	A	B	C	D	E	F
1	white Lupin proteoid root ESTs, sorted by categories					
2	I METABOLISM					
3	CARBON AND ENERGY METABOLISM: category 1					
4	CARBON METABOLISM: category 1a					
5						
6	**L#**	**GenBank accession #**	**bp**	**score**	**E-value**	**annotation**
7	E018	CA410748	535	198	1.00E-50	ENOLASE (EC 4.2.1.11)
8	E027	CA410757	464	152	1.00E-28	ALPHA-MANNOSIDASE
9	E047	CA410777	477	173	4.00E-43	PYRUVATE DESCARBOXYLASE ISOZYME (EC 4.1.1.1.)
10	E057	CA410786	514	159	5.00E-52	FRUCTOSE -BISPHPOSPHATE ALDOLASE
11	E068	CA410797	526	218	8.00E-57	PYRUVATE DEHYDROGENASE E1(EC 1.2.4.1)
12	E094	CA410820	455	75	2.00E-13	GLYCERALDEHYDE 3-PHPSPHATE DEHYDROGENASE
13	E100	CA410825	534	169	7.00E-42	GLYCERALDEHYDE 3-PHPSPHATE DEHYDROGENASE
14	E110	CA410835	489	141	2.00E-33	HYP. PROTEIN/UDP-galactose-4-epimerase
15	E111	CA410836	427	75	2.00E-13	GLYCERALDEHYDE 3-PHPSPHATE DEHYDROGENASE
16	E113	CA410838	458	151	2.00E-36	NAD-DEPENDENT MALIC ENZYME ISOFORM MITOCH
17	E119	CA410844	385	131	2.00E-30	BETA-GALACTOSIDASE (EC 2.2.1.23)
18	E125	CA410850	491	51	3.00E-06	RIBOSE 5-PHOSPHATE ISOMERASE (EC 5.3.1.6)
19	E136	CA410861	545	127	2.00E-29	TRANSALDOLASE-LIKE PROTEIN
20	E142	CA410867	514	180	2.00E-45	ISOCITRATE DEHYDROGENASE (NADP) (EC 1.1.1.42)
21	E147	CA410872	434	158	1.00E-38	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE
22	E170	CA526339	492	140	3.00E-33	P FRUCTOSE BISPHOSPHATE ALDOLASE
23	E171	CA410895	486	155	8.00E-38	CYTOSOLIC MALATE DEHYDROGENASE (EC 1.1.1.37)
24	E180	CA410904	468	116	2.00E-26	INOSITOL MONOPHOSPHATASE-LIKE PROTEIN
25	E185	CA410909	437	56	1.00E-07	PYRUVATE DEHYDROGENASE E1 BETA SUBUNIT
26	E241	CA410959	404	144	2.00E-34	2,3-BISPHOSPHOGLYCERATE-INDEPENDENT P-GLYCER
27	E242	CA410960	416	132	1.00E-30	FRUCTOSE-BISPHOSPHATE ALDOLASE
28	E285	CA411001	303	62	2.00E-09	ISOCITRATE DEHYDROGENASE (NAD+)
29	E292	CA411008	452	147	3.00E-35	FRUCTOSE-BISPHOSPHATE ALDOLASE
30	E295	CA411011	455	144	3.00E-34	FRUCTOSE-BISPHOSPHATE ALDOLASE
31	E304	CA411018	452	150	3.00E-36	FRUCTOSE BISPHOSPHATE ALDOLASE
32	E317	CA411029	494	174	2.00E-43	UDP-GLUCOSE PROTEIN TRANSGLUCOSYLASE
33	E318	CA411030	453	163	5.00E-40	UDP-GLUCOSE PROTEIN TRANSGLUCOSYLASE
34	E327	CA411039	434	156	4.00E-38	ALPHA-N-ACETYLGLUCOSAMINIDASE
35	E359	CA411071	459	185	1.00E-46	ISOCITRATE DEHYDROGENASE (NADP)
36	E379	CA411088	462	144	3.00E-34	FRUCTOSE-BISPHOSPHATE ALDOLASE
37	E393	CA411100	752	264	1.00E-70	BETA-GALACTOSIDASE (EC 3.2.1.23)
38	E395	CA411102	756	171	8.00E-43	PUTATIVE DEHYDROGENASE
39	E433	CA411140	750	247	1.00E-65	FRUCTOSE-BISPHOSPHATE ALDOLASE
40	E440	CA411147	741	238	5.00E-63	GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE
41	E441	CA411148	764	232	9.00E-61	DIHYDROLIPOAMIDE 5 ACETYLTRANSFERASE
42	E447	CA411154	704	79	9.00E-15	MALATE DEHYDROGENASE
43	E539	CA411244	555	163	4.00E-40	NAD-DEPENDIENT ISOCITRATE DEHYDROGENASE
44	E549	CA411254	614	119	6.00E-27	GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE
45	E625	CA411327	584	132	5.00E-38	GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE
46	E640	CA411342	706	229	3.00E-60	FRUCTOSE-BISPHOSPHATE ALDOLASE
47	E696	CA411397	636	115	9.00E-26	GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE
48	E697	CA411398	732	164	3.00E-40	DIHYDRODIPICOLINATE SYNTHASE (EC 4.2.1.5)
49	E713	CA411414	747	233	1.00E-62	TRANSKETOLASE, CHLOROPLAST
50	E724	CA411425	726	235	4.00E-62	FRUCTOSE-BISPHOSPHATE ALDOLASE
51	E736	CA411437	727	234	1.00E-61	FRUCTOSE-BISPHOSPHATE ALDOLASE
52	E746	CA411446	718	159	8.00E-39	ATP CITRATE-LYASE

	A	B	C	D	E	F
6	**L#**	**GenBank accession #**	**bp**	**score**	**E-value**	**annotation**
53	E788	CA411487	674	192	7..00E-49	INOSITOL MONOPHOSPHATASE-LIKE PROTEIN
54	E790	CA411489	715	218	9.00E-57	GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE
55	E819	CA411517	740	279	3.00E-75	PHOSPHOENOLPYRUVATE CARBOXYLASE
56	E845	CA411543	768	227	3.00E-59	SUCCINYL-COA-LIGASE BETA SUBUNIT
57						
58	ENERGY METABOLISM/Electron Transfer: category 1b					
59	E001	CA410731	537	135	1.00E-31	2-CYS PEROXIREDOXIN-LIKE PROTEIN
60	E005	CA410735	481	105	1.00E-36	NADH-UBIQUINONE REDUCTASE
61	E007	CA410737	464	106	8.00-23	
62	E033	CA410763	490	110	3.00E-24	2-CYS PEROXIREDOXIN-LIKE PROTEIN
63	E043	CA410773	492	91	3.00E-18	P ADENYLATE KINASE
64	E075	CA410802	534	210	3.00E-54	VACUOLAR ATP SYNTHASE SUBUNIT B
65	E108	CA410833	496	124	2.00E-28	VACUOLAR H+-ATP SYNTHASE PROTEOLIPID SUBUNIT
66	E179	CA410903	477	147	2.00E-35	ADENINE NUCLEOTIDE TRANSLOCATOR
67	E190	CA410912	446	129	1.00E-29	VACUOLAR H+-ATPASE B SUBUNIT
68	E226	CA410945	483	115	1.00E-25	ATP SYNTHASE GAMMA CHAIN
69	E227	CA410946	447	71	4.00E-12	14-3-3-LIKE PROTEIN
70	E279	CA410996	416	134	3.00E-21	BASIC BLUE COPPER PROTEIN
71	E289	CA411005	428	122	1.00E-27	VACUOLAR ATP SYNTHASE SUBUNIT B
72	E364	CA411075	453	155	1.00E-37	WHITE-FLY INDUCeD/respiratory burst oxidase F100
73	E376	CA411086	419	58	3.00E-08	ADP,ATP CARRIER PROTEIN
74	E461	CA411168	722	192	5.00E-49	CYTOCHROME B561
75	E491	CA411197	581	187	3.00E-47	14-3-3-LIKE PROTEIN
76	E531	CA411236	703	241	6.00E-64	VACUOLAR ATP SYNTHASE
77	E562	CA411267	649	196	4.00E-50	14-3-3-LIKE PROTEIN
78	E590	CA411294	687	171	1.00E-42	ATP SYNTHASE BETA CHAIN
79	E741	CA411442	709	219	4.00E-57	CYTOCHROME C1
80	E747	CA411447	649	132	6.00E-31	CYTOCHROME C OXIDASE
81	E752	CA411452	568	146	6.00E-35	CYTOCHROME C
82	E798	CA411497	730	111	1.00E-24	GLUTAREDOXIN-LIKE PROTEIN
83	E810	CA411508	751	236	2.00E-62	H(+)-TRANSPORTING ATPASE
84	E822	CA411520	716	219	4.00E-57	14-3-3 PROTEIN
85	E828	CA411526	693	151	1.00E-36	NADH DEHYDROGENASE CHAIN CI-18
86	E835	CA411533	438	80	6.00E-15	UBIQUINOL-CYTOCHROME-C REDUCTASE
87						
88	NUCLEOTIDE AND NUCLEIC ACID METABOLISM:2					
89	E009	CA410739	509	182	8.00E-46	60S RIBOSOMAL PROTEIN L12
90	E010	CA410740	551	174	2.00E-43	HISTONE H3
91	E022	CA410752	441	160	3.00E-39	UBIQUITIN
92	E035	CA410765	442	153	3.00E-37	HISTONE H3
93	E036	CA410766	295	69	1.00E-11	40S RIBOSOMAL PROTEIN S3
94	E037	CA410767	462	87	4.00E-17	ELONGATION FACTOR 1-BETA
95	E039	CA410769	490	153	5.00E-37	60S RIBOSOMAL PROTEIN-LIKE
96	E046	CA410776	474	163	5.00E-40	40S RIBOSOMAL PROTEIN S3
97	E056	CA410785	384	66	2.00E-10	RIBOSOMAL PROTEIN S30 HOMOLOG 40S RIBOS. S30
98	E060	CA410789	466	138	2.00E-32	40S RIBOSOMAL PROTEIN S18
99	E062	CA410791	451	102	1.00E-21	80S RIBOSOMAL PROTEIN L31
100	E069	CA410798	555	174	2.00E-43	60S RIBOSOMAL PROTEIN L17
101	E084	CA410811	515	180	4.00E-45	ELONGATION FACTOR 1-ALPHA
102	E088	CA410815	254	48	3.00E-05	UBIQUITIN PRECURSOR
103	E091	CA410818	591	88	2.00E-17	ARGININE METHYLTRANSFERASE-LIKE PROTEIN

	A	B	C	D	E	F
6	**L#**	**GenBank accession #**	**bp**	**score**	**E-value**	**annotation**
104	E099	CA526338	385	99	7.00E-21	UBIQUITIN
105	E105	CA410830	496	121	1.00E-27	60S RIBOSOMAL PROTEIN L37
106	E116	CA410841	400	146	8.00E-35	60S RIBOSOMAL PROTEIN L2
107	E130	CA410855	454	171	2.00E-42	RIBOSOMAL PROTEIN
108	E133	CA410858	501	141	2.00E-33	RIBOSOMAL PROTEIN S8
109	E140	CA410865	421	139	6.00E-33	60S RIBOSOMAL PROTEIN L27
110	E155	CA410880	469	163	5.00E-40	40S RIBOSOMAL PROTEIN S23
111	E162	CA410887	465	162	8.00E-40	UBIQUITIN/RIBOSOMAL PROTEIN
112	E193	CA410914	435	104	2.00E-22	HISTONE H2A
113	E196	CA410916	441	74	4.00E-13	UBIQUITIN-CONJUGATING ENZYME E2 (EC 6.3)
114	E201	CA410921	445	141	2.00E-33	40S RIBOSOMAL PROTEIN S7
115	E203	CA410923	432	154	2.00E-37	60S RIBOSOME PROTEIN L19-LIKE
116	E207	CA410926	450	171	2.00E-44	ARGININE DECARBOXYLASE (EC 4.1.1.19)
117	E209	CA410928	473	139	1.00E-32	UBIQUITIN-CONJUGATING ENZYME E2 (EC 6.3.2.19)
118	E210	CA410929	449	161	2.00E-39	60S RIBOSOMAL PROTEIN L24
119	E220	CA410939	462	171	2.00E-42	40S RIBOSOMAL PROTEIN S4
120	E221	CA410940	442	160	3.00E-39	40S RIBOSOMAL PROTEIN
121	E224	CA410943	461	149	1.00E-35	60S RIBOSOMAL PROTEIN L3
122	E225	CA410944	425	100	8.00E-21	RIBOSOMAL PROTEIN S27
123	E228	CA410947	453	111	2.00E-24	SUBTILISIN PRECURSOR
124	E246	CA410964	423	135	1.00E-35	60S RIBOSOMAL PROTEIN L1
125	E255	CA410973	431	125	9.00E-29	RIBOSOMAL PROTEIN S8
126	E258	CA410976	527	119	7.00E-27	RIBOSOMAL PROTEIN L26
127	E260	CA410978	439	149	1.00E-35	60S RIBOSOMAL PROTEIN L30
128	E264	CA410982	439	132	1.00E-30	RIBOSOMAL PROTEIN S8
129	E272	CA410990	399	69	1.00E-12	HISTONE H2B
130	E276	CA410994	429	127	3.00E-29	60S RIBOSOMAL PROTEIN L26
131	E278	CA526345	402	111	2.00E-24	60S RIBOSOMAL PROTEIN L7A
132	E280	CA526346	415	99	6.00E-21	CYSTEINE PROTEINASE
133	E281	CA410997	415	146	6.00E-35	60S RIBOSOMAL PROTEIN L17-1
134	E287	CA411003	413	140	4.00E-33	4OS RIBOSOMAL PROTEIN S20
135	E288	CA411004	417	156	7.00E-38	60S RIBOSOMAL PROTEIN LI3A
136	E291	CA411007	447	172	7.00E-43	RIBOSOMAL PROTEIN L18A
137	E302	CA411016	345	74	7.00E-15	TRANSLATION FACTOR SUI1
138	E311	CA411024	485	183	5.00E-46	POLYUBIQUITIN
139	E314	CA411026	450	108	1.00E-23	ALKYLATED DNA REPAIR PROTEIN
140	E316	CA411028	408	139	9.00E-36	40S RIBOSOMAL PROTEIN S4
141	E330	CA411042	405	145	2.00E-34	GUANINE NUCLEOTIDE-BINDING PROTEIN
142	E331	CA411043	429	150	5.00E-36	40S RIBOSOMAL PROTEIN S24
143	E339	CA411051	484	108	2.00E-23	60S RIBOSOMAL PROTEIN L22
144	E344	CA411056	436	161	2.00E-39	UBIQUITIN-CONJUGATING ENZYME
145	E350	CA411062	405	134	2.00E-31	RIBOSOMAL PROTEIN L32
146	E352	CA411064	464	127	3.00E-29	40S RIBOSOMAL PROTEIN S12
147	E354	CA411066	429	139	1.00E-32	L3 RIBOSOMAL PROTEIN
148	E363	CA411074	362	113	5.00E-25	ELONGATION FACTOR-1 ALPHA
149	E372	CA526349	435	148	1.00E-35	POLYUBIQUITIN
150	E388	CA411097	676	187	1.00E-47	ELONGATION FACTOR-1 ALPHA
151	E400	CA411107	739	202	5.00E-52	UBIQUITIN-CONJUGATING ENZYME (EC 6.3.2.19)
152	E401	CA411108	614	188	1.00E-47	40S RIBOSOMAL PROTEIN S23
153	E403	CA411110	750	216	2.00E-56	RIBOSOMAL PROTEIN S7
154	E407	CA411114	191	85	2.00E-16	60S RIBOSOMAL PROTEIN L10

	A	B	C	D	E	F
6	**L#**	**GenBank accession #**	**bp**	**score**	**E-value**	**annotation**
155	E425	CA411132	649	144	2.00E-24	RIBOSOMAL PROTEIN L23A
156	E426	CA411133	720	226	3.00E-59	60S RIBOSOMAL PROTEIN L15
157	E438	CA411145	656	244	1.00E-64	40S RIBOSOMAL PROTEIN SA
158	E442	CA411149	490	70	6.00E-12	60S ACIDIC RIBOSOMAL PROTEIN
159	E444	CA411151	671	192	7.00E-49	60S RIBOSOMAL PROTEIN L12
160	E448	CA411155	719	259	2.00E-69	60S RIBOSOMAL PROTEIN L13A
161	E451	CA411158	726	218	5.00E-57	40S RIBOSOMAL PROTEIN S2
162	E453	CA411160	737	234	7.00E-62	40S RIBOSOMAL PROTEIN S4
163	E454	CA411161	575	137	3.00E-32	40S RIBOSOMAL PROTEIN S2
164	E456	CA411163	700	122	5.00E-28	POLY (A) BINDING PROTEIN
165	E469	CA411175	738	192	6.00E-49	40S RIBOSOMAL PROTEIN S11
166	E470	CA411176	723	207	1.00E-53	ELONGATION FACTOR
167	E471	CA411177	636	149	4.00E-36	RIBOSOMAL PROTEIN L11
168	E476	CA411182	737	237	1.00E-62	40S RIBOSOMAL PROTEIN S9
169	E477	CA411183	706	140	2.00E-33	40S RIBOSOMAL PROTEIN S12
170	E482	CA411188	555	157	2.00E-38	60S RIBOSOMAL PROTEIN L26
171	E486	CA411192	655	115	7.00E-26	60S RIBOSOMAL PROTEIN
172	E494	CA411200	605	69	1.00E-11	60S ACIDIC RIBOSOMAL PROTEIN
173	E497	CA411203	723	280	1.00E-75	RIBOSOMAL PROTEIN L2
174	E503	CA411209	618	160	3.00E-39	RIBOSOMAL PROTEIN S9
175	E504	CA411210	634	149	4.00E-36	RIBOSOMAL PROTEIN L11
176	E506	CA526353	743	232	3.00E-61	60S RIBOSOMAL PROTEIN L1
177	E508	CA411213	722	189	7.00E-48	40S RIBOSOMAL PROTEIN S23
178	E510	CA411215	748	235	5.00E-62	60S RIBOSOMAL PROTEIN L9
179	E512	CA411217	687	130	3.00E-30	POLY (A) BINDING PROTEIN
180	E515	CA411220	708	198	6.00E-51	UBIQUITIN-CONJUGATING PROTEIN
181	E527	CA411232	530	166	4.00E-41	UBIQUITIN EXTENSION PROTEIN
182	E537	CA411242	626	121	1.00E-27	RIBOSOMAL PROTEIN L2
183	E557	CA411262	704	167	1.00E-41	40S RIBOSOMAL PROTEIN S11
184	E566	CA411271	454	90	5.00E-18	CYSTEINE PROTEINASE INHIBITOR
185	E578	CA411282	478	100	7.00E-21	RIBOSOMAL PROTEIN S27
186	E582	CA411286	392	64	4.00E-10	RIBOSOMAL PROTEIN S30
187	E585	CA411289	537	107	3.00E-23	HISTONE H2B
188	E594	CA411298	453	137	3.00E-32	40S RIBOSOMAL PROTEIN S17
189	E602	CA411305	672	170	2.00E-42	HISTONE H3
190	E605	CA411308	654	186	5.00E-47	40S RIBOSOMAL PROTEIN
191	E608	CA411311	749	198	6.00E-51	50S RIBOSOMAL PROTEIN L3
192	E611	CA411314	738	120	2.00E-38	RNA HELICASE
193	E628	CA411330	646	185	3.00E-47	CYTOPLASMIC RIBOSOMAL PROTEIN S13
194	E633	CA411335	604	173	1.00E-52	ELONGATION FACTOR 1-ALPHA
195	E641	CA411343	601	213	2.00E-55	60S RIBOSOMAL PROTEIN L10
196	E646	CA411348	665	238	1.00E-62	ASPARAGINE SYNTHETASE
197	E651	CA411353	612	129	7.00E-30	ELONGATION FACTOR 1-ALPHA
198	E655	CA411357	709	243	2.00E-64	RIBOSOMAL PROTEIN S4
199	E659	CA411361	669	174	2.00E-43	HISTONE H3
200	E666	CA411368	757	150	2.00E-36	40S RIBOSOMAL PROTEIN S14
201	E668	CA411370	707	189	4.00E-48	CYTOPLASMIC RIBOSOMAL PROTEIN S13
202	E670	CA411372	656	210	2.00E-54	RIBOSOMAL PROTEIN S6
203	E675	CA411377	609	116	1.00E-31	RIBOSOMAL PROTEIN S13
204	E678	CA411380	655	189	4.00E-49	CYTOPLASMIC RIBOSOMAL PROTEIN S13
205	E687	CA411388	673	169	5.00E-42	POLYUBIQUITIN

	A	B	C	D	E	F
6	**L#**	**GenBank accession #**	**bp**	**score**	**E-value**	**annotation**
206	E689	CA411390	732	279	3.00E-75	60S RIBOSOMAL PROTEIN L10
207	E693	CA411394	703	243	2.00E-64	60S RIBOSOMAL PROTEIN L13A
208	E694	CA411395	727	265	6.00E-71	60S RIBOSOMAL PROTEIN L10
209	E703	CA411404	738	196	2.00E-50	BIFUNCTIONAL NUCLEASE
210	E704	CA411405	733	196	3.00E-50	CYTOPLASMIC RIBOSOMAL PROTEIN S13
211	E707	CA411408	712	297	1.00E-77	60S RIBOSOMAL PROTEIN L10
212	E710	CA411411	724	275	4.00E-74	ASPARAGINE SYNTHETASE
213	E727	CA411428	699	145	6.00E-35	PROBABLE UBIQUITIN-CONJUGATING ENZYME
214	E731	CA411432	601	163	3.00E-40	HISTONE H3
215	E743	CA526356	696	210	2.00E-54	ASPARAGINE SYNTHETASE
216	E744	CA411444	323	64	5.00E-10	RIBOSOMAL PROTEIN S30
217	E755	CA411455	688	275	7.00E-74	HISTONE DEACETYLASE
218	E760	CA411461	723	126	4.00E-29	HISTONE H2A
219	E761	CA411462	571	66	9.00E-11	ACIDIC RIBOSOMAL PROTEIN P3
220	E766	CA411465	694	147	2.00E-35	ARGININE/SERINE-RICH SPLICING FACTOR
221	E769	CA411468	683	139	3.00E-55	CYSTEINE PROTEINASE PREDURSOR
222	E771	CA411470	686	60	3..00E-09	HISTONE H1
223	E773	CA411472	575	229	4.00E-60	RIBOSOMAL PROTEIN S9
224	E786	CA411485	665	196	5.00E-50	RIBOSOMAL PROTEIN S8
225	E797	CA411496	748	213	1.00E-55	RIBOSOMAL PROTEIN S30
226	E801	CA411500	759	251	8.00E-67	RIBOSOMAL PROTEIN L5
227	E805	CA411504	687	66	7.00E-11	RIBOSOMAL PROTEIN L10A
228	E806	CA411505	673	186	4.00E-47	RIBOSOMAL PROTEIN S16
229	E807	CA526358	725	264	6.00E-75	ELONGATIN FACTOR 1-ALPHA
230	E813	CA411511	709	214	1.00E-55	CYTOSOLIC CYSTEINE SYNTHASE
231	E817	CA411515	734	113	3.00E-25	P ALPHA NAC. ALPHA NAC-LIKE PROTEIN
232	E820	CA411518	601	64	2.003-10	60S ACIDIC RIBOSOMAL PROTEIN P3
233	E829	CA411527	728	222	6.00E-58	RIBOSOMAL PROTEIN L3
234	E847	CA411545	744	192	5.00E-49	NUCLEOSIDE DIPHOSPHATE KINASE I
235	E848	CA411546	740	248	7.00E-66	RUVB DNA HELICASE- LIKE PROTEIN
236						
237	AMINO ACID AND PROTEIN METABOLISM: category 3					
238	E025	CA410755	511	132	7.00E-31	SIMILARITY TO 40S RIBOSOMAL PROTEIN S10
239	E061	CA410790	482	158	2.00E-38	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (EC 5.2.1.8)
240	E188	CA410910	464	82	1.00E-15	NASCENT POLYPEPTIDE ASSOCIATED COMPLEX ALPH
241	E261	CA410979	438	95	2.00E-19	P LYSOSOMAL ACID LIPASE
242	E306	CA411020	264	44	1.00E-16	PAPAIN-LIKE CYSTEINE PROTEINASE
243	E505	CA411211	694	180	2.00E-45	PEPTIDYLPROPYL ISOMERASE FK506 BINDING PROT.
244	E519	CA411224	695	198	7.00E-51	PEPTIDYLPROPYL CIS-TRANS ISOMERASE
245	E763	CA411463	675	213	2.00E-55	HYP 34.0KDA PROT/phosphoglyceride transfer prot.
246	E526	CA411231	727	125	7.00E-29	NASCENT POLYPEPTIDE ASSOCIATED COMPLEX
247	E686	CA411387	667	206	3.00E-53	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE
248	E780	CA411479	730	278	7.00E-75	GLUTAMINE SYNTHETASE CYTOSOLIC ISOZYME
249						
250	FATTY ACID AND LIPID METABOLISM: category 4					
251	E049	CA410779	471	137	2.00E-32	LYSOPHOSPHOLIPASE-LIKE PROTEIN
252	E275	CA410993	432	118	1.00E-26	LIPASE-LIKE PROTEIN
253	E370	CA411081	460	165	1.00E-40	SQUALENE MONOOXYGENASE
254	E572	CA411276	729	256	2.00E-68	CTP: PHOSPHOCOLYNE CYTIDYLTRANSFERASE
255	E669	CA411371	702	106	4.00E-23	OMEGA6 FATTY ACID DESATURASE
256	E768	CA411467	708	138	7.00E-36	LIPASE/ACYLHIDROLASE

	A	B	C	D	E	F
6	**L#**	**GenBank accession #**	**bp**	**score**	**E-value**	**annotation**
257						
258	NUTRIENT ASSIMILATION (other than carbon): category 5					
259	E042	CA410772	513	197	3.00E-50	HYP. 28.9 KDA PROTEIN/alkaline phosphatase 56 6e-08
260	E166	CA410891	483	87	5.00E-17	ACID PHOSPHATASE PRECURSOR (EC 3.1.3.2)
261	E237	CA410956	420	94	4.00E-19	P ACID PHOSPHATASE
262	E369	CA411080	455	64	3.00E-10	PHOSPHATASE-LIKE PROTEIN
263						
264	SECONDARY METABOLISM: category 6					
265	E149	CA410874	456	99	1.00E-20	CARNITINE RACEMASE LIKE PROTEIN
266	E206	CA410925	458	179	7.00E-45	EPOXIDE HYDROLASE (EC 3.3.2.3)
267	E213	CA410932	213	166	2.00E-41	HYP. PROTEIN/methionyl trna formyltransferasa 83 7e-16
268	E231	CA410950	405	100	8.00E-21	THIAZOLE BIOSYNTHETIC ENZYME
269	E235	CA410954	416	100	8.00E-21	4-COUMARATE; COA LIGASE (EC 6.2.1.12)
270	E239	CA410957	429	125	2.00E-28	FLAVONOL GLUCOSYLTRANSFERASE
271	E267	CA410985	432	53	1.00E-06	S-ADENOSYL-L-METHIONINE DECARBOXYLASE
272	E320	CA411032	463	120	3.00E-27	CYTOCHROME P450/isoflavone synthase 114 3.00e-25
273	E402	CA411109	741	254	7.00E-68	EPOXIDE HYDROLASE
274	E404	CA411111	728	204	8.00E-53	CYTOCHROME P45/steroid 22-alpha hydrixylase 118 9e-27
275	E418	CA411125	777	140	4.00E-33	CYTHOCROMRE P450
276	E523	CA411228	710	271	2.00E-73	HYP. 49.0 PROT/similarity limonene cyclase 121 1e-27
277	E601	CA411304	694	126	4.00E-29	CYTOCHROME P450 71A10
278	E621	CA411324	730	195	6.00E-50	S-ADENOSYLMETHIONINE 2-DEMETHYLMENAQUINONE
279	E629	CA411331	686	108	1.00E-23	MANNOSYL-OLYGOSACHARIDE 1,2ALPHA MANNOSIDA
280	E657	CA411359	500	140	4.00E-33	ALLERGENIC ISOFLAVONE REDUCTASE-LIKE PROT.
281	E681	CA411383	714	260	3.OOE-39	UDP-GLUCOSE -STEROL GLUCOSYLTRANSFERASA
282	E685	CA411386	642	159	6.00E-39	CYTOCHROME P450
283	E709	CA411410	683	212	4.00E-55	THIAZOLE BIOSYNTHETIC ENZYME CHLOROPLAST
284	E717	CA411418	716	193	3.00E-49	THIAZOLE BIOSYNTHETIC ENZYME CHLOROPLAST
285	E787	CA411486	408	56	1.00E-12	CYTOCHROME P450 MONOOXYGENASE
286						
287	POSSIBLE FUNCTION(S) IN DIFFERENT AREAS of METABOLISM: category 7					
288	E012	CA410742	536	192	5.00E-49	S-ADENOSYLMETHIONINE SYNTHETASE 2 (EC 2.5.1.6)
289	E059	CA410788	460	135	1.00E-31	5-METHYL/TETRAHYDROPTEROYLTRIGLUTAMATE
290	E079	CA410806	534	142	3.00E-34	ENDOGLUCANASE (EC 3.2.1.4)
291	E083	CA410810	582	201	1.00E-51	CHAPERONIN
292	E090	CA410817	489	157	2.00E-38	ADP-RIBOSYLATION FACTOR
293	E107	CA410832	517	191	2.00E-48	5-METHYL/TETRAHYDROPTEROYLTRIGLUTAMATE
294	E109	CA410834	452	141	2.00E-33	5-METHYL/TETRAHYDROPTEROYLTRIGLUTAMATE
295	E159	CA410884	465	78	2.00E-14	SYNTAXIN RELATED PROTEIN
296	E167	CA410892	418	125	1.00E-28	ANNEXIN LIKE PROTEIN
297	E204	CA410924	464	145	1.00E-34	ANNEXIN PROTEIN
298	E249	CA410967	436	151	1.00E-36	P WD-40 REPEAT PROTEIN
299	E303	CA411017	443	134	2.00E-31	METHYLENETETRAHYDROFOLATE REDUCTASE 1.5.1.20
300	E307	CA411021	503	163	4.00E-40	ADP-RIBOSYLATION FACTOR
301	E325	CA411037	425	149	7.00E-36	METHIONINE SYNTHASE(EC 2.1.1.14)
302	E332	CA411044	443	126	8.00E-29	ENDOGLUCANASE (EC 3.2.1.4)
303	E355	CA411067	442	129	1.00E-29	S-ADENOSYLMETHIONINE SYNTHETASE (EC 2.5.1.6)
304	E378	CA411087	457	82	1.00E-15	HYDROLASE (contains an esterase/lipase/thioesterase
305	E434	CA411141	580	142	6.00E-34	THIOREDOXIN
306	E462	CA411169	746	122	5.00E-28	0-METHYLTRANSFERASE
307	E472	CA411178	741	263	2.00E-70	S-ADENOSYLMETHIONINE SYNTHETASE (EC 2.5.1.6)

	A	B	C	D	E	F
6	**L#**	**GenBank accession #**	**bp**	**score**	**E-value**	**annotation**
308	E475	CA411181	729	252	5.00E-67	S-ADENOSYLMETHIONINE SYNTHETASE
309	E480	CA411186	688	230	2.00E-80	5METHYLTETRAHYDROPTEROYLTRIGLUTAMATE
310	E489	CA411195	698	179	5.00E-45	5METHYLTETRAHYDROPTEROYLTRIGLUTAMATE
311	E513	CA411218	732	212	6.00E-55	SULFATE ADENYLTRANSFERASE (EC 2.7.7.4)
312	E530	CA411235	704	182	4.00E-46	AMINOTRANSFERASE
313	E588	CA411292	671	233	2.00E-61	S-ADENOSYLMETHIONINE SYNTHETASE
314	E596	CA411300	766	279	4.00E-75	S-ADENOSYLMETHIONINE SYNTHETASE
315	E609	CA411312	753	258	1.00E-68	S-ADENOSYLMETHIONINE SYNTHETASE (EC 2.5.1.1.6.)
316	E618	CA411321	749	229	3.00E-60	ATP SULFURYLASE/APS KINASE (EC 2.7.7.4)
317	E630	CA411332	709	139	3.00E-33	HISTIDINE CONTAINING PHOSPHOTRANSFER PROTEIN
318	E636	CA411338	719	94	2.00E-19	CARBONYL REDUCTASE-LIKE PROTEIN
319	E688	CA411389	713	271	8.00E-73	METHIONINE SYNTHASE (EC 2.1.1.14)
320	E764	CA526357	721	211	5.00E-56	SERYNE HYDROXYMETHYLTRANSFERASE (EC 2.1.2.1)
321	E784	CA411483	686	244	1.00E-64	SULFATE ADENYLYLTRANSFERASE
322	E792	CA411491	754	257	1.00E-68	ADENOSYLHOMOSYSTEINASE (EC 3.3.1.1)
323	E804	CA411503	737	219	3.00E-57	SULFATE ADENYLYLTRANSFERASE
324	E827	CA411525	727	243	2.00E-64	ENDOCGLUCANASE 1
325	E830	CA411528	737	278	7.00E-75	ADENOSYLHOMOSYSTEINASE (EC 3.3.1.1)
326	E832	CA411530	743	163	3.00E-39	P BETA-1,3-GLUCANASE
327						
328	II DEVELOPMENT					
329	CELL STRUCTURE, DIFFERENTIATION, CELL CYCLE: category 8					
330	E003	CA410733	484	165	1.00E-40	PECTINESTERASE (EC 3.1.1.11)
331	E013	CA410743	509	177	3.00E-44	TUBULIN ALPHA-1 CHAIN
332	E050	CA410780	478	153	3.00E-37	BETA-1,3 GLUCANASE PRECURSOR (EC 3.2.1.39)
333	E121	CA410846	446	168	2.00E-41	PECTINESTERASE (EC 3.1.1.11)
334	E131	CA410856	470	144	3.00E-34	TUBULIN ALPHA-2/ALPHA-4 CHAIN
335	E154	CA410879	501	100	5.00E-22	ACTIN
336	E176	CA410900	367	82	2.00E-15	ACTIN
337	E187	CA526341	459	156	7.00E-38	TUBULIN ALPHA-2/ALPHA-4 CHAIN
338	E197	CA410917	463	114	2.00E-25	EXPANSIN PROTEIN
339	E199	CA410919	456	93	7.00E-19	XYLOGLUCAN ENDO-TRANSGLYCOSYLASE LIKE-PROT
340	E200	CA410920	456	93	7.00E-19	XYLOGLUCAN ENDO-TRANSGLYCOSYLASE LIKE-PROT
341	E219	CA410938	447	118	1.00E-26	EXPANSIN PRECURSOR
342	E262	CA410980	429	175	2.00E-43	ACTIN
343	E274	CA410992	413	159	6.00E-39	TUBULIN BETA CHAIN
344	E319	CA411031	460	167	2.00E-41	TUBULIN BETA CHAIN
345	E394	CA411101	723	188	9.00E-48	BETA-1-3-GLUCANASE-LIKE PROTEIN
346	E405	CA411112	731	116	3.00E-26	FPF1 LIKE PROTEIN
347	E536	CA411241	741	177	1.00E-44	PECTINESTERASE PRECURSOR (EC 3.1.1.11)
348	E554	CA411259	643	130	3.00E-30	PECTINESTERASE PRECURSOR (EC 3.1.1.11)
349	E652	CA411354	702	212	5.00E-55	F-ACTIN CAPPING PROTEIN ALPHA SUBUNIT
350	E660	CA411362	688	263	2.00E-70	UDP-GLUCOSE DEHYDROGENASE
351	E671	CA411373	695	264	1.00E-70	TUBULIN ALPHA CHAIN
352	E680	CA411382	671	217	2.00E-56	TUBULIN ALPHA-2/ALPHA-4 CHAIN
353	E695	CA411396	724	165	8.00E-41	ACTIN-DEPOLYMERIZING FACTOR 2
354	E702	CA411403	690	106	4.00E-23	HMG 1 PROTEIN
355	E705	CA411406	706	283	1.00E-76	BETA TUBULIN
356	E732	CA411433	746	106	3.00E-23	HMG 1 PROTEIN
357	E818	CA411516	708	280	2.00E-75	ACTIN 11
358						

	A	B	C	D	E	F
6	**L#**	**GenBank accession #**	**bp**	**score**	**E-value**	**annotation**
359	PLANT DEVELOPMENT, NODULATION, SENESCENCE: category 9					
360	E004	CA410734	521	75	2.00E-13	AUXIN-REPRESSED PROTEIN
361	E073	CA410801	520	157	2.00E-38	BRASSINOSTEROID INSENSITIVE PROTEIN recp.prot.kina
362	E078	CA410805	492	102	1.00E-23	PUTATIVE AUXIN-REPRESSED PROTEIN
363	E080	CA410807	534	115	1.00E-35	ETHYLENE-RESPONSIVE SMALL GTPBINDING PROTEIN
364	E081	CA410808	425	77	5.00E-14	PUTATIVE SENESCENSE-ASSOCIATED PROTEIN
365	E087	CA410814	568	126	6.00E-29	HYP. PROTEIN/Home domain transcrip. Factor 85 1e-16
366	E112	CA410837	450	62	1.00E-09	PROLINE RICH SAC51
367	E123	CA410848	498	101	2.00E-21	PHYTOCHROME-ASSOCIATED/auxin responsive 96 7e-20
368	E139	CA410864	495	100	7.00E-21	AUXIN REPRESSED PROTEIN
369	E175	CA410899	515	152	7.00E-37	RIPENING RELATED PROTEIN
370	E186	CA526340	469	97	5.00E-20	WD-40 REPEAT PROTEIN LIKE
371	E282	CA410998	433	83	1.00E-15	HYP. PROT/ gibberellin- regulated protein 74 4e-13
372	E284	CA411000	420	96	7.00E-20	SIMILARITY TO EMBRYO-SPECIFIC PROTEIN
373	E309	CA411022	446	66	1.00E-10	HYP. PROT/ Similar to inhibitor of apoptosis protein
374	E313	CA526348	429	162	1.00E-39	PROTEASOME SUBUNIT ALPHA TYPE 5
375	E315	CA411027	444	133	5.00E-31	CS-IAA2/ auxin responsive protein IAA8 121 2e-27
376	E328	CA411040	458	150	3.00E-36	ASCORBATO PEROXIDASE
377	E341	CA411053	431	176	5.00E-44	LIPOXYGENASE L5
378	E348	CA411060	460	118	2.00E-26	P HYDROLASE/p ripeninig related protein 108 2e-23
379	E349	CA411061	408	95	2.00E-19	LIPOXYGENASE
380	E361	CA411072	459	114	3.00E-25	P 21 KDA PROTEIN/ ripeninig related protein 86 8e-17
381	E389	CA526351	741	114	1.00E-25	APA DOMAIN TRANSCRIPTION FACTOR
382	E399	CA411106	733	87	3.00E-17	ETHYLENE RESPONSIVE ELEMENT BINDING FACTOR
383	E423	CA411130	752	84	2.00E-16	Prolin rich F12F1.3 PROTEIN/ EXTENSIN-LIKE PROT
384	E429	CA411136	733	189	3.00E-48	WD-40 REPEAT PROTEIN MS12
385	E516	CA411221	727	158	8.00E-39	AUXIN-BINDING PROTEIN
386	E529	CA411234	710		6.00E-13	AP2 DOMAIN /ETHYLENE RESPONS ELEMT BINDING
387	E535	CA411240	647	110	3.00E-24	AUXIN-REPRESSED PROTEIN
388	E550	CA411255	729	264	1.00E-70	PROTEASOME BETA SUBUNIT (EC 3.4.99.46)
389	E595	CA411299	716	140	2.00E-33	EARLY NODULIN ENOD18
390	E598	CA411302	688	207	2.00E-53	1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE
391	E600	CA411303	744	194	1.00E-49	NODULIN LIKE PROTEIN
392	E631	CA411333	733	167	1.00E-41	PROFILIN
393	E638	CA411340	718	110	2.00E-24	AUXIN-REPRESSED PROTEIN
394	E648	CA411350	729	153	2.00E-37	RIPENING RELATED PROTEIN
395	E654	CA411356	727	153	2.00E-37	RIPENING RELATED PROTEIN
396	E662	CA411364	746	101	1.00E-21	DORMANCY-ASSOCIATED PROTEIN
397	E677	CA411379	709	83	3.00E-16	PROLINE RICH PROTEIN
398	E690	CA411391	662	181	9.00E-40	ACTIN-DEPOLYMERIZING FACTOR 2
399	E699	CA411400	722	133	2.00E-27	POLLEN SPECIFIC PROTEIN PRECURSOR
400	E740	CA411441	753	183	3.00E-46	HYP. 17.6 KDA PROT/seed maduratin protein 65 4e-11
401	E749	CA411449	724	118	1.00E-26	AUXIN RESPONSE FACTOR 9
402	E750	CA411450	707	127	2.00E-30	IAA7-LIKE PROTEIN
403	E757	CA411457	459	88	2.00E-17	PUTATIVE SENESENCE-ASSOCIATED PROTEIN
404	E775	CA411474	759	280	1.00E-75	SCARECROW
405	E778	CA411477	705	118	8.00E-27	LECTIN LIKE PROTEIN
406	E783	CA411482	672	104	2.00E-22	LECTIN LIKE PROTEIN
407	E796	CA411495	409	73	8.00E-13	Putative SENESCENCE-ASSOCIATED PROTEIN
408	E815	CA411513	710	107	2.00E-23	P AUXIN-REPRESSED PROTEIN
409	E841	CA411539	735	248	1.00E-67	AUXIN RESPONSE-LIKE PROTEIN

	A	B	C	D	E	F
6	**L#**	**GenBank accession #**	**bp**	**score**	**E-value**	**annotation**
410	E850	CA411548	724	133	2.00E-31	SIMILARITY TO EMBRYO-SPECIFIC PROTEIN 3
411						
412	III INTERACTION WITH THE ENVIRONMENT					
413	TRANSPORT, MEMBRANE PROTEINS: category 10					
414	E014	CA410744	514	139	5.00-33	PLASMA MEMBRANE INTRINSIC PROTEIN
415	E026	CA410756	508	211	2.00E-54	AQUAPORIN
416	E038	CA410768	508	156	4.00E-38	PLASMA MEMBRANE INTRINSIC PROTEIN
417	E065	CA410794	467	181	2.00E-45	WATER SELECTIVE TRANSPORT INTRINSIC MEMBRANE
418	E085	CA410812	529	169	5.00E-42	AQUAPORIN
419	E093	CA526337	577	49	9.00E-06	SMALL BASIC MEMBRANE PROTEIN Z
420	E095	CA410821	546	171	2.00E-42	AQUAPORIN
421	E096	CA410822	524	158	9.00E-39	AQUAPORIN
422	E101	CA410826	519	186	4.00E-47	CLATHRIN ASSEMBLY PROTEIN AP19
423	E122	CA410847	474	160	5.00E-39	GLUCOSE-6-PHOSPHATE/PHOSPHATE TRANSLOCATOR
424	E134	CA410859	493	76	7.00E-14	P MITOCHONDRIAL DICARBOXYLATE CARRRIER PROT.
425	E138	CA410863	496	155	1.00E-37	OUTER MITOCHONDRIAL MEMBRANE PROTEIN
426	E172	CA410896	457	166	4.00E-41	AQUAPORIN
427	E182	CA410906	489	168	1.00E-41	AQUAPORIN
428	E192	CA410913	313	123	5.00E-28	ENDOMEMBRANE PROTEIN EMP70PRECURSOR
429	E195	CA526343	472	124	2.00E-28	PROBABLE 28 KDA GOLGI SNARE PROTEIN
430	E198	CA410918	458	165	1.00E-40	AQUAPORIN
431	E208	CA410927	430	94	5.00E-19	PUTATIVE PLASMA MEMBRANE INTRINSIC PROTEIN
432	E232	CA410951	476	189	5.00E-48	AQUAPORIN
433	E236	CA410955	569	169	7.00E-42	P PLASMA MEMBRANE INTRINSIC PROTEIN
434	E252	CA410970	416	123	4.00E-28	AQUAPORIN
435	E253	CA410971	534	180	3.00E-45	AQUAPORIN
436	E265	CA410983	550	142	7.00E-42	AQUAPORIN
437	E293	CA411009	297	90	9.00E-18	PLASMA MEMBRANE INTRINSIC PROTEIN
438	E323	CA411035	463	120	5.00E-27	AQUAPORIN
439	E338	CA411050	508	75	1.00E-13	AQUAPORIN
440	E340	CA411052	403	75	1.00E-13	AQUAPORIN
441	E342	CA411054	453	184	2.00E-46	AQUAPORIN
442	E357	CA411069	468	112	8.00E-25	P MEMBRANE PROTEIN
443	E371	CA411082	465	187	2.00E-47	TRANSPORT PROTEIN PARTICLE
444	E375	CA411085	482	188	1.00E-47	IMPORTIN-BETA 2
445	E377	CA526350	444	99	1.00E-20	TONOPLAST INTRINSIC PROTEIN
446	E381	CA411090	457	169	8.00E-42	AQUAPORIN
447	E396	CA411103	737	202	5.00E-52	MRP LIKE ABC TRANSPORTER
448	E414	CA411121	658	205	5.00E-53	RAS-RELATED GTP-BINDING PROTEIN
449	E420	CA411127	742	220	2.00E-57	WATER CHANNEL PROTEIN
450	E428	CA411135	537	130	4.00E-30	AQUAPORIN
451	E431	CA411138	733	241	8.00E-64	WATER-SELECTIVE TRANSPORT INTRINSIC MEMBRANE
452	E445	CA411152	753	238	5.00E-63	PLASMA MEMBRANE INTRINSIC PROTEIN
453	E449	CA411156	730	202	6.00-52	
454	E452	CA411159	627	194	2.00E-49	AQUAPORIN
455	E487	CA411193	736	202	3.00E-52	CHLOROPLAST OUTER ENVELOPE PROTEIN
456	E488	CA411194	729	192	3.00E-52	WATER-SELECTIVE TRANSPORT INTRINSIC MEMBRANE
457	E495	CA411201	446	52	2.00E-06	WATER CHANNEL PROTEIN
458	E499	CA411205	698	255	4.00E-68	RAS-RELATED PROTEIN
459	E500	CA411206	671	174	1.00E-43	ENDOPLASMIC RETICULUM RETRIEVAL PROTEIN RER1A
460	E518	CA411223	770	166	6.00E-41	TRANSMEMBRANE PROTEIN

	A	B	C	D	E	F
6	**L#**	**GenBank accession #**	**bp**	**score**	**E-value**	**annotation**
461	E522	CA411227	675	152	7.00E-37	TONOPLAST MEMBRANE INTEGRAL PROTEIN
462	E524	CA411229	706	204	1.00E-52	COATOMER COMPLEX SUBUNIT
463	E547	CA411252	608	121	1.00E-27	P COMPONENT OF HIGH AFFINITY NITRTE TRANSPORT
464	E548	CA411253	561	173	4.00E-43	PLASMA MEMBRANE INTRINSIC PROTEIN
465	E555	CA411260	664	204	1.00E-52	PLASMA MEMBRANE INTRINSIC PROTEIN
466	E574	CA411278	530	168	1.00E-41	PLASMA MEMBRANE INTRINSIC PROTEIN
467	E576	CA411280	741	192	5.00E-49	TONOPLAST MEMBRANE INTEGRAL PROTEIN
468	E579	CA411283	629	110	2.00E-24	P NUCLEOSIDE TRANSPORTER
469	E581	CA411285	629	234	1.00E-61	AQUAPORIN
470	E591	CA411295	636	180	2.00E-45	VACUOLA-ASSOCIATED ANNEXIN
471	E592	CA411296	659	116	3.00E-26	PUTATIVE CARRIER PROTEIN
472	E603	CA411306	590	91	2.00E-18	TRANSMEMBRANE CHANNEL PROTEIN
473	E604	CA411307	754	219	3.00E-37	VPS28 PROTEIN/vacuolar sorting-associated proteim
474	E612	CA411315	733	314	7.00E-86	PHOSPHATE TRANSPORTER 2
475	E617	CA411320	710	234	1.00E-61	AQUAPORIN
476	E623	CA411326	741	204	1.00E-54	MITOCHONDRIAL CARRIER PROTEIN
477	E635	CA411337	725	271	9.00E-73	AQUAPORIN
478	E649	CA411351	692	94	3.00E-19	PEROXISOMAL ATP/ADP CARRIER PROTEIN
479	E672	CA411374	662	193	3.00E-49	PLASMA MEMBRANE INTRINSIC PROTEIN
480	E684	CA526355	656	121	9.00E-28	PHOSPHATE TRANSPORTER 2
481	E716	CA411417	685	182	4.00E-46	STEROID MEMBRANE BINDING PROTEIN
482	E720	CA411421	735	230	2.00E-60	WATER SELECTIVE TRANSPORT INTRINSIC MEMBRANE
483	E733	CA411434	736	95	8.00E-20	HYP. PROTEIN/membrane protein 76 4e-14
484	E759	CA411459	713	269	1.00E-63	AQUAPORIN
485	E776	CA411475	741	188	7.00E-48	PORINE
486	E799	CA411498	735	285	3.00E-77	AQUAPORIN
487	E823	CA411521	716	235	6.00E-62	AQUAPORIN
488	E833	CA411531	723	190	2.00E-50	WATER-SELECTIVE TRANSPORT INTRINSIC MEMBRANE
489	E834	CA411532	735	271	8.00E-73	AQUAPORIN
490	E836	CA411534	760	213	2.00E-55	GAMMA-SOLUBLE NSF ATTACHMENT PROTEIN
491	E843	CA411541	707	178	7.00E-45	VESICLE-ASSOCIATED MEMMBRANE PROTEIN
492						
493	SIGNAL TRANSDUCTION, REGULATION: category 11					
494	E002	CA410732	536	160	3.00E-39	GTP BINDING PROTEIN ARAC10
495	E011	CA410741	490	86	1.00E-16	CYCLIN-SPECIFIC UBIQUITIN CARRIER PROTEIN
496	E023	CA410753	526	160	2.00E-39	RAC GTP BINDING PROTEIN ARAC10
497	E030	CA410760	562	186	4.00E-47	GTP BINDING PROTEIN
498	E044	CA410774	459	130	5.00E-30	PROTEASOME ATPASE/REGULATOR
499	E051	CA410781	483	161	2.00E-39	CALMODULIN
500	E053	CA410783	497	110	3.00E-24	HYP. 120.4 KDA PROTEIN/ZINCFINGER PROTEIN 84 3e-16
501	E054	CA410784	509	162	7.00E-40	PREDICTED LEUCINE-RICH PROTEIN
502	E071	CA410799	577	61	2.00-09	
503	E092	CA410819	527	96	1.00E-19	DOF ZINC FINGER PROTEIN LIKE
504	E120	CA410845	486	156	7.00E-38	EUKARYOTIC RELEASE FACTOR 1
505	E135	CA410860	461	85	2.00E-16	PUTATIVE MYB FAMILY TRANSCRIPTION FACTOR
506	E144	CA410869	477	149	2.00E-35	ATRANBP1B PROTEIN/ Ran binding protein
507	E152	CA410877	509	84	3.00E-14	RNA AND EXPORT FACTOR BINDING PROTEIN
508	E164	CA410889	451	74	3.00E-13	EUKARYOTIC INITIATION FACTOR 4 EIF4 LIKE-PROTEIN
509	E173	CA410897	443	55	2.00E-07	SIMILARITY TO NITRATE-INDUCED NOI PROTEIN
510	E184	CA410908	471	161	2.00E-39	CALMODULIN
511	E189	CA410911	466	115	1.00E-25	P PROGESTERONE-BINDING PROTEIN

	A	B	C	D	E	F
6	**L#**	**GenBank accession #**	**bp**	**score**	**E-value**	**annotation**
512	E194	CA410915	467	98	3.00E-20	P HOMEBOX PROTEIN
513	E230	CA410949	425	157	3.00E-38	GTP-BINDING PROTEIN
514	E238	CA526344	559	121	1.00E-27	PROBABLE MITOCHONDRIAL IMPORT RECEPTOR
515	E248	CA410966	568	41	1.00E-08	ENBP1 PROTEIN (DNA_binding prtein)
516	E254	CA410972	434	68	2.00E-11	PROTEIN KINASE-LIKE PROTEIN
517	E257	CA410975	404	156	7.00E-38	CALMODULIN
518	E263	CA410981	543	80	5.00E-15	P RNA-BINDING PROTEIN
519	E266	CA410984	421	88	3.00E-17	PRLI-INTERACTING FACTOR K
520	E283	CA410999	409	80	6.00E-15	CALMODULIN
521	E343	CA411055	446	73	6.00E-13	RNA-BINDING PROTEIN
522	E345	CA411057	439	129	6.00E-30	EUKARYOTIC INITIATION FACTOR
523	E362	CA411073	442	130	3.00E-30	RNA POLYMERASE TRANSCRIPTIONAL REGULATION
524	E368	CA411079	466	116	6.00E-26	PROTEIN BINDING TO ENOD12B PROMOTOR
525	E373	CA411083	462	151	2.00E-36	PROBABLE MITOCHONDRIAL IMPORT RECEPTOR
526	E382	CA411091	455	56	1.00E-07	OSMOTIC STRESS INDUCED ZINC-FINGER PROTEIN
527	E384	CA411093	664	216	3.00E-56	PUR ALPHA 1 TRANSCRIPTIONAL ACTIVATOR PROTEIN
528	E397	CA411104	634	168	1.00E-41	CAA30303719.1 PROT/tubby-like protein 161 1e-39
529	E398	CA411105	439	84	3.00E-16	S-RECEPTOR KINASE-LIKE PROTEIN
530	E408	CA411115	726	118	7.00E-27	RING ZINC FINGER PROTEIN
531	E413	CA411120	612	153	3.00E-31	PROBABLE SIN3 ASSOCIATED POLYPEPTIDE
532	E416	CA411123	746	161	8.00E-40	S-RECEPTOR KINASE-LIKE PROTEIN
533	E436	CA411143	733	135	8.00E-32	ZH856.10 PROT/ DNA-directed RNA polymerase 70 2e-12
534	E439	CA411146	603	141	1.00E-33	RING ZINC FINGER PROTEIN
535	E450	CA411157	710	108	1.00E-22	ZINC-FINGER PROTEIN
536	E466	CA411172	361	153	5.00E-37	GIGANTEA PROTEIN
537	E473	CA411179	712	158	1.00E-38	RNA BINDING PROTEIN
538	E478	CA411184	361	153	5.00E-37	GIGANTEA PROTEIN
539	E481	CA411187	614	151	2.00E-36	PROTEIN KINASE/cell division control protein 147 2e-35
540	E485	CA411191	548	141	2.00E-33	RING FINGER PROTEIN
541	E492	CA411198	632	190	2.00E-49	INITIATION FACTOR 5A-4
542	E498	CA411204	712	190	2.00E-48	INITIATION FACTOR 5A-4
543	E502	CA411208	598	80	5.00E-15	TRANSCRIPTION INITIATION PROTEIN
544	E511	CA411216	730	211	1.00E-54	CASEIN KINASE II ALPHA SUBUNIT
545	E514	CA411219	656	77	2.00E-14	CALMODULIN-BINDING PROTEIN
546	E520	CA411225	707	88	2.00E-17	RING-H2 FINGER PROTEIN
547	E528	CA411233	702	59	6.00E-09	PUTATIVE MAP KINASE
548	E532	CA411237	752	75	7.00E-14	EPSIN-LIKE PROTEIN
549	E534	CA411239	767	218	1.00E-56	GTP-BINDING PROTEIN
550	E541	CA411246	604	203	2.00E-52	SAR DNA-BINDING PROTEIN
551	E552	CA411257	585	226	4.00E-59	SHAGGY-RELATED PROTEIN KINASE (EC 2.7.1.-)
552	E560	CA411265	708	236	3.00E-62	EUKARYOTIC INITIATION FACTOR 4A-15
553	E561	CA411266	578	97	3.00E-20	T27E13 PROT/P LEUCINE-RICH REPEAT PROTEIN
554	E564	CA411269	709	221	1.00E-57	AAD25141 PROT/phosphate-induced protein PHI-1 87 2e-27
555	E577	CA411281	477	133	4.00E-31	RAC G-PROTEIN
556	E583	CA411287	676	93	6.00E-19	MYB-RELATED TRANSCRIPTION ACTIVATOR-LIKE
557	E616	CA411319	704	191	1.00E-49	SERINE PROTEASE
558	E626	CA411328	745	254	3.00E-67	EUKARYOTIC INITIATION FACTOR 6
559	E627	CA411329	715	56	4.00E-08	C2H2-TYPE ZINC FINGER PROTEIN
560	E643	CA411345	667	139	5.00E-33	TRANSCRIPTION FACTOR BTF3
561	E647	CA411349	750	110	2.00E-24	DNA BINDING PROTEIN
562	E650	CA411352	687	66	9.00E-11	RECEPTOR KINASE

	A	B	C	D	E	F
6	**L#**	**GenBank accession #**	**bp**	**score**	**E-value**	**annotation**
563	E656	CA411358	726	266	2.00E-71	SERNE/THREONINE PROTEIN KINASE
564	E673	CA411375	685	130	2.00E-30	SERINE/THREONINE PROTEIN KINASE
565	E683	CA411385	700	157	2.00E-38	INITIATION FACTOR A
566	E701	CA411402	688	134	2.00E-31	SIGNAL RECOGNITION PARTICLE 9 KDA PROTEIN
567	E706	CA411407	685	97	3.00E-20	TRANSCRIPTION FACTOR EREBP
568	E712	CA411413	673	217	1.00E-36	CALNEXIN
569	E725	CA411426	680	101	2.00E-21	SERINE/THREONINE PROTEIN PHOSPHATASE
570	E742	CA411443	738	229	4.00E-60	LIM-DOMAIN SF3 PROTEIN
571	E745	CA411445	737	132	5.00E-31	ZINC FINGER PROTEIN
572	E765	CA411464	716	113	4.00E-25	CALCINEURIN B-LIKE PROTEIN
573	E781	CA411480	694	238	9.00E-63	PROT. KINASE/ CELL DIVISION CONTROL PROTEIN 2
574	E785	CA411484	727	76	6.00E-14	GAI PROTEIN
575	E816	CA411514	708	150	2.00E-36	SIMILARITY TO GTP-BINDING REGULATORY PROTEIN
576	E831	CA411529	600	118	9.00E-27	GLYCINE-RICH RNA-BINDING PROTEIN
577						
578	STRESS, DEFENSE:category 12					
579	E008	CA410738	488	167	3.00-41	HEAT SHOCK PROTEIN
580	E019	CA410749	379	98	2.00E-20	PEROXIDASE 1B (EC 1.11.1.7)
581	E029	CA410759	514	148	2.00E-35	INDUCED UPON WOUNDING STRESS
582	E032	CA410762	515	151	1.00E-36	INDUCED UPON WOUNDING STRESS
583	E040	CA410770	519	192	7.00E-49	THAUMATIN
584	E058	CA410787	504	148	1.00E-35	PEROXIDASE (EC 1.11.1.7)
585	E066	CA410795	515	94	4.00E-19	PATHOGENESIS-RELATED PROTEIN
586	E076	CA410803	536	89	8.00E-18	COLD ACLIMATION RESPONSIVE PROTEIN
587	E082	CA410809	573	94	4.00E-19	TUMOR-RELATED PROTEIN
588	E098	CA410824	485	151	1.00E-36	PR-10 PROTEIN/root hair protein RH2 116 4e-26
589	E102	CA410827	468	108	2.00E-23	PR-10 PROTEIN/stress-induced gene 83/ 6e-16
590	E115	CA410840	386	121	3.00E-27	GLUTATHIONE S-TRANSFERASE GST (EC 2.5.1.18)
591	E124	CA410849	455	155	2.00E-37	PR-10 PROTEIN
592	E128	CA410853	486	149	8.00E-36	PR-10 PROTEIN
593	E143	CA410868	431	103	6.00E-22	PEROXIDASE PRECURSOR
594	E177	CA410901	460	82	1.00E-15	PEROXIDASE ATP17A-LIKE PROTEIN
595	E215	CA410934	452	145	1.00E-34	PR-10 PROTEIN
596	E218	CA410937	437	125	1.00E-28	PEROXIDASE ATP17A-LIKE PROTEIN
597	E229	CA410948	431	81	4.00E-15	PEROXIDASE PRECURSOR
598	E271	CA410989	416	132	1.00E-30	PEROXIDASE ATP17A-LIKE PROTEIN
599	E277	CA410995	418	94	3.00E-23	PEROXIDASE ATP17A-LIKE PROTEIN
600	E294	CA411010	440	140	3.00E-33	THAUMATIN
601	E296	CA526347	411	122	1.00E-27	PR-10 PROTEIN
602	E300	CA411014	435	141	2.00E-33	PR-10 PROTEIN
603	E301	CA411015	457	146	5.00E-35	PATHOGENESIS-RELATED PROTEIN
604	E312	CA411025	406	100	4.00E-21	GERMIN LIKE PROTEIN
605	E346	CA411058	445	139	6.00E-36	PR-10 PROTEIN
606	E365	CA411076	488	140	3.00E-33	DIRIGENT PROTEIN/ disease resistance protein 129 8e-30
607	E380	CA411089	473	151	2.00E-36	PEROXIDASE PRECURSOR
608	E391	CA526352	700	208	2.00E-56	INDUCED UPON WOUNDING STRESS
609	E406	CA411113	746	234	1.00E-61	PEROXIDASE PRECURSOR
610	E410	CA411117	745	247	1.00E-65	HIGH MOLECULAR WEIGHT HEAT SHOCK PROTEIN
611	E417	CA411124	756	123	3.00E-28	TUMOR RELATED PROTEIN
612	E419	CA411126	778	224	2.00E-58	PEROXIDASE PRECURSOR
613	E427	CA411134	709	225	5.00E-59	PEROXIDASE PRECURSOR

	A	B	C	D	E	F
6	**L#**	**GenBank accession #**	**bp**	**score**	**E-value**	**annotation**
614	E432	CA411139	765	279	1.00E-74	THAUMATIN
615	E455	CA411162	762	223	4.00E-58	PEROXIDASE PRECURSOR
616	E465	CA411171	532	64	4.00E-10	METALLOTHIONEIN LIKE PROTEIN
617	E490	CA411196	519	102	7.00E-22	B12D PROTEIN (Ipomea batata)
618	E496	CA411202	594	64	4.00E-10	METALLOTHIONEIN LIKE PROTEIN
619	E517	CA411222	582	115	1.00E-25	BASIC CHITANASE
620	E525	CA411230	712	155	1.00E-37	F16B3 PROT/ similarity to salt-inducible prot. 53 7e-07
621	E540	CA411245	609	123	3.00E-28	PATHOGENESIS-RELATED PROTEIN
622	E543	CA411248	602	131	1.00E-30	LIGHT INDUCIBLE PROTEIN ATLS1
623	E565	CA411270	685	170	3.00E-44	PR-10 .2D PROTEIN
624	E570	CA411275	615	54	4.00E-07	DEHYDRATATION-INDUCED ERD15 PPROTEIN
625	E573	CA411277	682	216	2.00E-56	PEROXIDASE PRECURSOR
626	E587	CA411291	643	187	2.00E-47	PR-10 .2D PROTEIN
627	E597	CA411301	700	127	2.00E-59	GLUTATHIONE S-TRANSFERASE
628	E606	CA411309	398	79	2.00E-12	B12D PROTEIN
629	E607	CA411310	531	74	4.00E-13	METALLOTHIONEIN-LIKE PROTEIN
630	E620	CA411323	535	99	1.00E-37	THAUMATIN LIKE PROTEIN
631	E622	CA411325	590	103	3.00E-22	B12D PROTEIN
632	E637	CA411339	683	219	3.00E-57	PEROXIDASE
633	E639	CA411341	726	184	8.00E-47	PR-10 .2D PROTEIN
634	E642	CA411344	700	169	8.00E-42	PR-10 .2D PROTEIN
635	E644	CA411346	693	157	1.00E-38	STRESS-INDUCED PROTEIN
636	E658	CA411360	750	192	4.00E-49	PR-10 PROTEIN
637	E674	CA411376	729	185	6.00E-47	PR-10 2D PROTEIN
638	E676	CA411378	531	99	8.00E-21	STRESS-RESPONSIVE PROTEIN
639	E691	CA411392	711	90	2.00E-18	ELICITOR INDUCIBLE PROTEIN
640	E708	CA411409	694	260	2.00E-69	THAUMATIN LIKE PROTEIN
641	E723	CA411424	524	160	4.00E-39	PR-10 2D PROTEIN
642	E726	CA411427	706	170	2.00E-42	BERBERINE BRIDGE ENZYME
643	E730	CA411431	703	243	2.00E-64	HEAT SHOCK COGNATE PROTEIN
644	E76	CA411460	701	185	6.00E-47	PR-10 2D PROTEIN
645	E772	CA411471	692	133	2.00E-31	DIRIGENT PROTEIN PUTATIVE
646	E782	CA411481	723	184	1.00E-46	MONODEHYDROASCORBATE REDUCTASE
647	E791	CA411490	700	213	2.00E-55	PEROXIDASE
648	E795	CA411494	503	103	4.00E-22	B12D PROTEIN
649	E808	CA411506	721	207	1.00E-53	GLUTATHIONE S-TRANSFERASE 2
650	E814	CA411512	761	124	3.00E-28	PEROXIDASE 1 PRECURSOR
651	E821	CA411519	727	192	5.00E-49	PR-10 2D PROTEIN
652	E825	CA411523	701	187	2.00E-47	GLUTATHIONE PEROXIDASE
653	E838	CA411536	379	50	6.00E-06	METALLOTIONEIN
654	E839	CA411537	426	97	5.00E-20	STRESS RESPONSIVE PROTEIN HOMOLOG
655	E844	CA411542	709	278	7.00E-75	HEAT SHOCH PROTEIN 90
656	E851	CA411549	703	187	1.00E-47	PR-10 2D PROTEIN
657	E852	CA411550	714	275	6.00E-74	THAUMATIN-LIKE PROTEIN
658	E853	CA411551	718	185	6.00E-47	PR-10 2D PROTEIN
659						
660	IV UNKNOWN FUNCTION					
661	FUNCTION UNKNOWN IN PLANTS: category 13					
662	E045	CA410775	494	171	2.00E-42	TRANSLATIONALLY CONTROLLED TUMOR PROTEIN
663	E067	CA410796	517	60	6.00E-09	MYOSIN HEAVY CHAIN-LIKE
664	E072	CA410800	607	81	3.00E-15	SIMILAR TO DROSOPHILA COUCH POTATO PROTEIN

	A	B	C	D	E	F
6	**L#**	**GenBank accession #**	**bp**	**score**	**E-value**	**annotation**
665	E216	CA410935	437	129	6.00E-30	SIMILARITY TO HEPARANASE
666	E334	CA411046	507	171	1.00E-42	HYP. PROT./candidate tumor suppressor 124 2e-28
667	E586	CA411290	615	189	3.00E-48	TRANSLATIONALLY CONTROLLED TUMOR PROTEIN
668	E728	CA411429	729	134	1.00E-31	SURFEIT 1
669	E729	CA411430	717	134	1.00E-31	SURFEIT 1
670	E754	CA411454	677	93	3.00E-21	VIRf-INTERACTING PROTEIN FIP1 (A. t.)
671	E777	CA411476	709	210	2.00E-54	TRANSLATIONALLY CONTROLLED TUMOR PROTEIN H
672	E812	CA411510	705	72	1.00E-12	BRAIN SECRETORY PROTEIN HSEC10P
673						
674	UNKNOWN FUNCTION: 14					
675	E015	CA410745	515	80	4.00E-15	GENOMIC DNA, CHROMOSOME5, TAC CLONE
676	E016	CA410746	505	65	6.00E-11	HYP. PROTEIN
677	E021	CA410751	532	149	6.00E-36	HYP 30.5 KDA .PROTEIN/ S 24 KDA SEED MADURATION
678	E024	CA410754	527	117	2.00E-26	PRE-MRNA SPLICING FACTOR SF2
679	E028	CA410758	492	66	1.00E-10	HYP. 45.5 KDA PROTEIN (A.t)
680	E034	CA410764	513	129	6.00E-30	GEN AAF69699 AC016041 (A.t.)
681	E041	CA410771	518	65	2.00E-10	29 PROTEIN (A.t.)
682	E048	CA410778	502	79	1.00E-14	HYP. 82.1 KDA PROTEIN (A.t.)
683	E052	CA410782	509	79	1.00E-14	HYP 82.1 KDA .PROTEIN/
684	E064	CA410793	515	79	1.00E-14	HYP. 36.8 KDA PROTEIN (A.t)
685	E074	CA526336	501	87	4.00E-17	GENOMIC DNA, CHROMOSOME 5, P1 CLONE
686	E089	CA410816	583	60	5.00E-09	HYP. 65 KDA PROTEIN
687	E097	CA410823	517	114	2.00E-25	7 PROTEIN (A.t.)
688	E103	CA410828	539	53	7.00E-07	T5A14.10 PROTEIN
689	E104	CA410829	492	66	9.00E-11	HYP. PROTEIN
690	E117	CA410842	474	59	9.00E-09	GENOMIC DNA, CHROMOSOME 3 P1 CLONE
691	E118	CA410843	545	82	3.00E-17	AAD27719.GENE (A.t.)
692	E126	CA410851	477	105	1.00E-22	UNNAMED PROTEIN PRODUCT (Helianthus annus)
693	E127	CA410852	310	78	4.00E-14	HYP. PROTEIN
694	E129	CA410854	528	102	9.00E-22	HYP. 34.4 KDA PROTEIN
695	E145	CA410870	456	79	2.00E-14	MTN5 GENE PRECURSOR
696	E146	CA410871	490	137	2.00E-32	HYP. PROTEIN
697	E148	CA410873	451	151	1.00E-36	HYP. PROTEIN
698	E153	CA410878	490	84	3.00E-16	HYP. 39.2 KDA PROTEIN
699	E157	CA410882	491	93	6.00E-19	HYP. 30.6 KDA PROTEIN
700	E158	CA410883	470	99	1.00E-20	AAF32311 GENE (A.t.)
701	E161	CA410886	479	102	1.00E-21	HYP. 32.8 KDA PROTEIN
702	E163	CA410888	428	120	4.00E-27	EPSILON1-COP
703	E168	CA410893	502	172	7.00E-43	HYP. 23.7 KDA PROTEIN
704	E181	CA410905	526	84	2.00E-16	HYP. PROTEIN T18A20
705	E183	CA410907	452	69	2.00E-11	CODED FOR BY A. thaliana CDNA T22029
706	E191	CA526342	475	110	3.00E-24	T9I22.1 PROTEIN
707	E202	CA410922	440	178	1.00E-44	F5011.10 PROTEIN
708	E212	CA410931	476	106	5.00E-23	HYP. 20.5 KDA PROTEIN
709	E222	CA410941	442	153	4.00E-37	CSF-3 PROTEIN
710	E243	CA410961	411	80	7.00E-15	SYMILARITY TO UNKNOWN PROTEIN (A. t.)
711	E244	CA410962	425	103	4.00E-22	HYP. PROTEIN
712	E245	CA410963	428	91	3.00E-18	HYP. 22.7 KDA PROTEIN
713	E250	CA410968	439	170	4.00E-42	F25I18.4 PROTEIN (A. t.)
714	E251	CA410969	566	64	4.00E-10	F20H23.20 PROTEIN (A.t.)
715	E269	CA410987	437	129	7.00E-30	HYP. 49.9 KDA PROTEIN

	A	B	C	D	E	F
6	**L#**	**GenBank accession #**	**bp**	**score**	**E-value**	**annotation**
716	E270	CA410988	478	129	7.00E-30	AT2G25280 PROTEIN
717	E273	CA410991	422	47	7.00E-05	F6I1.13 PROTEIN
718	E286	CA411002	441	84	3.00E-16	HYP. PROTEIN
719	E299	CA411013	422	124	2.00E-28	HYP. 19.9 KDA PROTEIN
720	E305	CA411019	449	62	1.00E-09	GENOMIC DNA CHROMOSOME 5, TAC CLONE
721	E321	CA411033	465	100	3.00E-21	UNKNOWN PROTEIN
722	E322	CA411034	382	79	8.00E-18	F1E22.17 PROTEIN (A.t)
723	E329	CA411041	449	150	3.00E-36	T26B15 PROT/ probable carboxymethylenebutenollidase
724	E335	CA411047	419	97	4.00E-08	HYP. 44.2 KDA PROTEIN
725	E337	CA411049	492	132	7.00E-31	F21F23 PROTEIN
726	E356	CA411068	462	112	1.00E-24	HYP. PRTEIN
727	E367	CA411078	353	49	2.00E-05	HYP. 6.1 KDA PROTEIN
728	E383	CA411092	457	92	2.00E-18	RDA23 PROTEIN
729	E392	CA411099	729	178	7.00E-45	SIMILARITY TO UNKNOW PROTEIN
730	E409	CA411116	697	235	4.00E-62	F20B24 PROT/ ATP citrate lyase 109 5e-24
731	E411	CA411118	594	48	2.00E-05	GENOMIC DNA, CHROMOSOME 3 P1 CLONE
732	E415	CA411122	766	116	5.00E-26	F17L21 PROTEIN (A.t.)
733	E421	CA411128	773	97	6.00E-20	HYP. 31.O KDA PROTEIN
734	E422	CA411129	632	185	6.00-47	
735	E430	CA411137	658	80	4.00E-15	GENOMIC DNA, CHROMOSOME 3 P1 CLONE
736	E437	CA411144	609	127	2.00E-29	SIN3 ASSOCIATED POLYPEPTIDE
737	E443	CA411150	727	188	9.00E-48	SIMILARITY TO UNKNOW PROTEIN
738	E446	CA411153	634	145	9.00E-35	F5D14.18 PROTEIN (contain a PPR repeat domain)
739	E457	CA411164	464	82	2.00E-15	AT2G220490 PROTEIN
740	E458	CA411165	415	119	2.00E-26	HYP. PROTEIN (Oriza sativa)
741	E460	CA411167	758	59	6.00E-09	GENOMIC DNA, CHROMOSOME 5, BAC CLONE
742	E463	CA411170	662	105	3.00E-23	GH1 PROTEIN
743	E474	CA411180	729	96	6.00E-20	CG12128 PROTEIN
744	E479	CA411185	707	91	1.00E-18	AAD30228 PROTEIN
745	E484	CA411190	587	67	6.00E-11	GENOMIC DNA CHROMOSOME 5, P1 CLONE
746	E501	CA411207	656	161	2.00E-39	HYP. 26.2 KDA PROTEIN
747	E507	CA411212	503	79	1.00E-14	HYP. 7.3 KDA PROTEIN
748	E509	CA411214	723	147	1.00E-35	HYP. 62.5 KDA PROTEIN
749	E521	CA411226	736	156	2.00E-38	AAFE4232 PROTEIN
750	E538	CA411243	396	66	1.00E-16	F10A16 PROTEIN
751	E544	CA411249	570	88	2.00E-17	T12H1 PROTEIN
752	E546	CA411251	721	224	1.00E-58	F14P13 PROTEIN
753	E551	CA411256	526	98	3.00E-20	T12C22
754	E559	CA411264	721	125	6.00E-29	HYP. 71.4 KDA PROTEIN
755	E563	CA411268	726	192	6.00E-49	HYP. PROTEIN
756	E567	CA411272	727	185	7.00E-47	ESTS AU097575
757	E575	CA411279	647	70	3.00E-12	F411.12 PROTEIN
758	E580	CA411284	642	80	3.00E-15	HYP. 76.2 KDA PROTEIN
759	E589	CA411293	693	152	5.00E-37	HYP. 20.8 KDA PROTEIN
760	E593	CA411297	717	153	3.00E-37	AT2G15290 HYP. PROTEIN
761	E613	CA411316	526	62	4.00E-10	AT2G30270 HYP. PROTEIN
762	E614	CA411317	714	72	8.00E-13	HYP.21.5 KDA PROTEIN
763	E615	CA411318	745	206	2.00E-53	HYP. 29.4 KDA PROTEIN
764	E619	CA411322	736	88	9.00E-18	AT2G15590 PROTEIN
765	E632	CA411334	712	185	5.OOE-47	REIR1A PROTEIN
766	E634	CA411336	708	124	2.00E-28	GENOMIC DNA CHROMOSOME 3, P1 CLONE

	A	B	C	D	E	F
6	**L#**	**GenBank accession #**	**bp**	**score**	**E-value**	**annotation**
767	E645	CA411347	576	90	5.00E-18	CAB89373 PROTEIN
768	E653	CA411355	214	61	4.00E-09	ORF 107A A. t.
769	E661	CA411363	426	54	4.00E-07	AT2G33470 PROTEIN
770	E663	CA411365	582	171	2.00E-42	AT2G33470 PROTEIN
771	E664	CA411366	456	50	5.00E-06	HYP. 33.1 KDA PROTEIN
772	E679	CA411381	707	97	2.00E-20	AT2G15910 PROTEIN
773	E682	CA411384	678	51	2.00E-06	AAF81354 PROTEIN
774	E692	CA411393	630	97	3.00E-20	HYP. PROTEIN
775	E715	CA411416	722	67	2.00E-11	GENOMIC DNA CHROMOSOME 5, P1 CLONE
776	E722	CA411423	723	64	3.00E-10	AAD25786 PROTEIN
777	E734	CA411435	643	107	2.00E-23	HYP. 17.7 PROTEIN (Picea mariana)
778	E737	CA411438	639	81	2.00E-15	HYP. 313.3 KDA PROTEIN (A.t.)
779	E739	CA411440	641	83	7.00E-17	T15F16 PROTEIN
780	E751	CA411451	742	231	6.00E-61	GENOMIC DNA CHROMOSOME 5, P1 CLONE
781	E756	CA411456	731	79	5.00E-15	SIMILARITY TO UNKNOWN PROTEIN
782	E758	CA411458	711	53	4.00E-07	GENOMIC DNA CHROMOSOME 5, P1 CLONE
783	E767	CA411466	729	149	6.00E-36	F14D16 PROTEIN
784	E774	CA411473	726	204	9.00E-53	HYP. 28.8 KDA PROTEIN
785	E793	CA411492	692	110	3.00E-24	SIMILARITY TO UNKNOWN PROTEIN
786	E794	CA411493	700	80	2.00E-15	HYP. 15.6 KDA PROTEIN
787	E800	CA411499	727	49	6.00E-06	HYP. 70.7 KDA PROTEIN (Schizosaccharomyces pombe)
788	E803	CA411502	682	185	5.00E-47	PROTEIN L1R18B
789	E811	CA411509	713	108	7.00E-24	CAB70981 PROTEIN
790	E826	CA411524	708	141	1.00E-33	AT2G42620 PROTEIN
791	E837	CA411535	709	72	1.00E-12	AT2G17710 PROTEIN
792	E846	CA411544	549	97	4.00E-20	HYP. 8.7 KDA PROT.
793	E849	CA411547	735	145	7.00E-35	SIMILAR TO PHZF, CATALYZING THE HYDROXYLATION
794						
795	NO SIGNIFICANT HOMOLOGY: category 15					
796	E006	CA410736	267	30		NO SIGNIFICANT MATCH
797	E017	CA410747	501	32		NO SIGNIFICANT MATCH
798	E031	CA410761	456	46		NO SIGNIFICANT MATCH
799	E063	CA410792	453	32		NO SIGNIFICANT MATCH
800	E077	CA410804	564	35		NO SIGNIFICANT MATCH
801	E086	CA410813	441	44		NO SIGNIFICANT MATCH
802	E114	CA410839	478	37		NO SIGNIFICANT MATCH
803	E132	CA410857	286	31		NO SIGNIFICANT MATCH
804	E141	CA410866	306	32		NO SIGNIFICANT MATCH
805	E156	CA410881	447	32		NO SIGNIFICANT MATCH
806	E160	CA410885	437	33		NO SIGNIFICANT MATCH
807	E165	CA410890	475	31		NO SIGNIFICANT MATCH
808	E174	CA410898	238	35		NO SIGNIFICANT MATCH
809	E178	CA410902	482	41		NO SIGNIFICANT MATCH
810	E211	CA410930	401	157		NO SIGNIFICANT MATCH
811	E214	CA410933	291	33		NO SIGNIFICANT MATCH
812	E217	CA410936	447	45		NO SIGNIFICANT MATCH
813	E223	CA410942	424	37		NO SIGNIFICANT MATCH
814	E234	CA410953	477	335		NO SIGNIFICANT MATCH
815	E259	CA410977	357	30		NO SIGNIFICANT MATCH
816	E268	CA410986	430	32		NO SIGNIFICANT MATCH
817	E310	CA411023	489	45		NO SIGNIFICANT MATCH

	A	B	C	D	E	F
6	**L#**	**GenBank accession #**	**bp**	**score**	**E-value**	**annotation**
818	E324	CA411036	460	31		NO SIGNIFICANT MATCH
819	E326	CA411038	382	45		NO SIGNIFICANT MATCH
820	E333	CA411045	503	35		NO SIGNIFICANT MATCH
821	E336	CA411048	463	43		NO SIGNIFICANT MATCH
822	E347	CA411059	437	35		NO SIGNIFICANT MATCH
823	E351	CA411063	427	39		NO SIGNIFICANT MATCH
824	E353	CA411065	453	31		NO SIGNIFICANT MATCH
825	E358	CA411070	427	30		NO SIGNIFICANT MATCH
826	E374	CA411084	378	31		NO SIGNIFICANT MATCH
827	E385	CA411094	312	35		NO SIGNIFICANT MATCH
828	E387	CA411096	396	36		NO SIGNIFICANT MATCH
829	E390	CA411098	593	31		NO SIGNIFICANT MATCH
830	E412	CA411119	412	34		NO SIGNIFICANT MATCH
831	E424	CA411131	557	41		NO SIGNIFICANT MATCH
832	E435	CA411142	732	30		NO SIGNIFICANT MATCH
833	E467	CA411173	380	30		NO SIGNIFICANT MATCH
834	E468	CA411174	571	33		NO SIGNIFICANT MATCH
835	E483	CA411189	729	31		NO SIGNIFICANT MATCH
836	E493	CA411199	216	32		NO SIGNIFICANT MATCH
837	E533	CA411238	537	26		NO SIGNIFICANT MATCH
838	E542	CA411247	429	31		NO SIGNIFICANT MATCH
839	E558	CA411263	454	40		NO SIGNIFICANT MATCH
840	E584	CA411288	700	29		NO SIGNIFICANT MATCH
841	E610	CA411313	421	36		NO SIGNIFICANT MATCH
842	E624	CA526354	583	44		NO SIGNIFICANT MATCH
843	E665	CA411367	279	38		NO SIGNIFICANT MATCH
844	E667	CA411369	537	30		NO SIGNIFICANT MATCH
845	E700	CA411401	684	45		NO SIGNIFICANT MATCH
846	E711	CA411412	737	41		NO SIGNIFICANT MATCH
847	E714	CA411415	714	33		NO SIGNIFICANT MATCH
848	E719	CA411420	621	29		NO SIGNIFICANT MATCH
849	E721	CA411422	375	31		NO SIGNIFICANT MATCH
850	E738	CA411439	416	33		NO SIGNIFICANT MATCH
851	E748	CA411448	533	45		NO SIGNIFICANT MATCH
852	E753	CA411453	715	38		NO SIGNIFICANT MATCH
853	E770	CA411469	298	30		NO SIGNIFICANT MATCH
854	E779	CA411478	720	42		NO SIGNIFICANT MATCH
855	E789	CA411488	398	31		NO SIGNIFICANT MATCH
856	E802	CA411501	644	30		NO SIGNIFICANT MATCH
857	E824	CA411522	714	34		NO SIGNIFICANT MATCH
858	E840	CA411538	718	30		NO SIGNIFICANT MATCH
859	E842	CA411540	711	35		NO SIGNIFICANT MATCH
860						
861	NO HOMOLOGY FOUND: category 16					
862	E020	CA410750	357			NO HITS FOUND
863	E106	CA410831	479			NO HITS FOUND
864	E137	CA410862	481			NO HITS FOUND
865	E150	CA410875	515			NO HITS FOUND
866	E151	CA410876	475			NO HITS FOUND
867	E169	CA410894	194			NO HITS FOUND
868	E233	CA410952	155			NO HITS FOUND

	A	B	C	D	E	F
6	**L#**	**GenBank accession #**	**bp**	**score**	**E-value**	**annotation**
869	E240	CA410958	479			NO HITS FOUND
870	E256	CA410974	456			NO HITS FOUND
871	E290	CA411006	438			NO HITS FOUND
872	E297	CA411012	413			NO HITS FOUND
873	E366	CA411077	274			NO HITS FOUND
874	E386	CA411095	304			NO HITS FOUND
875	E459	CA411166	377			NO HITS FOUND
876	E545	CA411250	643			NO HITS FOUND
877	E553	CA411258	467			NO HITS FOUND
878	E556	CA411261	467			NO HITS FOUND
879	E568	CA411273	729			NO HITS FOUND
880	E569	CA411274	163			NO HITS FOUND
881	E698	CA411399	687			NO HITS FOUND
882	E718	CA411419	284			NO HITS FOUND
883	E735	CA411436	733			NO HITS FOUND
884	E809	CA411507	684			NO HITS FOUND