white Lupin proteoid root ESTs 12-14 DAE, sorted by categories

I METABOLISM

CARBON METABOLISM: category 1a

L#	GenBank accession #	bp	E-value	annotation
79	CA410532	387	1E-24	acetyl-CoA synthetase
1175	CA409634	176	7E-17	alcohol dehydrogenase (EC 1.1.1.1)
951	CA410685	523	2E-54	alcohol dehydrogenase 1 (EC 1.1.1.1.)
337	CA410077	431	3E-21	ATP-citrate lyase (EC 4.1.3.8)
1006	CA409471	273	7E-32	beta-galactosidase
1101	CA409565	557	4E-37	beta-glucosidase (EC 3.2.1.21)
1106	CA409569	562	2E-36	beta-glucosidase (EC 3.2.1.21)
832	CA410567	485	6E-35	beta-glucosidase like protein
284	CA410023	492	7E-21	citrate synthase (EC 4.1.3.7)
976	CA410707	585	1E-08	dihydrolipoamide S-acetyltransferase
867	CA410598	444	2E-18	D-ribulose-5-phosphate 3-epimerase
697	CA410428	481	2E-23	enolase
894	CA410626	579	4E-35	enolase (2-phospho-D-glycerate hydrolase, EC 4.2.1.11)
247	CA409983	457	2E-41	enolase (2-phosphoglycerate dehydratase)
508	CA410244	488	1E-68	enolase (2-phosphoglycerate dehydratase)
728	CA410460	460	1E-32	formate dehydrogenase, NAD dependent
218	CA409954	467	4E-32	formate dehydrogenase, NAD dependent, mitochondrial
109	CA409562	109	0.000009	formamidase (EC 3.5.1.49)
41	CA410157	591	1E-53	formamidase-like protein
187	CA409923	490	1E-49	formamidase (EC 3.5.1.49)
61	CA410348	422	3E-31	formamidase like protein
891	CA410623	564	5E-40	fructokinase
834	CA410569	489	8E-42	fructose-biphosphate aldolase, cytoplasmic
1399	CA409843	447	3E-23	fructose-bisphosphate aldolase (EC 4.1.2.13)
836	CA410571	497	5E-44	fructose-biphosphate aldolase, cytoplasmic
538	CA410271	163	2E-09	fructose bisphosphate aldolase
133	CA409784	276		fructose bisphosphate aldolase
647	CA410375	462	2E-26	fructose-biphosphate aldolase
350	CA410092	461	3E-30	fructose-biphosphate aldolase, cytoplasmic (EC 4.1.2.13)
896	CA410627	487	9E-34	fructose-biphosphate aldolase, cytoplasmic
786	CA410521	455	1E-41	fructose-biphosphate aldolase, cytoplasmic
948	CA410681	497	1E-37	fructose-biphosphate aldolase, cytoplasmic
750	CA410485	450	9E-38	fructose-bisphosphate aldolase
155	CA409893	363	4E-28	fructose-bisphosphate aldolase (EC 4.1.2.13)
152	CA409890	152	0.000004	fructose-bisphosphate aldolase, cytoplasmic
1088	CA409549	566	3E-27	6-phosphogluconolactonase, putative (3.1.1.31)
245	CA409981	469	8E-33	glucose-6-phosphate 1-dehydrogenase
216	CA409952	469	2E-53	glucose-6-phosphate 1-dehydrogenase
762	CA410497	461	8E-33	glucose-6-phosphate 1-dehydrogenase -- cytoplasmic I
567	CA410300	471	9E-42	glucose-6-phosphate isomerase (EC 5.3.1.9)
710	CA410442	461	0.000004	glucosidase homolog
1363	CA409805	538	6E-41	glyceraldehyde 3-phosphate dehydrogenase (EC 1.2.1.12)
1380	CA409824	510	6E-43	glyceraldehyde 3-phosphate dehydrogenase (EC 1.2.1.12)
263	CA410001	455	1E-43	glyceraldehyde 3-phosphate dehydrogenase, cytosolic
578	CA410309	434	1E-40	glyceraldehyde 3-phosphate dehydrogenase, cytosolic
418	CA410155	438	2E-42	glyceraldehyde 3-phosphate dehydrogenase, cytosolic (EC 1.2.1.12)
799	CA410531	438	2E-38	glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)
1265	CA409716	383	3E-34	glyceraldehyde 3-phosphate dehydrogenase (EC 1.2.1.12)
470	CA410203	464	4E-42	glyceraldehyde 3-phosphate dehydrogenase (EC 1.2.1.12)
199	CA409932	456	7E-42	glyceraldehyde 3-phosphate dehydrogenase
1141	CA409604	552	1E-40	glyceraldehyde 3-phosphate dehydrogenase (EC 1.2.1.12)
1293	CA409742	533	1E-45	glyceraldehyde 3-phosphate dehydrogenase (EC 1.2.1.12)
14	CA409888	358	9E-30	glyceraldehyde-3-phosphate dehydrogenase(cytosolic)
1094	CA409556	562	5E-15	granule-bound glycogen[starch] synthase, (EC 2.4.1.21)
543	CA410276	427	6E-36	hexokinase (EC 2.7.1.1) (glucokinase)
38	CA410125	414	8E-31	hyp. protein C5H10.03 / phosphoglycerate mutase
1349	CA409792	539	2E-40	hyp. protein T30F21.10, similar to dTDP-D-glucose 4,6-dehydratase
656	CA410385	277	2E-24	isocitrate dehydrogenase (NADP)
664	CA410394	429	6E-36	isocitrate dehydrogenase (NADP)
1145	CA409607	544	8E-48	isocitrate dehydrogenase [NADP] (EC 1.1.1.42)
626	CA410354	452	4E-38	malate dehydrogenase
1394	CA409839	528	1E-36	malate dehydrogenase (EC 1.1.1.37)
497	CA410231	346	4E-27	malate oxidoreductase (EC 1.1.1.40)
213	CA409949	476	2E-40	malate oxidoreductase
1142	CA409605	548	5E-42	malic enzyme (EC 1.1.1.40), NADP-dependent
771	CA410506	450	1E-44	malate synthase, glyoxysomal (EC 4.1.3.2)
1407	CA409851	554	2E-38	malate synthase, glyoxysomal (EC 4.1.3.2)
1251	CA409705	271	3E-09	probable oxalyl-CoA decarboxylase (EC 4.1.1.8)
1259	CA409710	311	0.000003	probable oxalyl-CoA decarboxylase (EC 4.1.1.8)
1283	CA409732	538	1E-21	2-hydroxyphytanoyl-CoA lyase / 2E-19 oxalyl-CoA decarboxylase
1035	CA409498	597	4E-57	phosphoenolpyruvate carboxylase (EC 4.1.1.31)
1156	CA409618	530	6E-48	phosphoenolpyruvate carboxylase (EC 4.1.1.31)
1263	CA409714	435	2E-36	phosphoglucomutase (EC 5.4.2.2)
47	CA410213	416	2E-17	phosphoglucomutase, cytosolic
490	CA410224	479	2E-36	phosphoglycerate kinase, cytosolic
415	CA410152	463	4E-40	phosphoglycerate kinase, cytosolic (EC2.7.2.3)
33	CA410080	412	4E-36	phosphoglycerate kinase, cytosolic
1000	CA409465	556	1E-45	phosphoglycerate kinase, cytosolic
1097	CA409559	586	1E-140	probable pyrophosphate--fructose-6-phosphate 1-phosphotransferase
103	CA840666			probable pyrophosphate--fructose-6-phosphate 1-phosphotransferase

375	CA410117	513	3E-29	pyrophosphate-dependent phosphofructo-1-kinase
1081	CA409542	550	4E-46	pyrophosphate-dependent phosphofructo-1-kinase homolog
9	CA410730	453	3E-39	pyrophosphate-dependent phosphofructose-1-kinase
244	CA409980	465	5E-40	pyrophosphate-dependent phosphofructo-1-kinase
1386	CA409830	606	2E-40	pyruvat decarboxylase (EC 4.1.1.1)
731	CA410464	456	4E-25	pyruvate decarboxylase (EC 4.1.1.1)
130	CA409759	445	2E-23	pyruvate decarboxylase isozyme (EC 4.1.1.1)
1378	CA409821	572	2E-17	pyruvat dehydrogenase E1 beta subunit (EC 1.2.4.1)
80	CA410544	438	0.000003	pyruvate dehydrogenase E1 beta subunit
186	CA409922	470	3E-26	pyruvate dehydrogenase E1component alpha subunit
666	CA410396	435	5E-19	succinate dehydrogenase iron protein su
672	CA410403	474	4E-24	succinate dehydrogenase iron -protein su
1246	CA409700	580	9E-30	succinyl-CoA-ligase alpha subunit (EC 6.2.1.4)
197	CA409931	491	2E-38	sucrose synthase
904	CA410636	618	2E-41	sucrose synthase
639	CA410367	290	2E-18	sucrose synthase (EC 2.4.1.13)
1216	CA409676	279	7E-22	sucrose synthase (EC 2.4.1.13), Glycine max
183	CA409919	480	9E-49	sucrose synthase (EC 2.4.1.14)
684	CA410415	494	1E-56	sucrose synthase (EC 2.4.1.14)
358	CA410100	517	2E-49	transaldolase (EC 2.2.1.2)
249	CA409985	468	3E-43	transaldolase (EC 2.2.1.2)
1080	CA409541	524	9E-27	transaldolase (EC 2.2.1.2)
143	CA409882	472	4E-46	transketolase, chloroplast (EC 2.2.1.1)
1413	CA409858	602	4E-30	triosephosphate isomerase (EC 5.3.1.1)
1211	CA409671	522	2E-38	triosephosphate isomerase (EC5.3.1.1)
1098	CA409560	537	2E-38	triosephosphate isomerase, cytosolic (EC 5.3.1.1)

ENERGY METABOLISM: category 1b

1222	CA409682	597	5E-51	adenine nucleotide translocator/ 3E-50 ADP,ATP carrier protein
298	CA410038	470	3E-28	adenine nucleotide translocator / ADP, ATP carrier protein precursor
1132	CA409595	561	5E-36	adenine nucleotide translocator/ 4E-24 ADP,ATP carrier protein
1248	CA409702	541	2E-16	adenylate kinase (EC2.7.4.3), putative
474	CA410207	519	3E-55	alternative oxidase 3 (EC 1.-.-.-)
1354	CA409798	579	4E-41	alternative respiratory pathway oxidase (EC1.-.-.-)
821	CA410555	390	5E-28	alternative respiratory pathway, oxidase
1227	CA409687	567	1E-50	ATP synthase beta chain
1278	CA409726	417	2E-10	ATP synthase beta chain
110	CA409573			ATP synthase beta chain
1138	CA409600	489	6E-13	ATP synthase beta chain, mitochondrial precursor.
1384	CA409828	571	6E-37	ATP synthase gamma chain
977	CA410708	538	2E-29	ATPsynthase (EC 3.6.1.34) gamma chain, mitochondr.
202	CA409937	497	3E-34	ATP synthase gamma chain, mitochondrial precursor
869	CA410600	532	3E-18	H+ transporting ATP synthase (EC 3.6.1.34)
627	CA410355	487	2E-33	vacuolar ATP synthase subunit D
92	CA410649	401	2E-25	F1-APTase delta chain
1117	CA409581	527	8E-34	basic blue copper protein
46	CA410202	429	1E-25	cytochrome c oxidase subunits 6b-1
19	CA409933	356	1E-09	electron transfer flavoprotein
906	CA410638	547	5E-50	hyp. protein / 2E-36 mitoch. respirat. chain compl. assembly
1322	CA409772	617	2E-53	hyp. protein T14P8, similar to ATPases
233	CA409969	480	4E-17	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3)
94	CA410683	411	8E-26	NADH dehydrogenase 24 kD subunit
1312	CA409761	505	3E-17	NADH-ubiquinone oxidoreductase (1.6.5.3) 18 kd subunit
795	CA410529	407	2E-45	NADH-ubiquinone oxidoreductase (EC 1.6.5.3)
990	CA410721	555	1E-43	NADH-ubiquinone oxidoreductase 75 kd subunit
271	CA410010	446	5E-28	NADH-ubiquinone oxireductase
259	CA409996	472	1E-33	NADH-ubiquinone oxireductase
317	CA410056	461	6E-36	NADPH: quinone oxidoreductase
318	CA410057	476	8E-37	NADPH: quinone oxidoreductase
330	CA410071	492	1E-37	NADPH: quinone oxidoreductase
675	CA410406	482	6E-29	putative mitochondrial uncoupling protein
1010	CA409474	548	1E-12	putative mitochondrial uncoupling protein
1389	CA409833	541	3E-34	ubiquinone biosynthesis protein, putative
770	CA410505	447	2E-40	14-3-3-like protein
1166	CA409627	471	5E-29	14-3-3-like protein
1192	CA409652	485	3E-35	14-3-3-like protein
814	CA410548	509	7E-47	14-3-3-like protein
926	CA410646	508	2E-31	14-3-3-like protein
1107	CA409570	501	4E-39	14-3-3-like protein B homolog SGF14B.

NUCLEOTIDE AND NUCLEIC ACID METABOLISM:category 2

876	CA410607	558	1E-36	adenine phosphoribosyltransferase 1 (EC 2.4.2.7)
1291	CA409740	556	0.000002	cytosine methyltransferase
445	CA410179	124	0.000001	DNA topoisomerase I (EC 5.99.1.2)
724	CA410457	219	2E-09	DNA-directed RNA polymerase Iia
544	CA410277	328	4E-25	guanine nucleotide binding protein beta subunit-like
545	CA410278	455	1E-45	histone H3.3 like protein
1325	CA409775	592	2E-46	histone H3.3-like protein, Arabidopsis / 8E-46 histone H3.2
542	CA410275	430	3E-34	hyp. protein F19B6.1A protein/uridine kinase
408	CA410145	510	4E-10	hyp. protein T20K18.110/ 2E-1RPA interacting protein alpha
875	CA410606	506	4E-41	hyp. protein T22K18 / 2E-8 endonuclease III
226	CA409962	509	1E-29	nucleosome assembly protein 1
266	CA410004	464	9E-49	nucleotide pyrophosphatase-like protein
145	CA409885	404		nucleotide sugar epimerase-like protein

225	CA409961	467		nucleotide sugar epimerase-like protein
562	CA410296	464	3E-19	nucleotide sugar epimerase-like protein
320	CA410060	433	2E-08	nucleotide sugar epimerase-like protein, putative
1376	CA409819	549	7E-45	o-acetylserine (thiol) lyase, cystein synthase (EC 4.2.99.8)
911	CA410658	477	3E-23	putative splicing factor
1201	CA409662	550	5E-52	putative splicing factor Prp8, Arabidopsis etc.
741	CA410475	488	5E-35	ribonuclease non-S (EC 3.1.-.-.) precursor
1100	CA409564	477	0.000008	ribonuclease PH
55	CA410293	388	0.000008	ribonuclease PH-like protein
1195	CA409654	564	2E-37	RNA helicase
1296	CA409745	577	4E-44	RNA helicase
924	CA410644	507	2E-31	RNA helicase (fragment)
949	CA410682	559	2E-22	RNA helicase (fragment)
695	CA410427	501	1E-45	RNA helicase, ATP-dependent
323	CA410063	479	4E-07	sugar nucleot. phosphorylase /glucose-1-phosph. thymidylyltransferase
763	CA410498	467	5E-41	xanthine dehydrogenase-like protein (EC 1.1.1.204)

AMINO ACID AND PROTEIN METABOLISM: category 3

414	CA410151	491	2E-37	26S protease regulatory subunit 7 (26S proteasome ATPase)
1348	CA409791	604	8E-54	26S protease regulatory subunit 8,
740	CA410474	477	1E-34	26S protease subunit 4, putative
918	CA410665	527	2E-49	proteinase homolog
1148	CA409610	567	3E-40	26S proteasome subunit athMOV34, putative
828	CA410562	444	1E-16	3-hydroxy-3-methylglutaryl-coenzyme A reductase (EC 1.1.1.34)
809	CA410543	261	6E-14	3-hydroxyisobutyryl-coenzyme A hydrolase
1221	CA409681	528	3E-45	3-hydroxyisobutyryl-coenzyme A hydrolase homolog T9E8.100
1317	CA409766	201	1E-14	3-hydroxyisobutyryl-coenzyme A hydrolase homolog T9E8.100
279	CA410017	439	7E-25	40S ribosomal protein S2
1237	CA409693	538	2E-37	40S ribosomal protein S2
1164	CA409626	550	1E-39	40S ribosomal protein S3A
421	CA410158	436	6E-43	40S ribosomal protein S4
60	CA410338	415	9E-34	40S ribosomal protein S6
555	CA410288	461	1E-34	40S ribosomal protein S8
1223	CA409683	571	6E-35	40S ribosomal protein S8
549	CA410282	441	3E-31	ribosomal protein S8
1309	CA409758	536	3E-16	60S acidic ribosomal protein P2
794	CA410528	496	3E-14	60S acidic ribosomal protein PI
922	CA410670	531	5E-43	60S ribosomal protein L1
326	CA410066	445	3E-38	60S ribosomal protein L11
1069	CA409531	443	9E-43	60S ribosomal protein L3
355	CA410097	498	5E-40	arginine decarboxylase (EC 4.1.1.19)
725	CA410458	469	3E-49	arginine decarboxylase (EC 4.1.1.19)
848	CA410583	482	4E-47	arginine decarboxylase (EC 4.1.1.19)
453	CA410186	433	3E-10	argininosuccinate synthase (EC 6.3.4.5)
1071	CA409533	455	8E-15	aspartate aminotransferase (EC 2.6.1.1)
663	CA410393	458	3E-12	aspartate aminotransferase-homolog
655	CA410384	452	1E-11	aspartate aminotransferase-homolog
8	CA410632	230	0.000006	ATP dependent CLP protease proteolytic subunit
200	CA409935	474	4E-27	ATP dependent CLP protease proteolytic subunit
116	CA409630	440	9E-33	cathepsin B-like cysteine proteinase
1185	CA409644	552	3E-22	cucumisin-like serin protease / subtilisin-like proteinase (EC 3.4.21.-),
1083	CA409544	503	1E-37	cystathionine-gamma-synthase precursor (EC 4.2.99.9)
1063	CA409525	543	3E-34	cystein proteinase
689	CA410420	471	2E-48	cysteine protease
81	CA410553	407	9E-40	cysteine proteinase
915	CA410662	485	1E-42	elongation factor 1-alpha (EF-1-alpha)
1111	CA409575	547	7E-41	elongation factor 1-alpha (EF-1-alpha)
1207	CA409666	541	9E-44	elongation factor 1-alpha (EF-1-alpha), Vicia faba etc.
1079	CA409539	541	5E-47	elongation factor 1-alpha, translation elongation factor eEF-1
1375	CA409818	534	5E-47	elongation factor 1-alpha, translation elongation factor eEF-1
322	CA410062	469	5E-48	translocation elongation factor eEF-1 alpha chain (EF-1-ALPHA)
286	CA410025	469	4E-32	elongation factor 1B gamma
1218	CA409677	93	8E-19	elongation factor 1-beta (EF-1-beta)
191	CA409927	468	3E-33	elongation factor 2 (EF-2)
1387	CA409831	567	6E-44	glutamine synthetase (EC 6.3.1.2)
764	CA410499	428	1E-39	glutamine synthetase (EC 6.3.1.2)
807	CA410541	497	4E-56	glutamine synthetase isozyme (cytosolic/ root/ nodule) (EC 6.3.1.2)
1366	CA409808	563	1E-46	glycine hydroxymethyltransferase (EC 2.1.2.1)
1320	CA409770	566	3E-42	homogenotisate 1,2-dioxygenase (EC 1.13.11.5)
979	CA410710	557	2E-33	hyp. protein F6F22/-10 prob. 60S ribos. protein
501	CA410237	501	3E-36	hyp. protein T24I21.7 /1E-32 EF-1 alpha-like protein
1370	CA409813	592	5E-19	importin alpha subunit (karyopherin alpha subunit), tomato etc.
850	CA410586	523	1E-29	ketol-acid reductoisomerase precursor (EC 1.1.1.86)
1077	CA409537	552	1E-14	lysyl-tRNA synthetase (EC 6.1.1.6)
838	CA410573	517	3E-25	microsomal signal peptidase subunit 18kD
426	CA410163	499	5E-29	mitochondrial LON protease homolog/ATP dependent protease LA2
246	CA409982	364	4E-18	mitochondrial processing peptidase
1257	CA409708	136		blastn: 6E-9 cathepsin B-like, putative
588	CA410318	483	2E-45	peptidyl-prolyl cis-trans isomerase
611	CA410340	127	6E-09	peptidyl-prolyl cis-trans isomerase
650	CA410379	419	6E-33	peptidylprolyl isomerase (5.2.1.8)
658	CA410387	534	5E-39	peptidylprolyl isomerase (5.2.1.8)
385	CA410120	391	2E-25	peptidylprolyl isomerase (EC 5.2.1.8)
386	CA410121	262	5E-19	peptidylprolyl isomerase (EC 5.2.1.8)
1114	CA409578	529	4E-17	poly (A) binding protein II

619	CA410347	459	2E-34	polyA binding protein
880	CA410612	418	1E-30	polyadenylate binding protein, poly-A binding protein
803	CA410537	482	2E-24	polyadenylate binding protein, poly-A binding protein
359	CA410101	461	2E-45	polyubiquitin
515	CA410252	486	2E-49	polyubiquitin
1345	CA409788	519	4E-44	ubiqitin, Arabidopsis etc. / 5E-44 polyubiquitin Acetabularia etc.
787	CA410522	433	7E-44	polyubiquitin
1359	CA409802	552	3E-55	polyubiquitin, parsley etc.
587	CA410317	438	2E-43	ubiquitin
820	CA410554	402	1E-34	polyubiquitin
518	CA410255	382	1E-29	ubiquitin precursor
833	CA410568	494	4E-48	polyubiquitin
1330	CA409780	610	4E-37	proline iminopeptidase
1217	CA840674	426	5E-34	proteasome 26S, probable, reg. Subunit S12
852	CA410588	528	0.000001	protein disulfide-isomerase (EC 5.3.4.1)
430	CA410168	484	1E-40	protein phosphatase 2C-like protein
4	CA410235	491	2E-40	protein phosphatase type 2C
945	CA410678	244	2E-10	ribosomal protein L10
486	CA410219	477	6E-45	ribosomal protein L12
907	CA410639	563	1E-41	ribosomal protein L19
252	CA409989	448	1E-42	ribosomal protein L24
373	CA410115	473	1E-34	ribosomal protein L4
431	CA410169	497	2E-28	ribosomal protein S24
432	CA410170	463	2E-30	ribosomal protein S5
454	CA410187	404	2E-38	ribosome protein L13 (BBC1 protein homolog)
461	CA410194	507	1E-37	ribosome protein L5
1096	CA409558	583	1E-23	similar to protein disulfide isomerase
272	CA410011	442	4E-18	subtilisin-like proteinase homolog F7L13.110
1052	CA409514	591	2E-46	translation initiation factor
276	CA410014	466	4E-28	translation initiation factor
987	CA410718	556	2E-43	translation initiation factor 5A, (EIF-5A)
295	CA410035	481	6E-42	translation initiation factor eIF3-like
888	CA410619	616	6E-41	translation initiation factor, (EIF-4A)
817	CA410550	498	1E-39	translation initiation factor, eukaryotic (EIF-4A)
1105	CA409568	554	3E-32	translocation elongation factor EF-Tu
726	CA410459	448	5E-39	ubiquitin extension protein
553	CA410286	479	2E-42	ubiquitin/ribosomal protein CEP52
1	CA409934	446	4E-43	ubiquitin/ribosome protein
522	CA410260	502	2E-56	ubiquitin conjugating enzyme E2-17 KD (EC 6.3.2.19)
479	CA410212	500	9E-34	ubiquitin-conjugating enzyme
712	CA410444	397	0.000003	ubiquitin-conjugating enzyme E2
280	CA410019	457	3E-37	ubiquitin-conjugating enzyme UBC7

FATTY ACID AND LIPID METABOLISM: category 4

509	CA410245	461	2E-50	24-sterol C-methyltransferase (EC 2.1.1.41)
1125	CA409589	586	3E-56	24-sterol C-methyltransferase (EC 2.1.1.41)
1046	CA409508	620	8E-24	2-hydroxyphytanoyl-CoA lyase/1E-23 prob. oxalyl-CoA decarboxylase
1183	CA409643	529	2E-21	oxalyl-CoA decarboxylase (EC 4.1.1.8)
443	CA410177	164	7E-09	acetyl -CoA carboxylase (EC 6.4.1.2)
1392	CA409837	582	5E-40	acetyl-CoA acyltransferase (EC 2.3.1.16)
1007	CA409472	576	9E-38	acetyl-CoA C-acyltransferase (EC 2.3.1.16), peroxisomal
1023	CA409486	567	2E-59	acetyl-CoA carboxylase (EC 6.4.1.2),
826	CA410560	487	3E-22	acyl carrier protein, mitochondrial precursor
1041	CA409504	590	2E-42	acyl-CoA oxidase (EC 1.3.3.6)
167	CA409904	488	3E-26	b-keto acyl reductase /steroid dehydrogenase
1199	CA409658	581	2E-31	b-keto acyl reductase (EC 1.1.-.-), probable
1238	CA409694	574	8E-27	choline kinase (EC 2.7.1.32)
412	CA410150	494	0.000002	fatty acid CoA ligase (EC 6.2.1.-)
1126	CA409590	566	2E-39	glycerophosphodiester phosphodiesterase (EC 3.1.4.46)
1391	CA409836	545	7E-34	hyp protein, lipase like, Arabidopsis etc.
1381	CA409825	564	6E-22	lysophospholipase isolog, Arabidopsis etc.
84	CA410585	412	2E-35	NADH-cytochrome b5 reductase
1346	CA409789	548	2E-30	phosphoglyceride transfer protein, putative
628	CA410356	456	5E-22	triacylglycerol lipase homolog

NUTRIENT ASSIMILATION (other than carbon): category 5

269	CA410007	465	2E-14	5'-adenylylsulfate reductase
419	CA410156	524	1E-21	5'-adenylylsulfate reductase (EC 2.8.2)
617	CA410345	375	5E-37	acid phosphatase
1030	CA409493	600	4E-62	ferredoxin--nitrite reductase (EC 1.7.7.1)
769	CA410503	452	1E-20	purple acid phosphatase (EC 3.1.3.2)
823	CA410557	500	1E-48	purple acid phosphatase (EC 3.1.3.2)
1146	CA409608	580	2E-45	purple acid phosphatase (EC 3.1.3.2)
1085	CA409546	580	8E-45	purple acid phosphatase (EC 3.1.3.2)
901	CA410634	568	2E-68	Putative acid phosphatase (novel acid phosphatase)

SECONDARY METABOLISM: category 6

734	CA410467	484	3E-45	trehalose-6-phosphate synthase homolog
345	CA410086	519	1E-07	12-oxophytodienoate reductase (EC 1.3.1.42)
707	CA410439	503	2E-43	12-oxophytodienoate reductase OPR1
688	CA410419	483	9E-38	12-oxophytodienoate reductase OPR1/CPRD8 protein
22	CA409965	237	3E-21	1-D-deoxyxylulose 5-phosphate synthase
1189	CA409648	565	5E-55	1-deoxyxylulose 5-phosphate synthase
1210	CA409670	531	3E-26	1-deoxy d-xylulose 5-phosphate reductoisomerase
717	CA410449	494	8E-44	1-doxyxylulose 5-phosphate synthase

239	CA409974	457	2E-22	2'-hydroxydihydrodaidzein reductase
158	CA409896	455	2E-50	phospho-2-dehydro-3-deoxyheptonate aldolase (EC 4.1.2.15)
397	CA410133	483	3E-43	phospho-2-dehydro-3-deoxyheptonate aldolase (EC 4.1.2.15)
31	CA410059	404	5E-08	3-deoxy-D-arabino-heplulosonate 7-phosphate synthase
873	CA410604	545	2E-18	3-deoxy-D-arabino-heplulosonate 7-phosphate synthase
168	CA409905	413	3E-40	3-deoxy-D-arabino-heptulosonate-7-phosphate synthase
860	CA410596	500	3E-36	3-methylcrotonyl-coa carboxylase precursor (EC 6.4.1.4)
475	CA410208	433	9E-20	4-nitrophenylphosphatase (EC 3.1.3.41)
1040	CA409503	576	1E-27	alpha-1,3-mannosyl-glycoprotein beta-,2 n-acetylglucosaminyltransfer.
789	CA410523	462	7E-40	caffeoyl-coa 3-O-methyltransferase (EC 2.1.1.10)
1129	CA409592	556	8E-40	caffeoyl-CoA O-methyltransferase (EC 2.1.1.10)
1112	CA409576	528	4E-39	caffeoyl-CoA O-methyltransferase, (EC 2.1.1.10)
733	CA410466	466	1E-42	cinnamoyl-CoA reductase (EC 1.2.1.44)
344	CA410085	501	1E-45	cinnamyl-alcohol dehydrogenase (EC 1.1.1.195)
996	CA410726	595	1E-44	cinnamyl-alcohol dehydrogenase (EC 1.1.1.195)
782	CA410517	480	5E-55	copper methylamine oxidase precursor, peroxisomal
747	CA410481	434	5E-20	dolichyl-di-phosphooligosaccharide-protein glycotransferase
505	CA410241	340	4E-23	dolichyl-phosphate beta-glucosyltransferase homolog F12L6.29
1267	CA409718	459	8E-40	epoxide hydrolase homolog (EC 3.3.2.3)
459	CA410191	539	1E-43	heme oxygenase 1 precursor
1122	CA409586	557	2E-44	hyp. 21.7 kd protein, GEN: 5031275 / 4E-24 1,4-benzquinone reductase
1186	CA409645	513	5E-38	hyp. 21.7 kd protein, GEN: 5031275 / 6E -22 1,4-benzoquinone reductase
1162	CA409625	453	3E-20	hyp. 21.7 kd protein, GEN: 5031275 / 6E -6 1,4-benzoquinone reductase
1432	CA409875	524	4E-43	hyp. 21.7 kd protein, GEN: 5031275 / 6E-24 1,4-benzoquinone reductase
1087	CA409548	596	4E-51	hyp. 21.7 kd protein, GEN: 5031275 / 7E-25 1,4-benzoquinone reductase
391	CA410127	509	8E-22	isoliquiritigenin 2'-O-methyltransferase
777	CA410512	540	3E-21	narbonin
23	CA409975	431	4E-10	polyphenol oxidase precursor
1379	CA409822	535	3E-15	protoporphyrinogen oxidase PX-1 (EC 1.3.3.4), Nicotiana tabacum
599	CA410329	511	2E-49	putative chloroplast prephenate dehydratase
301	CA410042	478	4E-19	putative chloroplast prephenate dehydratase (EC 4.2.1.51)
257	CA409994	485	0.000001	quinone oxidoreductase
1426	CA409869	548	1E-15	quinone oxidoreductase (EC 1.6.5.5)
1390	CA409835	398	6E-18	reticuline oxidase homolog, Arabidopsis
575	CA410306	444	3E-27	thiazole biosynthetic enzyme precursor (AG6)
1285	CA409734	483	2E-27	thiazole biosynthetic enzyme, thiamin biosynthesis protein thi1+E540

POSSIBLE FUNCTION(S) IN DIFFERENT AREAS of METABOLISM: category 7

936	CA410655	516	3E-43	probable NADP-dependent oxidoreductase (EC 1.6.5.5)
1133	CA409596	561	1E-36	probable NADP-dependent oxidoreductase (EC 1.6.5.5).
892	CA410624	569	8E-28	aldehyde dehydrogenase (NAD+)
40	CA410147	471	3E-17	esterase
1352	CA409796	610	4E-27	ferredoxin
1078	CA409538	582	1E-23	GDP-mannose pyrophosphorylase
455	CA410188	521	5E-29	mannose-1-phosphate guanyltransferase (EC 2.7.7.13)
1150	CA409613	544	1E-45	glucosyltransferase, putative
264	CA410002	469	7E-21	hydrolase
161	CA409899	454	1E-16	hydrolase, putative (cont. an esterase/lipase/thioesterase active site)
467	CA410199	534	6E-32	hyp. protein T3P18.13 / flavin-containing monooxygenase
1213	CA409673	546	2E-35	isomerase like prot./5E-22 2-hydroxyhepta-2,4 diene-1,7-dioate isomer.
886	CA410618	554	3E-48	nucleoside diphosphate kinase I (EC 2.7.4.6))
306	CA410047	487	1E-10	PrMC3 protein / putative hydrolase
742	CA410476	454	2E-20	ribose-phosphate pyrophosphokinase (EC 2.7.6.1)
824	CA410558	486	1E-44	methionine adenosyltransferase
984	CA410715	556	7E-41	methylenetetrahydrofolate reductase
943	CA410677	517	6E-51	5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase
1061	CA409523	550	3E-43	5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase
125	CA409711	437	3E-37	5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferas
947	CA410680	538	2E-42	5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase
743	CA410477	432	9E-35	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase
1084	CA409545	555	3E-47	5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase
1240	CA409697	582	3E-45	5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase
1323	CA409773	643	1E-61	5-Methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase
149	CA409889	151	2E-10	S-adenosylmethionine synthetase (EC 2.5.1.6)
231	CA409967	450	3E-42	S-adenosylmethionine synthetase (EC 2.5.1.6)
921	CA410669	540	1E-45	S-adenosylmethionine synthetase (EC 2.5.1.6)
589	CA410319	410	2E-35	methionine adenosyltransferase
958	CA410691	501	1E-32	S-adenosylmethionine synthetase (EC 2.5.1.6)
1019	CA409482	553	1E-52	S-adenosylmethionine synthetase (EC 2.5.1.6)
1198	CA409657	557	7E-50	S-adenosylmethionine synthetase (EC 2.5.1.6)
1301	CA409752	504	2E-47	S-adenosylmethionine synthetase (EC 2.5.1.6)
1401	CA409846	555	2E-47	S-adenosylmethionine synthetase (EC 2.5.1.6)
341	CA410082	488	2E-43	S-adenosyl-methionine synthetase / -transferase
1410	CA409855	559	2E-55	S-adenosylmethionine synthetase (EC 2.5.1.6)
354	CA410096	508	9E-50	adenosyl-homocysteinase (EC 3.3.1.1)
1404	CA409849	510	2E-43	adenosylhomocysteinase, S-adenosyl-L-homocysteine hydrolase
394	CA410130	427	1E-46	adenosylhomocysteinase (EC 3.3.1.1) (S-adenosyl -L-homocysteine)
981	CA410712	579	3E-32	sulfate adenylyltransferase (EC 2.7.7.4)
1367	CA409809	536	2E-30	sulfate adenylyltransferase (EC 2.7.7.4)
1249	CA409703	522	2E-55	ATP sulfurylase (EC 2.7.7.4)
761	CA410496	484	4E-47	ATP sylfurylase precursor (EC 2.7.7.4) (sulfate adenylyltransferase)
113	CA409602	341	2E-17	sulfate adenylyltransferase (EC 2.7.7.4)
986	CA410717	529	5E-28	thioredoxin h-type
278	CA410016	391	2E-19	thioredoxin M
991	CA410722	533	1E-07	UDP-glucuronyltransferase-like protein

681	CA410412	479	2E-17	UTP-glucose glucosyltransferase homolog A_IG002N01.15
417	CA410154	532	4E-39	glutathione synthetase precursor (EC 6.3.2.3) (glutathione synthase).

II DEVELOPMENT

CELL STRUCTURE, DIFFERENTIATION, CELL CYCLE: category 8

1099	CA409561	568	4E-48	actin depolymerizing factor
403	CA410141	530	3E-48	actin depolymerizing factor 1/2/4
303	CA410044	487	2E-21	Beta-1.3-endoglucanase homolog
1025	CA409488	576	7E-42	cell division protein FTSH isolog
20	CA409945	373	1E-23	cell elongation diminuto
73	CA410473	364	3E-35	cell elongation protein
1193	CA409653	523	8E-31	chloroplast protease / 1E-30 cell division protein FTSH-like protein
1161	CA409624	449	2E-22	chloroplast protease, Capsicum / 2E-22 cell division protein FTSH-like protein PFTF
1154	CA409616			chloroplast protease, Capsicum / 2E-22 cell division protein FTSH-like protein PFTF
566	CA410299	442	2E-27	glucan endo-1,3-beta-D-glucosidase homolog/beta-1,3-glucanase
484	CA410217	470	3E-28	kinesin like protein
718	CA410450	500	3E-09	kinesin-like protein
1326	CA409776	586	1E-32	nucleotide-binding protein NBP35, yeast etc.
1318	CA409767	578	5E-17	pectinesterase (EC 3.1.1.11)
1360	CA409804	547	5E-48	pectinesterase (EC 3.1.1.11)
938	CA410671	513	2E-36	pectinesterase (EC 3.1.1.11)
805	CA410539	514	2E-26	pectinesterase-like protein
85	CA410595	440	6E-34	PITSLRE protein kinase alpha subunit
101	CA409483	375	8E-07	polygalacturonase inhibitor
292	CA410032	454	8E-21	cellulase homolog precursor (3.2.1.4)
1082	CA409543	518	2E-38	probable DNA-binding protein
238	CA409973	492	1E-46	tubulin alpha-1 chain
468	CA410200	470	1E-43	tubulin alpha-1 chain
1066	CA409528	379	3E-24	tubulin alpha-2 / alpha-4 chain
1176	CA409635	531	5E-50	alpha-tubulin
1435	CA409877	288	0.000007	tubulin beta chain
105	CA409521	134	7E-11	tubulin beta-1 chain
205	CA409940	487	2E-24	tubulin beta-1 chain
903	CA410635	576	4E-45	UDP-glucose 6-dehydrogenase (EC 1.1.1.22)
1440	CA409883	572	3E-43	UDP-glucose 6-dehydrogenase (EC 1.1.1.22)
148	CA409887		7E-56	UDP-glucose 6-dehydrogenase (EC 1.1.1.22)
29	CA410040	423	3E-18	xyloglucan endo-1, 4-beta-D-glucanase
997	CA410727	534	5E-22	xyloglucan endo-1, 4-beta-D-glucanase (EC 3.2.1.-)
723	CA410456	442	7E-34	xyloglucan endo-1,4-beta-D-glucanase (EC 3.2.1.-)
228	CA409964	521	9E-32	xyloglucan endo-1,4-beta-D-glucanase homolog
237	CA409972	469	2E-48	xyloglucan endo-1,4-beta-D-glucanase homolog
236	CA409971	492	3E-52	xyloglucan endo-1,4-beta-D-glucanase homolog

PLANT DEVELOPMENT, NODULATION, SENESCENCE: category 9

1430	CA409873	561	2E-42	abscisic acid activated protein, alfalfa/5E-38 put. alcohol dehydr.
720	CA410453	490	2E-43	actin 2/7
51	CA410257	380	7E-21	alpha fucosidase precursor
365	CA410107	491	3E-17	AP2 domain containing protein
411	CA410149	470		no significant match
637	CA410365	186	4E-09	AP2 domain containing protein, putative
625	CA410353	478	6E-15	hyp. protein T30B22,18
425	CA410162	449	7E-34	AR401/SLL2 protein (S locus linked protein)
172	CA409909	460	4E-45	argonaute protein/pinhead/zwille protein
209	CA409944	495	1E-35	ascorbate oxidase-related/ pectinesterase homolog
937	CA410656	483	5E-18	pollen-specific protein / 3E-12 pectinesterase like prot.
954	CA410688	517	2E-25	pollen-specific protein / 5E-20 pectinesterase like prot.
288	CA410027	462	1E-47	ascorbate oxidase-related/ pectinesterase homolog
629	CA410357	528	1E-33	cell division cycle protein 48 homolog
1036	CA409499	573	9E-18	cytokinin oxidase
998	CA410728	587	2E-18	cytokinin oxidase
241	CA409977	515	2E-19	cytokinin oxidase
1032	CA409495	610	1E-22	cytokinin oxidase
847	CA410582	506	3E-15	cytokinin oxidase
925	CA410645	535	2E-23	dormancy associated protein/4E-19 auxin repressed prot.
923	CA410643	511	5E-32	ethylene receptor homolog
86	CA410601	415	9E-13	ethylene response element binding factor
53	CA410272	393	5E-13	ethylene responsive element binding factor 1
88	CA410621	391	6E-13	ethylene responsive element binding factor 1
739	CA410472	429	7E-11	ethylene responsive element binding factor 1
405	CA410142	488	4E-14	ethylene-responsive transcription factor ERF1
37	CA410119	435	1E-14	ethylene response element
285	CA410024	436	1E-14	ethylene responsive element binding protein
818	CA410551	484	9E-12	ethylene responsive small GTP-binding protein
1065	CA409527	513	2E-21	extensin-like protein / disease resistance protein Hcr2-5D
524	CA410262	485	4E-07	F11M21.27 prot./AP2 domain containing prot./ethylene respon. element binding prot.
1209	CA409668	568	2E-21	gibberellin oxidase-like protein
234	CA840670	871	1E-55	similar to NAM
399	CA410135	661	7E-54	GRAB1 protein/NAC domain protein
1102	CA409566	559	2E-40	GRAB1-like protein / NAM-like protein
1021	CA409485	586	6E-47	GRAB1-like / NAM-like protein (no apical meristem)
735	CA410468	459	7E-31	GRAB1/NAM protein
1402	CA409847	580	6E-25	high mobility group protein HMG-1
842	CA410577	515	0.000004	homeobox protein
504	CA410240	494	2E-46	hyp. protein ATGP1/7E-18 cell division control protein
70	CA410441	480	4E-21	IAA-Ala dehydrolase

173	CA409910	439	0.000006	indole-3-acetate beta-glucosyltransferase
1431	CA409874	561	1E-56	lipooxygenase (EC 1.13.11.12)
469	CA410201	426	2E-18	lipoxygenase (EC 1.13.11.12)
127	CA409728	408		lipoxygenase (EC 1.13.11.12)
999	CA410729	567	1E-51	lipoxygenase (EC 1.13.11.12)
1092	CA409554	523	4E-44	lipoxygenase (EC 1.13.11.12)
1208	CA409667	534	2E-40	lipoxygenase (EC 1.13.11.12)
965	CA410698	550	3E-33	seed lipoxygenase-3 (EC 1.13.11.12)
1076	CA409536	485	5E-18	seed lipoxygenase (EC 1.13.11.12)
970	CA410703	553	8E-26	seedlipoxygenase (EC 1.13.11.12)
738	CA410471	476	4E-23	pea seed lipoxygenase-3 (EC 1.13.11.12)
493	CA410227	487	7E-23	MADS box protein AGL20
521	CA410259	488	5E-12	mads box transcription activator (AGL20)
1089	CA409550	482	4E-21	MtN19 gene precursor
645	CA410373	505	8E-37	nodulin-like protein
660	CA410390	426	6E-12	nodulin-like protein / hyp. protein F20O9.30
652	CA410381	466	5E-15	nodulin/like protein/ hyp. protein F20O9.30
912	CA410659	501	3E-31	nodulin-like protein / E-43, hyp. Protein T12G13.140
872	CA410603	525	9E-27	nodulin-like protein
1421	CA409864	515	1E-17	nodulin-like protein, Arabidopsis etc.
1308	CA409757	513	7E-30	pollen allergen homolog / 7E-11 beta-expansin
346	CA410087	424	3E-22	putative pollen allergen / putative beta-expansin protein
868	CA410599	515	4E-10	proline-rich / (pEARLI / extensin-like / root specific protein / cell wall protein)
665	CA410395	414	0.000005	proline rich protein
357	CA410099	488	3E-41	proteasome beta/theta subunit (EC 3.4.99.46)
758	CA410492	482	3E-42	proteasome component C3 (EC 3.4.99.46)
208	CA409943	476	2E-32	proteosome subunit
371	CA410113	425	4E-10	putative cytokinin oxidase
651	CA410380	482	2E-13	ripening induced protein
659	CA410388	494	8E-12	ripening-induced protein
698	CA410429	479	3E-16	scarecrow-like 8
328	CA410068	456	4E-25	small GTP-binding protein / ethylene responsive
368	CA410110	458	7E-19	squamosa-promotor binding protein 1 homolog
1049	CA409511	574	1E-49	S-adenosylmethionine decarboxylase proenzym (EC 4.1.1.50)
1149	CA409611	556	0.000002	S-adenosylmethionine decarboxylase proenzym (EC 4.1.1.50)
390	CA410126	509	3E-23	zeatin O-glucosyltransferase
969	CA410701	564	7E-19	zeatin o-glucosyltransferase (EC 2.4.1.203)

III INTERACTION WITH THE ENVIRONMENT

TRANSPORT, MEMBRANE PROTEINS: category 10

131	CA409769	467		MATE
449	CA410182	508	3E-10	MATE
471	CA410204	505	5E-09	MATE
1281	CA409730	458	2E-10	MATE
584	CA410314	508	3E-12	MATE
685	CA410416	535	0.0001	MATE
1160	CA409623			MATE
1297	CA409746			MATE
1020	CA409484	515	9E-24	MATE
729	CA410461	190		MATE
398	CA410134	489	9E-48	ABC transporter
1220	CA409680	563	2E-46	ABC transporter (PDR5-like) isolog
184	CA409920	515	4E-52	ABC type transporter protein
119	CA409659	511	3E-25	PDR5-like ABC type transporter protein
714	CA410446	503	2E-20	amino acid transporter-like protein 1
283	CA410022	494	2E-32	ammonium transporter
96	CA410702	343	8E-32	aquaporin
940	CA410674	526	4E-45	aquaporin (fragment)
360	CA410102	481	6E-47	water-stress induced tonoplast intrinsic protein / white lupin aquaporin
1033	CA409496	558	2E-52	aquaporin (fragment)
1180	CA409640	353	7E-21	aquaporin, Lupinus albus etc.
256	CA409993	452	7E-28	aquaporin 2
1064	CA409526	369	2E-27	water channel protein MIPL / aquaporin TIP7
123	CA409696	451	2E-29	plasma membrane intrinsic protein 2C (water stress induced)
1219	CA409678	590	1E-20	probable membrane channel protein / 2E-19 aquaporin TIP7
1013	CA409476	557	4E-23	probable tonoplast intrinsic protein / 2E-22 aquaporin
201	CA409936	432	6E-20	tonoplast intrinsic protein/membrane channel protein
570	CA410304	455	1E-21	coatomer delta subunit (delta-coat protein)
576	CA410307	463	4E-28	coatomer delta subunit (delta-coat protein)
1057	CA409518	542	3E-15	glutathione-regulated potassium-efflux system protein kefB
825	CA410559	404	1E-15	high affinity sulphate transporter
585	CA410315	492	5E-11	high affinity sulphate transporter 2
189	CA409925	482	1E-11	hyp. protein / F441ABC transporter permease protein
327	CA410067	503	2E-17	hyp. protein / glucose transport protein
335	CA410075	404	1E-13	hyp. protein / Y69E1A.7
294	CA410034	510	3E-10	hyp. protein F19B11.7
989	CA410720	532	3E-17	hyp. protein F23A5.26, CorA-like Mg2+ transport protein family
1151	CA409614	591	5E-30	hyp. protein F9D12.14, Arab. / 1E-5 cation transport protein, E.coli
649	CA410377	467	4E-45	inorganic phosphate transporter
657	CA410386	415	6E-37	inorganic phosphate transporter
511	CA410248	470	9E-28	integral membrane protein/sugar transporter protein
395	CA410131	527	5E-10	MEI1/permease
128	CA409738	467	9E-20	mitochondrial solute carrier protein
753	CA410487	488	6E-11	Mitochondrial solute carrier protein homolog
121	CA409679	458	2E-46	multispanning membrane protein

3	CA410137	434	2E-34	Na+/K+/Cl- co transporter protein
556	CA410289	490	8E-39	Na+/K+/Cl-- cotransporter protein
1303	CA409753	494		no significant match / blastn: 9E -20 DdANN7 gene for annexin VII
956	CA410690	538	5E-46	PDR5-like ABC transporter
1245	CA409699	594	3E-51	PDR5-like ABC transporter
214	CA409950	464	3E-43	hyp. protein T2K10.8 / permease 1
222	CA409958	487	4E-38	permease 1 / hyp. protein T2K10
441	CA410175	510	1E-32	permease homolog
132	CA409779	464	2E-31	phosphate transporter protein G7-mitochondrial
1108	CA409571	577	2E-31	potassium channel, KCO-like protein, putative
812	CA410547	389	9E-34	potassium transport protein
1408	CA409852	601	9E-54	proline transporter
138	CA409834	477	5E-47	RAS related protein RAB7C/GTP binding protein
27	CA410018	552	2E-30	RAS-related protein RAB11D
722	CA410455	465	4E-14	Sec24A protein
24	CA409986	466	9E-18	soluble NSF attachment protein
250	CA409987	438	2E-26	sugar transporter protein
846	CA410581	496	4E-13	type 1 membrane protein
547	CA410280	450	6E-30	vacuole associated annexin p35/38

SIGNAL TRANSDUCTION, REGULATION: category 11

961	CA410695	573	2E-48	ADP-ribosylation factor
1247	CA409701	549	8E-43	ADP-ribosylation factor
968	CA410700	552	9E-28	calcineurin B-like protein / 7E-27 calcium sensor homol.
300	CA410041	473	2E-18	Calcium binding protein-like / calmodulin
342	CA410083	493	1E-38	calmodulin
343	CA410084	504	2E-39	calmodulin
427	CA410164	532	2E-45	calmodulin
845	CA410580	520	1E-10	calmodulin related protein
477	CA410210	289		calmodulin-like protein
1095	CA409557	564	2E-41	calnexin, Zea mays etc.
1018	CA409481	566	1E-48	calreticulin
529	CA410267	417	2E-34	calreticulin
112	CA409593	170	2E-13	casein kinase I
972	CA410705	552	2E-49	casein kinase, putative
811	CA410546	529	5E-18	CCR4-associated transcription factor
192	CA409928	438	3E-42	Cys3his zinc finger protein
713	CA410445	470	3E-22	Cys3His zinc finger protein isolog
752	CA410486	464	9E-51	Cys3His zinc finger protein isolog
1225	CA409685	330	0.000002	diacylglycerol kinase, putative
95	CA410693	351	3E-20	DNA binding protein
1412	CA409857	529	0.000007	DNA binding protein ACBF, Nicotiana / 7E-5: RNA binding protein homolog,
1428	CA409870	605	3E-26	DNA binding protein PD3, Pisum sativa / 3E-26: early nodulin binding protein
1003	CA409468	301	0.000006	eukaryiotic initiation factor 4A (EIF-4A)
773	CA410508	476	5E-46	GDP dissociation inhibitor
1311	CA409760	524	3E-51	GDP dissociation inhibitor
802	CA410536	470	2E-51	GTP-binding protein
808	CA410542	484	3E-53	GTP-binding protein
1054	CA409516	541	3E-36	GTP-binding protein
631	CA410359	419	5E-30	guanine nucleotide regulatory protein
916	CA410663	541	1E-29	guanine nucleotide regulatory protein/ 2E-29 GTP binding prot.
410	CA410148	481	0.000003	hnRNP-like protein (heterogenous nuclear ribonucleoprotein
1396	CA409840	428	7E-37	hyp 45.8 kD protein, putative protein kinase, Arabidopsis etc.
1172	CA409631	444	1E-08	hyp. protein AC005824/ 3E-5 zinc finger protein
134	CA409793	504	4E-51	hyp. protein F15I1.23 protein/(p)PPGPP 3-pyrophosphohydrolase
1294	CA409743	574	5E-49	hyp. protein F15I1.23 / 6E-15 GTP pyrophosphokinase (EC 2.7.6.5)
1027	CA409490	576	1E-26	hyp. protein F309.7, contains protein kinase domain
181	CA409917	482	8E-44	hyp. protein F4I18.19 /tyrosine protein kinase
235	CA409970	498	2E-48	ubiquitin-conjugating enzyme (EC 6.3.2.19)
1239	CA409695	593	3E-12	SER/Thr-specific protein kinase
243	CA409979	444	1E-10	SER/Thr-specific protein kinase
1048	CA409510	624	1E-14	inositol polyphosphate 5-phosphatase, putative
1093	CA409555	513	9E-22	MAP3-like protein kinase
159	CA409897	453	2E-24	membrane associated salt inducible protein
140	CA409854	475	2E-35	mitogen-activated protein kinase (EC 2.7.1.-)
362	CA410104	481	1E-33	mitogen-activated protein kinase homolog
363	CA410105	503	6E-37	mitogen-activated protein kinase homolog
1264	CA409715	245	2E-18	mitogen-activated protein kinase.
34	CA410091	367	0.000001	MtRHE/serine/threonine kinase
774	CA410509	477	3E-21	serine/threonine protein kinase
389	CA410124	450	9E-21	MYB related transcription activator (MYBST1) isolog
843	CA410578	509	2E-41	MYB-related transcriptional factor
783	CA410518	440	1E-27	MYB-related transcriptional factor
889	CA410620	532	6E-32	myB-related transcriptional factor
835	CA410570	555	1E-07	nova1-like RNA-binding protein (neuro-oncologic ventral antigen)
1372	CA409815	544	2E-11	P100 co-activator, Mus musculus etc.
1118	CA409582	570	0.000003	phaseolin G-box binding protein, putative
255	CA409992	442	2E-19	PHI-1 protein
1319	CA409768	581	2E-22	phi-1 protein, Nicotiana tabacum cells
844	CA410579	493	5E-54	phosphatidylinositol
682	CA410413	481	8E-43	phosphoinositide-specific phospholipase C
702	CA410435	474	6E-11	PHO85 protein - yeast-like
932	CA410652	536	4E-17	probable casein kinase (EC 2.7.1.-)
900	CA410633	577	1E-31	probable serine/threonine-specific protein kinase
1047	CA409509	574	4E-25	put. protein kinase /3 E-23 prob.SER/THR-specific prot. kinase

1042	CA409505	588	8E-38	protein kinase CK2, alpha subunit
790	CA410525	514	0.000008	protein kinase homolog, shaggy related
829	CA410563	457	2E-27	protein kinase homolog
953	CA410687	510	1E-11	protein kinase homolog
671	CA410402	469	4E-40	protein kinase homolog F16A16.30
1289	CA409737	517	2E-57	protein kinase PVK-1 homolog (EC 2.7.1.-), kidney bean etc.
89	CA410631	378	4E-30	protein kinase/ 2E-29 MAP-kinase
1115	CA409579	566	1E-16	protein kinase-like, Arabidopsis etc.
1055	CA409517	574	7E-16	put. protein kinase /2E-14 SER/THR-specific protein kinase G1008
1206	CA409665	546	3E-16	putative DNA-binding protein (RAV2-like)
1139	CA409601	554	6E-43	putative protein kinase./ 8E-24 brassinosteroid-insensitive protein BRI1
744	CA410478	459	3E-43	putative serine/threonine protein kinase
498	CA410232	490	8E-19	receptor protein kinase-like protein
1058	CA409519	474	7E-16	receptor-like protein kinase 5 homolog
372	CA410114	476	8E-32	Receptor-like protein kinase precursor
1382	CA409826	558	2E-09	ring H2 zinc finger protein ATL6, Arabidopsis
42	CA410167	520	3E-14	RNA binding protein
487	CA410220	509	1E-20	secretory protein/serine threonine kinase-like protein
488	CA410221	459	5E-35	secretory protein/serine threonine kinase-like protein
476	CA410209	483	3E-36	serine/threonine kinase MAK
444	CA410178	118	0.000003	cyclin dependent protein kinase/serine threonine protein kinase
472	CA410205	489	7E-27	serine/threonine kinase-like protein
560	CA410294	460	1E-42	serine/threonine specific protein kinase
554	CA410287	480	1E-46	serine/threonine-specific protein kinase
1123	CA409587	547	3E-16	serine/threonine-specific protein kinase (EC 2.7.1.-)
1364	CA409806	539	6E-47	serine/threonine-specific protein kinase homolog
931	CA410651	527	2E-28	signal recognition particle 19 kd protein subunit SRP19
387	CA410122	494	5E-14	signal recognition particle 68K protein
349	CA410090	483	0.000003	similarity to human 100 kDa coactivator / putative transcription factor
993	CA410723	575	7E-19	SPF1 protein
351	CA410093	801	4E-26	TOM (target of Myb1)- like protein
1053	CA409515	556	2E-23	transc. factor TINY-like protein/ cadmium induced / ethylene respons. elem. bind. fact.
719	CA410451	515	2E-21	transcription factor IIA large subunit
928	CA410648	528	3E-22	transcription factor, putative
369	CA410111	478	2E-12	transcription factor, putative / CCR4-associated factor homolog
90	CA410642	463	1E-41	tubby like protein
407	CA410144	494	3E-22	tubby like protein/F22K20.1 protein
756	CA410490	464	5E-26	Tubby-like protein
1333	CA409782	580	4E-48	tyrosine phosphatase (EC 3.1.3.48), Glycine max etc.
1204	CA409664	506	2E-15	zinc finger protein
448	CA410181	400	2E-07	zinc finger protein
670	CA410401	483	4E-20	zinc finger protein 1
267	CA410005	459	1E-14	zinc finger protein 1
1273	CA409724	495	1E-15	zinc fiinger protein 1
804	CA410538	470	2E-17	zinc finger-like protein, small
674	CA410405	455	6E-32	Contains similarity to C2-HC type zinc finger

STRESS, DEFENSE:category 12

332	CA410072	446	9E-48	2,4-D auxin inducible glutathione S-transferase
483	CA410216	137	0.000003	auxin-induced protein/glutathione S-transferase(EC 2.5.1.18)
422	CA410159	494	1E-42	glutathione s- transferase (EC 2.5.1.18)
76	CA410504	368	8E-28	glutathione s-transferase-like or auxin induced protein
1005	CA409470	598	3E-47	prob. glutathione S-transferase (EC 2.5.1.18)
884	CA410616	590	7E-41	probable glutathione s- transferase (EC 2.5.1.18)/1E-33 auxin induced protein
1109	CA409572	542	1E-42	probable glutathione s- transferase/2E-38 auxin induced prot.
1231	CA409691	400	8E-15	probable gluthatione S-transferase (2.5.1.18)
574	CA410305	476	7E-38	1-aminocyclopropane-1-carboxylate oxidase (EC 1.4.3.-)
1140	CA409603	573	2E-28	1-aminocyclopropane-1-carboxylate oxidase homolog (ACC),
500	CA410236	510	3E-32	hyp. protein/desacetoxyvindoline-4-hydroxylase (EC 1.14.11.-)
865	CA410597	503	1E-42	1-aminocyclopropane-1-carboxylate oxidase (EC 1.4.3.-)
1400	CA409845	480	5E-32	1-aminocyclopropane-1-carboxylate synthetase (EC 4.4.1.14)
494	CA410228	486	2E-30	1-aminocyclopropane-a-carboxylate oxidase/ethylene biosynthesis
502	CA410238	501	4E-46	4-coumarate -- CoA ligase (EC 6.2.1.12)
995	CA410725	635	4E-18	4-coumarate:CoA ligase (EC 6.2.1.12)
466	CA410198	464	1E-29	allene oxide synthase (EC 4.1.2.92) (Rubber particle protein)
525	CA410263	440	1E-33	aluminum-induced protein
745	CA410479	400	2E-31	hyp. protein ARG10 / Al-induced protein
1127	CA409591	537	3E-45	aspartic proteinase/ 3E-39 aspatic proteinase wound induced
1113	CA409577	537	3E-27	cationic peroxidase (EC 1.11.1.7).
1324	CA409774	571	4E-31	cationic peroxidase EC 1.11.1.7)
1120	CA409585	490	6E-49	chalcone synthase (EC 2.3.1.74)
439	CA840672			chalcone synthase (EC 2.3.1.74)
429	CA410166	508	7E-47	chalcone synthase (EC 2.3.1.74) (naringenin-chalcone synthase)
1332	CA409781	561	6E-56	chalcone synthase (EC 2.3.1.74), naringenin-chalcone synthase
393	CA410129	493	4E-40	chalcone synthase (EC2.3.1.74)
939	CA410672	526	6E-10	chalcone-flavone isomerase, (EC 5.5.1.6.)
1103	CA409567	582	3E-47	chalcone--flavonone isomerase (EC 5.5.1.6)
946	CA410679	493	3E-29	chitinase class 1 / 3E-28 endochitinase precursor
1344	CA409787	446	5E-21	class I chitinase (EC 3.2.1.14)
1155	CA409617	280	1E-13	endochitinase (EC 3.2.1.14)
1228	CA409688	325	1E-33	class I chitinase (EC 3.2.1.14)
885	CA410617	569	7E-38	cold acclimation protein, wheat
1062	CA409524	544	1E-52	cyanogenic beta-glucosidase, (EC 3.2.1.21)
261	CA409999	466	9E-24	cytochrome p450
815	CA410549	488	2E-13	cytochrome P450 (EC 1.14.-.-)

520	CA410258	506	1E-13	cytochrome P450 76B1 (EC 1.14.-.-.) (7-ethoxycoumar)
910	CA410657	569	3E-23	cytochrome P450 (EC 1.14.-.-)
507	CA410243	491	6E-24	cytochrome P450 monooxygenase (EC 1.14.-.-)
374	CA410116	489	1E-25	Cytochrome P450/ ferrulate-5-hydroxylase
1134	CA409597	583	6E-28	cytosolic class II small heat shock protein HCT2
679	CA410409	499	2E-29	dehydration responsive element binding factor
52	CA410268	403	5E-08	disease resistant response protein
25	CA409997	456	2E-27	DNA J protein
1290	CA409739	542	8E-17	dTDP glucose 4-6-dehydratase homolog,
827	CA410561	476	1E-22	DTDP-D-glucose 4,6-dehydratase (EC 4.2.1.46)
1011	CA409475	578	9E-49	dTDP-glucose 4-6-dehydratase
93	CA410673	400	2E-09	elicitor response element binding protein
353	CA410095	477	5E-17	elicitor response protein, AVR9
1178	CA409637	553	4E-48	glyoxylase, lactoylglutathione lyase (EC 4.4.1.5),
485	CA410218	481	1E-14	GT2 gene/DNA binding protein GT-2
1182	CA409642	509	1E-08	heat shock [transcription] factor protein HSF30
1300	CA409751	514	4E-33	heat shock 70 kd protein, dnaK-type molecular chaperone precursor
1136	CA409598	534	2E-46	heat shock cognate protein HSP80, tomato etc.
6	CA410432	492	2E-41	heat shock protein
893	CA410625	527	2E-33	heat shock protein (82)
262	CA410000	485	1E-24	heat shock protein 101
612	CA410341	436	4E-30	heat shock protein 17.7
614	CA410343	466	3E-31	heat shock protein 17.7
623	CA410351	452	3E-30	heat shock protein 17.7
959	CA410692	509	5E-31	heat shock protein 70
169	CA409906	470	4E-34	heat shock protein 70 cognate
1316	CA409765	622	8E-56	heat shock protein 83 (90, 81, 82) , Arabidopsis etc.
11	CA409660	541	8E-55	heat shock protein
613	CA410342	511	2E-51	heat shock protein 83
122	CA409690	448	4E-32	heat shock transcription factor
160	CA409898	420	2E-28	heat shock transcription factor
1215	CA409675	559	2E-24	hyp. protein F15I1.13 protein/ 5E-16 heat shock protein 17.0
165	CA409903	461	5E-36	L-ascorbate peroxidase (EC 1.11.1.11)
1001	CA409466	553	7E-42	L-ascorbate peroxidase (EC 1.11.1.11) glyoxysomal
985	CA410716	502	6E-30	L-ascorbate peroxidase (EC 1.11.1.11.) glyoxysomal
952	CA410686	538	3E-44	L-ascorbate peroxidase (EC 1.11.1.11.), cytosolic
290	CA410030	476	4E-50	L-ascorbate peroxidase, cytosolic (EC 1.11.1.11)
1295	CA409744	520	4E-12	ascorbat peroxidase (1.11.1.11)
282	CA410021	456	6E-14	ascorbate peroxidase
1050	CA409512	569	7E-19	mitoch. heat shock 22 kd protein precursor
1119	CA409583	541	1E-49	monodehydroascorbate reductase (NADH) (EC 1.6.5.4)
1425	CA409868	590		8E -8 heat shock transcription factor 34
388	CA410123	453	1E-42	oxygenase --pathogen induced
91	CA410667	426	1E-15	peroxidase
1067	CA409529	340	2E-17	peroxidase (EC 1.11.1.7)
1224	CA409684	522	1E-37	peroxidase (EC 1.11.1.7)
736	CA410469	462	2E-27	peroxidase 1
1411	CA409856	597	2E-43	peroxidase (EC 1.11.1.7)
206	CA409941	477	7E-45	peroxidase 1 precursor
837	CA410572	493	2E-32	peroxidase precursor
340	CA410081	503	5E-34	peroxidase precursor, putative
1039	CA409502	533	2E-22	phenylalanine ammonia-lyase (EC 4.3.1.5)
973	CA410706	540	2E-42	glutathione peroxidase (EC 1.11.1.9)
312	CA410051	480	1E-48	phospholipid-hydroperoxide glutathione peroxidase
179	CA409916	524	6E-11	phospholipid-hydroperoxide glutathione peroxidase 2 (EC 1.11.1.9)
1015	CA409478	603	6E-55	phospholipid-hydroperoxide glutathione peroxidase
43	CA410173	425	9E-43	phospholipid-hydroperoxide glutathione peroxidase
967	CA410699	528	1E-36	PR-10 protein, Lupinus albus
1256	CA409707	498	6E-07	PR-10 protein, Lupinus albus
1284	CA409733	519	6E-38	PR-10 protein, Lupinus albus
1286	CA409735	517	3E-39	PR-10 protein, Lupinus albus
1307	CA409756	531	3E-37	PR-10 protein, Lupinus albus
1334	CA409783	587	1E-47	PR-10 protein, Lupinus albus
1373	CA409816	262	2E-11	PR-10 protein, Lupinus albus
97	CA410711	201	3E-17	PR-10 protein, Lupinus albus
115	CA409622	427	7E-39	PR-10 protein, Lupinus albus
316	CA410055	458	5E-38	PR-10 protein, Lupinus albus
517	CA410254	487	2E-40	PR-10 protein, Lupinus albus
705	CA410437	484	1E-38	PR-10 protein, Lupinus albus
541	CA410274			PR-10 protein, Lupinus albus
100	CA840665	445	2.00E-13	PR-10 protein, Lupinus albus
1137	CA409599	418	2E-18	pathogenesis-related protein, Lupinus albus etc.
1266	CA409717	472	5E-12	probable aldose 1-epimerase (EC 5.1.3.3)/ 3E-10 fungal stress protein
822	CA410556	358	1E-12	proline-rich protein
1191	CA409651	552	4E-09	RJS protein, mouse / 7E-7 UVB resistance protein UVR8
765	CA410500	471	5E-39	safener-induced In2.1-like protein
830	CA410565	484	3E-33	SGR1-like protein
1130	CA409594	536	2E-27	sim. to PHZ
1179	CA409638	547	8E-22	similar to PHZF.
1255	CA409706	877	7E-08	oxylase like protein
909	CA410641	530	1E-28	stress-induced protein sti1-like
297	CA410037	213	0.000005	superoxide dismutase (EC 1.15.1.1)
1159	CA409621	486	5E-12	UVB-resistance protein UVR8, Arabidopsis
1028	CA409491	593	2E-08	WIZZ / 2E-10 F23A5.19 protein, similar to gb\Z48431 DNA-binding prot.

IV UNKNOWN FUNCTION

FUNCTION UNKNOWN IN PLANTS: category 13

409	CA410146	508	2E-09	brain and reproductive organ-expressed protein
1313	CA409762	350	3E-25	CaLB protein, Arabidopsis etc.
667	CA410397	401	0.000002	CG1-141 protein
1327	CA409777	617	2E-13	CGI-29 protein
897	CA410628	579	4E-12	density regulated protein drp1
1321	CA409771	564	9E-22	Dreg-2 like protein
185	CA409921	444	6E-09	erythoblast macrophage protein EMP/Tnp1 Tam1 transposon protein
170	CA409907	464	2E-09	erythroblast macrophage protein EMP / hypothetical protein
1226	CA409686	512	5E-21	erythroblast macrophageprotein EMP
841	CA410576	476	2E-13	extracellular dermal glycoprotein precursor
59	CA410330	332	2E-11	extracellular dermal glycoprotein precursor (EDGP)
117	CA409639	430	2E-30	extracellular dermal glycoprotein precursor/F15K9.17
56	CA410303	400	4E-35	fernesylated protein GMFP7
503	CA410239	498	3E-22	HS1pro-1 related protein isolog
839	CA410574	473	4E-26	HS1pro-1 related protein isolog
1419	CA409861	543	2E-26	myosine heavy chain, putative
63	CA410368	418	1E-33	translationally controlled tumor protein
1157	CA409619	499	6E-30	translationally controlled tumor protein (TCTP) homolog

UNKNOWN FUNCTION: 14

1002	CA409467	548	1E-09	1E -9 Arabidopsis genomic DNA, chr. 5, blastn
1397	CA409841	424	2E-09	ESTs gb/ H37295 and gb/ R64895 come from this gene
1356	CA409800	567	4E-12	hyp 40.4 kD protein, GEN: 3482980 AL031369, Arabidopsis
1236	CA409692	589	9E-10	hyp protein F22K20.
955	CA410689	432	9E-13	hyp protein similar to Bacillus CotA
1388	CA409832	587	4E-13	hyp protein sll1188, GEN: 1651934 D90901, Synechocystis sp.
851	CA410587	522	2E-09	hyp. 16.6 kD protein, EMB:CAB52039
1147	CA409609	565	9E-41	hyp. 19.9 kd protein, GEN: 5738361 AL021637, Arabidopsis
1212	CA409672	511	2E-26	hyp. 21.1 kd protein, GEN:5924062 AF158699, Burkholderia cepacia
797	CA410530	525	5E-24	hyp. 28.2 kD protein, EMB: CAB43697
1368	CA409810	586	7E-54	hyp. 31.4 kd protein, GEN: 3928150 AJ131049, Cicer arietinum
737	CA410470	459	1E-22	hyp. 36.4 KD protein
10	CA409563	495	3E-28	hyp. protein 36.4 kd
190	CA409926	485	3E-12	hyp. 40.6 kD protein, PIR: A71410
1187	CA409646	511		hyp. 40.6 kD protein, PIR: A71410
1429	CA409871	547	7E-16	hyp. 43.1 kd protein, GEN: 2852640 AF007157, Homo sapiens
370	CA410112	514	2E-22	hyp. 49.9 kD Zinc finger protein C2F3.16
1014	CA409477	555	2E-12	hyp. 6.6 kd protein, GEN: 6522622 AL133298, Arabidopsis
1158	CA409620	531	4E-13	hyp. protein (clone TPP15)
356	CA410098	498	3E-27	hyp. protein / F10A8.29 protein
364	CA410106	493	4E-31	hyp. protein / F10A8.29 protein
715	CA410447	511		hyp. protein 108.0 KD
692	CA410424	476	4E-09	hyp. protein 17.6 KD
1439	CA409881	463	0.000004	adrenal gland protein AD-003
590	CA410321	504	2E-23	hyp. protein 39.1 kd
609	CA410337	360	8E-15	hyp. protein T29H11,70, 43.4 kd
615	CA410344	519	7E-29	hyp. protein T29H11.70
305	CA410046	469	1E-15	hyp. protein 4C15.10
605	CA410334	381	7E-15	hyp. protein 75.3 kd
1268	CA409719	517	3E-09	hyp. protein AJ225026
1177	CA409636	418		hyp. protein AJ225026
1091	CA409553	466	6E-16	hyp. protein AL162651
1124	CA409588	566	5E-09	hyp. protein AL162875
307	CA410048	491	0.000002	hyp. protein AR781
171	CA409908	829	4E-64	hyp. protein T22K7.10
577	CA410308	462	1E-24	hyp. protein CPRD8
748	CA410482	491	1E-07	hyp. protein DJ167A19.1
749	CA410483	481	2E-08	hyp. protein DJ167A19.1
1280	CA409729	506	1E-19	hyp. protein EIF4B
779	CA410514	430	2E-08	hyp. protein F10A8.22
853	CA410589	501	8E-26	hyp. protein F10M10.130
700	CA410433	521	1E-14	hyp. protein F10M10.5
701	CA410434	531	1E-14	hyp. protein F10M10.5
450	CA410183	411	4E-21	hyp. protein F11F19.23
583	CA410313	214	0.000005	hyp. protein F11F19.23
274	CA410012	486	2E-09	hyp. protein F12L6.15
210	CA409946	461	5E-25	hyp. protein F13A10.13 Ca ++ binding protein
558	CA410291	451	2E-11	hyp. protein F13H10.21
878	CA410609	493	2E-18	hyp. protein F14.P13.8
1086	CA409547	551	9E-29	hyp. protein F14B2.18
296	CA410036	467	2E-28	hyp. protein F14M19.130
1051	CA409513	593	5E-47	hyp. protein F15H11.2
1004	CA409469	549	5E-12	hyp. protein F15H18.9
690	CA410422	480	9E-12	hyp. protein F15I1.16 protein/1E-11 putative nucleolysin
428	CA410165	496	6E-37	hyp. protein F15I1.16/putative nucleolysin/TIA1 related protein
406	CA410143	497	8E-32	hyp. protein F15K9.15
621	CA410349	477	3E-30	hyp. protein F15K9.15
1196	CA409655	571	3E-24	hyp. protein F16B22.26
908	CA410640	590	1E-19	hyp. protein F16N3.26
633	CA410361	468	7E-49	hyp. protein F16N3.6
313	CA410052	481	9E-12	hyp. protein F17H15.23 / F3N11.19
1298	CA409747	551	6E-31	hyp. protein F18E5.190
781	CA410516	508	1E-09	hyp. protein F19F18.140

746	CA410480	746	2E-11	hyp. protein F19G10.9
785	CA410520	480	1E-27	hyp. protein F1N21.5
240	CA409976	479	2E-42	hyp. protein F20D21.14
212	CA409948	496	4E-31	hyp. protein F20D21.14
776	CA410511	488	6E-24	hyp. protein F20D22.14
598	CA410328	415	4E-12	hyp. protein F20D22.15
1436	CA409878	533	3E-36	hyp. protein F20D22.3
268	CA410006	463	1E-34	hyp. protein F20M13.160
321	CA410061	502	5E-12	hyp. protein F21B7.22 / anthocyanine 5-aromatic acyltransferase
217	CA409953	454	1E-08	hyp. protein F21M12
854	CA410590	517	6E-27	hyp. protein F24L7.16
1038	CA409501	549	1E-09	hyp. protein F25A4.8
361	CA410103	497		hyp. protein F25A4+E216
819	CA410552	462	1E-07	hyp. protein F26P21.170
49	CA410234	428	6E-35	hyp. protein F27B13.20
706	CA410438	509	3E-12	hyp. protein F28M20.80
135	CA409803	460	4E-11	hyp. protein F28P10.70/T16B24.14
596	CA410326	430	1E-11	hyp. protein F3F19.22
591	CA410322	227		hyp. protein F3N11.12
416	CA410153	515	2E-15	hyp. protein F3O9.4
669	CA410399	492	2E-19	hyp. protein F3O9.4
935	CA410654	568	9E-24	hyp. protein F4P13.19
193	CA409929	172	5E-16	hyp. protein F5A8.2 / F19F18.30 protein
396	CA410132	396	2E-40	hyp. protein, F5A8.2 protein
248	CA409984	416	2E-09	hyp. protein F5A8.8
856	CA410592	502	2E-23	hyp. protein F5o8.30
677	CA410407	482	0.000005	hyp. protein F6E13.26
732	CA410465	450	1E-10	hyp. protein F6P23.13
636	CA410364	525	2E-47	hyp. protein F8A5.3
757	CA410491	500	5E-21	hyp. protein F8F16.150+E34
711	CA410443	479	2E-08	hyp. protein F9D12.1
424	CA410161	523	1E-14	hyp. protein F9L1.44
643	CA410371	489	7E-18	hyp. protein F9L1.44 protein
942	CA410676	539	4E-28	hyp. protein M4E13.100
1090	CA409552	433		early nodulin
65	CA410389	429		early nodulin
1059	CA409520	260	3E-53	early nodulin
1377	CA409820	563	9E-21	hyp. Protein M4I22.130, GEN 3269293 AL030978, Arabidopsis
950	CA410684	533	2E-16	hyp. protein MJB20.6
630	CA410358	776	3E-27	hyp. protein F12M16.12
1044	CA409507	602	0.000003	hyp. protein SPBC15D4.10c
601	CA410332	498	0.000001	hyp. protein T11J7.17
687	CA410418	267	2E-07	hyp. protein T12M4.1
30	CA410049	425	3E-19	hyp. protein T14P8.16
1383	CA409827	581	6E-38	hyp. protein T16H5.20, Arab. / 4E-28: hyp protein F20B18.230*
579	CA410310	579	1E-17	hyp. protein T17F15.8
792	CA410526	509	8E-44	hyp. protein T18c20.9
800	CA410534	520	1E-44	hyp. protein T18c20.9
801	CA410535	502	4E-41	hyp. protein T18c20.9
642	CA410370	488	1E-34	hyp. protein T19P19.50
224	CA409960	512	1E-35	hyp. protein T1F15.13
1288	CA409736	551	5E-50	hyp. protein T1J1.5
1188	CA409647	570	2E-30	hyp. protein T1J8.2
48	CA410223	428	2E-18	hyp. protein T20K18.240
347	CA410088	472	9E-27	hyp. protein T21L14.16
1262	CA409713	515	1E-26	hyp. protein T22A6.120
1024	CA409487	593	8E-10	hyp. protein T23K23.1
32	CA410070	457	2E-31	hyp. protein T24P15.12
75	CA410494	735	1E-20	hyp. protein T10K17.100
1365	CA409807	510	4E-08	hyp. protein T26J14.6
568	CA410301	502	5E-38	hyp. protein T28I24.5
251	CA409988	400	0.000002	hyp. protein T29H11.40
230	CA409966	423	4E-26	hyp. protein T2N18.13
1073	CA409534	469	3E-30	hyp. protein T2P11.4
877	CA410608	557	1E-13	hyp. protein T30D6.8
1043	CA409506	575	9E-19	hyp. protein T31J12.4
1328	CA409778	604	2E-07	hyp. protein T3F17.20
646	CA410374	455	3E-10	hyp. protein T3G21.17
1190	CA409650	591	2E-08	hyp.protein T3G21.19
491	CA410225	515	0.000005	hyp. protein T3G21.19
329	CA410069	476	0.000005	hyp. protein T4M8.7
118	CA409649	466	2E-09	hyp. protein T3G21.19
232	CA409968	496	2E-24	hyp. protein T3G21.19
324	CA410064	506	5E-39	hyp. protein T4I9.18 / T9J23.23
859	CA410594	492	7E-33	hyp. protein T5I8.21
632	CA410360	508	7E-20	hyp. protein T6A23.6
683	CA410414	462	6E-34	hyp. protein T6K21.210
311	CA410050	455	6E-37	hyp. protein T6K21.80 / F9H16.1 / F17F8.25.
1009	CA409473	591	4E-17	hyp. protein T7A14.14
978	CA410709	567	1E-18	hyp. protein T8O11
308	CA840671	465	2E-21	hyp. protein T9A21.
971	CA410704	571	5E-27	hyp. protein T9E8.170
754	CA410488	489	2E-19	hyp. protein T9H9.19
1034	CA409497	549	6E-17	hyp. protein T9H9.19
849	CA410584	480	3E-14	hyp. protein T9I22

260	CA409998	475	0.000005	hyp. protein ykrt
898	CA410629	576	6E-22	hyp. protein YML27
638	CA410366	437	9E-14	hyp. protein YUP8H12R.13
919	CA410666	533	4E-30	hyp. protein, Arabidopsis, GEN 6119520 AC011560
930	CA410650	513	4E-16	hyp. protein, Arabidopsis, GEN 6119520 AC011560
557	CA410290	475	5E-11	hyp. protein, EMB: BAA76827
569	CA410302	444	6E-09	hyp. protein, EMB: BAA76827
367	CA410109	466	2E-14	hyp. protein, F18B3.30 / F13C5.60
1424	CA409867	576	4E-07	hyp. protein, GEN: 5777631 AJ245900
905	CA410637	620	3E-14	hyp. protein, GEN:5777621 AJ245900
550	CA410284	480	1E-41	hyp. protein, unknown function / F8K7.9
129	CA409749	458	5E-12	hyp. protein/F309.11 fragment
451	CA410184	465	3E-28	hyp. protein/RIF1 protein
452	CA410185	480	2E-31	hyp. protein/SRC2-like protein
1405	CA409850	418	5E-10	hyp.43.8 kd protein
1341	CA409786	604	6E-35	hyp.protein F21M11.17
1214	CA409674	569	2E-09	hyp.protein F9D16.280
634	CA410362	162		hyp.protein F9D16.280
1167	CA409628	481		no conv. match/blastn: E -8 subtellomeric satellite DNA, Pagellus
72	CA410462	727	1E-30	hyp. protien AAF50915.1
874	CA410605	528		no significant match / blastn: 2E -5 Arabidopsis genomic DNA, chr. 5
1369	CA409811	407		no significant match / blastn: 4E-19 Anopholes transposon Minos
1385	CA409829			no significant match / blastn: 4E-19 Anopholes transposon Minos
1358	CA409801	552		no significant match / blastn: 5e-12 Arabidopsis genom. DNA, chr. 3
57	CA410311	364		no match / blastn: 2E-16 farnesylated protein GMFP7
5	CA410331	480	3E-19	not 56 like protein
602	CA410333	427		hyp. protein 42c
1351	CA409795			hyp. protein AL138646
1350	CA409794	579	2E-12	hyp. protein AL138646

NO SIGNIFICANT HOMOLOGY: category 15

7	CA410533			no significant match
481	CA410215	469		no significant match
899	CA410630	560		no significant match
12	CA409750	363		no significant match
680	CA410411	460		no match
920	CA410668	542		no significant match
21	CA409956	214		no significant match
26	CA410008	431		no significant match
28	CA410029	438		no significant match
50	CA410246	472		no significant match
54	CA410283	389		no significant match
58	CA410320	291		no significant match
68	CA410421	427		no significant match
69	CA410431	428		no significant match
74	CA410484	427		no significant match
78	CA410524	225		no significant match
87	CA410611	433		no significant match
108	CA409551	460		no significant match
111	CA409584	150		no significant match
120	CA409669	464		no significant match
124	CA409704	494		no significant match
136	CA409812	439		no significant match
137	CA409823	482		no significant match
141	CA409862	481		no significant match
144	CA409884	471		no significant match
147	CA409886	295		no significant match
153	CA409891	286		no significant match
157	CA409895	462		no significant match
162	CA409900	415		no significant match
178	CA409915	414		no significant match
164	CA409902	496		no significant match
174	CA409911	449		no significant match
175	CA409912	482		no significant match
176	CA409913	499		no significant match
177	CA409914	449		no significant match
204	CA409939	357		no significant match
207	CA409942	503		no significant match
211	CA409947	486		no significant match
223	CA409959	484		no significant match
215	CA409951	452		no significant match
221	CA409957	488		no significant match
242	CA409978	480		no significant match
275	CA410013	486		no significant match
277	CA410015	470		no significant match
299	CA410039	475		no significant match
304	CA410045	451		no significant match
319	CA410058	493		no significant match
348	CA410089	488		no significant match
392	CA410128	507		no significant match
400	CA410138	532		no significant match
654	CA410383	456		no significant match
662	CA410392	464		no significant match
401	CA410139	493		no significant match
423	CA410160	489		no significant match

447	CA410180	131	no significant match
456	CA410189	471	no significant match
473	CA410206	329	no significant match
478	CA410211	565	no significant match
492	CA410226	479	no significant match
495	CA410229	463	no significant match
496	CA410230	325	no significant match
512	CA410249	467	no significant match
527	CA410265	430	no significant match
546	CA410279	453	no significant match
548	CA410281	436	no significant match
552	CA410285	476	no significant match
582	CA410312	398	no significant match
597	CA410327	401	no significant match
607	CA410335	504	no significant match
624	CA410352	488	no significant match
640	CA410369	469	no significant match
644	CA410372	504	no significant match
653	CA410382	469	no significant match
635	CA410363	210	no significant match
661	CA410391	470	no significant match
686	CA410417	495	no significant match
691	CA410423	440	no significant match
693	CA410425	509	no significant match
694	CA410426	483	no significant match
716	CA410448	458	no significant match
730	CA410463	439	no significant match
759	CA410493	472	no significant match
760	CA410495	462	no significant match
767	CA410502	470	no significant match
775	CA410510	234	no significant match
778	CA410513	128	no significant match
784	CA410519	444	no significant match
831	CA410566	475	no significant match
855	CA410591	524	no significant match
890	CA410622	550	no significant match
914	CA410661	554	no significant match
917	CA410664	467	no significant match
927	CA410647	519	no significant match
941	CA410675	543	no significant match
960	CA410694	479	no significant match
962	CA410696	534	no significant match
963	CA410697	573	no significant match
988	CA410719	533	no significant match
1016	CA409479	555	no significant match
1070	CA409532	347	no significant match
1110	CA409574	456	no significant match
1116	CA409580	541	no significant match
1181	CA409641	492	no significant match
1229	CA409689	509	no significant match
1232	CA840675	457	no significant match
1244	CA409698	577	no significant match
1270	CA409721	508	no significant match
1272	CA409723	445	no significant match
1276	CA409725	490	no significant match
1279	CA409727	406	no significant match
1282	CA409731	581	no significant match
1292	CA409741	551	no significant match
1299	CA409748	396	no significant match
1304	CA409754	512	no significant match
1306	CA409755	581	no significant match
1314	CA409763	234	no significant match
1315	CA409764	559	no significant match
1347	CA409790	586	no significant match
1353	CA409797	571	no significant match
1371	CA409814	603	no significant match
1398	CA409842	533	no significant match
1403	CA409848	558	no significant match
1417	CA409859	577	no significant match
1420	CA409863	527	no significant match
1422	CA409865	506	no significant match
1423	CA409866	560	no significant match
1434	CA409876	547	no significant match
1437	CA409879	557	no significant match
1438	CA409880	583	no significant match
107	CA409540	467	no significant match
163	CA409901	453	no significant match
188	CA409924	471	no significant match
339	CA410079	483	no significant match
376	CA410118	475	no significant match
510	CA410247	476	no significant match
622	CA410350	519	no significant match
1074	CA409535	455	no significant match
270	CA410009	450	no significant match
289	CA410028	211	no significant match

499	CA410233	485	no significant match
883	CA410615	552	no significant match
1031	CA409494	585	no significant match
594	CA410325	481	no significant match
442	CA410176	112	no significant match
810	CA410545	554	no significant match
648	CA410376	505	no significant match
258	CA409995	470	no significant match
39	CA410136	476	no significant match
618	CA410346	132	no significant match
514	CA410251	306	no significant match
673	CA410404	365	no significant match
563	CA410297	454	no significant match
114	CA409612	121	no significant match
593	CA410324	7	no significant match
561	CA410295	366	no significant match
64	CA410378	140	no significant match
142	CA409872	483	no significant match
1026	CA409489	587	no significant match
516	CA410253	487	no significant match
1409	CA409853	570	no significant match
302	CA410043	489	no significant match
755	CA410489	449	no significant match
82	CA410564	450	no significant match
1203	CA409663	542	no significant match
293	CA410033	463	no significant match
1261	CA409712	352	no significant match
333	CA410073	272	no significant match
465	CA410197	475	no significant match
291	CA410031	162	no significant match
526	CA410264	490	no significant match
336	CA410076	116	no significant match
1393	CA409838	534	no significant match
281	CA410020	474	no significant match
45	CA410192	456	no significant match
66	CA410400	412	no significant match
523	CA410261	507	no significant match
440	CA410174	472	no significant match
433	CA410171		no significant match
352	CA410094	479	no significant match
254	CA409991	451	no significant match
106	CA840667	103	no significant match
1200	CA409661	527	no significant match
196	CA840669	112	no significant match
813	CA840673	90	no significant match
325	CA410065	482	no significant match
1017	CA409480	613	no significant match
1418	CA409860	536	no significant match
994	CA410724	533	no significant match
1197	CA409656	552	no significant match
1143	CA409606	576	no significant match
721	CA410454	400	no significant match
709	CA410440	504	no significant match
704	CA410436	489	no significant match
265	CA410003	306	no significant match
882	CA410614	560	no significant match
219	CA409955	473	no significant match
83	CA410575	402	no significant match
668	CA410398	468	no significant match
933	CA410653	500	no significant match
227	CA409963	484	no significant match
1355	CA409799	524	no significant match
806	CA410540	458	no significant match
314	CA410053	484	no significant match
462	CA410195	226	no significant match
870	CA410602	517	no significant match
1169	CA409629	526	no significant match
1374	CA409817	545	no significant match
67	CA410410	406	no significant match
71	CA410452	415	no significant match
203	CA409938	502	no significant match
402	CA410140	516	no significant match
253	CA409990	378	no significant match
1060	CA409522	526	no significant match
457	CA410190	271	no significant match
610	CA410339	361	no significant match
334	CA410074		no significant match
460	CA410193		no significant match

NO HOMOLOGY FOUND: category 16

126	CA409720	430	no match
879	CA410610	463	no match
139	CA409844	492	no match
154	CA409892	137	no match
146	CA840668	86	no match

156	CA409894	466	no match
182	CA409918	456	no match
194	CA409930	487	no match
287	CA410026	480	no match
315	CA410054	496	no match
338	CA410078	458	no match
366	CA410108	792	no match
438	CA410172	213	no match
464	CA410196	292	no match
489	CA410222	385	no match
506	CA410242	471	no match
559	CA410292	333	no match
565	CA410298	420	no match
586	CA410316	462	no match
592	CA410323	470	no match
608	CA410336	452	no match
699	CA410430	491	no match
772	CA410507	475	no match
480	CA410214	527	no match
793	CA410527	517	no match
881	CA410613	579	no match
913	CA410660	544	no match
983	CA410714	499	no match
1068	CA409530	551	no match
1258	CA409709	453	no match