68414.m00490 hydroxyproline-rich glycoprotein family protein Common family member: At2g32840 [Arabidopsis thaliana]
356723	1	3933	1	1	8033	1	1	At1g05720	2,00E-26	68414.m00596 selenoprotein family protein contains Prosite PS00190: Cytochrome c family heme-binding site signature; similar to 15 kDa selenoprotein (GI:12314088) {Homo sapiens}
353743	5	3949	1	1	8164	1	1	At1g07830	1,00E-51	68414.m00849 ribosomal protein L29 family protein similar to GB:CAA83057 from [Saccharomyces cerevisiae]
358074	1	3962	1	1	8402	1	1	At1g08780	4,00E-40	68414.m00977 prefoldin, putative similar to Swiss-Prot:Q9NQP4 prefoldin subunit 4 (Protein C-1) [Homo sapiens]
355209	1	3963	1	1	242	1	1	At1g09010	1,00E-13	68414.m01005 glycoside hydrolase family 2 protein low similarity to mannosidase [gi:5359712] from Cellulomonas fimi
355758	1	3966	1	1	3592	1	1	At1g09450	7,00E-26	68414.m01057 haspin-related similar to haspin (GI:9229937) {Mus musculus} and haploid germ cell-specific nuclear protein kinase (GI:13561418) {Mus musculus}
354367	2	3968	1	1	7012	1	1	At1g09760	8,00E-36	68414.m01095 U2 small nuclear ribonucleoprotein A, putative identical to U2 small nuclear ribonucleoprotein A' (U2 snRNP-A') [Arabidopsis thaliana] SWISS-PROT:P43333; supported by cDNA:gi_16649064_gb_AY059902.1_
353449	2	3975	1	1	9170	1	1	At1g10522	1,00E-29	68414.m01185 expressed protein

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356784	1	3977	1	1	4812	1	1	At1g10840	1,00E-72	68414.m01245 eukaryotic translation initiation factor 3 subunit 3 / eIF-3 gamma / eIF3h (TIF3H1) identical to SP|Q9C5Z2 Eukaryotic translation initiation factor 3 subunit 3 (eIF-3 gamma) (eIF3 p38 subunit) (eIF3h) {Arabidopsis thaliana}; contains Pfam profile PF01398: Mov34/MPN/PAD-1 family
357220	1	3977	1	1	4812	1	1	At1g10840	5,00E-13	68414.m01245 eukaryotic translation initiation factor 3 subunit 3 / eIF-3 gamma / eIF3h (TIF3H1) identical to SP|Q9C5Z2 Eukaryotic translation initiation factor 3 subunit 3 (eIF-3 gamma) (eIF3 p38 subunit) (eIF3h) {Arabidopsis thaliana}; contains Pfam profile PF01398: Mov34/MPN/PAD-1 family
359715	1	3981	1	1	8810	1	1	At1g11400	8,00E-14	68414.m01310 expressed protein
353802	2	3984	1	1	2329	1	1	At1g12050	8,00E-162	68414.m01391 fumarylacetoacetase, putative similar to fumarylacetoacetase (Fumarylacetoacetate hydrolase, Beta-diketonase, FAA)[Rattus norvegicus] SWISS-PROT:P25093
355430	1	3986	1	1	3550	1	1	At1g12230	5,00E-08	68414.m01415 transaldolase, putative similar to Swiss-Prot:P30148 transaldolase B (EC 2.2.1.2) [Escherichia coli O157:H7]
359710	1	3993	1	1	6593	1	1	At1g13330	6,00E-60	68414.m01547 expressed protein similar to nuclear receptor coactivator GT198 (GI:16506273) {Rattus norvegicus}; similar to TBP-1 interacting protein (GI:7328534) [Homo sapiens]
355768	1	4001	1	1	6532	1	1	At1g14620	4,00E-07	68414.m01738 expressed protein
359151	1	4004	1	1	3378	1	1	At1g14810	2,00E-87	68414.m01770 semialdehyde dehydrogenase family protein similar to SP:O31219 Aspartate-semialdehyde dehydrogenase (EC 1.2.1.11) (ASA dehydrogenase) (ASADH) {Legionella pneumophila}; contains Pfam profiles PF02774: Semialdehyde dehydrogenase dimerisation domain, PF01118: Semialdehyde dehydrogenase NAD binding domain
359903	1	4004	1	1	3378	1	1	At1g14810	9,00E-12	68414.m01770 semialdehyde dehydrogenase family protein similar to SP:O31219 Aspartate-semialdehyde dehydrogenase (EC 1.2.1.11) (ASA dehydrogenase) (ASADH) {Legionella pneumophila}; contains Pfam profiles PF02774: Semialdehyde dehydrogenase dimerisation domain, PF01118: Semialdehyde dehydrogenase NAD binding domain
359891	1	4005	1	1	93	1	1	At1g14850	3,00E-39	68414.m01776 non-repetitive/WGA-negative nucleoporin family protein contains Pfam profile: PF03177 non-repetitive/WGA-negative nucleoporin

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356189	1	4009	1	1	10307	1	2	At1g15230	3,00E-14	68414.m01823 expressed protein ESTs gb|R30529, gb|Z48463, gb|Z48467, gb|AA597369 and gb|AA394772 come from this gene
354995	1	4010	1	1	7540	1	1	At1g15410	8,00E-12	68414.m01846 aspartate-glutamate racemase family contains Pfam profile PF|01177 Aspartate-glutamate racemase family; contains TIGRFAM TIGR00035: aspartate racemase; similar to aspartate racemase (GI:5458794){Pyrococcus abyssi}
358804	1	4015	1	1	5860	1	1	At1g16070	2,00E-09	68414.m01928 tubby family protein similar to Tubby related protein 1 (Tubby-like protein 1) (Swiss-Prot:Q9Z273) [Mus musculus]; low similarity to Tubby related protein 1 (Tubby-like protein 1) (Swiss-Prot:O0029) {Homo sapiens}; similar to phosphodiesterase (GI:467578) [Mus musculus]; contains Pfam profile PF01167: Tub family
356829	1	4029	1	1	5481	1	1	At1g18340	2,00E-38	68414.m02292 basal transcription factor complex subunit-related similar to TFIIH basal transcription factor complex p34 subunit (Basic transcription factor 2 34 kDa subunit) (BTF2-p34) (General transcription factor IIH polypeptide 3) (SP:Q8VD76) {Mus musculus}; contains Pfam PF03850: Transcription factor Tfb4
353476	2	4033	1	1	8614	1	1	At1g18850	1,00E-35	68414.m02347 expressed protein
359624	1	4049	1	1				At1g21570	1,00E-30	68414.m02697 zinc finger (CCCH-type) family protein contains Pfam domain, PF00642: Zinc finger C-x8-C-x5-C-x3-H type (and similar)
359443	1	4057	1	1	3156	1	1	At1g22660	3,00E-41	68414.m02832 tRNA-nucleotidyltransferase, putative / tRNA adenylyltransferase, putative similar to tRNA nucleotidyltransferase [Lupinus albus] GI:1139585; contains Pfam profile PF01743: polyA polymerase family protein
358604	1	4060	1	1	326	1	1	At1g22770	1,00E-16	68414.m02845 gigantea protein (GI) identical to gigantea protein SP:Q9SQI2 from [Arabidopsis thaliana]
357977	1	4061	1	1	5534	1	1	At1g22800	8,00E-33	68414.m02848 expressed protein similar to Biotin synthesis protein bioC. {Serratia marcescens} (SP:P36571); ESTs gb|Z34075, gb|Z34835 and gb|AA404888 come from this gene
354321	3	4062	1	1	1051	1	1	At1g22860	9,00E-59	68414.m02854 TGF beta receptor associated protein-related contains weak similarity to TGF beta receptor associated protein-1 [Homo sapiens] gi|3150052|gb|AAC16903

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359911	1	4063	1	1	2508	1	1	At1g22940	1,00E-80	68414.m02867 thiamin biosynthesis protein, putative strong similarity to hydroxymethylpyrimidine kinase/thiamin-phosphate pyrophosphorylase (BTH1) GI:7488455 from [Brassica napus]
357400	1	4071	1	1	9653	1	1	At1g24450	2,00E-29	68414.m03080 ribonuclease III family protein contains similarity to Swiss-Prot:P51837 ribonuclease III (EC 3.1.26.3) (RNase III) [Coxiella burnetii]
358274	1	4074	1	1	3887	1	1	At1g25375	1,00E-52	68414.m03149 metallo-beta-lactamase family protein
354905	1	4080	1	1	4294	1	1	At1g26330	9,00E-08	68414.m03211 hypothetical protein
354322	2	4081	1	1	2282	1	1	At1g26460	2,00E-44	68414.m03227 pentatricopeptide (PPR) repeat-containing protein contains Pfam profile PF01535: PPR repeat
354922	1	4086	1	1	9169	1	1	At1g26660	1,00E-39	68414.m03246 c-myc binding protein, putative / prefoldin, putative similar to Swiss-Prot:Q99471 prefoldin subunit 5 (C-myc binding protein Mm-1) (Myc modulator 1) [Homo sapiens]
355052	1	4098	1	1	9945	1	1	At1g28250	9,00E-12	68414.m03467 expressed protein
356078	1	4101	1	1	8993	1	1	At1g29040	1,00E-26	68414.m03555 expressed protein
359447	1	4111	1	1	8487	1	1	At1g29990	2,00E-21	68414.m03668 prefoldin, putative similar to Swiss-Prot:O15212 prefoldin subunit 6 (Protein Ke2) [Homo sapiens]
356096	1	4118	1	1	4598	1	1	At1g30480	7,00E-16	68414.m03726 DNA-damage-repair/toleration protein, chloroplast (DRT111) nearly identical to SP|P42698 DNA-damage-repair/toleration protein DRT111, chloroplast precursor {Arabidopsis thaliana}; contains Pfam profiles PF01585: G-patch domain, PF00076: RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
355588	1	4125	1	1	4387	1	1	At1g31660	2,00E-80	68414.m03887 bystin family contains Pfam profile: PF05291 Bystin
356643	1	4128	1	1	3687	1	1	At1g31870	5,00E-25	68414.m03917 expressed protein
355485	1	4129	1	1	3505	1	1	At1g32200	3,00E-26	68414.m03961 glycerol-3-phosphate acyltransferase, chloroplast (ATS1) identical to SP|Q43307|PLSB_ARATH Glycerol-3-phosphate acyltransferase, chloroplast precursor (EC 2.3.1.15) (GPAT) (ATS1) {Arabidopsis thaliana}; contains Pfam profile PF01553: Acyltransferase
357605	1	4133	1	1	8167	1	1	At1g32730	1,00E-45	68414.m04036 expressed protein
359450	1	4137	1	1	839	1	1	At1g33410	4,00E-21	68414.m04136 expressed protein
358726	1	4141	1	1	9821	1	1	At1g34000	3,00E-10	68414.m04216 light stress-responsive one-helix protein (OHP2) contains similarity to photosystem II 22 kDa protein GI:6006279 from [Arabidopsis thaliana]

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353711	3	4145	1	1	7059	1	1	At1g34770	1,00E-41	68414.m04328 MAGE-8 antigen-related contains weak similarity to Swiss-Prot:P43361 melanoma-associated antigen 8 (MAGE-8 antigen) [Homo sapiens]
356030	1	4160	1	1	4293	1	1	At1g43860	3,00E-35	68414.m05053 expressed protein
359962	1	4160	1	1	4293	1	1	At1g43860	2,00E-42	68414.m05053 expressed protein
354511	1	4184	1	1	2686	1	1	At1g48850	1,00E-32	68414.m05469 chorismate synthase, putative / 5-enolpyruvylshikimate-3-phosphate phospholyase, putative similar to chorismate synthase from Lycopersicon esculentum [SP|Q42884], Corydalis sempervirens [SP|P27793]; contains Pfam chorismate synthase domain PF01264
354184	2	4191	1	1	5346	1	1	At1g49870	3,00E-07	68414.m05591 expressed protein ; expression supported by MPSS
358152	1	4191	1	1	5346	1	1	At1g49870	9,00E-16	68414.m05591 expressed protein ; expression supported by MPSS
353001	2	4200	1	1	4102	1	1	At1g50710	5,00E-108	68414.m05702 expressed protein
359048	1	4203	1	1	4395	1	1	At1g50940	5,00E-65	68414.m05727 electron transfer flavoprotein alpha subunit family protein contains Pfam profile: PF00766 electron transfer flavoprotein, alpha subunit
358987	1	4211	1	1	4600	1	1	At1g51610	1,00E-45	68414.m05814 cation efflux family protein / metal tolerance protein, putative (MTPc4) member of the cation diffusion facilitator (CDF) family, or cation efflux (CE) family, PMID:11500563
357343	1	4215	1	1	5303	1	1	At1g52530	9,00E-16	68414.m05930 expressed protein ; expression supported by MPSS
355178	1	4221	1	1	5482	1	1	At1g53120	3,00E-32	68414.m06015 RNA-binding S4 domain-containing protein
355972	1	4236	1	1	7564	1	1	At1g54990	1,00E-39	68414.m06281 expressed protein
358264	1	4239	1	1	547	1	1	At1g55090	3,00E-33	68414.m06292 carbon-nitrogen hydrolase family protein low similarity to SP|P71911 Glutamine-dependent NAD(+) synthetase (EC 6.3.5.1) {Mycobacterium tuberculosis}; contains Pfam profile PF00795: hydrolase, carbon-nitrogen family
354401	2	4243	1	1	16	1	1	At1g55350	4,00E-65	68414.m06326 calpain-type cysteine protease family identical to calpain-like protein GI:20268660 from [Arabidopsis thaliana]; contains Pfam profiles: PF00648 Calpain family cysteine protease, PF01067 Calpain large subunit,domain III; identical to cDNA calpain-like protein GI:20268659
357844	1	4244	1	1	5187	1	1	At1g55480	6,00E-26	68414.m06346 expressed protein
359992	1	4244	1	1	5187	1	1	At1g55480	5,00E-34	68414.m06346 expressed protein

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357097	1	4256	1	1	6265	1	1	At1g60430	6,00E-15	68414.m06803 ARP2/3 complex 21 kDa subunit family contains Pfam PF04062: P21-ARC (ARP2/3 complex 21 kDa subunit); similar to Arp2/3 complex subunit p21-Arc (GI:6983853) [Mus musculus]; similar to ARP2/3 complex 21 kDa subunit (P21-ARC) (Actin-related protein 2/3 complex subunit 3) (Swiss-Prot:O15145) [Homo sapiens]; similar to Chain E, Crystal Structure Of Arp23 COMPLEX Length(GI:17943203) [
353893	2	4257	1	1	5634	1	1	At1g60600	2,00E-53	68414.m06821 UbiA prenyltransferase family protein contains Pfam profile PF01040: UbiA prenyltransferase family
357658	1	4260	1	1	3421	1	1	At1g61040	4,00E-23	68414.m06872 plus-3 domain-containing protein contains Pfam profile PF03126: Plus-3 domain
358063	1	4276	1	1	5692	1	1	At1g63980	1,00E-06	68414.m07247 D111/G-patch domain-containing protein contains Pfam profile PF01585: G-patch domain
355114	1	4287	1	1	8509	1	1	At1g64510	7,00E-59	68414.m07313 ribosomal protein S6 family protein similar to plastid ribosomal protein S6 precursor GB:AAF64311 GI:7582401 from [Spinacia oleracea]
353221	2	4294	1	1	6522	1	1	At1g65030	1,00E-33	68414.m07371 transducin family protein / WD-40 repeat family protein contains 5 WD-40 repeats (PF00400); similar to PAK/PLC-interacting protein 1 (GI:14211689) [Homo sapiens]
353486	2	4298	1	1	6552	1	1	At1g65270	2,00E-76	68414.m07401 expressed protein
353616	2	4300	1	1	8175	1	1	At1g65820	4,00E-60	68414.m07469 microsomal glutathione s-transferase, putative similar to MGST3_HUMAN SP:O14880
356912	1	4305	1	1	4458	1	1	At1g66520	9,00E-57	68414.m07558 formyltransferase, putative similar to methionyl-tRNA formyltransferase [strain N315-Staphylococcus aureus] SWISS-PROT:Q99UQ2
358267	1	4312	1	1	3898	1	1	At1g67320	1,00E-52	68414.m07662 DNA primase, large subunit family contains Pfam profile PF04104: Eukaryotic-type DNA primase, large subunit; similar to DNA primase large subunit (EC 2.7.7.-) (DNA primase 58 kDa subunit) (p58) (Swiss-Prot:P49643) [Homo sapiens]
354189	2	4318	1	1	4411	1	1	At1g67960	5,00E-82	68414.m07763 expressed protein AT-AC non-consensus splice sites at intron 6
359691	1	4332	1	1	7236	1	1	At1g70590	1,00E-38	68414.m08131 F-box family protein contains Pfam PF00646: F-box domain; similar to SKP1 interacting partner 2 (SKIP2) TIGR_Ath1:At5g67250
358913	1	4344	1	1	9616	1	1	At1g71760	6,00E-06	68414.m08294 hypothetical protein
353418	3	4346	1	1	383	1	1	At1g71820	9,00E-152	68414.m08300 expressed protein

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
353157	2	4359	1	1	6560	1	1	At1g73740	3,00E-12	68414.m08538 glycosyl transferase family 28 protein similar to UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide)-pyrophosphoryl-undecaprenol N-acetylglucosamine transferase GB:O07670 [SP|O07670] from Enterococcus hirae,]SP|O07109] from Enterococcus faecalis; contains Pfam profile PF04101: Glycosyltransferase family 28 C-terminal domain
359125	1	4359	1	1	6560	1	1	At1g73740	1,00E-15	68414.m08538 glycosyl transferase family 28 protein similar to UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide)-pyrophosphoryl-undecaprenol N-acetylglucosamine transferase GB:O07670 [SP|O07670] from Enterococcus hirae,]SP|O07109] from Enterococcus faecalis; contains Pfam profile PF04101: Glycosyltransferase family 28 C-terminal domain
354560	1	4363	1	1	487	1	1	At1g73960	3,00E-15	68414.m08565 expressed protein similar to TATA binding protein associated factor (GI:2827282) [Homo sapiens]; similar to Transcription initiation factor TFIID 150 kDa subunit (TAFII-150) (TAFII150) (Swiss-Prot:Q24325) [Drosophila melanogaster]
356948	1	4363	1	1	487	1	1	At1g73960	5,00E-07	68414.m08565 expressed protein similar to TATA binding protein associated factor (GI:2827282) [Homo sapiens]; similar to Transcription initiation factor TFIID 150 kDa subunit (TAFII-150) (TAFII150) (Swiss-Prot:Q24325) [Drosophila melanogaster]
355624	1	4364	1	1	5096	1	1	At1g73970	7,00E-09	68414.m08567 expressed protein
355236	1	4371	1	1	7267	1	1	At1g75150	1,00E-07	68414.m08729 expressed protein ; expression supported by MPSS
359063	1	4371	1	1	7267	1	1	At1g75150	6,00E-08	68414.m08729 expressed protein ; expression supported by MPSS
355933	1	4374	1	1	8949	1	1	At1g75670	4,00E-20	68414.m08791 expressed protein similar to DNA-dependent RNA polymerase 19 kDa polypeptide (EC 2.7.7.6) (A43) (Swiss-Prot:O43036) [Schizosaccharomyces pombe]
353694	2	4389	1	1	638	1	1	At1g77550	1,00E-71	68414.m09030 tubulin-tyrosine ligase family protein contains tubulin-tyrosine ligase family domain, Pfam:PF03133
353678	2	4390	1	1	8857	1	1	At1g77710	2,00E-42	68414.m09048 expressed protein similar to hypothetical protein GB:P34661 [Caenorhabditis elegans]
353748	2	4393	1	1	6201	1	1	At1g78620	8,00E-65	68414.m09163 integral membrane family protein contains Pfam domain PF01940: Integral membrane protein

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358844	1	4394	1	1	6510	1	1	At1g78650	2,00E-16	68414.m09166 expressed protein weak similarity to DNA polymerase delta subunit 3 (DNA polymerase delta subunit p66) (Swiss-Prot:Q15054) [Homo sapiens]
358958	1	4400	1	1	576	1	1	At1g79690	2,00E-71	68414.m09294 MutT/nudix family protein contains Pfam NUDIX domain [PF00293]; very low similarity to Chain A and Chain B of Escherichia coli isopentenyl diphosphate:dimethylallyl diphosphate isomerase [gi:15826361] [gi:15826360]
359532	1	4403	1	1	6496	1	1	At1g79810	7,00E-70	68414.m09319 Pex2/Pex12 N-terminal domain-containing protein / zinc finger (C3HC4-type RING finger) family protein contains Pfam profiles PF00097: zinc finger C3HC4 type (RING finger), PF04757: Pex2/Pex12 amino terminal region
357436	1	4408	2		10484	2	1	At1g80245	2,00E-12	68414.m09392 expressed protein
359198	1	4418	1	1	9082	1	1	At2g01120	4,00E-25	68415.m00020 origin recognition complex subunit 4, putative (ORC4) similar to origin recognition complex subunit 4 (GI:15866782) [Zea mays]
354981	1	4424	1	1	9486	1	1	At2g02050	1,00E-31	68415.m00140 NADH-ubiquinone oxidoreductase B18 subunit, putative contains Pfam PF05676: NADH-ubiquinone oxidoreductase B18 subunit (NDUFB7); similar to NADH-ubiquinone oxidoreductase B18 subunit (EC 1.6.5.3) (EC 1.6.99.3) (Complex I-B18) (CI-B18) (Cell adhesion protein SQM1) (Swiss-Prot:P17568) [Homo sapiens]; similar to NADH:ubiquinoe oxidoreductase NDUFB7 subunit (GI:9651635) [Homo sapiens]
356615	1	4427	1	1	6547	1	1	At2g02590	4,00E-12	68415.m00199 expressed protein
358051	1	4434	1	1	6837	1	1	At2g03780	4,00E-29	68415.m00338 translin family protein similar to SP|Q99598 Translin-associated protein X (Translin-associated factor X) {Homo sapiens}; contains Pfam profile PF01997: Translin family
354988	1	4435	1	1	8937	1	1	At2g03870	4,00E-30	68415.m00349 small nuclear ribonucleoprotein, putative / snRNP, putative / Sm protein, putative similar to U6 snRNA-associated Sm-like protein LSm7 [Homo sapiens] SWISS-PROT:Q9UK45
358161	1	4439	1	1	4191	1	1	At2g04305	1,00E-64	68415.m00423 magnesium transporter CorA-like protein-related
358218	1	4444	1	1	727	1	1	At2g04660	1,00E-69	68415.m00475 E3 ubiquitin ligase, putative E3, ubiquitin ligase; contains similarity to anaphase-promoting complex subunit 2 GI:6180009 from [Homo sapiens]
358706	1	4451	1	1	8462	1	1	At2g04900	4,00E-43	68415.m00509 expressed protein
354247	2	4452	1	1	546	1	1	At2g05120	1,00E-81	68415.m00539 expressed protein

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359976	1	4453	1	1	257	1	1	At2g05170	8,00E-59	68415.m00544 vacuolar protein sorting 11 family protein / VPS11 family protein similar to Vacuolar protein sorting 11 (hVPS11) (PP3476) (Swiss-Prot:Q9H270) [Homo sapiens]; similar to Vacuolar biogenesis protein END1 (PEP5 protein) (Vacuolar protein sorting 11) (Swiss-Prot:P12868) [Saccharomyces cerevisiae]
357269	1	4454	1	1	3428	1	1	At2g05320	1,00E-56	68415.m00560 beta-1,2-N-acetylglucosaminyltransferase II identical to beta-1,2-N-acetylglucosaminyltransferase II GI:10183645 from [Arabidopsis thaliana]
354710	1	4469	1	1	1828	1	1	At2g11000	1,00E-22	68415.m01176 natC N(alpha)-terminal acetyltransferase, Mak10 subunit family protein contains Pfam PF04112: Mak10 subunit, NatC N(alpha)-terminal acetyltransferase; similar to corneal wound healing related protein (GI:8926320) [Rattus norvegicus]; weak similarity to Glucose repressible protein MAK10 (Swiss-Prot:Q02197) [Saccharomyces cerevisiae]
354506	1	4476	1	1	602	1	1	At2g13540	5,00E-46	68415.m01493 mRNA cap-binding protein (ABH1) identical to mRNA cap binding protein [Arabidopsis thaliana] GI:15192738; contains Pfam profile PF02854: MIF4G domain; identical to cDNA nuclear cap-binding protein CBP80 GI:8515770
357582	1	4478	1	1	9247	1	1	At2g14045	6,00E-31	68415.m01562 expressed protein
358089	1	4484	1	1	8231	1	1	At2g14835	8,00E-70	68415.m01682 zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)
356637	1	4485	2					At4g34265	5,00E-06	68417.m04871 expressed protein
357804	1	4485	2					At4g34265	1,00E-13	68417.m04871 expressed protein
358482	1	4487	1	1	8638	1	1	At2g15270	7,00E-24	68415.m01741 expressed protein
353574	2	4496	1	1	5740	1	1	At2g16860	2,00E-14	68415.m01939 GCIP-interacting family protein similar to GCIP-interacting protein mp29 (GI:27372623) [Mus musculus]; similar to GCIP-interacting protein P29 (GI:11967379) [Homo sapiens]
357042	1	4515	1	1	1650	1	1	At2g19880	7,00E-52	68415.m02324 ceramide glucosyltransferase, putative similar to ceramide glucosyltransferase (GI:14718995) [Gossypium arboreum]; weak similarity to Ceramide glucosyltransferase (Glucosylceramide synthase) (GCS) (UDP-glucose:N-acylsphingosine D-glucosyltransferase) (GLCT-1) (Swiss-Prot:Q16739) [Homo sapiens]

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
357745	1	4517	1	1	5149	1	1	At2g20210	4,00E-37	68415.m02363 leucine-rich repeat family protein contains leucine rich repeat (LRR) domains, Pfam:PF00560
357384	1	4518	1	1	3558	1	1	At2g20280	4,00E-51	68415.m02369 zinc finger (CCCH-type) family protein contains Pfam domain, PF00642: Zinc finger C-x8-C-x5-C-x3-H type (and similar)
357346	1	4520	1	1				At2g20410	2,00E-41	68415.m02382 activating signal cointegrator-related similar to ASC-1 (GI:6581062) [Mus musculus]; similar to Activating signal cointegrator 1 (ASC-1) (Thyroid receptor interacting protein 4) (TRIP-4) (Swiss-Prot:Q15650) [Homo sapiens]
358764	1	4521	1	1	1847	1	1	At2g20420	1,00E-113	68415.m02383 succinyl-CoA ligase [GDP-forming] beta-chain, mitochondrial, putative / succinyl-CoA synthetase, beta chain, putative / SCS-beta, putative identical to SP|O82662 Succinyl-CoA ligase [GDP-forming] beta-chain, mitochondrial precursor (EC 6.2.1.4) (Succinyl-CoA synthetase, beta chain) (SCS- beta) {Arabidopsis thaliana}; similar to SP|O97580 Succinyl-CoA ligase [ADP-forming] beta-chain, mitochondrial precursor (EC 6.2.1.5) {Sus scrofa}; contains Pfam profiles PF00549: CoA-ligase, PF02222: ATP-grasp domain
353376	4	4532	1	1	4382	1	1	At2g21070	3,00E-67	68415.m02501 expressed protein
355140	1	4532	1	1	4382	1	1	At2g21070	2,00E-29	68415.m02501 expressed protein
357835	1	4542	1	1	6991	1	1	At2g21870	2,00E-54	68415.m02599 expressed protein
356294	1	4546	1	1	6204	1	1	At2g22370	8,00E-09	68415.m02654 expressed protein
357089	1	4549	1	1	6061	1	1	At2g22650	4,00E-24	68415.m02684 FAD-dependent oxidoreductase family protein
354502	1	4552	1	1	9370	1	1	At2g23090	2,00E-31	68415.m02753 expressed protein
355462	1	4552	1	1	9370	1	1	At2g23090	1,00E-32	68415.m02753 expressed protein
354900	1	4557	1	1	9489	1	1	At2g24090	5,00E-10	68415.m02877 ribosomal protein L35 family protein contains Pfam profile PF01632: ribosomal protein L35
360054	1	4560	1	1	9842	1	1	At2g24970	5,00E-34	68415.m02986 expressed protein
355214	1	4561	1	1	4708	1	1	At2g25100	2,00E-80	68415.m03003 ribonuclease HII family protein contains Pfam profile: PF01351 ribonuclease HII
357776	1	4565	1	1	5411	1	1	At2g25570	2,00E-83	68415.m03062 expressed protein
354498	1	4575	1	1	8717	1	1	At2g26210	2,00E-35	68415.m03147 ankyrin repeat family protein contains ankyrin repeats, Pfam:PF00023
356383	1	4576	1	1	9432	1	1	At2g26340	8,00E-43	68415.m03160 expressed protein
354742	1	4585	2		10435	2	1	At2g27385	8,00E-06	68415.m03304 expressed protein

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353661	2	4597	1	1	8737	1	1	At2g30410	3,00E-40	68415.m03704 tubulin folding cofactor A (KIESEL) identical to cDNA tubulin folding cofactor A, GI:20514256, SP|O04350 Tubulin-specific chaperone A (Tubulin-folding cofactor A) (CFA) (TCP1-chaperonin cofactor A homolog) {Arabidopsis thaliana}
356431	1	4597	1	1	8737	1	1	At2g30410	6,00E-28	68415.m03704 tubulin folding cofactor A (KIESEL) identical to cDNA tubulin folding cofactor A, GI:20514256, SP|O04350 Tubulin-specific chaperone A (Tubulin-folding cofactor A) (CFA) (TCP1-chaperonin cofactor A homolog) {Arabidopsis thaliana}
355820	1	4606	1	1	4651	1	1	At2g32080	5,00E-24	68415.m03921 PUR alpha-1 protein identical to PUR alpha-1 GI:5081612 from [Arabidopsis thaliana]; contains Pfam profile: PF04845 PurA ssDNA and RNA-binding protein
353686	2	4609	1	1	5316	1	1	At2g32520	1,00E-111	68415.m03973 dienelactone hydrolase family protein low similarity to dienelactone hydrolase [Pseudomonas resinovorans] GI:13094163; contains Pfam profile PF01738: Dienelactone hydrolase family
357025	1	4613	1	1	4242	1	1	At2g32900	6,00E-55	68415.m04033 centromere/kinetochore protein, putative (ZW10) identical to centromere/kinetochore protein zw10 homolog SP:O48626 from [Arabidopsis thaliana]
357560	1	4614	1	1	5889	1	1	At2g32980	4,00E-46	68415.m04042 expressed protein
357208	1	4624	1	1	4000	1	1	At2g34470	3,00E-14	68415.m04231 urease accessory protein (UREG) identical to urease accessory protein UREG GI:4324678 from [Arabidopsis thaliana]; contains Pfam profile: PF01495 HypB/UreG nucleotide-binding domain
358203	1	4624	1	1	4000	1	1	At2g34470	7,00E-27	68415.m04231 urease accessory protein (UREG) identical to urease accessory protein UREG GI:4324678 from [Arabidopsis thaliana]; contains Pfam profile: PF01495 HypB/UreG nucleotide-binding domain
353014	2	4625	1	1	7738	1	1	At2g34570	8,00E-29	68415.m04247 expressed protein contains Pfam profile: PF04900 protein of unknown function, DUF652
357663	1	4625	1	1	7738	1	1	At2g34570	9,00E-13	68415.m04247 expressed protein contains Pfam profile: PF04900 protein of unknown function, DUF652
354563	1	4630	1	1	8395	1	1	At2g34860	1,00E-43	68415.m04280 chaperone protein dnaJ-related contains Pfam PF00684 : DnaJ central domain (4 repeats); similar to Chaperone protein dnaJ (Heat shock protein 40) (SP:Q9UXR9) {Methanosarcina thermophila}
357225	1	4631	1	1	4610	1	1	At2g34980	4,00E-22	68415.m04292 phosphatidylinositolglycan synthase family protein similar to SP|Q92535 Phosphatidylinositol-glycan biosynthesis, class C protein (PIG-C) {Homo sapiens}

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359360	1	4633	1	1	924	1	1	At2g35040	2,00E-99	68415.m04299 AICARFT/IMPCHase bienzyme family protein similar to SP|P12048 Bifunctional purine biosynthesis protein purH [Includes: Phosphoribosylaminoimidazolecarboxamide formyltransferase (EC 2.1.2.3) (AICAR transformylase); IMP cyclohydrolase (EC 3.5.4.10) (Inosinicase) (IMP synthetase) (ATIC)] {Bacillus subtilis}; contains Pfam profiles PF01808: AICARFT/IMPCHase bienzyme, PF02142: MGS-like domain
354829	1	4634	1	1	132	1	1	At2g35110	3,00E-67	68415.m04307 HEM protein-related weak similarity to Membrane-associated protein Hem (Dhem-2) (Swiss-Prot:P55162) [Drosophila melanogaster]; weak similarity to Nck-associated protein 1 (NAP 1) (p125Nap1) (Membrane-associated protein HEM-2) (Swiss-Prot:P55161) [Rattus norvegicus]
355364	1	4637	1	1	5696	1	1	At2g35450	5,00E-22	68415.m04343 amidohydrolase family similar to fluorene degradation (FldB) protein (GI:7573256) [Sphingomonas sp. LB126]; similar to 2-pyrone-4,6-dicarboxylic acid hydrolase (GI:3738249) [Sphingomonas paucimobilis]; contains Pfam PF04909: Amidohydrolase family
358199	1	4644	1	1	7761	1	1	At2g36230	3,00E-63	68415.m04447 N'-5'-phosphoribosyl-formimino-5-aminoimidazole-4-carboxamide ribonucleotide isomerase identical to N'-5'-phosphoribosyl-formimino-5-aminoimidazole-4-carboxamide ribonucleotide isomerase GI:3449284 from [Arabidopsis thaliana]; contains Pfam profile: PF00977 histidine biosynthesis protein
355184	1	4657	1	1	10165	1	1	At2g37195	2,00E-11	68415.m04563 expressed protein
355641	1	4663	2					At2g37960	4,00E-06	68415.m04659 expressed protein
355593	1	4666	1	1	10018	1	1	At2g38140	4,00E-17	68415.m04682 chloroplast 30S ribosomal protein S31 (PSRP4)
357055	1	4670	1	1	9802	1	1	At2g38580	4,00E-16	68415.m04739 expressed protein ; expression supported by MPSS
354227	2	4674	1	1	8982	1	1	At2g39170	2,00E-33	68415.m04811 expressed protein
358773	1	4677	1	1	10358	1	1	At2g39705	6,00E-08	68415.m04871 expressed protein
353944	2	4681	1	1	7582	1	1	At2g39950	1,00E-18	68415.m04909 expressed protein
357677	1	4683	1	1	8391	1	1	At2g40316	2,00E-23	68415.m04968 expressed protein
353144	2	4684	1	1	1205	1	1	At2g40360	1,00E-58	68415.m04977 transducin family protein / WD-40 repeat family protein contains 4 WD-40 repeats (PF00400); similar to block of proliferation protein Bop1 (GI:1679772) [Mus musculus]

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358236	1	4684	1	1	1205	1	1	At2g40360	2,00E-28	68415.m04977 transducin family protein / WD-40 repeat family protein contains 4 WD-40 repeats (PF00400); similar to block of proliferation protein Bop1 (GI:1679772) [Mus musculus]
355851	1	4690	1	1	1067	1	1	At2g40980	3,00E-10	68415.m05062 expressed protein
357553	1	4697	1	1	3194	1	1	At2g42120	2,00E-26	68415.m05210 DNA polymerase delta small subunit-related similar to DNA polymerase delta small subunit SP:Q9LRE5 from [Oryza sativa]
358182	1	4697	1	1	3194	1	1	At2g42120	6,00E-38	68415.m05210 DNA polymerase delta small subunit-related similar to DNA polymerase delta small subunit SP:Q9LRE5 from [Oryza sativa]
355629	1	4706	1	1	6909	1	1	At2g43210	1,00E-20	68415.m05371 UBX domain-containing protein contains Pfam profile PF00789: UBX domain
353855	4	4724	1	1	8340	1	1	At2g45640	6,00E-47	68415.m05675 sin3 associated polypeptide p18 family protein similar to Sin3 associated polypeptide p18 (2HOR0202) (Swiss-Prot:O00422) [Homo sapiens]
357639	1	4724	1	1	8340	1	1	At2g45640	2,00E-49	68415.m05675 sin3 associated polypeptide p18 family protein similar to Sin3 associated polypeptide p18 (2HOR0202) (Swiss-Prot:O00422) [Homo sapiens]
353986	2	4726	1	1	4568	1	1	At2g45730	2,00E-27	68415.m05688 eukaryotic initiation factor 3 gamma subunit family protein contains Pfam profile PF04189: Eukaryotic initiation factor 3, gamma subunit
356200	1	4730	1	1	8966	1	1	At2g46000	2,00E-07	68415.m05722 expressed protein
354937	1	4732	1	1	4288	1	1	At2g46090	2,00E-80	68415.m05733 diacylglycerol kinase family protein contains INTERPRO domain, IPR001206, DAG-kinase catalytic domain
353973	3	4747	1	1	468	1	1	At2g47980	5,00E-72	68415.m06004 expressed protein
356494	1	4767	1	1	8002	1	1	At3g02820	1,00E-12	68416.m00274 zinc knuckle (CCHC-type) family protein contains Pfam domain, PF00098: Zinc knuckle
355208	1	4769	1	1	9439	1	1	At3g03070	3,00E-34	68416.m00303 NADH-ubiquinone oxidoreductase-related contains weak similarity to NADH-ubiquinone oxidoreductase 13 kDa-A subunit, mitochondrial precursor (EC 1.6.5.3) (EC 1.6.99.3) (Complex I-13KD-A) (CI-13KD-A) (Swiss-Prot:P23934) [Bos taurus]
353141	2	4790	1	1	6550	1	1	At3g05520	4,00E-49	68416.m00605 F-actin capping protein alpha subunit family protein contains Pfam profile: PF01267 F-actin capping protein alpha subunit
356280	1	4797	2					At5g18790	4,00E-18	68418.m02232 ribosomal protein L33 family protein ribosomal protein L33, Rickettsia prowazekii, PIR:E71650
353863	2	4798	1	1	330	1	1	At3g06530	5,00E-102	68416.m00757 BAP28-related similar to Protein BAP28 (Swiss-Prot:Q9H583) [Homo sapiens]

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353469	4	4800	1	1	1840	1	1	At3g06580	2,00E-164	68416.m00764 galactokinase (GAL1) identical to galactokinase (Galactose kinase) [Arabidopsis thaliana] SWISS-PROT:Q9SEE5
358464	1	4800	1	1	1840	1	1	At3g06580	9,00E-62	68416.m00764 galactokinase (GAL1) identical to galactokinase (Galactose kinase) [Arabidopsis thaliana] SWISS-PROT:Q9SEE5
355334	1	4815	1	1	3313	1	1	At3g07790	4,00E-14	68416.m00951 DGCR14-related similar to DGCR14 protein (DiGeorge syndrome critical region 14) (ES2 protein) (Swiss-Prot:Q96DF8) [Homo sapiens]
359274	1	4818	1	1	4419	1	1	At3g08505	3,00E-18	68416.m00987 zinc finger (CCCH-type/C3HC4-type RING finger) family protein contains zinc finger C-x8-C-x5-C-x3-H type (and similar) domains, Pfam:PF00642 and zinc finger, C3HC4 type (RING finger) domain, Pfam:PF00097
359448	1	4827	1	1	6683	1	1	At3g09180	2,00E-43	68416.m01090 expressed protein
355193	1	4830	2		9745	2	1	At3g09390	2,00E-16	68416.m01115 metallothionein protein, putative (MT2A) identical to Swiss-Prot:P25860 metallothionein-like protein 2A (MT-2A) (MT-K) (MT-1G) [Arabidopsis thaliana]
357845	1	4832	1	1	4688	1	1	At3g09850	2,00E-29	68416.m01175 D111/G-patch domain-containing protein contains Pfam profile PF01585: G-patch domain
356980	1	4841	1	1	3331	1	1	At3g10630	9,00E-51	68416.m01278 glycosyl transferase family 1 protein contains Pfam glycosyl transferase, group 1 family protein domain PF00534; C-terminal portion similar to mannosyltransferase GB:BAA28328 [Escherichia coli]
359585	1	4849	1	1	2108	1	1	At3g12010	1,00E-56	68416.m01488 expressed protein contains Prosite PS00626: Regulator of chromosome condensation (RCC1) signature 2
358671	1	4854	1	1	8574	1	1	At3g12260	2,00E-34	68416.m01531 complex 1 family protein / LVR family protein contains Pfam PF05347: Complex 1 protein (LYR family)
358139	1	4855	1	1	5890	1	1	At3g12300	2,00E-44	68416.m01535 expressed protein
359100	1	4859	1	1	7318	1	1	At3g12530	1,00E-33	68416.m01559 DNA replication protein-related similar to DNA replication protein Psf2 (GI:29365481) [Xenopus laevis]; contains Pfam profile PF04128: Domain of unknown function (DUF392)
358301	1	4860	1	1	518	1	1	At3g12590	3,00E-11	68416.m01568 expressed protein
356192	1	4862	1	1	5606	1	1	At3g13200	5,00E-23	68416.m01652 Cwf15 / Cwc15 cell cycle control family protein contains Pfam profile PF04889: Cwf15/Cwc15 cell cycle control protein; similar to Cell cycle control protein cwf15 (Swiss-Prot:P78794) [Schizosaccharomyces pombe]

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
357821	1	4865	1	1	3060	1	1	At3g13235	5,00E-56	68416.m01666 ubiquitin family protein contains INTERPRO:IPR000626 ubiquitin domain
353538	2	4866	1	1	55	1	1	At3g13330	2,00E-72	68416.m01678 expressed protein
359945	1	4871	1	1	311	1	1	At3g14120	3,00E-44	68416.m01786 expressed protein similar to Nuclear pore complex protein Nup107 (Nucleoporin Nup107) (107 kDa nucleoporin) (p105) (Swiss-Prot:P52590) [Rattus norvegicus]
359155	1	4875	1	1	8605	1	1	At3g15095	5,00E-10	68416.m01909 expressed protein
354878	1	4876	1	1	8036	1	1	At3g15110	4,00E-19	68416.m01911 expressed protein
357568	1	4880	1	1	9293	1	1	At3g15190	1,00E-43	68416.m01920 chloroplast 30S ribosomal protein S20, putative contains Pfam profile: PF01649 ribosomal protein S20
359313	1	4886	1	1	2434	1	1	At3g16270	7,00E-61	68416.m02053 expressed protein gene model
358280	1	4896	1	1	2146	1	1	At3g17740	5,00E-33	68416.m02264 expressed protein
356071	1	4898	1	1	8546	1	1	At3g17930	3,00E-14	68416.m02283 expressed protein
358465	1	4898	1	1	8546	1	1	At3g17930	6,00E-22	68416.m02283 expressed protein
354703	1	4904	1	1	9083	1	1	At3g18760	9,00E-42	68416.m02381 ribosomal protein S6 family protein contains TIGRFAM profile TIGR00166: ribosomal protein S6
360031	1	4904	1	1	9083	1	1	At3g18760	1,00E-14	68416.m02381 ribosomal protein S6 family protein contains TIGRFAM profile TIGR00166: ribosomal protein S6
357830	1	4906	1	1	8796	1	1	At3g18800	2,00E-07	68416.m02388 expressed protein
359408	1	4914	1	1	811	1	1	At3g19820	6,00E-56	68416.m02511 cell elongation protein / DWARF1 / DIMINUTO (DIM) identical to GB:S71189 [SP|Q39085] from [Arabidopsis thaliana]; contains Pfam FAD binding domain PF01565
359985	1	4915	1	1	1228	1	1	At3g19870	1,00E-38	68416.m02516 expressed protein
355332	1	4917	1	1	6137	1	1	At3g20320	1,00E-22	68416.m02575 mce-related family protein contains Pfam PF02470: mce related protein
356090	1	4922	1	1	597	1	1	At3g20720	2,00E-07	68416.m02622 expressed protein
357970	1	4924	1	1	4588	1	1	At3g20790	2,00E-50	68416.m02629 oxidoreductase family protein weak similarity to SP|Q07982 Glucose--fructose oxidoreductase precursor (EC 1.1.99.28) {Zymomonas mobilis}; contains Pfam profiles PF01408: Oxidoreductase family NAD-binding Rossmann fold, PF02894: Oxidoreductase family C-terminal alpha/beta domain

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
356286	1	4927	1	1	3606	1	1	At3g21110	4,00E-68	68416.m02668 phosphoribosylamidoimidazole-succinocarboxamide synthase / SAICAR synthetase (PUR7) identical to phosphoribosylamidoimidazole-succinocarboxamide synthase, chloroplast [precursor] SP:P38025 from [Arabidopsis thaliana]
353847	2	4930	1	1	6155	1	1	At3g21350	8,00E-56	68416.m02696 RNA polymerase transcriptional regulation mediator-related contains weak similarity to RNA polymerase transcriptional regulation mediator, subunit 6 homolog (Activator-recruited cofactor 33 kDa component) (ARC33) (NY-REN-28 antigen) (Swiss-Prot:O75586) [Homo sapiens]
353412	2	4937	1	1	5918	1	1	At3g22660	6,00E-59	68416.m02860 rRNA processing protein-related contains weak similarity to rRNA processing protein EBP2 (EBNA1-binding protein homolog) (Swiss-Prot:P36049) [Saccharomyces cerevisiae]
358633	1	4939	1	1	2701	1	1	At3g22990	3,00E-24	68416.m02899 expressed protein
353396	7	4948	2					At4g32295	1,00E-60	68417.m04595 expressed protein
355464	1	4954	1	1	5720	1	1	At3g25470	1,00E-18	68416.m03166 bacterial hemolysin-related similar to hemolysine GB:AAD36643 from [Thermotoga maritima], contains Pfam profile: PF01479 S4 domain
354070	2	4969	1	1	4327	1	1	At3g26950	1,00E-57	68416.m03374 expressed protein
358521	1	4975	1	1	4658	1	1	At3g27325	2,00E-39	68416.m03415 expressed protein
356754	1	5000	2		10095	1	2	At5g21940	9,00E-12	68418.m02547 expressed protein supported by full length cDNA GI:22531282 from [Arabidopsis thaliana]
356672	1	5006	1	1	9164	1	1	At3g44890	2,00E-20	68416.m04836 50S ribosomal protein L9, chloroplast (CL9) contains Pfam profile PF03948: Ribosomal protein L9, C-terminal domain; contains Pfam profile PF01281: ribosomal protein L9, N-terminal domain; contains TIGRfam profile TIGR00158: ribosomal protein L9
356786	1	5014	1	1	5751	1	1	At3g46200	8,00E-29	68416.m05001 MutT/nudix family protein similar to head organizer protein P17F11 GI:17976973 from [Xenopus laevis]; contains a NUDIX hydrolase domain IPR000086
359770	1	5015	1	1	3782	1	1	At3g46220	2,00E-55	68416.m05003 expressed protein
359790	1	5017	2					At3g46580	6,00E-15	68416.m05056 methyl-CpG-binding domain-containing protein weak similarity to SP|P51608 Methyl-CpG-binding protein 2 (MeCP-2 protein) (MeCP2) {Homo sapiens}; contains Pfam profile PF01429: Methyl-CpG binding domain

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
353355	2	5018	1	1	7696	1	1	At3g46940	2,00E-60	68416.m05095 deoxyuridine 5'-triphosphate nucleotidohydrolase family contains Pfam profile: PF00692 deoxyuridine 5'-triphosphate nucleotidohydrolase
355113	1	5020	1	1	9390	1	1	At3g47650	9,00E-33	68416.m05187 bundle-sheath defective protein 2 family / bsd2 family similar to bundle sheath defective protein 2 [Zea mays] GI:4732091
353464	2	5021	1	1	6125	1	1	At3g47810	5,00E-80	68416.m05210 calcineurin-like phosphoesterase family protein contains Pfam profile: PF00149 calcineurin-like phosphoesterase
353082	2	5024	1	1	246	1	1	At3g48110	3,00E-31	68416.m05246 aminoacyl-t-RNA synthetase, putative similar to aminoacyl-t-RNA synthetase GI:2654226 from [Arabidopsis thaliana]; contains Pfam profiles: PF02092 glycyl-tRNA synthetase beta subunit,PF02091 glycyl-tRNA synthetase alpha subunit
354437	2	5024	1	1	246	1	1	At3g48110	5,00E-69	68416.m05246 aminoacyl-t-RNA synthetase, putative similar to aminoacyl-t-RNA synthetase GI:2654226 from [Arabidopsis thaliana]; contains Pfam profiles: PF02092 glycyl-tRNA synthetase beta subunit,PF02091 glycyl-tRNA synthetase alpha subunit
356930	1	5024	1	1	246	1	1	At3g48110	6,00E-15	68416.m05246 aminoacyl-t-RNA synthetase, putative similar to aminoacyl-t-RNA synthetase GI:2654226 from [Arabidopsis thaliana]; contains Pfam profiles: PF02092 glycyl-tRNA synthetase beta subunit,PF02091 glycyl-tRNA synthetase alpha subunit
359136	1	5024	1	1	246	1	1	At3g48110	1,00E-10	68416.m05246 aminoacyl-t-RNA synthetase, putative similar to aminoacyl-t-RNA synthetase GI:2654226 from [Arabidopsis thaliana]; contains Pfam profiles: PF02092 glycyl-tRNA synthetase beta subunit,PF02091 glycyl-tRNA synthetase alpha subunit
358543	1	5027	1	1	2225	1	1	At3g48380	6,00E-06	68416.m05281 expressed protein
359861	1	5027	1	1	2225	1	1	At3g48380	1,00E-37	68416.m05281 expressed protein
354768	1	5028	1	1	2024	1	1	At3g48500	2,00E-54	68416.m05294 expressed protein
357792	1	5035	1	1	8454	1	1	At3g49900	1,00E-23	68416.m05455 BTB/POZ domain-containing protein contains BTB/POZ domain, INTERPRO:IPR000210
355643	1	5052	1	1	6687	1	1	At3g51610	3,00E-30	68416.m05656 expressed protein
356509	1	5054	1	1	2943	1	1	At3g51820	2,00E-24	68416.m05683 chlorophyll synthetase, putative identical to gi:972938 putative chlorophyll synthetase from Arabidopsis thaliana
359194	1	5055	1	1	5854	1	1	At3g52030	7,00E-09	68416.m05707 F-box family protein / WD-40 repeat family protein

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
355349	1	5060	1	1	5173	1	1	At3g52120	6,00E-30	68416.m05721 SWAP (Suppressor-of-White-APricot)/surp domain-containing protein / D111/G-patch domain-containing protein contains Pfam profiles PF01585: G-patch domain, PF01805: Surp module
358447	1	5060	1	1	5173	1	1	At3g52120	2,00E-35	68416.m05721 SWAP (Suppressor-of-White-APricot)/surp domain-containing protein / D111/G-patch domain-containing protein contains Pfam profiles PF01585: G-patch domain, PF01805: Surp module
359719	1	5061	1	1	7628	1	1	At3g52155	1,00E-46	68416.m05725 expressed protein
358271	1	5064	1	1	9453	1	1	At3g52300	2,00E-40	68416.m05748 ATP synthase D chain-related contains weak similarity to ATP synthase D chain, mitochondrial (EC 3.6.3.14) (Swiss-Prot:P31399) [Rattus norvegicus]
359988	1	5065	1	1	4698	1	1	At3g52640	2,00E-10	68416.m05800 nicastrin-related contains weak similarity to Nicastrin precursor (Swiss-Prot:Q92542) [Homo sapiens]
353123	2	5070	1	1	9162	1	1	At3g53440	1,00E-08	68416.m05898 expressed protein
354778	1	5071	1	1	3678	1	1	At3g53580	1,00E-45	68416.m05918 diaminopimelate epimerase family protein contains Pfam profile PF01678: Diaminopimelate epimerase
353880	3	5076	1	1	175	1	1	At3g54440	5,00E-148	68416.m06023 glycoside hydrolase family 2 protein similar to beta-galactosidase (lactase) from Alteromonas haloplanktis [SP|P81650]; contains Pfam glycoside hydrolase domains PF02836, PF02837, PF02929, PF02930
359788	1	5081	1	1	8254	1	1	At3g54970	4,00E-17	68416.m06097 expressed protein
354206	2	5089	1	1	7987	1	1	At3g56210	1,00E-47	68416.m06247 expressed protein
357765	1	5093	1	1	7813	1	1	At3g56820	1,00E-34	68416.m06319 expressed protein
354035	2	5096	1	1	2239	1	1	At3g56940	1,00E-43	68416.m06334 dicarboxylate diiron protein, putative (Crd1) similar to leucine-containing zipper protein At103 GP:6911864; contains Pfam profile PF05447: Copper response defect 1 (CRD1)
359676	1	5098	1	1	6594	1	1	At3g57000	6,00E-44	68416.m06345 nucleolar essential protein-related contains weak similarity to Nucleolar essential protein 1 (Essential for mitotic growth 1) (Swiss-Prot:Q06287) [Saccharomyces cerevisiae]
358192	1	5109	1	1	8094	1	1	At3g59090	2,00E-33	68416.m06588 expressed protein
359256	1	5109	1	1	8094	1	1	At3g59090	1,00E-17	68416.m06588 expressed protein
358485	1	5119	1	1	651	1	1	At3g60740	5,00E-109	68416.m06795 tubulin folding cofactor D identical to tubulin folding cofactor D GI:20514263 from [Arabidopsis thaliana]
355574	1	5121	1	1	2849	1	1	At3g60850	3,00E-12	68416.m06807 expressed protein

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358455	1	5121	1	1	2849	1	1	At3g60850	7,00E-28	68416.m06807 expressed protein
359727	1	5125	1	1	86	1	1	At3g62010	1,00E-85	68416.m06964 expressed protein
357508	1	5128	1	1	9560	1	1	At3g62190	2,00E-08	68416.m06987 DNAJ heat shock N-terminal domain-containing protein similar to SP|P39101 CAJ1 protein Saccharomyces cerevisiae; contains Pfam profile PF00226 DnaJ domain
354992	1	5130	1	1	5117	1	1	At3g62330	9,00E-40	68416.m07002 zinc knuckle (CCHC-type) family protein contains Pfam domain, PF00098: Zinc knuckle
356219	1	5130	1	1	5117	1	1	At3g62330	4,00E-25	68416.m07002 zinc knuckle (CCHC-type) family protein contains Pfam domain, PF00098: Zinc knuckle
359889	1	5130	1	1	5117	1	1	At3g62330	2,00E-17	68416.m07002 zinc knuckle (CCHC-type) family protein contains Pfam domain, PF00098: Zinc knuckle
355785	1	5131	1	1	259	1	1	At3g62360	3,00E-42	68416.m07005 expressed protein
357985	1	5132	1	1	4206	1	1	At3g62370	5,00E-52	68416.m07006 expressed protein
358309	1	5137	1	1	3381	1	1	At4g00090	1,00E-72	68417.m00009 transducin family protein / WD-40 repeat family protein similar to Transducin beta-like 2 protein (WS beta-transducin repeats protein) (WS-betaTRP) (Williams-Beuren syndrome chromosome region 13 protein) (SP:Q9Y4P3) {Homo sapiens}
355326	1	5143	1	1	4670	1	1	At4g01040	4,00E-47	68417.m00141 glycosyl hydrolase family 18 protein contains Pfam profile PF00704: Glycosyl hydrolases family 18
353733	2	5153	1	1	1352	1	1	At4g02030	5,00E-67	68417.m00273 expressed protein
353237	2	5157	1	1	8334	1	1	At4g02530	2,00E-29	68417.m00346 chloroplast thylakoid lumen protein SP:022773 ;TL16_ARATH
354316	2	5159	1	1	9688	1	1	At4g02620	4,00E-54	68417.m00356 vacuolar ATPase subunit F family protein contains weak similarity to vacuolar ATP synthase subunit F (EC 3.6.3.14) (V-ATPase F subunit) (Vacuolar proton pump F subunit) (V-ATPase 14 kDa subunit) (Swiss-Prot:P50408) [Rattus norvegicus]; contains Pfam PF01990: ATP synthase (F/14-kDa) subunit
353081	2	5163	1	1	8198	1	1	At4g03120	1,00E-17	68417.m00425 proline-rich family protein similar to U1 small nuclear ribonucleoprotein C; contains proline rich extensin domains, INTERPRO:IPR002965
357709	1	5166	1	1	807	1	1	At4g03200	2,00E-49	68417.m00437 expressed protein contains Pfam PF03190: Protein of unknown function, DUF255
355836	1	5169	1	1	893	1	1	At4g03560	6,00E-55	68417.m00488 two-pore calcium channel (TPC1) identical to two-pore calcium channel (TPC1) [Arabidopsis thaliana] gi|14041819|dbj|BAB55460

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
355568	1	5179	1	1	4025	1	1	At4g08960	1,00E-33	68417.m01476 phosphotyrosyl phosphatase activator (PTPA) family protein similar to Protein phosphatase 2A, regulatory subunit B' (PP2A, subunit B', PR53 isoform) (Phosphotyrosyl phosphatase activator) (PTPA) (Swiss-Prot:Q28717) [Oryctolagus cuniculus]
353200	2	5195	1	1	6964	1	1	At4g11790	6,00E-31	68417.m01878 Ran-binding protein 1 domain-containing protein / RanBP1 domain-containing protein contains Pfam profile PF00638: RanBP1 domain
359916	1	5197	1	1	5504	1	1	At4g12130	4,00E-52	68417.m01925 glycine cleavage T family protein / aminomethyl transferase family protein contains Pfam profile: PF01571 glycine cleavage T-protein (aminomethyl transferase)
355878	1	5198	1	1	6570	1	1	At4g12230	4,00E-30	68417.m01940 esterase/lipase/thioesterase family protein low similarity to 2-hydroxy-6-ketonona-2,4-dienedoic acid hydrolase; OhpC [Rhodococcus sp.] GI:8926386; contains Interpro entry IPR000379
355175	1	5209	1	1	6706	1	1	At4g13720	7,00E-64	68417.m02130 inosine triphosphate pyrophosphatase, putative / HAM1 family protein contains Pfam profile PF01725: Ham1 family; similar to inosine triphosphate pyrophosphatase (GI:13398328) [Homo sapiens]
356926	1	5219	1	1	8532	1	1	At4g15030	5,00E-34	68417.m02309 expressed protein
354108	3	5223	1	1	9677	1	1	At4g15790	8,00E-10	68417.m02403 expressed protein
358154	1	5227	1	1	24	1	1	At4g16340	7,00E-60	68417.m02476 adapter protein SPIKE1 (SPK1) One model reflects the alignment of a full-length cDNA sequence gi:18496702. There are multiple frame shifts in the gene model resulting in a truncated protein. The alternate model includes modifications in exons 14, 17 and 29 to compensate for frame shifts and maximize the protein length. It is not based on EST data. adapter protein SPIKE1 [Arabidopsis thaliana] GI:18496703
353292	2	5231	1	1	8720	1	1	At4g16450	1,00E-43	68417.m02492 expressed protein
357547	1	5237	1	1	6568	1	1	At4g17050	2,00E-61	68417.m02571 expressed protein
359292	1	5237	1	1	6568	1	1	At4g17050	1,00E-08	68417.m02571 expressed protein
359046	1	5252	1	1	7457	1	1	At4g18460	2,00E-13	68417.m02739 D-Tyr-tRNA(Tyr) deacylase family protein contains Pfam profile: PF02580 D-Tyr-tRNA(Tyr) deacylase
356902	1	5256	1	1	9593	1	1	At4g19350	3,00E-21	68417.m02850 expressed protein
359554	1	5258	1	1	815	1	1	At4g19490	9,00E-54	68417.m02867 expressed protein
357402	1	5261	1	1	9279	1	1	At4g20150	7,00E-31	68417.m02948 expressed protein
359082	1	5263	1	1	9572	1	1	At4g20350	2,00E-20	68417.m02970 expressed protein hypothetical protein - Caenorhabditis elegans,SPTREMBL:Q17527

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356218	1	5270	1	1	6243	1	1	At4g21320	4,00E-60	68417.m03079 (2R)-phospho-3-sulfolactate synthase-related contains weak similarity to Swiss-Prot:Q57703 (2R)-phospho-3-sulfolactate synthase (PSL synthase) [Methanococcus jannaschii]
359777	1	5276	1	1	8205	1	1	At4g22000	3,00E-24	68417.m03184 expressed protein
356800	1	5277	1	1	4816	1	1	At4g22330	1,00E-34	68417.m03228 alkaline phytoceramidase family / aPHC family contains Pfam profile: PF05875: alkaline phytoceramidase (aPHC)
358995	1	5277	1	1	4816	1	1	At4g22330	4,00E-13	68417.m03228 alkaline phytoceramidase family / aPHC family contains Pfam profile: PF05875: alkaline phytoceramidase (aPHC)
358212	1	5285	1	1	3347	1	1	At4g24040	1,00E-35	68417.m03454 glycosyl hydrolase family protein 37 / trehalase, putative similar to trehalase 1 GMTRE1 GI:4559292 from [Glycine max]
352919	2	5287	1	1	3385	1	1	At4g24160	6,00E-95	68417.m03466 hydrolase, alpha/beta fold family protein contains Pfam profile PF00561: hydrolase, alpha/beta fold family
358486	1	5287	1	1	3385	1	1	At4g24160	4,00E-27	68417.m03466 hydrolase, alpha/beta fold family protein contains Pfam profile PF00561: hydrolase, alpha/beta fold family
357472	1	5294	1	1	861	1	1	At4g25120	7,00E-23	68417.m03614 UvrD/REP helicase family protein contains Pfam PF00580: UvrD/REP helicase
355736	1	5303	2		10464	2	2	At4g26960	8,00E-07	68417.m03879 expressed protein
357216	1	5305	1	1	7990	1	1	At4g27120	4,00E-51	68417.m03898 expressed protein
359835	1	5313	1	1	5309	1	1	At4g28020	5,00E-49	68417.m04019 expressed protein contains Pfam PF01980: Uncharacterised protein family
354079	3	5314	1	1	9871	1	1	At4g28025	3,00E-18	68417.m04020 expressed protein
356724	1	5316	1	1	5620	1	1	At4g28260	2,00E-26	68417.m04048 expressed protein
352932	2	5317	1	1	2104	1	1	At4g28450	2,00E-58	68417.m04071 transducin family protein / WD-40 repeat family protein SOF1 (involved in rRNA processing) protein-yeast
353415	3	5317	1	1	2104	1	1	At4g28450	1,00E-85	68417.m04071 transducin family protein / WD-40 repeat family protein SOF1 (involved in rRNA processing) protein-yeast
354575	1	5328	1	1	7717	1	1	At4g29860	8,00E-54	68417.m04250 transducin family protein / WD-40 repeat family protein contains 3 WD-40 repeats (PF00400); WDVCF variant 1 (gi:12006981) [Mus musculus]
357238	1	5334	1	1	2975	1	1	At4g30150	8,00E-44	68417.m04287 expressed protein
359099	1	5335	1	1	1505	1	1	At4g30310	2,00E-39	68417.m04309 ribitol kinase, putative similar to ribitol kinase [Klebsiella pneumoniae] gi|2905643|gb|AAC26495
356395	1	5338	1	1	745	1	1	At4g30790	9,00E-26	68417.m04362 expressed protein

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
356065	1	5339	1	1	6351	1	1	At4g30840	1,00E-29	68417.m04375 WD-40 repeat protein family
353260	3	5343	1	1	1145	1	1	At4g31120	2,00E-54	68417.m04418 Skb1 methyltransferase family protein contains Pfam profile: PF05185 Skb1 methyltransferase
353061	2	5345	1	1	195	1	1	At4g31160	1,00E-35	68417.m04423 transducin family protein / WD-40 repeat family protein contains 2 WD-40 repeats (PF00400); KIAA0800 protein, Homo sapiens GI:3882321 EMBL:AB018343
355945	1	5346	1	1	2016	1	1	At4g31200	1,00E-07	68417.m04431 SWAP (Suppressor-of-White-APricot)/surp domain-containing protein related to DAN26 [Homo sapiens] gi|1770394|emb|CAA69591
357452	1	5350	1	1	3382	1	1	At4g31770	2,00E-76	68417.m04508 calcineurin-like phosphoesterase family protein contains Pfam profile: PF00149 calcineurin-like phosphoesterase
353420	3	5356	1	1	9825	1	1	At4g32680	5,00E-07	68417.m04652 expressed protein
358336	1	5359	1	1	2951	1	1	At4g32770	4,00E-45	68417.m04662 tocopherol cyclase, chloroplast / vitamin E deficient 1 (VTE1) / sucrose export defective 1 (SXD1) identical to SP|Q94FY7 Tocopherol cyclase, chloroplast precursor (Vitamin E deficient 1) (Sucrose export defective 1) {Arabidopsis thaliana}
353210	2	5360	1	1	253	1	1	At4g32820	3,00E-60	68417.m04668 expressed protein ; expression supported by MPSS
354341	2	5362	1	1	9518	1	1	At4g32915	1,00E-27	68417.m04684 expressed protein
359409	1	5363	1	1	1676	1	1	At4g33030	3,00E-41	68417.m04699 UDP-sulfoquinovose synthase / sulfite:UDP-glucose sulfotransferase / sulfolipid biosynthesis protein (SQD1) identical to gi:2736155
357074	1	5364	1	1	10236	1	1	At4g33100	5,00E-16	68417.m04716 expressed protein contains Pfam PF05254: Uncharacterised protein family (UPF0203)
357861	1	5364	1	1	10236	1	1	At4g33100	3,00E-22	68417.m04716 expressed protein contains Pfam PF05254: Uncharacterised protein family (UPF0203)
357717	1	5365	1	1	6128	1	1	At4g33250	2,00E-44	68417.m04732 eukaryotic translation initiation factor 3 subunit 11 / eIF-3 p25 / eIF3k (TIF3K1) identical to Swiss-Prot:Q9SZA3 eukaryotic translation initiation factor 3 subunit 11 (eIF-3 p25) (eIF3k) [Arabidopsis thaliana]; identical to cDNA initiation factor 3k GI:12407752
354973	1	5366	1	1	8764	1	1	At4g33480	6,00E-76	68417.m04755 expressed protein
353305	2	5370	1	1	3960	1	1	At4g33945	8,00E-43	68417.m04817 armadillo/beta-catenin repeat family protein contains Pfam profile: PF00514 armadillo/beta-catenin-like repeat

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
354477	1	5371	1	1	1078	1	1	At4g34030	3,00E-54	68417.m04829 methylcrotonyl-CoA carboxylase beta chain, mitochondrial / 3-methylcrotonyl-CoA carboxylase 2 (MCCB) identical to SP|Q9LDD8 Methylcrotonyl-CoA carboxylase beta chain, mitochondrial precursor (EC 6.4.1.4) (3-Methylcrotonyl-CoA carboxylase 2) (MCCase beta subunit) (3-methylcrotonyl-CoA:carbon dioxide ligase beta subunit) {Arabidopsis thaliana}; contains Pfam profile: PF01039 carboxyl transferase domain
357029	1	5371	1	1	1078	1	1	At4g34030	5,00E-12	68417.m04829 methylcrotonyl-CoA carboxylase beta chain, mitochondrial / 3-methylcrotonyl-CoA carboxylase 2 (MCCB) identical to SP|Q9LDD8 Methylcrotonyl-CoA carboxylase beta chain, mitochondrial precursor (EC 6.4.1.4) (3-Methylcrotonyl-CoA carboxylase 2) (MCCase beta subunit) (3-methylcrotonyl-CoA:carbon dioxide ligase beta subunit) {Arabidopsis thaliana}; contains Pfam profile: PF01039 carboxyl transferase domain
357123	1	5373	1	1	906	1	1	At4g34260	3,00E-36	68417.m04869 expressed protein
359320	1	5373	1	1	906	1	1	At4g34260	3,00E-53	68417.m04869 expressed protein
354205	2	5375	1	1	948	1	1	At4g34310	6,00E-57	68417.m04876 expressed protein
357326	1	5381	1	1	2657	1	1	At4g35250	5,00E-82	68417.m05010 vestitone reductase-related low similarity to vestitone reductase [Medicago sativa subsp. sativa] GI:973249
353778	2	5382	1	1	9700	1	1	At4g35530	3,00E-25	68417.m05050 phosphatidylinositolglycan-related contains weak similarity to Swiss-Prot:Q14442 phosphatidylinositol-glycan biosynthesis, class H protein (PIG-H) [Homo sapiens]
358395	1	5393	1	1	9618	1	1	At4g37090	1,00E-09	68417.m05254 expressed protein
355494	1	5395	1	1	7194	1	1	At4g37210	4,00E-28	68417.m05267 tetratricopeptide repeat (TPR)-containing protein low similarity to SP|Q02508 Protein HGV2 Halocynthia roretzi; contains Pfam profile PF00515 TPR Domain
353757	2	5398	1	1	9435	1	1	At4g37830	5,00E-23	68417.m05352 cytochrome c oxidase-related contains weak similarity to cytochrome c oxidase polypeptide VIa-liver, mitochondrial precursor (EC 1.9.3.1) (Swiss-Prot:P10818) [Rattus norvegicus]
354670	1	5404	1	1	932	1	1	At4g38440	2,00E-24	68417.m05432 expressed protein
355037	1	5404	1	1	932	1	1	At4g38440	7,00E-08	68417.m05432 expressed protein
355111	1	5404	1	1	932	1	1	At4g38440	1,00E-18	68417.m05432 expressed protein
359199	1	5404	1	1	932	1	1	At4g38440	9,00E-51	68417.m05432 expressed protein

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
353798	2	5407	1	1	4017	1	1	At4g39280	4,00E-107	68417.m05563 phenylalanyl-tRNA synthetase, putative / phenylalanine--tRNA ligase, putative similar to SP|Q9Y285 Phenylalanyl-tRNA synthetase alpha chain (EC 6.1.1.20) (Phenylalanine- -tRNA ligase alpha chain) (PheRS) {Homo sapiens}; contains Pfam profile PF01409: tRNA synthetases class II core domain (F)
356138	1	5407	1	1	4017	1	1	At4g39280	2,00E-28	68417.m05563 phenylalanyl-tRNA synthetase, putative / phenylalanine--tRNA ligase, putative similar to SP|Q9Y285 Phenylalanyl-tRNA synthetase alpha chain (EC 6.1.1.20) (Phenylalanine- -tRNA ligase alpha chain) (PheRS) {Homo sapiens}; contains Pfam profile PF01409: tRNA synthetases class II core domain (F)
353897	2	5409	1	1				At4g39630	5,00E-40	68417.m05601 expressed protein
359854	1	5415	1	1	3817	1	1	At5g01010	2,00E-32	68418.m00001 expressed protein
355893	1	5417	1	1	7430	1	1	At5g01470	3,00E-34	68418.m00060 expressed protein
355059	1	5420	1	1	3344	1	1	At5g02410	6,00E-22	68418.m00164 DIE2/ALG10 family contains Pfam PF04922: DIE2/ALG10 family
358080	1	5423	1	1	9642	1	1	At5g02770	7,00E-26	68418.m00219 expressed protein
357936	1	5436	1	1	6595	1	1	At5g04920	2,00E-42	68418.m00519 vacuolar protein sorting 36 family protein / VPS36 family protein contains Pfam PF04132: Vacuolar protein sorting 36
356372	1	5437	1	1	165	1	1	At5g05560	2,00E-39	68418.m00604 E3 ubiquitin ligase, putative E3, ubiquitin ligase; contains similarity to Apc1/Tsg24 protein, the largest subunit of human anaphase-promoting complex (APC/C) GI:11967711 from [Homo sapiens]
359526	1	5443	1	1	4570	1	1	At5g06360	4,00E-70	68418.m00712 ribosomal protein S8e family protein contains Pfam profile PF01201: Ribosomal protein S8e
354831	1	5450	1	1	6095	1	1	At5g07380	3,00E-28	68418.m00845 hypothetical protein
358571	1	5453	1	1	1702	1	1	At5g07590	8,00E-65	68418.m00870 WD-40 repeat protein family contains 3 WD-40 repeats (PF00400); similarity to WD-repeat protein 8 (WDR8)(SP:Q9P2S5) [HOMO SAPIENS]
359725	1	5453	1	1	1702	1	1	At5g07590	3,00E-55	68418.m00870 WD-40 repeat protein family contains 3 WD-40 repeats (PF00400); similarity to WD-repeat protein 8 (WDR8)(SP:Q9P2S5) [HOMO SAPIENS]
357085	1	5463	1	1	1565	1	1	At5g08450	3,00E-13	68418.m00996 expressed protein KED, Nicotiana tabacum, EMBL:AB009883
353120	11	5469	1	1	8642	1	1	At5g09680	5,00E-32	68418.m01120 cytochrome b5 domain-containing protein flavohemoprotein b5+b5R, Homo sapiens, EMBL:AF169803

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
354323	3	5469	1	1	8642	1	1	At5g09680	4,00E-19	68418.m01120 cytochrome b5 domain-containing protein flavohemoprotein b5+b5R, Homo sapiens, EMBL:AF169803
353067	3	5471	1	1	1385	1	1	At5g09860	2,00E-138	68418.m01140 nuclear matrix protein-related low similarity to nuclear matrix protein p84 [Homo sapiens] GI:550058
353188	2	5484	1	1	6183	1	1	At5g11450	3,00E-54	68418.m01337 oxygen-evolving complex-related 23 kDa polypeptide of water-oxidizing complex of photosystem II, Nicotiana tabacum, EMBL:NT23WOP2B
358081	1	5485	1	1	618	1	1	At5g11560	1,00E-103	68418.m01348 PQQ enzyme repeat-containing protein contains Pfam profile PF01011: PQQ enzyme repeat
358847	1	5485	1	1	618	1	1	At5g11560	7,00E-51	68418.m01348 PQQ enzyme repeat-containing protein contains Pfam profile PF01011: PQQ enzyme repeat
354115	2	5493	1	1	1486	1	1	At5g11980	8,00E-73	68418.m01401 conserved oligomeric Golgi complex component-related / COG complex component-related similar to SP|Q96MW5 Conserved oligomeric Golgi complex component 8 {Homo sapiens}; contains Pfam profile PF04124: Dor1-like family
354906	1	5497	1	1	958	1	1	At5g13030	1,00E-59	68418.m01494 expressed protein contains Pfam profile PF02696: Uncharacterized ACR, YdiU/UPF0061 family
354779	1	5498	1	1	6845	1	1	At5g13050	2,00E-29	68418.m01496 5-formyltetrahydrofolate cyclo-ligase (5-FCL) nearly identical to gi:22087553
359543	1	5499	1	1	8511	1	1	At5g13190	3,00E-40	68418.m01510 expressed protein
359553	1	5501	1	1	6969	1	1	At5g13240	2,00E-34	68418.m01521 expressed protein prdeicted proteins, Schizosaccharomyces pombe
357424	1	5502	1	1	393	1	1	At5g13390	4,00E-20	68418.m01542 expressed protein
353906	6	5503	1	1	2636	1	1	At5g13420	4,00E-107	68418.m01545 transaldolase, putative similar to transaldolase [Solanum tuberosum] gi|2078350|gb|AAB54016
355040	1	5503	1	1	2636	1	1	At5g13420	2,00E-23	68418.m01545 transaldolase, putative similar to transaldolase [Solanum tuberosum] gi|2078350|gb|AAB54016
354449	2	5504	1	1	5500	1	1	At5g13570	8,00E-91	68418.m01568 MutT/nudix family protein similar to mRNA-decapping enzyme [Homo sapiens] GI:23268269; contains Pfam profile PF00293: NUDIX domain
358912	1	5504	1	1	5500	1	1	At5g13570	2,00E-44	68418.m01568 MutT/nudix family protein similar to mRNA-decapping enzyme [Homo sapiens] GI:23268269; contains Pfam profile PF00293: NUDIX domain
353713	5	5509	1	1	2573	1	1	At5g14050	1,00E-111	68418.m01644 transducin family protein / WD-40 repeat family protein contains 4 WD-40 repeats (PF00400); similar to unknown protein (ref|NP_057085.1)

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
354889	1	5512	1	1	1457	1	1	At5g14520	2,00E-67	68418.m01702 pescadillo-related similar to pescadillo [Zebrafish, Danio rerio] SWISS-PROT:P79741
353087	2	5514	1	1	9674	1	1	At5g14910	3,00E-27	68418.m01749 heavy-metal-associated domain-containing protein Pfam profile PF00403: Heavy-metal-associated domain
359484	1	5518	1	1	6842	1	1	At5g15750	6,00E-52	68418.m01842 RNA-binding S4 domain-containing protein 40S RIBOSOMAL PROTEINs - different species
357429	1	5524	1	1	405	1	1	At5g16210	5,00E-37	68418.m01894 HEAT repeat-containing protein contains Pfam profile PF02985: HEAT repeat
355993	1	5526	1	1	460	1	1	At5g16280	7,00E-31	68418.m01901 expressed protein
357641	1	5527	1	1	917	1	1	At5g16300	2,00E-35	68418.m01906 expressed protein
358335	1	5529	1	1	4490	1	1	At5g16520	2,00E-06	68418.m01932 expressed protein
353049	2	5531	1	1	5546	1	1	At5g16620	2,00E-10	68418.m01946 hydroxyproline-rich glycoprotein family protein contains proline rich extensin domains, INTERPRO:IPR002965
355096	1	5533	1	1	6807	1	1	At5g16850	1,00E-21	68418.m01974 telomerase reverse transcriptase (TERT) identical to telomerase reverse transcriptase [Arabidopsis thaliana] GI:5880683
359993	1	5537	1	1	5484	1	1	At5g17290	1,00E-25	68418.m02025 autophagy protein Apg5 family contains Pfam profile: PF04106 autophagy protein Apg5
357876	1	5541	1	1	4180	1	1	At5g17620	7,00E-28	68418.m02066 expressed protein
359749	1	5541	1	1	4180	1	1	At5g17620	1,00E-30	68418.m02066 expressed protein
353080	4	5544	1	1	4400	1	1	At5g17990	7,00E-36	68418.m02110 anthranilate phosphoribosyltransferase identical to anthranilate phosphoribosyltransferase, chloroplast precursor (EC 2.4.2.18) SP:Q02166 from [Arabidopsis thaliana]
355289	1	5545	1	1	2469	1	1	At5g18070	3,00E-62	68418.m02120 phosphoglucosamine mutase-related similar to SP|Q9P4V2 Phosphoacetylglucosamine mutase (EC 5.4.2.3) (PAGM) (Acetylglucosamine phosphomutase) (N-acetylglucosamine-phosphate mutase) {Candida albicans}; contains Pfam profiles PF00408: Phosphoglucomutase/phosphomannomutase C-terminal domain, PF02878: Phosphoglucomutase/phosphomannomutase alpha/beta/alpha domain I
357599	1	5547	1	1	1047	1	1	At5g18230	1,00E-62	68418.m02139 transcription regulator NOT2/NOT3/NOT5 family protein contains Pfam domain PF04153: NOT2 / NOT3 / NOT5 family
354598	1	5552	1	1	4030	1	1	At5g19050	4,00E-50	68418.m02265 expressed protein
358394	1	5565	1	1	3296	1	1	At5g20170	6,00E-08	68418.m02402 expressed protein

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
356405	1	5569	1	1	3943	1	1	At5g20930	6,00E-37	68418.m02486 protein kinase, putative nearly identical to protein kinase tousled gi|433052|gb|AAA32874
354635	1	5571	1	1	1912	1	1	At5g20990	3,00E-21	68418.m02495 molybdopterin biosynthesis CNX1 protein / molybdenum cofactor biosynthesis enzyme CNX1 (CNX1) identical to SP|Q39054 Molybdopterin biosynthesis CNX1 protein (Molybdenum cofactor biosynthesis enzyme CNX1) {Arabidopsis thaliana}
356139	1	5572	1	1	2907	1	1	At5g21040	2,00E-25	68418.m02503 F-box family protein / WD-40 repeat family protein contains G-protein beta WD-40 repeats
353799	2	5577	1	1	8307	1	1	At5g22120	1,00E-29	68418.m02575 expressed protein
357627	1	5580	1	1	7127	1	1	At5g22820	6,00E-32	68418.m02668 expressed protein
358351	1	5585	1	1	8080	1	1	At5g23290	7,00E-07	68418.m02725 c-myc binding protein, putative / prefoldin, putative similar to Swiss-Prot:Q99471 prefoldin subunit 5 (C-myc binding protein Mm-1) (Myc modulator 1) [Homo sapiens]
354705	1	5586	1	1	1965	1	1	At5g23300	3,00E-73	68418.m02726 dihydroorotate dehydrogenase, mitochondrial / dihydroorotate oxidase / DHOdehase (PYRD) nearly identical to SP|P32746 Dihydroorotate dehydrogenase, mitochondrial precursor (EC 1.3.3.1) (Dihydroorotate oxidase) (DHOdehase) {Arabidopsis thaliana}; identical to cDNA pyrD mRNA for dihydroorotate dehydrogenase GI:16448
359461	1	5592	1	1	71	1	1	At5g24350	4,00E-12	68418.m02870 expressed protein weak similarity to neuroblastoma-amplified protein [Homo sapiens] GI:4337460
358975	1	5595	1	1	9690	1	1	At5g24670	1,00E-19	68418.m02916 cytidine/deoxycytidylate deaminase family protein similar to SP|Q9URQ3 tRNA-specific adenosine deaminase 3 (EC 3.5.4.-) (tRNA-specific adenosine-34 deaminase subunit TAD3) {Saccharomyces cerevisiae}; contains Pfam profile PF00383: Cytidine and deoxycytidylate deaminase zinc-binding region
359319	1	5600	1	1	7815	1	1	At5g25480	5,00E-30	68418.m03032 C-5 cytosine-specific DNA methylase family protein contains Pfam profile PF00145: C-5 cytosine-specific DNA methylase
359789	1	5607	1	1	7767	1	1	At5g26880	6,00E-74	68418.m03206 tRNA/rRNA methyltransferase (SpoU) family protein low similarity to tRNA (Gm18) methyltransferase [Thermus thermophilus] GI:11079208; contains Pfam profile PF00588: SpoU rRNA Methylase (RNA methyltransferase, TrmH) family

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
353834	2	5610	1	1	4785	1	1	At5g27450	3,00E-38	68418.m03277 mevalonate kinase (MK) identical to mevalonate kinase [Arabidopsis thaliana] SWISS-PROT:P46086
356908	1	5615	1	1	9427	1	2	At5g27860	1,00E-11	68418.m03342 expressed protein
353598	2	5618	1	1	2729	1	1	At5g32470	9,00E-31	68418.m03828 expressed protein
357644	1	5619	1	1	9571	1	1	At5g35080	1,00E-27	68418.m04151 expressed protein
359504	1	5620	1	1	3152	1	1	At5g35430	1,00E-17	68418.m04213 expressed protein
358265	1	5621	1	1	3363	1	1	At5g35460	2,00E-61	68418.m04217 expressed protein
358862	1	5622	1	1	9872	1	1	At5g35520	5,00E-30	68418.m04224 kinetochore protein-related contains Pfam PF05859: Mis12 protein
357598	1	5629	1	1	429	1	1	At5g37510	3,00E-27	68418.m04518 NADH-ubiquinone dehydrogenase, mitochondrial, putative similar to NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial from Solanum tuberosum [SP|Q43644]
358148	1	5632	1	1	904	1	1	At5g37630	6,00E-30	68418.m04532 chromosome condensation family protein contains pfam profile: PF04154 chromosome condensation protein 3, C-terminal region
356628	1	5636	1	1	6214	1	1	At5g38660	2,00E-76	68418.m04675 expressed protein similar to unknown protein (pir||S75762)
357116	1	5639	1	1	7414	1	1	At5g38890	5,00E-45	68418.m04703 exoribonuclease-related similar to SP|P53859 3'-5' exoribonuclease CSL4 (EC 3.1.13.-) {Saccharomyces cerevisiae}
353914	2	5642	1	1	6966	1	1	At5g39250	2,00E-21	68418.m04754 F-box family protein ; similar to SKP1 interacting partner 2 (SKIP2) TIGR_Ath1:At5g67250
356024	1	5643	1	1	2761	1	1	At5g39410	3,00E-22	68418.m04774 expressed protein
359288	1	5649	1	1	6598	1	1	At5g40530	3,00E-09	68418.m04918 expressed protein contains Pfam profile PF05148: Protein of unknown function (DUF691)
355564	1	5652	1	1	4234	1	1	At5g40850	7,00E-23	68418.m04960 urophorphyrin III methylase (UPM1) identical to urophorphyrin III methylase (GI:1146165) [Arabidopsis thaliana]; similar to s-adenosyl-L-methionine-dependent uroporphyrinogen III methyltransferase (GI:1490606) [Arabidopsis thaliana]; similar to Diphthine synthase (Diphtamide biosynthesis methyltransferase) (DPH5) (SP:P32469) [Saccharomyces cerevisiae]; contains Pfam PF00590 : Tetrapyrrole (Corrin/Porphyrin) Methylases domain; contains TIGRFAM PF00590: Tetrapyrrole (Corrin/Porphyrin) Methylases
356622	1	5654	1	1	3287	1	1	At5g41190	7,00E-45	68418.m05006 expressed protein ; expression supported by MPSS

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
359826	1	5654	1	1	3287	1	1	At5g41190	4,00E-50	68418.m05006 expressed protein ; expression supported by MPSS
356730	1	5656	1	1	5438	1	1	At5g41880	2,00E-61	68418.m05099 DNA primase small subunit family contains Pfam profile: PF01896 DNA primase small subunit
355163	1	5657	1	1	8705	1	1	At5g41960	2,00E-38	68418.m05109 expressed protein
357485	1	5684	1	1	6289	1	1	At5g45360	3,00E-57	68418.m05569 F-box family protein similar to SKP1 interacting partner 2 (SKIP2) TIGR_Ath1:At5g67250
358892	1	5685	1	1	9707	1	1	At5g45590	4,00E-22	68418.m05601 expressed protein
358724	1	5693	1	1	8316	1	1	At5g47570	4,00E-36	68418.m05872 expressed protein
358548	1	5695	1	1	9472	1	1	At5g47830	3,00E-33	68418.m05909 expressed protein
357689	1	5705	1	1				At5g48830	2,00E-14	68418.m06041 expressed protein
357920	1	5705	1	1				At5g48830	2,00E-22	68418.m06041 expressed protein
357198	1	5710	1	1	6776	1	1	At5g49400	3,00E-20	68418.m06113 zinc knuckle (CCHC-type) family protein contains Pfam domain, PF00098: Zinc knuckle
353096	3	5712	1	1	6640	1	1	At5g49510	3,00E-75	68418.m06127 VHL binding protein, putative / prefoldin, putative similar to Swiss-Prot:Q15765 prefoldin subunit 3 (Von Hippel-Lindau binding protein 1; VHL binding protein-1; VBP-1; HIBBJ46) [Mus musculus]
357299	1	5714	1	1	9367	1	1	At5g49550	4,00E-23	68418.m06132 expressed protein
358858	1	5715	1	1	1877	1	1	At5g49555	4,00E-06	68418.m06133 amine oxidase-related contains Pfam profile PF01593: amine oxidase, flavin-containing
359160	1	5716	1	1	1393	1	1	At5g49570	3,00E-59	68418.m06135 transglutaminase-like family protein low similarity to peptide:N-glycanase PNGase [Mus musculus] GI:8347622; contains Pfam profile PF01841: Transglutaminase-like superfamily
356825	1	5718	1	1	732	1	1	At5g49810	1,00E-34	68418.m06169 methionine S-methyltransferase identical to methionine S-methyltransferase [Arabidopsis thaliana] GI:5733429
356316	1	5725	1	1	4500	1	1	At5g50375	3,00E-94	68418.m06239 cyclopropyl isomerase (CPI1)
355708	1	5732	1	1	5336	1	1	At5g51020	1,00E-06	68418.m06325 expressed protein similar to unknown protein (pir||S76207)
355759	1	5733	1	1	8336	1	1	At5g51040	2,00E-43	68418.m06327 expressed protein
355373	1	5736	1	1	65	1	1	At5g51200	7,00E-10	68418.m06349 expressed protein
359351	1	5739	1	1	5261	1	1	At5g51340	2,00E-39	68418.m06366 expressed protein
359431	1	5741	1	1	9252	1	1	At5g51510	5,00E-12	68418.m06388 expressed protein
355531	1	5745	1	1	8071	1	1	At5g51840	3,00E-18	68418.m06427 expressed protein
353928	2	5748	1	1	7206	1	1	At5g52110	2,00E-16	68418.m06468 expressed protein similar to unknown protein (pir||S76150)
353548	2	5764	1	1	4423	1	1	At5g53620	7,00E-13	68418.m06662 expressed protein

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
356839	1	5765	1	1	3024	1	1	At5g53850	1,00E-50	68418.m06693 haloacid dehalogenase-like hydrolase family protein low similarity to enolase-phosphatase E-1 enzyme [Klebsiella oxytoca] GI:401712; contains InterPro accession IPR005834: Haloacid dehalogenase-like hydrolase
353485	7	5766	1	1	9675	1	1	At5g53930	2,00E-11	68418.m06710 expressed protein
358821	1	5768	1	1	804	1	1	At5g54440	5,00E-68	68418.m06780 expressed protein
357780	1	5782	1	1	2080	1	1	At5g56290	1,00E-65	68418.m07026 peroxisomal targeting signal type 1 receptor (PEX5) identical to GI:3603353; contains Pfam profile PF00515 TPR Domain
358646	1	5786	1	1	8748	1	1	At5g57120	5,00E-29	68418.m07132 expressed protein weak similarity to SP|Q14978 Nucleolar phosphoprotein p130 {Homo sapiens}
359138	1	5788	1	1	7079	1	1	At5g57280	2,00E-56	68418.m07156 expressed protein
356967	1	5791	1	1	2042	1	1	At5g57460	1,00E-34	68418.m07181 expressed protein
359682	1	5792	1	1	1454	1	1	At5g57655	1,00E-50	68418.m07204 xylose isomerase family protein contains similarity to Xylose isomerase (EC 5.3.1.5) (Swiss-Prot:P22842) [Thermoanaerobacter ethanolicus]
358981	1	5798	1	1	7576	1	1	At5g58200	8,00E-20	68418.m07285 expressed protein
356168	1	5801	1	1	7042	1	1	At5g58260	1,00E-28	68418.m07294 expressed protein
353765	2	5802	1	1	262	1	1	At5g58410	1,00E-09	68418.m07314 expressed protein contains similarity to hypothetical proteins
355350	1	5804	1	1	9774	1	1	At5g58575	3,00E-30	68418.m07339 expressed protein
354839	1	5813	1	1	3959	1	1	At5g59960	4,00E-42	68418.m07520 expressed protein
355250	1	5813	1	1	3959	1	1	At5g59960	2,00E-37	68418.m07520 expressed protein
354904	1	5815	1	1	386	1	1	At5g60600	6,00E-53	68418.m07603 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate synthase, putative / GcpE family protein similar to GcpE [Plasmodium falciparum] GI:13094969; contains Pfam profile PF04551: GcpE protein; supporting cDNA gi|27462471|gb|AF434673.1
357694	1	5816	1	1	5660	1	1	At5g61330	3,00E-64	68418.m07696 rRNA processing protein-related contains weak similarity to rRNA processing protein EBP2 (EBNA1-binding protein homolog) (Swiss-Prot:P36049) [Saccharomyces cerevisiae]
358480	1	5817	1	1	4859	1	1	At5g61530	7,00E-68	68418.m07721 small G protein family protein / RhoGAP family protein contains Pfam domain, PF00620: RhoGAP domain
356561	1	5818	1	1	5387	1	1	At5g61770	2,00E-68	68418.m07752 brix domain-containing protein contains Pfam domain, PF04427: Brix domain
353114	6	5823	1	1	9207	1	1	At5g62550	2,00E-39	68418.m07850 expressed protein

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
359840	1	5829	1	1	9900	1	1	At5g63135	2,00E-09	68418.m07927 expressed protein
359303	1	5831	1	1	6059	1	1	At5g63220	1,00E-48	68418.m07936 expressed protein contains Pfam PF04190: Protein of unknown function (DUF410)
353399	3	5841	1	1	8595	1	1	At5g64180	1,00E-10	68418.m08058 expressed protein
354055	2	5854	1	1	1231	1	1	At5g65950	8,00E-26	68418.m08302 expressed protein
359049	1	5856	1	1	7925	1	1	At5g66090	4,00E-30	68418.m08326 expressed protein
354186	2	5857	1	1	2392	1	1	At5g66120	7,00E-125	68418.m08330 3-dehydroquinate synthase, putative similar to aroB [Neisseria gonorrhoeae][GI:2661441]; contains 3-dehydroquinate synthase domain PF01761
359451	1	5857	1	1	2392	1	1	At5g66120	2,00E-23	68418.m08330 3-dehydroquinate synthase, putative similar to aroB [Neisseria gonorrhoeae][GI:2661441]; contains 3-dehydroquinate synthase domain PF01761
354092	2	5864	1	1	2135	1	1	At5g66810	2,00E-26	68418.m08423 expressed protein similar to unknown protein (gb|AAB71479.1|)
354617	1	6622	1		10402	1	2	At1g01730	7,00E-09	68414.m00092 expressed protein
353298	2	6645	1		2670	1	4	At1g05350	6,00E-18	68414.m00542 thiF family protein low similarity to SP|P30138 Adenylyltransferase thiF (EC 2.7.7.-) {Escherichia coli}; contains Pfam profile PF00899: ThiF family
354572	1	6645	1		2670	1	4	At1g05350	3,00E-06	68414.m00542 thiF family protein low similarity to SP|P30138 Adenylyltransferase thiF (EC 2.7.7.-) {Escherichia coli}; contains Pfam profile PF00899: ThiF family
353617	2	6689	1					At1g13870	8,00E-89	68414.m01628 expressed protein similar to KTI12 protein (SP:P34253) {Saccharomyces cerevisiae}; contains Prosite PS00070: Aldehyde dehydrogenases cysteine active site
356254	1	6723	1					At1g20050	1,00E-58	68414.m02510 C-8,7 sterol isomerase identical to C-8,7 sterol isomerase GI:11279073 from [Arabidopsis thaliana] (Plant Mol. Biol. 38 (5), 807-815 (1998))
358678	1	6723	1					At1g20050	5,00E-29	68414.m02510 C-8,7 sterol isomerase identical to C-8,7 sterol isomerase GI:11279073 from [Arabidopsis thaliana] (Plant Mol. Biol. 38 (5), 807-815 (1998))
357257	1	6725	1					At1g20575	2,00E-16	68414.m02567 dolichyl-phosphate beta-D-mannosyltransferase, putative / dolichol-phosphate mannosyltransferase, putative / mannose-P-dolichol synthase, putative similar to DPM1 from Homo sapiens [SP|O60762]; member of glycosyltransferase family 2
358357	1	6749	1		8670	18	1	At1g23720	4,00E-10	68414.m02994 proline-rich extensin-like family protein contains proline-rich extensin domains, INTERPRO:IPR002965

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356288	1	6770	1					At1g28135	6,00E-06	68414.m03450 expressed protein
353459	3	6844	1					At1g42960	6,00E-33	68414.m04946 expressed protein
353930	4	6844	1					At1g42960	5,00E-28	68414.m04946 expressed protein
357813	1	6844	1					At1g42960	8,00E-17	68414.m04946 expressed protein
355419	1	6880	1					At1g49245	1,00E-11	68414.m05521 expressed protein
355008	1	6884	1					At1g49510	3,00E-16	68414.m05549 expressed protein
358842	1	6884	1					At1g49510	4,00E-12	68414.m05549 expressed protein
355554	1	6917	1					At1g55365	1,00E-08	68414.m06328 hypothetical protein
359421	1	7008	1		10370	1	1	At1g70350	3,00E-09	68414.m08093 expressed protein
353089	2	7022	1		9577	2	1	At1g72790	2,00E-11	68414.m08415 hydroxyproline-rich glycoprotein family protein contains proline-rich extensin domains, INTERPRO:IPR002965
353029	2	7042	1					At1g77030	3,00E-39	68414.m08970 glycine-rich protein
353051	2	7102	1					At2g07687	6,00E-133	68415.m00937 cytochrome c oxidase subunit 3 identical to cytochrome c oxidase subunit 3 (GI:15215914) [Arabidopsis thaliana]; similar to Cytochrome c oxidase polypeptide III (EC 1.9.3.1) (Swiss-Prot:P92514) [Arabidopsis thaliana]
354738	1	7115	1					At2g07715	9,00E-06	68415.m00965 ribosomal protein L2, putative similar to ribosomal protein L2 [Gossypium arboreum] GI:17933133; contains Pfam profile PF00181: Ribosomal Proteins L2, RNA binding domain
352975	2	7202	1					At2g20490	7,00E-25	68415.m02392 nucleolar RNA-binding Nop10p family protein similar to Nop10p (GI:8096260) [Homo sapiens]
358758	1	7202	1					At2g20490	2,00E-14	68415.m02392 nucleolar RNA-binding Nop10p family protein similar to Nop10p (GI:8096260) [Homo sapiens]
355763	1	7206	1		10437	1	1	At2g20820	2,00E-08	68415.m02451 expressed protein .
353940	4	7237	1					At2g26810	8,00E-29	68415.m03217 expressed protein and genefinder
359549	1	7253	1					At2g28820	3,00E-23	68415.m03504 ribosomal protein L16 family protein contains Pfam PF00252 domain ribosomal protein L16
356154	1	7271	1					At2g31130	2,00E-08	68415.m03801 expressed protein
358505	1	7272	1		10185	1	1	At2g31305	8,00E-25	68415.m03822 expressed protein
354069	2	7316	1					At2g38040	1,00E-11	68415.m04670 acetyl co-enzyme A carboxylase carboxyltransferase alpha subunit family contains Pfam profile: PF03255: Acetyl co-enzyme A carboxylase carboxyltransferase alpha subunit
355333	1	7316	1					At2g38040	2,00E-14	68415.m04670 acetyl co-enzyme A carboxylase carboxyltransferase alpha subunit family contains Pfam profile: PF03255: Acetyl co-enzyme A carboxylase carboxyltransferase alpha subunit

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
357313	1	7344	1					At2g41950	2,00E-40	68415.m05190 expressed protein
354467	2	7379	1					At3g02120	2,00E-10	68416.m00178 hydroxyproline-rich glycoprotein family protein
357569	1	7446	1					At3g14280	5,00E-10	68416.m01807 expressed protein
357536	1	7456	1		10479	1	1	At3g15420	2,00E-10	68416.m01956 expressed protein
354876	1	7687	1					At3g57570	6,00E-16	68416.m06410 expressed protein
357368	1	7687	1					At3g57570	2,00E-34	68416.m06410 expressed protein
355926	1	7706	1		3052	1	1	At3g61540	9,00E-35	68416.m06893 peptidase family protein similar to prolyl aminopeptidase (proline iminopeptidase) from Aeromonas sobria SP|P46547, Propionibacterium freudenreichii subsp. shermanii GI:2415704, Hafnia alvei GI:1754489
355215	1	7722	1		10438	1	1	At4g00525	4,00E-09	68417.m00072 expressed protein
357411	1	7753	1		4341	1	1	At4g04880	5,00E-06	68417.m00710 adenosine/AMP deaminase family protein low similarity to SP|P03958 Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase) {Mus musculus}; contains Pfam profile PF00962: Adenosine/AMP deaminase
357788	1	7753	1		4341	1	1	At4g04880	3,00E-06	68417.m00710 adenosine/AMP deaminase family protein low similarity to SP|P03958 Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase) {Mus musculus}; contains Pfam profile PF00962: Adenosine/AMP deaminase
356787	1	7807	1		10322	1	226	At4g13320	3,00E-10	68417.m02082 expressed protein
354191	2	7825	1					At4g15802	2,00E-16	68417.m02405 expressed protein contains non-consensus AT-AC splice sites at intron 4
357976	1	7826	1		4950	1	1	At4g15840	3,00E-22	68417.m02409 expressed protein
352942	5	7871	1					At4g21150	1,00E-104	68417.m03057 ribophorin II (RPN2) family protein contains Pfam domain PF05817: Ribophorin II (RPN2)
356841	1	7871	1					At4g21150	5,00E-24	68417.m03057 ribophorin II (RPN2) family protein contains Pfam domain PF05817: Ribophorin II (RPN2)
353149	2	7954	1					At4g32570	4,00E-07	68417.m04636 expressed protein
355130	1	7954	1					At4g32570	5,00E-21	68417.m04636 expressed protein
354715	1	8062	1					At5g11630	1,00E-12	68418.m01360 expressed protein
353782	2	8119	1					At5g22640	1,00E-12	68418.m02645 MORN (Membrane Occupation and Recognition Nexus) repeat-containing protein contains Pfam profile PF02493: MORN repeat
355398	1	8293	1					At5g53860	3,00E-72	68418.m06698 expressed protein
359610	1	8337	1		10289	1	1	At5g57910	4,00E-13	68418.m07244 expressed protein similar to unknown protein (emb|CAB79781.1)

ID	# ESTS	TRIBE	# ATH	# OSA	INPAR	# ATH	# OSA	BEST ATH	EVALUE	DESC
354426	2	8371	1					At5g63050	4,00E-18	68418.m07910 expressed protein
358113	1	8371	1					At5g63050	2,00E-33	68418.m07910 expressed protein
353391	2	8376	1					At5g64010	4,00E-16	68418.m08037 expressed protein