Nr.	**Fragment**	**Länge [bp]**	**Beschreibung**	**Organismus**	**AGI Code/ Accession#**	**BlastX**	**GO-Biologischer Prozess**
2	PC1-2	260	putative RNA helicase (see 473-2)	Oryza sativa	AAO72375	14/33	-
3	PC1-3	262	ATP binding / ATP-dependent helicase	Arabidopsis thaliana	At3g18600	31/78	-
4	PC2-1	155	polyprotein	Potato virus Y	ABC70481	14/33	-
5	PC2-2	156	polyprotein	Potato virus Y	ABC70481	14/33	-
9	PC3H-2	143	peroxidase precursor (see 113-2)	Petroselinum crispum	AAA98491	19/25	response to oxidative stress
14	PC4-3	116	structural constituent of ribosome (see 182-4)	Arabidopsis thaliana	At1g15250	30/36	protein biosynthesis, ribosome biogenesis
15	PC5-1	81	putative senescence-associated protein	Pisum sativum	BAB33421	26/26	-
16	PC5-2	81	putative senescence-associated protein	Pisum sativum	BAB33421	26/26	-
19	PC6	394	unknown protein	Arabidopsis thaliana	At3g01740	26/70	biological_process unknown
20	PC8	139	unknown protein (see 10)	Arabidopsis thaliana	At2g39530	16/29	biological_process unknown
21	PC9-1	123	HSP70; ATP binding (see 21-1)	Arabidopsis thaliana	At3g12580	39/40	protein folding; response to heat; response to virus
22	PC9-2	123	HSP70; ATP binding (see 21-1)	Arabidopsis thaliana	At3g12580	39/40	protein folding; response to heat; response to virus
23	PC9-3	123	HSP70; ATP binding (see 21-1)	Arabidopsis thaliana	At3g12580	39/40	protein folding; response to heat; response to virus
24	PC9-4	123	HSP70; ATP binding (see 21-1)	Arabidopsis thaliana	At3g12580	39/40	protein folding; response to heat; response to virus
25	PC10-1	141	integral membrane protein (see 25)	Arabidopsis thaliana	At2g39530	17/31	biological_process unknown
26	PC10-2	141	integral membrane protein (see 25)	Arabidopsis thaliana	At2g39530	17/31	biological_process unknown
27	PC10-4	141	integral membrane protein (see 25)	Arabidopsis thaliana	At2g39530	17/31	biological_process unknown
28	PC10-3	123	HSP70; ATP binding (see 21-1)	Arabidopsis thaliana	At3g12580	39/40	protein folding; response to heat; response to virus
33	PC12	102	transferase, transferring glycosyl groups (see 43-3)	Arabidopsis thaliana	At1g05170	18/20	protein amino acid glycosylation
42	PC15-1	67	ADL1D; GTP binding / GTPase	Arabidopsis thaliana	At2g44590	19/21	biological process unknown
43	PC15-2	76	unknown protein	Arabidopsis thaliana	At3g55840	12/22	biological_process unknown
44	PC15-3	76	unknown protein	Arabidopsis thaliana	At3g55840	14/21	biological_process unknown
50	PC17-3	118	catalytic/ protein phosphatase type 2C	Arabidopsis thaliana	At1g79630	14/18	N-terminal protein myristoylation
52	PC20-3	141	integral membrane protein (see 10)	Arabidopsis thaliana	At2g39530	17/31	biological process unknown
53	PC20-4	177	integral membrane protein (see 8)	Arabidopsis thaliana	At2g39530	18/32	biological process unknown
54	PC21-1	123	HSP70; ATP binding (see 9)	Arabidopsis thaliana	At3g12580	39/40	protein folding; response to heat; response to virus
55	PC21-2	123	HSP70; ATP binding (see 9)	Arabidopsis thaliana	At3g12580	39/40	protein folding; response to heat; response to virus
56	PC21-3	123	HSP70; ATP binding (see 9)	Arabidopsis thaliana	At3g12580	39/40	protein folding; response to heat; response to virus
57	PC21-4	123	HSP70; ATP binding (see 34)	Arabidopsis thaliana	At3g12580	39/40	protein folding; response to heat; response to virus
59	PC23-2	253	unknown protein	Arabidopsis thaliana	At2g31410	56/79	-
60	PC23-3	253	unknown protein	Arabidopsis thaliana	At2g31410	56/79	-
62	PC24-1	156	down syndrome cell adhesion molecule	Aedes aegypti	EAT37388	15/41	-
63	PC24-2	156	down syndrome cell adhesion molecule	Aedes aegypti	EAT37388	15/41	-
65	PC24-4	158	structural constituent of ribosome	Arabidopsis thaliana	At5g20290	44/51	protein biosynthesis ; ribosome biogenesis
66	PC25-1	141	integral membrane protein (see 20)	Arabidopsis thaliana	At2g39530	17/31	biological process unknown
67	PC25-2	141	integral membrane protein (see 20)	Arabidopsis thaliana	At2g39530	17/31	biological process unknown
68	PC25-3	141	integral membrane protein (see 20)	Arabidopsis thaliana	At2g39530	17/31	biological process unknown
69	PC25-4	141	integral membrane protein (see 20)	Arabidopsis thaliana	At2g39530	17/31	biological process unknown
77	PC27-4	123	transferase, transferring glycosyl groups	Arabidopsis thaliana	At5g41460	32/40	biological process unknown
78	PC28-1	103	ATMRP5	Arabidopsis thaliana	At1g04120	31/34	transport
82	PC29-2	86	aspartic-type endopeptidase/ pepsin A	Arabidopsis thaliana	At3g51340	15/23	proteolysis
83	PC29-3	85	aspartic-type endopeptidase/ pepsin A	Arabidopsis thaliana	At3g51340	16/28	proteolysis
101	PC34	155	HSP70; ATP binding	Arabidopsis thaliana	At3g12580	18/19	protein folding; response to heat; response to virus
106	PC36-1	114	putative leucine-rich repeat transmembrane protein kinase	Arabidopsis thaliana	At1g14390	18/36	protein amino acid phosphorylation

107	PC36-4	114	putative leucine-rich repeat transmembrane protein kinase	Arabidopsis thaliana	At1g14390	18/36	protein amino acid phosphorylation
108	PC36-2	111	phosphoinositide 5-phosphatase	Arabidopsis thaliana	At3g43220	25/36	biological process unknown
109	PC36-3	111	nucleotide binding	Arabidopsis thaliana	At4g01860	18/35	biological process unknown
114	PC38-1	59	oxidoreductase/ zinc ion binding	Arabidopsis thaliana	At3g56460	16/19	-
133	PC43-3	101	transferase, transferring glycosyl groups (see 12)	Arabidopsis thaliana	At1g05170	28/31	protein amino acid glycosylation
136	PC44-2	120	unknown protein	Arabidopsis thaliana	At4g01400	20/36	biological process unknown
137	PC44-3	111	phosphoinositide 5-phosphatase (see 36-2)	Arabidopsis thaliana	At3g43220	25/36	biological process unknown
138	PC44-4	111	phosphoinositide 5-phosphatase (see 36-2)	Arabidopsis thaliana	At3g43220	25/36	biological process unknown
139	PC45-1	104	amino acid permease	Arabidopsis thaliana	At3g30390	26/34	amino acid transport
149	PC48-1	111	catalytic/ epoxide hydrolase/ hydrolase	Arabidopsis thaliana	At4g02340	21/36	aromatic compound metabolism
150	PC48-2	111	catalytic/ epoxide hydrolase/ hydrolase	Arabidopsis thaliana	At4g02340	21/36	aromatic compound metabolism
151	PC48-3	111	catalytic/ epoxide hydrolase/ hydrolase	Arabidopsis thaliana	At4g02340	21/36	aromatic compound metabolism
152	PC48-4	111	catalytic/ epoxide hydrolase/ hydrolase	Arabidopsis thaliana	At4g02340	21/36	aromatic compound metabolism
156	PC49-4	102	unknown protein	Arabidopsis thaliana	At3g54190	31/33	biological process unknown
177	PC55-1	196	pectinesterase	Arabidopsis thaliana	At2g47550	28/44	cell wall modification
178	PC55-2	155	ATP binding / casein kinase I	Arabidopsis thaliana	At5g44100	50/51	protein amino acid phosphorylation
179	PC55-3	155	ATP binding / casein kinase I	Arabidopsis thaliana	At5g44100	50/51	protein amino acid phosphorylation
180	PC55-4	196	pectinesterase	Arabidopsis thaliana	At2g47550	28/44	cell wall modification
184	PC56-3	179	oxidoreductase	Arabidopsis thaliana	At1g59960	24/51	-
185	PC57-1	137	iron ion binding / lipoxygenase	Arabidopsis thaliana	At1g72520	24/50	defense response, jasmonic acid biosynthesis
187	PC57-3	137	iron ion binding / lipoxygenase	Arabidopsis thaliana	At1g72520	24/50	defense response, jasmonic acid biosynthesis
188	PC57-4	137	iron ion binding / lipoxygenase	Arabidopsis thaliana	At1g72520	24/50	defense response, jasmonic acid biosynthesis
197	PC60-1	51	structural constituent of ribosome (see 95-4)	Arabidopsis thaliana	At1g67430	16/16	protein biosynthesis
198	PC60-2	51	structural constituent of ribosome (see 95-4)	Arabidopsis thaliana	At1g67430	16/16	protein biosynthesis
200	PC60-4	51	structural constituent of ribosome (see 95-4)	Arabidopsis thaliana	At1g67430	16/16	protein biosynthesis
216	PC64-4	250	similar to hydrocephalus-inducing protein	Rattus norvegicus	XP_226468	25/77	-
218	PC65-2	203	GTP cyclohydrolase I	Arabidopsis thaliana	At3g07270	20/23	biosynthesis
220	PC65-4	116	unknown protein O-linked GlcNAc transferase like protein	Arabidopsis thaliana	At3g04830	32/38	biological process unknown
230	PC68-2	94	protein serine/threonine kinase/ protein-tyrosine kinase	Arabidopsis thaliana	At2g17220	25/31	protein amino acid phosphorylation
231	PC68-3	94	protein serine/threonine kinase/ protein-tyrosine kinase	Arabidopsis thaliana	At2g17220	26/31	protein amino acid phosphorylation
232	PC68-4	94	protein serine/threonine kinase/ protein-tyrosine kinase	Arabidopsis thaliana	At2g17220	26/31	protein amino acid phosphorylation
233	PC69-1	106	similar to UPF2 regulator of nonsense transcripts homolog	Strongylocentrotus p.	XP_795243	14/25	-
234	PC69-2	179	putative gag-pol polyprotein	Solanum demissum	AAT38758	36/57	DNA integration
235	PC69-3	179	putative gag-pol polyprotein	Solanum demissum	AAT38758	36/57	DNA integration
237	PC70-1	148	ATP binding / microtubule motor	Arabidopsis thaliana	At3g49650	16/22	microtubule-based movement
238	PC70-2	190	calcium ion binding	Arabidopsis thaliana	At5g28900	42/46	biological process unknown
239	PC70-3	142	cysteine protease (see 131-4)	Vigna mungo	BAA92495	15/17	proteolysis
240	PC70-4	146	calcium ion binding	Arabidopsis thaliana	At5g61790	30/37	-
242	PC71-2	135	transferase/ transferase, transferring glycosyl groups	Arabidopsis thaliana	At4g02500	22/34	biological process unknown
244	PC71-4	116	transferase, transferring glycosyl groups	Arabidopsis thaliana	At1g53290	29/38	protein amino acid glycosylation
249	PC74-2	79	POP2 (POLLEN-PISTIL INCOMPATIBILITY 2)	Arabidopsis thaliana	At3g22200	19/22	biotin biosynthesis; pollen tube adhesion
255	PC76-1	140	endoxyloglucantransferase	Daucus carota	AF349963	23/27	carbohydrate metabolism, glucan metabolism
256	PC76-2	140	endoxyloglucantransferase	Daucus carota	AF349963	23/27	carbohydrate metabolism, glucan metabolism
258	PC76-4	140	endoxyloglucantransferase	Daucus carota	AF349963	23/27	carbohydrate metabolism, glucan metabolism
271	PC80-1	140	ubiquitin-protein ligase/ zinc ion binding	Arabidopsis thaliana	At1g61620	15/17	protein ubiquitination
273	PC80-3	140	ubiquitin-protein ligase/ zinc ion binding	Arabidopsis thaliana	At1g61620	15/17	protein ubiquitination

274	PC80-4	140	ubiquitin-protein ligase/ zinc ion binding	Arabidopsis thaliana	At1g61620	15/17	protein ubiquitination
291	PC85-1	55	RHM1 (see 86-3)	Arabidopsis thaliana	At1g78570	14/17	nucleotide-sugar metabolism
293	PC85-3	134	antiporter/ drug transporter (see pc87-1)	Arabidopsis thaliana	At5g10420	34/44	multidrug transport, ripening
294	PC85-4	109	serine rich protein	Arachis hypogaea	ABH09320	20/25	-
296	PC86-2	132	ATP binding / nucleoside-triphosphatase/ nucleotide binding	Arabidopsis thaliana	At1g67120	13/17	-
297	PC86-3	55	RHM1 (see 85-1)	Arabidopsis thaliana	At1g78570	14/17	nucleotide-sugar metabolism
298	PC86-4	174	oxidoreductase/ zinc ion binding (see 162-2)	Arabidopsis thaliana	At1g23740	42/56	-
299	PC87-1	136	antiporter/ drug transporter (see pc85-3)	Arabidopsis thaliana	At5g10420	23/30	multidrug transport, ripening
300	PC87-2	136	CIPK17 (CBL-interacting protein kinase 17)	Arabidopsis thaliana	At1g48260	14/19	protein amino acid phosphorylation; signal transduction
303	PC88-1-1	161	ATGLR2.8 (see 252-1)	Arabidopsis thaliana	At2g29110	25/52	calcium ion homeostasis; response to light stimulus
304	PC88-1-2	275	transferase	Arabidopsis thaliana	At5g07860	48/91	biological process unknown
307	PC88-2-1	343	unknown protein	Arabidopsis thaliana	At4g24310	38/61	biological process unknown
314	PC89-1-2	299	structural constituent of ribosome (see 100-2-1)	Arabidopsis thaliana	At1g74270	51/61	protein biosynthesis, ribosome biogenesis
316	PC89-3-1	178	ATEXPB2 (ARABIDOPSIS THALIANA EXPANSIN B2)	Arabidopsis thaliana	At1g65680	34/53	cell wall modification during multidimensional cell growth
318	PC90-1	159	ATGLR2.8 (see 88-1-1)	Arabidopsis thaliana	At2g29110	21/47	calcium ion homeostasis; response to light stimulus
319	PC90-2	206	peptidyl-prolyl cis-trans isomerase	Arabidopsis thaliana	At2g21130	47/56	protein folding
320	PC90-3	206	hydrolase (see 92-2)	Arabidopsis thaliana	At2g01670	42/68	biological process unknown
323	PC91-3	178	ATEXPB2 (ARABIDOPSIS THALIANA EXPANSIN B2)	Arabidopsis thaliana	At1g65680	35/56	cell wall modification during multidimensional cell growth
325	PC92-1	160	ATGLR2.8 (see 88-1-1)	Arabidopsis thaliana	At2g29110	21/47	calcium ion homeostasis; response to light stimulus
326	PC92-2	206	hydrolase (see 90-3)	Arabidopsis thaliana	At2g01670	42/68	biological process unknown
338	PC95-4	51	structural constituent of ribosome (see 60-1)	Arabidopsis thaliana	At1g67430	16/16	protein biosynthesis
339	PC96-1	48	transcription factor (see 545-1-4)	Arabidopsis thaliana	At2g40140	13/15	regulation of transcription
347	PC100-1-1	298	ATGCH	Arabidopsis thaliana	At5g64300	75/87	riboflavin biosynthesis
348	PC100-1-2	299	unknown protein	Arabidopsis thaliana	At2g20940	14/17	biological process unknown
349	PC100-1-3	289	structural constituent of ribosome	Arabidopsis thaliana	At2g47610	27/28	protein biosynthesis [pmid 11598216]
351	PC100-2-1	181	structural constituent of ribosome (see 89-1-2)	Arabidopsis thaliana	At1g74270	50/60	protein biosynthesis, ribosome biogenesis
352	PC100-2-2	181	structural constituent of ribosome (see 89-1-2)	Arabidopsis thaliana	At1g74270	50/60	protein biosynthesis, ribosome biogenesis
354	PC100-2-4	134	hypothetical protein PdenDRAFT_2922 (see 623-4)	Paracoccus denitrificans	ZP_00630617	27/34	-
355	PC102-1	181	structural constituent of ribosome (see 89-1-2)	Arabidopsis thaliana	At1g74270	50/60	protein biosynthesis, ribosome biogenesis
356	PC102-2	181	structural constituent of ribosome (see 89-1-2)	Arabidopsis thaliana	At1g74270	50/60	protein biosynthesis, ribosome biogenesis
357	PC102-3	181	structural constituent of ribosome (see 89-1-2)	Arabidopsis thaliana	At1g74270	50/60	protein biosynthesis, ribosome biogenesis
358	PC102-4	181	structural constituent of ribosome (see 89-1-2)	Arabidopsis thaliana	At1g74270	50/60	protein biosynthesis, ribosome biogenesis
363	PC107-1-1	295	trans-cinnamate 4 monooxygease (C4H)	Petroselinum crispum	Q43033	95/98	Lignin biosynthesis; Phenylpropanoid metabolism
364	PC107-1-2	165	cyclophilin (see 670-2-3)	Euphorbia esula	AAF65770	50/52	protein folding
365	PC107-1-3	287	NHL25 (NDR1/HIN1-LIKE 25)	Arabidopsis thaliana	At5g36970	35/62	defense response to pathogen
366	PC107-1-4	292	peroxidase (see 108-1-2)	Arabidopsis thaliana	At5g05340	49/62	response to oxidative stress
367	PC107-2-1	165	cyclophilin (see 107-1-2)	Euphorbia esula	AAF65770	50/52	protein folding
368	PC107-2-2	164	cyclophilin (see 107-1-2)	Euphorbia esula	AAF65770	50/52	protein folding
369	PC107-2-3	161	cyclophilin (see 107-1-2)	Euphorbia esula	AAF65770	50/52	protein folding
370	PC107-2-4	165	cyclophilin (see 107-1-2)	Euphorbia esula	AAF65770	50/52	protein folding
371	PC108-1-1	165	cyclophilin (see 107-1-2)	Euphorbia esula	AAF65770	50/52	protein folding
372	PC108-1-2	291	peroxidase (see 107-1-4)	Arabidopsis thaliana	At5g05340	49/79	response to oxidative stress
373	PC108-1-4	291	peroxidase (see 107-1-4)	Arabidopsis thaliana	At5g05340	48/79	response to oxidative stress
375	PC108-2-1	164	cyclophilin (see 107-1-2)	Euphorbia esula	AAF65770	50/52	protein folding
376	PC108-2-2	164	cyclophilin (see 107-1-2)	Euphorbia esula	AAF65770	50/52	protein folding
377	PC108-2-3	135	cyclophilin (see 107-1-2)	Euphorbia esula	AAF65770	50/52	protein folding

378	PC108-2-4	164	cyclophilin (see 107-1-2)	Euphorbia esula	AAF65770	50/52	protein folding
379	PC110-1	?	polyubiquitin	Zea mays	AAB21993	39/48	protein modification
380	PC110-2	297	peroxidase (see 107-1-4)	Arabidopsis thaliana	At5g05340	21/56	response to oxidative stress
381	PC110-3	275	conserved hypothetical protein	Medicago truncatula	ABE80754	23/59	-
382	PC110-4	143	cytochrome P450 71D8	Glycine max	CAA71517	22/32	Secondary metabolites biosynthesis, transport & catabolism
383	PC113-1	339	ribose-5-phosphate isomerase	Arabidopsis thaliana	At3g04790	21/25	5-phosphoribose 1-diphosphate biosynthesis
384	PC113-2	381	anionic peroxidase (see 535-1)	Petroselinum crispum	AAA98491	88/89	response to oxidative stress
385	PC113-3	/	anionic peroxidase (see 535-1)	Petroselinum crispum	AAA98491	88/89	response to oxidative stress
386	PC113-4	384	cysteine-type endopeptidase/ cysteine-type peptidase	Arabidopsis thaliana	At1g02305	21/25	proteolysis
387	PC114-1	328	AALP	Arabidopsis thaliana	At5g60360	37/52	proteolysis
388	PC114-2	314	putative Ac transposase	Arabidopsis thaliana	AAF19546	51/103	-
389	PC114-3	180	cytochrome P450 (CYP94A1)	Vicia sativa	AAD10204	43/59	Secondary metabolites biosynthesis, transport & catabolism
390	PC114-4	313	hydrolase/ protein serine/threonine phosphatase	Arabidopsis thaliana	At1g13750	52/66	biological process unknown
391	PC115-1	297	unknown protein	Arabidopsis thaliana	At5g35690	34/62	-
392	PC115-4	297	unknown protein	Arabidopsis thaliana	At5g35690	34/62	-
394	PC115-3	297	(S)-reticuline oxidase-like protein (see 397-1)	Daucus carota	BAB68539	34/64	electron transport
395	PC116-1	288	similar to vacuolar ATP-synthase subunit B isoform	Arabidopsis thaliana	At4g38510	42/42	ATP biosynthesis, ATP synthesis coupled proton transport
398	PC116-3	292	peroxidase (see 107-1-4)	Arabidopsis thaliana	At5g05340	49/79	response to oxidative stress
399	PC117-1	223	structural constituent of ribosome	Arabidopsis thaliana	At5g62300	33/34	protein biosynthesis
401	PC117-3	218	Os01g0790200 (ev. see 408-2)	Oryza sativa	BAF06404	16/16	-
402	PC117-4	219	UBP16 (UBIQUITIN-SPECIFIC PROTEASE 16)	Arabidopsis thaliana	At4g24560	27/43	ubiquitin-dependent protein catabolism
411	PC120-1	187	60S acidic ribosomal protein PO	Euphorbia esula	AF227622	45/61	protein biosynthesis, ribosome biogenesis
414	PC120-4	286	RNA binding / structural constituent of ribosome	Arabidopsis thaliana	At5g20160	60/63	protein biosynthesis; ribosome biogenesis and assembly
415	PC121-1	91	fatty acid desaturase/hydroxylase-like protein ELI7.1 (see 256-4)	Petroselinum crispum	AAG24521	24/24	fatty acid biosynthesis; fatty acid desaturation
416	PC121-4	91	fatty acid desaturase/hydroxylase-like protein ELI7.1 (see 256-4)	Petroselinum crispum	AAG24521	24/24	fatty acid biosynthesis; fatty acid desaturation
417	PC121-2	90	peptidyl-prolyl cis-trans isomerase	Arabidopsis thaliana	At2g21130	27/29	protein folding
419	PC125-1	281	kinase/ ribokinase	Arabidopsis thaliana	At5g51830	52/72	acetate fermentation; sucrose biosynthesis; sucrose catabolism
420	PC125-2	281	kinase/ ribokinase	Arabidopsis thaliana	At5g51830	52/72	acetate fermentation; sucrose biosynthesis; sucrose catabolism
421	PC125-3	281	kinase/ ribokinase	Arabidopsis thaliana	At5g51830	52/72	acetate fermentation; sucrose biosynthesis; sucrose catabolism
422	PC125-4	281	kinase/ ribokinase	Arabidopsis thaliana	At5g51830	52/72	acetate fermentation; sucrose biosynthesis; sucrose catabolism
423	PC126-1	292	peroxidase (see 107-1-4)	Arabidopsis thaliana	At5g05340	47/78	response to oxidative stress
424	PC126-2	281	kinase/ ribokinase (see 125)	Arabidopsis thaliana	At5g51830	51/72	acetate fermentation; sucrose biosynthesis; sucrose catabolism
425	PC126-3	280	kinase/ ribokinase (see 125)	Arabidopsis thaliana	At5g51830	51/72	acetate fermentation; sucrose biosynthesis; sucrose catabolism
426	PC126-4	292	S1 self-incompatibility locus-linked pollen 3.15 protein	Petunia inflata	AAQ09997	15/33	-
427	PC129-1	264	protein AX1108-carrot (embryogenesis-associated protein)	Daucus carota	BAA03455	59/87	electron transport; metabolism
428	PC129-2	289	PREDICTED: similar to CG30266-PA isoform 2	Apis mellifera	XP_623643	21/77	-
431	PC130-1	279	copper ion binding	Arabidopsis thaliana	At2g40370	21/49	-
434	PC131-1	218	unknown protein	Arabidopsis thaliana	At2g48110	49/71	biological process unknown
435	PC131-2	175	unknown protein	Arabidopsis thaliana	At5g51570	55/58	N-terminal protein myristoylation [pmid 12912986]
436	PC131-3	216	subtilisin-like protease C1 (see 235)	Glycine max	AAD02075	29/50	negative regulation of enzyme activity; proteolysis
437	PC131-4	168	Cysteine protease (see 70-3)	Vigna mungo	BAA92495	15/17	proteolysis
439	PC132-2	97	anionic peroxidase, putative	Arabidopsis thaliana	At1g14540	13/20	response to oxidative stress
442	PC133-1	46	omega-3 fatty acid desaturase (see 764-1)	Petroselinum crispum	AAB72241	15/15	fatty acid biosynthesis; fatty acid desaturation
443	PC133-2	46	omega-3 fatty acid desaturase (see 764-1)	Petroselinum crispum	AAB72241	15/15	fatty acid biosynthesis; fatty acid desaturation
445	PC133-4	46	omega-3 fatty acid desaturase (see 764-1)	Petroselinum crispum	AAB72241	15/15	fatty acid biosynthesis; fatty acid desaturation
447	PC134-2	92	sucrose synthase isoform I	Daucus carota	CAA76056	23/24	-

448	PC134-3	93	ATTIM44-2	Arabidopsis thaliana	At2g36110	16/28	protein targeting to mitochondrion
449	PC134-4	65	unknown protein	Arabidopsis thaliana	At3g57420	18/21	-
454	PC137-1	291	peroxidase (see 107-1-4)	Arabidopsis thaliana	At5g05340	29/44	response to oxidative stress
455	PC137-3	291	peroxidase (see 107-1-4)	Arabidopsis thaliana	At5g05340	32/51	response to oxidative stress
456	PC137-4	292	peroxidase (see 107-1-4)	Arabidopsis thaliana	At5g05340	49/79	response to oxidative stress
457	PC137-2	288	ATBPM1	Arabidopsis thaliana	At5g19000	46/68	biological process unknown
458	PC138-1	283	RSZ33 (see 139-1)	Arabidopsis thaliana	At2g37340	65/94	nuclear mRNA splicing, via spliceosome; spliceosome assembly
459	PC138-2	97	unknown protein (see 139-2)	Arabidopsis thaliana	At2g27660	16/30	-
460	PC138-3	283	RSZ33 (see 139-1)	Arabidopsis thaliana	At2g37340	71/94	nuclear mRNA splicing, via spliceosome; spliceosome assembly
461	PC138-4	283	RSZ33 (see 139-1)	Arabidopsis thaliana	At2g37340	71/94	nuclear mRNA splicing, via spliceosome; spliceosome assembly
462	PC139-1	283	RSZ33 (see 138-1)	Arabidopsis thaliana	At2g37340	72/94	nuclear mRNA splicing, via spliceosome; spliceosome assembly
463	PC139-2	97	unknown protein (see 138-2)	Arabidopsis thaliana	At2g27660	16/30	-
464	PC139-3	217	protein serine/threonine kinase/ protein-tyrosine kinase	Arabidopsis thaliana	At3g04690	28/65	protein amino acid phosphorylation
466	PC140-1	283	RSZ33 (see 139-1)	Arabidopsis thaliana	At2g37340	72/94	nuclear mRNA splicing, via spliceosome; spliceosome assembly
467	PC140-2	282	RSZ33 (see 139-1)	Arabidopsis thaliana	At2g37340	72/94	nuclear mRNA splicing, via spliceosome; spliceosome assembly
468	PC140-3	274	pathogenesis-related protein PR1-3 (PR1)	Petroselinum crispum	P19418	63/71	defense response
469	PC140-4	97	unknown protein (see 138-2)	Arabidopsis thaliana	At2g27660	16/30	-
470	PC141-1	168	PREDICTED: similar to otogelin; MLEMP	Danio rerio	XP_688432	14/45	-
471	PC141-2	165	unknown protein	Arabidopsis thaliana	At5g11090	38/51	biological process unknown
472	PC141-3	165	unknown protein	Arabidopsis thaliana	At5g11090	38/51	biological process unknown
473	PC141-4	165	unknown protein	Arabidopsis thaliana	At5g11090	38/51	biological process unknown
474	PC142-1	93	calcium ion binding	Arabidopsis thaliana	At1g09210	26/30	-
475	PC142-3	93	calcium ion binding	Arabidopsis thaliana	At1g09210	26/30	-
476	PC142-2	87	LRX2 (LEUCINE-RICH REPEAT/EXTENSIN 2)	Arabidopsis thaliana	At1g62440	20/28	cellular morphogenesis during differentiation
477	PC142-4	87	LRX2 (LEUCINE-RICH REPEAT/EXTENSIN 2)	Arabidopsis thaliana	At1g62440	20/28	cellular morphogenesis during differentiation
480	PC143-3	454	(+)-pulegone reductase	Mentha x piperita	AAQ75423	29/58	-
481	PC144-1	293	oxidoreductase (see 145-3)	Arabidopsis thaliana	At5g06060	55/82	metabolism
482	PC144-2	293	oxidoreductase (see 145-3)	Arabidopsis thaliana	At5g06060	55/82	metabolism
483	PC144-3	292	oxidoreductase (see 596-1)	Arabidopsis thaliana	At5g06060	55/82	metabolism
485	PC145-1	292	peroxidase (see 107-1-4)	Arabidopsis thaliana	At5g05340	49/79	response to oxidative stress
486	PC145-4	292	peroxidase (see 107-1-4)	Arabidopsis thaliana	At5g05340	49/79	response to oxidative stress
487	PC145-2	310	FLA9 (fasciclin-like arabinogalactan-protein 9)	Arabidopsis thaliana	At1g03870	59/101	cell adhesion
488	PC145-3	377	oxidoreductase (see 144-1)	Arabidopsis thaliana	At5g06060	35/50	metabolism
489	PC146-1	293	oxidoreductase (see 144-1)	Arabidopsis thaliana	At5g06060	55/85	metabolism
490	PC146-2	293	oxidoreductase (see 144-1)	Arabidopsis thaliana	At5g06060	56/85	metabolism
492	PC146-4	293	oxidoreductase (see 144-1)	Arabidopsis thaliana	At5g06060	56/85	metabolism
493	PC147-1	154	ATP binding	Arabidopsis thaliana	At5g48620	21/42	apoptosis; defense response; defense response to pathogen
494	PC147-2	153	ATP binding	Arabidopsis thaliana	At5g48620	21/42	apoptosis; defense response; defense response to pathogen
495	PC147-3	153	ATP binding	Arabidopsis thaliana	At5g48620	21/42	apoptosis; defense response; defense response to pathogen
496	PC147-4	153	ATP binding	Arabidopsis thaliana	At5g48620	23/43	apoptosis; defense response; defense response to pathogen
497	PC148-1	153	ATP binding (see 147)	Arabidopsis thaliana	At5g48620	22/43	apoptosis; defense response; defense response to pathogen
498	PC148-2	153	ATP binding (see 147)	Arabidopsis thaliana	At5g48620	23/43	apoptosis; defense response; defense response to pathogen
499	PC148-3	153	ATP binding (see 147)	Arabidopsis thaliana	At5g48620	23/43	apoptosis; defense response; defense response to pathogen
500	PC148-4	153	ATP binding (see 147)	Arabidopsis thaliana	At5g48620	23/43	apoptosis; defense response; defense response to pathogen
501	PC149-1	417	unknown protein	Arabidopsis thaliana	At1g56290	69/116	-
502	PC149-3	414	unknown protein	Arabidopsis thaliana	At1g56290	61/138	-

503	PC149-4	414	unknown protein	Arabidopsis thaliana	At1g56290	84/134	-
507	PC150-3	259	PHR2 (PHOTOLYASE/BLUE-LIGHT RECEPTOR 2)	Arabidopsis thaliana	At2g47590	36/48	DNA repair
508	PC150-4	400	Glutamine synthetase, chloroplast precursor, GS2	Daucus carota	AAB71693	47/67	-
509	PC152-1	296	glutamine-fructose-6-phosphate transaminase (isomerizing)	Arabidopsis thaliana	At3g24090	91/98	carbohydrate biosynthesis; carbohydrate metabolism; metabolism
511	PC152-3	296	oxidoreductase	Arabidopsis thaliana	At1g16720	40/52	metabolism
512	PC152-4	87	elongation factor 1-alpha	Schistosoma japonicum	AAQ16109	15/26	-
516	PC154-4	77	mtHSC70-2 (HEAT SHOCK PROTEIN 70)	Arabidopsis thaliana	At5g09590	17/18	protein folding; response to heat; response to virus
517	PC155-1	46	omega-3 fatty acid desaturase (see 764-1)	Petroselinum crispum	AAB72241	15/15	fatty acid biosynthesis; fatty acid desaturation
524	PC156-4	46	omega-3 fatty acid desaturase (see 764-1)	Petroselinum crispum	AAB72241	15/15	fatty acid biosynthesis; fatty acid desaturation
529	PC158-1	247	ATP binding / protein binding (see 206-3)	Arabidopsis thaliana	At5g26360	44/47	cellular protein metabolism
530	PC158-4	247	ATP binding / protein binding (see 206-3)	Arabidopsis thaliana	At5g26360	44/47	cellular protein metabolism
536	PC159-4	294	zinc finger DNA-binding protein	Catharanthus roseus	CAF74934	53/85	-
538	PC161-2	174	oxidoreductase/ zinc ion binding (see 162-2)	Arabidopsis thaliana	At1g23740	30/39	-
539	PC161-4	223	oxidoreductase/ zinc ion binding (see 162-2)	Arabidopsis thaliana	At1g23740	42/61	-
540	PC161-3	224	conserved hypothetical protein	Medicago truncatula	ABE92227	17/29	-
542	PC162-2	174	oxidoreductase/ zinc ion binding (see 161-4)	Arabidopsis thaliana	At1g23740	42/56	-
547	PC163-2	174	oxidoreductase/ zinc ion binding (see 162-2)	Arabidopsis thaliana	At1g23740	30/39	-
548	PC163-4	174	oxidoreductase/ zinc ion binding (see 162-2)	Arabidopsis thaliana	At1g23740	30/39	-
549	PC164-1-1	176	oxidoreductase/ zinc ion binding (see 162-2)	Arabidopsis thaliana	At1g23740	42/56	-
550	PC164-1-2	174	oxidoreductase/ zinc ion binding (see 162-2)	Arabidopsis thaliana	At1g23740	42/56	-
551	PC164-1-3	174	oxidoreductase/ zinc ion binding (see 162-2)	Arabidopsis thaliana	At1g23740	42/56	-
552	PC164-1-4	176	oxidoreductase/ zinc ion binding (see 162-2)	Arabidopsis thaliana	At1g23740	42/56	-
553	PC164-2-2	174	oxidoreductase/ zinc ion binding (see 162-2)	Arabidopsis thaliana	At1g23740	42/56	-
554	PC164-2-1	118	copper ion binding	Arabidopsis thaliana	At3g09220	18/39	-
555	PC164-2-4	118	copper ion binding	Arabidopsis thaliana	At3g09220	24/39	-
557	PC167-1	315	unknown protein (see 470-1)	Arabidopsis thaliana	At2g46150	31/80	biological process unknown
558	PC167-2	322	transferase, transferring hexosyl groups	Arabidopsis thaliana	At3g28340	68/105	carbohydrate biosynthesis
559	PC167-3	322	transferase, transferring hexosyl groups	Arabidopsis thaliana	At3g28340	68/105	carbohydrate biosynthesis
560	PC167-4	322	transferase, transferring hexosyl groups	Arabidopsis thaliana	At3g28340	68/105	carbohydrate biosynthesis
561	PC168-1	238	unknown protein	Arabidopsis thaliana	At1g49000	37/54	biological process unknown
562	PC168-2	236	protein serine/threonine kinase/ protein-tyrosine kinase	Arabidopsis thaliana	At2g18470	21/71	protein amino acid phosphorylation
563	PC168-3	238	oxidoreductase/ zinc ion binding (see 162-2)	Arabidopsis thaliana	At1g23740	30/58	-
570	PC175-2	191	SEN1 (DARK INDUCIBLE 1)	Arabidopsis thaliana	At4g35770	33/54	aging; response to light stimulus; response to sucrose stimulus
572	PC175-4	219	SEN1 (DARK INDUCIBLE 1)	Arabidopsis thaliana	At4g35770	38/55	aging; response to light stimulus; response to sucrose stimulus
573	PC177-1	233	unknown protein (see 216-1)	Arabidopsis thaliana	At2g15220	49/62	defense response to pathogen
574	PC177-2	141	70 kD heatshockprotein (see 182-2)	Medicago sativa	CAA67588	16/21	-
575	PC177-3	209	ubiquitin-protein ligase (see 388-3)	Arabidopsis thaliana	At2g35930	42/69	protein ubiquitination
576	PC177-4	216	Phenylalanine ammonia-lyase 1 (see 596-2)	Petroselinum crispum	CAA34715	69/71	Phenylpropanoid biosynthesis; first step
578	PC178-2	229	SGS3 (SUPPRESSOR OF GENE SILENCING 3) (see 280-4)	Arabidopsis thaliana	At5g23570	19/46	virus induced gene silencing
579	PC178-3	237	malate dehydrogenase/ oxidoreductase	Arabidopsis thaliana	At5g43330	56/70	malate metabolism; tricarboxylic acid cycle intermediate metabolism
580	PC178-4	216	Phenylalanine ammonia-lyase 1 (see 177-4)	Petroselinum crispum	CAA34715	69/71	Phenylpropanoid biosynthesis; first step
581	PC180-1	217	unknown protein	Arabidopsis thaliana	At1g26850	55/71	-
582	PC180-2	171	ATPUP3 (see 345-4)	Arabidopsis thaliana	At1g28220	17/39	-
583	PC180-3	133	kinase	Arabidopsis thaliana	At3g51550	28/37	protein amino acid phosphorylation
584	PC180-4	171	catalytic/ intramolecular transferase, phosphotransferases	Arabidopsis thaliana	At1g22170	13/18	glycolysis; metabolism
586	PC182-2	141	70 kD heatshockprotein (see 727-4)	Medicago sativa	CAA67588	16/21	-

587	PC182-3	142	electron carrier (ev. 543-3)	Arabidopsis thaliana	At1g30740	17/27	electron transport
588	PC182-4	135	structural constituent of ribosome (see 4-3)	Arabidopsis thaliana	At1g15250	31/39	protein biosynthesis, ribosome biogenesis
589	PC184-1	235	unknown protein (see 470-1)	Arabidopsis thaliana	At2g46150	31/79	biological process unknown
590	PC184-2	235	unknown protein (see470-1)	Arabidopsis thaliana	At2g46150	31/79	biological process unknown
591	PC184-4	235	unknown protein (see470-1)	Arabidopsis thaliana	At2g46150	31/79	biological process unknown
593	PC185-1	174	oxidoreductase/ zinc ion binding (see 162-2)	Arabidopsis thaliana	At1g23740	42/56	-
594	PC185-2	169	unknown protein (see 216-1)	Arabidopsis thaliana	At2g15220	47/58	defense response to pathogen
595	PC185-3	170	unknown protein (see 216-1)	Arabidopsis thaliana	At2g15220	47/58	defense response to pathogen
596	PC185-4	169	unknown protein (see 216-1)	Arabidopsis thaliana	At2g15220	47/58	defense response to pathogen
597	PC187-2	235	unknown protein (see470-1)	Arabidopsis thaliana	At2g46150	31/79	biological process unknown
605	PC190-1	169	unknown protein (see 216-1)	Arabidopsis thaliana	At2g15220	47/58	defense response to pathogen
606	PC190-2	203	protein tyrosine/serine/threonine phosphatase	Arabidopsis thaliana	At5g56610	53/67	protein amino acid dephosphorylation
608	PC190-4	174	hydrogen-exporting ATPase	Arabidopsis thaliana	At5g08670	57/57	ATP biosynthesis; ATP synthesis coupled proton transport
609	PC191-1	169	unknown protein (see 216-1)	Arabidopsis thaliana	At2g15220	47/58	defense response to pathogen
610	PC191-4	169	unknown protein	Arabidopsis thaliana	At2g15220	47/58	defense response to pathogen
611	PC191-2	171	trans-cinnamate 4 monooxygease (C4H)	Petroselinum crispum	TCMO_PETCI	26/26	Lignin biosynthesis; Phenylpropanoid metabolism; second step
612	PC191-3	163	hypothetical protein	Methanococcus j.	NP_247974	17/41	-
613	PC195-1	409	ATGPAT6/GPAT6; acyltransferase (see 797-2)	Arabidopsis thaliana	At2g38110	102/133	metabolism
614	PC195-2	406	ATGPAT6/GPAT6; acyltransferase (see 797-2)	Arabidopsis thaliana	At2g38110	88/122	metabolism
616	PC195-4	174	S-norcoclaurine synthase 2	Papaver somniferum	AAX56304	17/48	-
618	PC196-2	349	ubiquitin-protein ligase	Arabidopsis thaliana	At3g52450	52/86	protein ubiquitination
619	PC196-3	350	ubiquitin-protein ligase	Arabidopsis thaliana	At3g52450	52/86	protein ubiquitination
621	PC197-2	378	HSP81-3	Arabidopsis thaliana	At5g56010	42/60	protein folding; response to heat
623	PC197-4	373	Eli7.7, andere Eli7 (see 287-4)	Petroselinum crispum	AF239832	14/15	fatty acid biosynthesis; fatty acid desaturation
624	PC197-5	364	unknown protein (see 470-1)	Arabidopsis thaliana	At2g46150	33/82	biological process unknown
625	PC198-1	238	component of 9-1-1 complex	Dictyostelium d.	XP_644078	15/49	-
626	PC198-2	237	protein serine/threonine kinase/ protein-tyrosine kinase (see 228-4)	Arabidopsis thaliana	At5g40540	72/78	protein amino acid phosphorylation
628	PC198-4	245	amino acid permease/ amino acid transporter	Arabidopsis thaliana	At4g38250	35/86	amino acid transport
636	PC200-4	174	S-norcoclaurine synthase 2	Papaver somniferum	AAX56304	17/48	-
637	PC201-1	178	pathogenesis-related 10 protein PR10-2	Papaver somniferum	AAX56076	14/43	-
638	PC201-2	174	S-norcoclaurine synthase 2	Papaver somniferum	AAX56304	17/48	-
639	PC201-4	174	S-norcoclaurine synthase 2	Papaver somniferum	AAX56304	17/48	-
641	PC202-1	?	S-norcoclaurine synthase 2 (BUT apo at 183)	Papaver somniferum	AAX56304	17/48	-
642	PC202-2	154	oxidoreductase	Arabidopsis thaliana	At1g01800	27/45	metabolism
643	PC202-3	156	oxidoreductase	Arabidopsis thaliana	At1g01800	28/48	metabolism
644	PC202-4	156	oxidoreductase	Arabidopsis thaliana	At1g01800	28/48	metabolism
654	PC206-3	140	ATP binding / protein binding (see 158-1)	Arabidopsis thaliana	At5g26360	43/46	cellular protein metabolism
655	PC206-4	156	RPS15A (RIBOSOMAL PROTEIN S15A)	Arabidopsis thaliana	At1g07770	34/40	protein biosynthesis
656	PC207-1	143	RNA polymerase II transcription factor	Arabidopsis thaliana	At3g10330	21/27	regulation of transcription, DNA-dependent; transcription initiation
657	PC207-2	140	ATP binding / protein binding (see 158-1)	Arabidopsis thaliana	At5g26360	43/46	cellular protein metabolism
658	PC207-3	140	protein serine/threonine kinase/ protein-tyrosine kinase	Arabidopsis thaliana	At1g16670	30/38	protein amino acid phosphorylation
668	PC210-1	141	hypothetical protein PTD2_09632	Pseudoalteromonas t.	ZP_01136035	14/33	-
669	PC210-2	324	oxidoreductase/ zinc ion binding (see 417-1)	Arabidopsis thaliana	At1g23740	27/46	-
670	PC210-3	235	oxidoreductase/ zinc ion binding (see 417-1)	Arabidopsis thaliana	At1g23740	27/46	-
671	PC210-4	225	14 KD proline-rich protein DC2.15 precursor	Daucus carota	CAA33476	37/39	May be connected with the initiation of embryogenesis
673	PC211-2	168	ATPase/ nucleoside-triphosphatase/ nucleotide binding	Arabidopsis thaliana	At4g02480	18/24	-

675	PC211-4	160	unknown protein (see 212-3)	Arabidopsis thaliana	At1g70505	29/50	biological process unknown
678	PC212-3	160	unknown protein (see 211-4)	Arabidopsis thaliana	At1g70505	29/50	biological process unknown
680	PC215-1	419	putative beta-amyrin synthase (see 245-3)	Centella asiatica	AAS01523	101/139	metabolism
681	PC215-2	432	hypothetical protein	Magnetospirillum g.	CAJ30048	37/41	-
682	PC215-3	169	unknown protein (see 216-1)	Arabidopsis thaliana	At2g15220	45/56	defense response to pathogen
683	PC215-4	189	membrane alanyl aminopeptidase	Arabidopsis thaliana	At1g63770	40/62	proteolysis
684	PC216-1	168	unknown protein (see 177-1)	Arabidopsis thaliana	At2g15220	28/36	defense response to pathogen
685	PC216-3	168	unknown protein (see 177-1)	Arabidopsis thaliana	At2g15220	28/36	defense response to pathogen
686	PC216-2	277	unknown protein	Arabidopsis thaliana	At1g54320	58/83	biological process unknown
687	PC216-4	276	unknown protein	Arabidopsis thaliana	At1g54320	58/83	biological process unknown
688	PC217-1	242	oxidoreductase/ zinc ion binding (see 162-2 & 210-2)	Arabidopsis thaliana	At1g23740	42/56	-
689	PC217-2	252	quercetin 3-O-glucoside-6"-O-malonyltransferase	Verbena x hybrida	AAS77403	32/71	-
690	PC217-3	250	unknown protein (see 216-1)	Arabidopsis thaliana	At2g15220	49/61	defense response to pathogen
691	PC217-4	244	Tyrosin-Decarboxylase (see 312-1)	Petroselinum crispum	AAA33861	40/40	-
692	PC218-1	235	unknown protein (see 470-1)	Arabidopsis thaliana	At2g46150	31/79	biological process unknown
693	PC218-2	235	unknown protein (see 470-1)	Arabidopsis thaliana	At2g46150	31/79	biological process unknown
694	PC218-3	234	unknown protein (see 470-1)	Arabidopsis thaliana	At2g46150	31/79	biological process unknown
696	PC219-1	201	APS1	Arabidopsis thaliana	At3g22890	59/66	dissimilatory sulfate reduction; sulfate assimilation
697	PC219-2	201	APS1	Arabidopsis thaliana	At3g22890	59/66	dissimilatory sulfate reduction; sulfate assimilation
698	PC219-3	212	protein Ser/Thr kinase/ protein Tyr kinase/ sugar binding (see 661-2)	Arabidopsis thaliana	At4g27300	27/69	protein amino acid phosphorylation
699	PC219-4	211	2,3-bisphosphoglycerate-independent phosphoglycerate mutase	Arabidopsis thaliana	At3g08590	50/57	acetate fermentation; aerobic glycerol catabolism
700	PC220-1	168	unknown protein (see 216-1)	Arabidopsis thaliana	At2g15220	28/36	defense response to pathogen
701	PC220-2	168	unknown protein (see 216-1)	Arabidopsis thaliana	At2g15220	28/36	defense response to pathogen
702	PC220-3	173	ACS1 (ACC SYNTHASE 1) (see 246-1)	Arabidopsis thaliana	At3g61510	32/39	ethylene biosynthesis
704	PC221-2	171	unknown protein (see 216-1)	Arabidopsis thaliana	At2g15220	41/50	defense response to pathogen
705	PC221-3	173	unknown protein (see 216-1)	Arabidopsis thaliana	At2g15220	40/45	defense response to pathogen
706	PC221-4	169	unknown protein (see 216-1)	Arabidopsis thaliana	At2g15220	26/31	defense response to pathogen
707	PC222-1	170	unknown protein (see 216-1)	Arabidopsis thaliana	At2g15220	43/57	defense response to pathogen
708	PC222-2	169	unknown protein (see 216-1)	Arabidopsis thaliana	At2g15220	43/57	defense response to pathogen
709	PC222-3	169	unknown protein (see 216-1)	Arabidopsis thaliana	At2g15220	43/57	defense response to pathogen
712	PC223-2	169	unknown protein (see 216-1)	Arabidopsis thaliana	At2g15220	46/58	defense response to pathogen
713	PC223-3	169	unknown protein (see 216-1)	Arabidopsis thaliana	At2g15220	46/57	defense response to pathogen
717	PC224-3	102	PWD (PHOSPHOGLUCAN WATER DIKINASE)	Arabidopsis thaliana	At5g26570	16/30	starch metabolism, protein amino acid autophosphorylation
722	PC225-2	81	X-Pro dipeptidase-like protein (see 249-2)	Arabidopsis thaliana	At4g29500	20/26	-
727	PC228-1	72	putative cinnamyl-alcohol dehydrogenase (see 580-1)	Arabidopsis thaliana	At1g72680	16/24	lignin biosynthesis [pmid 8219046]
728	PC228-2	235	ATSK11	Arabidopsis thaliana	At5g26751	75/77	meristem organization; phosphorylation
729	PC228-3	202	hypothetical protein RoseRSDRAFT_4270	Roseiflexus sp. RS-1	ZP_01355879	14/34	-
730	PC228-4	237	protein serine/threonine kinase/ protein-tyrosine kinase (see 198-2)	Arabidopsis thaliana	At5g40540	51/54	protein amino acid phosphorylation
731	PC229-1	170	unknown protein	Arabidopsis thaliana	At3g44100	13/29	biological process unknown
732	PC229-3	170	unknown protein	Arabidopsis thaliana	At3g44100	19/40	biological process unknown
733	PC229-2	169	unknown protein	Arabidopsis thaliana	At3g44100	13/29	biological process unknown
736	PC230-2	159	BXL2 (BETA-XYLOSIDASE 2)	Arabidopsis thaliana	At1g02640	37/52	carbohydrate metabolism
738	PC230-4	160	protein serine/threonine kinase/ protein-tyrosine kinase	Arabidopsis thaliana	At3g20860	25/39	protein amino acid phosphorylation
739	PC232-1	145	MUR3 (MURUS 3)	Arabidopsis thaliana	At2g20370	38/47	endomembrane organization; fucose biosynthesis
740	PC232-2	137	alcohol acyltransferase	Fragaria x ananassa	AF193789	13/18	-
743	PC233-1	91	SKIP4 (SKP1 INTERACTING PARTNER 4)	Arabidopsis thaliana	At3g61350	21/25	biological process unknown

744	PC233-2	91	SKIP4 (SKP1 INTERACTING PARTNER 4)	Arabidopsis thaliana	At3g61350	21/25	biological process unknown
747	PC234-1	223	COR413-PM2	Arabidopsis thaliana	At3g50830	20/31	response to stress
748	PC234-2	225	oxidoreductase/ zinc ion binding	Arabidopsis thaliana	At5g24760	60/74	-
749	PC234-3	225	oxidoreductase/ zinc ion binding	Arabidopsis thaliana	At5g24760	60/74	-
751	PC235-1	130	subtilisin-like protease C1 (see 131-3)	Glycine max	AAD02075	21/44	negative regulation of enzyme activity; proteolysis
752	PC235-2	130	subtilisin-like protease C1 (see 131-3)	Glycine max	AAD02075	21/44	negative regulation of enzyme activity; proteolysis
753	PC235-3	130	subtilisin-like protease C1 (see 131-3)	Glycine max	AAD02075	21/44	negative regulation of enzyme activity; proteolysis
754	PC235-4	130	subtilisin-like protease C1 (see 131-3)	Glycine max	AAD02075	21/44	negative regulation of enzyme activity; proteolysis
761	PC237-2	84	CYP86A2; oxygen binding	Arabidopsis thaliana	At4g00360	22/27	fatty acid metabolism
764	PC238-2	70	1-phosphatidylinositol-4-phosphate 5-kinase/ zinc ion binding	Arabidopsis thaliana	At4g33240	19/22	-
765	PC238-3	66	LACS6 (LONG-CHAIN ACYL-COA SYNTHETASE 6)	Arabidopsis thaliana	At3g05970	18/22	fatty acid oxidation; metabolism; n-octane oxidation
766	PC238-4	66	(S)-reticuline oxidase-like protein (see 397-1)	Daucus carota	BAB68539	17/21	electron transport
767	PC239-1	315	transcription factor	Arabidopsis thaliana	At1g50600	15/27	regulation of transcription
768	PC239-2	336	RBOHD (RESPIRATORY BURST OXIDASE PROTEIN D)	Arabidopsis thaliana	At5g47910	56/68	defense response; oxygen and reactive oxygen species metabolism
769	PC239-4	336	RBOHD (RESPIRATORY BURST OXIDASE PROTEIN D)	Arabidopsis thaliana	At5g47910	56/68	defense response; oxygen and reactive oxygen species metabolism
770	PC239-3	356	unknown protein	Arabidopsis thaliana	At3g52370	73/103	cell adhesion
771	PC240-2	281	Phenylalanine ammonia-lyase 1 (see 690-1)	Petroselinum crispum	CAA34715	74/74	Phenylpropanoid biosynthesis; first step
772	PC240-3	280	protein binding / ubiquitin-protein ligase/ zinc ion binding	Arabidopsis thaliana	At4g34100	66/92	protein ubiquitination
773	PC240-4	277	L-aspartate oxidase/ disulfide oxidoreductase/ oxidoreductase	Arabidopsis thaliana	At5g14760	49/57	electron transport; NAD biosynthesis
774	PC240-5	277	L-aspartate oxidase/ disulfide oxidoreductase/ oxidoreductase	Arabidopsis thaliana	At5g14760	49/57	electron transport; NAD biosynthesis
775	PC241-1	235	unknown protein (see 470-1)	Arabidopsis thaliana	At2g46150	31/79	biological process unknown
776	PC241-2	279	oxidoreductase/ zinc ion binding (see 162-2 & 210-2)	Arabidopsis thaliana	At1g23740	21/29	-
777	PC241-4	265	oxidoreductase/ zinc ion binding (see 162-2 & 210-2)	Arabidopsis thaliana	At1g23740	41/56	-
779	PC243-1	164	carboxylic ester hydrolase/ hydrolase, acting on ester bonds	Arabidopsis thaliana	At5g45670	45/54	lipid metabolism
780	PC243-2	160	immediate-early fungal elicitor protein CMPG1, Eli17 (see 334-4)	Petroselinum crispum	AAK69402	14/17	protein ubiquitination
781	PC243-3	235	unknown protein (see 470-1)	Arabidopsis thaliana	At2g46150	30/79	biological process unknown
785	PC245-3	419	putative beta-amyrin synthase (see 215-1)	Centella asiatica	AAS01523	104/139	metabolism
786	PC245-4	419	putative beta-amyrin synthase (see 215-1)	Centella asiatica	AAS01523	104/139	metabolism
787	PC246-1	196	ACS1 (ACC SYNTHASE 1) (see 220-3)	Arabidopsis thaliana	At3g61510	51/60	ethylene biosynthesis
788	PC246-2	174	ACS1 (ACC SYNTHASE 1) (see 220-3)	Arabidopsis thaliana	At3g61510	50/58	ethylene biosynthesis
789	PC246-3	230	unknown protein	Arabidopsis thaliana	At3g53990	17/31	response to stress
790	PC246-4	155	ubiquitin-protein ligase/ zinc ion binding (see 247-3)	Arabidopsis thaliana	At1g65430	48/51	protein ubiquitination
792	PC247-2	174	ACS1 (ACC SYNTHASE 1) (see 220-3)	Arabidopsis thaliana	At3g61510	50/58	ethylene biosynthesis
793	PC247-4	175	ACS1 (ACC SYNTHASE 1) (see 220-3)	Arabidopsis thaliana	At3g61510	50/58	ethylene biosynthesis
794	PC247-3	156	ubiquitin-protein ligase/ zinc ion binding (see 246-4)	Arabidopsis thaliana	At1g65430	49/51	protein ubiquitination
799	PC249-1	81	protein binding	Arabidopsis thaliana	At1g03440	19/25	signal transduction
800	PC249-3	81	protein binding	Arabidopsis thaliana	At1g03440	19/25	signal transduction
801	PC249-2	81	X-Pro dipeptidase-like protein (see 225-2)	Arabidopsis thaliana	At4g29500	21/26	-
802	PC249-4	81	X-Pro dipeptidase-like protein (see 225-2)	Arabidopsis thaliana	At4g29500	21/26	-
803	PC250-1	72	cinnamyl-alcohol dehydrogenase (CAD) (see 580-1)	Arabidopsis thaliana	At1g72860	16/24	lignin biosynthesis [pmid 8219046]
804	PC250-2	189	omega-6 fatty acid desaturase (EC 1.14.99.-) (see 355-1)	Petroselinum crispum	AAB80696	29/35	fatty acid biosynthesis; fatty acid desaturation
806	PC250-4	189	unknown protein	Arabidopsis thaliana	At1g27760	31/43	biological process unknown
807	PC251-1	281	(S)-reticuline oxidase-like protein (see 397-1)	Daucus carota	BAB68539	48/94	electron transport
808	PC251-2	281	(S)-reticuline oxidase-like protein (see 397-1)	Daucus carota	BAB68539	48/94	electron transport
809	PC251-4	289	electron carrier (see 397-1)	Arabidopsis thaliana	At1g26420	18/47	electron transport
811	PC252-1	98	ATGLR2.8	Arabidopsis thaliana	At2g29110	20/32	calcium ion homeostasis; response to light stimulus

812	PC252-2	98	ATGLR2.8	Arabidopsis thaliana	At2g29110	20/32	calcium ion homeostasis; response to light stimulus
815	PC253-1	277	conserved hypothetical protein (see 664-2-3)	Paracoccus denitrificans	ZP_00630616	46/65	-
816	PC253-2	283	unknown protein	Arabidopsis thaliana	At5g47570	18/21	biological process unknown
817	PC253-3	283	unknown protein	Arabidopsis thaliana	At5g47570	18/21	biological process unknown
818	PC253-4	283	unknown protein	Arabidopsis thaliana	At5g47570	18/21	biological process unknown
819	PC254-1	270	anionic peroxidase (see 113-2)	Petroselinum crispum	AAA98491	41/46	response to oxidative stress
820	PC254-4	ca 208	anionic peroxidase (see 113-2)	Petroselinum crispum	AAA98491	39/40	response to oxidative stress
821	PC254-2	270	APX1	Arabidopsis thaliana	At1g07890	57/65	response to reactive oxygen species
822	PC254-3	265	similar to zinc finger protein 91 (HPF7, HTF10)	Danio rerio	XP_694208	31/96	-
823	PC255-1-1	468	BPF-1a protein	Petroselinum crispum	CAA48413	85/116	protein modification; regulation of transcription
824	PC255-1-2	469	BPF-1a protein	Petroselinum crispum	CAA48413	103/158	protein modification; regulation of transcription
825	PC255-1-3	472	BPF-1a protein	Petroselinum crispum	CAA48413	71/95	protein modification; regulation of transcription
826	PC255-1-4	466	BPF-1a protein	Petroselinum crispum	CAA48413	103/151	protein modification; regulation of transcription
828	PC255-2-2	260	electron carrier (see pc300-3)	Arabidopsis thaliana	At1g30760	43/72	electron transport
829	PC255-2-3	258	WNK8	Arabidopsis thaliana	At5g41990	14/24	protein amino acid phosphorylation
830	PC255-2-4	287	tyrosin/dopa decarboxylase	Papaver somniferum	AAC61842	33/81	amino acid and derivative metabolism; carboxylic acid metabolism
831	PC256-1	171	protein transporter (see 289-1)	Arabidopsis thaliana	At5g16880	30/56	intra-Golgi transport; intracellular protein transport
832	PC256-2	172	protein transporter (see 289-1)	Arabidopsis thaliana	At5g16880	30/56	intra-Golgi transport; intracellular protein transport
833	PC256-3	166	GAD2 (GLUTAMATE DECARBOXYLASE 2) (see 445-4)	Arabidopsis thaliana	At1g65960	43/55	glutamate metabolism; nitrogen compound metabolism
834	PC256-4	171	fatty acid desaturase/hydroxylase-like protein Eli7.1 (see 289-3)	Petroselinum crispum	AAG24521	49/50	fatty acid biosynthesis; fatty acid desaturation
839	PC258-1	281	AGC2-1 (OXIDATIVE SIGNAL-INDUCIBLE1)	Arabidopsis thaliana	At3g25250	39/59	protein amino acid phosphorylation
840	PC258-2	212	Tyr-DC (Eli 5) (see 312-1)	Petroselinum crispum	AAA33861	70/70	-
843	PC259-1	272	SQD2 (SULFOQUINOVOSYLDIACYLGLYCEROL 2)	Arabidopsis thaliana	At5g01220	49/55	cellular response to phosphate starvation; glycolipid biosynthesis
845	PC259-3	272	protein transporter	Arabidopsis thaliana	At4g16143	44/50	intracellular protein transport; protein import into nucleus
846	PC259-4	265	UBP6 (UBIQUITIN-SPECIFIC PROTEASE 6)	Arabidopsis thaliana	At1g51710	74/86	protein deubiquitination
847	PC261-1	269	anionic peroxidase (see 113-2)	Petroselinum crispum	AAA98491	43/43	response to oxidative stress
848	PC261-2	272	pectate lyase	Arabidopsis thaliana	At1g67750	46/52	biological process unknown
850	PC261-4	269	calcium ion binding	Arabidopsis thaliana	At1g53210	29/81	-
851	PC262-1	212	SHD (SHEPHERD)	Arabidopsis thaliana	At4g24190	29/34	protein folding; regulation of meristem organization
853	PC262-3	203	nicotinate-nucleotide diphosphorylase (carboxylating)	Arabidopsis thaliana	At2g01350	48/52	NAD biosynthesis; pyridine nucleotide biosynthesis
854	PC262-4	206	Putative NADPH HC toxin reductase	Oryza sativa	BAC79712	34/68	cellular metabolism
855	PC263-1	98	protein serine/threonine kinase/ protein-tyrosine kinase	Arabidopsis thaliana	At1g06840	26/32	protein amino acid phosphorylation
856	PC263-2	89	TIM50	Arabidopsis thaliana	At1g55900	21/29	biological process unknown
857	PC263-3	98	NRPD2a	Arabidopsis thaliana	At3g23780	15/21	DNA methylation; RNA interference, production of siRNA; transcription
858	PC263-4	98	NRPD2a	Arabidopsis thaliana	At3g23780	15/21	DNA methylation; RNA interference, production of siRNA; transcription
859	PC264-1	70	(S)-reticuline oxidase-like protein (see 397-1)	Daucus carota	BAB68539	16/22	electron transport
860	PC264-2	70	(S)-reticuline oxidase-like protein (see 397-1)	Daucus carota	BAB68539	16/22	electron transport
863	PC265-1	287	copper ion binding	Arabidopsis thaliana	At4g39830	20/39	-
864	PC265-2	277	ARA7	Arabidopsis thaliana	At4g19640	19/22	intracellular protein transport;small GTPase mediated signal transduction
865	PC265-3	290	unknown protein	Arabidopsis thaliana	At2g18740	32/33	mRNA processing
866	PC265-4	273	F-box protein family (see 347-2)	Arabidopsis thaliana	At4g22030	13/26	biological process unknown
868	PC266-2	233	structural constituent of ribosome	Arabidopsis thaliana	At5g35530	43/60	protein biosynthesis
869	PC266-3	166	serine-type endopeptidase inhibitor (see 301-2)	Arabidopsis thaliana	At5g43580	14/21	response to wounding
870	PC266-4	165	serine-type endopeptidase inhibitor (see 301-2)	Arabidopsis thaliana	At5g43580	12/21	response to wounding
876	PC268-2	165	electron carrier (see 718-4) (BUT no taq)	Arabidopsis thaliana	At5g44400	16/27	electron transport
877	PC268-3	140	ALDH3H1; aldehyde dehydrogenase	Arabidopsis thaliana	At1g44170	21/36	metabolism

883	PC271-1	274	nucleotide binding signal recognition particle 54KD protein 2 (SRP54)	Arabidopsis thaliana	At1g48900	79/90	protein targeting
889	PC273-3	182	protein serine/threonine kinase/ protein-tyrosine kinase/ sugar binding	Arabidopsis thaliana	At4g03230	27/36	protein amino acid phosphorylation
895	PC275-1	281	hypothetical protein	Plasmodium chabaudi c.	XP_745411	18/65	-
896	PC275-2	276	DC2.15 like protein	Daucus carota	BAA99575	38/44	lipid transport
897	PC275-3	276	DC2.15 like protein	Daucus carota	BAA99575	38/44	lipid transport
899	PC276-1	271	protein serine/threonine kinase/ protein-tyrosine kinase (see 564-1)	Arabidopsis thaliana	At2g28590	30/43	protein amino acid phosphorylation
900	PC276-2	271	hypothetical protein CYB_0720	Synechococcus sp.	YP_476967	13/35	-
901	PC276-3	271	ATGPX6 (GLUTATHIONE PEROXIDASE 6)	Arabidopsis thaliana	At4g11600	48/66	response to oxidative stress
902	PC276-4	275	ubiquitin-protein ligase (see 564-4)	Arabidopsis thaliana	At2g44900	23/30	ubiquitin-dependent protein catabolism
903	PC277-1	207	putative chromosome partition protein SmC	Treponema denticola	NP_972102	16/50	-
904	PC277-2	221	EDGP precursor (see 566-2)	Daucus carota	BAA03413	41/51	proteolysis
907	PC278-1	95	calmodulin binding (see 787-2)	Arabidopsis thaliana	At2g26190	25/28	N-terminal protein myristoylation
908	PC278-2	95	calmodulin binding (see 787-2)	Arabidopsis thaliana	At2g26190	25/28	N-terminal protein myristoylation
909	PC278-4	95	calmodulin binding (see 787-2)	Arabidopsis thaliana	At2g26190	25/28	N-terminal protein myristoylation
910	PC278-3	96	GTP binding / translation initiation factor	Arabidopsis thaliana	At2g05830	27/31	cellular biosynthesis; translational initiation
911	PC279-1	54	spermidine synthase (see 446-4)	Malus x domestica	BAC20170	14/17	-
915	PC280-1	281	ATP-dependent helicase/ nucleic acid binding / transcription regulator	Arabidopsis thaliana	At2g46020	86/93	biological process unknown
916	PC280-2	280	ATP-dependent helicase/ nucleic acid binding / transcription regulator	Arabidopsis thaliana	At2g46020	87/93	biological process unknown
917	PC280-3	212	Tyr-DC (Eli 5) (see 312-1)	Petroselinum crispum	AAA33861	70/70	-
918	PC280-4	282	SGS3 (SUPPRESSOR OF GENE SILENCING 3) (see 178-2)	Arabidopsis thaliana	At5g23570	18/51	virus induced gene silencing
923	PC282-1	71	secreted glycoprotein EP4, 47K, precursor	Daucus carota	AAA98926	21/23	lipid metabolism
924	PC282-4	71	secreted glycoprotein EP4, 47K, precursor	Daucus carota	AAA98926	21/23	lipid metabolism
926	PC282-3	69	unknown protein	Arabidopsis thaliana	At4g11860	21/22	biological process unknown
928	PC283-2	350	acyltransferase-like protein (see 774-3)	Arabidopsis thaliana	At3g26040	38/79	biological process unknown
929	PC283-3	340	unknown protein	Arabidopsis thaliana	At3g07090	73/107	biological process unknown
936	PC285-2	128	CNBT1 (CYCLIC NUCLEOTIDE-BINDING TRANSPORTER 1) (see290-2)	Arabidopsis thaliana	At3g17700	30/40	ion transport
941	PC287-3	211	(S)-reticuline oxidase-like protein (see 397-1)	Daucus carota	BAB68539	29/59	electron transport
942	PC287-4	303	Eli7.7 (see 197-4)	Petroselinum crispum	AF239832	65/87	fatty acid biosynthesis; fatty acid desaturation
945	PC288-2	272	unknown protein	Arabidopsis thaliana	At2g28310	47/61	biological process unknown
946	PC288-4	271	putative ammonium transporter	Oryza sativa	NP_915679	79/89	transport
947	PC289-1	172	protein transporter (see 256-1)	Arabidopsis thaliana	At5g16880	25/45	intra-Golgi transport; intracellular protein transport
948	PC289-4	171	protein transporter (see 256-1)	Arabidopsis thaliana	At5g16880	30/56	intra-Golgi transport; intracellular protein transport
949	PC289-2	171	hypothetical protein Badol_01000417	Bifidobacterium a.	ZP_01029720	15/40	-
950	PC289-3	172	fatty acid desaturase/hydroxylase-like protein Eli7.1 (see 256-4)	Petroselinum crispum	AAG24521	49/50	fatty acid biosynthesis; fatty acid desaturation
952	PC290-2	128	CNBT1 (CYCLIC NUCLEOTIDE-BINDING TRANSPORTER 1) (see285-2)	Arabidopsis thaliana	At3g17700	30/40	ion transport
953	PC290-3	128	CNBT1 (CYCLIC NUCLEOTIDE-BINDING TRANSPORTER 1) (see285-2)	Arabidopsis thaliana	At3g17700	30/40	ion transport
954	PC290-4	124	unknown	Petroselinum crispum	AAG09294	14/14	-
963	PC293-1	255	PP2A-1	Arabidopsis thaliana	At1g59830	59/72	biological process unknown
966	PC293-4	212	Tyr-DC (Eli 5) (see 312-1)	Petroselinum crispum	AAA33861	69/70	-
967	PC294-1	254	putative 3-ketoacyl-acyl carrier protein reductase	Oryza sativa	BAC57400	25/47	metabolism
968	PC294-2	212	Tyr-DC (Eli 5) (see 312-1)	Petroselinum crispum	AAA33861	69/70	-
969	PC294-3	212	Tyr-DC (Eli 5) (see 312-1)	Petroselinum crispum	AAA33861	68/70	-
970	PC294-4	211	Tyr-DC (Eli 5) (see 312-1)	Petroselinum crispum	AAA33861	63/64	-
971	PC295-1	213	Tyr-DC (Eli 5) (see 312-1)	Petroselinum crispum	AAA33861	68/71	-
982	PC297-4	/	unknown protein	Arabidopsis thaliana	At5g61820	68/132	biological process unknown
985	PC298-3	270	hydroxymethylbilane synthase (HMBS)	Pisum sativum	CAA51820	46/66	Porphyrin biosynthesis by the C5 pathway

987	PC299-1	289	bergaptol O-methyltransferase	Ammi majus	AAR24096	58/62	lignin biosynthesis; regulation of transcription, DNA-dependent
988	PC299-2	283	ACT7	Arabidopsis thaliana	At5g09810	70/71	cytoskeleton organization and biogenesis; response to auxin stimulus
991	PC300-1	210	protein binding / ubiquitin-protein ligase/ zinc ion binding (see 569-1)	Arabidopsis thaliana	At2g02960	40/61	protein ubiquitination
992	PC300-2	153	catalytic/ protein phosphatase type 2C (see 569-2)	Arabidopsis thaliana	At3g62260	30/47	-
993	PC300-3	211	electron carrier (see364-3)	Arabidopsis thaliana	At1g30760	29/59	electron transport
994	PC300-4	269	CYP72A11; monooxygenase/ oxygen binding (BUT no apo)	Arabidopsis thaliana	At3g14650	38/73	electron transport
995	PC301-1	210	extra-large guanine nucleotide binding protein, putative	Arabidopsis thaliana	At1g31930	52/57	-
996	PC301-2	213	serine-type endopeptidase inhibitor (see 266-3)	Arabidopsis thaliana	At5g43580	14/21	response to wounding
998	PC301-4	213	cell attachment protein in somatic embryogenesis (see 372-3)	Daucus carota	BAD24818	51/26	-
999	PC303-1	147	Avr9/Cf-9 rapidly elicited protein 231 (see 315)	Arabidopsis thaliana	At1g19300	36/47	carbohydrate biosynthesis
1000	PC303-2	144	cytochrome P450	Petunia x hybrida	BAC53892	26/46	Anthocyanin biosynthesis
1001	PC303-4	144	cytochrome P450	Petunia x hybrida	BAC53892	26/46	Anthocyanin biosynthesis
1002	PC303-3	134	probable 60S ribosomal protein L27a	Picea mariana	AAC32151	32/43	protein biosynthesis
1010	PC307-4	161	GTP binding	Arabidopsis thaliana	At4g18800	22/25	intracellular protein transport; mall GTPase mediated signal transduction
1011	PC308-1	166	serine-type endopeptidase inhibitor (see 266-3)	Arabidopsis thaliana	At5g43580	14/21	response to wounding
1012	PC308-2	171	hAT family dimerisation domain, putative	Medicago truncatula	ABE88160	29/55	-
1013	PC308-3	172	hAT family dimerisation domain, putative	Medicago truncatula	ABE88160	32/59	-
1014	PC308-4	172	hAT family dimerisation domain, putative	Medicago truncatula	ABE88160	32/59	-
1019	PC310-1	301	ATL3	Arabidopsis thaliana	At1g72310	43/85	protein ubiquitination
1020	PC310-2	271	Tyrosin-Decarboxylase (see 312-1)	Petroselinum crispum	AAA33861	68/69	-
1021	PC310-3	280	electron carrier (see 432-3)	Arabidopsis thaliana	At1g26420	49/88	electron transport
1022	PC310-4	299	electron carrier (see 432-3)	Arabidopsis thaliana	At1g26420	53/98	electron transport
1025	PC311-3	122	oxidoreductase/ sphingolipid delta-4 desaturase	Arabidopsis thaliana	At3g61580	28/40	lipid metabolism
1026	PC311-4	212	Tyr-DC (Eli5) (see 312-1)	Petroselinum crispum	AAA33861	70/70	-
1027	PC312-1	246	Tyr-DC (Eli5) (see 311-4)	Petroselinum crispum	AAA33861	72/72	-
1028	PC312-2	269	fructose-bisphosphate aldolase	Arabidopsis thaliana	At2g01140	79/89	pentose-phosphate shunt
1030	PC312-4	248	isoflavone reductase related protein	Pyrus communis	AAC24001	23/26	regulation of nitrogen utilization
1031	PC313-1	213	protein binding / ubiquitin-protein ligase/ zinc ion binding	Arabidopsis thaliana	At2g42350	24/31	protein ubiquitination
1032	PC313-2	212	protein binding / ubiquitin-protein ligase/ zinc ion binding	Arabidopsis thaliana	At2g42350	29/61	protein ubiquitination
1033	PC313-3	212	protein binding / ubiquitin-protein ligase/ zinc ion binding	Arabidopsis thaliana	At2g42350	29/61	protein ubiquitination
1034	PC313-4	213	protein binding / ubiquitin-protein ligase/ zinc ion binding	Arabidopsis thaliana	At2g42350	24/31	protein ubiquitination
1036	PC314-2	179	Eli 7.5 (see 352-3)	Petroselinum crispum	AAG23926	59/59	fatty acid biosynthesis; fatty acid desaturation
1039	PC315-1	147	Avr9/Cf-9 rapidly elicited protein 231 (glycosyltransferase) (303-1)	Arabidopsis thaliana	At1g19300	37/47	carbohydrate biosynthesis
1040	PC315-3	147	Avr9/Cf-9 rapidly elicited protein 231 (glycosyltransferase) (303-1)	Arabidopsis thaliana	At1g19300	37/47	carbohydrate biosynthesis
1041	PC315-4	147	Avr9/Cf-9 rapidly elicited protein 231 (glycosyltransferase) (303-1)	Arabidopsis thaliana	At1g19300	37/47	carbohydrate biosynthesis
1042	PC315-2	144	calmodulin binding (see 787-2)	Arabidopsis thaliana	At2g26190	21/22	N-terminal protein myristoylation
1051	PC318-1	105	serine-type endopeptidase inhibitor (see 360-3)	Arabidopsis thaliana	At3g61980	16/22	biological process unknown
1053	PC318-3	70	(S)-reticuline oxidase-like protein (see 397-1)	Daucus carota	BAB68539	16/22	electron transport
1062	PC320-3	135	SGS3 (SUPPRESSOR OF GENE SILENCING 3) (see 178-2)	Arabidopsis thaliana	At5g23570	17/43	virus induced gene silencing
1063	PC321-2	205	expressed protein	Arabidopsis thaliana	At1g31940	19/24	-
1065	PC321-4	257	probable urea transport protein	Bacteroides fragilis	BAD48607	17/33	-
1066	PC321-6	262	hypothetical protein	Arabidopsis thaliana	At2g36430	61/86	biological process unknown
1067	PC322-1	226	serine/threonine protein kinase-like	Arabidopsis thaliana	At5g35960	51/73	protein amino acid phosphorylation
1068	PC322-2	226	serine/threonine protein kinase-like	Arabidopsis thaliana	At5g35960	51/73	protein amino acid phosphorylation
1069	PC322-3	226	serine/threonine protein kinase-like	Arabidopsis thaliana	At5g35960	51/73	protein amino acid phosphorylation
1070	PC322-4	226	serine/threonine protein kinase-like	Arabidopsis thaliana	At5g35960	51/73	protein amino acid phosphorylation

1071	PC323-1	152	unknown protein	Arabidopsis thaliana	At3g57400	37/49	N-terminal protein myristoylation
1072	PC323-4	152	unknown protein	Arabidopsis thaliana	At3g57400	37/49	N-terminal protein myristoylation
1073	PC323-2	154	RNA binding / aconitate hydratase/ hydro-lyase/ iron ion binding / lyase	Arabidopsis thaliana	At2g05710	19/21	metabolism
1075	PC324-1	95	calmodulin binding (see 787-2)	Arabidopsis thaliana	At2g26190	24/28	N-terminal protein myristoylation
1079	PC325-1	57	unknown protein	Arabidopsis thaliana	At2g42700	15/19	biological process unknown
1084	PC326-2	196	PHS1 (PROPYZAMIDE-HYPERSENSITIVE 1)	Arabidopsis thaliana	At5g23720	52/65	protein amino acid dephosphorylation
1085	PC326-3	199	cytochrome P450 (see 454-3)	Nicotiana tabacum	AAD47832	41/64	electron transport
1091	PC328-1	250	PAD2	Arabidopsis thaliana	At5g66140	58/73	ubiquitin-dependent protein catabolism
1092	PC328-2	257	PAD2	Arabidopsis thaliana	At5g66140	39/74	ubiquitin-dependent protein catabolism
1093	PC328-3	250	PAD2	Arabidopsis thaliana	At5g66140	39/52	ubiquitin-dependent protein catabolism
1095	PC329-1	239	unknown protein	Arabidopsis thaliana	At1g15030	45/71	biological process unknown
1096	PC329-2	239	putative protein kinase	Oryza sativa	AAK27806	22/72	protein amino acid phosphorylation
1097	PC329-4	238	unknown protein	Arabidopsis thaliana	At1g15030	47/79	biological process unknown
1098	PC329-3	240	ADA2A	Arabidopsis thaliana	At3g07740	29/53	biological process unknown
1099	PC330-1	205	SMP2	Arabidopsis thaliana	At4g37120	48/68	positive regulation of cell proliferation; RNA splicing
1100	PC330-2	205	SMP2	Arabidopsis thaliana	At4g37120	48/68	positive regulation of cell proliferation; RNA splicing
1101	PC330-3	205	SMP2	Arabidopsis thaliana	At4g37120	48/68	positive regulation of cell proliferation; RNA splicing
1109	PC332-3	103	binding / transporter	Arabidopsis thaliana	At2g37890	26/34	mitochondrial transport; transport
1115	PC334-1	328	conserved hypothetical protein (see 664-2-3)	Paracoccus denitrificans	ZP_00630616	42/61	-
1116	PC334-2	327	conserved hypothetical protein (see 664-2-3)	Paracoccus denitrificans	ZP_00630616	42/56	-
1118	PC334-4	328	immediate-early fungal elicitor protein CMPG1, Eli17 (see 243-2)	Petroselinum crispum	AAK69402	46/50	protein ubiquitination
1119	PC335-1	140	ubiquitin	Glomus mosseae	CAB96869	20/21	-
1122	PC335-3	139	putative ACC-synthase 1	Lactuca sativa	AAP14019	42/46	biosynthesis; ethylene biosynthesis; ripening
1123	PC336-1-1	340	protein binding / ubiquitin-protein ligase/ zinc ion binding (see 628-3)	Arabidopsis thaliana	At5g01960	100/113	protein ubiquitination
1124	PC336-1-4	340	protein binding / ubiquitin-protein ligase/ zinc ion binding (see 628-3)	Arabidopsis thaliana	At5g01960	101/113	protein ubiquitination
1125	PC336-1-2	140	unknown protein	Arabidopsis thaliana	At4g31880	17/35	-
1127	PC336-2-1	241	unknown protein	Arabidopsis thaliana	At3g62650	22/61	biological process unknown
1128	PC336-2-2	241	unknown protein	Arabidopsis thaliana	At3g62650	23/61	biological process unknown
1129	PC336-2-4	241	unknown protein	Arabidopsis thaliana	At3g62650	23/61	biological process unknown
1130	PC336-2-3	236	putative hydroxyproline-rich glycoprotein	Oryza sativa	AAN04190	23/72	-
1132	PC340-3	640 ?	unknown protein (see 630-1-1)	Arabidopsis thaliana	At5g06370	15/28	biological process unknown
1137	PC345-1	141	carnitine racemase/ catalytic	Arabidopsis thaliana	At4g14440	15/21	metabolism
1139	PC345-4	108	ATPUP3 (see 180-2)	Arabidopsis thaliana	At1g28220	12/22	-
1140	PC346-1	83	transposase	Pisum sativum	AAX51974	23/27	-
1141	PC346-2	83	transposase	Pisum sativum	AAX51974	23/27	-
1144	PC347-1	376	ATTPS8	Arabidopsis thaliana	At1g70290	107/123	metabolism; trehalose biosynthesis
1145	PC347-3	376	EDGP precursor (see 763-4)	Daucus carota	BAA03413	89/113	proteolysis
1146	PC347-2	380	F-box protein family (see 796-4)	Arabidopsis thaliana	At4g22030	51/113	biological process unknown
1147	PC347-4	376	trehalose-phosphate synthase [UDP-forming]	Arabidopsis thaliana	At1g70290	110/123	metabolism; trehalose biosynthesis
1148	PC348-1	325	F-box protein family (see 796-4)	Arabidopsis thaliana	At4g22030	50/111	biological process unknown
1149	PC348-2	325	F-box protein family (see 796-4)	Arabidopsis thaliana	At4g22030	52/111	biological process unknown
1150	PC348-3	326	F-box protein family (see 796-4)	Arabidopsis thaliana	At4g22030	35/71	biological process unknown
1151	PC348-4	326	F-box protein family (see 796-4)	Arabidopsis thaliana	At4g22030	44/103	biological process unknown
1152	PC349-1	208	protein ser/thr kinase/ protein-tyr kinase/ sugar binding (see 654)	Arabidopsis thaliana	At4g27290	19/59	protein amino acid phosphorylation
1153	PC349-2	210	protein ser/thr kinase/ protein-tyr kinase/ sugar binding (see 654)	Arabidopsis thaliana	At4g27290	17/35	protein amino acid phosphorylation
1154	PC349-3	211	protein ser/thr kinase/ protein-tyr kinase/ sugar binding (see 654)	Arabidopsis thaliana	At4g27290	31/63	protein amino acid phosphorylation

1155	PC349-4	210	protein ser/thr kinase/ protein-tyr kinase/ sugar binding (see 654)	Arabidopsis thaliana	At4g27290	23/59	protein amino acid phosphorylation
1156	PC350-1	131	retrotransposon protein, putative, unclassified	Oryza sativa	ABF97084	24/32	-
1158	PC350-3	146	protein serine/threonine kinase/ protein-tyrosine kinase	Arabidopsis thaliana	At3g09830	21/44	protein amino acid phosphorylation
1159	PC350-4	139	catalytic	Arabidopsis thaliana	At5g61840	39/45	biological process unknown
1160	PC351-1	239	PHT5	Arabidopsis thaliana	At2g32830	40/60	phosphate transport; transport
1161	PC351-2	78	kinase	Arabidopsis thaliana	At4g08850	17/25	protein amino acid phosphorylation
1162	PC351-3	237	AHA4	Arabidopsis thaliana	At3g47950	39/41	cation transport; metabolism; proton transport
1163	PC351-4	236	PHT5	Arabidopsis thaliana	At2g32830	30/49	phosphate transport; transport
1166	PC352-3	181	Eli 7.5 (see 314-2)	Petroselinum crispum	AAG23926	36/36	fatty acid biosynthesis; fatty acid desaturation
1167	PC352-4	182	calcium ion binding	Arabidopsis thaliana	At5g61790	24/29	-
1168	PC353-1	102	Esterase/lipase/thioesterase (see 358-3)	Medicago truncatula	ABE88701	22/33	-
1169	PC353-2	102	Esterase/lipase/thioesterase (see 358-3)	Medicago truncatula	ABE88701	22/33	-
1170	PC353-3	102	Esterase/lipase/thioesterase (see 358-3)	Medicago truncatula	ABE88701	22/33	-
1171	PC353-4	102	Esterase/lipase/thioesterase (see 358-3)	Medicago truncatula	ABE88701	22/33	-
1176	PC355-1	324	omega-6 fatty acid desaturase (EC 1.14.99.-) (see 355-3)	Petroselinum crispum	AAB80696	61/63	fatty acid biosynthesis; fatty acid desaturation
1177	PC355-3	324	omega-6 fatty acid desaturase (EC 1.14.99.-) (see 355-1)	Petroselinum crispum	AAB80696	63/75	fatty acid biosynthesis; fatty acid desaturation
1178	PC355-2	320	TUB6 (BETA-6 TUBULIN)	Arabidopsis thaliana	At5g12250	56/56	microtubule-based process; response to cold
1179	PC355-4	320	TUB6 (BETA-6 TUBULIN)	Arabidopsis thaliana	At5g12250	56/56	microtubule-based process; response to cold
1180	PC356-1	305	ARP2/RPL3B	Arabidopsis thaliana	At1g61580	50/61	protein biosynthesis
1181	PC356-2	324	CIP1 (COP1-INTERACTIVE PROTEIN 1)	Arabidopsis thaliana	At5g41790	32/57	regulation of protein import into nucleus
1182	PC356-3	113	UBQ3 (POLYUBIQUITIN 3)	Arabidopsis thaliana	At5g03240	37/37	response to light stimulus; ubiquitin-dependent protein catabolism
1183	PC356-4	113	UBQ3 (POLYUBIQUITIN 3)	Arabidopsis thaliana	At5g03240	37/37	response to light stimulus; ubiquitin-dependent protein catabolism
1184	PC357-1	262	peroxidase	Populus alba	BAE16616	40/66	response to oxidative stress
1186	PC357-3	262	peroxidase	Populus alba	BAE16616	41/62	response to oxidative stress
1187	PC357-4	263	peroxidase	Populus alba	BAE16616	59/79	response to oxidative stress
1190	PC358-3	118	Esterase/lipase/thioesterase (see 353-1)	Medicago truncatula	ABE88701	18/30	-
1192	PC359-1	71	protein serine/threonine kinase/ protein-tyrosine kinase/ sugar binding	Arabidopsis thaliana	At4g27290	20/23	protein amino acid phosphorylation
1193	PC359-2	213	senescence-associated cysteine protease	Brassica oleracea	AAL60580	54/71	proteolysis
1194	PC359-3	213	senescence-associated cysteine protease	Brassica oleracea	AAL60580	56/71	proteolysis
1195	PC359-4	214	MLO8	Arabidopsis thaliana	At2g17480	53/70	cell death; defense response
1198	PC360-3	106	serine-type endopeptidase inhibitor (see 318-1)	Arabidopsis thaliana	At3g61980	16/22	biological process unknown
1200	PC361-1	408	ATP binding / glycine-tRNA ligase/ tRNA ligase	Arabidopsis thaliana	At1g29880	119/135	glycyl-tRNA aminoacylation; protein biosynthesis
1201	PC361-2	408	ATP binding / glycine-tRNA ligase/ tRNA ligase	Arabidopsis thaliana	At1g29880	87/138	glycyl-tRNA aminoacylation; protein biosynthesis
1202	PC361-3	407	ATP binding / glycine-tRNA ligase/ tRNA ligase	Arabidopsis thaliana	At1g29880	118/135	glycyl-tRNA aminoacylation; protein biosynthesis
1204	PC362-1	358	AT2 (see 489-1)	Arabidopsis thaliana	At1g22360	28/39	metabolism
1205	PC362-2	177	unknown protein	Arabidopsis thaliana	At4g15610	23/47	biological process unknown
1206	PC362-3	90	SKIP2 (SKP1 INTERACTING PARTNER 2)	Arabidopsis thaliana	At5g67250	22/29	N-terminal protein myristoylation
1209	PC363-2	227	similar to SCO-spondin	Rattus norvegicus	CAF33425	14/36	-
1210	PC363-3	227	similar to SCO-spondin	Rattus norvegicus	CAF33425	14/36	-
1213	PC364-2	209	pathogenesis-related protein-like protein 2	Daucus carota	BAD04048	34/39	defense response
1214	PC364-3	158	electron carrier (see255-2-2)	Arabidopsis thaliana	At1g30760	26/52	electron transport
1216	PC365-1	256	unknown protein	Arabidopsis thaliana	At2g32980	74/85	-
1220	PC366-1	158	electron carrier	Arabidopsis thaliana	At2g34790	30/52	electron transport
1221	PC366-2	158	electron carrier	Arabidopsis thaliana	At2g34790	26/47	electron transport
1222	PC366-3	158	electron carrier (beste Sequenz)	Arabidopsis thaliana	At2g34790	31/52	electron transport
1223	PC366-4	159	electron carrier	Arabidopsis thaliana	At2g34790	32/53	electron transport

1226	PC367-3	435	YLS9 (YELLOW-LEAF-SPECIFIC GENE 9)	Arabidopsis thaliana	At2g35980	67/132	response to pathogen
1227	PC367-4	436	YLS9 (YELLOW-LEAF-SPECIFIC GENE 9)	Arabidopsis thaliana	At2g35980	67/132	response to pathogen
1232	PC368-2-1	243	RPS6 (RIBOSOMAL PROTEIN S6) (see 369-2)	Arabidopsis thaliana	At4g31700	64/67	protein biosynthesis
1233	PC368-2-2	243	RPS6 (RIBOSOMAL PROTEIN S6) (see 369-2)	Arabidopsis thaliana	At4g31700	63/67	protein biosynthesis
1234	PC368-2-3	243	RPS6 (RIBOSOMAL PROTEIN S6) (see 369-2)	Arabidopsis thaliana	At4g31700	61/67	protein biosynthesis
1235	PC368-2-4	244	RPS6 (RIBOSOMAL PROTEIN S6) (see 369-2)	Arabidopsis thaliana	At4g31700	71/80	protein biosynthesis
1236	PC369-1	209	DNA-binding response regulator, LuxR family	Caulobacter crescentus	NP_419575	14/44	-
1237	PC369-2	244	RPS6 (RIBOSOMAL PROTEIN S6) (see 368-2-1)	Arabidopsis thaliana	At4g31700	67/80	protein biosynthesis
1238	PC369-3	244	RPS6 (RIBOSOMAL PROTEIN S6) (see 380-2)	Arabidopsis thaliana	At4g31700	67/80	protein biosynthesis
1239	PC369-4	244	putative ribosomal protein	Brassica rapa	BAA11393	34/41	protein biosynthesis
1244	PC371-1	199	unknown protein (see 411-1-2)	Arabidopsis thaliana	At1g32690	28/81	biological process unknown
1249	PC372-2	295	hydrolase, hydrolyzing O-glycosyl compounds	Arabidopsis thaliana	At2g26600	32/39	carbohydrate metabolism
1250	PC372-3	243	cell attachment protein in somatic embryogenesis (see 375-1)	Daucus carota	BAD24818	26/67	-
1251	PC372-4	292	peroxidase (see 107-1-4)	Nicotiana tabacum	NP_196153	49/79	response to oxidative stress
1253	PC373-2	256	acyltransferase	Arabidopsis thaliana	At4g00400	38/66	metabolism
1254	PC373-3	278	ALATS (ALANYL-TRNA SYNTHETASE)	Arabidopsis thaliana	At1g50200	53/92	alanyl-tRNA aminoacylation
1255	PC373-4	279	ALATS (ALANYL-TRNA SYNTHETASE)	Arabidopsis thaliana	At1g50200	52/83	alanyl-tRNA aminoacylation
1260	PC375-1	244	cell attachment protein in somatic embryogenesis (see 638-3)	Daucus carota	BAD24818	71/80	-
1261	PC375-2	244	cell attachment protein in somatic embryogenesis (see 638-3)	Daucus carota	BAD24818	71/80	-
1262	PC375-4	244	cell attachment protein in somatic embryogenesis (see 638-3)	Daucus carota	BAD24818	71/80	-
1266	PC376-3	130	1-aminocyclopropane-1-carboxylate oxidase	Artemisia annua	CAA04872	28/33	Ethylene biosynthesis; last step
1268	PC377-1	69	dihydroorotase (see 602-3)	Beta vulgaris	CAC80990	16/21	pyrimidine nucleotide biosynthesis
1279	PC380-2	147	RPS6 (RIBOSOMAL PROTEIN S6) (see 368-2-1)	Arabidopsis thaliana	At4g31700	33/35	protein biosynthesis
1281	PC381-2	194	conserved hypothetical protein	Shewanella oneidensis	NP_717426	21/69	-
1283	PC381-4	194	unknown protein	Arabidopsis thaliana	At2g46900	39/69	biological process unknown
1285	PC382-2	235	electron carrier	Arabidopsis thaliana	At4g20840	28/31	electron transport
1292	PC384-1	175	dihydrolipoamide dehydrogenase precursor	Lycopersicon esculentum	AAN23154	38/44	electron transport
1295	PC384-4	180	ubiquitin-protein ligase (see 394)	Arabidopsis thaliana	At3g07370	21/42	protein ubiquitination
1298	PC385-3	123	Proteinase inhibitor I13, potato inhibitor I	Medicago truncatula	ABE83038	30/40	-
1299	PC385-4	122	Proteinase inhibitor I13, potato inhibitor I	Medicago truncatula	ABE83038	29/40	-
1303	PC386-2	197	structural constituent of ribosome / transcription regulator	Arabidopsis thaliana	At2g44120	58/65	protein biosynthesis
1304	PC387-1	179	copper ion binding	Arabidopsis thaliana	At3g09220	15/28	-
1305	PC387-2	181	DNA-dependent ATPase/nucleotide binding	Arabidopsis thaliana	At2g16440	54/59	DNA replication initiation
1307	PC387-4	179	unknown protein	Arabidopsis thaliana	At3g56040	27/36	biological process unknown
1311	PC388-3	157	ubiquitin-protein ligase (see 177-3)	Arabidopsis thaliana	At2g35930	23/51	protein ubiquitination
1312	PC389-1	95	WRKY4 (see 508-4)	Petroselinum crispum	AAG35658	30/30	regulation of transcription
1313	PC389-2	94	WRKY4 (see 508-4)	Petroselinum crispum	AAG35658	30/30	regulation of transcription
1314	PC389-3	94	WRKY4 (see 508-4)	Petroselinum crispum	AAG35658	30/30	regulation of transcription
1316	PC390-1	232	(S)-reticuline oxidase-like protein (see 397-1)	Daucus carota	BAB68539	32/74	electron transport
1322	PC391-3	171	ubiquitin-protein ligase/ zinc ion binding	Arabidopsis thaliana	At5g60250	16/41	protein ubiquitination
1327	PC392-4	141	copia-type reverse transcriptase-like protein	Arabidopsis thaliana	CAB75469	33/47	-
1328	PC393-1	207	putative glucosyltransferase-2	Oryza sativa	BAC57706	37/68	metabolism
1329	PC393-4	181	putative glucosyltransferase-2	Oryza sativa	BAC57706	27/68	metabolism
1332	PC394-1	136	ubiquitin-protein ligase (see 384-4)	Arabidopsis thaliana	At3g07370	19/38	protein ubiquitination
1333	PC394-2	135	ubiquitin-protein ligase (see 384-4)	Arabidopsis thaliana	At3g07370	19/38	protein ubiquitination
1334	PC394-3	135	ubiquitin-protein ligase (see 384-4)	Arabidopsis thaliana	At3g07370	19/38	protein ubiquitination

1335	PC394-4	135	ubiquitin-protein ligase (see 384-4)	Arabidopsis thaliana	At3g07370	19/38	protein ubiquitination
1336	PC395-1	180	SYP124; t-SNARE	Arabidopsis thaliana	At1g61290	17/30	intracellular protein transport; membrane fusion
1337	PC395-2	144	oxidoreductase (see 591-1)	Arabidopsis thaliana	At4g23420	37/47	metabolism
1341	PC396-2	173	EMB2386 (see 817-2)	Arabidopsis thaliana	At1g02780	21/22	protein biosynthesis; ribosome biogenesis
1342	PC396-3	176	patatin-like protein I, see (399-1)	Nicotiana tabacum	AAF98369	31/57	lipid metabolism
1344	PC397-1	122	(S)-reticuline oxidase-like protein (see 748-2)	Daucus carota	BAB68539	22/32	electron transport
1345	PC397-3	122	(S)-reticuline oxidase-like protein (see 748-2)	Daucus carota	BAB68539	22/32	electron transport
1346	PC397-2	125	putative signal peptidase I	Arabidopsis thaliana	At2g30440	28/35	proteolysis
1347	PC397-4	125	putative signal peptidase I	Arabidopsis thaliana	At2g30440	28/35	proteolysis
1352	PC399-1	176	patatin-like protein I or 3, (see 396-3)	Nicotiana tabacum	AAF98369	32/57	lipid metabolism
1353	PC399-2	177	patatin-like protein I or 3, (see 396-3)	Nicotiana tabacum	AAF98369	32/57	lipid metabolism
1354	PC399-3	175	patatin-like protein I or 3, (see 396-3)	Nicotiana tabacum	AAF98369	32/57	lipid metabolism
1355	PC399-4	175	patatin-like protein I or 3, (see 396-3)	Nicotiana tabacum	AAF98369	32/57	lipid metabolism
1356	PC400-1-1	159	disulfide oxidoreductase/ monooxygenase/ oxidoreductase	Arabidopsis thaliana	At5g61290	18/37	electron transport
1357	PC400-1-2	166	protein binding	Arabidopsis thaliana	At5g21090	44/53	signal transduction
1358	PC400-1-3	92	unknown protein (see 401-2-	Arabidopsis thaliana	At2g21270	26/30	ubiquitin-dependent protein catabolism
1360	PC400-2-1	83	unknown protein	Arabidopsis thaliana	At1g17630	17/26	biological process unknown
1361	PC400-2-2	76	hypothetical protein LOC_Os11g16310 (ident. mit 401-1-4)	Oryza sativa	ABA92487	12/23	-
1362	PC400-2-3	85	DPE2 (DISPROPORTIONATING ENZYME 2)	Arabidopsis thaliana	At2g40840	18/27	maltose metabolism
1363	PC400-2-4	78	ATP binding / transmembrane receptor	Arabidopsis thaliana	At5g17880	16/25	apoptosis; defense response; defense response to pathogen
1364	PC401-1-1	122	(S)-reticuline oxidase-like protein (see 397-1)	Daucus carota	BAB68539	22/32	electron transport
1365	PC401-1-2	132	OSJNBa0052O12.20 (putative reverse transcriptase)	Oryza sativa	NP_914902	19/39	-
1367	PC401-1-4	76	hypothetical protein LOC_Os11g16310 (ident. mit 401-1-4)	Oryza sativa	ABA92487	12/23	-
1368	PC401-2-1	76	hypothetical protein LOC_Os11g16310 (ident. mit 401-1-4)	Oryza sativa	ABA92487	12/23	-
1369	PC401-2-2	76	hypothetical protein LOC_Os11g16310 (ident. mit 401-1-4)	Oryza sativa	ABA92487	12/23	-
1370	PC401-2-3	76	hypothetical protein LOC_Os11g16310 (ident. mit 401-1-4)	Oryza sativa	ABA92487	12/23	-
1371	PC401-2-4	92	unknown protein (see 400-1-3)	Arabidopsis thaliana	At2g21270	26/30	ubiquitin-dependent protein catabolism
1372	PC402-1	308	Pathogenesis-related protein	Petroselinum crispum	AAB47235	15/16	defense response
1373	PC402-2	312	structural constituent of ribosome	Arabidopsis thaliana	At1g04480	58/61	protein biosynthesis
1374	PC402-3	320	putative peroxidase	Solanum tuberosum	CAJ77506	53/76	response to oxidative stress
1375	PC402-4	314	unknown protein	Arabidopsis thaliana	At5g55060	45/100	-
1376	PC403-1	178	S-adenosylmethionine-dependent methyltransferase	Arabidopsis thaliana	At3g15530	35/50	-
1377	PC403-2	199	putative peroxidase	Zinnia elegans	CAI54302	33/49	-
1378	PC403-4	173	S-adenosylmethionine-dependent methyltransferase	Arabidopsis thaliana	At3g15530	14/19	-
1379	PC403-3	173	unknown protein	Arabidopsis thaliana	At3g16590	17/42	biological process unknown
1380	PC404-1	65	unknown	Arabidopsis thaliana	At3g55840	15/19	biological process unknown
1384	PC405-1-1	387	HSP81-2	Arabidopsis thaliana	At5g56030	121/128	protein folding
1388	PC405-2-1	552	hypothetical protein predicted by FGENESH etc.	Oryza sativa	NP_910689	22/25	-
1389	PC405-2-2	421	catalytic	Arabidopsis thaliana	At4g33850	56/76	fatty acid biosynthesis
1390	PC405-2-3	361	rac GTPase activating protein 3 (see 406)	Lotus japonicus	AAC62626	40/97	-
1391	PC405-2-4	128	ethylene-responsive element binding protein 1 homolog	Matricaria chamomilla	BAA87068	38/42	regulation of transcription, DNA-dependent
1392	PC406-1	361	rac GTPase activating protein 3 (see 405-2-3)	Lotus japonicus	AAC62626	40/97	-
1393	PC406-3	361	rac GTPase activating protein 3 (see 405-2-3)	Lotus japonicus	AAC62626	42/97	-
1394	PC406-4	360	rac GTPase activating protein 3 (see 405-2-3)	Lotus japonicus	AAC62626	41/86	-
1396	PC407-1	118	IAR4	Arabidopsis thaliana	At1g24180	38/39	metabolism
1397	PC407-2	119	IAR4	Arabidopsis thaliana	At1g24180	29/30	metabolism

1398	PC407-3	118	IAR4	Arabidopsis thaliana	At1g24180	38/39	metabolism
1400	PC408-1	112	RNA binding / nucleic acid binding / protein transporter (see 590-2)	Arabidopsis thaliana	At3g25150	22/36	nucleocytoplasmic transport; protein import into nucleus
1401	PC408-2	112	conserved hypothetical protein (see 665-2-2)	Corynebacterium efficiens	NP_738153	17/23	-
1402	PC408-3	114	beta-glucan binding protein	Phaseolus vulgaris	AAF19265	18/26	-
1408	PC411-1-1	94	putative protein	Arabidopsis thaliana	At5g16470	19/26	regulation of transcription
1409	PC411-1-2	196	unknown protein (see 371-1)	Arabidopsis thaliana	At1g32690	23/82	biological process unknown
1410	PC411-1-4	199	unknown protein (see 371-1)	Arabidopsis thaliana	At1g32690	28/82	biological process unknown
1416	PC412-1	157	ubiquitin (see 597-4)	Lycopersicon esculentum	CAA51679	46/50	protein modification
1417	PC412-2	336	unknown protein	Arabidopsis thaliana	At4g16146	16/23	-
1418	PC412-4	336	unknown protein	Arabidopsis thaliana	At4g16146	16/23	-
1419	PC412-3	69	putative S-receptor kinase (see 414-2-4)	Oryza sativa	BAD82381	15/22	protein amino acid phosphorylation
1420	PC413-1	300	plasma membrane H+-ATPase	Daucus carota	BAD16685	94/99	cation transport; metabolism; proton transport
1421	PC413-2	300	plasma membrane H+-ATPase	Daucus carota	BAD16685	94/99	cation transport; metabolism; proton transport
1422	PC413-3	300	plasma membrane H+-ATPase	Daucus carota	BAD16685	94/99	cation transport; metabolism; proton transport
1423	PC413-4	300	plasma membrane H+-ATPase	Daucus carota	BAD16685	94/99	cation transport; metabolism; proton transport
1424	PC414-1-1	266	putative helicase (see 414-2-1)	Arabidopsis thaliana	At2g05080	34/70	biological process unknown
1425	PC414-1-3	266	putative helicase (see 414-2-1)	Arabidopsis thaliana	At2g05080	34/70	biological process unknown
1426	PC414-1-2	268	ANAC092; transcription factor	Arabidopsis thaliana	At5g39610	54/68	development
1427	PC414-1-4	269	ANAC092; transcription factor	Arabidopsis thaliana	At5g39610	74/89	development
1428	PC414-2-1	265	putative helicase (see 414-1-1)	Arabidopsis thaliana	At2g05080	34/70	biological process unknown
1429	PC414-2-2	139	ribonuclease/ transcriptional repressor (see 416-1)	Arabidopsis thaliana	At5g10960	35/44	negative regulation of transcription; RNA modification
1430	PC414-2-3	139	ribonuclease/ transcriptional repressor (see 416-1)	Arabidopsis thaliana	At5g10960	35/44	negative regulation of transcription; RNA modification
1431	PC414-2-4	70	putative S-receptor kinase (see 412-3)	Oryza sativa	BAD82381	18/22	protein amino acid phosphorylation
1432	PC416-1	139	ribonuclease/ transcriptional repressor (see 414-2)	Arabidopsis thaliana	At5g10960	35/44	negative regulation of transcription; RNA modification
1433	PC416-2	139	ribonuclease/ transcriptional repressor (see 414-2)	Arabidopsis thaliana	At5g10960	35/44	negative regulation of transcription; RNA modification
1434	PC416-3	139	ribonuclease/ transcriptional repressor (see 414-2)	Arabidopsis thaliana	At5g10960	35/44	negative regulation of transcription; RNA modification
1436	PC417-1	107	oxidoreductase/ zinc ion binding (see 210-3)	Arabidopsis thaliana	At1g23740	15/20	-
1438	PC417-3	142	putative phosphate transporter OsPT8	Oryza sativa	AAN39049	28/46	phosphate transport; transport
1439	PC417-4	109	ATSR1 (SERINE/THREONINE PROTEIN KINASE 1)	Arabidopsis thaliana	At5g01820	22/41	protein amino acid phosphorylation; signal transduction
1448	PC422-1	54	unknown protein (see 512-1)	Arabidopsis thaliana	At5g01750	14/17	biological process unknown
1484	PC431-1	290	unknown protein	Arabidopsis thaliana	At1g19180	33/118	biological process unknown
1485	PC431-2	290	unknown protein	Arabidopsis thaliana	At1g19180	35/118	biological process unknown
1486	PC431-3	290	unknown protein	Arabidopsis thaliana	At1g19180	35/118	biological process unknown
1487	PC431-4	292	unknown protein	Arabidopsis thaliana	At1g19180	33/118	biological process unknown
1489	PC432-2	83	ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding	Arabidopsis thaliana	At5g40010	24/27	-
1490	PC432-3	119	electron carrier (see 310-3)	Arabidopsis thaliana	At1g26420	20/39	electron transport
1491	PC432-4	225	nuclease/ nucleic acid binding	Arabidopsis thaliana	At5g61780	57/74	biological process unknown
1492	PC433-1	187	PREDICTED: similar to dysfusion CG32474-PA	Apis mellifera	XP_624744	13/37	-
1493	PC433-2	187	PREDICTED: similar to dysfusion CG32474-PA	Apis mellifera	XP_624744	13/37	-
1494	PC433-3	187	PREDICTED: similar to dysfusion CG32474-PA	Apis mellifera	XP_624744	13/37	-
1497	PC434-2	80	ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding	Arabidopsis thaliana	At3g28580	16/27	-
1499	PC434-4	107	ATP-dependent helicase/chromatin binding/protein binding/zinc ion binding	Arabidopsis thaliana	At5g44800	17/33	chromatin assembly or disassembly; regulation of transcription
1500	PC435-1	76	lactoylglutathione lyase	Arabidopsis thaliana	At1g15380	15/18	carbohydrate metabolism
1503	PC435-4	76	lactoylglutathione lyase	Arabidopsis thaliana	At1g15380	15/18	carbohydrate metabolism
1507	PC436-4	311	ribosomal protein L15	Oryza sativa	AAN08216	72/82	protein biosynthesis
1516	PC439-1	81	pre-mRNA splicing factor, putative	Arabidopsis thaliana	At3g49430	24/26	biological process unknown

1517	PC439-2	81	pre-mRNA splicing factor, putative	Arabidopsis thaliana	At3g49430	24/26	biological process unknown
1518	PC439-4	81	pre-mRNA splicing factor, putative	Arabidopsis thaliana	At3g49430	24/26	biological process unknown
1532	PC445-1	46	germin (oxalate oxidase) -like protein	Oryza sativa	NP_914653	12/14	-
1533	PC445-2	103	CDC25	Arabidopsis thaliana	At5g03455	25/33	protein amino acid phosphorylation
1535	PC445-4	166	GAD2 (GLUTAMATE DECARBOXYLASE 2) (see 256-3)	Arabidopsis thaliana	At1g65960	43/55	glutamate metabolism; nitrogen compound metabolism
1537	PC446-2	46	germin-like protein 3 (see 448-2)	Oryza sativa	AAC04834	12/14	-
1538	PC446-3	44	germin-like protein 3 (see 448-2)	Oryza sativa	AAC04834	12/14	-
1539	PC446-4	67	spermidine synthase (see 279-1)	Malus x domestica	BAC20170	15/18	-
1540	PC448-1	44	germin-like protein 3 (see 446-2)	Oryza sativa	AAC04834	12/14	-
1541	PC448-2	44	germin-like protein 3 (see 446-2)	Oryza sativa	AAC04834	12/14	-
1542	PC448-4	46	germin-like protein 3 (see 446-2)	Oryza sativa	AAC04834	12/14	-
1549	PC450-2	115	DRT100 (DNA-DAMAGE REPAIR/TOLERATION 100)	Arabidopsis thaliana	At3g12610	25/37	signal transduction
1550	PC450-3	115	DRT100 (DNA-DAMAGE REPAIR/TOLERATION 100)	Arabidopsis thaliana	At3g12610	25/37	signal transduction
1551	PC450-4	115	DRT100 (DNA-DAMAGE REPAIR/TOLERATION 100)	Arabidopsis thaliana	At3g12610	25/37	signal transduction
1552	PC451-1	358	protein serine/threonine kinase/ protein-tyrosine kinase	Arabidopsis thaliana	At2g32850	43/77	protein amino acid phosphorylation
1554	PC451-3	130	cytochrome P450 (see 326-3)	Nicotiana tabacum	AAD47832	19/42	electron transport
1556	PC452-1	217	catalytic	Arabidopsis thaliana	At1g34340	47/66	biological process unknown
1557	PC452-2	219	catalytic	Arabidopsis thaliana	At1g34340	47/66	biological process unknown
1558	PC452-4	218	catalytic	Arabidopsis thaliana	At1g34340	47/66	biological process unknown
1559	PC452-3	216	catalytic	Arabidopsis thaliana	At1g34340	27/46	biological process unknown
1560	PC453-1	154	calcium ion binding	Arabidopsis thaliana	At1g24620	31/50	biological process unknown
1561	PC453-2	158	protein binding	Arabidopsis thaliana	At2g28650	25/44	exocytosis; vesicle docking during exocytosis
1562	PC453-3	158	protein binding	Arabidopsis thaliana	At2g28650	25/44	exocytosis; vesicle docking during exocytosis
1564	PC454-1	75	structural constituent of ribosome	Arabidopsis thaliana	At2g47610	18/21	protein biosynthesis
1565	PC454-2	107	TOM20-3	Arabidopsis thaliana	At3g27080	13/19	protein targeting to mitochondrion
1566	PC454-3	129	cytochrome P450 (see 326-3)	Nicotiana tabacum	AAD47832	18/40	electron transport
1569	PC455-2	254	unknown protein (see 456-1)	Arabidopsis thaliana	At5g40720	24/58	biological process unknown
1572	PC456-1	255	unknown protein (see 455-2)	Arabidopsis thaliana	At5g40720	28/82	biological process unknown
1573	PC456-4	255	unknown protein (see 455-2)	Arabidopsis thaliana	At5g40720	30/82	biological process unknown
1575	PC456-3	257	unknown protein	Arabidopsis thaliana	At5g01710	18/31	-
1578	PC457-3	199	ATP binding / nucleoside-triphosphatase/ nucleotide binding	Arabidopsis thaliana	At2g27600	52/68	-
1581	PC458-2	137	calmodulin binding	Arabidopsis thaliana	At3g58480	24/38	biological process unknown
1582	PC458-3	134	calmodulin binding	Arabidopsis thaliana	At3g58480	24/38	biological process unknown
1583	PC458-4	137	calmodulin binding	Arabidopsis thaliana	At3g58480	24/38	biological process unknown
1584	PC459-1	188	Hypothetical protein CBG02772	Caenorhabditis briggsae	CAE59408	16/47	-
1585	PC459-2	188	Hypothetical protein CBG02772	Caenorhabditis briggsae	CAE59408	16/47	-
1586	PC459-3	188	Hypothetical protein CBG02772	Caenorhabditis briggsae	CAE59408	16/47	-
1587	PC459-4	187	Hypothetical protein CBG02772	Caenorhabditis briggsae	CAE59408	16/47	-
1588	PC460-1	162	unknown protein (see 470-1)	Arabidopsis thaliana	At2g46150	18/24	biological process unknown
1589	PC460-2	166	catalytic	Arabidopsis thaliana	At3g23540	34/39	-
1590	PC460-3	<193	unknown protein	Arabidopsis thaliana	At1g14990	11/17	biological process unknown
1591	PC460-4	166	cytochrome P450 (see 326-3)	Nicotiana tabacum	AAD47832	20/45	electron transport
1592	PC461-1	147	protein binding/ ubiquitin-protein ligase/ zinc ion binding (see 569-1)	Arabidopsis thaliana	At2g02960	22/28	protein ubiquitination
1593	PC461-2	139	unknown protein	Arabidopsis thaliana	At3g06250	24/37	response to red or far red light
1594	PC461-3	120	protein transporter/ transporter	Arabidopsis thaliana	At1g62020	29/33	ER to Golgi transport; intracellular protein transport
1595	PC461-4	131	unknown protein (see 470-1)	Arabidopsis thaliana	At2g46150	20/35	biological process unknown

1596	PC462-1	119	putative glutamyl-tRNA reductase	Oryza sativa	AAG13620	26/38	porphyrin biosynthesis by the C5 pathway
1602	PC463-3	94	unknown protein (see 470-1)	Arabidopsis thaliana	At2g46150	18/24	biological process unknown
1604	PC464-1	67	cytochrome P450	Panax ginseng	BAD15331	17/21	electron transport
1605	PC464-2	67	cytochrome P450	Panax ginseng	BAD15331	17/21	electron transport
1606	PC464-3	67	cytochrome P450	Panax ginseng	BAD15331	17/21	electron transport
1607	PC464-4	67	cytochrome P450	Panax ginseng	BAD15331	17/21	electron transport
1609	PC465-2	71	cytochrome P450	Panax ginseng	BAD15331	19/23	electron transport
1624	PC470-1	191	unknown protein (see 471-3)	Arabidopsis thaliana	At2g46150	31/61	biological process unknown
1625	PC470-2	191	unknown protein (see 471-3)	Arabidopsis thaliana	At2g46150	31/61	biological process unknown
1626	PC470-3	191	unknown protein (see 471-3)	Arabidopsis thaliana	At2g46150	31/61	biological process unknown
1627	PC470-4	191	unknown protein (see 471-3)	Arabidopsis thaliana	At2g46150	31/61	biological process unknown
1628	PC471-1	155	ubiquitin-protein ligase	Arabidopsis thaliana	At3g52450	37/49	protein ubiquitination
1629	PC471-2	154	high molecular weight heat shock protein	Malus x domestica	AAF34134	33/44	protein folding; response to unfolded protein
1630	PC471-3	191	unknown protein (see 470)	Arabidopsis thaliana	At2g46150	31/61	biological process unknown
1631	PC471-4	156	ubiquitin-protein ligase	Arabidopsis thaliana	At3g52450	37/47	protein ubiquitination
1634	PC472-3	191	unknown protein (see 470)	Arabidopsis thaliana	At2g46150	31/61	biological process unknown
1635	PC472-4	137	hydrolase, hydrolyzing O-glycosyl compounds	Arabidopsis thaliana	At1g19940	18/24	carbohydrate metabolism
1636	PC473-1	217	anionic peroxidase (see 261-1)	Petroselinum crispum	AAA98491	30/37	response to oxidative stress
1637	PC473-2	260	putative RNA helicase (see 1-2)	Oryza sativa	AAO72375	14/33	-
1643	PC474-3	67	oxidoreductase	Arabidopsis thaliana	At3g51680	16/21	metabolism
1648	PC476-1	409	unknown protein (see 766-1)	Arabidopsis thaliana	At4g04480	61/133	-
1652	PC477-1	271	unknown protein	Arabidopsis thaliana	At5g23040	29/41	biological process unknown
1655	PC477-3	262	ATPase, coupled to transmembrane movement of substances	Arabidopsis thaliana	At2g36380	37/50	-
1657	PC478-2	252	homogentisate phytylprenyltransferase	Glycine max	AAX56086	19/33	-
1658	PC478-4	252	homogentisate phytylprenyltransferase	Glycine max	AAX56086	19/33	-
1659	PC478-3	237	ABC 1 protein	Nicotiana plumbaginifolia	CAC40990	51/78	-
1663	PC479-4	179	Lifr protein	Mus musculus	AAH31929	15/42	-
1665	PC480-2	<171	hypothetical protein	Mus musculus	XP_156355	16/44	-
1669	PC481-2	396	EDGP precursor (see 763-4)	Daucus carota	BAA03413	59/92	proteolysis
1670	PC481-3	259	PAPS-reductase-like protein (see 651-2)	Catharanthus roseus	AAB05871	68/85	metabolism; sulfate reduction, APS pathway
1671	PC481-4	440	EDGP precursor (see 763-4)	Daucus carota	BAA03413	59/93	proteolysis
1672	PC482-1	332	protein binding (BUT no apo)	Arabidopsis thaliana	At4g18670	42/55	-
1673	PC482-2	340	catalytic/ protein phosphatase type 2C (BUT no apo)	Arabidopsis thaliana	At4g33920	30/67	-
1678	PC483-3	303	anionic peroxidase (see 261-1) (BUT no taq)	Petroselinum crispum	AAA98491	72/87	response to oxidative stress
1679	PC483-4	278	S-adenosylmethionine decarboxylase (BUT no apo)	Nicotiana tabacum	AAB88854	18/36	Amine and polyamine biosynthesis
1681	PC484-2	177	transcription factor similar to VPI/AB13 family regulatory protein	Arabidopsis thaliana	At4g32010	27/58	regulation of transcription
1684	PC485-1	93	ubiquitin-protein ligase	Arabidopsis thaliana	At5g43190	16/26	ubiquitin-dependent protein catabolism
1685	PC485-2	133	RPL27A (RIBOSOMAL PROTEIN L27A)	Arabidopsis thaliana	At1g23290	21/21	protein biosynthesis
1686	PC485-3	130	cytochrome P450 (see PC674-4)	Nicotiana tabacum	AAD47832	15/42	electron transport
1698	PC488-3	416	unknown protein (see 456-4)	Arabidopsis thaliana	At5g40720	26/65	biological process unknown
1699	PC488-4	231	AT2 (see 362-1)	Arabidopsis thaliana	At1g22360	29/70	metabolism
1700	PC489-1	229	AT2 (see 488-4)	Arabidopsis thaliana	At1g22360	39/73	metabolism
1701	PC489-2	289	EP4b	Daucus carota	AAA98927	25/52	lipid metabolism
1702	PC489-3	285	subtilisin-like protein C1 (see 608-1)	Glycine max	AAN12272	34/73	negative regulation of enzyme activity; proteolysis
1703	PC489-4	285	catalytic/ hydrolase (see 608-4)	Arabidopsis thaliana	At3g62860	82/94	aromatic compound metabolism
1706	PC490-3	187	Anthocyanin 5-aromatic acyltransferase (5AT)	Gentiana triflora	BAA74428	22/54	development

1707	PC490-4	145	CYP86A7; oxygen binding	Arabidopsis thaliana	At1g63710	22/36	fatty acid metabolism
1708	PC491-1	268	ATSGS1	Arabidopsis thaliana	At1g10930	13/16	DNA metabolism
1709	PC491-2	270	unknown protein	Arabidopsis thaliana	At5g52590	38/49	biological process unknown
1710	PC491-3	264	GTP binding / GTPase	Arabidopsis thaliana	At2g14120	26/42	-
1712	PC492-1	155	transferase, transferring glycosyl groups	Arabidopsis thaliana	At5g47780	27/34	carbohydrate biosynthesis
1713	PC492-2	214	RLK902 (see 611-2)	Arabidopsis thaliana	At3g17840	37/70	protein amino acid phosphorylation
1714	PC492-3	214	RLK902 (see 611-2)	Arabidopsis thaliana	At3g17840	37/70	protein amino acid phosphorylation
1715	PC492-4	214	RLK902 (see 611-2)	Arabidopsis thaliana	At3g17840	37/70	protein amino acid phosphorylation
1720	PC494-1	153	dnaK-type molecular chaperone hsp70	Oryza sativa	AAX95352	19/19	-
1722	PC494-3	153	dnaK-type molecular chaperone hsp70	Oryza sativa	AAX95352	20/33	-
1724	PC495-1	112	S-locus receptor-like kinase RLK 11	Oryza sativa	AAM90696	22/31	protein amino acid phosphorylation
1725	PC495-2	112	S-locus receptor-like kinase RLK 11	Oryza sativa	AAM90696	23/32	protein amino acid phosphorylation
1727	PC495-4	112	S-locus receptor-like kinase RLK 11	Oryza sativa	AAM90696	20/31	protein amino acid phosphorylation
1728	PC496-1	246	J20 (DNAJ-LIKE 20)	Arabidopsis thaliana	At4g13830	11/23	protein folding
1729	PC496-3	246	J20 (DNAJ-LIKE 20)	Arabidopsis thaliana	At4g13830	11/23	protein folding
1730	PC496-4	248	J20 (DNAJ-LIKE 20)	Arabidopsis thaliana	At4g13830	11/23	protein folding
1732	PC497-1	130	beta-galactosidase/ hydrolase, hydrolyzing O-glycosyl compounds	Arabidopsis thaliana	At3g54440	21/42	carbohydrate metabolism
1733	PC497-2	130	beta-galactosidase/ hydrolase, hydrolyzing O-glycosyl compounds	Arabidopsis thaliana	At3g54440	21/42	carbohydrate metabolism
1734	PC497-3	131	beta-galactosidase/ hydrolase, hydrolyzing O-glycosyl compounds	Arabidopsis thaliana	At3g54440	21/42	carbohydrate metabolism
1735	PC497-4	129	beta-galactosidase/ hydrolase, hydrolyzing O-glycosyl compounds	Arabidopsis thaliana	At3g54440	21/42	carbohydrate metabolism
1736	PC498-1	100	unknown protein	Arabidopsis thaliana	At4g13350	28/33	regulation of GTPase activity
1737	PC498-2	100	unknown protein	Arabidopsis thaliana	At4g13350	28/33	regulation of GTPase activity
1738	PC498-3	101	unknown protein	Arabidopsis thaliana	At4g13350	28/33	regulation of GTPase activity
1739	PC498-4	100	unknown protein	Arabidopsis thaliana	At4g13350	28/33	regulation of GTPase activity
1740	PC499-1	94	1-aminocyclopropane-1-carboxylate synthase	Solanum tuberosum	CAA81749	27/31	Ethylene biosynthesis; last step
1741	PC499-2	94	1-aminocyclopropane-1-carboxylate synthase	Solanum tuberosum	CAA81749	27/31	Ethylene biosynthesis; last step
1742	PC499-3	94	1-aminocyclopropane-1-carboxylate synthase	Solanum tuberosum	CAA81749	27/31	Ethylene biosynthesis; last step
1743	PC499-4	94	1-aminocyclopropane-1-carboxylate synthase	Solanum tuberosum	CAA81749	27/31	Ethylene biosynthesis; last step
1744	PC500-1	92	putative pectinesterase	Oryza sativa	AAT38097	15/30	cell wall modification
1745	PC500-2	100	unknown protein	Arabidopsis thaliana	At4g13350	28/33	regulation of GTPase activity
1746	PC500-3	100	unknown protein	Arabidopsis thaliana	At4g13350	28/33	regulation of GTPase activity
1747	PC500-4	73	SDH2-1	Arabidopsis thaliana	At3g27380	20/21	mitochondrial electron transport, succinate to ubiquinone
1748	PC501-1	263	immediate-early fungal elicitor protein CMPG1, Eli17 (see 334-4)	Petroselinum crispum	AAK69402	43/50	protein ubiquitination
1749	PC501-2	263	immediate-early fungal elicitor protein CMPG1, Eli17 (see 334-4)	Petroselinum crispum	AAK69402	43/50	protein ubiquitination
1750	PC501-3	263	immediate-early fungal elicitor protein CMPG1, Eli17 (see 334-4)	Petroselinum crispum	AAK69402	43/50	protein ubiquitination
1751	PC501-4	263	immediate-early fungal elicitor protein CMPG1, Eli17 (see 334-4)	Petroselinum crispum	AAK69402	43/50	protein ubiquitination
1752	PC502-1	175	rhodopsin-like receptor	Arabidopsis thaliana	At4g34150	39/58	G-protein coupled receptor protein signaling pathway
1753	PC502-2	169	transcription factor	Arabidopsis thaliana	At1g13290	43/52	-
1755	PC502-3	168	transcription factor (see 503-1)	Arabidopsis thaliana	At3g55980	28/60	regulation of transcription
1756	PC503-1	170	transcription factor (see 502-3)	Arabidopsis thaliana	At3g55980	17/23	regulation of transcription
1757	PC503-2	168	transcription factor (see 502-3)	Arabidopsis thaliana	At3g55980	29/60	regulation of transcription
1758	PC503-4	168	transcription factor (see 502-3)	Arabidopsis thaliana	At3g55980	29/60	regulation of transcription
1762	PC504-3	150	DEK1	Arabidopsis thaliana	At1g55350	30/49	cell fate specification; embryonic development
1765	PC505-2	127	DNA binding / transcription factor (see 524-1)	Arabidopsis thaliana	At5g64750	22/36	regulation of transcription, DNA-dependent
1766	PC505-3	127	DNA binding / transcription factor (see 524-1)	Arabidopsis thaliana	At5g64750	22/36	regulation of transcription, DNA-dependent
1767	PC505-4	127	DNA binding / transcription factor (see 524-1)	Arabidopsis thaliana	At5g64750	22/36	regulation of transcription, DNA-dependent

1768	PC506-1	124	ADH2 (see 525-1)	Verbascum thapsus	AAL08686	27/39	-
1769	PC506-2	124	ADH2 (see 525-1)	Verbascum thapsus	AAL08686	27/39	-
1770	PC506-3	124	ADH2 (see 525-1)	Verbascum thapsus	AAL08686	27/39	-
1771	PC506-4	124	ADH2 (see 525-1)	Verbascum thapsus	AAL08686	27/39	-
1776	PC508-1	381	EDS1 (ENHANCED DISEASE SUSCEPTIBILITY 1)	Arabidopsis thaliana	At3g48090	53/102	defense response; lipid metabolism; systemic acquired resistance
1777	PC508-2	260	hydroxy cinnamoyl transferase (see 521-1-2)	Nicotiana tabacum	CAD47830	69/77	-
1778	PC508-3	269	expressed protein	Arabidopsis thaliana	At1g70480	28/42	biological process unknown
1779	PC508-4	252	WRKY4 (see 389-1)	Petroselinum crispum	AAG35658	29/37	regulation of transcription
1781	PC509-2	87	translation elongation factor (see 533-2-3)	Arabidopsis thaliana	At1g57720	24/28	translational elongation
1782	PC509-3	87	translation elongation factor (see 533-2-3)	Arabidopsis thaliana	At1g57720	24/28	translational elongation
1786	PC510-3	81	antiporter/ drug transporter/ transporter	Arabidopsis thaliana	At4g23030	18/27	multidrug transport
1787	PC510-4	81	antiporter/ drug transporter/ transporter	Arabidopsis thaliana	At4g23030	18/27	multidrug transport
1788	PC511-1	181	Thiamine biosynthesis protein ThiC	Burkholderia vietnamensis	ZP_00426125	16/47	-
1790	PC511-4	178	transferase, transferring glycosyl groups	Arabidopsis thaliana	At1g70090	32/35	carbohydrate biosynthesis
1791	PC512-1	89	unknown protein (see 422-1)	Arabidopsis thaliana	At5g01750	13/27	biological process unknown
1792	PC512-2	90	unknown protein (see 422-1)	Arabidopsis thaliana	At5g01750	16/29	biological process unknown
1793	PC512-3	90	unknown protein (see 422-1)	Arabidopsis thaliana	At5g01750	16/29	biological process unknown
1794	PC512-4	91	protein serine/threonine kinase/protein-tyrosine kinase/ sugar binding	Arabidopsis thaliana	At4g21390	16/29	protein amino acid phosphorylation
1795	PC513-1	287	unknown protein	Arabidopsis thaliana	At2g42760	17/40	-
1796	PC513-2	282	unknown protein	Arabidopsis thaliana	At2g42760	13/24	-
1797	PC513-3	287	unknown protein	Arabidopsis thaliana	At2g42760	17/40	-
1798	PC513-4	286	unknown protein	Arabidopsis thaliana	At2g42760	28/55	-
1799	PC514-1	228	BIN2 (BRASSINOSTEROID-INSENSITIVE 2)	Arabidopsis thaliana	At4g18710	57/58	brassinosteroid mediated signaling
1800	PC514-2	217	unknown protein	Arabidopsis thaliana	At1g74790	21/34	biological process unknown
1801	PC514-3	243	immediate-early fungal elicitor protein CMPG1, Eli17 (see 334-4)	Petroselinum crispum	AAK69402	18/20	protein ubiquitination
1803	PC515-1	167	unknown protein	Arabidopsis thaliana	At5g38200	30/44	biological process unknown
1804	PC515-3	170	unknown protein	Arabidopsis thaliana	At5g38200	31/47	biological process unknown
1805	PC515-2	162	ATP binding / ATP-dependent helicase/ helicase/ nucleic acid binding	Arabidopsis thaliana	At2g47680	18/30	nucleobase, nucleoside, nucleotide and nucleic acid metabolism
1807	PC516-1	174	electron carrier (see 707-4)	Arabidopsis thaliana	At1g30700	17/29(58)	electron transport
1808	PC516-2	128	plasma membrane H+-ATPase	Daucus carota	BAD16688	25/26	cation transport; metabolism; proton transport
1809	PC516-4	129	plasma membrane H+-ATPase	Daucus carota	BAD16688	41/42	cation transport; metabolism; proton transport
1810	PC516-3	121	ribosomal protein S18	Drosophila melanogaster	NP_476964	36/42	protein biosynthesis
1819	PC519-1-1	366	unknown protein	Arabidopsis thaliana	At2g36220	17/30	biological process unknown
1820	PC519-1-4	354	glycosyl transferase, family 2	Verminephrobacter eiseniae	EAT71611	23/70	-
1822	PC519-1-3	376	nucleic acid binding / transcription factor/ zinc ion binding	Arabidopsis thaliana	At2g23740	30/65	chromatin modification
1823	PC519-2-1	251	putative uclacyanin 3 (see 529-3)	Oryza sativa	BAD24983	21/46	electron transport
1824	PC519-2-2	248	putative uclacyanin 3 (see 529-3)	Oryza sativa	BAD24983	25/64	electron transport
1825	PC519-2-3	246	putative uclacyanin 3	Oryza sativa	BAD24983	28/69	electron transport
1826	PC519-2-4	243	putative uclacyanin 3 (see 529-3)	Oryza sativa	BAD24983	20/36	electron transport
1827	PC520-1	198	phosphorylase/ transferase, transferring glycosyl groups	Arabidopsis thaliana	At3g29320	24/47	carbohydrate metabolism
1828	PC520-2	246	hydroxy cinnamoyl transferase (see 521-1-2)	Nicotiana tabacum	CAD47830	67/75	-
1829	PC520-3	98	unknown protein	Arabidopsis thaliana	At1g45688	15/27	biological process unknown
1830	PC520-4	263	immediate-early fungal elicitor protein CMPG1, Eli17 (see 334-2)	Petroselinum crispum	AAK69402	42/50	protein ubiquitination
1831	PC521-1-2	238	hydroxy cinnamoyl transferase (see 508-2)	Nicotiana tabacum	CAD47830	25/37	-
1832	PC521-1-3	239	hydroxy cinnamoyl transferase (see 508-2)	Nicotiana tabacum	CAD47830	33/68	-
1833	PC521-1-1	196	patatin-like protein 3 (see 399)	Nicotiana tabacum	AAF98369	36/48	lipid metabolism

1834	PC521-1-4	196	patatin-like protein 3 (see 399)	Nicotiana tabacum	AAF98369	31/56	lipid metabolism
1835	PC521-2-1	194	patatin-like protein 3 (see 399)	Nicotiana tabacum	AAF98369	38/57	lipid metabolism
1836	PC521-2-2	194	patatin-like protein 3 (see 399)	Nicotiana tabacum	AAF98369	47/61	lipid metabolism
1837	PC521-2-3	191	patatin-like protein 3 (see 399)	Nicotiana tabacum	AAF98369	47/61	lipid metabolism
1838	PC521-2-4	194	patatin-like protein 3 (see 399)	Nicotiana tabacum	AAF98369	38/57	lipid metabolism
1839	PC522-1-1	195	patatin-like protein 3 (see 399)	Nicotiana tabacum	AAF98369	36/49	lipid metabolism
1840	PC522-1-2	191	patatin-like protein 3 (see 399)	Nicotiana tabacum	AAF98369	36/49	lipid metabolism
1841	PC522-1-3	193	patatin-like protein 3 (see 399)	Nicotiana tabacum	AAF98369	47/61	lipid metabolism
1843	PC522-2-1	100	unknown protein	Arabidopsis thaliana	At1g45688	13/18	biological process unknown
1844	PC522-2-2	99	unknown protein (see 520-3)	Arabidopsis thaliana	At1g45688	15/30	biological process unknown
1847	PC523-1	87	catalytic/ hydrolase	Arabidopsis thaliana	At3g48410	14/21	biological process unknown
1848	PC523-2	247	H+-exporting ATPase (EC 3.6.3.6), plasmamembrane	Prunus persica	CAB69824	71/77	cation transport; metabolism; proton transport
1849	PC523-3	244	pleiotropic drug resistance (PDR) like protein (see 812-2)	Nicotiana tabacum	BAB92011	28/34	general defense
1850	PC523-4	91	FAD binding / aldehyde-lyase/ oxidoreductase (see 526-1)	Arabidopsis thaliana	At5g51950	23/29	electron transport
1851	PC524-1	127	DNA binding / transcription factor (see 505-2)	Arabidopsis thaliana	At5g64750	21/36	regulation of transcription, DNA-dependent
1854	PC524-4	125	ADH2 (see 525-1)	Verbascum thapsus	AAL08686	19/32	-
1855	PC525-1	124	ADH2 (see 506-1)	Verbascum thapsus	AAL08686	26/39	-
1856	PC525-4	124	ADH2 (see 506-1)	Verbascum thapsus	AAL08686	26/39	-
1859	PC526-1	91	FAD binding / aldehyde-lyase/ oxidoreductase (see 523-4)	Arabidopsis thaliana	At5g51950	23/29	electron transport
1863	PC527-1	148	receptor related protein kinase-like (LRR)	Arabidopsis thaliana	At5g25930	27/49	protein amino acid phosphorylation
1864	PC527-3	148	receptor related protein kinase-like (LRR)	Arabidopsis thaliana	At5g25930	27/49	protein amino acid phosphorylation
1865	PC527-2	147	acyl-CoA oxidase	Aedes aegypti	EAT48670	10/18	-
1866	PC527-4	148	hydroperoxide lyase	Medicago sativa	CAB54847	22/34	electron transport
1867	PC528-1	164	transcription factor	Arabidopsis thaliana	At5g52510	32/54	regulation of transcription
1868	PC528-2	163	transcription factor	Arabidopsis thaliana	At5g52510	32/54	regulation of transcription
1869	PC528-3	163	transcription factor	Arabidopsis thaliana	At5g52510	32/54	regulation of transcription
1870	PC528-4	164	transcription factor	Arabidopsis thaliana	At5g52510	32/54	regulation of transcription
1871	PC529-1	249	EIG-I24	Nicotiana tabacum	BAB16426	40/56	-
1872	PC529-2	221	transcription factor Pti 4	Lycopersicon esculentum	AAC50047	32/46	regulation of transcription, DNA-dependent
1873	PC529-3	291	putative uclacyanin 3 (see 519-2-2)	Oryza sativa	BAD24983	37/66	electron transport
1874	PC529-4	192	pathogenesis-related protein-like protein 1	Daucus carota	BAD04841	12/14	defense response
1879	PC531-1	135	leucine-rich repeat receptor-like protein kinase	Pyrus pyrifolia	AAT28309	20/35	protein amino acid phosphorylation
1881	PC531-3	161	elicitor induced glycoprotein iEP4	Daucus carota	AAB50843	26/48	lipid metabolism
1882	PC531-4	198	patatin-like protein 3 (see 521-1-1)	Nicotiana tabacum	AAF98369	33/38	lipid metabolism
1886	PC532-1-4	139	unknown protein (see 533-1-1)	Arabidopsis thaliana	At2g36090	23/46	biological process unknown
1891	PC533-1-1	139	unknown protein (see 532-1-4)	Arabidopsis thaliana	At2g36090	22/46	biological process unknown
1892	PC533-1-2	139	unknown protein (see 532-1-4)	Arabidopsis thaliana	At2g36090	14/25	biological process unknown
1893	PC533-1-3	138	unknown protein (see 532-1-4)	Arabidopsis thaliana	At2g36090	14/25	biological process unknown
1894	PC533-1-4	137	unknown protein (see 532-1-4)	Arabidopsis thaliana	At2g36090	14/25	biological process unknown
1897	PC533-2-3	87	translation elongation factor (see 509-2)	Arabidopsis thaliana	At1g57720	24/28	translational elongation
1898	PC533-2-4	71	alcohol dehydrogenase	Calamus usitatus	AAB17255	21/23	-
1903	PC535-1	194	anionic peroxidase (see 113-2)	Petroselinum crispum	AAA98491	63/64	response to oxidative stress
1905	PC535-4	192	unknown protein	Arabidopsis thaliana	At1g53280	37/63	biological process unknown
1906	PC536-3	202	put. 4-methyl-5(B-hydroxyethyl)-thiazol monophosphate biosynthesis enzyme	Oryza sativa	BAD54224	25/48	-
1907	PC536-4	188	glycine dehydrogenase A	Flaveria pringlei	CAA81076	38/40	-
1909	PC538-3	153	protein binding / voltage-gated potassium channel	Arabidopsis thaliana	At5g41330	22/29	potassium ion transport

1910	PC538-4	153	protein binding / voltage-gated potassium channel	Arabidopsis thaliana	At5g41330	22/29	potassium ion transport
1912	PC539-2	133	ATP binding / nucleoside-triphosphatase/ nucleotide binding	Arabidopsis thaliana	At4g24850	15/24	-
1923	PC543-1	165	electron carrier/ oxidoreductase	Arabidopsis thaliana	At5g44360	16/36	electron transport
1927	PC544-1	260	calmodulin-binding protein	Arabidopsis thaliana	At4g31000	34/85	-
1928	PC544-2	260	calmodulin-binding protein	Arabidopsis thaliana	At4g31000	34/85	-
1929	PC544-4	260	calmodulin-binding protein	Arabidopsis thaliana	At4g31000	34/85	-
1930	PC544-3	260	LIP1	Arabidopsis thaliana	At2g20860	45/46	glycine catabolism; lipoic acid biosynthesis
1931	PC545-1-1	201	T17H7.4	Arabidopsis thaliana	AAD32929	17/19	-
1932	PC545-1-4	60	transcription factor (see 96-1)	Arabidopsis thaliana	At2g40140	17/19	regulation of transcription
1938	PC545-2-2	198	oxidoreductase	Arabidopsis thaliana	At2g36690	31/45	biosynthesis
1939	PC546-1	159	calreticulin precursor	Nicotiana plumbaginifolia	CAA95999	48/52	-
1940	PC546-2	159	calreticulin precursor	Nicotiana plumbaginifolia	CAA95999	48/52	-
1941	PC546-4	159	calreticulin precursor	Nicotiana plumbaginifolia	CAA95999	48/52	-
1942	PC546-3	151	putative protein phosphatase	Oryza sativa	BAB12036	36/49	protein amino acid dephosphorylation
1943	PC547-1-1	144	IAR3 (IAA-ALANINE RESISTANT 3); metallopeptidase	Arabidopsis thaliana	At1g51760	41/46	proteolysis
1944	PC547-1-4	144	IAR3 (IAA-ALANINE RESISTANT 3); metallopeptidase	Arabidopsis thaliana	At1g51760	41/46	proteolysis
1945	PC547-1-2	143	unknown protein	Arabidopsis thaliana	At1g15060	27/37	-
1946	PC547-1-3	415	isoflavone reductase related protein	Pyrus communis	AAC24001	80/103	regulation of nitrogen utilization
1948	PC547-2-2	140	IAR3 (IAA-ALANINE RESISTANT 3); metallopeptidase	Arabidopsis thaliana	At1g51760	40/45	proteolysis
1949	PC547-2-3	144	IAR3 (IAA-ALANINE RESISTANT 3); metallopeptidase	Arabidopsis thaliana	At1g51760	40/46	proteolysis
1950	PC547-2-4	140	IAR3 (IAA-ALANINE RESISTANT 3); metallopeptidase	Arabidopsis thaliana	At1g51760	40/45	proteolysis
1952	PC549-3	65	unknown protein	Arabidopsis thaliana	At1g44960	18/21	biological process unknown
1957	PC550-1-3	146	ATP binding	Arabidopsis thaliana	At5g43730	15/26	apoptosis; defense response; defense response to pathogen
1962	PC550-2-3	144	RPS5 (RESISTANT TO P. SYRINGAE 5) (similar to 550-1-3)	Arabidopsis thaliana	At1g12220	18/40	defense response; hypersensitive response
1963	PC551-1	107	protein serine/threonine kinase/ protein-tyrosine kinase	Arabidopsis thaliana	At5g15730	27/32	protein amino acid phosphorylation
1964	PC551-2	108	protein serine/threonine kinase/ protein-tyrosine kinase	Arabidopsis thaliana	At5g15730	28/33	protein amino acid phosphorylation
1965	PC551-3	107	protein serine/threonine kinase/ protein-tyrosine kinase	Arabidopsis thaliana	At5g15730	28/33	protein amino acid phosphorylation
1966	PC551-4	107	protein serine/threonine kinase/ protein-tyrosine kinase	Arabidopsis thaliana	At5g15730	28/33	protein amino acid phosphorylation
1967	PC552-1	175	ubiquitin-protein ligase	Arabidopsis thaliana	At1g20780	40/55	protein ubiquitination
1968	PC552-3	175	ubiquitin-protein ligase	Arabidopsis thaliana	At1g20780	40/55	protein ubiquitination
1969	PC552-4	175	ubiquitin-protein ligase	Arabidopsis thaliana	At1g20780	40/55	protein ubiquitination
1970	PC552-2	136	oxidoreductase	Arabidopsis thaliana	At4g23430	18/23	metabolism
1976	PC554-2	161	PDF1	Arabidopsis thaliana	At3g25800	47/53	regulation of phosphorylation
1980	PC555-2	130	protein transporter	Arabidopsis thaliana	At3g15980	23/44	intracellular protein transport
1988	PC557-2	81	expressed protein (see 796-3)	Arabidopsis thaliana	At3g46430	20/26	biological process unknown
1989	PC557-3	368	anionic peroxidase (see 113-2)	Petroselinum crispum	AAA98491	33/36	response to oxidative stress
2000	PC560-2	269	transporter	Arabidopsis thaliana	At5g35160	21/33	transport
2004	PC561-2	216	phenylcoumaran benzylic ether reductase homolog F2	Forsythia x intermedia	AAF64175	18/29	regulation of nitrogen utilization
2015	PC564-1	271	protein serine/threonine kinase/ protein-tyrosine kinase (see 276-1)	Arabidopsis thaliana	At2g28590	30/43	protein amino acid phosphorylation
2017	PC564-3	271	ATGPX6 (GLUTATHIONE PEROXIDASE 6)	Arabidopsis thaliana	At4g11600	51/66	response to oxidative stress
2018	PC564-4	277	ubiquitin-protein ligase putative arm repeat protein (see 276-4)	Arabidopsis thaliana	At2g44900	37/55	ubiquitin-dependent protein catabolism
2020	PC566-2	221	EDGP precursor (see 763-4)	Daucus carota	BAA03413	31/39	proteolysis
2024	PC567-2	198	Int1	Citrobacter freundii	AAL59385	15/16	-
2027	PC568-1	481	ATP binding / kinase/ protein kinase/ protein serine/threonine	Arabidopsis thaliana	At1g77280	63/116	protein amino acid phosphorylation; response to stress
2028	PC568-2	455	Mal d 1-associated protein	Malus x domestica	AAP86780	55/107	-
2029	PC568-3	473	structural constituent of ribosome / transcription regulator	Arabidopsis thaliana	At3g13580	64/98	protein biosynthesis

2031	PC569-1	209	protein binding / ubiquitin-protein ligase/ zinc ion binding (see 300-1)	Arabidopsis thaliana	At2g02960	47/70	protein ubiquitination
2032	PC569-2	152	catalytic/ protein phosphatase type 2C (see 300-2)	Arabidopsis thaliana	At3g62260	30/47	-
2034	PC569-4	209	cytochrome P450 monooxygenase CYP72A68	Glycine max	ABC68405	43/69	electron transport
2039	PC575-1	129	ACLA-3	Arabidopsis thaliana	At1g09430	41/43	acetyl-CoA biosynthesis
2040	PC575-2	570	Pirin	Lycopersicon esculentum	AAF22236	82/124	-
2041	PC575-3	137	probable epoxide hydrolase (EC 3.3.2.3)	Solanum tuberosum	AAA81891	16/22	-
2042	PC575-4	562	Pirin	Lycopersicon esculentum	AAF22236	85/124	-
2044	PC576-2	373	expressed protein	Arabidopsis thaliana	At5g24740	32/80	-
2046	PC576-4	376	unknown protein	Arabidopsis thaliana	At2g39690	74/93	biological process unknown
2047	PC577-1	143	transferase, transferring glycosyl groups	Arabidopsis thaliana	At1g05170	41/47	protein amino acid glycosylation
2048	PC577-2	282	unknown protein	Oryza sativa	XP_466550	42/92	-
2049	PC577-3	371	unknown protein	Arabidopsis thaliana	At1g35350	36/58	-
2050	PC577-4	229	unknown protein	Arabidopsis thaliana	At1g28100	55/73	biological process unknown
2051	PC578-1	198	PPI1 (PROTON PUMP INTERACTOR 1)	Arabidopsis thaliana	At4g27500	19/40	regulation of proton transport
2052	PC578-2	187	unknown protein (see 579-1)	Arabidopsis thaliana	At4g16144	29/51	biological process unknown
2053	PC578-3	187	unknown protein (see 579-1)	Arabidopsis thaliana	At4g16144	28/51	biological process unknown
2054	PC578-4	199	PPI1 (PROTON PUMP INTERACTOR 1)	Arabidopsis thaliana	At4g27500	18/32	regulation of proton transport
2055	PC579-1	187	unknown protein (see 578-2)	Arabidopsis thaliana	At4g16144	27/51	biological process unknown
2056	PC579-2	181	MGD1 (MONOGALACTOSYLDIACYLGLYCEROL SYNTHASE 1)	Arabidopsis thaliana	At4g31780	45/60	galactolipid biosynthesis; glycolipid biosynthesis
2057	PC579-3	187	protein binding / ubiquitin-protein ligase/ zinc ion binding	Arabidopsis thaliana	At1g73760	17/39	protein ubiquitination
2058	PC579-4	187	unknown protein (see 578-2)	Arabidopsis thaliana	At4g16144	28/51	biological process unknown
2059	PC580-1	171	oxidoreductase (see 228-1)	Arabidopsis thaliana	At1g72680	35/55	lignin biosynthesis
2061	PC580-3	<296	ILR1 (IAA-LEUCINE RESISTANT 1) (BUT no apo)	Arabidopsis thaliana	At3g02875	52/78	auxin metabolism; proteolysis
2062	PC580-3'	266	putative IAA amido hydrolase	Oryza sativa	BAC20815	43/61	proteolysis
2065	PC581-2	59	kinesin motor protein-related	Arabidopsis thaliana	At2g21380	15/17	microtubule-based movement
2066	PC581-3	83	protein serine/threonine kinase/ protein-tyrosine kinase	Arabidopsis thaliana	At1g56145	17/26	protein amino acid phosphorylation
2067	PC581-4	83	protein serine/threonine kinase/ protein-tyrosine kinase	Arabidopsis thaliana	At1g56145	17/26	protein amino acid phosphorylation
2068	PC582-1	310	PAB8	Arabidopsis thaliana	At1g49760	27/46	-
2069	PC582-2	310	PAB8	Arabidopsis thaliana	At1g49760	45/84	-
2070	PC582-3	308	PAB8	Arabidopsis thaliana	At1g49760	39/80	-
2071	PC582-4	303	Proteasome component region PCI	Medicago truncatula	ABE93374	38/49	-
2072	PC583-1	323	XPO1A	Arabidopsis thaliana	At5g17020	20/21	protein export from nucleus; protein import into nucleus, docking
2075	PC583-4	198	heat shock protein 70	Rhynchopus sp.	AAQ24864	22/65	-
2076	PC584-1	<320	oxidoreductase (see 395-2) (BUT no taq)	Arabidopsis thaliana	At4g23420	18/23	metabolism
2077	PC584-2	<307	tumor-related protein (BUT no apo)	Nicotiana glanca x N.langsdorfi	BAA05475	18/30	-
2078	PC584-3	<303	anionic peroxidase (see 113-2)	Petroselinum crispum	AAA98491	33/46	response to oxidative stress
2079	PC584-4	<237	coatomer alpha subunit-like protein	Lotus corniculatus var. Japonicu	CAE45585	16/36	ER to Golgi vesicle-mediated transport; intracellular protein transport
2082	PC585-3	249	anionic peroxidase (see 589-4)	Petroselinum crispum	AAA98491	34/35	response to oxidative stress
2084	PC586-1	131	unknown protein (see 764-4)	Arabidopsis thaliana	At1g73430	26/35	intracellular protein transport
2085	PC586-2	128	conserved hypothetical protein (ähnlich 664-1-1) (see 738)	Corynebacterium efficiens	NP_738153	13/15	-
2088	PC588-1	438	G protein beta subunit 2	Solanum tuberosum	AAL07488	66/76	signal transduction
2089	PC588-2	438	G protein beta subunit 2	Solanum tuberosum	AAL07488	66/76	signal transduction
2090	PC588-3	446	isocitrate dehdrogenase (NADP+)	Apium graveolens	CAA73139	143/148	glyoxylate cycle; isocitrate metabolism; metabolism
2091	PC588-4	450	protein binding / ubiquitin-protein ligase/ zinc ion binding	Arabidopsis thaliana	At1g73950	54/104	protein ubiquitination
2092	PC589-1	385	ABI1L1	Arabidopsis thaliana	At2g46225	35/54	actin nucleation; trichome morphogenesis (sensu Magnoliophyta)
2093	PC589-2	233	acitic chitinase	Glycine max	BAA77676	27/41	carbohydrate metabolism

2095	PC589-4	381	peroxidase precursor (see 113-2)	Petroselinum crispum	AAA98491	31/31	response to oxidative stress
2096	PC590-1	311	NADH-glutamate synthase	Medicago sativa	AAB46617	49/55	Glutamine synthetase/GOGAT pathway /assimilation of ammonia
2097	PC590-2	317	RNA binding / nucleic acid binding / protein transporter (see 408-1)	Arabidopsis thaliana	At3g25150	16/21	nucleocytoplasmic transport; protein import into nucleus
2099	PC590-4	317	CDC48 (CELL DIVISION CYCLE 48)	Arabidopsis thaliana	At3g09840	39/48	-
2100	PC591-1	223	oxidoreductase (see 395-2)	Arabidopsis thaliana	At4g23420	15/23	metabolism
2102	PC591-3	215	glycosyltransferase NTGT5b	Nicotiana tabacum	BAD93690	30/46	metabolism
2103	PC591-4	221	oxidoreductase	Arabidopsis thaliana	At4g23340	34/51	metabolism
2105	PC593-2	388	probable transposase - soybean transposon mariner element Soymar1	Medicago truncatula	ABE81132	21/46	-
2106	PC593-3	385	probable transposase - soybean transposon mariner element Soymar1	Medicago truncatula	ABE81132	25/74	-
2107	PC593-4	390	CRT3 (CALRETICULIN 3)	Arabidopsis thaliana	At1g08450	85/107	biological process unknown
2108	PC594-1	249	ERHC3048	Homo sapiens	AAQ88908	16/37	-
2109	PC594-2	250	gamete-specific homeodomain protein (see 595-1)	Chlamydomonas reinhardtii	AAL14119	17/40	-
2110	PC594-3	249	ERHC3048	Homo sapiens	AAQ88908	16/37	-
2112	PC595-1	250	gamete-specific homeodomain protein (see 594-2)	Chlamydomonas reinhardtii	AAL14119	17/40	-
2113	PC595-2	249	hypothetical protein SAV5905	Streptomyces avermitilis	NP_827082	15/41	-
2114	PC595-3	267	gamete-specific homeodomain protein (see 594-2)	Chlamydomonas reinhardtii	AAL14119	16/37	-
2115	PC595-4	251	ERHC3048	Homo sapiens	AAQ88908	16/37	-
2116	PC596-1	229	oxidoreductase	Arabidopsis thaliana	At5g06060	44/75	metabolism
2117	PC596-2	231	Phenylalanine ammonia-lyase 1 (see 240-2)	Petroselinum crispum	CAA34715	31/36	Phenylpropanoid biosynthesis; first step
2118	PC596-3	229	TATA-binding protein	Zea mays	AAA65942	73/76	Transcription
2119	PC596-4	229	TATA-binding protein	Zea mays	AAA65942	73/76	Transcription
2120	PC597-1	211	Rab geranylgeranyl transferase beta subunit	Metasequoia glyptostroboides	BAB91474	61/70	-
2121	PC597-2	194	eukaryotic translation initiation factor 2 beta subunit-like chain	Solanum tuberosum	ABB86256	26/29	translational initiation
2122	PC597-3	222	Rab geranylgeranyl transferase beta subunit	Metasequoia glyptostroboides	BAB91474	59/68	-
2123	PC597-4	224	ubiquitin (see 412-1)	Lycopersicon esculentum	CAA51679	47/47	protein modification
2124	PC598-1	144	ubiquitin-protein ligase/ zinc ion binding	Arabidopsis thaliana	At1g12470	43/47	protein ubiquitination
2127	PC598-4	153	peroxisomal membrane protein 22 kDa (PMP22)	Arabidopsis thaliana	At4g04470	27/35	biological process unknown
2132	PC600-2-1	436	nucleotide binding	Arabidopsis thaliana	At1g72960	47/70	biological process unknown
2133	PC600-2-2	433	unknown protein	Arabidopsis thaliana	At4g27720	54/72	-
2134	PC600-2-3	388	unknown protein	Arabidopsis thaliana	At1g64650	26/51	-
2135	PC600-2-4	437	heat shock protein binding / unfolded protein binding	Arabidopsis thaliana	At3g08970	86/144	protein folding
2138	PC602-1	176	unknown protein	Arabidopsis thaliana	At4g14746	27/62	biological process unknown
2139	PC602-2	176	unknown protein	Arabidopsis thaliana	At4g14746	27/62	biological process unknown
2140	PC602-3	175	dihydroorotase (see 377-1)	Beta vulgaris	CAC80990	21/23	pyrimidine nucleotide biosynthesis
2141	PC602-4	176	unknown protein	Arabidopsis thaliana	At4g14746	26/62	biological process unknown
2144	PC603-3	153	pleiotropic drug resistance (PDR)-type ABC transporter (see 523-3)	Nicotiana tabacum	BAD07483	36/51	general defense
2146	PC604-1	140	beta-amylase PCT-BMYI (see 786-2)	Solanum tuberosum	AAK84008	19/36	carbohydrate metabolism; polysaccharide catabolism
2147	PC604-2	138	putative MtN19 (see 628-4)	Oryza sativa	BAD01246	24/37	-
2152	PC605-3	73	S-adenosylmethionine decarboxylase proenzyme	Ipomoea nil	Q96471	20/23	Amine and polyamine biosynthesis
2155	PC606-2	637	ATZW10	Arabidopsis thaliana	At2g32900	98/164	chromosome segregation
2156	PC607-1	299	B1 type cyclin	Daucus carota	BAC15746	23/24	cell cycle; cell division; regulation of progression through cell cycle
2157	PC607-2	297	kinase (see 610-2)	Arabidopsis thaliana	At1g19390	69/98	protein amino acid phosphorylation
2158	PC607-3	297	kinase (see 610-2)	Arabidopsis thaliana	At1g19390	69/98	protein amino acid phosphorylation
2159	PC607-4	297	kinase (see 610-2)	Arabidopsis thaliana	At1g19390	69/98	protein amino acid phosphorylation
2160	PC608-1	285	subtilisin-like protease C1 (see 489-3)	Glycine max	AAN12272	34/73	negative regulation of enzyme activity; proteolysis
2161	PC608-2	289	probable cell-wall-bound EP4 protein, 45K, precursor	Daucus carota	S56181	25/52	lipid metabolism

2162	PC608-3	285	subtilisin-like protease C1 (see 489-3)	Glycine max	AAN12272	34/73	negative regulation of enzyme activity; proteolysis
2163	PC608-4	285	catalytic/ hydrolase (see 489-4)	Arabidopsis thaliana	At3g62860	82/94	aromatic compound metabolism
2164	PC609-1	260	unknown protein	Oryza sativa	NP_922728	55/90	-
2165	PC609-2	260	unknown protein	Oryza sativa	NP_922728	55/90	-
2166	PC609-3	260	unknown protein	Oryza sativa	NP_922728	53/90	-
2167	PC609-4	260	unknown protein	Oryza sativa	NP_922728	53/90	-
2169	PC610-2	305	kinase (see 607-2) (BUT no Apo)	Arabidopsis thaliana	At1g19390	60/98	protein amino acid phosphorylation
2170	PC610-3	260	Nod-factor receptor 1a	Lotus corniculatus var. Japonicu	CAE02591	22/38	cell wall catabolism; protein amino acid phosphorylation
2171	PC610-4	247	DNA binding	Arabidopsis thaliana	At1g51060	41/43	chromosome organization and biogenesis; nucleosome assembly
2173	PC611-2	214	RLK902 (see 492-1)	Arabidopsis thaliana	At3g17840	37/70	protein amino acid phosphorylation
2174	PC611-3	214	RLK902 (see 492-1)	Arabidopsis thaliana	At3g17840	37/70	protein amino acid phosphorylation
2175	PC611-4	214	RLK902 (see 492-1)	Arabidopsis thaliana	At3g17840	32/70	protein amino acid phosphorylation
2176	PC614-1	186	F-box	Prunus mume	BAC66626	23/69	-
2177	PC614-2	153	elicitor induced glycoprotein iEP4	Daucus carota	AAB50843	22/47	lipid metabolism
2178	PC614-3	153	elicitor induced glycoprotein iEP4	Daucus carota	AAB50843	23/47	lipid metabolism
2179	PC614-4	153	SAB (SABRE)	Arabidopsis thaliana	At1g58250	38/50	multidimensional cell growth
2184	PC617-1	94	MAP1C (METHIONINE AMINOPEPTIDASE 1B)	Arabidopsis thaliana	At1g13270	24/30	N-terminal protein amino acid modification; proteolysis
2185	PC617-2	94	MAP1C (METHIONINE AMINOPEPTIDASE 1B)	Arabidopsis thaliana	At1g13270	23/30	N-terminal protein amino acid modification; proteolysis
2186	PC617-3	94	putative polyprotein-related	Medicago truncatula	ABE77847	22/31	-
2188	PC618-2-1	305	ACRE 74 (U-box, homologous to PC CMPG1) (see 620-3)	Nicotiana tabacum	AAP03884	48/106	protein ubiquitination
2189	PC618-2-2	209	putative cinnamyl alcohol dehydrogenase (Os10g0194200) (see 701-2-4)	Oryza sativa	NP_001064283	37/46	-
2190	PC618-2-3	315	metal ion binding	Arabidopsis thaliana	At4g14710	78/90	biological process unknown
2191	PC618-2-4	374	probable retroelement polyprotein	Arabidopsis thaliana	AAG10812	25/75	DNA integration
2192	PC620-1	306	ACRE 74 (U-box, homologous to PC CMPG1) (see 618-2-1)	Nicotiana tabacum	AAP03884	32/78	protein ubiquitination
2193	PC620-2	304	ACRE 74 (U-box, homologous to PC CMPG1) (see 618-2-1)	Nicotiana tabacum	AAP03884	39/80	protein ubiquitination
2194	PC620-3	305	ACRE 74 (U-box, homologous to PC CMPG1) (see 618-2-1)	Nicotiana tabacum	AAP03884	47/105	protein ubiquitination
2195	PC620-4	304	ACRE 74 (U-box, homologous to PC CMPG1) (see 618-2-1)	Nicotiana tabacum	AAP03884	39/78	protein ubiquitination
2198	PC621-3	238	mutator-like transposase-like protein	Arabidopsis thaliana	BAB10320	39/71	-
2200	PC623-1	485	SRC2	Glycine max	BAA19769	29/66	-
2201	PC623-2	485	SRC2	Glycine max	BAA19769	31/61	-
2202	PC623-3	182	oxidoreductase	Arabidopsis thaliana	At5g64250	38/49	metabolism
2203	PC623-4	128	hypothetical protein PdenDRAFT_2922 (see 100-2-4)	Paracoccus denitrificans	ZP_00630617	25/30	-
2204	PC624-1	315	putative receptor-like protein kinase	Oryza sativa	AAM91884	50/69	protein amino acid phosphorylation
2205	PC624-2	303	4-coumarate--CoA ligase (4Cl-1)	Petroselinum crispum	P14912	20/24	general phenylpropanoid metabolism
2207	PC624-4	312	MAPKKK19 (see 628-1)	Arabidopsis thaliana	At5g67080	15/20	protein amino acid phosphorylation
2208	PC625-1	253	PAPS-reductase-like protein (see 481-3)	Catharanthus roseus	AAB05871	25/51	metabolism; sulfate reduction, APS pathway
2209	PC625-2	252	unknown protein (see 651-1)	Arabidopsis thaliana	At4g30010	29/52	biological process unknown
2210	PC625-3	252	PAPS-reductase-like protein (see 481-3)	Catharanthus roseus	AAB05871	40/88	metabolism; sulfate reduction, APS pathway
2211	PC625-4	252	PAPS-reductase-like protein (see 481-3)	Catharanthus roseus	AAB05871	33/88	metabolism; sulfate reduction, APS pathway
2212	PC628-1	313	MAPKKK19 (see 624-4)	Arabidopsis thaliana	At5g67080	15/20	protein amino acid phosphorylation
2213	PC628-2	253	PAPS-reductase-like protein (see 625-3)	Catharanthus roseus	AAB05871	34/57	metabolism; sulfate reduction, APS pathway
2214	PC628-3	340	protein binding / ubiquitin-protein ligase/ zinc ion binding (see 336-1-1)	Arabidopsis thaliana	At5g01960	100/113	protein ubiquitination
2215	PC628-4	327	putative MtN19 (see 604-2)	Oryza sativa	BAD01246	27/45	-
2216	PC629-1	162	protein serine/threonine kinase/protein-tyrosine kinase	Arabidopsis thaliana	At1g74360	39/54	protein amino acid phosphorylation
2218	PC629-3	162	protein serine/threonine kinase/protein-tyrosine kinase	Arabidopsis thaliana	At1g74360	39/54	protein amino acid phosphorylation
2219	PC629-4	128	CYP83A1 (CYTOCHROME P450 83A1); oxygen binding	Arabidopsis thaliana	At4g13770	15/34	glucosinolate biosynthesis; response to UV

2220	PC630-1-1	701	unknown protein (see 340-3) (BUT 2x taq)	Arabidopsis thaliana	At5g06370	136/174	biological process unknown
2221	PC630-1-2	74	OSJNBa0039G19.7 (see 634-1)	Oryza sativa	XP_474637	17/24	-
2222	PC630-1-3	701	unknown protein (see 340-3) (BUT 2x taq)	Arabidopsis thaliana	At5g06370	134/174	biological process unknown
2224	PC630-2-1	383	CSLD3 (CELLULOSE SYNTHASE-LIKE 3)	Arabidopsis thaliana	At3g03050	99/127	cell wall biosynthesis; cellulose biosynthesis
2225	PC630-2-2	383	CSLD3 (CELLULOSE SYNTHASE-LIKE 3)	Arabidopsis thaliana	At3g03050	103/127	cell wall biosynthesis; cellulose biosynthesis
2226	PC630-2-3	383	CSLD3 (CELLULOSE SYNTHASE-LIKE 3)	Arabidopsis thaliana	At3g03050	103/127	cell wall biosynthesis; cellulose biosynthesis
2227	PC630-2-4	383	CSLD3 (CELLULOSE SYNTHASE-LIKE 3)	Arabidopsis thaliana	At3g03050	102/127	cell wall biosynthesis; cellulose biosynthesis
2228	PC631-1	234	oxidoreductase	Arabidopsis thaliana	At2g36690	42/61	biosynthesis
2229	PC631-2	233	S-adenosylmethionine decarboxylase uORF	Daucus carota	AAR84407	25/40	-
2230	PC631-3	233	S-adenosylmethionine decarboxylase uORF	Daucus carota	AAR84407	20/20	-
2231	PC631-4	234	oxidoreductase	Arabidopsis thaliana	At2g36690	42/61	biosynthesis
2232	PC632-1	207	protein binding / ubiquitin-protein ligase/ zinc ion binding	Arabidopsis thaliana	At1g28040	24/64	protein ubiquitination
2233	PC632-2	206	OSJNBa0004N05.26	Oryza sativa	XP_473162	41/65	-
2234	PC632-3	207	Pathogenesis-related protein A (PR1-1)	Petroselinum crispum	CAA31086	56/59	defense response
2235	PC632-4	206	OSJNBa0004N05.26	Oryza sativa	XP_473162	41/65	-
2236	PC634-1	186	OSJNBa0039G19.7 (see 630-1-2)	Oryza sativa	XP_474637	18/26	-
2237	PC634-2	185	unknown protein	Arabidopsis thaliana	At1g47550	25/32	biological process unknown
2239	PC634-4	101	expansin S2 precursor	Cucumis sativus	AAB37749	32/33	cell wall organization and biogenesis (sensu Magnoliophyta)
2240	PC637-1	101	expansin S2 precursor	Cucumis sativus	AAB37749	22/25	cell wall organization and biogenesis (sensu Magnoliophyta)
2241	PC637-2	145	unknown protein	Arabidopsis thaliana	At1g65720	18/27	biological process unknown
2243	PC637-4	152	strictosidine synthase	Arabidopsis thaliana	At3g51450	17/37	alkaloid biosynthesis; biosynthesis
2244	PC638-1	294	Biotin synthase protein (EC 2.8.1.6),gene: BIOB	Azoarcus sp. EbN1	CAI06685	15/51	-
2246	PC638-3	242	cell attachment protein in somatic embryogenesis	Daucus carota	BAD24818	57/65	-
2248	PC639-1	394	unknown protein (BUT no taq)	Arabidopsis thaliana	At1g45150	84/115	biological process unknown
2249	PC639-2	274	hypothetical protein, conserved (BUT no apo)	Leishmania major	CAJ02928	20/52	-
2250	PC639-3	322	hypothetical protein, conserved (BUT no taq)	Leishmania major	CAJ02928	20/58	-
2251	PC639-4	406	unknown protein (BUT no taq)	Arabidopsis thaliana	At1g45150	49/77	biological process unknown
2252	PC640-1	244	unknown protein	Arabidopsis thaliana	At1g05575	23/44	biological process unknown
2253	PC640-2	245	unknown protein	Arabidopsis thaliana	At1g05575	28/49	biological process unknown
2254	PC640-3	226	putative phosphate transporter OsPT 12	Oryza sativa	AAN39053	29/42	phosphate transport; transport
2255	PC640-4	249	rab-type small GTP-binding protein	Cicer arietinum	BAA76426	75/82	protein biosynthesis
2256	PC642-1	172	catalytic/ hydrolase	Arabidopsis thaliana	At2g32150	25/49	metabolism
2257	PC642-2	169	binding	Arabidopsis thaliana	At3g03790	23/37	biological process unknown
2258	PC642-3	169	binding	Arabidopsis thaliana	At3g03790	35/55	biological process unknown
2260	PC643-1	227	lipoxygenase (EC 1.13.11.12) (BUT 2x apo)	Nicotiana tabacum	CAA58859	22/31	electron transport; fatty acid biosynthesis
2261	PC643-2	149	lipoxygenase (EC 1.13.11.12)	Nicotiana tabacum	CAA58859	32/43	electron transport; fatty acid biosynthesis
2262	PC643-3	129	WRKY1	Petroselinum crispum	AAD55974	39/39	regulation of transcription
2264	PC644-1	157	putative cytosolic tRNA-Ala synthetase	Oryza sativa	ABG65948	21/24	-
2266	PC644-3	125	ATDGK1/DGK1 (DIACYLGLYCEROL KINASE 1)	Arabidopsis thaliana	At5g07920	38/42	intracellular signaling cascade; protein kinase C activation
2272	PC649-1	<409	zinc ion binding (BUT no taq)	Arabidopsis thaliana	At1g19270	75/101	-
2274	PC651-1	253	unknown protein (see 625-2)	Arabidopsis thaliana	At4g30010	56/81	biological process unknown
2275	PC651-2	254	PAPS-reductase-like protein (see 481-3)	Catharanthus roseus	AAB05871	43/70	metabolism; sulfate reduction, APS pathway
2276	PC651-3	252	cytoplasmic malate dehydrogenase (see 790-2)	Oryza sativa	NP_921996	63/70	-
2277	PC651-4	254	unknown protein	Arabidopsis thaliana	At5g13500	50/71	biological process unknown
2279	PC652-2	214	unknown protein	Arabidopsis thaliana	At3g21190	24/32	-
2280	PC652-3	185	Acyl-ACP thioesterase	Helianthus annus	CAC80371	56/60	fatty acid biosynthesis

2282	PC654-1	95	protein ser/thr kinase/ protein-tyr kinase/ sugar binding (see 349)	Arabidopsis thaliana	At4g27290	23/31	protein amino acid phosphorylation
2283	PC654-2	95	protein ser/thr kinase/ protein-tyr kinase/ sugar binding (see 349)	Arabidopsis thaliana	At4g27290	23/31	protein amino acid phosphorylation
2284	PC654-3	95	protein ser/thr kinase/ protein-tyr kinase/ sugar binding (see 349)	Arabidopsis thaliana	At4g27290	23/31	protein amino acid phosphorylation
2285	PC654-4	92	putative Serine carboxypeptidase III	Arabidopsis thaliana	At3g45010	22/29	-
2294	PC660-1	116	unknown protein	Arabidopsis thaliana	At5g54370	29/37	biological process unknown
2295	PC660-2	97	protein ser/thr kinase/ protein-tyr kinase/ sugar binding (see 349)	Arabidopsis thaliana	At4g27290	15/20	protein amino acid phosphorylation
2296	PC660-3	116	unknown protein	Arabidopsis thaliana	At5g54370	29/37	biological process unknown
2297	PC660-4	116	unknown protein	Arabidopsis thaliana	At5g54370	29/37	biological process unknown
2298	PC661-1	359	OSJNBb0017I01.25	Oryza sativa	XP_474384	13/41	-
2299	PC661-2	354	protein ser/thr kinase/ protein-tyr kinase/ sugar binding (see 349)	Arabidopsis thaliana	At4g27300	34/53	protein amino acid phosphorylation
2300	PC661-3	187	anionic peroxidase (see 113-2)	Petroselinum crispum	AAA98491	55/61	response to oxidative stress
2301	PC661-4	358	NADH glutamate dehydrogenase	Nicotiana plumbaginifolia	CAA69600	49/56	-
2302	PC662-1	288	KU80	Arabidopsis thaliana	At1g48050	46/93	double-strand break repair via nonhomologous end-joining
2303	PC662-2	288	KU80	Arabidopsis thaliana	At1g48050	45/93	double-strand break repair via nonhomologous end-joining
2304	PC662-3	291	KU80	Arabidopsis thaliana	At1g48050	17/35	double-strand break repair via nonhomologous end-joining
2305	PC662-4	288	KU80	Arabidopsis thaliana	At1g48050	46/93	double-strand break repair via nonhomologous end-joining
2306	PC663-1	273	hypothetical protein MtrDRAFT_AC151668g16v1	Medicago truncatula	ABE87175	19/30	-
2307	PC663-2	278	hypothetical protein MtrDRAFT_AC151668g16v1	Medicago truncatula	ABE87175	20/30	-
2308	PC663-3	277	nucleic acid binding	Arabidopsis thaliana	At1g19860	28/45	biological process unknown
2309	PC663-4	272	hypothetical protein MtrDRAFT_AC151668g16v1	Medicago truncatula	ABE87175	20/30	-
2310	PC664-1-1	243	conserved hypothetical protein (see 334-1)	Paracoccus denitrificans	ZP_00630616	42/56	-
2311	PC664-1-2	337	zinc finger (C3HH4-type RING finger) family protein	Arabidopsis thaliana	At3g46620	57/115	-
2312	PC664-1-3	243	conserved hypothetical protein (see 253-1)	Paracoccus denitrificans	ZP_00630616	43/61	-
2313	PC664-1-4	243	conserved hypothetical protein (see 664-2-3)	Paracoccus denitrificans	ZP_00630616	42/56	-
2314	PC664-2-1	243	conserved hypothetical protein (see 664-1-3)	Paracoccus denitrificans	ZP_00630616	28/57	-
2315	PC664-2-2	246	conserved hypothetical protein (see 664-1-3)	Paracoccus denitrificans	ZP_00630616	32/81	-
2316	PC664-2-3	244	conserved hypothetical protein (see 664-1-3)	Paracoccus denitrificans	ZP_00630616	42/83	-
2317	PC664-2-4	242	conserved hypothetical protein (see 664-1-3)	Corynebacterium efficiens	BAC18353	13/14	-
2318	PC665-1-1	243	conserved hypothetical protein (see 664-1-3)	Paracoccus denitrificans	ZP_00630616	43/61	-
2319	PC665-1-2	201	peroxidase (see 722-2)	Linum usitatissimum	AAB02926	56/66	response to oxidative stress
2320	PC665-1-3	243	conserved hypothetical protein (see 664-1-3)	Paracoccus denitrificans	ZP_00630616	42/56	-
2321	PC665-1-4	243	conserved hypothetical protein (see 664-1-3)	Paracoccus denitrificans	ZP_00630616	38/80	-
2323	PC665-2-2	238	conserved hypothetical protein (ähnlich 664-1-1) (see 738)	Corynebacterium efficiens	NP_738153	21/38	-
2324	PC665-2-3	196	peroxidase, cationic (ähnlich 665-1-2)	Vigna angularis	BAA01950	36/45	response to oxidative stress
2325	PC665-2-4	238	conserved hypothetical protein (ähnlich 664-1-1) (see 738)	Corynebacterium efficiens	NP_738153	10/16	-
2327	PC666-2	239	conserved hypothetical protein (ähnlich 664-1-1) (see 738)	Corynebacterium efficiens	NP_738153	13/14	-
2329	PC666-4	220	peroxidase (see 722-2)	Linum usitatissimum	AAB02926	60/78	response to oxidative stress
2330	PC667-1	234	E-class P450, group I (BUT no taq)	Medicago truncatula	ABE81445	16/32	-
2334	PC668-1	155	bacterial-induced class III peroxidase (see 691-1-4)	Gossypium hirsutum	AAL93154	29/38	response to oxidative stress
2337	PC668-4	175	matrix metalloproteinase	Cucumis sativus	CAB76364	20/32	peptidoglycan metabolism; proteolysis
2339	PC669-2	100	catalytic	Arabidopsis thaliana	At3g05170	23/26	metabolism
2340	PC669-3	89	putative RNA-binding protein	Oryza sativa	AAG21903	21/29	-
2341	PC669-4	90	putative RNA-binding protein	Oryza sativa	AAG21903	25/29	-
2342	PC670-1-1	164	cyclophilin	Euphorbia esula	AAF65770	43/49	protein folding
2343	PC670-2-1	162	Cyclophilin (see 108-1-1)	Euphorbia esula	AAF65770	32/34	protein folding
2345	PC670-2-3	162	Cyclophilin (see 108-1-1)	Euphorbia esula	AAF65770	33/34	protein folding

2346	PC670-2-4	47	ATP binding / cysteine-tRNA ligase	Arabidopsis thaliana	At3g56300	14/15	cysteinyl-tRNA aminoacylation
2347	PC672-1	160	bacterial-induced class III peroxidase (see 691-1-4)	Gossypium hirsutum	AAL93154	28/38	response to oxidative stress
2349	PC672-3	263	peroxidase (see 722-2)	Linum usitatissimum	AAB02926	58/68	response to oxidative stress
2351	PC674-1	204	transferase/ transferase, transferring glycosyl groups	Arabidopsis thaliana	At5g01250	22/43	biological process unknown
2354	PC674-4	198	cytochrome P450 (see 326-3)	Nicotiana tabacum	AAD47832	19/33	electron transport
2355	PC675-1	194	protein serine/threonine kinase/ protein-tyrosine kinase	Arabidopsis thaliana	At3g57120	36/48	protein amino acid phosphorylation
2356	PC675-2	195	protein serine/threonine kinase/ protein-tyrosine kinase	Arabidopsis thaliana	At3g57120	36/48	protein amino acid phosphorylation
2357	PC675-3	197	Zinc finger, RING-type; Thioredoxin-related	Medicago truncatula	ABE85589	36/57	-
2358	PC675-4	197	Zinc finger, RING-type; Thioredoxin-related	Medicago truncatula	ABE85589	36/57	-
2359	PC676-1	156	Tyr-DC 2	Petroselinum crispum	Q06086	29/31	-
2360	PC676-2	156	Tyr-DC 2	Petroselinum crispum	Q06086	30/31	-
2361	PC676-3	157	Tyr-DC 2	Petroselinum crispum	Q06086	51/51	-
2362	PC676-4	156	Tyr-DC 2	Petroselinum crispum	Q06086	30/31	-
2363	PC677-1	296	conserved hypothetical protein (see 684-1)	Paracoccus denitrificans	ZP_00630616	43/61	-
2364	PC677-2	148	oxidoreductase (see 724-3)	Arabidopsis thaliana	At3g13610	29/37	secondary metabolism
2369	PC678-3	142	NPC4 (NONSPECIFIC PHOSPHOLIPASE C4)	Arabidopsis thaliana	At3g03530	25/39	phospholipid catabolism
2370	PC678-4	146	GTP binding (see 735-1)	Arabidopsis thaliana	At3g62290	15/16	N-terminal protein myristoylation
2375	PC683-1	125	unknown protein	Arabidopsis thaliana	At2g16650	24/40	biological process unknown
2377	PC683-3	125	unknown protein	Arabidopsis thaliana	At2g16650	24/40	biological process unknown
2378	PC683-4	152	ammonium transporter	Arabidopsis thaliana	At3g24290	39/45	transport
2379	PC684-1	260	conserved hypothetical protein (see 685-2)	Paracoccus denitrificans	ZP_00630616	40/83	-
2380	PC684-2	258	NADH glutamate dehydrogenase	Vitis vinifera	CAC18730	29/41	amino acid metabolism
2381	PC684-3	243	conserved hypothetical protein (see 685-2)	Paracoccus denitrificans	ZP_00630616	43/61	-
2382	PC684-4	257	conserved hypothetical protein (see 685-2)	Paracoccus denitrificans	ZP_00630616	44/61	-
2383	PC685-1	150	oxidoreductase (see 724-3)	Arabidopsis thaliana	At3g13610	36/49	secondary metabolism
2384	PC685-2	243	conserved hypothetical protein (see 687-1)	Paracoccus denitrificans	ZP_00630616	44/61	-
2385	PC685-3	232	ECA1; calcium-transporting ATPase	Arabidopsis thaliana	At1g07810	26/34	manganese ion homeostasis; response to manganese ion
2386	PC685-4	252	Ser/Thr protein kinase	Lotus japonicus	BAD95981	45/82	protein amino acid phosphorylation
2387	PC686-1	244	pyrophosphate-dependent phosphofructokinase beta subunit	Citrus x paradisi	AAC67586	26/27	glycolysis
2388	PC686-2	186	serpin-like protein	Citrus x paradisi	AAN76362	38/61	-
2389	PC686-3	244	60S ribosomal protien L27a	Panax ginseng	BAA96068	35/47	protein biosynthesis, ribosome biogenesis
2390	PC686-4	186	serpin-like protein	Citrus x paradisi	AAN76362	38/61	-
2391	PC687-1	243	conserved hypothetical protein (see 691-1-1)	Paracoccus denitrificans	ZP_00630616	42/61	-
2392	PC687-2	244	conserved hypothetical protein (see 691-1-1)	Paracoccus denitrificans	ZP_00630616	40/81	-
2393	PC687-3	243	conserved hypothetical protein (see 691-1-1)	Paracoccus denitrificans	ZP_00630616	43/61	-
2394	PC687-4	243	conserved hypothetical protein (see 691-1-1)	Paracoccus denitrificans	ZP_00630616	42/61	-
2395	PC689-1	194	protein binding	Arabidopsis thaliana	At4g32640	24/28	ER to Golgi transport; intracellular protein transport
2397	PC689-3	149	enoyl-CoA-hydratase	Avicennia marina	AAF01467	21/27	metabolism
2398	PC689-4	207	cytochrome P450	Asparagus officinalis	BAB40323	34/51	electron transport
2399	PC690-1	198	Phenylalanine ammonia-lyase 1 (see 240-2)	Petroselinum crispum	CAA34715	33/33	Phenylpropanoid biosynthesis; first step
2400	PC690-2	210	Tyr-DC (see 312-1)	Petroselinum crispum	AAA33861	26/38	-
2401	PC690-3	237	inositol or phosphatidylinositol kinase/ phosphotransferase	Arabidopsis thaliana	At2g03890	36/78	-
2402	PC690-4	201	peroxidase (see 672-3)	Linum usitatissimum	AAB02926	57/66	response to oxidative stress
2403	PC691-1-1	246	conserved hypothetical protein (see 692-2)	Paracoccus denitrificans	ZP_00630616	42/56	-
2404	PC691-1-2	241	conserved hypothetical protein (see 692-2)	Paracoccus denitrificans	ZP_00630616	22/32	-
2406	PC691-1-4	147	bacterial-induced class III peroxidase (see 672-1)	Gossypium hirsutum	AAL93154	41/44	response to oxidative stress

2409	PC691-2-3	160	GTP binding (see 735-1)	Arabidopsis thaliana	At3g62290	32/40	N-terminal protein myristoylation
2412	PC692-2	172	conserved hypothetical protein (see 677-1)	Paracoccus denitrificans	ZP_00630616	15/24	-
2413	PC692-3	234	conserved hypothetical protein (see 677-1)	Paracoccus denitrificans	ZP_00630616	15/24	-
2414	PC692-4	233	conserved hypothetical protein (see 677-1)	Paracoccus denitrificans	ZP_00630616	15/24	-
2415	PC693-1	115	eucaroytic translation initiation factor 4A-1	Elaeis oleifera	AAK74073	38/38	-
2416	PC693-2	121	eucaroytic translation initiation factor 4A-1	Elaeis oleifera	AAK74073	31/40	-
2417	PC693-3	115	eucaroytic translation initiation factor 4A-1	Elaeis oleifera	AAK74073	37/38	-
2418	PC693-4	115	eucaroytic translation initiation factor 4A-1	Elaeis oleifera	AAK74073	38/38	-
2423	PC695-1	134	putative helicase	Oryza sativa	AAK54302	17/37	-
2426	PC695-4	160	hypothetical protein Ecan 02000441	Ehrlichia canis str. Jake	ZP_00211102	28/42	-
2427	PC696-1	202	HUA enhancer 2 (HEN2)/DexH-box RNA helicase, putative	Arabidopsis thaliana	At2g06990	60/66	RNA metabolism; specification of floral organ identity
2429	PC696-3	200	PAA2; endopeptidase/ peptidase/ threonine endopeptidase (see 697-1)	Arabidopsis thaliana	At2g05840	57/65	ubiquitin-dependent protein catabolism
2430	PC696-4	200	PAA2; endopeptidase/ peptidase/ threonine endopeptidase (see 697-1)	Arabidopsis thaliana	At2g05840	56/65	ubiquitin-dependent protein catabolism
2431	PC697-1	200	PAA2; endopeptidase/ peptidase/ threonine endopeptidase (see 696-3)	Arabidopsis thaliana	At2g05840	56/65	ubiquitin-dependent protein catabolism
2432	PC697-2	200	PAA2; endopeptidase/ peptidase/ threonine endopeptidase (see 696-3)	Arabidopsis thaliana	At2g05840	55/65	ubiquitin-dependent protein catabolism
2433	PC697-3	200	PAA2; endopeptidase/ peptidase/ threonine endopeptidase (see 696-3)	Arabidopsis thaliana	At2g05840	56/65	ubiquitin-dependent protein catabolism
2434	PC697-4	200	PAA2; endopeptidase/ peptidase/ threonine endopeptidase (see 696-3)	Arabidopsis thaliana	At2g05840	57/65	ubiquitin-dependent protein catabolism
2435	PC699-1	222	putative DNA-binding protein (ethylene responsive)	Oryza sativa	AAP44742	30/39	regulation of transcription, DNA-dependent
2438	PC699-4	225	calcium-transporting ATPase/ calmodulin binding	Arabidopsis thaliana	At3g63380	68/74	calcium ion transport; cation transport; metabolism; proton transport
2439	PC700-1	140	SIGF (RNA POLYMERASE SIGMA-70 FACTOR)	Arabidopsis thaliana	At2g36990	15/26	positive regulation of transcription
2442	PC700-4	139	putative MtN19 (see 604-2)	Oryza sativa	BAD01246	17/30	-
2444	PC701-1-2	325	protein binding	Arabidopsis thaliana	At2g28840	56/104	-
2446	PC701-1-4	323	protein binding	Arabidopsis thaliana	At2g28840	45/61	-
2447	PC701-2-1	328	CPK30; calcium- and calmodulin-dependent protein kinase (see 832-2)	Arabidopsis thaliana	At1g74740	75/109	abscisic acid mediated signaling; N-terminal protein myristoylation
2448	PC701-2-2	130	nucleic acid binding (see 709-4)	Arabidopsis thaliana	At5g32450	35/43	-
2449	PC701-2-3	328	CPK30; calcium- and calmodulin-dependent protein kinase (see 832-2)	Arabidopsis thaliana	At1g74740	75/109	abscisic acid mediated signaling; N-terminal protein myristoylation
2450	PC701-2-4	159	putative cinnamyl alcohol dehydrogenase (Os10g0194200) (see 618-2-2)	Oryza sativa	NP_001064283	31/46	-
2451	PC704-1	130	ATP binding	Arabidopsis thaliana	At1g58807	21/41	apoptosis; defense response; defense response to pathogen
2452	PC704-2	130	ATP binding	Arabidopsis thaliana	At1g58807	16/36	apoptosis; defense response; defense response to pathogen
2453	PC704-3	130	ATP binding	Arabidopsis thaliana	At1g58807	20/41	apoptosis; defense response; defense response to pathogen
2455	PC705-1	104	homeobox leucine zipper protein Hb-2, dehydration-inducible	Craterostigma plantagineum	T09784	20/35	regulation of transcription, DNA-dependent
2457	PC705-3	104	homeobox leucine zipper protein Hb-2, dehydration-inducible	Craterostigma plantagineum	T09784	17/31	regulation of transcription, DNA-dependent
2458	PC705-4	104	homeobox leucine zipper protein Hb-2, dehydration-inducible	Craterostigma plantagineum	T09784	17/31	regulation of transcription, DNA-dependent
2461	PC707-3	182	retrotransposon protein, putative, Ty3-gypsy subclass	Oryza sativa	ABA95229	35/56	DNA integration; RNA-dependent DNA replication
2462	PC707-4	174	electron carrier (see 516-1)	Arabidopsis thaliana	At1g30700	18/33	electron transport
2468	PC709-2	130	exostosin family protein	Arabidopsis thaliana	At5g62220	34/44	biological process unknown
2469	PC709-3	133	ATATH7; ATPase, coupled to transmembrane movement of substances	Arabidopsis thaliana	At3g47750	21/23	N-terminal protein myristoylation
2470	PC709-4	130	nucleic acid binding (see 701-2-2)	Arabidopsis thaliana	At5g32450	37/43	-
2474	PC711-4	150	NtEIG-E80 (elicitor inducible gene product)	Nicotiana tabacum	BAB16427	27/45	-
2475	PC712-1	103	PERK1-like protein kinase (proline extensin-like receptor kinase)	Nicotiana tabacum	BAD06582	16/22	protein amino acid phosphorylation
2476	PC712-2	103	PERK1-like protein kinase (proline extensin-like receptor kinase)	Nicotiana tabacum	BAD06582	14/19	protein amino acid phosphorylation
2480	PC713-1-2	202	bacterial-induced class III peroxidase (see 691-1-4)	Gossypium hirsutum	AAL93154	27/38	response to oxidative stress
2482	PC713-1-4	202	cytochrome P450 (see 326-3)	Nicotiana tabacum	AAD47832	15/29	electron transport
2483	PC713-2-1	149	oxidoreductase (see 685-1)	Arabidopsis thaliana	At3g13610	37/48	secondary metabolism
2484	PC713-2-2	149	oxidoreductase (see 685-1)	Arabidopsis thaliana	At3g13610	37/48	secondary metabolism
2491	PC716-1	149	oxidoreductase (see 685-1)	Arabidopsis thaliana	At3g13610	37/48	secondary metabolism

2492	PC716-2	149	oxidoreductase (see 685-1)	Arabidopsis thaliana	At3g13610	36/48	secondary metabolism
2493	PC716-3	149	oxidoreductase (see 685-1)	Arabidopsis thaliana	At3g13610	37/48	secondary metabolism
2494	PC716-4	149	oxidoreductase (see 685-1)	Arabidopsis thaliana	At3g13610	36/47	secondary metabolism
2495	PC717-1	177	AMP binding / catalytic (see 740-4)	Arabidopsis thaliana	At3g48990	42/54	flavonoid biosynthesis; metabolism
2496	PC717-2	176	AMP binding / catalytic (see 740-4)	Arabidopsis thaliana	At3g48990	36/48	flavonoid biosynthesis; metabolism
2497	PC717-3	177	AMP binding / catalytic (see 740-4)	Arabidopsis thaliana	At3g48990	39/54	flavonoid biosynthesis; metabolism
2500	PC718-2	202	cytochrome P450 (see 326-3)	Nicotiana tabacum	AAD47832	17/29	electron transport
2501	PC718-3	204	bacterial-induced class III peroxidase (see 691-1-4)	Gossypium hirsutum	AAL93154	27/38	response to oxidative stress
2502	PC718-4	224	electron carrier (see 268-2)	Arabidopsis thaliana	At5g44400	55/73	electron transport
2504	PC719-2	176	AMP binding / catalytic (see 740-3)	Arabidopsis thaliana	At3g48990	34/48	flavonoid biosynthesis; metabolism
2505	PC719-3	194	unknown protein	Arabidopsis thaliana	At3g61800	24/41	-
2506	PC719-4	194	expressed protein	Arabidopsis thaliana	At3g61800	42/63	-
2507	PC720-1	194	expressed protein	Arabidopsis thaliana	At3g61800	42/63	-
2508	PC720-2	154	bacterial-induced class III peroxidase (see 691-1-4)	Gossypium hirsutum	AAL93154	29/38	response to oxidative stress
2509	PC720-3	147	protein binding	Arabidopsis thaliana	At2g04740	41/47	-
2510	PC720-4	146	mannitol dehydrogenase (NAD-dependent mannitol DH), Eli 3	Petroselinum crispum	P42754	22/23	-
2511	PC721-1	181	carbohydrate transporter/ sugar porter (see 724-1)	Arabidopsis thaliana	At2g20780	44/59	carbohydrate transport; transport
2512	PC721-2	181	carbohydrate transporter/ sugar porter (see 724-1)	Arabidopsis thaliana	At2g20780	44/59	carbohydrate transport; transport-
2513	PC721-3	181	carbohydrate transporter/ sugar porter (see 724-1)	Arabidopsis thaliana	At2g20780	34/58	carbohydrate transport; transport
2514	PC721-4	201	peroxidase (see 672-3)	Linum usitatissimum	AAB02926	58/66	response to oxidative stress
2515	PC722-1	202	peroxidase (see 672-3)	Linum usitatissimum	AAB02926	47/55	response to oxidative stress
2516	PC722-2	201	peroxidase (see 672-3)	Linum usitatissimum	AAB02926	57/66	response to oxidative stress
2517	PC722-3	201	peroxidase (see 672-3)	Linum usitatissimum	AAB02926	56/66	response to oxidative stress
2518	PC722-4	202	cytochrome P450 (see 326-3)	Nicotiana tabacum	AAD47832	27/54	electron transport
2519	PC723-1	152	putative guanine nucleotide exchange factor	Arabidopsis thaliana	AAL74193	41/50	-
2521	PC723-3	156	putative guanine nucleotide exchange factor	Arabidopsis thaliana	AAL74193	40/49	-
2522	PC723-4	151	putative guanine nucleotide exchange factor	Arabidopsis thaliana	AAL74193	40/49	-
2523	PC724-1	180	carbohydrate transporter/ sugar porter (see 721-1)	Arabidopsis thaliana	At2g20780	38/52	carbohydrate transport; transport
2524	PC724-2	149	GTP binding (see 735-1)	Arabidopsis thaliana	At3g62290	33/33	N-terminal protein myristoylation
2525	PC724-3	149	oxidoreductase (see 685-1)	Arabidopsis thaliana	At3g13610	37/48	secondary metabolism
2527	PC726-1	129	pyruvate dehydrogenase (acetyl-transferring)	Arabidopsis thaliana	At5g50850	34/43	-
2528	PC726-2	128	pyruvate dehydrogenase (acetyl-transferring)	Arabidopsis thaliana	At5g50850	23/28	-
2529	PC726-3	129	pyruvate dehydrogenase (acetyl-transferring)	Arabidopsis thaliana	At5g50850	38/43	-
2530	PC726-4	153	structural constituent of ribosome	Arabidopsis thaliana	At3g49910	20/26	protein biosynthesis
2534	PC727-4	109	dnaK-type molecular chaperone hsp70 (see 177-2)	Medicago sativa	T09535	17/20	-
2535	PC729-1	128	GTP binding (see 735-1)	Arabidopsis thaliana	At3g62290	31/31	N-terminal protein myristoylation
2536	PC729-2	128	GTP binding (see 735-1)	Arabidopsis thaliana	At3g62290	30/31	N-terminal protein myristoylation
2537	PC729-3	128	GTP binding (see 735-1)	Arabidopsis thaliana	At3g62290	31/31	N-terminal protein myristoylation
2541	PC730-3	128	GTP binding (see 735-1)	Arabidopsis thaliana	At3g62290	29/29	N-terminal protein myristoylation
2543	PC735-1	201	GTP binding (see 678-4)	Arabidopsis thaliana	At3g62290	38/52	N-terminal protein myristoylation
2544	PC735-2	238	cytochrome P450 (see 326-3)	Nicotiana tabacum	AAD47832	34/54	electron transport
2545	PC735-3	244	cytochrome P450 (see 326-3)	Nicotiana tabacum	AAD47832	25/46	electron transport
2547	PC738-1	243	conserved hypothetical protein (see 665-2-2)	Corynebacterium efficiens	NP_738153	28/71	-
2548	PC738-2	244	conserved hypothetical protein (see 665-2-2)	Corynebacterium efficiens	NP_738153	33/97	-
2549	PC738-3	249	IDH -1 (isocitrate dehydrogenase subunit 1) (NAD+ dependent)	Arabidopsis thaliana	At4g35260	46/53	-
2550	PC738-4	244	conserved hypothetical protein (see 665-2-2)	Corynebacterium efficiens	NP_738153	36/97	-

2551	PC739-1	201	peroxidase (see 722-2)	Linum usitatissimum	AAB02926	56/66	response to oxidative stress
2552	PC739-2	201	peroxidase (see 722-2)	Linum usitatissimum	AAB02926	56/66	response to oxidative stress
2553	PC739-3	205	peroxidase (see 722-2)	Linum usitatissimum	AAB02926	29/43	response to oxidative stress
2556	PC740-2	152	EDGP precursor (see 763-4)	Daucus carota	BAA03413	35/44	proteolysis
2557	PC740-3	150	AMP binding / catalytic (see 717-1)	Arabidopsis thaliana	At3g48990	31/38	flavonoid biosynthesis; metabolism
2559	PC742-1	324	bacterial-induced class III peroxidase (see 691-1-4)	Gossypium hirsutum	AAL93154	29/38	response to oxidative stress
2562	PC742-4	466	hydrolase/ isopentenyl-diphosphate delta-isomerase	Arabidopsis thaliana	At1g79690	106/155	isoprenoid biosynthesis
2563	PC743-1	225	translation initiation factor eIF-4A.14	Nicotiana tabacum	CAA55641	66/74	Protein biosynthesis
2564	PC743-2	225	translation initiation factor eIF-4A.14	Nicotiana tabacum	CAA55641	71/74	Protein biosynthesis
2565	PC743-3	227	gb protein	Sorghum bicolor	AAL68853	26/37	-
2567	PC745-1	150	cationic peroxidase 2 precursor (PNPC2)	Arachis hypogaea	AAA32676	26/43	-
2568	PC745-2	151	Tyr-DC (see 312-1)	Petroselinum crispum	AAA33861	31/34	-
2575	PC747-1	418	Cyclophilin D	Dictyostelium discoideum	AAD50375	51/135	-
2576	PC747-2	431	cytochrome c-type biogenesis protein	Aquifex aeolicus	NP_213502	26/78	-
2577	PC747-3	411	putative LRR protein	Oryza sativa	AAO23085	19/25	-
2578	PC747-4	65	PAL3 (PHENYL ALANINE AMMONIA-LYASE 3)	Arabidopsis thaliana	At5g04230	19/20	defense response; response to wounding
2579	PC748-1	140	suppressor of K+ transport growth defekt-like protein	Musa acuminata	AAL16668	46/46	-
2580	PC748-2	208	(S)-reticuline oxidase-like protein (see 397-1)	Daucus carota	BAB68539	33/66	electron transport
2582	PC748-4	117	phi-1 (phosphate-induced) (see 749-2)	Nicotiana tabacum	BAA33810	24/38	-
2583	PC749-1	232	hydro-lyase/ lyase	Arabidopsis thaliana	At4g13430	53/77	amino acid metabolism; metabolism
2584	PC749-4	231	hydro-lyase/ lyase	Arabidopsis thaliana	At4g13430	44/61	amino acid metabolism; metabolism
2585	PC749-2	117	phi-1 (phosphate-induced) (see 748-4)	Nicotiana tabacum	BAA33810	26/38	-
2586	PC749-3	230	vf 14-3-3 d protein	Vicia faba	BAB17822	19/23	-
2587	PC750-1	208	(S)-reticuline oxidase-like protein (see 397-1)	Daucus carota	BAB68539	32/66	electron transport
2588	PC750-2	207	(S)-reticuline oxidase-like protein (see 397-1)	Daucus carota	BAB68539	27/55	electron transport
2589	PC750-3	117	60 S ribosomal protein L4 (L1)	Prunus armeniaca	Q9XF97	21/26	protein biosynthesis
2591	PC751-1	175	peroxidase 2	Scutellaria baicalensis	BAA77388	33/43	response to oxidative stress
2592	PC751-2	209	(S)-reticuline oxidase-like protein (see 397-1)	Daucus carota	BAB68539	23/48	electron transport
2596	PC752-1-2	155	receptor protein kinase	Ipomoea trifida	AAC23542	19/29	protein amino acid phosphorylation
2597	PC752-1-3	208	(S)-reticuline oxidase-like protein (see 397-1)	Daucus carota	BAB68539	32/66	electron transport
2598	PC752-1-4	155	COG0477: Permeases of the major facilitator superfamily	Yersinia intermedia ATCC	ZP_00834542	20/47	-
2606	PC753-4	125	putative cinnamoyl-alcohol-dehydrogenase (CAD)	Arabidopsis thaliana	At5g19440	23/41	-
2607	PC754-1	110	expressed protein	Arabidopsis thaliana	At1g66860	23/34	-
2608	PC754-2	194	coatomer alpha subunit	Arabidopsis thaliana	At2g21390	31/37	-
2609	PC754-4	111	coatomer alpha subunit	Arabidopsis thaliana	At2g21390	29/36	-
2611	PC755-1	117	phi-1 (phosphate-induced) (see 748-4)	Nicotiana tabacum	BAA33810	26/38	-
2623	PC758-1	469	binding (see 811-3)	Arabidopsis thaliana	At2g01600	80/145	N-terminal protein myristoylation
2624	PC758-4	477	binding (see 811-3)	Arabidopsis thaliana	At2g01600	85/162	N-terminal protein myristoylation
2625	PC758-2	314	cell attachment protein in somatic embryogenesis (see 759-3)	Daucus carota	BAD24818	102/104	-
2629	PC759-3	314	cell attachment protein in somatic embryogenesis (see 758-2)	Daucus carota	BAD24818	102/104	-
2631	PC760-1-1	314	cell attachment protein in somatic embryogenesis (see 758-2)	Daucus carota	BAD24818	102/104	-
2632	PC760-1-2	314	cell attachment protein in somatic embryogenesis (see 758-2)	Daucus carota	BAD24818	101/104	-
2633	PC760-1-3	314	cell attachment protein in somatic embryogenesis (see 758-2)	Daucus carota	BAD24818	98/104	-
2634	PC760-1-4	261	(S)-reticuline oxidase-like protein (see 397-1)	Daucus carota	BAB68539	38/80	electron transport
2635	PC760-2-1	314	cell attachment protein in somatic embryogenesis (see 758-2)	Daucus carota	BAD24818	101/104	-
2636	PC760-2-2	314	cell attachment protein in somatic embryogenesis (see 758-2)	Daucus carota	BAD24818	100/104	-

2637	PC760-2-3	314	cell attachment protein in somatic embryogenesis (see 758-2)	Daucus carota	BAD24818	101/104	-
2638	PC760-2-4	314	cell attachment protein in somatic embryogenesis (see 758-2)	Daucus carota	BAD24818	101/104	-
2640	PC761-1-2	314	cell attachment protein in somatic embryogenesis (see 758-2)	Daucus carota	BAD24818	102/104	-
2641	PC761-1-3	314	cell attachment protein in somatic embryogenesis (see 758-2)	Daucus carota	BAD24818	102/104	-
2642	PC761-1-4	314	cell attachment protein in somatic embryogenesis (see 758-2)	Daucus carota	BAD24818	102/104	-
2643	PC761-2-1	314	cell attachment protein in somatic embryogenesis (see 758-2)	Daucus carota	BAD24818	101/104	-
2644	PC761-2-2	315	cell attachment protein in somatic embryogenesis (see 758-2)	Daucus carota	BAD24818	75/76	-
2645	PC761-2-3	314	cell attachment protein in somatic embryogenesis (see 758-2)	Daucus carota	BAD24818	101/104	-
2646	PC761-2-4	314	cell attachment protein in somatic embryogenesis (see 758-2)	Daucus carota	BAD24818	98/104	-
2650	PC762-4	231	(S)-reticuline oxidase-like protein (see 397-1)	Daucus carota	BAB68539	33/74	electron transport
2651	PC763-1	228	ATGSL03 (GLUCAN SYNTHASE-LIKE 3);	Arabidopsis thaliana	At2g31960	61/75	beta-1,3 glucan biosynthesis
2653	PC763-3	228	electron carrier	Arabidopsis thaliana	At4g28570	54/74	electron transport
2654	PC763-4	229	EDGP precursor (see 808-4)	Daucus carota	BAA03413	46/49	proteolysis
2655	PC764-1	175	omega-3 fatty acid desaturase (EC 1.14.99.) (see 156-1)	Petroselinum crispum	AAB72241	58/58	fatty acid biosynthesis; fatty acid desaturation
2656	PC764-2	176	26S proteasome regulatory non-ATPase subunit 8	Oryza sativa	BAB78487	37/40	26S proteasome/ATP-dependent degradation of ubiquitinated proteins
2657	PC764-3	175	putative threonyl-tRNA synthetase	Oryza sativa	BAD01219	27/39	electron transport; protein biosynthesis; threonyl-tRNA aminoacylation
2658	PC764-4	174	unknown protein (586-1)	Arabidopsis thaliana	At1g73430	13/15	intracellular protein transport
2659	PC765-1	168	unknown protein	Arabidopsis thaliana	At2g22660	15/34	biological process unknown
2661	PC765-3	161	pectinesterase	Lycopersicon esculentum	CAB08077	25/35	-
2663	PC766-1	157	unknown protein (see 476-1)	Arabidopsis thaliana	At4g04480	18/49	-
2667	PC767-1	201	ferredoxin-nitrite reductase, chloroplast precursor	Spinacia oleracea	P05314	59/66	Nitrate assimilation (denitrification); second step
2668	PC767-2	153	PMZ (see 781-1)	Arabidopsis thaliana	At3g28210	26/42	biological process unknown
2669	PC767-3	152	hypothetical protein CaO19_7420	Candida albicans	XP_716085	17/42	-
2671	PC768-1	198	40 S ribosomal protein S4	Prunus armeniaca	O81363	45/48	protein biosynthesis
2675	PC769-1	228	unknown protein	Arabidopsis thaliana	At2g46420	43/69	biological process unknown
2677	PC769-3	110	acyltransferase homolog	Gentiana triflora	BAA93452	13/23	-
2678	PC769-4	217	hypothetical protein	Oryza sativa	NP_922520	43/48	-
2679	PC770-1	98	CYP71B6 (CYTOCHROME P450 71B6)	Arabidopsis thaliana	At2g24180	17/32	electron transport
2680	PC770-2	97	oxidoreductase (see 782-4)	Arabidopsis thaliana	At4g11410	14/20	metabolism
2683	PC771-1	90	transport inhibitor response 1 (TIR1), AtFBL1	Arabidopsis thaliana	At3g62980	23/29	response to auxin stimulus; ubiquitin-dependent protein catabolism
2684	PC771-2	90	transport inhibitor response 1 (TIR1), AtFBL2	Arabidopsis thaliana	At3g62980	23/29	response to auxin stimulus; ubiquitin-dependent protein catabolism
2691	PC773-1	229	GTP binding / translation elongation factor	Arabidopsis thaliana	At2g31060	26/37	protein biosynthesis
2692	PC773-2	229	AP2 domain-containing transcription factor (ethylene response)	Nicotiana tabacum	CAC12822	32/58	regulation of transcription, DNA-dependent
2694	PC773-4	232	3-isopropylmalate dehydratase large subunit	Trichodesmium erythraeum	ZP_00074911	29/53	-
2696	PC774-2	225	unknown protein	Arabidopsis thaliana	At2g39170	36/53	biological process unknown
2697	PC774-3	238	acyltransferase-like protein (see 283-2)	Arabidopsis thaliana	At3g26040	21/38	biological process unknown
2698	PC774-4	220	putative polyprotein	Arabidopsis thaliana	At4g04410	33/54	-
2700	PC776-2	197	SCL21 (SCARECROW-LIKE 21); transcription factor	Arabidopsis thaliana	At2g04890	42/61	regulation of transcription
2701	PC776-3	195	PR1-1	Petroselinum crispum	S04552	17/19	plant defense
2703	PC777-1	457	PHO1-like protein	Arabidopsis thaliana	At1g14040	86/103	biological process unknown
2704	PC777-2	456	PHO1-like protein	Arabidopsis thaliana	At1g14040	93/113	biological process unknown
2705	PC777-3	405	protein translation factor SUI1 homolog	Pimpinella brachycarpa	AAC61599	94/107	-
2706	PC777-4	262	60 S ribosomal protein L7A (RPL7aB)	Arabidopsis thaliana	At3g62870	77/86	protein biosynthesis
2707	PC778-1	309	Tyrosine protein kinase, active site	Medicago truncatula	ABE81354	34/51	-
2708	PC778-2	309	Tyrosine protein kinase, active site	Medicago truncatula	ABE81354	35/51	-
2709	PC778-4	309	Tyrosine protein kinase, active site	Medicago truncatula	ABE81354	35/51	-

2710	PC778-3	<349	unknown protein	Arabidopsis thaliana	At5g64400	42/74	biological process unknown
2711	PC779-1	245	ATGCN4	Arabidopsis thaliana	At3g54540	54/60	-
2712	PC779-2	246	ATGCN4	Arabidopsis thaliana	At3g54540	72/81	-
2715	PC780-1	131	hypothetical protein	Oryza sativa	NP_918208	17/38	-
2716	PC780-3	131	hypothetical protein	Oryza sativa	NP_918208	17/38	-
2717	PC780-4	131	hypothetical protein	Oryza sativa	NP_918208	16/38	-
2719	PC781-1	113	PMZ (see 767-2)	Arabidopsis thaliana	At3g28210	24/33	biological process unknown
2720	PC781-2	113	PMZ (see 767-2)	Arabidopsis thaliana	At3g28210	24/33	biological process unknown
2721	PC781-4	113	PMZ (see 767-2)	Arabidopsis thaliana	At3g28210	24/33	biological process unknown
2726	PC782-4	76	oxidoreductase (see 770-2)	Arabidopsis thaliana	At4g11410	13/20	metabolism
2731	PC784-1	90	carbohydrate oxidase	Lactuca sativa	AAL77102	20/27	electron transport
2732	PC784-3	90	carbohydrate oxidase	Lactuca sativa	AAL77102	22/28	electron transport
2733	PC784-4	90	carbohydrate oxidase	Lactuca sativa	AAL77102	22/28	electron transport
2736	PC785-2	90	carbohydrate oxidase	Lactuca sativa	AAL77102	22/28	electron transport
2737	PC785-3	90	carbohydrate oxidase	Lactuca sativa	AAL77102	22/28	electron transport
2738	PC785-4	90	carbohydrate oxidase	Lactuca sativa	AAL77102	18/27	electron transport
2739	PC786-1	356	putative xyloglucanase inhibitor (see 787-1)	Solanum tuberosum	AAP84703	79/118	proteolysis
2740	PC786-3	356	putative xyloglucanase inhibitor (see 787-1)	Solanum tuberosum	AAP84703	85/118	proteolysis
2741	PC786-2	353	beta-amylase PCT-BMYI (see 604-1)	Solanum tuberosum	AAK84008	66/72	carbohydrate metabolism; polysaccharide catabolism
2742	PC786-4	356	calmodulin binding (see 787-2)	Arabidopsis thaliana	At2g26190	42/54	N-terminal protein myristoylation
2743	PC787-1	356	putative xyloglucanase inhibitor (see 786-1)	Solanum tuberosum	AAP84703	88/118	proteolysis
2744	PC787-2	358	calmodulin binding (see 278-2)	Arabidopsis thaliana	At2g26190	81/110	N-terminal protein myristoylation
2745	PC787-3	356	putative xyloglucanase inhibitor (see 786-1)	Solanum tuberosum	AAP84703	81/118	proteolysis
2746	PC787-4	356	putative xyloglucanase inhibitor (see 786-1)	Solanum tuberosum	AAP84703	82/118	proteolysis
2747	PC789-1	476	unknown protein (F9L1_1)	Arabidopsis thaliana	At1g15070	98/155	-
2749	PC789-3	71	putative cathepsin B-like cysteine protease	Arabidopsis thaliana	At4g01610	19/22	proteolysis
2750	PC789-4	71	putative cathepsin B-like cysteine protease	Arabidopsis thaliana	At4g01610	19/22	proteolysis
2751	PC790-1	71	putative cathepsin B-like cysteine protease	Arabidopsis thaliana	At4g01610	19/22	proteolysis
2752	PC790-2	229	cytoplasmic malate dehydrogenase (see 651-3)	Oryza sativa	NP_921996	62/69	-
2754	PC790-4	71	putative cathepsin B-like cysteine protease	Arabidopsis thaliana	At4g01610	19/22	proteolysis
2755	PC791-1	228	cytoplasmic malate dehydrogenase (see 651-3)	Oryza sativa	NP_921996	61/69	-
2756	PC791-2	428	unknown protein	Arabidopsis thaliana	At2g44260	75/136	-
2757	PC791-3	428	unknown protein	Arabidopsis thaliana	At2g44260	76/136	-
2758	PC791-4	232	cytoplasmic malate dehydrogenase (see 651-3)	Oryza sativa	NP_921996	49/56	-
2760	PC792-2	243	protein serine/threonine kinase/ protein-tyrosine kinase/ sugar binding	Arabidopsis thaliana	At4g27290	23/62	protein amino acid phosphorylation
2764	PC793-2	229	SHM4 (SERINE HYDROXYMETHYLTRANSFERASE 4)	Arabidopsis thaliana	At4g13930	35/49	glycine metabolism; L-serine metabolism
2766	PC793-4	230	F-box protein family (see 347-2)	Arabidopsis thaliana	At4g22030	35/78	biological process unknown
2767	PC794-1	224	unknown protein	Arabidopsis thaliana	At1g13570	31/47	biological process unknown
2768	PC794-2	227	peroxidase	Arabidopsis thaliana	At1g14550	47/74	response to oxidative stress
2769	PC794-3	226	peroxidase	Arabidopsis thaliana	At1g14550	35/58	response to oxidative stress
2771	PC796-1	174	putative cation transporter	Beta procumbens	CAD38520	29/34	-
2773	PC796-3	174	expressed protein (see 557-2)	Arabidopsis thaliana	At3g46430	33/48	biological process unknown
2774	PC796-4	231	unknown protein (see 793-4)	Arabidopsis thaliana	At4g22030	26/40	biological process unknown
2775	PC797-1	412	CPK2 (Calmodulin-domain protein kinase CDPK ISOFORM 2)	Arabidopsis thaliana	At3g10660	96/136	N-terminal protein myristoylation; protein amino acid phosphorylation
2776	PC797-2	408	ATGPAT6/GPAT6; 1-acylglycerol-3-phosphate O-acyltransferase (see 195-1)	Arabidopsis thaliana	At2g38110	60/82	metabolism
2777	PC797-3	412	CPK2 (Calmodulin-domain protein kinase CDPK ISOFORM 2)	Arabidopsis thaliana	At3g10660	103/136	N-terminal protein myristoylation; protein amino acid phosphorylation

2779	PC798-1	344	unknown protein	Oryza sativa	BAC79895	64/113	-
2780	PC798-2	341	CYP94B1; iron ion binding / monooxygenase/ oxygen binding	Arabidopsis thaliana	At5g63450	42/60	electron transport
2781	PC798-3	341	CYP94B1; iron ion binding / monooxygenase/ oxygen binding	Arabidopsis thaliana	At5g63450	39/60	electron transport
2782	PC798-4	343	unknown protein	Oryza sativa	BAC79895	35/67	-
2783	PC799-1	249	secreted glycoprotein 3	Ipomoea trifida	AAA97903	40/78	-
2784	PC799-2	249	secreted glycoprotein 3	Ipomoea trifida	AAA97903	39/80	-
2785	PC799-3	249	secreted glycoprotein 3	Ipomoea trifida	AAA97903	40/78	-
2786	PC799-4	252	unknown protein	Arabidopsis thaliana	At1g19720	24/41	biological process unknown
2787	PC800-1	174	putative disease resistance protein (CC-NBS-LRR class)	Arabidopsis thaliana	At1g33560	25/50	-
2788	PC800-2	170	cytochrome P450 monooxygenase CYP83H2	Medicago truncatula	ABC59082	15/23	electron transport
2789	PC800-3	175	ethylene-response factor 1 (ERF1)	Arabidopsis thaliana	At3g23240	36/41	-
2792	PC801-2	114	oxidoreductase family (see pc802-3)	Arabidopsis thaliana	At1g12550	19/29	L-serine biosynthesis
2793	PC801-3	114	oxidoreductase family (see pc802-3)	Arabidopsis thaliana	At1g12550	19/29	L-serine biosynthesis
2794	PC801-4	116	putative heat shock protein	Arabidopsis thaliana	At3g47940	26/37	protein folding
2795	PC802-1	108	peroxidase	Zea mays	CAC21393	14/19	response to oxidative stress
2797	PC802-3	114	oxidoreductase family (see 801-2)	Arabidopsis thaliana	At1g12550	19/29	L-serine biosynthesis
2798	PC802-4	108	peroxidase	Zea mays	CAC21393	14/19	response to oxidative stress
2799	PC803-1	114	oxidoreductase family (see 801-2)	Arabidopsis thaliana	At1g12550	19/29	L-serine biosynthesis
2800	PC803-2	114	oxidoreductase family (see 801-2)	Arabidopsis thaliana	At1g12550	18/29	L-serine biosynthesis
2801	PC803-3	110	unknown protein	Arabidopsis thaliana	At3g43240	34/36	-
2804	PC804-1	304	hypothetical protein	Nicotiana benthamiana	BAF02552	36/95	-
2806	PC804-3	304	hypothetical protein	Nicotiana benthamiana	BAF02552	31/83	-
2817	PC808-2	139	no apical meristem (NAM)-like protein (see 830-1)	Glycine max	AAN03466	42/45	regulation of transcription
2818	PC808-3	139	no apical meristem (NAM)-like protein (see 830-1)	Glycine max	AAN03466	43/45	regulation of transcription
2819	PC808-4	143	EDGP precursor (see 277-2)	Daucus carota	BAA03413	44/47	proteolysis
2820	PC809-1	126	putative protein kinase	Arabidopsis thaliana	At3g22750	34/41	-
2821	PC809-2	126	putative protein kinase	Arabidopsis thaliana	At3g22750	39/41	-
2822	PC809-3	99	glutamine-fructose-6-phosphate transaminase 2	Arabidopsis thaliana	BAB03027	15/24	carbohydrate biosynthesis; carbohydrate metabolism; metabolism
2823	PC809-4	125	putative protein kinase	Arabidopsis thaliana	At3g22750	27/29	-
2824	PC810-1	91	expressed protein	Arabidopsis thaliana	At5g56120	24/30	-
2825	PC810-3	72	CYP76C1; heme binding / iron ion binding / monooxygenase	Arabidopsis thaliana	At2g45560	16/23	electron transport
2826	PC810-4	90	carbohydrate oxidase (see 784)	Lactuca sativa	AAL77102	22/28	electron transport
2827	PC811-1	468	unknown protein	Oryza sativa	NP_914373	88/139	-
2828	PC811-2	468	unknown protein	Oryza sativa	NP_914373	89/139	-
2829	PC811-3	140	expressed protein (see 758-1)	Arabidopsis thaliana	At2g01600	34/39	N-terminal protein myristoylation
2830	PC811-4	443	transporter	Arabidopsis thaliana	At4g12650	64/104	transport
2831	PC812-1	358	PD1-like protein	Quercus suber	CAC87937	27/75	electron transport
2832	PC812-2	346	pleiotropic drug resistance (PDR) like protein (see 523-3)	Nicotiana tabacum	BAB92011	29/38	general defense
2833	PC812-3	350	putative xyloglucanase inhibitor (see 786-1)	Solanum tuberosum	AAP84703	47/69	proteolysis
2834	PC812-4	356	putative xyloglucanase inhibitor (see 786-1)	Solanum tuberosum	AAP84703	84/118	proteolysis
2835	PC813-1	316	unknown protein	Arabidopsis thaliana	At3g15395	29/45	biological process unknown
2836	PC813-2	317	ALATS (ALANYL-TRNA SYNTHETASE)	Arabidopsis thaliana	At1g50200	28/35	alanyl-tRNA aminoacylation
2840	PC814-2	232	unknown protein	Arabidopsis thaliana	At5g14310	17/18	biological process unknown
2841	PC814-3	230	RNA binding / nucleic acid binding	Arabidopsis thaliana	At3g52120	51/94	RNA processing
2842	PC814-4	233	RNA binding / nucleic acid binding	Arabidopsis thaliana	At3g52120	44/63	RNA processing
2843	PC815-1	204	putative 2-oxoglutarate-dependent dioxygenase	Arabidopsis thaliana	At1g06650	25/51	-

2844	PC815-2	205	putative 2-oxoglutarate-dependent dioxygenase	Arabidopsis thaliana	At1g06650	30/65	-
2845	PC815-3	205	putative 2-oxoglutarate-dependent dioxygenase	Arabidopsis thaliana	At1g06650	30/65	-
2846	PC815-4	205	putative 2-oxoglutarate-dependent dioxygenase	Arabidopsis thaliana	At1g06650	25/51	-
2847	PC816-1	193	nectarin 5	Nicotiana langsdorffii x Nic	AAP30840	35/63	electron transport
2848	PC816-2	193	nectarin 5	Nicotiana langsdorffii x Nic	AAP30840	35/63	electron transport
2849	PC816-3	188	expressed protein	Arabidopsis thaliana	At1g13360	20/28	-
2850	PC816-4	193	nectarin 5	Nicotiana langsdorffii x Nic	AAP30840	35/63	electron transport
2851	PC817-1	170	unknown protein	Arabidopsis thaliana	At3g14870	16/25	biological process unknown
2852	PC817-2	173	EMB2386 (see 396-2)	Arabidopsis thaliana	At1g02780	24/25	protein biosynthesis, ribosome biogenesis
2853	PC817-3	171	EMB2386 (see 396-2)	Arabidopsis thaliana	At1g02780	24/25	protein biosynthesis, ribosome biogenesis
2855	PC818-1	122	unknown protein (see 820-4)	Arabidopsis thaliana	At1g18740	19/37	biological process unknown
2856	PC818-2	122	unknown protein (see 820-4)	Arabidopsis thaliana	At1g18740	20/37	biological process unknown
2857	PC818-3	124	unknown protein (see 820-1)	Arabidopsis thaliana	At1g74450	21/39	biological process unknown
2858	PC818-4	113	acidic cellulase (EC 3.2.1.4) (see 819-1)	Citrus sinensis	AAB65155	25/36	carbohydrate metabolism
2859	PC819-1	114	acidic cellulase (EC 3.2.1.4) (see 820-2)	Citrus sinensis	AAB65155	26/36	carbohydrate metabolism
2860	PC819-2	117	stress enhanced protein 2 (SEP2)	Arabidopsis thaliana	At2g21970	25/38	photosynthesis light harvesting
2861	PC819-3	119	stress enhanced protein 2 (SEP2)	Arabidopsis thaliana	At2g21970	26/31	photosynthesis light harvesting
2862	PC819-4	119	stress enhanced protein 2 (SEP2)	Arabidopsis thaliana	At2g21970	26/31	photosynthesis light harvesting
2863	PC820-1	120	unknown protein (see 818-3)	Arabidopsis thaliana	At1g74450	18/34	biological process unknown
2864	PC820-2	114	acidic cellulase (EC 3.2.1.4) (see 818-4)	Citrus sinensis	AAB65155	25/36	carbohydrate metabolism
2865	PC820-3	123	unknown protein (see 818-3)	Arabidopsis thaliana	At1g74450	18/40	biological process unknown
2866	PC820-4	124	unknown protein (see 818-1)	Arabidopsis thaliana	At1g18740	16/28	biological process unknown
2871	PC822-1	555	AGO4-1 (see 823-4)	Nicotiana benthamiana	ABC61504	87/187	-
2872	PC822-2	555	AGO4-1 (see 823-4)	Nicotiana benthamiana	ABC61504	85/125	-
2873	PC822-3	566	protein serine/threonine kinase/ protein-tyrosine kinase	Arabidopsis thaliana	At5g01850	133/145	protein amino acid phosphorylation
2874	PC822-4	564	protein serine/threonine kinase/ protein-tyrosine kinase	Arabidopsis thaliana	At5g01850	126/136	protein amino acid phosphorylation
2877	PC823-3	555	AGO4-2 or AGO4-1	Nicotiana benthamiana	ABC61505	126/180	-
2878	PC823-4	554	AGO4-1	Nicotiana benthamiana	ABC61504	76/115	-
2880	PC824-2	222	DNA-binding protein WRKY 3	Petroselinum crispum	S72445	34/38	regulation of transcription
2882	PC824-4	342	Trypsin family protein, expressed	Oryza sativa	ABA92346	31/85	proteolysis
2883	PC825-1	243	S. cerevisiae SEC31-like 2 isoform a	Homo sapiens	NP_056305	17/38	-
2885	PC825-3	248	ATP-sulfurylase	Allium cepa	AAF18998	27/35	sulfate assimilation
2886	PC825-4	243	nucleotide binding / transmembrane receptor	Arabidopsis thaliana	At5g17970	17/36	apoptosis; defense response; defense response to pathogen
2887	PC826-1	235	Tyr-DC (see 312-1)	Petroselinum crispum	AAA33861	39/65	-
2888	PC826-2	224	putative oxysterol binding protein	Oryza sativa	AAM97165	54/74	steroid metabolism
2890	PC826-4	236	polygalakturonase inhibiting protein	Prunus persica	AAQ56728	37/69	-
2891	PC827-1	224	putative oxysterol binding protein	Oryza sativa	AAM97165	56/74	steroid metabolism
2893	PC827-3	234	GDP dissociation inhibitor	Medicago truncatula	CAF02075	31/50	protein transport; regulation of GTPase activity
2898	PC828-4	224	putative oxysterol binding protein	Oryza sativa	AAM97165	49/74	steroid metabolism
2902	PC829-4	176	patatin-like protein 3 (see 521-1-1)	Nicotiana tabacum	AAF98369	26/57	lipid metabolism
2903	PC830-1	139	no apical meristem (NAM)-like protein (see 808-2)	Glycine max	AAN03466	30/45	regulation of transcription
2904	PC830-2	139	no apical meristem (NAM)-like protein (see 808-2)	Glycine max	AAN03466	29/44	regulation of transcription
2911	PC832-1	276	ATCDPK1; calcium- and calmodulin-dependent protein kinase	Arabidopsis thaliana	At1g18890	19/26	abscisic acid mediated signaling; N-terminal protein myristoylation
2912	PC832-2	277	CPK30; calcium- and calmodulin-dependent protein kinase (see 701-2-1)	Arabidopsis thaliana	At1g74740	19/27	abscisic acid mediated signaling; N-terminal protein myristoylation
2913	PC832-3	278	CPK30; calcium- and calmodulin-dependent protein kinase (see 701-2-1)	Arabidopsis thaliana	At1g74740	19/27	abscisic acid mediated signaling; N-terminal protein myristoylation
2914	PC832-4	276	CPK30; calcium- and calmodulin-dependent protein kinase (see 701-2-1)	Arabidopsis thaliana	At1g74740	23/32	abscisic acid mediated signaling; N-terminal protein myristoylation

2915	PC833-1	207	epoxide hydrolase	Nicotiana tabacum	AAB02006	23/40	aromatic compound metabolism
2916	PC833-2	276	CPK30; calcium- and calmodulin-dependent protein kinase (see 832-2)	Arabidopsis thaliana	At1g74740	19/30	abscisic acid mediated signaling; N-terminal protein myristoylation
2917	PC833-3	214	putative transmembrane transport protein	Streptomyces avermitilis	NP_824731	17/46	-
2918	PC833-4	276	CPK30; calcium- and calmodulin-dependent protein kinase (see 832-2)	Arabidopsis thaliana	At1g74740	23/32	abscisic acid mediated signaling; N-terminal protein myristoylation
2919	PC835-1	230	inner mitochondrial membrane protein	Arabidopsis thaliana	At1g72750	45/90	-
2921	PC835-3	230	inner mitochondrial membrane protein	Arabidopsis thaliana	At1g72750	49/90	-
2923	PC836-1	243	fatty acid desaturase/hydroxylase-like protein Eli7.1 (see 256-4)	Petroselinum crispum	AAG24521	48/61	fatty acid biosynthesis; fatty acid desaturation
2924	PC836-4	240	fatty acid desaturase/hydroxylase-like protein Eli7.1 (see 256-4)	Petroselinum crispum	AAG24521	22/26	fatty acid biosynthesis; fatty acid desaturation
2926	PC836-3	298	GTP binding	Arabidopsis thaliana	At1g08410	24/45	biological process unknown
2927	PC837-1	226	omega-6 fatty acid desaturase (EC 1.14.99.-) (see 355-1)	Petroselinum crispum	AAB80696	24/35	fatty acid biosynthesis; fatty acid desaturation
2929	PC837-3	230	GTP binding (see 735-1, protein level)	Arabidopsis thaliana	At3g62290	63/70	N-terminal protein myristoylation
2930	PC837-4	237	Epidermis-specific secreted glycoprotein EP1 precursor	Daucus carota	Q39688	41/48	water transport

Bemerkung
ATP-dependent RNA helicase C1F7.02c, putative, expressed
DEAD/DEAH box helicase, putative
-
-
-
60S ribosomal protein L37 (RPL37A)
-
-
expressed protein
integral membrane protein, putative, contains 3 transmembrane domains; contains Pfam PF04535 : Domain of unknown function (DUF588); similar to putative ethylene responsive element binding protein (GI:22135858) (Arabidopsis thaliana)
heat shock cognate 70 kDa protein 1 (HSC70-1) (HSP70-1)
heat shock cognate 70 kDa protein 1 (HSC70-1) (HSP70-1)
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integral membrane protein, putative, contains 3 transmembrane domains; contains Pfam PF04535 : Domain of unknown function (DUF588); similar to putative ethylene responsive element binding protein (GI:22135858) (Arabidopsis thaliana)
heat shock cognate 70 kDa protein 1 (HSC70-1) (HSP70-1)
putative AVR9 elicitor response protein, galactosyltransferase family protein
dynamin-like protein D (DL1D)
nematode resistance protein Hs1pro-1
nematode resistance protein Hs1pro-1
protein phosphatase 2C family protein
integral membrane protein, putative, contains 3 transmembrane domains; contains Pfam PF04535 : Domain of unknown function (DUF588); similar to putative ethylene responsive element binding protein (GI:22135858) (Arabidopsis thaliana)
integral membrane protein, putative, contains 3 transmembrane domains; contains Pfam PF04535 : Domain of unknown function (DUF588); similar to putative ethylene responsive element binding protein (GI:22135858) (Arabidopsis thaliana)
heat shock cognate 70 kDa protein 1 (HSC70-1) (HSP70-1)
heat shock cognate 70 kDa protein 1 (HSC70-1) (HSP70-1)
heat shock cognate 70 kDa protein 1 (HSC70-1) (HSP70-1)
heat shock cognate 70 kDa protein 1 (HSC70-1) (HSP70-1)
expressed protein
expressed protein
-
-
40S ribosomal protein S8 (RPS8A)
integral membrane protein, putative, contains 3 transmembrane domains; contains Pfam PF04535 : Domain of unknown function (DUF588); similar to putative ethylene responsive element binding protein (GI:22135858) (Arabidopsis thaliana)
integral membrane protein, putative, contains 3 transmembrane domains; contains Pfam PF04535 : Domain of unknown function (DUF588); similar to putative ethylene responsive element binding protein (GI:22135858) (Arabidopsis thaliana)
integral membrane protein, putative, contains 3 transmembrane domains; contains Pfam PF04535 : Domain of unknown function (DUF588); similar to putative ethylene responsive element binding protein (GI:22135858) (Arabidopsis thaliana)
integral membrane protein, putative, contains 3 transmembrane domains; contains Pfam PF04535 : Domain of unknown function (DUF588); similar to putative ethylene responsive element binding protein (GI:22135858) (Arabidopsis thaliana)
fringe-related protein
ABC transporter family protein
aspartyl protease family protein
aspartyl protease family protein
heat shock cognate 70 kDa protein 1 (HSC70-1) (HSP70-1)
-

-
phosphoinositide phosphatase family protein
transducin family protein / WD-40 repeat family protein
oxidoreductase, zinc-binding dehydrogenase family protein
putative AVR9 elicitor response protein, galactosyltransferase family protein
pentatricopeptide (PPR) repeat-containing protein
phosphoinositide phosphatase family protein
phosphoinositide phosphatase family protein
amino acid transporter family protein
epoxide hydrolase, putative
epoxide hydrolase, putative
epoxide hydrolase, putative
epoxide hydrolase, putative
expressed protein, GTP-binding regulatory protein beta chain, Dictyostelium discoideum, PIR:A47370
pectinesterase family protein
casein kinase, putative
casein kinase, putative
pectinesterase family protein
aldo/keto reductase, putative
lipoxygenase, putative, similar to lipoxygenase gi:1495804 (Solanum tuberosum)
lipoxygenase, putative, similar to lipoxygenase gi:1495804 (Solanum tuberosum)
lipoxygenase, putative, similar to lipoxygenase gi:1495804 (Solanum tuberosum)
60S ribosomal protein L17 (RPL17B)
60S ribosomal protein L17 (RPL17B)
60S ribosomal protein L17 (RPL17B)
-
-
expressed protein
protein kinase, putative, similar to protein kinase APK1A (Arabidopsis thaliana) Swiss-Prot:Q06548
protein kinase, putative, similar to protein kinase APK1A (Arabidopsis thaliana) Swiss-Prot:Q06548
protein kinase, putative, similar to protein kinase APK1A (Arabidopsis thaliana) Swiss-Prot:Q06548
-
-
-
kinesin motor protein-related, several kinesin-like proteins
calcium-binding EF hand family protein, contains Pfam profile: PF00036 EF hand
-
calnexin 1 (CNX1), identical to calnexin homolog 1, Arabidopsis thaliana, EMBL:AT08315 (SP|P29402)
galactosyl transferase GMA12/MNN10 family protein, low similarity to alpha-1,2-galactosyltransferase, Schizosaccharomyces pombe (SP|Q09174)
galactosyltransferase family protein, contains Pfam profile: PF01762 galactosyltransferase ;contains similarity to Avr9 elicitor response protein GI:4138265 from (Nicotiana tabacum)
4-aminobutyrate aminotransferase / gamma-amino-N-butyrate transaminase / GABA transaminase
-
-
-
expressed protein, contains Pfam profile: PF01363 FYVE zinc finger
expressed protein, contains Pfam profile: PF01363 FYVE zinc finger

expressed protein, contains Pfam profile: PF01363 FYVE zinc finger
NAD-dependent epimerase/dehydratase family protein
ripening-responsive protein, putative
-
midasin-related, similar to Midasin (MIDAS-containing protein) (Swiss-Prot:Q12019) (Saccharomyces cerevisiae)
NAD-dependent epimerase/dehydratase family protein
oxidoreductase, zinc-binding dehydrogenase family protein, contains Pfam profile PF00107: oxidoreductase, zinc-binding dehydrogenase family
ripening-responsive protein, putative
CBL-interacting protein kinase 17 (CIPK17), identical to CBL-interacting protein kinase 17 (Arabidopsis thaliana) gi|14571553|gb|AAK64513
glutamate receptor family protein (GLR2.8) (GLUR9), plant glutamate receptor family, PMID:11379626
transferase family protein, similar to anthranilate N-hydroxycinnamoyl/benzoyltransferase, Dianthus caryophyllus (gi:2239091)
expressed protein
60S ribosomal protein L35a (RPL35aC)
similar to beta-expansin, putative (EXPB4)[Arabidopsis thaliana] (TAIR:At2g45110.1)
glutamate receptor family protein (GLR2.8) (GLUR9), plant glutamate receptor family, PMID:11379626
peptidyl-prolyl cis-trans isomerase / cyclophilin (CYP2) / rotamase, identical to cyclophilin (Arabidopsis thaliana) gi|2443757|gb|AAB71402
MutT/nudix family protein
similar to beta-expansin, putative (EXPB4)[Arabidopsis thaliana] (TAIR:At2g45110.1)
glutamate receptor family protein (GLR2.8) (GLUR9), plant glutamate receptor family, PMID:11379626
MutT/nudix family protein
60S ribosomal protein L17 (RPL17B)
putative CCCH-type zinc finger protein
similar to riboflavin biosynthesis protein, putative [Arabidopsis thaliana] (TAIR:At2g22450.1)
expressed protein
60S ribosomal protein L7A (RPL7aA)
60S ribosomal protein L35a (RPL35aC)
60S ribosomal protein L35a (RPL35aC)
-
60S ribosomal protein L35a (RPL35aC)
60S ribosomal protein L35a (RPL35aC)
60S ribosomal protein L35a (RPL35aC)
60S ribosomal protein L35a (RPL35aC)
Belongs to the cytochrome P450 family
cyclophilin_ABH_like: Cyclophilin A, B and H-like cyclophilin-type peptidylprolyl cis- trans isomerase (PPIase) domain
harpin-induced protein-related / HIN1-related / harpin-responsive protein-related, weak similarity to harpin inducing protein (hin1), Nicotiana tabacum, EMBL:AF212183, GI:1619321
peroxidase, putative, similar to peroxidase (Nicotiana tabacum) gi|5381253|dbj|BAA82306
cyclophilin_ABH_like: Cyclophilin A, B and H-like cyclophilin-type peptidylprolyl cis- trans isomerase (PPIase) domain
cyclophilin_ABH_like: Cyclophilin A, B and H-like cyclophilin-type peptidylprolyl cis- trans isomerase (PPIase) domain
cyclophilin_ABH_like: Cyclophilin A, B and H-like cyclophilin-type peptidylprolyl cis- trans isomerase (PPIase) domain
cyclophilin_ABH_like: Cyclophilin A, B and H-like cyclophilin-type peptidylprolyl cis- trans isomerase (PPIase) domain
cyclophilin_ABH_like: Cyclophilin A, B and H-like cyclophilin-type peptidylprolyl cis- trans isomerase (PPIase) domain
peroxidase, putative, similar to peroxidase (Nicotiana tabacum) gi|5381253|dbj|BAA82306
peroxidase, putative, similar to peroxidase (Nicotiana tabacum) gi|5381253|dbj|BAA82306
cyclophilin_ABH_like: Cyclophilin A, B and H-like cyclophilin-type peptidylprolyl cis- trans isomerase (PPIase) domain
cyclophilin_ABH_like: Cyclophilin A, B and H-like cyclophilin-type peptidylprolyl cis- trans isomerase (PPIase) domain
cyclophilin_ABH_like: Cyclophilin A, B and H-like cyclophilin-type peptidylprolyl cis- trans isomerase (PPIase) domain

cyclophilin_ABH_like: Cyclophilin A, B and H-like cyclophilin-type peptidylprolyl cis- trans isomerase (PPIase) domain
-
peroxidase, putative, similar to peroxidase (Nicotiana tabacum) gi|5381253|dbj|BAA82306
-
induced by fungal elicitor
ribose 5-phosphate isomerase-related
-
-
cathepsin B-like cysteine protease, putative
cysteine proteinase, putative / AALP protein(AALP), identical to AALP protein GI:7230640 from (Arabidopsis thaliana)
hAT family dimerisation domain
May play a minor role in cutin synthesis and could be involved in plant defense
calcineurin-like phosphoesterase family
expressed protein
expressed protein
-
-
peroxidase, putative, similar to peroxidase (Nicotiana tabacum) gi|5381253|dbj|BAA82306
40S ribosomal protein S20 (RPS20C)
-
ubiquitin-specific protease 16, putative (UBP16)
-
ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein
-
-
peptidyl-prolyl cis-trans isomerase / cyclophilin (CYP2) / rotamase, identical to cyclophilin (Arabidopsis thaliana) gi|2443757|gb|AAB71402
pfkB-type carbohydrate kinase family protein
pfkB-type carbohydrate kinase family protein
pfkB-type carbohydrate kinase family protein
pfkB-type carbohydrate kinase family protein
peroxidase, putative, similar to peroxidase (Nicotiana tabacum) gi|5381253|dbj|BAA82306
pfkB-type carbohydrate kinase family protein
pfkB-type carbohydrate kinase family protein
-
-
-
laccase, putative / diphenol oxidase, putative, similar to laccase (Populus balsamifera subsp. trichocarpa)(GI:3805960)
expressed protein
band 7 family protein, similar to hypersensitive-induced response protein (Zea mays)
light-responsive
-
-
-
-
-
Belongs to the glycosyltransferase 1 family. Plant sucrose synthase subfamily

mitochondrial import inner membrane translocase subunit TIM44, putative
expressed protein
peroxidase, putative, similar to peroxidase (Nicotiana tabacum) gi|5381253|dbj|BAA82306
peroxidase, putative, similar to peroxidase (Nicotiana tabacum) gi|5381253|dbj|BAA82306
peroxidase, putative, similar to peroxidase (Nicotiana tabacum) gi|5381253|dbj|BAA82306
similar to speckle-type POZ protein-related [Arabidopsis thaliana] (TAIR:At3g06190.1)
splicing factor RSZ33 (RSZ33)
DC 1 domain-containing protein
splicing factor RSZ33 (RSZ33)
splicing factor RSZ33 (RSZ33)
splicing factor RSZ33 (RSZ33)
DC 1 domain-containing protein
similar to PC180-3 (AT3G51550)
splicing factor RSZ33 (RSZ33)
splicing factor RSZ33 (RSZ33)
belongs to the BetVI family
DC 1 domain-containing protein
-
serine-rich protein-related
serine-rich protein-related
serine-rich protein-related
-
calreticulin 2 (CRT2)
leucine-rich repeat family protein / extensin family protein, similar to extensin-like protein (Lycopersicon esculentum)
leucine-rich repeat family protein / extensin family protein, similar to extensin-like protein (Lycopersicon esculentum)
-
tropinone reductase, putative
tropinone reductase, putative
tropinone reductase, putative
peroxidase, putative, similar to peroxidase (Nicotiana tabacum) gi|5381253|dbj|BAA82306
peroxidase, putative, similar to peroxidase (Nicotiana tabacum) gi|5381253|dbj|BAA82306
-
tropinone reductase, putative
tropinone reductase, putative
tropinone reductase, putative
tropinone reductase, putative
putative disease resistance protein (CC-NBS-LRR)
putative disease resistance protein (CC-NBS-LRR)
putative disease resistance protein (CC-NBS-LRR)
putative disease resistance protein (CC-NBS-LRR)
putative disease resistance protein (CC-NBS-LRR class)
putative disease resistance protein (CC-NBS-LRR class)
putative disease resistance protein (CC-NBS-LRR class)
putative disease resistance protein (CC-NBS-LRR class)
CwfJ-like family protein
CwfJ-like family protein

CwfJ-like family protein
-
Belongs to the glutamine synthetase family.
-
expressed protein
-
heat shock protein mtHsc 70-2 (Hsc70-5)
-
-
chaperonin, putative, similar to SWISS-PROT:P50143- T-complex protein 1, gamma subunit (TCP-1-gamma) (Xenopus laevis)
chaperonin, putative, similar to SWISS-PROT:P50143- T-complex protein 1, gamma subunit (TCP-1-gamma) (Xenopus laevis)
zct2
oxidoreductase, zinc-binding dehydrogenase family protein, contains Pfam profile PF00107: oxidoreductase, zinc-binding dehydrogenase family
oxidoreductase, zinc-binding dehydrogenase family protein, contains Pfam profile PF00107: oxidoreductase, zinc-binding dehydrogenase family
-
oxidoreductase, zinc-binding dehydrogenase family protein, contains Pfam profile PF00107: oxidoreductase, zinc-binding dehydrogenase family
oxidoreductase, zinc-binding dehydrogenase family protein, contains Pfam profile PF00107: oxidoreductase, zinc-binding dehydrogenase family
oxidoreductase, zinc-binding dehydrogenase family protein, contains Pfam profile PF00107: oxidoreductase, zinc-binding dehydrogenase family
oxidoreductase, zinc-binding dehydrogenase family protein, contains Pfam profile PF00107: oxidoreductase, zinc-binding dehydrogenase family
oxidoreductase, zinc-binding dehydrogenase family protein, contains Pfam profile PF00107: oxidoreductase, zinc-binding dehydrogenase family
oxidoreductase, zinc-binding dehydrogenase family protein, contains Pfam profile PF00107: oxidoreductase, zinc-binding dehydrogenase family
oxidoreductase, zinc-binding dehydrogenase family protein, contains Pfam profile PF00107: oxidoreductase, zinc-binding dehydrogenase family
oxidoreductase, zinc-binding dehydrogenase family protein, contains Pfam profile PF00107: oxidoreductase, zinc-binding dehydrogenase family
-
laccase family protein / diphenol oxidase family protein, similar to laccase (Pinus taeda)
Harpin-induced protein 1 (Hin1); pfam07320
galactinol synthase, putative
galactinol synthase, putative
galactinol synthase, putative
expressed protein
protein kinase family protein, contains Pfam PF00069: Protein kinase domain
oxidoreductase, zinc-binding dehydrogenase family protein, contains Pfam profile PF00107: oxidoreductase, zinc-binding dehydrogenase family
senescence-associated protein (SEN1), identical to senescence-associated protein GI:1046270 from (Arabidopsis thaliana)
senescence-associated protein (SEN1), identical to senescence-associated protein GI:1046270 from (Arabidopsis thaliana)
secretory protein, putative, similar to NtPRp27 (Nicotiana tabacum) GI:5360263
-
U-box domain-containing protein, similar to immediate-early fungal elicitor protein CMPG1 (Petroselinum crispum) GI:14582200
Belongs to the PAL/histidase family
XS domain-containing protein / XS zinc finger domain-containing protein-related
malate dehydrogenase, cytosolic, putative, strong similarity to cytosolic malate dehydrogenase (EC 1.1.1.37) SP|O24047 {Mesembryanthemum crystallinum}
phenylalanine ammonia-lyase (AA 137 - 716) (1 is 3rd base in codon)
dehydration -induced protein family
purine permease; putative purine permease (or PR1-2 from Pc)
protein kinase family protein
phosphoglycerate/bisphosphoglycerate mutase family protein
-

FAD-linked oxidoreductase family
60S ribosomal protein L37 (RPL37A)
Harpin-induced protein 1 (Hin1); pfam07320
Harpin-induced protein 1 (Hin1); pfam07320
Harpin-induced protein 1 (Hin1); pfam07320
oxidoreductase, zinc-binding dehydrogenase family protein, contains Pfam profile PF00107: oxidoreductase, zinc-binding dehydrogenase family
secretory protein, putative, similar to NtPRp27 (Nicotiana tabacum) GI:5360263
secretory protein, putative, similar to NtPRp27 (Nicotiana tabacum) GI:5360263
secretory protein, putative, similar to NtPRp27 (Nicotiana tabacum) GI:5360263
Harpin-induced protein 1 (Hin1); pfam07320
secretory protein, putative, similar to NtPRp27 (Nicotiana tabacum) GI:5360263
dual specificity protein phosphatase family protein, contains Pfam profile: PF00782 dual specificity phosphatase, catalytic domain
ATP synthase beta chain 1, mitochondrial, identical to SP|P83483 ATP synthase beta chain 1, mitochondrial precursor (EC 3.6.3.14) {Arabidopsis thaliana}
secretory protein, putative, similar to NtPRp27 (Nicotiana tabacum) GI:5360263
secretory protein, putative, similar to NtPRp27 (Nicotiana tabacum) GI:5360263
Belongs to the cytochrome P450 family
-
phospholipid/glycerol acyltransferase family protein
phospholipid/glycerol acyltransferase family protein
-
U-box domain-containing protein, similar to immediate-early fungal elicitor protein CMPG1 (Petroselinum crispum) GI:14582200; contains Pfam profile PF04564: U-box domain
U-box domain-containing protein, similar to immediate-early fungal elicitor protein CMPG1 (Petroselinum crispum) GI:14582200; contains Pfam profile PF04564: U-box domain
heat shock protein, putative, strong similarity to SP|P55737 Heat shock protein 81-2 (HSP81-2) {Arabidopsis thaliana}
similar to fatty acid desaturases/hydroxylases
Harpin-induced protein 1 (Hin1); pfam07320
-
protein kinase, putative, similar to protein kinase ATN1 (Arabidopsis thaliana) gi|1054633|emb|CAA63387
amino acid transporter family protein
-
almost identical to pc200-4
pc201-1~pc201-2=pc201-4
pc201-1~pc201-2=pc201-4
similar to pc200-4 or pc201-1
short-chain dehydrogenase/reductase (SDR) family protein, similar to carbonyl reductase GI:1049108 from (Mus musculus)
short-chain dehydrogenase/reductase (SDR) family protein, similar to carbonyl reductase GI:1049108 from (Mus musculus)
short-chain dehydrogenase/reductase (SDR) family protein, similar to carbonyl reductase GI:1049108 from (Mus musculus)
chaperonin, putative, similar to SWISS-PROT:P50143- T-complex protein 1, gamma subunit (TCP-1-gamma) (Xenopus laevis)
40S ribosomal protein S15A (RPS15aA)
Transcription initiation factor IIB (AtTGIIB2)
chaperonin, putative, similar to SWISS-PROT:P50143- T-complex protein 1, gamma subunit (TCP-1-gamma) (Xenopus laevis)
protein kinase family protein
-
oxidoreductase, zinc-binding dehydrogenase family protein, contains Pfam profile PF00107: oxidoreductase, zinc-binding dehydrogenase family
oxidoreductase, zinc-binding dehydrogenase family protein, contains Pfam profile PF00107: oxidoreductase, zinc-binding dehydrogenase family
-
AAA-type ATPase family protein

expressed protein
expressed protein
Squalene cyclase [Lipid metabolism]
-
secretory protein, putative, similar to NtPRp27 (Nicotiana tabacum) GI:5360263
peptidase M1 family protein, similar to SP|P04825 Aminopeptidase N (EC 3.4.11.2) (Alpha-aminoacylpeptide hydrolase) {Escherichia coli}
secretory protein, putative, similar to NtPRp27 (Nicotiana tabacum) GI:5360263
secretory protein, putative, similar to NtPRp27 (Nicotiana tabacum) GI:5360263
LEM3 (ligand-effect modulator 3) family protein
LEM3 (ligand-effect modulator 3) family protein
oxidoreductase, zinc-binding dehydrogenase family protein, contains Pfam profile PF00107: oxidoreductase, zinc-binding dehydrogenase family
-
secretory protein, putative, similar to NtPRp27 (Nicotiana tabacum) GI:5360263
Belongs to the group II decarboxylase family
Harpin-induced protein 1 (Hin1); pfam07320
Harpin-induced protein 1 (Hin1); pfam07320
Harpin-induced protein 1 (Hin1); pfam07320
sulfate adenylyltransferase 1 / ATP-sulfurylase 1 (APS1), nearly identical to ATP sulfurylase (APS1) (Arabidopsis thaliana) GI:6606509
sulfate adenylyltransferase 1 / ATP-sulfurylase 1 (APS1), nearly identical to ATP sulfurylase (APS1) (Arabidopsis thaliana) GI:6606509
S-locus protein kinase, putative, similar to receptor protein kinase (Ipomoea trifida)
strong similarity to SP|Q42908 2,3-bisphosphoglycerate-independent phosphoglycerate mutase (EC 5.4.2.1) (Phosphoglyceromutase) {Mesembryanthemum crystallinum}
secretory protein, putative, similar to NtPRp27 (Nicotiana tabacum) GI:5360263
secretory protein, putative, similar to NtPRp27 (Nicotiana tabacum) GI:5360263
putataive 1-aminocyclopropane-1-carboxylate synthase
secretory protein, putative, similar to NtPRp27 (Nicotiana tabacum) GI:5360263
secretory protein, putative, similar to NtPRp27 (Nicotiana tabacum) GI:5360263
secretory protein, putative, similar to NtPRp27 (Nicotiana tabacum) GI:5360263
secretory protein, putative, similar to NtPRp27 (Nicotiana tabacum) GI:5360263
secretory protein, putative, similar to NtPRp27 (Nicotiana tabacum) GI:5360263
secretory protein, putative, similar to NtPRp27 (Nicotiana tabacum) GI:5360263
secretory protein, putative, similar to NtPRp27 (Nicotiana tabacum) GI:5360263
secretory protein, putative, similar to NtPRp27 (Nicotiana tabacum) GI:5360263
in plants expressed in root, inflorescence, stem, rosette leaf
-
putative cinnamoyl-alcohol dehydrogenase
shaggy-related protein kinase alpha / ASK-alpha (ASK1), identical to shaggy-related protein kinase alpha SP:P43288 GI:460832 from (Arabidopsis thaliana)
-
protein kinase, putative, similar to protein kinase ATN1 (Arabidopsis thaliana) gi|1054633|emb|CAA63387
MD-2-related lipid recognition domain-containing protein
MD-2-related lipid recognition domain-containing protein
MD-2-related lipid recognition domain-containing protein
glycosyl hydrolase family 3 protein
protein kinase family protein
exostosin family protein
-
SKP1 interacting partner 4 (SKIP4), almost idential to SKP1 interacting partner 4 GI:10716953 from (Arabidopsis thaliana)

SKP1 interacting partner 4 (SKIP4), almost idential to SKP1 interacting partner 4 GI:10716953 from (Arabidopsis thaliana)
stress-responsive protein, putative, similar to cold acclimation WCOR413-like protein gamma form (Hordeum vulgare) gi|18449100|gb|AAL69988
alcohol dehydrogenase, putative, similar to alcohol dehydrogenase from Solanum tuberosum (SP|p14673)
alcohol dehydrogenase, putative, similar to alcohol dehydrogenase from Solanum tuberosum (SP|p14673)
light-responsive
light-responsive
light-responsive
light-responsive
putative P450 cytochrome
phosphatidylinositol-4-phosphate 5-kinase family protein
long-chain acyl-CoA synthetase/AMP binding protein
-
scarecrow-like transcription factor 5 (SCL5)
respiratory burst oxidase protein D (RbohD) / NADPH oxidase
respiratory burst oxidase protein D (RbohD) / NADPH oxidase
beta-Ig-H3 domain-containing protein / fasciclin domain-containing protein, weak similarity to osteoblast specific factor 2 (Homo sapiens) GI:393319
phenylalanine ammonia-lyase (AA 137 - 716) (1 is 3rd base in codon)
zinc finger (C3HC4-type RING finger) family protein
-
-
Harpin-induced protein 1 (Hin1); pfam07320
oxidoreductase, zinc-binding dehydrogenase family protein, contains Pfam profile PF00107: oxidoreductase, zinc-binding dehydrogenase family
oxidoreductase, zinc-binding dehydrogenase family protein, contains Pfam profile PF00107: oxidoreductase, zinc-binding dehydrogenase family
GDSL-motif ligase/hydrolase-like protein
-
Harpin-induced protein 1 (Hin1); pfam07320
Squalene cyclase [Lipid metabolism]
Squalene cyclase [Lipid metabolism]
putataive 1-aminocyclopropane-1-carboxylate synthase
putataive 1-aminocyclopropane-1-carboxylate synthase
universal stress protein (USP) family protein
zinc finger protein-related
putataive 1-aminocyclopropane-1-carboxylate synthase
putataive 1-aminocyclopropane-1-carboxylate synthase
zinc finger protein-related
leucine-rich repeat family protein
leucine-rich repeat family protein
-
-
putative cinnamoyl-alcohol dehydrogenase
-
interferon-related developmental regulator family protein
-
-
FAD-binding domain-containing protein, similar to SP|P30986 reticuline oxidase precursor (Berberine-bridge-forming enzyme) (BBE)
glutamate receptor family protein (GLR2.8) (GLUR9), plant glutamate receptor family, PMID:11379626

glutamate receptor family protein (GLR2.8) (GLUR9), plant glutamate receptor family, PMID:11379626
-
expressed protein
expressed protein
expressed protein
-
-
L-ascorbate peroxidase 1, cytosolic (APX1)
-
-
-
-
-
FAD-binding domain-containing protein, similar to SP|P30986 reticuline oxidase precursor (Berberine-bridge-forming enzyme) (BBE) (Tetrahydroprotoberberine synthase) (Eschscholzia californica); contains PF01565 FAD binding domain
protein kinase family protein
Belongs to the group II decarboxylase family
VHS domain-containing protein / GAT domain-containing protein, weak similarity to hepatocyte growth factor-regulated tyrosine kinase substrate (Homo sapiens) GI:2731383
VHS domain-containing protein / GAT domain-containing protein, weak similarity to hepatocyte growth factor-regulated tyrosine kinase substrate (Homo sapiens) GI:2731383
similar to glutamate decarboxylase 1 (GAD 1) [Arabidopsis thaliana] (TAIR:At5g17330.1)
-
protein kinase family protein, contains protein kinase domain, Pfam:PF00069
Belongs to the group II decarboxylase family
UDP-sulfoquinovose:DAG sulfoquinovosyltransferase / sulfolipid synthase (SQD2), identical to GI:20302857
importin alpha-2, putative (IMPA-2), similar to importin alpha 2 (Capsicum annuum) GI:13752562
ubiquitin-specific protease 6, putative (UBP6) similar to GI:11993465
-
pectate lyase family protein, similar to pectate lyase GI:14289169 from (Salix gilgiana)
sodium/calcium exchanger family protein / calcium-binding EF hand family protein
shepherd protein (SHD) / clavata formation protein, putative, nearly identical to SHEPHERD (Arabidopsis thaliana) GI:19570872
quinolinate phosphoribosyl transferase family protein, contains Pfam profile: PF01729 quinolinate phosphoribosyl transferase, C-terminal domain
Os07g0601100
leucine-rich repeat transmembrane protein kinase, putative, similar to receptor protein kinase GB:BAA11869 GI:1389566 from (Arabidopsis thaliana)
NL1 interacting factor (NIF) family protein
putative DNA-dirceted RNA polymerase
putative DNA-dirceted RNA polymerase
-
-
L-ascorbate oxidase, putative, similar to SP|P14133 L-ascorbate oxidase precursor (EC 1.10.3.3) (Ascorbase) {Cucumis sativus}
Ras-related GTP-binding protein, putative, similar to GTP-binding protein RAB5A GI:1370178 from (Lotus japonicus)
small nuclear ribonucleoprotein E, putative / snRNP-E, putative / Sm protein E, putative
F-box family protein, PF0064: F-box domain
40S ribosomal protein S3 (RPS3C)
protease inhibitor, putative, similar to SP|P19873 Inhibitor of trypsin and hageman factor (CMTI-V) {Cucurbita maxima}
protease inhibitor, putative, similar to SP|P19873 Inhibitor of trypsin and hageman factor (CMTI-V) {Cucurbita maxima}
FAD-binding domain-containing protein (Berberine-bridge-forming enzyme) (BBE)
-

signal recognition particle 54 kDa protein 3 /SRP54 (SRP-54C), identical to SP|P49967 Signal recognition particle 54 kDa protein 3 (SRP54) {Arabidopsis thaliana}
S-locus lectin protein kinase family protein
-
-
-
protein kinase family
-
putative glutathione peroxidase
armadillo/beta-catenin repeat family protein / F-box family protein, contains similarity to F-box protein FBL2 GI:6010699 from (Rattus norvegicus)
-
dermal glycoprotein precursor, extracellular
calmodulin-binding family protein
calmodulin-binding family protein
calmodulin-binding family protein
eukaryotic translation initiation factor 2B family protein / eIF-2B family protein, similar to CIG2 (Nicotiana tabacum) GI:15216226
-
transcription regulatory protein SNF2, putative
transcription regulatory protein SNF2, putative
Belongs to the group II decarboxylase family
XS domain-containing protein / XS zinc finger domain-containing protein-related
-
-
expressed protein
-
expressed protein
cyclic nucleotide-binding transporter 1 / CNBT1 (CNGC20), identical to cyclic nucleotide-binding transporter 1 (CNBT1) GI:8131898 from (Arabidopsis thaliana)
-
similar to fatty acid desaturases/hydroxylases
expressed protein
-
VHS domain-containing protein / GAT domain-containing protein, weak similarity to hepatocyte growth factor-regulated tyrosine kinase substrate (Homo sapiens) GI:2731383
VHS domain-containing protein / GAT domain-containing protein, weak similarity to hepatocyte growth factor-regulated tyrosine kinase substrate (Homo sapiens) GI:2731383
-
-
cyclic nucleotide-binding transporter 1 / CNBT1 (CNGC20), identical to cyclic nucleotide-binding transporter 1 (CNBT1) GI:8131898 from (Arabidopsis thaliana)
cyclic nucleotide-binding transporter 1 / CNBT1 (CNGC20), identical to cyclic nucleotide-binding transporter 1 (CNBT1) GI:8131898 from (Arabidopsis thaliana)
-
serine/threonine protein phosphatase PP2A-2 catalytic subunit (PP2A2), identical to SP|Q07099 Serine/threonine protein phosphatase PP2A-2 catalytic subunit (EC 3.1.3.16) {Arabidopsis thaliana}
Belongs to the group II decarboxylase family
Belongs to the short-chain dehydrogenases/reductases (SDR) family
Belongs to the group II decarboxylase family
Belongs to the group II decarboxylase family
Belongs to the group II decarboxylase family
Belongs to the group II decarboxylase family
expressed protein, MtN19, Medicago truncatula (immer nur ein Primer vorhanden)
belongs to the HMBS family

-
actin 7 (ACT7) / actin 2, identical to SP|P53492 Actin 7 (Actin-2) {Arabidopsis thaliana}
zinc finger (C3HC4-type RING finger) family protein
protein phosphatase 2C, putative / PP2C, putative, phosphoprotein phosphatase (EC 3.1.3.16) 1A-alpha - Homo sapiens, PIR:S22423
FAD-binding domain-containing protein, similar to SP|P30986 reticuline oxidase precursor (Berberine-bridge-forming enzyme) (BBE) (Tetrahydroprotoberberine synthase) (Eschscholzia californica); contains PF01565 FAD binding domain
putative cytochrome P450
-
protease inhibitor, putative, similar to SP|P19873 Inhibitor of trypsin and hageman factor (CMTI-V) {Cucurbita maxima}
possible involvement in somatic embryo development
-
-
-
belongs to the ribosomal protein L15P family
ras-related GTP-binding protein, putative
protease inhibitor, putative, similar to SP|P19873 Inhibitor of trypsin and hageman factor (CMTI-V) {Cucurbita maxima}
-
-
-
zinc finger (C3HC4-type RING finger) family protein (ATL3) or similar to Avr9/Cf-9 rapidly elicited protein 132 (Nicotiana tabacum)
Belongs to the group II decarboxylase family
FAD-binding domain-containing protein, similar to SP|P30986 reticuline oxidase precursor (Berberine-bridge-forming enzyme) (BBE)
FAD-binding domain-containing protein, similar to SP|P30986 reticuline oxidase precursor (Berberine-bridge-forming enzyme) (BBE)
delta8 sphingolipid desaturase (EC 1.14.99.)
Belongs to the group II decarboxylase family
Belongs to the group II decarboxylase family
fructose-bisphosphate aldolase, putative, similar to plastidic aldolase NPALDP1 from Nicotiana paniculata (GI:4827251)
-
zinc finger (C3HC4-type RING finger) family protein
zinc finger (C3HC4-type RING finger) family protein
zinc finger (C3HC4-type RING finger) family protein
zinc finger (C3HC4-type RING finger) family protein
similar to fatty acid desaturases/hydroxylases
-
-
-
calmodulin-binding family protein
serine protease inhibitor, Kazal-type family protein
-
XS domain-containing protein / XS zinc finger domain-containing protein-related
-
-
-
-
-
-
-

expressed protein
expressed protein
putative aconitate hydratase, cytoplasmic
calmodulin-binding family protein
expressed protein
dual specificity protein phosphatase family protein, contains Pfam profile: PF00782 dual specificity phosphatase, catalytic domain
Secondary metabolites biosynthesis, transport, and catabolism
20S proteasome alpha subunit D2 (PRS1) PRC6)
20S proteasome alpha subunit D2 (PRS1) PRC6)
20S proteasome alpha subunit D2 (PRS1) PRC6)
expressed protein
-
expressed protein
transcriptional adaptor (ADA2a) protein
expressed protein; step II splicing factor-like protein
expressed protein; step II splicing factor-like protein
expressed protein; step II splicing factor-like protein
mitochondrial substrate carrier family protein
-
-
-
-
-
zinc finger (C3HC4-type RING finger) family protein
zinc finger (C3HC4-type RING finger) family protein
expressed protein
expressed protein
expressed protein
expressed protein
Transposon protein, putative, CACTA, En/Spm sub-class
NC domain-containing protein
enoyl-CoA hydratase/isomerase family protein, low similarity to PhaB (Pseudomonas putida) GI:3253198, SP|P31551 Carnitine racemase {Escherichia coli}
purine permease; putative purine permease (or PR1-2 from Pc)
Glucuronate isomerase [Carbohydrate transport and metabolism]
Glucuronate isomerase [Carbohydrate transport and metabolism]
trehalose-6-phosphate synthase, putative, similar to Alpha,alpha-trehalose-phosphate synthase (UDP-forming) (EC 2.4.1.15)
dermal glycoprotein precursor, extracellular
F-box family protein, PF0064: F-box domain
trehalose-6-phosphate synthase, putative, similar to Alpha,alpha-trehalose-phosphate synthase (UDP-forming) (EC 2.4.1.15)
F-box family protein, PF0064: F-box domain
F-box family protein, PF0064: F-box domain
F-box family protein, PF0064: F-box domain
F-box family protein, PF0064: F-box domain
S-locus protein kinase, putative, similar to S-receptor kinase gi|392557|gb|AAA62232
S-locus protein kinase, putative, similar to S-receptor kinase gi|392557|gb|AAA62232
S-locus protein kinase, putative, similar to S-receptor kinase gi|392557|gb|AAA62232

S-locus protein kinase, putative, similar to S-receptor kinase gi|392557|gb|AAA62232
-
putative protein kinase
exostosin family protein
inorganic phosphate transporter (PHT5)
leucine-rich repeat family protein
putative ATPase, plasma membrane-type / proton pump
inorganic phosphate transporter (PHT5)
similar to fatty acid desaturases/hydroxylases
calnexin 1 (CNX1), identical to calnexin homolog 1, Arabidopsis thaliana, EMBL:AT08315 (SP|P29402)
-
-
-
-
-
-
tubulin beta-6 chain (TUB6), nearly identical to SP|P29514 Tubulin beta-6 chain {Arabidopsis thaliana}
tubulin beta-6 chain (TUB6), nearly identical to SP|P29514 Tubulin beta-6 chain {Arabidopsis thaliana}
60 S ribosmal protein L3 (RPL3B)
COP1-interactive protein 1 / CIP1, almost identical to CIP1 (GI:836950) (Arabidopsis thaliana)
polyubiquitin (UBQ3), identical to GI:928809
polyubiquitin (UBQ3), identical to GI:928809
-
-
-
-
S-locus protein kinase, putative, similar to S-receptor kinase gi|392557|gb|AAA62232
Belongs to the peptidase C1 family
Belongs to the peptidase C1 family
seven transmembrane MLO family protein/MLO-like protein 8 (MLO8)
serine protease inhibitor, Kazal-type family protein
glycyl-tRNA synthetase / glycine--tRNA ligase, identical to SP|O23627 Glycyl-tRNA synthetase (EC 6.1.1.14) (Glycine--tRNA ligase) (GlyRS) {Arabidopsis thaliana}
glycyl-tRNA synthetase / glycine--tRNA ligase, identical to SP|O23627 Glycyl-tRNA synthetase (EC 6.1.1.14) (Glycine--tRNA ligase) (GlyRS) {Arabidopsis thaliana}
glycyl-tRNA synthetase / glycine--tRNA ligase, identical to SP|O23627 Glycyl-tRNA synthetase (EC 6.1.1.14) (Glycine--tRNA ligase) (GlyRS) {Arabidopsis thaliana}
UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase
integral membrane family protein
SKP1 interacting partner 2 (SKIP2), identical to SKP1 interacting partner 2 GI:10716949 from (Arabidopsis thaliana)
-
-
-
FAD-binding domain-containing protein, similar to SP|P30986 reticuline oxidase precursor (Berberine-bridge-forming enzyme) (BBE) (Tetrahydroprotoberberine synthase) (Eschscholzia californica); contains PF01565 FAD binding domain
expressed protein
FAD-binding domain-containing protein, similar to SP|P30986 reticuline oxidase precursor (Berberine-bridge-forming enzyme) (BBE) (Tetrahydroprotoberberine synthase) (Eschscholzia californica); contains PF01565 FAD binding domain
FAD-binding domain-containing protein, similar to SP|P30986 reticuline oxidase precursor (Berberine-bridge-forming enzyme) (BBE) (Tetrahydroprotoberberine synthase) (Eschscholzia californica); contains PF01565 FAD binding domain
FAD-binding domain-containing protein, similar to SP|P30986 reticuline oxidase precursor (Berberine-bridge-forming enzyme) (BBE) (Tetrahydroprotoberberine synthase) (Eschscholzia californica); contains PF01565 FAD binding domain
FAD-binding domain-containing protein, similar to SP|P30986 reticuline oxidase precursor (Berberine-bridge-forming enzyme) (BBE) (Tetrahydroprotoberberine synthase) (Eschscholzia californica); contains PF01565 FAD binding domain

harpin-induced family protein (YLS9) / HIN1 family protein / harpin-responsive family protein, similar to harpin-induced protein hin1 (GI:1619321) (Nicotiana tabacum)
harpin-induced family protein (YLS9) / HIN1 family protein / harpin-responsive family protein, similar to harpin-induced protein hin1 (GI:1619321) (Nicotiana tabacum)
40 S ribosomal protein S6
-
40 S ribosomal protein S6
40 S ribosomal protein S6
-
40 S ribosomal protein S6
40 S ribosomal protein S6
-
expressed protein
glycosyl hydrolase family 17 protein
possible involvement in somatic embryo development
peroxidase, putative, similar to peroxidase (Nicotiana tabacum) gi|5381253|dbj|BAA82306
phospholipid/glycerol acyltransferase family protein
aminoacyl-tRNA synthetase family protein
aminoacyl-tRNA synthetase family protein
possible involvement in somatic embryo development
possible involvement in somatic embryo development
possible involvement in somatic embryo development
-
-
40 S ribosomal protein S6
-
expressed protein
FAD-binding domain-containing protein, similar to SP|P30986 reticuline oxidase precursor (Berberine-bridge-forming enzyme) (BBE) (Tetrahydroprotoberberine synthase) (Eschscholzia californica); contains PF01565 FAD binding domain
-
tetratricopeptide repeat (TPR)-containing protein
-
-
60 S ribosmal protein L7 (RPL7C)
laccase family protein / diphenol oxidase family protein, similar to laccase (Pinus taeda)
DNA replication licensing factor (CDC21)
expressed protein
U-box domain-containing protein, similar to immediate-early fungal elicitor protein CMPG1 (Petroselinum crispum) GI:14582200
-
-
-
-
zinc finger (C3HC4-type RING finger) family protein
strong similarity to several reverse transcriptases
Belongs to the UDP-glycosyltransferase family
Belongs to the UDP-glycosyltransferase family
ligasetetratricopeptide repeat (TPR)-containing protein
tetratricopeptide repeat (TPR)-containing protein
tetratricopeptide repeat (TPR)-containing protein

tetratricopeptide repeat (TPR)-containing protein
synthaxin SYP124 (in PEN1)
short-chain dehydrogenase/reductase (SDR) family protein, similar to WW-domain oxidoreductase
60S ribosomal protein L19 (RPL19A)
Patatin-like phospholipase; pfam01734
-
-
-
-
Patatin-like phospholipase; pfam01734
Patatin-like phospholipase; pfam01734
Patatin-like phospholipase; pfam01734
Patatin-like phospholipase; pfam01734
flavin-containing monooxygenase family protein
leucine-rich repeat protein
ubiquitin fusion degradation UFD1 family protein, similar to SP|P70362 Ubiquitin fusion degradation protein 1 homolog (UB fusion protein 1) {Mus musculus}
pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat
-
4-alpha glucanotransferase
putative disease resistance protein (TIR-NBS-LRR class)
-
-
-
-
-
-
ubiquitin fusion degradation UFD1 family protein, similar to SP|P70362 Ubiquitin fusion degradation protein 1 homolog (UB fusion protein 1) {Mus musculus}
-
60S ribosomal protein L23 (RPL23A)
-
similar to expressed protein [Arabidopsis thaliana] (TAIR:At5g58510.1)
-
belongs to the peroxidase family. Classical plant (class III) peroxidase subfamily.
-
-
proteinputative Hs1pro-1 homolog
heat shock protein 81-2 (HSP81-2)
-
long-chain-fatty-acid--CoA ligase (acyl-CoA synthetase)
-
-
-
-
-
pyruvate dehydrogenase E1 alpha subunit
pyruvate dehydrogenase E1 alpha subunit

pyruvate dehydrogenase E1 alpha subunit
putative NTF2-containing RNA-binding protein
-
putative receptor family
nucleic acid binding / transcription factor/ zinc ion binding
expressed protein
expressed protein
-
-
-
belongs to the Ser/Thr protein kinase family
-
-
-
-
-
-
No apical meristem (NAM) protein; pfam02365
No apical meristem (NAM) protein; pfam02365
-
CCR4-NOT transcription complex protein, putative, similar to SWISS-PROT:Q9UFF9 CCR4-NOT transcription complex, subunit 8 (CAF1-like protein, CALIFp) (Homo sapiens)
CCR4-NOT transcription complex protein, putative, similar to SWISS-PROT:Q9UFF9 CCR4-NOT transcription complex, subunit 8 (CAF1-like protein, CALIFp) (Homo sapiens)
belongs to the Ser/Thr protein kinase family
CCR4-NOT transcription complex protein, putative, similar to SWISS-PROT:Q9UFF9 CCR4-NOT transcription complex, subunit 8 (CAF1-like protein, CALIFp) (Homo sapiens)
CCR4-NOT transcription complex protein, putative, similar to SWISS-PROT:Q9UFF9 CCR4-NOT transcription complex, subunit 8 (CAF1-like protein, CALIFp) (Homo sapiens)
CCR4-NOT transcription complex protein, putative, similar to SWISS-PROT:Q9UFF9 CCR4-NOT transcription complex, subunit 8 (CAF1-like protein, CALIFp) (Homo sapiens)
oxidoreductase, zinc-binding dehydrogenase family protein, contains Pfam profile PF00107: oxidoreductase, zinc-binding dehydrogenase family
-
CBL-interacting protein kinase 14 (CIPK14)
expressed protein
expressed protein
expressed protein
expressed protein
expressed protein
AAA-type ATPase family
FAD-binding domain-containing protein, similar to SP|P30986 reticuline oxidase precursor (Berberine-bridge-forming enzyme) (BBE)
tudor domain-containing protein / nuclease family protein, contains Pfam domains PF00567: Tudor domain and PF00565: Staphylococcal nuclease homologue
-
-
-
mitochondrial protein-like
chromodomain-helicase-DNA-binding family protein
lactoylglutathione lyase family protein / glyoxalase I family protein
lactoylglutathione lyase family protein / glyoxalase I family protein
-
pre-mRNA splicing factor, putative, strong similarity to SP|O22315 Pre-mRNA splicing factor SF2 (SR1 protein) {Arabidopsis thaliana}

pre-mRNA splicing factor, putative, strong similarity to SP|O22315 Pre-mRNA splicing factor SF2 (SR1 protein) {Arabidopsis thaliana}
pre-mRNA splicing factor, putative, strong similarity to SP|O22315 Pre-mRNA splicing factor SF2 (SR1 protein) {Arabidopsis thaliana}
-
rhodanese-like domain protein
similar to glutamate decarboxylase 1 (GAD 1) [Arabidopsis thaliana] (TAIR:At5g17330.1)
-
-
-
-
-
-
putative DNA-damage-repair/toleration protein (ORT 100)
putative DNA-damage-repair/toleration protein (ORT 100)
putative DNA-damage-repair/toleration protein (ORT 100)
protein kinase family (putative ser/thr protein kinase)
Secondary metabolites biosynthesis, transport, and catabolism
esterase/lipase/thioesterase family protein, similar to late embryogenesis abundant protein
esterase/lipase/thioesterase family protein, similar to late embryogenesis abundant protein
esterase/lipase/thioesterase family protein, similar to late embryogenesis abundant protein
esterase/lipase/thioesterase family protein, similar to late embryogenesis abundant protein
putative polcalein (calcium-binding pollen allergen)
exocyst subunit EXO70 family
exocyst subunit EXO70 family
60S ribosomal protein L7A (RPL7aA)
mitochondrial import receptor subunit TOM20-3 / translocase of outer membrane 20 kDa subunit 3 (TOM20-3)
Secondary metabolites biosynthesis, transport, and catabolism
expressed protein
expressed protein
expressed protein
expressed protein
AAA-type ATPase family protein / vacuolar sorting protein-related
-
-
-
-
-
-
-
Harpin-induced protein 1 (Hin1); pfam07320
similar to expressed protein [Arabidopsis thaliana] (TAIR:At4g14290.1)
expressed protein
Secondary metabolites biosynthesis, transport, and catabolism
zinc finger (C3HC4-type RING finger) family protein
far-red impaired responsive protein, putative
putative coatomer protein complex, subunit alpha
Harpin-induced protein 1 (Hin1); pfam07320

Belongs to the glutamyl-tRNA reductase family
Harpin-induced protein 1 (Hin1); pfam07320
Secondary metabolites biosynthesis, transport, and catabolism
Secondary metabolites biosynthesis, transport, and catabolism
Secondary metabolites biosynthesis, transport, and catabolism
Secondary metabolites biosynthesis, transport, and catabolism
Secondary metabolites biosynthesis, transport, and catabolism
Harpin-induced protein 1 (Hin1); pfam07320
Harpin-induced protein 1 (Hin1); pfam07320
Harpin-induced protein 1 (Hin1); pfam07320
Harpin-induced protein 1 (Hin1); pfam07320
U-box domain-containing protein, similar to immediate-early fungal elicitor protein CMPG1 (Petroselinum crispum) GI:14582200; contains Pfam profile PF04564: U-box domain
Belongs to the heat shock protein 70 family
Harpin-induced protein 1 (Hin1); pfam07320
U-box domain-containing protein, similar to immediate-early fungal elicitor protein CMPG1 (Petroselinum crispum) GI:14582200; contains Pfam profile PF04564: U-box domain
Harpin-induced protein 1 (Hin1); pfam07320
glycosyl hydrolase family 9
-
ATP-dependent RNA helicase C1F7.02c, putative, expressed
short-chain dehydrogenase/reductase family protein
expressed protein
expressed protein
ABC transporter family protein, related to multidrug resistance proteins and P-glycoproteins
Coenzyme metabolism
Coenzyme metabolism
similar to pc477-3
similar to soluble D-factor/LIF receptor
-
dermal glycoprotein precursor, extracellular
-
dermal glycoprotein precursor, extracellular
leucine rich repeat family protein
-
-
Belongs to the eukaryotic AdoMetDC family
transcriptional factor B3 family protein, low similarity to FUSCA3 (Arabidopsis thaliana) GI:3582518
F-box protein family (FBX 6)
60S ribosomal protein L27A
Secondary metabolites biosynthesis, transport, and catabolism
expressed protein
UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase
UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase
secreted protein; probable cell wall-bound EP4 protein, 45K, precursor
light-responsive
esterase/lipase/thioesterase family protein
-

putative cytochrome P450
DNA helicase (RECQl4A), nearly identical to DNA Helicase (Arabidopsis thaliana) GI:11121449
RabGAP/TBC domain-containing protein
dynamin-like protein 2B (ADL2b)
glycosyl transferase family 8 protein
putative leucine-rich repeat transmembrane protein kinase
putative leucine-rich repeat transmembrane protein kinase
putative leucine-rich repeat transmembrane protein kinase
-
-
-
-
-
DNAJ heat shock N-terminal domain-containing protein (J20), identical to DnaJ-like protein GI:6691127
DNAJ heat shock N-terminal domain-containing protein (J20), identical to DnaJ-like protein GI:6691127
DNAJ heat shock N-terminal domain-containing protein (J20), identical to DnaJ-like protein GI:6691127
glycoside hydrolase family 2 protein, similar to beta-galactosidase (lactase) from Alteromonas haloplanktis (SP|P81650)
glycoside hydrolase family 2 protein, similar to beta-galactosidase (lactase) from Alteromonas haloplanktis (SP|P81650)
glycoside hydrolase family 2 protein, similar to beta-galactosidase (lactase) from Alteromonas haloplanktis (SP|P81650)
glycoside hydrolase family 2 protein, similar to beta-galactosidase (lactase) from Alteromonas haloplanktis (SP|P81650)
human Rev interacting-like protein-related / hRIP protein-related
human Rev interacting-like protein-related / hRIP protein-related
human Rev interacting-like protein-related / hRIP protein-related
human Rev interacting-like protein-related / hRIP protein-related
-
-
-
-
-
human Rev interacting-like protein-related / hRIP protein-related
human Rev interacting-like protein-related / hRIP protein-related
putative succinate dehydrogenase iron-protein subunit
-
-
-
-
C2 domain-containing protein
zinc finger (C2H2 type) family protein
zinc finger (CCCH-type) family protein, contains Pfam domain, PF00642: Zinc finger C-x8-C-x5-C-x3-H type (and similar) and Pfam domain, PF00023: Ankyrin repeat
zinc finger (CCCH-type) family protein, contains Pfam domain, PF00642: Zinc finger C-x8-C-x5-C-x3-H type (and similar) and Pfam domain, PF00023: Ankyrin repeat
zinc finger (CCCH-type) family protein, contains Pfam domain, PF00642: Zinc finger C-x8-C-x5-C-x3-H type (and similar) and Pfam domain, PF00023: Ankyrin repeat
zinc finger (CCCH-type) family protein, contains Pfam domain, PF00642: Zinc finger C-x8-C-x5-C-x3-H type (and similar) and Pfam domain, PF00023: Ankyrin repeat
calpain-type cysteine protease family
putative AP2 domain-containing transcription factor
putative AP2 domain-containing transcription factor
putative AP2 domain-containing transcription factor

Zn-dependent alcohol dehydrogenases, class III [Energy production and conversion]; COG1062
Zn-dependent alcohol dehydrogenases, class III [Energy production and conversion]; COG1062
Zn-dependent alcohol dehydrogenases, class III [Energy production and conversion]; COG1062
Zn-dependent alcohol dehydrogenases, class III [Energy production and conversion]; COG1062
disease resistance protein (EDS1)
-
expressed protein
-
elongation factor 1B-gamma (eEF-1B gamma)
elongation factor 1B-gamma (eEF-1B gamma)
MATE - efflux protein-related
MATE - efflux protein-related
-
glycosyl transferase family 8
expressed protein
expressed protein
expressed protein
S-locus lectin protein kinase family protein
expressed protein
expressed protein
expressed protein
expressed protein
shaggy-related protein kinase eta / ASK-eta (ASK7)
expressed protein, contains similarity to hedgehog-interacting protein GI:4868122 from (Mus musculus)
-
similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g66860.1)
similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g66860.1)
zinc finger (CCCH type) helicase family protein
FAD-binding domain-containing protein
-
-
-
expressed protein
nt-sequence similar to pc519-1-1
zinc finger (C2H2 type) protein family
blue-copper binging protein III
blue-copper binging protein III
blue-copper binging protein III
blue-copper binging protein III
glucan phosphorylase, putative, similar to alpha-glucan phosphorylase, L isozyme 1 precursor GB:P04045 from (Solanum tuberosum) (J. Biochem. 106 (4), 691-695 (1989))
-
Harpin-induced protein 1 (Hin1)
-
-
-
Patatin-like phospholipase; pfam01734

Patatin-like phospholipase; pfam01734
Patatin-like phospholipase; pfam01734
Patatin-like phospholipase; pfam01734
Patatin-like phospholipase; pfam01734
Patatin-like phospholipase; pfam01734
Patatin-like phospholipase; pfam01734
Patatin-like phospholipase; pfam01734
Patatin-like phospholipase; pfam01734
Harpin-induced protein 1 (Hin1)
Harpin-induced protein 1 (Hin1)
hydrolase alpha/beta fold family
-
belongs to the ABC transporter family. PDR subfamily; contains 2 ABC transmembrane type-2 domains; contains 2 ABC transporter domains
Glucose-methanol-choline (GMC) oxidoreductase family protein, similar to mandelonitrile lyase from Prunus serotina (SP|P52706, SP|P52707)
putative AP2 domain-containing transcription factor
Zn-dependent alcohol dehydrogenases, class III [Energy production and conversion]; COG1062
Zn-dependent alcohol dehydrogenases, class III [Energy production and conversion]; COG1062
Zn-dependent alcohol dehydrogenases, class III [Energy production and conversion]; COG1062
Glucose-methanol-choline (GMC) oxidoreductase family protein, similar to mandelonitrile lyase from Prunus serotina (SP|P52706, SP|P52707)
-
-
-
Belongs to the cytochrome P450 family
scarecrow-like transcription factor (SCL 8)
scarecrow-like transcription factor (SCL 8)
scarecrow-like transcription factor (SCL 8)
scarecrow-like transcription factor (SCL 8)
elicitor inducible gene product EIG-I24
-
blue-copper binging protein III
-
Belongs to the Ser/Thr protein kinase family
-
Patatin-like phospholipase; pfam01734
F-box protein family
F-box protein family
F-box protein family
F-box protein family
F-box protein family
elongation factor 1B-gamma (eEF-1B gamma)
-
-
Type 1 glutamine amidotransferase (GATase1)-like domain found in Human DJ-1; cd03135
-
belongs to the gcvP family
potassium channel tetramerisation domain-containing protein, contains Pfam profile PF02214: K+ channel tetramerisation domain

potassium channel tetramerisation domain-containing protein, contains Pfam profile PF02214: K+ channel tetramerisation domain
AAA-type ATPase family protein, contains Pfam profile PF00004: ATPase, AAA family
FAD-linked oxidoreductase family (berberine bridge enzyme)
-
-
-
lipoic acid synthase (LIP1)
-
putative CCCH-type zinc finger protein
probable gibberllin beta-hydroxylase
-
-
-
-
(JR3 protein) IAA-Ala hydrolase (IAR3)
(JR3 protein) IAA-Ala hydrolase (IAR3)
expressed protein
-
(JR3 protein) IAA-Ala hydrolase (IAR3)
(JR3 protein) IAA-Ala hydrolase (IAR3)
(JR3 protein) IAA-Ala hydrolase (IAR3)
expressed protein
disease resistance protein (CC-NBS-LRR class)
disease resistance protein RPS5 (CC-NBS-LRR class)
similar to ser/thr-specific protein kinase NPK15 (Nicotiana tabacum) gi|505146|dbj|BAA06538
similar to ser/thr-specific protein kinase NPK15 (Nicotiana tabacum) gi|505146|dbj|BAA06538
similar to ser/thr-specific protein kinase NPK15 (Nicotiana tabacum) gi|505146|dbj|BAA06538
similar to ser/thr-specific protein kinase NPK15 (Nicotiana tabacum) gi|505146|dbj|BAA06538
-
-
-
-
ser/thr protein phosphatase 2A (regulatory chain)
putative coatomer complex subunit
-
-
endomembrane protein 70, putative, p76, Homo sapiens, EMBL:HSU81006
-
protein kinase family
glutathione peroxidase
armadillo/beta-catenin repeat family protein / F-box family protein, contains similarity to F-box protein FBL2 GI:6010699 from (Rattus norvegicus)
extracellular dermal glycoprotein
IntI (E2) integrases, site-specific tyrosine recombinases, DNA breaking-rejoining enzymes, N- and C-terminal domains; cd01193
protein kinase family protein, contains Pfam domain, PF00069: Protein kinase domain
associated with the major allergen Mal d 1
60S ribosomal protien L7 (RPL7D)

zinc finger (C3HC4-type RING finger) family protein
protein phosphatase 2C, putative / PP2C, putative, phosphoprotein phosphatase (EC 3.1.3.16) 1A-alpha - Homo sapiens, PIR:S22423
ytochrome P450 [Secondary metabolites biosynthesis, transport, and catabolism
putative ATP-citrate synthase (ATP-citrate(pro-S)-lyase/citrate cleavage enzyme)
Belongs to the pirin family
-
Belongs to the pirin family
Vacuolar protein sorting-associated protein [Intracellular trafficking and secretion]; COG5043
expressed protein
galactosyltransferase family protein
-
EXS family protein/ ERD1/XPR1 (PHO1-like)/SYG1 family protein
expressed protein
expressed protein, non-consensus GA donor splice site at exon 6
expressed protein
expressed protein
expressed protein, non-consensus GA donor splice site at exon 6
expressed protein
putative 1,2-diacylglycerol 3-beta-galactosyltransferase
zinc finger (C3HC4-type RING finger) family protein
expressed protein
putative cinnamoyl-alcohol dehydrogenase
IAA-aminoacid hydrolase I (ILR1)
-
-
leucine-rich repeat family protein/protein kinase family protein
leucine-rich repeat family protein/protein kinase family protein
polyadenylate-binding protein, putative / PABP, putative, similar to poly(A)-binding protein GB:AAF66825 GI:7673359 from (Nicotiana tabacum)
polyadenylate-binding protein, putative / PABP, putative, similar to poly(A)-binding protein GB:AAF66825 GI:7673359 from (Nicotiana tabacum)
polyadenylate-binding protein, putative / PABP, putative, similar to poly(A)-binding protein GB:AAF66825 GI:7673359 from (Nicotiana tabacum)
26S proteasome regulatory complex component [Posttranslational modification, protein turnover, chaperones]; COG5159
exportin 1 (XPO1)
-
short-chain dehydrogenase/reductase (SDR) family protein
-
-
-
-
sec34-like family protein (vesicle docking protein)
-
-
-
-
zinc finger (C3HC4-type RING finger) family protein
expressed protein
Glycosyl hydrolase family 9; pfam00759

-
glutamate synthase [NADH], chloroplast precursor
nuclear transport factor 2 (NTF2) family protein
cell division cycle protein 48 (CDC 48A)
short-chain dehydrogenase/reductase (SDR) family protein, similar to WW-domain oxidoreductase
-
oxidoreductase, 2 OG-Fe(II) oxygenase family protein
-
-
-
-
nt sequence very similar to pc594-1 or pc594-3
-
nt sequence very similar to pc594-1 or pc594-3
nt sequence very similar to pc594-1 or pc594-3
nt sequence very similar to pc594-1 or pc594-3
-
tropinone reductase, putative
phenylalanine ammonia-lyase (AA 137 - 716) (1 is 3rd base in codon)
Belongs to the TBP family
Belongs to the TBP family
-
-
-
-
Pep3/Vsp18/deep orange family protein
-
root hair defect 3 GTP-binding (RHD3) family protein
expressed protein
expressed protein (putative DNA J protein)
DNAJ heat shock N-terminal domain-containing protein
-
-
-
-
belongs to the ABC transporter family
-
MtN19=Medicago tuncatula Nodulin 19
Belongs to the eukaryotic AdoMetDC family
putative cetromere/kinetochore protein (ZW10)
-
putative wall-associated kinase
putative wall-associated kinase
putative wall-associated kinase
light-responsive
-

light-responsive
esterase/lipase/thioesterase family protein
-
-
-
-
putative wall-associated kinase
-
putative histone H2A
putative leucine-rich repeat transmembrane protein kinase
putative leucine-rich repeat transmembrane protein kinase
putative leucine-rich repeat transmembrane protein kinase
-
-
-
-
metallopeptidase M24 family protein
metallopeptidase M24 family protein
-
-
-
putative iron-deficiency-responsive protein
-
-
-
-
-
-
soybean cold-regulated gene
soybean cold-regulated gene
2-nitropropane dioxygenase family/NPD family
-
Belongs to the Ser/Thr protein kinase family
-
protein kinase family protein
-
-
-
-
protein kinase family protein
-
zinc finger (C3HC4-type RING finger) family protein
MtN19=Medicago tuncatula Nodulin 19
putative leucine-rich repeat transmembrane protein kinase, similar to brassinosteroid insensitive 1
putative leucine-rich repeat transmembrane protein kinase, similar to brassinosteroid insensitive 1
cytochrome P450 family protein

NC domain-containing protein
-
NC domain-containing protein
cellulose synthase family protein (CslD3), similar to cellulose synthase catalytic subunit gi:2827143
cellulose synthase family protein (CslD3), similar to cellulose synthase catalytic subunit gi:2827143
cellulose synthase family protein (CslD3), similar to cellulose synthase catalytic subunit gi:2827143
cellulose synthase family protein (CslD3), similar to cellulose synthase catalytic subunit gi:2827143
probable gibberllin beta-hydroxylase
-
-
probable gibberllin beta-hydroxylase
zinc finger (C3HC4-type RING finger) family protein
-
-
-
-
expressed protein
-
-
expressed protein
strictosidine synthase family protein
-
possible involvement in somatic embryo development
expressed protein
-
-
expressed protein
expressed protein
expressed protein
-
-
haloacid dehalogenase-like hydrolase family protein
ankyrin repeat family protein, regulator of chromosomal condensation (RCC1) family protein
ankyrin repeat family protein, regulator of chromosomal condensation (RCC1) family protein
Contains 1 PLAT domain
Contains 1 PLAT domain
zinc-finger
Os10g0182000
diacylglycerol kinase 1 (DGK1)
short-chain dehydrogenase/reductase (SDR) family protein
expressed protein
-
CATALYTIC ACTIVITY: (S)-malate + NAD+ = oxaloacetate + NADH
expressed protein
expressed protein
-

S-locus protein kinase, putative, similar to S-receptor kinase gi|392557|gb|AAA62232
S-locus protein kinase, putative, similar to S-receptor kinase gi|392557|gb|AAA62232
S-locus protein kinase, putative, similar to S-receptor kinase gi|392557|gb|AAA62232
-
late embryogenesis abundant protein-related
S-locus protein kinase, putative, similar to S-receptor kinase gi|392557|gb|AAA62232
late embryogenesis abundant protein-related
late embryogenesis abundant protein-related
-
S-locus protein kinase, putative, similar to receptor protein kinase (Ipomoea trifida)
-
glutamate dehydrogenase A (GDH A)
Ku 80 family protein
Ku 80 family protein
Ku 80 family protein
Ku 80 family protein
-
-
zinc finger (CCCH-type) family protein
-
-
-
-
-
-
-
-
but very similar to PC664-2-1
-
-
-
-
-
-
-
-
-
cytochrome P450
Secretory peroxidase
-
phosphoglycerate/bisphosphoglycerate mutase family protein
-
-
cyclophilin_ABH_like: Cyclophilin A, B and H-like cyclophilin-type peptidylprolyl cis- trans isomerase (PPIase) domain
cyclophilin_ABH_like: Cyclophilin A, B and H-like cyclophilin-type peptidylprolyl cis- trans isomerase (PPIase) domain
cyclophilin_ABH_like: Cyclophilin A, B and H-like cyclophilin-type peptidylprolyl cis- trans isomerase (PPIase) domain

tRNA synthetase class I (C) family protein
Secretory peroxidase
-
alpha-1,4-glycosyltransferase family protein
Secondary metabolites biosynthesis, transport, and catabolism
protein kinase family protein
protein kinase family protein
-
-
Belongs to the group II decarboxylase family
Belongs to the group II decarboxylase family
Belongs to the group II decarboxylase family
Belongs to the group II decarboxylase family
-
oxidoreductase, 2OG-Fe(II) oxygenase family protein
phosphoesterase family protein
ADP-ribosylation factor
similar to MATE efflux family protein
similar to MATE efflux family protein
putative ammonium transporter
-
-
-
-
oxidoreductase, 2OG-Fe(II) oxygenase family protein
-
calcium-transporting ATPase 1, endoplasmic reticulum-type (ECA1)
Serine/Threonine protein kinases, catalytic domain
-
Belongs to the serpin family
-
Belongs to the serpin family
-
-
-
-
sec23/sec24 treansport protein-related
-
Secondary metabolites biosynthesis, transport, and catabolism
phenylalanine ammonia-lyase (AA 137 - 716) (1 is 3rd base in codon)
Belongs to the group II decarboxylase family
-
-
-
-
Secretory peroxidase

ADP ribosylation factor
-
-
-
-
-
-
-
-
-
-
20S proteasome alpha subunit A2 (PAA2)
20S proteasome alpha subunit A2 (PAA2)
20S proteasome alpha subunit A2 (PAA2)
20S proteasome alpha subunit A2 (PAA2)
20S proteasome alpha subunit A2 (PAA2)
20S proteasome alpha subunit A2 (PAA2)
-
putative Calcium-transporting ATPase, plasmamembrane-type
RNA polymerase sigma subunit SigF (SigF)
MtN19=Medicago tuncatula Nodulin 19
ankyrin repeat family protein (putative RING zinc finger)
ankyrin repeat family protein (putative RING zinc finger)
putative Calcium-dependent protein kinase (CDPK)
RNA recognition motif (RRM)-containing protein
-
-
putative disease resistance protein (CC-NBS-LRR class)
putative disease resistance protein (CC-NBS-LRR class)
putative disease resistance protein (CC-NBS-LRR class)
-
-
-
-
FAD-binding domain-containing protein
-
ABC transporter family protein
RNA recognition motif (RRM)-containing protein
-
-
-
Secretory peroxidase
Secondary metabolites biosynthesis, transport, and catabolism
oxidoreductase, 2OG-Fe(II) oxygenase family protein
oxidoreductase, 2OG-Fe(II) oxygenase family protein
oxidoreductase, 2OG-Fe(II) oxygenase family protein

oxidoreductase, 2OG-Fe(II) oxygenase family protein
oxidoreductase, 2OG-Fe(II) oxygenase family protein
oxidoreductase, 2OG-Fe(II) oxygenase family protein
AMP-dependent synthetase & ligase family protein
AMP-dependent synthetase & ligase family protein
AMP-dependent synthetase & ligase family protein
Secondary metabolites biosynthesis, transport, and catabolism
Secretory peroxidase
FAD-binding domain-containing protein (Berberine-bridge-forming enzyme) (BBE)
AMP-dependent synthetase & ligase family protein
expressed protein
-
-
Secretory peroxidase
ankyrin repeat family protein (ankyrin repeats mediate)
Belongs to the zinc-containing alcohol dehydrogenase family
putative mannitol transporter
putative mannitol transporter
putative mannitol transporter
-
-
-
-
Secondary metabolites biosynthesis, transport, and catabolism
regulator of epidermal morphogenesis; similar to catalytic domain of DOCK-family exchange factors
regulator of epidermal morphogenesis; similar to catalytic domain of DOCK-family exchange factors
regulator of epidermal morphogenesis; similar to catalytic domain of DOCK-family exchange factors
putative mannitol transporter
ADP ribosylation factor
oxidoreductase, 2OG-Fe(II) oxygenase family protein
pyruvate dehydrogenase E1 component beta subunit, mitochondrial
pyruvate dehydrogenase E1 component beta subunit, mitochondrial
pyruvate dehydrogenase E1 component beta subunit, mitochondrial
60 S ribosomal protein L26 (RPL26A)
-
ADP ribosylation factor
ADP ribosylation factor
ADP ribosylation factor
ADP ribosylation factor
ADP ribosylation factor
Secondary metabolites biosynthesis, transport, and catabolism
Secondary metabolites biosynthesis, transport, and catabolism
-
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dermal glycoprotein precursor, extracellular
AMP-dependent synthetase & ligase family protein
Secretory peroxidase
MutT/nudix family protein
Belongs to the DEAD box helicase family. eIF4A subfamily; Contains 1 helicase ATP-binding domain; Contains 1 helicase C-terminal domain
Belongs to the DEAD box helicase family. eIF4A subfamily; Contains 1 helicase ATP-binding domain; Contains 1 helicase C-terminal domain
-
Belongs to the peroxidase family. Classical plant (class III) peroxidase subfamily
Belongs to the group II decarboxylase family
-
-
BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1, putative, expressed
similar to PAL1 or PAL2
Belongs to the AAA ATPase family
-
-
aconitase family
aconitase family
-
Belongs to the 14-3-3 family
-
-
-
-
-
belongs to the Ser/Thr protein kinase family
-
-
-
-
-
-
-
epsin N-terminal homology (ENTH) domain-containing protein, contains Pfam PF01417: ENTH domain
epsin N-terminal homology (ENTH) domain-containing protein, contains Pfam PF01417: ENTH domain
possible involvement in somatic embryo development
possible involvement in somatic embryo development
possible involvement in somatic embryo development
possible involvement in somatic embryo development
possible involvement in somatic embryo development
-
possible involvement in somatic embryo development
possible involvement in somatic embryo development

possible involvement in somatic embryo development
possible involvement in somatic embryo development
possible involvement in somatic embryo development
possible involvement in somatic embryo development
possible involvement in somatic embryo development
possible involvement in somatic embryo development
possible involvement in somatic embryo development
possible involvement in somatic embryo development
possible involvement in somatic embryo development
-
glycosyl transferase family 48 protein,
alcohol oxidase-related
extracellular dermal glycoprotein
-
-
-
sec34-like family protein (vesicle docking protein)
similar to glycine-rich protein
-
expressed protein
INDUCTION: By nitrate
zinc finger (AN1-like) family protein, contains Pfam profile: PF01428 AN1-like zinc finger
-
-
expressed protein
-
-
cytochrome P450 family
short-chain dehydrogenase/reductase family protein
-
-
-
-
-
expressed protein
-
-
scarecrow-like transcription factor 21 (SCL21)
belongs to the BetVI family
EXS family protein / ERD1/XPR1/SYG1 family protein
EXS family protein / ERD1/XPR1/SYG1 family protein
belongs to the SUI1 family.
-
-
-
-

expressed protein
ABC transporter family
ABC transporter family
OSJNBa0065J17.16
OSJNBa0065J17.16
OSJNBa0065J17.16
zinc finger (AN1-like) family protein, contains Pfam profile: PF01428 AN1-like zinc finger
zinc finger (AN1-like) family protein, contains Pfam profile: PF01428 AN1-like zinc finger
zinc finger (AN1-like) family protein, contains Pfam profile: PF01428 AN1-like zinc finger
short-chain dehydrogenase/reductase family protein
-
-
-
-
-
-
contains aspartyl protease-like domain
or similar to nectarin IV [Nicotiana langsdorffii x Nicotiana sanderae]; AAX81588
-
calmodulin-binding family protein
or similar to nectarin IV [Nicotiana langsdorffii x Nicotiana sanderae]; AAX81588
calmodulin-binding family protein
or similar to nectarin IV [Nicotiana langsdorffii x Nicotiana sanderae]; AAX81588
or similar to nectarin IV [Nicotiana langsdorffii x Nicotiana sanderae]; AAX81588
-
-
-
-
CATALYTIC ACTIVITY: (S)-malate + NAD+ = oxaloacetate + NADH
-
CATALYTIC ACTIVITY: (S)-malate + NAD+ = oxaloacetate + NADH
expressed protein
expressed protein
CATALYTIC ACTIVITY: (S)-malate + NAD+ = oxaloacetate + NADH
S-locus protein kinase, putative, similar to S-receptor kinase gi|392557|gb|AAA62232
glycine hydroxymethyltransferase
F-box family protein, PF0064: F-box domain
F-box family protein
putative anionic peroxidase
putative anionic peroxidase
-
-
F-box family protein, PF0064: F-box domain
calcium- and calmodulin-dependent protein kinase/ kinase
phospholipid/glycerol acyltransferase family protein
calcium- and calmodulin-dependent protein kinase/ kinase

-
putative cytochrome P450
putative cytochrome P450
-
-
-
-
pentatricopeptide (PPR) repeat-containing protein
-
Cytochrome P450 [Secondary metabolites biosynthesis, transport, and catabolism]
-
oxidoreductase, acting on the CH-OH group of donors, NAD or NADP as acceptor
oxidoreductase, acting on the CH-OH group of donors, NAD or NADP as acceptor
DNAJ heat shock protein, putative, similar to SP|O89114 DnaJ homolog subfamily B member 5 (Heat shock protein Hsp40-3) {Mus musculus}
belongs to the peroxidase family
oxidoreductase, acting on the CH-OH group of donors, NAD or NADP as acceptor
-
oxidoreductase, acting on the CH-OH group of donors, NAD or NADP as acceptor
oxidoreductase, acting on the CH-OH group of donors, NAD or NADP as acceptor
-
Modified RING finger domain; Modified RING finger domain, without the full complement of Zn2+-binding ligands. Probable involvement in E2-dependent ubiquitination; smart00504
Modified RING finger domain; Modified RING finger domain, without the full complement of Zn2+-binding ligands. Probable involvement in E2-dependent ubiquitination; smart00504
-
-
extracellular dermal glycoprotein
-
-
-
-
-
cytochrome P450
-
P0698H10.19
P0698H10.19
epsin N-terminal homology (ENTH) domain-containing protein, contains Pfam PF01417: ENTH domain
putative endomembrane protein 70, TM4 family
protein disulfide isomerase (PDI)-like protein
belongs to the ABC transporter family
-
or similar to nectarin IV [Nicotiana langsdorffii x Nicotiana sanderae]; AAX81588
expressed protein
mitochondrial tRNA-Ala synthetase
expressed protein; Esterase/lipase
SWAP (Suppressor-of-White-APricot)/surp domain-containing protein
SWAP (Suppressor-of-White-APricot)/surp domain-containing protein
-

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-
-
-
-
expressed protein, similar to expressed protein
60S ribosomal protien L19 (RPL19A)
60S ribosomal protien L19 (RPL19A)
expressed protein, very similar to PC818-3
expressed protein, very similar to PC818-3
expressed protein
Glycosyl hydrolase family 9; pfam00759
Glycosyl hydrolase family 9; pfam00759
-
-
-
expressed protein
Glycosyl hydrolase family 9; pfam00759
expressed protein
expressed protein, very similar to PC818-3
argonaute protein
argonaute protein
-
-
argonaute protein
argonaute protein
-
-
-
-
putative disease resistance protein (TIR-NBS-LRR class)
Belongs to the group II decarboxylase family
contains 1 PH domain
Leucine-rich repeat; repeat
contains 1 PH domain
-
contains 1 PH domain
Patatin-like phospholipase; pfam01734
-
-
but very similar to pc832-2 und pc701-2-1
-
-
-

induced during the resistance response to TMV
-
Sodium:solute symporter family
-
-
-
-
-
GTP-binding family protein
-
ADP ribosylation factor
-

Nr.	**Fragment**	**Länge**	**Beschreibung**	**AGI Code**	**Identität**	**GO-Biologischer Prozess**
3	PC1-3	262	ATP binding / ATP-dependent helicase	At3g18600	31/78 (39%)	-
14	PC4-3	116	structural constituent of ribosome (see 182-4)	At1g15250	30/36 (83%)	protein biosynthesis, ribosome biogenesis
19	PC6	394	unknown protein	At3g01740	26/70 (37%)	biological_process unknown
20	PC8	139	unknown protein (see 10)	At2g39530	16/29 (55%)	biological_process unknown
21	PC9-1	123	HSP70; ATP binding (see 21-1)	At3g12580	39/40 (97%)	protein folding [pmid 11402207]; response to heat [pmid 11402207];
22	PC9-2	123	HSP70; ATP binding (see 21-1)	At3g12580	39/40 (97%)	protein folding [pmid 11402207]; response to heat [pmid 11402207];
23	PC9-3	123	HSP70; ATP binding (see 21-1)	At3g12580	39/40 (97%)	protein folding [pmid 11402207]; response to heat [pmid 11402207];
24	PC9-4	123	HSP70; ATP binding (see 21-1)	At3g12580	39/40 (97%)	protein folding [pmid 11402207]; response to heat [pmid 11402207];
25	PC10-1	141	unknown protein (see 25)	At2g39530	17/31 (54%)	biological_process unknown
26	PC10-2	141	unknown protein (see 25)	At2g39530	17/31 (54%)	biological_process unknown
27	PC10-4	141	unknown protein (see 25)	At2g39530	17/31 (54%)	biological_process unknown
28	PC10-3	123	HSP70; ATP binding (see 21-1)	At3g12580	39/40 (97%)	protein folding [pmid 11402207]; response to heat [pmid 11402207];
33	PC12	102	transferase, transferring glycosyl groups / transferase, transferring hexosy	At1g05170	18/20 (90%)	protein amino acid glycosylation
42	PC15-1	67	ADL1D; GTP binding / GTPase	At2g44590	19/21 (90%)	biological process unknown
43	PC15-2	76	unknown protein	At3g55840	12/22 (54%)	biological_process unknown
44	PC15-3	76	unknown protein	At3g55840	14/21 (66%)	biological_process unknown
50	PC17-3	118	catalytic/ protein phosphatase type 2C	At1g79630	14/18 (77%)	N-terminal protein myristoylation [pmid 12912986]
52	PC20-3	141	unknown protein (see 10)	At2g39530	17/31 (54%)	biological process unknown
53	PC20-4	177	unknown protein (see 8)	At2g39530	18/32 (56%)	biological process unknown
54	PC21-1	123	HSP70; ATP binding (see 9)	At3g12580	39/40 (97%)	protein folding [pmid 11402207]; response to heat [pmid 11402207];
55	PC21-2	123	HSP70; ATP binding (see 9)	At3g12580	39/40 (97%)	protein folding [pmid 11402207]; response to heat [pmid 11402207];
56	PC21-3	123	HSP70; ATP binding (see 9)	At3g12580	39/40 (97%)	protein folding [pmid 11402207]; response to heat [pmid 11402207];
57	PC21-4	123	HSP70; ATP binding (see 34)	At3g12580	39/40 (97%)	protein folding [pmid 11402207]; response to heat [pmid 11402207];
59	PC23-2	253	unknown protein	At2g31410	56/79 (70%)	-
60	PC23-3	253	unknown protein	At2g31410	56/79 (70%)	-
65	PC24-4	158	structural constituent of ribosome	At5g20290	44/51 (86%)	protein biosynthesis [pmid 11598216]; ribosome biogenesis
66	PC25-1	141	unknown protein (see 20)	At2g39530	17/31 (54%)	biological process unknown
67	PC25-2	141	unknown protein (see 20)	At2g39530	17/31 (54%)	biological process unknown
68	PC25-3	141	unknown protein (see 20)	At2g39530	17/31 (54%)	biological process unknown
69	PC25-4	141	unknown protein (see 20)	At2g39530	17/31 (54%)	biological process unknown
77	PC27-4	123	transferase, transferring glycosyl groups	At5g41460	32/40 (80%)	biological process unknown
78	PC28-1	103	ATMRP5	At1g04120	31/34 (91%)	transport
82	PC29-2	86	aspartic-type endopeptidase/ pepsin A	At3g51340	15/23 (65%)	proteolysis
83	PC29-3	85	aspartic-type endopeptidase/ pepsin A	At3g51340	16/28 (57%)	proteolysis
101	PC34	155	HSP70; ATP binding	At3g12580	18/19 (94%)	protein folding [pmid 11402207]; response to heat [pmid 11402207];
106	PC36-1	114	putative leucine-rich repeat transmembrane protein kinase	At1g14390	18/36 50%	protein amino acid phosphorylation, transmembrane receptor protein t
107	PC36-4	114	putative leucine-rich repeat transmembrane protein kinase	At1g14390	18/36 50%	protein amino acid phosphorylation, transmembrane receptor protein t
108	PC36-2	111	phosphoinositide 5-phosphatase	At3g43220	25/36 (69%)	biological process unknown
109	PC36-3	111	nucleotide binding	At4g01860	18/35 (51%)	biological process unknown
114	PC38-1	59	oxidoreductase/ zinc ion binding	At3g56460	16/19 (84%)	-
133	PC43-3	101	transferase, transferring glycosyl groups / transferase, transferring hexosy	At1g05170	28/31 (90%	protein amino acid glycosylation
136	PC44-2	120	unknown protein	At4g01400	20/36 (55%)	biological process unknown
137	PC44-3	111	phosphoinositide 5-phosphatase (see 36-2)	At3g43220	25/36 (69%	biological process unknown
138	PC44-4	111	phosphoinositide 5-phosphatase (see 36-2)	At3g43220	25/36 (69%	biological process unknown
139	PC45-1	104	amino acid permease	At3g30390	26/34 (76%)	amino acid transport
149	PC48-1	111	catalytic/ epoxide hydrolase/ hydrolase	At4g02340	21/36 (58%)	aromatic compound metabolism
150	PC48-2	111	catalytic/ epoxide hydrolase/ hydrolase	At4g02340	21/36 (58%)	aromatic compound metabolism
151	PC48-3	111	catalytic/ epoxide hydrolase/ hydrolase	At4g02340	21/36 (58%)	aromatic compound metabolism
152	PC48-4	111	catalytic/ epoxide hydrolase/ hydrolase	At4g02340	21/36 (58%)	aromatic compound metabolism
156	PC49-4	102	unknown protein	At3g54190	31/33 (93%)	biological process unknown
177	PC55-1	196	pectinesterase	At2g47550	28/44 (63%)	cell wall modification

178	PC55-2	155	ATP binding / casein kinase I	At5g44100	50/51 (98%)	protein amino acid phosphorylation
179	PC55-3	155	ATP binding / casein kinase I	At5g44100	50/51 (98%)	protein amino acid phosphorylation
180	PC55-4	196	pectinesterase	At2g47550	28/44 (63%)	cell wall modification
184	PC56-3	179	oxidoreductase	At1g59960	24/51 (47%)	-
185	PC57-1	137	iron ion binding / lipoxygenase	At1g72520	24/50 (48%)	defense response, jasmonic acid biosynthesis, response to wounding,
187	PC57-3	137	iron ion binding / lipoxygenase	At1g72520	24/50 (48%)	defense response, jasmonic acid biosynthesis, response to wounding,
188	PC57-4	137	iron ion binding / lipoxygenase	At1g72520	24/50 (48%)	defense response, jasmonic acid biosynthesis, response to wounding,
197	PC60-1	51	structural constituent of ribosome (see 95-4)	At1g67430	16/16 (100%)	protein biosynthesis
198	PC60-2	51	structural constituent of ribosome (see 95-4)	At1g67430	16/16 (100%)	protein biosynthesis
200	PC60-4	51	structural constituent of ribosome (see 95-4)	At1g67430	16/16 (100%)	protein biosynthesis
218	PC65-2	203	GTP cyclohydrolase I	At3g07270	20/23 (86%)	biosynthesis
220	PC65-4	116	unknown protein O-linked GlcNAc transferase like protein	At3g04830	32/38 (84%)	biological process unknown
230	PC68-2	94	ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ pro	At2g17220	25/31 (80%)	protein amino acid phosphorylation
231	PC68-3	94	ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ pro	At2g17220	26/31 (83%)	protein amino acid phosphorylation
232	PC68-4	94	ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ pro	At2g17220	26/31 (83%)	protein amino acid phosphorylation
237	PC70-1	148	ATP binding / microtubule motor	At3g49650	16/22 (72%)	microtubule-based movement
238	PC70-2	190	calcium ion binding	At5g28900	42/46 (91%)	biological process unknown
240	PC70-4	146	calcium ion binding	At5g61790	30/37 (81%)	-
242	PC71-2	135	transferase/ transferase, transferring glycosyl groups	At4g02500	22/34 (64%)	biological process unknown
244	PC71-4	116	transferase, transferring glycosyl groups	At1g53290	29/38 (76%)	protein amino acid glycosylation
249	PC74-2	79	POP2 (POLLEN-PISTIL INCOMPATIBILITY 2)	At3g22200	19/22 (86%)	biotin biosynthesis; pollen tube adhesion [pmid 8929415]; pollen tube
271	PC80-1	140	ubiquitin-protein ligase/ zinc ion binding	At1g61620	15/17 (88%)	protein ubiquitination
273	PC80-3	140	ubiquitin-protein ligase/ zinc ion binding	At1g61620	15/17 (88%)	protein ubiquitination
274	PC80-4	140	ubiquitin-protein ligase/ zinc ion binding	At1g61620	15/17 (88%)	protein ubiquitination
291	PC85-1	55	RHM1 (see 86-3)	At1g78570	14/17 (82%)	nucleotide-sugar metabolism
293	PC85-3	134	antiporter/ drug transporter (see pc87-1)	At5g10420	34/44 (77%)	multidrug transport, ripening
296	PC86-2	132	ATP binding / nucleoside-triphosphatase/ nucleotide binding	At1g67120	13/17 (76%)	-
297	PC86-3	55	RHM1 (see 85-1)	At1g78570	14/17 (82%)	nucleotide-sugar metabolism
298	PC86-4	174	oxidoreductase/ zinc ion binding (see 162-2)	At1g23740	42/56 (75%)	-
299	PC87-1	136	antiporter/ drug transporter (see pc85-3)	At5g10420	23/30 (76%)	multidrug transport, ripening
300	PC87-2	136	CIPK17 (CBL-interacting protein kinase 17)	At1g48260	14/19 (73%)	protein amino acid phosphorylation; signal transduction
303	PC88-1-1	161	ATGLR2.8 (see 252-1)	At2g29110	25/52 (48%)	calcium ion homeostasis [pmid 11379626]; response to light stimulus
304	PC88-1-2	275	transferase	At5g07860	48/91 (52%)	biological process unknown
307	PC88-2-1	343	unknown protein	At4g24310	38/61 (62%)	biological process unknown
314	PC89-1-2	299	structural constituent of ribosome (see 100-2-1)	At1g74270	51/61 (83%)	protein biosynthesis, ribosome biogenesis
316	PC89-3-1	178	ATEXPB2 (ARABIDOPSIS THALIANA EXPANSIN B2)	At1g65680	34/53 (64%)	cell wall loosening (sensu Magnoliophyta) [pmid 11641069]; cell wal
318	PC90-1	159	ATGLR2.8 (see 88-1-1)	At2g29110	21/47 (44%)	calcium ion homeostasis [pmid 11379626]; response to light stimulus
319	PC90-2	206	peptidyl-prolyl cis-trans isomerase	At2g21130	47/56 (83%)	protein folding
320	PC90-3	206	hydrolase (see 92-2)	At2g01670	42/68 (61%)	biological process unknown
323	PC91-3	178	ATEXPB2 (ARABIDOPSIS THALIANA EXPANSIN B2)	At1g65680	35/56 (62%)	cell wall loosening (sensu Magnoliophyta) [pmid 11641069]; cell wal
325	PC92-1	160	ATGLR2.8 (see 88-1-1)	At2g29110	21/47 (44%)	calcium ion homeostasis [pmid 11379626]; response to light stimulus
326	PC92-2	206	hydrolase (see 90-3)	At2g01670	42/68 (61%)	biological process unknown
338	PC95-4	51	structural constituent of ribosome (see 60-1)	At1g67430	16/16 (100%)	protein biosynthesis
339	PC96-1	48	transcription factor (see 545-1-4)	At2g40140	13/15 (86%)	regulation of transcription [pmid 11118137]
347	PC100-1-1	298	ATGCH	At5g64300	75/87 (86%)	riboflavin biosynthesis
348	PC100-1-2	299	unknown protein	At2g20940	14/17 (82%)	biological process unknown
349	PC100-1-3	289	structural constituent of ribosome	At2g47610	27/28 (96%)	protein biosynthesis [pmid 11598216]
351	PC100-2-1	181	structural constituent of ribosome (see 89-1-2)	At1g74270	50/60 (83%)	protein biosynthesis, ribosome biogenesis
352	PC100-2-2	181	structural constituent of ribosome (see 89-1-2)	At1g74270	50/60 (83%)	protein biosynthesis, ribosome biogenesis
355	PC102-1	181	structural constituent of ribosome (see 89-1-2)	At1g74270	50/60 (83%)	protein biosynthesis, ribosome biogenesis
356	PC102-2	181	structural constituent of ribosome (see 89-1-2)	At1g74270	50/60 (83%)	protein biosynthesis, ribosome biogenesis
357	PC102-3	181	structural constituent of ribosome (see 89-1-2)	At1g74270	50/60 (83%)	protein biosynthesis, ribosome biogenesis

358	PC102-4	181	structural constituent of ribosome (see 89-1-2)	At1g74270	50/60 (83%)	protein biosynthesis, ribosome biogenesis
365	PC107-1-3	287	NHL25 (NDR1/HIN1-LIKE 25)	At5g36970	35/62 (56%)	defense response to pathogen, incompatible interaction, salicylic acid
366	PC107-1-4	292	peroxidase (see 108-1-2)	At5g05340	49/62 (62%)	response to oxidative stress
372	PC108-1-2	291	peroxidase (see 107-1-4)	At5g05340	49/79 (62%)	response to oxidative stress
373	PC108-1-4	291	peroxidase (see 107-1-4)	At5g05340	48/79 (60%)	response to oxidative stress
380	PC110-2	297	peroxidase (see 107-1-4)	At5g05340	21/56 (37%)	response to oxidative stress
383	PC113-1	339	ribose-5-phosphate isomerase	At3g04790	21/25 (84%)	5-phosphoribose 1-diphosphate biosynthesis; D-ribose catabolism; gl
386	PC113-4	384	cysteine-type endopeptidase/ cysteine-type peptidase	At1g02305	21/25 (84%)	proteolysis
387	PC114-1	328	AALP	At5g60360	37/52 (71%)	proteolysis
390	PC114-4	313	hydrolase/ protein serine/threonine phosphatase	At1g13750	52/66 (78%)	biological process unknown
391	PC115-1	297	unknown protein	At5g35690	34/62 (54%)	-
392	PC115-4	297	unknown protein	At5g35690	34/62 (54%)	-
395	PC116-1	288	similar to vacuolar ATP-synthase subunit B isoform	At4g38510	42/42 (100%)	ATP biosynthesis, ATP synthesis coupled proton transport, energy co
398	PC116-3	292	peroxidase (see 107-1-4)	At5g05340	49/79 (62%)	response to oxidative stress
399	PC117-1	223	structural constituent of ribosome	At5g62300	33/34 (97%)	protein biosynthesis
402	PC117-4	219	UBP16 (UBIQUITIN-SPECIFIC PROTEASE 16)	At4g24560	27/43 (62%)	ubiquitin-dependent protein catabolism
414	PC120-4	286	RNA binding / structural constituent of ribosome	At5g20160	60/63 (95%)	protein biosynthesis; ribosome biogenesis and assembly
417	PC121-2	90	peptidyl-prolyl cis-trans isomerase	At2g21130	27/29 (93%)	protein folding
419	PC125-1	281	kinase/ ribokinase	At5g51830	52/72 (72%)	acetate fermentation; D-ribose metabolism; sucrose biosynthesis; sucr
420	PC125-2	281	kinase/ ribokinase	At5g51830	52/72 (72%)	acetate fermentation; D-ribose metabolism; sucrose biosynthesis; sucr
421	PC125-3	281	kinase/ ribokinase	At5g51830	52/72 (72%)	acetate fermentation; D-ribose metabolism; sucrose biosynthesis; sucr
422	PC125-4	281	kinase/ ribokinase	At5g51830	52/72 (72%)	acetate fermentation; D-ribose metabolism; sucrose biosynthesis; sucr
423	PC126-1	292	peroxidase (see 107-1-4)	At5g05340	47/78 (60%)	response to oxidative stress
424	PC126-2	281	kinase/ ribokinase (see 125)	At5g51830	51/72 (70%)	acetate fermentation; D-ribose metabolism; sucrose biosynthesis; sucr
425	PC126-3	280	kinase/ ribokinase (see 125)	At5g51830	51/72 (70%)	acetate fermentation; D-ribose metabolism; sucrose biosynthesis; sucr
431	PC130-1	279	copper ion binding	At2g40370	21/49 (42%)	-
434	PC131-1	218	unknown protein	At2g48110	49/71 (69%)	biological process unknown
435	PC131-2	175	unknown protein	At5g51570	55/58 (94%)	N-terminal protein myristoylation [pmid 12912986]
439	PC132-2	97	anionic peroxidase, putative	At1g14540	13/20 (65%)	response to oxidative stress
448	PC134-3	93	ATTIM44-2	At2g36110	16/28 (57%)	protein targeting to mitochondrion [pmid 12692332]
449	PC134-4	65	unknown protein	At3g57420	18/21 (85%)	-
454	PC137-1	291	peroxidase (see 107-1-4)	At5g05340	29/44 (65%)	response to oxidative stress
455	PC137-3	291	peroxidase (see 107-1-4)	At5g05340	32/51 (62%)	response to oxidative stress
456	PC137-4	292	peroxidase (see 107-1-4)	At5g05340	49/79 (62%)	response to oxidative stress
457	PC137-2	288	ATBPM1	At5g19000	46/68 (67%)	biological process unknown
458	PC138-1	283	RSZ33 (see 139-1)	At2g37340	65/94 (69%)	nuclear mRNA splicing, via spliceosome [pmid 12176998]; spliceoso
459	PC138-2	97	unknown protein (see 139-2)	At2g27660	16/30 (53%)	-
460	PC138-3	283	RSZ33 (see 139-1)	At2g37340	71/94 (75%)	nuclear mRNA splicing, via spliceosome [pmid 12176998]; spliceoso
461	PC138-4	283	RSZ33 (see 139-1)	At2g37340	71/94 (75%)	nuclear mRNA splicing, via spliceosome [pmid 12176998]; spliceoso
462	PC139-1	283	RSZ33 (see 138-1)	At2g37340	72/94 (76%)	nuclear mRNA splicing, via spliceosome [pmid 12176998]; spliceoso
463	PC139-2	97	unknown protein (see 138-2)	At2g27660	16/30 (53%)	-
464	PC139-3	217	ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ pro	At3g04690	28/65 (43%)	protein amino acid phosphorylation
466	PC140-1	283	RSZ33 (see 139-1)	At2g37340	72/94 (76%)	nuclear mRNA splicing, via spliceosome [pmid 12176998]; spliceoso
467	PC140-2	282	RSZ33 (see 139-1)	At2g37340	72/94 (76%)	nuclear mRNA splicing, via spliceosome [pmid 12176998]; spliceoso
469	PC140-4	97	unknown protein (see 138-2)	At2g27660	16/30 (53%)	-
471	PC141-2	165	unknown protein	At5g11090	38/51 (74%)	biological process unknown
472	PC141-3	165	unknown protein	At5g11090	38/51 (74%)	biological process unknown
473	PC141-4	165	unknown protein	At5g11090	38/51 (74%)	biological process unknown
474	PC142-1	93	calcium ion binding	At1g09210	26/30 (86%)	-
475	PC142-3	93	calcium ion binding	At1g09210	26/30 (86%)	-
476	PC142-2	87	LRX2 (LEUCINE-RICH REPEAT/EXTENSIN 2)	At1g62440	20/28 (71%)	cellular morphogenesis during differentiation [pmid 12834403]
477	PC142-4	87	LRX2 (LEUCINE-RICH REPEAT/EXTENSIN 2)	At1g62440	20/28 (71%)	cellular morphogenesis during differentiation [pmid 12834403]

481	PC144-1	293	oxidoreductase (see 145-3)	At5g06060	55/82 (67%)	metabolism
482	PC144-2	293	oxidoreductase (see 145-3)	At5g06060	55/82 (67%)	metabolism
483	PC144-3	292	oxidoreductase (see 596-1)	At5g06060	55/82 (67%)	metabolism
485	PC145-1	292	peroxidase (see 107-1-4)	At5g05340	49/79 (62%)	response to oxidative stress
486	PC145-4	292	peroxidase (see 107-1-4)	At5g05340	49/79 (62%)	response to oxidative stress
487	PC145-2	310	FLA9 (fasciclin-like arabinogalactan-protein 9)	At1g03870	59/101 (58%)	cell adhesion
488	PC145-3	377	oxidoreductase (see 144-1)	At5g06060	35/50 (70%)	metabolism
489	PC146-1	293	oxidoreductase (see 144-1)	At5g06060	55/85 (64%)	metabolism
490	PC146-2	293	oxidoreductase (see 144-1)	At5g06060	56/85 (65%)	metabolism
492	PC146-4	293	oxidoreductase (see 144-1)	At5g06060	56/85 (65%)	metabolism
493	PC147-1	154	ATP binding	At5g48620	21/42 (50%)	apoptosis; defense response; defense response to pathogen
494	PC147-2	153	ATP binding	At5g48620	21/42 (50%)	apoptosis; defense response; defense response to pathogen
495	PC147-3	153	ATP binding	At5g48620	21/42 (50%)	apoptosis; defense response; defense response to pathogen
496	PC147-4	153	ATP binding	At5g48620	23/43 (53%)	apoptosis; defense response; defense response to pathogen
497	PC148-1	153	ATP binding (see 147)	At5g48620	22/43 (51%)	apoptosis; defense response; defense response to pathogen
498	PC148-2	153	ATP binding (see 147)	At5g48620	23/43 (53%)	apoptosis; defense response; defense response to pathogen
499	PC148-3	153	ATP binding (see 147)	At5g48620	23/43 (53%)	apoptosis; defense response; defense response to pathogen
500	PC148-4	153	ATP binding (see 147)	At5g48620	23/43 (53%)	apoptosis; defense response; defense response to pathogen
501	PC149-1	417	unknown protein	At1g56290	69/116 (59%)	-
502	PC149-3	414	unknown protein	At1g56290	61/138 (44%)	-
503	PC149-4	414	unknown protein	At1g56290	84/134 (62%)	-
507	PC150-3	259	PHR2 (PHOTOLYASE/BLUE-LIGHT RECEPTOR 2)	At2g47590	36/48 (75%)	DNA repair
509	PC152-1	296	glutamine-fructose-6-phosphate transaminase (isomerizing)	At3g24090	91/98 (92%)	carbohydrate biosynthesis; carbohydrate metabolism; metabolism
511	PC152-3	296	oxidoreductase	At1g16720	40/52 (76%)	metabolism
516	PC154-4	77	mtHSC70-2 (HEAT SHOCK PROTEIN 70)	At5g09590	17/18 (94%)	protein folding [pmid 11402207]; response to heat [pmid 11402207];
529	PC158-1	247	ATP binding / protein binding (see 206-3)	At5g26360	44/47 (93%)	cellular protein metabolism
530	PC158-4	247	ATP binding / protein binding (see 206-3)	At5g26360	44/47 (93%)	cellular protein metabolism
538	PC161-2	174	oxidoreductase/ zinc ion binding (see 162-2)	At1g23740	30/39 (76%)	-
539	PC161-4	223	oxidoreductase/ zinc ion binding (see 162-2)	At1g23740	42/61 (68%)	-
542	PC162-2	174	oxidoreductase/ zinc ion binding (see 161-4)	At1g23740	42/56 (75%)	-
547	PC163-2	174	oxidoreductase/ zinc ion binding (see 162-2)	At1g23740	30/39 (76%)	-
548	PC163-4	174	oxidoreductase/ zinc ion binding (see 162-2)	At1g23740	30/39 (76%)	-
549	PC164-1-1	176	oxidoreductase/ zinc ion binding (see 162-2)	At1g23740	42/56 (75%)	-
550	PC164-1-2	174	oxidoreductase/ zinc ion binding (see 162-2)	At1g23740	42/56 (75%)	-
551	PC164-1-3	174	oxidoreductase/ zinc ion binding (see 162-2)	At1g23740	42/56 (75%)	-
552	PC164-1-4	176	oxidoreductase/ zinc ion binding (see 162-2)	At1g23740	42/56 (75%)	-
553	PC164-2-2	174	oxidoreductase/ zinc ion binding (see 162-2)	At1g23740	42/56 (75%)	-
554	PC164-2-1	118	copper ion binding	At3g09220	18/39 (46%)	-
555	PC164-2-4	118	copper ion binding	At3g09220	24/39 (61%)	-
557	PC167-1	315	unknown protein (see 470-1)	At2g46150	31/80 (38%)	biological process unknown
558	PC167-2	322	transferase, transferring hexosyl groups	At3g28340	68/105 (64%)	carbohydrate biosynthesis
559	PC167-3	322	transferase, transferring hexosyl groups	At3g28340	68/105 (64%)	carbohydrate biosynthesis
560	PC167-4	322	transferase, transferring hexosyl groups	At3g28340	68/105 (64%)	carbohydrate biosynthesis
561	PC168-1	238	unknown protein	At1g49000	37/54 (68%)	biological process unknown
562	PC168-2	236	ATP binding / protein kinase/ protein serine/threonine kinase/ protein-tyr	At2g18470	21/71 (29%)	protein amino acid phosphorylation
563	PC168-3	238	oxidoreductase/ zinc ion binding (see 162-2)	At1g23740	30/58 (51%)	-
570	PC175-2	191	SEN1 (DARK INDUCIBLE 1)	At4g35770	33/54 (61%)	aging [pmid 8624406] [pmid 8624406]; response to light stimulus [p
572	PC175-4	219	SEN1 (DARK INDUCIBLE 1)	At4g35770	38/55 (69%)	aging [pmid 8624406] [pmid 8624406]; response to light stimulus [p
573	PC177-1	233	unknown protein (see 216-1)	At2g15220	49/62 (79%)	defense response to pathogen
575	PC177-3	209	ubiquitin-protein ligase (see 388-3)	At2g35930	42/69 (60%)	protein ubiquitination
578	PC178-2	229	SGS3 (SUPPRESSOR OF GENE SILENCING 3) (see 280-4)	At5g23570	19/46 (41%)	virus induced gene silencing [pmid 10850495]
579	PC178-3	237	malate dehydrogenase/ oxidoreductase	At5g43330	56/70 (80%)	malate metabolism; tricarboxylic acid cycle intermediate metabolism

581	PC180-1	217	unknown protein	At1g26850	55/71 (77%)	-
582	PC180-2	171	ATPUP3 (see 345-4)	At1g28220	17/39 (43%)	-
583	PC180-3	133	kinase	At3g51550	28/37 (75%)	protein amino acid phosphorylation
584	PC180-4	171	catalytic/ intramolecular transferase, phosphotransferases	At1g22170	13/18 (72%)	glycolysis; metabolism
587	PC182-3	142	electron carrier (ev. 543-3)	At1g30740	17/27 (62%)	electron transport
588	PC182-4	135	structural constituent of ribosome (see 4-3)	At1g15250	31/39 (79%)	protein biosynthesis, ribosome biogenesis
589	PC184-1	235	unknown protein (see 470-1)	At2g46150	31/79 (39%)	biological process unknown
590	PC184-2	235	unknown protein (see470-1)	At2g46150	31/79 (39%)	biological process unknown
591	PC184-4	235	unknown protein (see470-1)	At2g46150	31/79 (39%)	biological process unknown
593	PC185-1	174	oxidoreductase/ zinc ion binding (see 162-2)	At1g23740	42/56 (75%)	-
594	PC185-2	169	unknown protein (see 216-1)	At2g15220	47/58 (81%)	defense response to pathogen
595	PC185-3	170	unknown protein (see 216-1)	At2g15220	47/58 (81%)	defense response to pathogen
596	PC185-4	169	unknown protein (see 216-1)	At2g15220	47/58 (81%)	defense response to pathogen
597	PC187-2	235	unknown protein (see470-1)	At2g46150	31/79 (39%)	biological process unknown
605	PC190-1	169	unknown protein (see 216-1)	At2g15220	47/58 (81%)	defense response to pathogen
606	PC190-2	203	phosphoprotein phosphatase/ protein tyrosine/serine/threonine phosphatas	At5g56610	53/67 (79%)	protein amino acid dephosphorylation
608	PC190-4	174	hydrogen-exporting ATPase	At5g08670	57/57 (100%)	ATP biosynthesis; ATP synthesis coupled proton transport
609	PC191-1	169	unknown protein (see 216-1)	At2g15220	47/58 (81%)	defense response to pathogen
610	PC191-4	169	unknown protein	At2g15220	47/58 (81%)	defense response to pathogen
613	PC195-1	409	ATGPAT6/GPAT6; 1-acylglycerol-3-phosphate O-acyltransferase/ acyltr	At2g38110	102/133 (76%)	metabolism
614	PC195-2	406	ATGPAT6/GPAT6; 1-acylglycerol-3-phosphate O-acyltransferase/ acyltr	At2g38110	88/122 (72%)	metabolism
618	PC196-2	349	ubiquitin-protein ligase	At3g52450	52/86 (60%)	protein ubiquitination
619	PC196-3	350	ubiquitin-protein ligase	At3g52450	52/86 (60%)	protein ubiquitination
621	PC197-2	378	HSP81-3	At5g56010	42/60 (70%)	protein folding; response to heat [pmid 7697294]
624	PC197-5	364	unknown protein (see 470-1)	At2g46150	33/82 (40%)	biological process unknown
626	PC198-2	237	ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ pro	At5g40540	72/78 (92%)	protein amino acid phosphorylation
628	PC198-4	245	amino acid permease/ amino acid transporter	At4g38250	35/86 (40%)	amino acid transport
642	PC202-2	154	oxidoreductase	At1g01800	27/45 (60%)	metabolism
643	PC202-3	156	oxidoreductase	At1g01800	28/48 (68%)	metabolism
644	PC202-4	156	oxidoreductase	At1g01800	28/48 (68%)	metabolism
654	PC206-3	140	ATP binding / protein binding (see 158-1)	At5g26360	43/46 (93%)	cellular protein metabolism
655	PC206-4	156	RPS15A (RIBOSOMAL PROTEIN S15A)	At1g07770	34/40 (85%)	protein biosynthesis [pmid 11598216]
656	PC207-1	143	RNA polymerase II transcription factor	At3g10330	21/27 (77%)	regulation of transcription, DNA-dependent; transcription initiation
657	PC207-2	140	ATP binding / protein binding (see 158-1)	At5g26360	43/46 (93%)	cellular protein metabolism
658	PC207-3	140	ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ pro	At1g16670	30/38 (78%)	protein amino acid phosphorylation
669	PC210-2	324	oxidoreductase/ zinc ion binding (see 417-1)	At1g23740	27/46 (58%)	-
670	PC210-3	235	oxidoreductase/ zinc ion binding (see 417-1)	At1g23740	27/46 (58%)	-
673	PC211-2	168	ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding	At4g02480	18/24 (75%)	-
675	PC211-4	160	unknown protein (see 212-3)	At1g70505	29/50 (58%)	biological process unknown
678	PC212-3	160	unknown protein (see 211-4)	At1g70505	29/50 (58%)	biological process unknown
682	PC215-3	169	unknown protein (see 216-1)	At2g15220	45/56 (80%)	defense response to pathogen
683	PC215-4	189	membrane alanyl aminopeptidase	At1g63770	40/62 (64%)	proteolysis
684	PC216-1	168	unknown protein (see 177-1)	At2g15220	28/36 (77%)	defense response to pathogen
685	PC216-3	168	unknown protein (see 177-1)	At2g15220	28/36 (77%)	defense response to pathogen
686	PC216-2	277	unknown protein	At1g54320	58/83 (69%)	biological process unknown
687	PC216-4	276	unknown protein	At1g54320	58/83 (69%)	biological process unknown
688	PC217-1	242	oxidoreductase/ zinc ion binding (see 162-2 & 210-2)	At1g23740	42/56 (75%)	-
690	PC217-3	250	unknown protein (see 216-1)	At2g15220	49/61 (80%)	defense response to pathogen
692	PC218-1	235	unknown protein (see 470-1)	At2g46150	31/79 (39%)	biological process unknown
693	PC218-2	235	unknown protein (see 470-1)	At2g46150	31/79 (39%)	biological process unknown
694	PC218-3	234	unknown protein (see 470-1)	At2g46150	31/79 (39%)	biological process unknown
696	PC219-1	201	APS1	At3g22890	59/66 (89%)	dissimilatory sulfate reduction; sulfate assimilation; sulfate assimilatic

697	PC219-2	201	APS1	At3g22890	59/66 (89%)	dissimilatory sulfate reduction; sulfate assimilation; sulfate assimilatio
698	PC219-3	212	ATP binding / carbohydrate binding / kinase/ protein kinase/protein serine	At4g27300	27/69 (39%)	protein amino acid phosphorylation
699	PC219-4	211	2,3-bisphosphoglycerate-independent phosphoglycerate mutase	At3g08590	50/57 (87%)	acetate fermentation; aerobic glycerol catabolism; aerobic glycerol de
700	PC220-1	168	unknown protein (see 216-1)	At2g15220	28/36 (77%)	defense response to pathogen
701	PC220-2	168	unknown protein (see 216-1)	At2g15220	28/36 (77%)	defense response to pathogen
702	PC220-3	173	ACS1 (ACC SYNTHASE 1) (see 246-1)	At3g61510	32/39 (82%)	ethylene biosynthesis [pmid 8566772]
704	PC221-2	171	unknown protein (see 216-1)	At2g15220	41/50 (82%)	defense response to pathogen
705	PC221-3	173	unknown protein (see 216-1)	At2g15220	40/45 (88%)	defense response to pathogen
706	PC221-4	169	unknown protein (see 216-1)	At2g15220	26/31 (83%)	defense response to pathogen
707	PC222-1	170	unknown protein (see 216-1)	At2g15220	43/57 (75%)	defense response to pathogen
708	PC222-2	169	unknown protein (see 216-1)	At2g15220	43/57 (75%)	defense response to pathogen
709	PC222-3	169	unknown protein (see 216-1)	At2g15220	43/57 (75%)	defense response to pathogen
712	PC223-2	169	unknown protein (see 216-1)	At2g15220	46/58 (79%)	defense response to pathogen
713	PC223-3	169	unknown protein (see 216-1)	At2g15220	46/57 (80%)	defense response to pathogen
717	PC224-3	102	PWD (PHOSPHOGLUCAN WATER DIKINASE)	At5g26570	16/30 (53%)	starch catabolism, starch metabolism, protein amino acid autophospho
722	PC225-2	81	X-Pro dipeptidase-like protein (see 249-2)	At4g29500	20/26 (76%)	-
727	PC228-1	72	putative cinnamyl-alcohol dehydrogenase (see 580-1)	At1g72680	16/24 (66%)	lignin biosynthesis [pmid 8219046]
728	PC228-2	235	ATSK11	At5g26751	75/77 (97%)	meristem organization [pmid 10758494]; phosphorylation [pmid 7509
730	PC228-4	237	ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ pro	At5g40540	51/54 (94%)	protein amino acid phosphorylation
731	PC229-1	170	unknown protein	At3g44100	13/29 (44%)	biological process unknown
732	PC229-3	170	unknown protein	At3g44100	19/40 (47%)	biological process unknown
733	PC229-2	169	unknown protein	At3g44100	13/29 (44%)	biological process unknown
736	PC230-2	159	BXL2 (BETA-XYLOSIDASE 2)	At1g02640	37/52 (71%)	carbohydrate metabolism
738	PC230-4	160	ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ pro	At3g20860	25/39 (64%)	protein amino acid phosphorylation
739	PC232-1	145	MUR3 (MURUS 3)	At2g20370	38/47 (80%)	endomembrane organization [pmid 15863516]; fucose biosynthesis [p
743	PC233-1	91	SKIP4 (SKP1 INTERACTING PARTNER 4)	At3g61350	21/25 (84%)	biological process unknown
744	PC233-2	91	SKIP4 (SKP1 INTERACTING PARTNER 4)	At3g61350	21/25 (84%)	biological process unknown
747	PC234-1	223	COR413-PM2	At3g50830	20/31 (64%)	response to stress [pmid 12746512]
748	PC234-2	225	oxidoreductase/ zinc ion binding	At5g24760	60/74 (81%)	-
749	PC234-3	225	oxidoreductase/ zinc ion binding	At5g24760	60/74 (81%)	-
761	PC237-2	84	CYP86A2; oxygen binding	At4g00360	22/27 (81%)	fatty acid metabolism [pmid 15709153]
764	PC238-2	70	1-phosphatidylinositol-4-phosphate 5-kinase/ zinc ion binding	At4g33240	19/22 (86%)	-
765	PC238-3	66	LACS6 (LONG-CHAIN ACYL-COA SYNTHETASE 6)	At3g05970	18/22 (81%)	fatty acid oxidation; metabolism; n-octane oxidation
767	PC239-1	315	transcription factor	At1g50600	15/27 (55%)	regulation of transcription [pmid 11118137]
768	PC239-2	336	RBOHD (RESPIRATORY BURST OXIDASE PROTEIN D)	At5g47910	56/68 (82%)	defense response [pmid 11756663]; oxygen and reactive oxygen speci
769	PC239-4	336	RBOHD (RESPIRATORY BURST OXIDASE PROTEIN D)	At5g47910	56/68 (82%)	defense response [pmid 11756663]; oxygen and reactive oxygen speci
770	PC239-3	356	unknown protein	At3g52370	73/103 (70%)	cell adhesion
772	PC240-3	280	protein binding / ubiquitin-protein ligase/ zinc ion binding	At4g34100	66/92 (71%)	protein ubiquitination
773	PC240-4	277	L-aspartate oxidase/ disulfide oxidoreductase/ oxidoreductase	At5g14760	49/57 (85%)	electron transport; NAD biosynthesis
774	PC240-5	277	L-aspartate oxidase/ disulfide oxidoreductase/ oxidoreductase	At5g14760	49/57 (85%)	electron transport; NAD biosynthesis
775	PC241-1	235	unknown protein (see 470-1)	At2g46150	31/79 (39%)	biological process unknown
776	PC241-2	279	oxidoreductase/ zinc ion binding (see 162-2 & 210-2)	At1g23740	21/29 (72%)	-
777	PC241-4	265	oxidoreductase/ zinc ion binding (see 162-2 & 210-2)	At1g23740	41/56 (73%)	-
779	PC243-1	164	carboxylic ester hydrolase/ hydrolase, acting on ester bonds	At5g45670	45/54 (80%)	lipid metabolism
781	PC243-3	235	unknown protein (see 470-1)	At2g46150	30/79 (37%)	biological process unknown
787	PC246-1	196	ACS1 (ACC SYNTHASE 1) (see 220-3)	At3g61510	51/60 (85%)	ethylene biosynthesis [pmid 8566772]
788	PC246-2	174	ACS1 (ACC SYNTHASE 1) (see 220-3)	At3g61510	50/58 (86%)	ethylene biosynthesis [pmid 8566772]
789	PC246-3	230	unknown protein	At3g53990	17/31 (54%)	response to stress
790	PC246-4	155	ubiquitin-protein ligase/ zinc ion binding (see 247-3)	At1g65430	48/51 (94%)	protein ubiquitination
792	PC247-2	174	ACS1 (ACC SYNTHASE 1) (see 220-3)	At3g61510	50/58 (86%)	ethylene biosynthesis [pmid 8566772]
793	PC247-4	175	ACS1 (ACC SYNTHASE 1) (see 220-3)	At3g61510	50/58 (86%)	ethylene biosynthesis [pmid 8566772]
794	PC247-3	156	ubiquitin-protein ligase/ zinc ion binding (see 246-4)	At1g65430	49/51 (96%)	protein ubiquitination

799	PC249-1	81	protein binding	At1g03440	19/25 (76%)	signal transduction [pmid 11751054]
800	PC249-3	81	protein binding	At1g03440	19/25 (76%)	signal transduction [pmid 11751054]
801	PC249-2	81	X-Pro dipeptidase-like protein (see 225-2)	At4g29500	21/26 (80%)	-
802	PC249-4	81	X-Pro dipeptidase-like protein (see 225-2)	At4g29500	21/26 (80%)	-
803	PC250-1	72	cinnamyl-alcohol dehydrogenase (CAD) (see 580-1)	At1g72860	16/24 (66%)	lignin biosynthesis [pmid 8219046]
806	PC250-4	189	unknown protein	At1g27760	31/43 (72%)	biological process unknown
809	PC251-4	289	electron carrier (see 397-1)	At1g26420	18/47 (38%)	electron transport
811	PC252-1	98	ATGLR2.8	At2g29110	20/32 (62%)	calcium ion homeostasis [pmid 11379626]; response to light stimulus
812	PC252-2	98	ATGLR2.8	At2g29110	20/32 (62%)	calcium ion homeostasis [pmid 11379626]; response to light stimulus
816	PC253-2	283	unknown protein	At5g47570	18/21 (85%)	biological process unknown
817	PC253-3	283	unknown protein	At5g47570	18/21 (85%)	biological process unknown
818	PC253-4	283	unknown protein	At5g47570	18/21 (85%)	biological process unknown
821	PC254-2	270	APX1	At1g07890	57/65 (89%)	response to reactive oxygen species [pmid 15608336]
828	PC255-2-2	260	electron carrier (see pc300-3)	At1g30760	43/72 (59%)	electron transport
829	PC255-2-3	258	WNK8	At5g41990	14/24 (58%)	protein amino acid phosphorylation [pmid 12506983]
831	PC256-1	171	protein transporter (see 289-1)	At5g16880	30/56 (56%)	intra-Golgi transport; intracellular protein transport
832	PC256-2	172	protein transporter (see 289-1)	At5g16880	30/56 (53%)	intra-Golgi transport; intracellular protein transport
833	PC256-3	166	GAD2 (GLUTAMATE DECARBOXYLASE 2) (see 445-4)	At1g65960	43/55 (78%)	glutamate metabolism [pmid 9700069] [pmid 9701597]; nitrogen com
839	PC258-1	281	AGC2-1 (OXIDATIVE SIGNAL-INDUCIBLE1)	At3g25250	39/59 (66%)	protein amino acid phosphorylation
843	PC259-1	272	SQD2 (SULFOQUINOVOSYLDIACYLGLYCEROL 2)	At5g01220	49/55 (89%)	cellular response to phosphate starvation [pmid 11960029]; glycolipid
845	PC259-3	272	protein transporter	At4g16143	44/50 (88%)	intracellular protein transport; protein import into nucleus
846	PC259-4	265	UBP6 (UBIQUITIN-SPECIFIC PROTEASE 6)	At1g51710	74/86 (86%)	protein deubiquitination [pmid 15987637]
848	PC261-2	272	pectate lyase	At1g67750	46/52 (88%)	biological process unknown
850	PC261-4	269	calcium ion binding	At1g53210	29/81 (35%)	-
851	PC262-1	212	SHD (SHEPHERD)	At4g24190	29/34 (85%)	protein folding; regulation of meristem organization [pmid 11867518]
853	PC262-3	203	nicotinate-nucleotide diphosphorylase (carboxylating)	At2g01350	48/52 (92%)	NAD biosynthesis; pyridine nucleotide biosynthesis
855	PC263-1	98	ATP binding / protein kinase/ protein serine/threonine kinase/ protein-tyr	At1g06840	26/32 (81%)	protein amino acid phosphorylation; transmembrane receptor protein t
856	PC263-2	89	TIM50	At1g55900	21/29 (72%)	biological process unknown
857	PC263-3	98	NRPD2a	At3g23780	15/21 (71%)	DNA methylation [pmid 15766525]; RNA interference, production of
858	PC263-4	98	NRPD2a	At3g23780	15/21 (71%)	DNA methylation [pmid 15766525]; RNA interference, production of
863	PC265-1	287	copper ion binding	At4g39830	20/39 (51%)	-
864	PC265-2	277	ARA7	At4g19640	19/22 (86%)	intracellular protein transport; protein transport; small GTPase mediat
865	PC265-3	290	unknown protein	At2g18740	32/33 (96%)	mRNA processing
866	PC265-4	273	F-box protein family (see 347-2)	At4g22030	13/26 (50%)	biological process unknown
868	PC266-2	233	structural constituent of ribosome	At5g35530	43/60 (71%)	protein biosynthesis [pmid 11598216]
869	PC266-3	166	serine-type endopeptidase inhibitor (see 301-2)	At5g43580	14/21 (66%)	response to wounding
870	PC266-4	165	serine-type endopeptidase inhibitor (see 301-2)	At5g43580	12/21 (57%)	response to wounding
876	PC268-2	165	electron carrier (see 718-4) (BUT no taq)	At5g44400	16/27 (59%)	electron transport
877	PC268-3	140	ALDH3H1; aldehyde dehydrogenase	At1g44170	21/36 (58%)	metabolism
883	PC271-1	274	7S RNA binding / GTP binding / RNA binding / mRNA binding / nucleo	At1g48900	79/90 (87%)	protein targeting; SRP-dependent cotranslational protein targeting to
889	PC273-3	182	ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ pro	At4g03230	27/36 (75%)	protein amino acid phosphorylation
899	PC276-1	271	ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ pro	At2g28590	30/43 (69%)	protein amino acid phosphorylation
901	PC276-3	271	ATGPX6 (GLUTATHIONE PEROXIDASE 6)	At4g11600	48/66 (72%)	response to oxidative stress
902	PC276-4	275	ubiquitin-protein ligase (see 564-4)	At2g44900	23/30 (76%)	ubiquitin-dependent protein catabolism [pmid 11019805] [pmid 1107
907	PC278-1	95	calmodulin binding (see 787-2)	At2g26190	25/28 (89%)	N-terminal protein myristoylation [pmid 12912986]
908	PC278-2	95	calmodulin binding (see 787-2)	At2g26190	25/28 (89%)	N-terminal protein myristoylation [pmid 12912986]
909	PC278-4	95	calmodulin binding (see 787-2)	At2g26190	25/28 (89%)	N-terminal protein myristoylation [pmid 12912986]
910	PC278-3	96	GTP binding / translation initiation factor	At2g05830	27/31 (87%)	cellular biosynthesis; translational initiation
915	PC280-1	281	ATP binding / ATP-dependent helicase/ DNA binding / helicase/ nucleic	At2g46020	86/93 (92%)	biological process unknown
916	PC280-2	280	ATP binding / ATP-dependent helicase/ DNA binding / helicase/ nucleic	At2g46020	87/93 (93%)	biological process unknown
918	PC280-4	282	SGS3 (SUPPRESSOR OF GENE SILENCING 3) (see 178-2)	At5g23570	18/51 (35%)	virus induced gene silencing [pmid 10850495]
926	PC282-3	69	unknown protein	At4g11860	21/22 (95%)	biological process unknown

928	PC283-2	350	acyltransferase-like protein (see 774-3)	At3g26040	38/79 (48%)	biological process unknown
929	PC283-3	340	unknown protein	At3g07090	73/107 (68%)	biological process unknown
936	PC285-2	128	CNBT1 (CYCLIC NUCLEOTIDE-BINDING TRANSPORTER 1) (see2	At3g17700	30/40 (75%)	ion transport
945	PC288-2	272	unknown protein	At2g28310	47/61 (77%)	biological process unknown
947	PC289-1	172	protein transporter (see 256-1)	At5g16880	25/45 (55%)	intra-Golgi transport; intracellular protein transport
948	PC289-4	171	protein transporter (see 256-1)	At5g16880	30/56 (53%)	intra-Golgi transport; intracellular protein transport
952	PC290-2	128	CNBT1 (CYCLIC NUCLEOTIDE-BINDING TRANSPORTER 1) (see2	At3g17700	30/40 (75%)	ion transport
953	PC290-3	128	CNBT1 (CYCLIC NUCLEOTIDE-BINDING TRANSPORTER 1) (see2	At3g17700	30/40 (75%)	ion transport
963	PC293-1	255	PP2A-1	At1g59830	59/72 (81%)	biological process unknown
982	PC297-4	/	unknown protein	At5g61820	68/132 (51%)	biological process unknown
988	PC299-2	283	ACT7	At5g09810	70/71 (98%)	cytoskeleton organization and biogenesis; response to auxin stimulus |
991	PC300-1	210	protein binding / ubiquitin-protein ligase/ zinc ion binding (see 569-1)	At2g02960	40/61 (65%)	protein ubiquitination
992	PC300-2	153	catalytic/ protein phosphatase type 2C (see 569-2)	At3g62260	30/47 (63%)	-
993	PC300-3	211	electron carrier (see364-3)	At1g30760	29/59 (49%)	electron transport
994	PC300-4	269	CYP72A11; heme binding / iron ion binding / monooxygenase/ oxygen b	At3g14650	38/73 (52%)	electron transport
995	PC301-1	210	extra-large guanine nucleotide binding protein, putative	At1g31930	52/57 (91%)	-
996	PC301-2	213	serine-type endopeptidase inhibitor (see 266-3)	At5g43580	14/21 (66%)	response to wounding
999	PC303-1	147	Avr9/Cf-9 rapidly elicited protein 231 (see 315)	At1g19300	36/47 (76%)	carbohydrate biosynthesis
1010	PC307-4	161	GTP binding	At4g18800	22/25 (88%)	intracellular protein transport; protein transport; small GTPase mediat
1011	PC308-1	166	serine-type endopeptidase inhibitor (see 266-3)	At5g43580	14/21 (66%)	response to wounding
1019	PC310-1	301	ATL3	At1g72310	43/85 (50%)	protein ubiquitination
1021	PC310-3	280	electron carrier (see 432-3)	At1g26420	49/88 (55%)	electron transport
1022	PC310-4	299	electron carrier (see 432-3)	At1g26420	53/98 (54%)	electron transport
1025	PC311-3	122	oxidoreductase/ sphingolipid delta-4 desaturase	At3g61580	28/40 (70%)	lipid metabolism [pmid 9786850]
1028	PC312-2	269	fructose-bisphosphate aldolase	At2g01140	79/89 (88%)	pentose-phosphate shunt
1031	PC313-1	213	protein binding / ubiquitin-protein ligase/ zinc ion binding	At2g42350	24/31 (77%)	protein ubiquitination
1032	PC313-2	212	protein binding / ubiquitin-protein ligase/ zinc ion binding	At2g42350	29/61 (47%)	protein ubiquitination
1033	PC313-3	212	protein binding / ubiquitin-protein ligase/ zinc ion binding	At2g42350	29/61 (47%)	protein ubiquitination
1034	PC313-4	213	protein binding / ubiquitin-protein ligase/ zinc ion binding	At2g42350	24/31 (77%)	protein ubiquitination
1039	PC315-1	147	Avr9/Cf-9 rapidly elicited protein 231 (glycosyltransferase) (303-1)	At1g19300	37/47 (78%)	carbohydrate biosynthesis
1040	PC315-3	147	Avr9/Cf-9 rapidly elicited protein 231 (glycosyltransferase) (303-1)	At1g19300	37/47 (78%)	carbohydrate biosynthesis
1041	PC315-4	147	Avr9/Cf-9 rapidly elicited protein 231 (glycosyltransferase) (303-1)	At1g19300	37/47 (78%)	carbohydrate biosynthesis
1042	PC315-2	144	calmodulin binding (see 787-2)	At2g26190	21/22 (95%)	N-terminal protein myristoylation [pmid 12912986]
1051	PC318-1	105	serine-type endopeptidase inhibitor (see 360-3)	At3g61980	16/22 (72%)	biological process unknown
1062	PC320-3	135	SGS3 (SUPPRESSOR OF GENE SILENCING 3) (see 178-2)	At5g23570	17/43 (39%)	virus induced gene silencing [pmid 10850495]
1063	PC321-2	205	expressed protein	At1g31940	19/24 (79%)	-
1066	PC321-6	262	hypothetical protein	At2g36430	61/86 (70%)	biological process unknown
1067	PC322-1	226	serine/threonine protein kinase-like	At5g35960	51/73 (69%)	protein amino acid phosphorylation
1068	PC322-2	226	serine/threonine protein kinase-like	At5g35960	51/73 (69%)	protein amino acid phosphorylation
1069	PC322-3	226	serine/threonine protein kinase-like	At5g35960	51/73 (69%)	protein amino acid phosphorylation
1070	PC322-4	226	serine/threonine protein kinase-like	At5g35960	51/73 (69%)	protein amino acid phosphorylation
1071	PC323-1	152	unknown protein	At3g57400	37/49 (75%)	N-terminal protein myristoylation [pmid12912986]
1072	PC323-4	152	unknown protein	At3g57400	37/49 (75%)	N-terminal protein myristoylation [pmid12912986]
1073	PC323-2	154	RNA binding / aconitate hydratase/ hydro-lyase/ iron ion binding / lyase	At2g05710	19/21 (90%)	metabolism
1075	PC324-1	95	calmodulin binding (see 787-2)	At2g26190	24/28 (85%)	N-terminal protein myristoylation [pmid 12912986]
1079	PC325-1	57	unknown protein	At2g42700	15/19 (78%)	biological process unknown
1084	PC326-2	196	PHS1 (PROPYZAMIDE-HYPERSENSITIVE 1)	At5g23720	52/65 (80%)	protein amino acid dephosphorylation
1091	PC328-1	250	PAD2	At5g66140	58/73 (79%)	ubiquitin-dependent protein catabolism [pmid 9611183] [pmid 96111
1092	PC328-2	257	PAD2	At5g66140	39/74 (52%)	ubiquitin-dependent protein catabolism [pmid 9611183] [pmid 96111
1093	PC328-3	250	PAD2	At5g66140	39/52 (75%)	ubiquitin-dependent protein catabolism [pmid 9611183] [pmid 96111
1095	PC329-1	239	unknown protein	At1g15030	45/71 (63%)	biological process unknown
1097	PC329-4	238	unknown protein	At1g15030	47/79 (59%)	biological process unknown

1098	PC329-3	240	ADA2A	At3g07740	29/53 (54%)	biological process unknown
1099	PC330-1	205	SMP2	At4g37120	48/68 (70%)	positive regulation of cell proliferation[pmid 15937226]; RNA splicin
1100	PC330-2	205	SMP2	At4g37120	48/68 (70%)	positive regulation of cell proliferation[pmid 15937226]; RNA splicin
1101	PC330-3	205	SMP2	At4g37120	48/68 (70%)	positive regulation of cell proliferation[pmid 15937226]; RNA splicin
1109	PC332-3	103	binding / transporter	At2g37890	26/34 (76%)	mitochondrial transport; transport
1123	PC336-1-1	340	protein binding / ubiquitin-protein ligase/ zinc ion binding (see 628-3)	At5g01960	100/113 (89%)	protein ubiquitination
1124	PC336-1-4	340	protein binding / ubiquitin-protein ligase/ zinc ion binding (see 628-3)	At5g01960	101/113 (89%)	protein ubiquitination
1125	PC336-1-2	140	unknown protein	At4g31880	17/35 (48%)	-
1127	PC336-2-1	241	unknown protein	At3g62650	22/61 (36%)	biological process unknown
1128	PC336-2-2	241	unknown protein	At3g62650	23/61 (37%)	biological process unknown
1129	PC336-2-4	241	unknown protein	At3g62650	23/61 (37%)	biological process unknown
1132	PC340-3	640 ?	unknown protein (see 630-1-1)	At5g06370	15/28 (53%)	biological process unknown
1137	PC345-1	141	carnitine racemase/ catalytic	At4g14440	15/21 (71%)	metabolism
1139	PC345-4	108	ATPUP3 (see 180-2)	At1g28220	12/22 (54%)	-
1144	PC347-1	376	ATTPS8	At1g70290	107/123 (86%)	metabolism; trehalose biosynthesis
1146	PC347-2	380	F-box protein family (see 796-4)	At4g22030	51/113 (45%)	biological process unknown
1147	PC347-4	376	trehalose-phosphate synthase [UDP-forming]	At1g70290	110/123 (89%)	metabolism; trehalose biosynthesis
1148	PC348-1	325	F-box protein family (see 796-4)	At4g22030	50/111 (45%)	biological process unknown
1149	PC348-2	325	F-box protein family (see 796-4)	At4g22030	52/111 (46%)	biological process unknown
1150	PC348-3	326	F-box protein family (see 796-4)	At4g22030	35/71 (49%)	biological process unknown
1151	PC348-4	326	F-box protein family (see 796-4)	At4g22030	44/103 (42%)	biological process unknown
1152	PC349-1	208	ATP binding / protein kinase/ protein serine/threonine kinase/ protein-tyr	At4g27290	19/59 (32%)	protein amino acid phosphorylation
1153	PC349-2	210	ATP binding / protein kinase/ protein serine/threonine kinase/ protein-tyr	At4g27290	17/35 (48%)	protein amino acid phosphorylation
1154	PC349-3	211	ATP binding / protein kinase/ protein serine/threonine kinase/ protein-tyr	At4g27290	31/63 (49%)	protein amino acid phosphorylation
1155	PC349-4	210	ATP binding / protein kinase/ protein serine/threonine kinase/ protein-tyr	At4g27290	23/59 (38%)	protein amino acid phosphorylation
1158	PC350-3	146	ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ pro	At3g09830	21/44 (47%)	protein amino acid phosphorylation
1159	PC350-4	139	catalytic	At5g61840	39/45 (86%)	biological process unknown
1160	PC351-1	239	PHT5	At2g32830	40/60 (66%)	phosphate transport; transport
1161	PC351-2	78	kinase	At4g08850	17/25 (68%)	protein amino acid phosphorylation
1162	PC351-3	237	AHA4	At3g47950	39/41 (95%)	cation transport; metabolism; proton transport
1163	PC351-4	236	PHT5	At2g32830	30/49 (61%)	phosphate transport; transport
1167	PC352-4	182	calcium ion binding	At5g61790	24/29 (82%)	-
1178	PC355-2	320	TUB6 (BETA-6 TUBULIN)	At5g12250	56/56 (100%)	microtubule-based process [pmid 1498609]; response to cold [pmid 1
1179	PC355-4	320	TUB6 (BETA-6 TUBULIN)	At5g12250	56/56 (100%)	microtubule-based process [pmid 1498609]; response to cold [pmid 1
1180	PC356-1	305	ARP2/RPL3B	At1g61580	50/61 (81%)	protein biosynthesis
1181	PC356-2	324	CIP1 (COP1-INTERACTIVE PROTEIN 1)	At5g41790	32/57 (56%)	regulation of protein import into nucleus [pmid 7753789]
1182	PC356-3	113	UBQ3 (POLYUBIQUITIN 3)	At5g03240	37/37 (100%)	protein modification; response to light stimulus [pmid 9193073]; resp
1183	PC356-4	113	UBQ3 (POLYUBIQUITIN 3)	At5g03240	37/37 (100%)	protein modification; response to light stimulus [pmid 9193073]; resp
1192	PC359-1	71	ATP binding / protein kinase/ protein serine/threonine kinase/ protein-tyr	At4g27290	20/23 (86%)	protein amino acid phosphorylation
1195	PC359-4	214	MLO8	At2g17480	53/70 (75%)	cell death; defense response
1198	PC360-3	106	serine-type endopeptidase inhibitor (see 318-1)	At3g61980	16/22 (72%)	biological process unknown
1200	PC361-1	408	ATP binding / glycine-tRNA ligase/ tRNA ligase	At1g29880	119/135 (88%)	glycyl-tRNA aminoacylation; protein biosynthesis; tRNA aminoacyla
1201	PC361-2	408	ATP binding / glycine-tRNA ligase/ tRNA ligase	At1g29880	87/138 (63%)	glycyl-tRNA aminoacylation; protein biosynthesis; tRNA aminoacyla
1202	PC361-3	407	ATP binding / glycine-tRNA ligase/ tRNA ligase	At1g29880	118/135 (87%)	glycyl-tRNA aminoacylation; protein biosynthesis; tRNA aminoacyla
1204	PC362-1	358	AT2 (see 489-1)	At1g22360	28/39 (71%)	metabolism
1205	PC362-2	177	unknown protein	At4g15610	23/47 (48%)	biological process unknown
1206	PC362-3	90	SKIP2 (SKP1 INTERACTING PARTNER 2)	At5g67250	22/29 (75%)	N-terminal protein myristoylation [pmid 12912986]
1214	PC364-3	158	electron carrier (see255-2-2)	At1g30760	26/52 (50%)	electron transport
1216	PC365-1	256	unknown protein	At2g32980	74/85 (87%)	-
1220	PC366-1	158	electron carrier	At2g34790	30/52 (57%)	electron transport
1221	PC366-2	158	electron carrier	At2g34790	26/47 (55%)	electron transport
1222	PC366-3	158	electron carrier (beste Sequenz)	At2g34790	31/52 (59%)	electron transport

1223	PC366-4	159	electron carrier	At2g34790	32/53 (60%)	electron transport
1226	PC367-3	435	YLS9 (YELLOW-LEAF-SPECIFIC GENE 9)	At2g35980	67/132 (50%)	response to pathogen [pmid 11230571]
1227	PC367-4	436	YLS9 (YELLOW-LEAF-SPECIFIC GENE 9)	At2g35980	67/132 (50%)	response to pathogen [pmid 11230571]
1232	PC368-2-1	243	RPS6 (RIBOSOMAL PROTEIN S6) (see 369-2)	At4g31700	64/67 (95%)	protein biosynthesis [pmid 11598216]
1233	PC368-2-2	243	RPS6 (RIBOSOMAL PROTEIN S6) (see 369-2)	At4g31700	63/67 (94%)	protein biosynthesis
1234	PC368-2-3	243	RPS6 (RIBOSOMAL PROTEIN S6) (see 369-2)	At4g31700	61/67 (91%)	protein biosynthesis [pmid 11598216]
1235	PC368-2-4	244	RPS6 (RIBOSOMAL PROTEIN S6) (see 369-2)	At4g31700	71/80 (88%)	protein biosynthesis [pmid 11598216]
1237	PC369-2	244	RPS6 (RIBOSOMAL PROTEIN S6) (see 368-2-1)	At4g31700	67/80 (83%)	protein biosynthesis [pmid 11598216]
1238	PC369-3	244	RPS6 (RIBOSOMAL PROTEIN S6) (see 380-2)	At4g31700	67/80 (83%)	protein biosynthesis [pmid 11598216]
1244	PC371-1	199	unknown protein (see 411-1-2)	At1g32690	28/81 (34%)	biological process unknown
1249	PC372-2	295	hydrolase, hydrolyzing O-glycosyl compounds	At2g26600	32/39 (82%)	carbohydrate metabolism
1253	PC373-2	256	acyltransferase	At4g00400	38/66 (57%)	metabolism
1254	PC373-3	278	ALATS (ALANYL-TRNA SYNTHETASE)	At1g50200	53/92 (57%)	alanyl-tRNA aminoacylation
1255	PC373-4	279	ALATS (ALANYL-TRNA SYNTHETASE)	At1g50200	52/83 (62%)	alanyl-tRNA aminoacylation
1279	PC380-2	147	RPS6 (RIBOSOMAL PROTEIN S6) (see 368-2-1)	At4g31700	33/35 (94%)	protein biosynthesis [pmid 11598216]
1283	PC381-4	194	unknown protein	At2g46900	39/69 (56%)	biological process unknown
1285	PC382-2	235	electron carrier	At4g20840	28/31 (90%)	electron transport
1295	PC384-4	180	ubiquitin-protein ligase (see 394)	At3g07370	21/42 (50%)	protein ubiquitination
1303	PC386-2	197	structural constituent of ribosome / transcription regulator	At2g44120	58/65 (89%)	protein biosynthesis
1304	PC387-1	179	copper ion binding	At3g09220	15/28 (53%)	-
1305	PC387-2	181	ATP binding / DNA binding / DNA-dependent ATPase/nucleoside-tripho	At2g16440	54/59 (91%)	DNA replication initiation
1307	PC387-4	179	unknown protein	At3g56040	27/36 (75%)	biological process unknown
1311	PC388-3	157	ubiquitin-protein ligase (see 177-3)	At2g35930	23/51 (45%)	protein ubiquitination
1322	PC391-3	171	ubiquitin-protein ligase/ zinc ion binding	At5g60250	16/41 (39%)	protein ubiquitination
1332	PC394-1	136	ubiquitin-protein ligase (see 384-4)	At3g07370	19/38 (50%)	protein ubiquitination
1333	PC394-2	135	ubiquitin-protein ligase (see 384-4)	At3g07370	19/38 (50%)	protein ubiquitination
1334	PC394-3	135	ubiquitin-protein ligase (see 384-4)	At3g07370	19/38 (50%)	protein ubiquitination
1335	PC394-4	135	ubiquitin-protein ligase (see 384-4)	At3g07370	19/38 (50%)	protein ubiquitination
1336	PC395-1	180	SYP124; t-SNARE	At1g61290	17/30 (56%)	intracellular protein transport [pmid 11115874]; membrane fusion [pn
1337	PC395-2	144	oxidoreductase (see 591-1)	At4g23420	37/47 (78%)	metabolism
1341	PC396-2	173	EMB2386 (see 817-2)	At1g02780	21/22 (95%)	protein biosynthesis; ribosome biogenesis
1346	PC397-2	125	putative signal peptidase I	At2g30440	28/35 (80%)	proteolysis
1347	PC397-4	125	putative signal peptidase I	At2g30440	28/35 (80%)	proteolysis
1356	PC400-1-1	159	disulfide oxidoreductase/ monooxygenase/ oxidoreductase	At5g61290	18/37 (48%)	electron transport
1357	PC400-1-2	166	protein binding	At5g21090	44/53 (83%)	signal transduction [pmid 11751054]
1358	PC400-1-3	92	unknown protein (see 401-2-	At2g21270	26/30 (86%)	ubiquitin-dependent protein catabolism
1360	PC400-2-1	83	unknown protein	At1g17630	17/26 (65%)	biological process unknown
1362	PC400-2-3	85	DPE2 (DISPROPORTIONATING ENZYME 2)	At2g40840	18/27 (66%)	maltose metabolism [pmid 14593480]
1363	PC400-2-4	78	ATP binding / transmembrane receptor	At5g17880	16/25 (64%)	apoptosis; defense response; defense response to pathogen
1371	PC401-2-4	92	unknown protein (see 400-1-3)	At2g21270	26/30 (86%)	ubiquitin-dependent protein catabolism
1373	PC402-2	312	structural constituent of ribosome	At1g04480	58/61 (95%)	protein biosynthesis
1375	PC402-4	314	unknown protein	At5g55060	45/100 (45%)	-
1376	PC403-1	178	S-adenosylmethionine-dependent methyltransferase/ methyltransferase	At3g15530	35/50 (70%)	-
1378	PC403-4	173	S-adenosylmethionine-dependent methyltransferase/ methyltransferase	At3g15530	14/19 (73%)	-
1379	PC403-3	173	unknown protein	At3g16590	17/42 (40%)	biological process unknown
1380	PC404-1	65	unknown	At3g55840	15/19 (78%)	biological process unknown
1384	PC405-1-1	387	HSP81-2	At5g56030	121/128 (94%)	protein folding
1389	PC405-2-2	421	catalytic	At4g33850	56/76 (73%)	fatty acid biosynthesis [pmid 9106514]
1396	PC407-1	118	IAR4	At1g24180	38/39 (97%)	metabolism
1397	PC407-2	119	IAR4	At1g24180	29/30 (96%)	metabolism
1398	PC407-3	118	IAR4	At1g24180	38/39 (97%)	metabolism
1400	PC408-1	112	RNA binding / nucleic acid binding / protein transporter (see 590-2)	At3g25150	22/36 (61%)	nucleocytoplasmic transport; protein import into nucleus

1408	PC411-1-1	94	putative protein	At5g16470	19/26 (73%)	regulation of transcription [pmid 11118137]
1409	PC411-1-2	196	unknown protein (see 371-1)	At1g32690	23/82 (28%)	biological process unknown
1410	PC411-1-4	199	unknown protein (see 371-1)	At1g32690	28/82 (34%)	biological process unknown
1417	PC412-2	336	unknown protein	At4g16146	16/23 (56%)	-
1418	PC412-4	336	unknown protein	At4g16146	16/23 (56%)	-
1424	PC414-1-1	266	putative helicase (see 414-2-1)	At2g05080	34/70 (48%)	biological process unknown
1425	PC414-1-3	266	putative helicase (see 414-2-1)	At2g05080	34/70 (48%)	biological process unknown
1426	PC414-1-2	268	ANAC092; transcription factor	At5g39610	54/68 (79%)	development
1427	PC414-1-4	269	ANAC092; transcription factor	At5g39610	74/89 (83%)	development
1428	PC414-2-1	265	putative helicase (see 414-1-1)	At2g05080	34/70 (48%)	biological process unknown
1429	PC414-2-2	139	ribonuclease/ transcriptional repressor (see 416-1)	At5g10960	35/44 (79%)	negative regulation of transcription; RNA modification
1430	PC414-2-3	139	ribonuclease/ transcriptional repressor (see 416-1)	At5g10960	35/44 (79%)	negative regulation of transcription; RNA modification
1432	PC416-1	139	ribonuclease/ transcriptional repressor (see 414-2)	At5g10960	35/44 (79%)	negative regulation of transcription; RNA modification
1433	PC416-2	139	ribonuclease/ transcriptional repressor (see 414-2)	At5g10960	35/44 (79%)	negative regulation of transcription; RNA modification
1434	PC416-3	139	ribonuclease/ transcriptional repressor (see 414-2)	At5g10960	35/44 (79%)	negative regulation of transcription; RNA modification
1436	PC417-1	107	oxidoreductase/ zinc ion binding (see 210-3)	At1g23740	15/20 (75%)	-
1439	PC417-4	109	ATSR1 (SERINE/THREONINE PROTEIN KINASE 1)	At5g01820	22/41 (53%)	protein amino acid phosphorylation; signal transduction
1448	PC422-1	54	unknown protein (see 512-1)	At5g01750	14/17 (82%)	biological process unknown
1484	PC431-1	290	unknown protein	At1g19180	33/118 (27%)	biological process unknown
1485	PC431-2	290	unknown protein	At1g19180	35/118 (29%)	biological process unknown
1486	PC431-3	290	unknown protein	At1g19180	35/118 (29%)	biological process unknown
1487	PC431-4	292	unknown protein	At1g19180	33/118 (27%)	biological process unknown
1489	PC432-2	83	ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding	At5g40010	24/27 (88%)	-
1490	PC432-3	119	electron carrier (see 310-3)	At1g26420	20/39 (51%)	electron transport
1491	PC432-4	225	nuclease/ nucleic acid binding	At5g61780	57/74 (77%)	biological process unknown
1497	PC434-2	80	ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding	At3g28580	16/27 (59%)	-
1499	PC434-4	107	ATP binding / ATP-dependent helicase/ DNA binding / chromatin bindin	At5g44800	17/33 (51%)	chromatin assembly or disassembly; regulation of transcription, DNA-
1500	PC435-1	76	lactoylglutathione lyase	At1g15380	15/18 (83%)	carbohydrate metabolism
1503	PC435-4	76	lactoylglutathione lyase	At1g15380	15/18 (83%)	carbohydrate metabolism
1516	PC439-1	81	pre-mRNA splicing factor, putative	At3g49430	24/26 (92%)	biological process unknown
1517	PC439-2	81	pre-mRNA splicing factor, putative	At3g49430	24/26 (92%)	biological process unknown
1518	PC439-4	81	pre-mRNA splicing factor, putative	At3g49430	24/26 (92%)	biological process unknown
1533	PC445-2	103	CDC25	At5g03455	25/33 (75%)	protein amino acid phosphorylation [pmid 15336525]
1535	PC445-4	166	GAD2 (GLUTAMATE DECARBOXYLASE 2) (see 256-3)	At1g65960	43/55 (78%)	glutamate metabolism [pmid 9700069] [pmid 9701597]; nitrogen com
1549	PC450-2	115	DRT100 (DNA-DAMAGE REPAIR/TOLERATION 100)	At3g12610	25/37 (67%)	response to chemical stimulus [pmid 1518832]; response to drug [pmi
1550	PC450-3	115	DRT100 (DNA-DAMAGE REPAIR/TOLERATION 100)	At3g12610	25/37 (67%)	response to chemical stimulus [pmid 1518832]; response to drug [pmi
1551	PC450-4	115	DRT100 (DNA-DAMAGE REPAIR/TOLERATION 100)	At3g12610	25/37 (67%)	response to chemical stimulus [pmid 1518832]; response to drug [pmi
1552	PC451-1	358	ATP binding / protein kinase/ protein serine/threonine kinase/ protein-tyr	At2g32850	43/77 (55%)	protein amino acid phosphorylation
1556	PC452-1	217	catalytic	At1g34340	47/66 (71%)	biological process unknown
1557	PC452-2	219	catalytic	At1g34340	47/66 (71%)	biological process unknown
1558	PC452-4	218	catalytic	At1g34340	47/66 (71%)	biological process unknown
1559	PC452-3	216	catalytic	At1g34340	27/46 (58%)	biological process unknown
1560	PC453-1	154	calcium ion binding	At1g24620	31/50 (62%)	biological process unknown
1561	PC453-2	158	protein binding	At2g28650	25/44 (56%)	exocytosis; vesicle docking during exocytosis
1562	PC453-3	158	protein binding	At2g28650	25/44 (56%)	exocytosis; vesicle docking during exocytosis
1564	PC454-1	75	structural constituent of ribosome	At2g47610	18/21 (85%)	protein biosynthesis [pmid 11598216]
1565	PC454-2	107	TOM20-3	At3g27080	13/19 (68%)	protein targeting to mitochondrion [pmid 11161051]
1569	PC455-2	254	unknown protein (see 456-1)	At5g40720	24/58 (41%)	biological process unknown
1572	PC456-1	255	unknown protein (see 455-2)	At5g40720	28/82 (34%)	biological process unknown
1573	PC456-4	255	unknown protein (see 455-2)	At5g40720	30/82 (36%)	biological process unknown
1575	PC456-3	257	unknown protein	At5g01710	18/31 (58%)	-
1578	PC457-3	199	ATP binding / nucleoside-triphosphatase/ nucleotide binding	At2g27600	52/68 (76%)	-

1581	PC458-2	137	calmodulin binding	At3g58480	24/38 (63%)	biological process unknown
1582	PC458-3	134	calmodulin binding	At3g58480	24/38 (63%)	biological process unknown
1583	PC458-4	137	calmodulin binding	At3g58480	24/38 (63%)	biological process unknown
1588	PC460-1	162	unknown protein (see 470-1)	At2g46150	18/24 (75%)	biological process unknown
1589	PC460-2	166	catalytic	At3g23540	34/39 (87%)	-
1590	PC460-3	<193	unknown protein	At1g14990	11/17 (64%)	biological process unknown
1592	PC461-1	147	protein binding / ubiquitin-protein ligase/ zinc ion binding(see 569-1)	At2g02960	22/28 (78%)	protein ubiquitination
1593	PC461-2	139	unknown protein	At3g06250	24/37 (64%)	response to red or far red light
1594	PC461-3	120	protein transporter/ transporter	At1g62020	29/33 (87%)	ER to Golgi transport; intracellular protein transport
1595	PC461-4	131	unknown protein (see 470-1)	At2g46150	20/35 (57%)	biological process unknown
1602	PC463-3	94	unknown protein (see 470-1)	At2g46150	18/24 (75%)	biological process unknown
1624	PC470-1	191	unknown protein (see 471-3)	At2g46150	31/61 (50%)	biological process unknown
1625	PC470-2	191	unknown protein (see 471-3)	At2g46150	31/61 (50%)	biological process unknown
1626	PC470-3	191	unknown protein (see 471-3)	At2g46150	31/61 (50%)	biological process unknown
1627	PC470-4	191	unknown protein (see 471-3)	At2g46150	31/61 (50%)	biological process unknown
1628	PC471-1	155	ubiquitin-protein ligase	At3g52450	37/49 (75%)	protein ubiquitination
1630	PC471-3	191	unknown protein (see 470)	At2g46150	31/61 (50%)	biological process unknown
1631	PC471-4	156	ubiquitin-protein ligase	At3g52450	37/47 (78%)	protein ubiquitination
1634	PC472-3	191	unknown protein (see 470)	At2g46150	31/61 (50%)	biological process unknown
1635	PC472-4	137	hydrolase, hydrolyzing O-glycosyl compounds	At1g19940	18/24 (75%)	carbohydrate metabolism
1643	PC474-3	67	oxidoreductase	At3g51680	16/21 (76%)	metabolism
1648	PC476-1	409	unknown protein (see 766-1)	At4g04480	61/133 (45%)	-
1652	PC477-1	271	unknown protein	At5g23040	29/41 (70%)	biological process unknown
1655	PC477-3	262	ATPase, coupled to transmembrane movement of substances	At2g36380	37/50 (74%)	-
1672	PC482-1	332	protein binding (BUT no apo)	At4g18670	42/55 (76%)	-
1673	PC482-2	340	catalytic/ protein phosphatase type 2C (BUT no apo)	At4g33920	30/67 (44%)	-
1681	PC484-2	177	transcription factor similar to VPI/AB13 family regulatory protein	At4g32010	27/58 (46%)	regulation of transcription [pmid 11118137]
1684	PC485-1	93	ubiquitin-protein ligase	At5g43190	16/26 (61%)	ubiquitin-dependent protein catabolism
1685	PC485-2	133	RPL27A (RIBOSOMAL PROTEIN L27A)	At1g23290	21/21 (100%)	protein biosynthesis
1698	PC488-3	416	unknown protein (see 456-4)	At5g40720	26/65 (40%)	biological process unknown
1699	PC488-4	231	AT2 (see 362-1)	At1g22360	29/70 (41%)	metabolism
1700	PC489-1	229	AT2 (see 488-4)	At1g22360	39/73 (53%)	metabolism
1703	PC489-4	285	catalytic/ hydrolase (see 608-4)	At3g62860	82/94 (87%)	aromatic compound metabolism
1707	PC490-4	145	CYP86A7; oxygen binding	At1g63710	22/36 (61%)	fatty acid metabolism
1708	PC491-1	268	ATSGS1	At1g10930	13/16 (81%)	DNA metabolism
1709	PC491-2	270	unknown protein	At5g52590	38/49 (77%)	biological process unknown
1710	PC491-3	264	GTP binding / GTPase	At2g14120	26/42 (61%)	-
1712	PC492-1	155	transferase, transferring glycosyl groups	At5g47780	27/34 (79%)	carbohydrate biosynthesis
1713	PC492-2	214	RLK902 (see 611-2)	At3g17840	37/70 (52%)	protein amino acid phosphorylation; transmembrane receptor protein t
1714	PC492-3	214	RLK902 (see 611-2)	At3g17840	37/70 (52%)	protein amino acid phosphorylation; transmembrane receptor protein t
1715	PC492-4	214	RLK902 (see 611-2)	At3g17840	37/70 (52%)	protein amino acid phosphorylation; transmembrane receptor protein t
1728	PC496-1	246	J20 (DNAJ-LIKE 20)	At4g13830	11/23 (47%)	protein folding
1729	PC496-3	246	J20 (DNAJ-LIKE 20)	At4g13830	11/23 (47%)	protein folding
1730	PC496-4	248	J20 (DNAJ-LIKE 20)	At4g13830	11/23 (47%)	protein folding
1732	PC497-1	130	beta-galactosidase/ hydrolase, hydrolyzing O-glycosyl compounds	At3g54440	21/42 (50%)	carbohydrate metabolism
1733	PC497-2	130	beta-galactosidase/ hydrolase, hydrolyzing O-glycosyl compounds	At3g54440	21/42 (50%)	carbohydrate metabolism
1734	PC497-3	131	beta-galactosidase/ hydrolase, hydrolyzing O-glycosyl compounds	At3g54440	21/42 (50%)	carbohydrate metabolism
1735	PC497-4	129	beta-galactosidase/ hydrolase, hydrolyzing O-glycosyl compounds	At3g54440	21/42 (50%)	carbohydrate metabolism
1736	PC498-1	100	unknown protein	At4g13350	28/33 (84%)	regulation of GTPase activity
1737	PC498-2	100	unknown protein	At4g13350	28/33 (84%)	regulation of GTPase activity
1738	PC498-3	101	unknown protein	At4g13350	28/33 (84%)	regulation of GTPase activity
1739	PC498-4	100	unknown protein	At4g13350	28/33 (84%)	regulation of GTPase activity

1745	PC500-2	100	unknown protein	At4g13350	28/33 (84%)	regulation of GTPase activity
1746	PC500-3	100	unknown protein	At4g13350	28/33 (84%)	regulation of GTPase activity
1747	PC500-4	73	SDH2-1	At3g27380	20/21 (95%)	mitochondrial electron transport, succinate to ubiquinone [pmid 1144
1752	PC502-1	175	rhodopsin-like receptor	At4g34150	39/58 (67%)	G-protein coupled receptor protein signaling pathway
1753	PC502-2	169	transcription factor	At1g13290	43/52 (82%)	-
1755	PC502-3	168	transcription factor (see 503-1)	At3g55980	28/60 (46%)	regulation of transcription
1756	PC503-1	170	transcription factor (see 502-3)	At3g55980	17/23 (73%)	regulation of transcription
1757	PC503-2	168	transcription factor (see 502-3)	At3g55980	29/60 (48%)	regulation of transcription
1758	PC503-4	168	transcription factor (see 502-3)	At3g55980	29/60 (48%)	regulation of transcription
1762	PC504-3	150	DEK1	At1g55350	30/49 (61%)	cell fate specification [pmid 15647902]; embryonic development (sen
1765	PC505-2	127	DNA binding / transcription factor (see 524-1)	At5g64750	22/36 (61%)	regulation of transcription, DNA-dependent
1766	PC505-3	127	DNA binding / transcription factor (see 524-1)	At5g64750	22/36 (61%)	regulation of transcription, DNA-dependent
1767	PC505-4	127	DNA binding / transcription factor (see 524-1)	At5g64750	22/36 (61%)	regulation of transcription, DNA-dependent
1776	PC508-1	381	EDS1 (ENHANCED DISEASE SUSCEPTIBILITY 1)	At3g48090	53/102 (51%)	defense response; lipid metabolism; systemic acquired resistance, sali
1778	PC508-3	269	expressed protein	At1g70480	28/42 (66%)	biological process unknown
1781	PC509-2	87	translation elongation factor (see 533-2-3)	At1g57720	24/28 (85%)	translational elongation
1782	PC509-3	87	translation elongation factor (see 533-2-3)	At1g57720	24/28 (85%)	translational elongation
1786	PC510-3	81	antiporter/ drug transporter/ transporter	At4g23030	18/27 (66%)	multidrug transport
1787	PC510-4	81	antiporter/ drug transporter/ transporter	At4g23030	18/27 (66%)	multidrug transport
1790	PC511-4	178	transferase, transferring glycosyl groups / transferase, transferring hexosy	At1g70090	32/35 (91%)	carbohydrate biosynthesis
1791	PC512-1	89	unknown protein (see 422-1)	At5g01750	13/27 (48%)	biological process unknown
1792	PC512-2	90	unknown protein (see 422-1)	At5g01750	16/29 (55%)	biological process unknown
1793	PC512-3	90	unknown protein (see 422-1)	At5g01750	16/29 (55%)	biological process unknown
1794	PC512-4	91	ATP binding / protein kinase/ protein serine/threonine kinase/protein-tyro	At4g21390	16/29 (55%)	protein amino acid phosphorylation
1795	PC513-1	287	unknown protein	At2g42760	17/40 (42%)	-
1796	PC513-2	282	unknown protein	At2g42760	13/24 (54%)	-
1797	PC513-3	287	unknown protein	At2g42760	17/40 (42%)	-
1798	PC513-4	286	unknown protein	At2g42760	28/55 (50%)	-
1799	PC514-1	228	BIN2 (BRASSINOSTEROID-INSENSITIVE 2)	At4g18710	57/58 (98%)	brassinosteroid mediated signaling [pmid 11553730]; detection of bra
1800	PC514-2	217	unknown protein	At1g74790	21/34 (61%)	biological process unknown
1803	PC515-1	167	unknown protein	At5g38200	30/44 (68%)	biological process unknown
1804	PC515-3	170	unknown protein	At5g38200	31/47 (65%)	biological process unknown
1805	PC515-2	162	ATP binding / ATP-dependent helicase/ helicase/ nucleic acid binding	At2g47680	18/30 (60%)	nucleobase, nucleoside, nucleotide and nucleic acid metabolism
1807	PC516-1	174	electron carrier (see 707-4)	At1g30700	17/29(58)	electron transport
1819	PC519-1-1	366	unknown protein	At2g36220	17/30 (56%)	biological process unknown
1822	PC519-1-3	376	nucleic acid binding / transcription factor/ zinc ion binding	At2g23740	30/65 (46%)	chromatin modification
1827	PC520-1	198	phosphorylase/ transferase, transferring glycosyl groups	At3g29320	24/47 (51%)	carbohydrate metabolism
1829	PC520-3	98	unknown protein	At1g45688	15/27 (55%)	biological process unknown
1843	PC522-2-1	100	unknown protein	At1g45688	13/18 72%	biological process unknown
1844	PC522-2-2	99	unknown protein (see 520-3)	At1g45688	15/30 (50%)	biological process unknown
1847	PC523-1	87	catalytic/ hydrolase	At3g48410	14/21 66%	biological process unknown
1850	PC523-4	91	FAD binding / aldehyde-lyase/ oxidoreductase (see 526-1)	At5g51950	23/29 79%	electron transport
1851	PC524-1	127	DNA binding / transcription factor (see 505-2)	At5g64750	21/36 (58%)	regulation of transcription, DNA-dependent
1859	PC526-1	91	FAD binding / aldehyde-lyase/ oxidoreductase (see 523-4)	At5g51950	23/29 (79%)	electron transport
1863	PC527-1	148	receptor related protein kinase-like (LRR)	At5g25930	27/49 (55%)	protein amino acid phosphorylation
1864	PC527-3	148	receptor related protein kinase-like (LRR)	At5g25930	27/49 (55%)	protein amino acid phosphorylation
1867	PC528-1	164	transcription factor	At5g52510	32/54 (59%)	regulation of transcription [pmid 11118137]
1868	PC528-2	163	transcription factor	At5g52510	32/54 (59%)	regulation of transcription [pmid 11118137]
1869	PC528-3	163	transcription factor	At5g52510	32/54 (59%)	regulation of transcription [pmid 11118137]
1870	PC528-4	164	transcription factor	At5g52510	32/54 (59%)	regulation of transcription [pmid 11118137]
1886	PC532-1-4	139	unknown protein (see 533-1-1)	At2g36090	23/46 (50%)	biological process unknown
1891	PC533-1-1	139	unknown protein (see 532-1-4)	At2g36090	22/46 (47%)	biological process unknown

1892	PC533-1-2	139	unknown protein (see 532-1-4)	At2g36090	14/25 (56%)	biological process unknown
1893	PC533-1-3	138	unknown protein (see 532-1-4)	At2g36090	14/25 (56%)	biological process unknown
1894	PC533-1-4	137	unknown protein (see 532-1-4)	At2g36090	14/25 (56%)	biological process unknown
1897	PC533-2-3	87	translation elongation factor (see 509-2)	At1g57720	24/28 (85%)	translational elongation
1905	PC535-4	192	unknown protein	At1g53280	37/63 (58%)	biological process unknown
1909	PC538-3	153	protein binding / voltage-gated potassium channel	At5g41330	22/29 (75%)	potassium ion transport
1910	PC538-4	153	protein binding / voltage-gated potassium channel	At5g41330	22/29 (75%)	potassium ion transport
1912	PC539-2	133	ATP binding / nucleoside-triphosphatase/ nucleotide binding	At4g24850	15/24 (56%)	-
1923	PC543-1	165	electron carrier/ oxidoreductase	At5g44360	16/36 (44%)	electron transport
1927	PC544-1	260	calmodulin-binding protein	At4g31000	34/85 (40%)	-
1928	PC544-2	260	calmodulin-binding protein	At4g31000	34/85 (40%)	-
1929	PC544-4	260	calmodulin-binding protein	At4g31000	34/85 (40%)	-
1930	PC544-3	260	LIP1	At2g20860	45/46 (97%)	glycine catabolism [pmid 9808738]; lipoic acid biosynthesis [pmid 98
1932	PC545-1-4	60	transcription factor (see 96-1)	At2g40140	17/19 (89%)	regulation of transcription [pmid 11118137]
1938	PC545-2-2	198	oxidoreductase	At2g36690	31/45 (68%)	biosynthesis
1943	PC547-1-1	144	IAR3 (IAA-ALANINE RESISTANT 3); metallopeptidase	At1g51760	41/46 (89%)	proteolysis
1944	PC547-1-4	144	IAR3 (IAA-ALANINE RESISTANT 3); metallopeptidase	At1g51760	41/46 (89%)	proteolysis
1945	PC547-1-2	143	unknown protein	At1g15060	27/37 (72%)	-
1948	PC547-2-2	140	IAR3 (IAA-ALANINE RESISTANT 3); metallopeptidase	At1g51760	40/45 (88%)	proteolysis
1949	PC547-2-3	144	IAR3 (IAA-ALANINE RESISTANT 3); metallopeptidase	At1g51760	40/46 (86%)	proteolysis
1950	PC547-2-4	140	IAR3 (IAA-ALANINE RESISTANT 3); metallopeptidase	At1g51760	40/45 (88%)	proteolysis
1952	PC549-3	65	unknown protein	At1g44960	18/21 (85%)	biological process unknown
1957	PC550-1-3	146	ATP binding	At5g43730	15/26 (57%)	apoptosis; defense response; defense response to pathogen
1962	PC550-2-3	144	RPS5 (RESISTANT TO P. SYRINGAE 5) (similar to 550-1-3)	At1g12220	18/40 (45%)	defense response [pmid 9724691] [pmid 11846877]; hypersensitive re
1963	PC551-1	107	ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ pro	At5g15730	27/32 (84%)	protein amino acid phosphorylation
1964	PC551-2	108	ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ pro	At5g15730	28/33 (84%)	protein amino acid phosphorylation
1965	PC551-3	107	ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ pro	At5g15730	28/33 (84%)	protein amino acid phosphorylation
1966	PC551-4	107	ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ pro	At5g15730	28/33 (84%)	protein amino acid phosphorylation
1967	PC552-1	175	ubiquitin-protein ligase	At1g20780	40/55 (72%)	protein ubiquitination
1968	PC552-3	175	ubiquitin-protein ligase	At1g20780	40/55 (72%)	protein ubiquitination
1969	PC552-4	175	ubiquitin-protein ligase	At1g20780	40/55 (72%)	protein ubiquitination
1970	PC552-2	136	oxidoreductase	At4g23430	18/23 (78%)	metabolism
1976	PC554-2	161	PDF1	At3g25800	47/53 (88%)	regulation of phosphorylation [pmid 7811971]
1980	PC555-2	130	protein transporter	At3g15980	23/44 (52%)	intracellular protein transport
1988	PC557-2	81	expressed protein (see 796-3)	At3g46430	20/26 (76%)	biological process unknown
2000	PC560-2	269	transporter	At5g35160	21/33 (93%)	transport
2015	PC564-1	271	ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ pro	At2g28590	30/43 (69%)	protein amino acid phosphorylation
2017	PC564-3	271	ATGPX6 (GLUTATHIONE PEROXIDASE 6)	At4g11600	51/66 (77%)	response to oxidative stress
2018	PC564-4	277	ubiquitin-protein ligase putative arm repeat protein (see 276-4)	At2g44900	37/55 (67%)	ubiquitin-dependent protein catabolism [pmid 11019805] [pmid 1107
2027	PC568-1	481	ATP binding / kinase/ protein kinase/ protein serine/threonine	At1g77280	63/116 (54%)	protein amino acid phosphorylation; response to stress
2029	PC568-3	473	structural constituent of ribosome / transcription regulator	At3g13580	64/98 (65%)	protein biosynthesis
2031	PC569-1	209	protein binding / ubiquitin-protein ligase/ zinc ion binding (see 300-1)	At2g02960	47/70 (67%)	protein ubiquitination
2032	PC569-2	152	catalytic/ protein phosphatase type 2C (see 300-2)	At3g62260	30/47 (63%)	-
2039	PC575-1	129	ACLA-3	At1g09430	41/43 (95%)	acetyl-CoA biosynthesis [pmid 12376641]
2044	PC576-2	373	expressed protein	At5g24740	32/80 (40%)	-
2046	PC576-4	376	unknown protein	At2g39690	74/93 (79%)	biological process unknown
2047	PC577-1	143	transferase, transferring glycosyl groups / transferase, transferring hexosy	At1g05170	41/47 (87%)	protein amino acid glycosylation
2049	PC577-3	371	unknown protein	At1g35350	36/58 (62%)	-
2050	PC577-4	229	unknown protein	At1g28100	55/73 (75%)	biological process unknown
2051	PC578-1	198	PPI1 (PROTON PUMP INTERACTOR 1)	At4g27500	19/40 (47%)	regulation of proton transport [pmid 12182706]
2052	PC578-2	187	unknown protein (see 579-1)	At4g16144	29/51 (56%)	biological process unknown
2053	PC578-3	187	unknown protein (see 579-1)	At4g16144	28/51 (54%)	biological process unknown

2054	PC578-4	199	PPI1 (PROTON PUMP INTERACTOR 1)	At4g27500	18/32 (56%)	regulation of proton transport [pmid 12182706]
2055	PC579-1	187	unknown protein (see 578-2)	At4g16144	27/51 (52%)	biological process unknown
2056	PC579-2	181	MGD1 (MONOGALACTOSYLDIACYLGLYCEROL SYNTHASE 1)	At4g31780	45/60 (75%)	galactolipid biosynthesis [pmid 10869420]; glycolipid biosynthesis [p
2057	PC579-3	187	protein binding / ubiquitin-protein ligase/ zinc ion binding	At1g73760	17/39 (43%)	protein ubiquitination
2058	PC579-4	187	unknown protein (see 578-2)	At4g16144	28/51 (54%)	biological process unknown
2059	PC580-1	171	oxidoreductase (see 228-1)	At1g72680	35/55 (63%)	lignin biosynthesis [pmid 8219046]
2061	PC580-3	<296	ILR1 (IAA-LEUCINE RESISTANT 1) (BUT no apo)	At3g02875	52/78 (66%)	auxin metabolism [pmid 7792599]; proteolysis
2065	PC581-2	59	kinesin motor protein-related	At2g21380	15/17 (88%)	microtubule-based movement
2066	PC581-3	83	ATP binding / protein kinase/ protein serine/threonine kinase/ protein-tyr	At1g56145	17/26 (65%)	protein amino acid phosphorylation
2067	PC581-4	83	ATP binding / protein kinase/ protein serine/threonine kinase/ protein-tyr	At1g56145	17/26 (65%)	protein amino acid phosphorylation
2068	PC582-1	310	PAB8	At1g49760	27/46 (58%)	-
2069	PC582-2	310	PAB8	At1g49760	45/84 (53%)	-
2070	PC582-3	308	PAB8	At1g49760	39/80 (48%)	-
2072	PC583-1	323	XPO1A	At5g17020	20/21 (95%)	protein export from nucleus [pmid 10652141]; protein import into nuc
2076	PC584-1	<320	oxidoreductase (see 395-2) (BUT no taq)	At4g23420	18/23 (78%)	metabolism
2084	PC586-1	131	unknown protein (see 764-4)	At1g73430	26/35 (74%)	intracellular protein transport
2091	PC588-4	450	protein binding / ubiquitin-protein ligase/ zinc ion binding	At1g73950	54/104 (51%)	protein ubiquitination
2092	PC589-1	385	ABI1L1	At2g46225	35/54 (64%)	actin nucleation [pmid 15653407]; trichome morphogenesis (sensu M
2097	PC590-2	317	RNA binding / nucleic acid binding / protein transporter (see 408-1)	At3g25150	16/21 (76%)	nucleocytoplasmic transport; protein import into nucleus
2099	PC590-4	317	CDC48 (CELL DIVISION CYCLE 48)	At3g09840	39/48 (81%)	-
2100	PC591-1	223	oxidoreductase (see 395-2)	At4g23420	15/23 (65%)	metabolism
2103	PC591-4	221	oxidoreductase	At4g23340	34/51 (66%)	metabolism
2107	PC593-4	390	CRT3 (CALRETICULIN 3)	At1g08450	85/107 (79%)	biological process unknown
2116	PC596-1	229	oxidoreductase	At5g06060	44/75 (58%)	metabolism
2124	PC598-1	144	ubiquitin-protein ligase/ zinc ion binding	At1g12470	43/47 (91%)	protein ubiquitination
2127	PC598-4	153	peroxisomal membrane protein 22 kDa (PMP22)	At4g04470	27/35 (77%)	biological process unknown
2132	PC600-2-1	436	nucleotide binding	At1g72960	47/70 (67%)	biological process unknown
2133	PC600-2-2	433	unknown protein	At4g27720	54/72 (75%)	-
2134	PC600-2-3	388	unknown protein	At1g64650	26/51 (50%)	-
2135	PC600-2-4	437	heat shock protein binding / unfolded protein binding	At3g08970	86/144 (59%)	protein folding
2138	PC602-1	176	unknown protein	At4g14746	27/62 (43%)	biological process unknown
2139	PC602-2	176	unknown protein	At4g14746	27/62 (43%)	biological process unknown
2141	PC602-4	176	unknown protein	At4g14746	26/62 (41%)	biological process unknown
2155	PC606-2	637	ATZW10	At2g32900	98/164 (59%)	chromosome segregation [pmid 9298984]
2157	PC607-2	297	kinase (see 610-2)	At1g19390	69/98 (70%)	protein amino acid phosphorylation
2158	PC607-3	297	kinase (see 610-2)	At1g19390	69/98 (70%)	protein amino acid phosphorylation
2159	PC607-4	297	kinase (see 610-2)	At1g19390	69/98 (70%)	protein amino acid phosphorylation
2163	PC608-4	285	catalytic/ hydrolase (see 489-4)	At3g62860	82/94 (87%)	aromatic compound metabolism
2169	PC610-2	305	kinase (see 607-2) (BUT no Apo)	At1g19390	60/98 (61%)	protein amino acid phosphorylation
2171	PC610-4	247	DNA binding	At1g51060	41/43 (95%)	chromosome organization and biogenesis (sensu Eukaryota); nucleos
2173	PC611-2	214	RLK902 (see 492-1)	At3g17840	37/70 (52%)	protein amino acid phosphorylation; transmembrane receptor protein t
2174	PC611-3	214	RLK902 (see 492-1)	At3g17840	37/70 (52%)	protein amino acid phosphorylation; transmembrane receptor protein t
2175	PC611-4	214	RLK902 (see 492-1)	At3g17840	32/70 (45%)	protein amino acid phosphorylation; transmembrane receptor protein t
2179	PC614-4	153	SAB (SABRE)	At1g58250	38/50 (76%)	multidimensional cell growth
2184	PC617-1	94	MAP1C (METHIONINE AMINOPEPTIDASE 1B)	At1g13270	24/30 (80%)	N-terminal protein amino acid modification [pmid 15681659]; proteol
2185	PC617-2	94	MAP1C (METHIONINE AMINOPEPTIDASE 1B)	At1g13270	23/30 (76%)	N-terminal protein amino acid modification [pmid 15681659]; proteol
2190	PC618-2-3	315	metal ion binding	At4g14710	78/90 (86%)	biological process unknown
2202	PC623-3	182	oxidoreductase	At5g64250	38/49 (77%)	metabolism
2207	PC624-4	312	MAPKKK19 (see 628-1)	At5g67080	15/20 (75%)	protein amino acid phosphorylation
2209	PC625-2	252	unknown protein (see 651-1)	At4g30010	29/52 (55%)	biological process unknown
2212	PC628-1	313	MAPKKK19 (see 624-4)	At5g67080	15/20 (75%)	protein amino acid phosphorylation
2214	PC628-3	340	protein binding / ubiquitin-protein ligase/ zinc ion binding (see 336-1-1) (	At5g01960	100/113 (88%)	protein ubiquitination

2216	PC629-1	162	ATP binding / protein kinase/ protein serine/threonine kinase/protein-tyro	At1g74360	39/54 (72%)	protein amino acid phosphorylation; transmembrane receptor protein t
2218	PC629-3	162	ATP binding / protein kinase/ protein serine/threonine kinase/protein-tyro	At1g74360	39/54 (72%)	protein amino acid phosphorylation; transmembrane receptor protein t
2219	PC629-4	128	CYP83A1 (CYTOCHROME P450 83A1); oxygen binding	At4g13770	15/34 (44%)	glucosinolate biosynthesis [pmid 11553739]; response to UV
2220	PC630-1-1	701	unknown protein (see 340-3) (BUT 2x taq)	At5g06370	136/174 (78%)	biological process unknown
2222	PC630-1-3	701	unknown protein (see 340-3) (BUT 2x taq)	At5g06370	134/174 (77%)	biological process unknown
2224	PC630-2-1	383	CSLD3 (CELLULOSE SYNTHASE-LIKE 3)	At3g03050	99/127 (77%)	cell wall biosynthesis (sensu Magnoliophyta); cellulose biosynthesis;
2225	PC630-2-2	383	CSLD3 (CELLULOSE SYNTHASE-LIKE 3)	At3g03050	103/127 (81%)	cell wall biosynthesis (sensu Magnoliophyta); cellulose biosynthesis;
2226	PC630-2-3	383	CSLD3 (CELLULOSE SYNTHASE-LIKE 3)	At3g03050	103/127 (81%)	cell wall biosynthesis (sensu Magnoliophyta); cellulose biosynthesis;
2227	PC630-2-4	383	CSLD3 (CELLULOSE SYNTHASE-LIKE 3)	At3g03050	102/127 (80%)	cell wall biosynthesis (sensu Magnoliophyta); cellulose biosynthesis;
2228	PC631-1	234	oxidoreductase	At2g36690	42/61 (68%)	biosynthesis
2231	PC631-4	234	oxidoreductase	At2g36690	42/61 (68%)	biosynthesis
2232	PC632-1	207	protein binding / ubiquitin-protein ligase/ zinc ion binding	At1g28040	24/64 (37%)	protein ubiquitination
2237	PC634-2	185	unknown protein	At1g47550	25/32 (78%)	biological process unknown
2241	PC637-2	145	unknown protein	At1g65720	18/27 (66%)	biological process unknown
2243	PC637-4	152	strictosidine synthase	At3g51450	17/37 (45%)	alkaloid biosynthesis; biosynthesis
2248	PC639-1	394	unknown protein (BUT no taq)	At1g45150	84/115 (73%)	biological process unknown
2251	PC639-4	406	unknown protein (BUT no taq)	At1g45150	49/77 (64%)	biological process unknown
2252	PC640-1	244	unknown protein	At1g05575	23/44 (52%)	biological process unknown
2253	PC640-2	245	unknown protein	At1g05575	28/49 (57%)	biological process unknown
2256	PC642-1	172	catalytic/ hydrolase	At2g32150	25/49 (51%)	metabolism
2257	PC642-2	169	binding	At3g03790	23/37 (62%)	biological process unknown
2258	PC642-3	169	binding	At3g03790	35/55 (63%)	biological process unknown
2266	PC644-3	125	ATDGK1/DGK1 (DIACYLGLYCEROL KINASE 1, DIACYLGLYCER	At5g07920	38/42 (90%)	intracellular signaling cascade; protein kinase C activation
2272	PC649-1	<409	zinc ion binding (BUT no taq)	At1g19270	75/101 (74%)	-
2274	PC651-1	253	unknown protein (see 625-2)	At4g30010	56/81 (69%)	biological process unknown
2277	PC651-4	254	unknown protein	At5g13500	50/71 (70%)	biological process unknown
2279	PC652-2	214	unknown protein	At3g21190	24/32 (75%)	-
2282	PC654-1	95	ATP binding / protein kinase/ protein serine/threonine kinase/ protein-tyr	At4g27290	23/31 (74%)	protein amino acid phosphorylation
2283	PC654-2	95	ATP binding / protein kinase/ protein serine/threonine kinase/ protein-tyr	At4g27290	23/31 (74%)	protein amino acid phosphorylation
2284	PC654-3	95	ATP binding / protein kinase/ protein serine/threonine kinase/ protein-tyr	At4g27290	23/31 (74%)	protein amino acid phosphorylation
2285	PC654-4	92	putative Serine carboxypeptidase III	At3g45010	22/29 (75%)	-
2294	PC660-1	116	unknown protein	At5g54370	29/37 (78%)	biological process unknown
2295	PC660-2	97	ATP binding / protein kinase/ protein serine/threonine kinase/ protein-tyr	At4g27290	15/20 (75%)	protein amino acid phosphorylation
2296	PC660-3	116	unknown protein	At5g54370	29/37 (78%)	biological process unknown
2297	PC660-4	116	unknown protein	At5g54370	29/37 (78%)	biological process unknown
2299	PC661-2	354	ATP binding / carbohydrate binding / kinase/ protein kinase/protein serin	At4g27300	34/53 (64%)	protein amino acid phosphorylation
2302	PC662-1	288	KU80	At1g48050	46/93 (49%)	double-strand break repair via nonhomologous end-joining [pmid 121
2303	PC662-2	288	KU80	At1g48050	45/93 (48%)	double-strand break repair via nonhomologous end-joining [pmid 121
2304	PC662-3	291	KU80	At1g48050	17/35 (48%)	double-strand break repair via nonhomologous end-joining [pmid 121
2305	PC662-4	288	KU80	At1g48050	46/93 (49%)	double-strand break repair via nonhomologous end-joining [pmid 121
2308	PC663-3	277	nucleic acid binding	At1g19860	28/45 (62%)	biological process unknown
2311	PC664-1-2	337	zinc finger (C3HH4-type RING finger) family protein	At3g46620	57/115 (49%)	-
2339	PC669-2	100	catalytic	At3g05170	23/26 (88%)	metabolism
2346	PC670-2-4	47	ATP binding / cysteine-tRNA ligase	At3g56300	14/15 (93%)	cysteinyl-tRNA aminoacylation
2351	PC674-1	204	transferase/ transferase, transferring glycosyl groups	At5g01250	22/43 (51%)	biological process unknown
2355	PC675-1	194	ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ pro	At3g57120	36/48 (75%)	protein amino acid phosphorylation
2356	PC675-2	195	ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ pro	At3g57120	36/48 (75%)	protein amino acid phosphorylation
2364	PC677-2	148	oxidoreductase (see 724-3)	At3g13610	29/37 (78%)	secondary metabolism
2369	PC678-3	142	NPC4 (NONSPECIFIC PHOSPHOLIPASE C4)	At3g03530	25/39 (64%)	phospholipid catabolism [pmid 15618226]
2370	PC678-4	146	GTP binding (see 735-1)	At3g62290	15/16 (93%)	N-terminal protein myristoylation [pmid 12912986]
2375	PC683-1	125	unknown protein	At2g16650	24/40 (60%)	biological process unknown
2377	PC683-3	125	unknown protein	At2g16650	24/40 (60%)	biological process unknown

2378	PC683-4	152	ammonium transporter	At3g24290	39/45 (86%)	transport
2383	PC685-1	150	oxidoreductase (see 724-3)	At3g13610	36/49 (73%)	secondary metabolism
2385	PC685-3	232	ECA1; calcium-transporting ATPase	At1g07810	26/34 (76%)	manganese ion homeostasis [pmid 9238019];manganese ion homeosta
2395	PC689-1	194	protein binding	At4g32640	24/28 (85%)	ER to Golgi transport; intracellular protein transport
2401	PC690-3	237	inositol or phosphatidylinositol kinase/ phosphotransferase	At2g03890	36/78 (46%)	-
2409	PC691-2-3	160	GTP binding (see 735-1)	At3g62290	32/40 (80%)	N-terminal protein myristoylation [pmid 12912986]
2427	PC696-1	202	HUA enhancer 2 (HEN2)/DexH-box RNA helicase, putative	At2g06990	60/66 (90%)	RNA metabolism [pmid 12119159]; specification of floral organ ident
2429	PC696-3	200	PAA2; endopeptidase/ peptidase/ threonine endopeptidase (see 697-1)	At2g05840	57/65 (87%)	ubiquitin-dependent protein catabolism [pmid 10363660]
2430	PC696-4	200	PAA2; endopeptidase/ peptidase/ threonine endopeptidase (see 697-1)	At2g05840	56/65 (86%)	ubiquitin-dependent protein catabolism [pmid 10363660]
2431	PC697-1	200	PAA2; endopeptidase/ peptidase/ threonine endopeptidase (see 696-3)	At2g05840	56/65 (86%)	ubiquitin-dependent protein catabolism [pmid 10363660]
2432	PC697-2	200	PAA2; endopeptidase/ peptidase/ threonine endopeptidase (see 696-3)	At2g05840	55/65 (84%)	ubiquitin-dependent protein catabolism [pmid 10363660]
2433	PC697-3	200	PAA2; endopeptidase/ peptidase/ threonine endopeptidase (see 696-3)	At2g05840	56/65 (86%)	ubiquitin-dependent protein catabolism [pmid 10363660]
2434	PC697-4	200	PAA2; endopeptidase/ peptidase/ threonine endopeptidase (see 696-3)	At2g05840	57/65 (87%)	ubiquitin-dependent protein catabolism [pmid 10363660]
2438	PC699-4	225	calcium-transporting ATPase/ calmodulin binding	At3g63380	68/74 (91%)	calcium ion transport; cation transport; metabolism; proton transport
2439	PC700-1	140	SIGF (RNA POLYMERASE SIGMA-70 FACTOR)	At2g36990	15/26 (57%)	positive regulation of transcription [pmid 15807777]; regulation of tra
2444	PC701-1-2	325	protein binding	At2g28840	56/104 (53%)	-
2446	PC701-1-4	323	protein binding	At2g28840	45/61 (73%)	-
2447	PC701-2-1	328	CPK30; calcium- and calmodulin-dependent protein kinase (see 832-2)	At1g74740	75/109 (68%)	abscisic acid mediated signaling [pmid 8943201]; N-terminal protein
2448	PC701-2-2	130	nucleic acid binding (see 709-4)	At5g32450	35/43 (81%)	-
2449	PC701-2-3	328	CPK30; calcium- and calmodulin-dependent protein kinase (see 832-2)	At1g74740	75/109 (68%)	abscisic acid mediated signaling [pmid 8943201]; N-terminal protein
2451	PC704-1	130	ATP binding	At1g58807	21/41 (51%)	apoptosis; defense response; defense response to pathogen
2452	PC704-2	130	ATP binding	At1g58807	16/36 (44%)	apoptosis; defense response; defense response to pathogen
2453	PC704-3	130	ATP binding	At1g58807	20/41 (48%)	apoptosis; defense response; defense response to pathogen
2462	PC707-4	174	electron carrier (see 516-1)	At1g30700	18/33 (54%)	electron transport
2468	PC709-2	130	exostosin family protein	At5g62220	34/44 (77%)	biological process unknown
2469	PC709-3	133	ATATH7; ATPase, coupled to transmembrane movement of substances	At3g47750	21/23 (91%)	N-terminal protein myristoylation [pmid 12912986]
2470	PC709-4	130	nucleic acid binding (see 701-2-2)	At5g32450	37/43 (86%)	-
2483	PC713-2-1	149	oxidoreductase (see 685-1)	At3g13610	37/48 (77%)	secondary metabolism
2484	PC713-2-2	149	oxidoreductase (see 685-1)	At3g13610	37/48 (77%)	secondary metabolism
2491	PC716-1	149	oxidoreductase (see 685-1)	At3g13610	37/48 (77%)	secondary metabolism
2492	PC716-2	149	oxidoreductase (see 685-1)	At3g13610	36/48 (75%)	secondary metabolism
2493	PC716-3	149	oxidoreductase (see 685-1)	At3g13610	37/48 (77%)	secondary metabolism
2494	PC716-4	149	oxidoreductase (see 685-1)	At3g13610	36/47 (76%)	secondary metabolism
2495	PC717-1	177	AMP binding / catalytic (see 740-4)	At3g48990	42/54 (77%)	flavonoid biosynthesis; metabolism
2496	PC717-2	176	AMP binding / catalytic (see 740-4)	At3g48990	36/48 (75%)	flavonoid biosynthesis; metabolism
2497	PC717-3	177	AMP binding / catalytic (see 740-4)	At3g48990	39/54 (72%)	flavonoid biosynthesis; metabolism
2502	PC718-4	224	electron carrier (see 268-2)	At5g44400	55/73 (75%)	electron transport
2504	PC719-2	176	AMP binding / catalytic (see 740-3)	At3g48990	34/48 (70%)	flavonoid biosynthesis; metabolism
2505	PC719-3	194	unknown protein	At3g61800	24/41 (58%)	-
2506	PC719-4	194	expressed protein	At3g61800	42/63 (66%)	-
2507	PC720-1	194	expressed protein	At3g61800	42/63 (66%)	-
2509	PC720-3	147	protein binding	At2g04740	41/47 (87%)	-
2511	PC721-1	181	carbohydrate transporter/ sugar porter (see 724-1)	At2g20780	44/59 (74%)	carbohydrate transport; transport
2512	PC721-2	181	carbohydrate transporter/ sugar porter (see 724-1)	At2g20780	44/59 (74%)	carbohydrate transport; transport-
2513	PC721-3	181	carbohydrate transporter/ sugar porter (see 724-1)	At2g20780	34/58 (58%)	carbohydrate transport; transport
2523	PC724-1	180	carbohydrate transporter/ sugar porter (see 721-1)	At2g20780	38/52 (73%)	carbohydrate transport; transport
2524	PC724-2	149	GTP binding (see 735-1)	At3g62290	33/33 (100%)	N-terminal protein myristoylation [pmid 12912986]
2525	PC724-3	149	oxidoreductase (see 685-1)	At3g13610	37/48 (77%)	secondary metabolism
2527	PC726-1	129	pyruvate dehydrogenase (acetyl-transferring)	At5g50850	34/43 (79%)	-
2528	PC726-2	128	pyruvate dehydrogenase (acetyl-transferring)	At5g50850	23/28 (82%)	-
2529	PC726-3	129	pyruvate dehydrogenase (acetyl-transferring)	At5g50850	38/43 (88%)	-
2530	PC726-4	153	structural constituent of ribosome	At3g49910	20/26 (76%)	protein biosynthesis

2535	PC729-1	128	GTP binding (see 735-1)	At3g62290	31/31 (100%)	N-terminal protein myristoylation [pmid 12912986]
2536	PC729-2	128	GTP binding (see 735-1)	At3g62290	30/31 (96%)	N-terminal protein myristoylation [pmid 12912986]
2537	PC729-3	128	GTP binding (see 735-1)	At3g62290	31/31 (100%)	N-terminal protein myristoylation [pmid 12912986]
2541	PC730-3	128	GTP binding (see 735-1)	At3g62290	29/29 (100%)	N-terminal protein myristoylation [pmid 12912986]
2543	PC735-1	201	GTP binding (see 678-4)	At3g62290	38/52 (73%)	N-terminal protein myristoylation [pmid 12912986]
2549	PC738-3	249	IDH -1 (isocitrate dehydrogenase subunit 1) (NAD+ dependent)	At4g35260	46/53 (86%)	-
2557	PC740-3	150	AMP binding / catalytic (see 717-1)	At3g48990	31/38 (81%)	flavonoid biosynthesis; metabolism
2562	PC742-4	466	hydrolase/ isopentenyl-diphosphate delta-isomerase (BUT no taq)	At1g79690	106/155 (68%)	isoprenoid biosynthesis
2578	PC747-4	65	PAL3 (PHENYL ALANINE AMMONIA-LYASE 3)	At5g04230	19/20 (95%)	defense response [pmid 7888622]; response to wounding [pmid 78886
2583	PC749-1	232	hydro-lyase/ lyase	At4g13430	53/77 (68%)	amino acid metabolism; metabolism
2584	PC749-4	231	hydro-lyase/ lyase	At4g13430	44/61 (72%)	amino acid metabolism; metabolism
2606	PC753-4	125	putative cinnamoyl-alcohol-dehydrogenase (CAD)	At5g19440	23/41 (56%)	-
2607	PC754-1	110	expressed protein	At1g66860	23/34 (67%)	-
2608	PC754-2	194	coatomer alpha subunit	At2g21390	31/37 (83%)	-
2609	PC754-4	111	coatomer alpha subunit	At2g21390	29/36 (80%)	-
2623	PC758-1	469	binding (see 811-3)	At2g01600	80/145 (55%)	N-terminal protein myristoylation [pmid 12912986]
2624	PC758-4	477	binding (see 811-3)	At2g01600	85/162 (52%)	N-terminal protein myristoylation [pmid 12912986]
2651	PC763-1	228	ATGSL03 (GLUCAN SYNTHASE-LIKE 3); 1,3-beta-glucan synthase/tr	At2g31960	61/75 (81%)	beta-1,3 glucan biosynthesis
2653	PC763-3	228	electron carrier	At4g28570	54/74 (72%)	electron transport
2658	PC764-4	174	unknown protein (586-1)	At1g73430	13/15 (86%)	intracellular protein transport
2659	PC765-1	168	unknown protein	At2g22660	15/34 (77%)	biological process unknown
2663	PC766-1	157	unknown protein (see 476-1)	At4g04480	18/49 (36%)	-
2668	PC767-2	153	PMZ (see 781-1)	At3g28210	26/42 (61%)	biological process unknown
2675	PC769-1	228	unknown protein	At2g46420	43/69 (62%)	biological process unknown
2679	PC770-1	98	CYP71B6 (CYTOCHROME P450 71B6); heme binding / iron ion bindin	At2g24180	17/32 (53%)	electron transport
2680	PC770-2	97	oxidoreductase (see 782-4)	At4g11410	14/20 (70%)	metabolism
2683	PC771-1	90	transport inhibitor response 1 (TIR1), AtFBL1	At3g62980	23/29 (79%)	response to auxin stimulus [pmid 10398681]; ubiquitin-dependent pro
2684	PC771-2	90	transport inhibitor response 1 (TIR1), AtFBL2	At3g62980	23/29 (79%)	response to auxin stimulus [pmid 10398681]; ubiquitin-dependent pro
2691	PC773-1	229	GTP binding / translation elongation factor	At2g31060	26/37 (70%)	protein biosynthesis
2696	PC774-2	225	unknown protein	At2g39170	36/53 (67%)	biological process unknown
2697	PC774-3	238	acyltransferase-like protein (see 283-2)	At3g26040	21/38 (55%)	biological process unknown
2698	PC774-4	220	putative polyprotein	At4g04410	33/54 (61%)	-
2700	PC776-2	197	SCL21 (SCARECROW-LIKE 21); transcription factor	At2g04890	42/61 (68%)	regulation of transcription [pmid 11118137]
2703	PC777-1	457	PHO1-like protein	At1g14040	86/103 (83%)	biological process unknown
2704	PC777-2	456	PHO1-like protein	At1g14040	93/113 (82%)	biological process unknown
2706	PC777-4	262	60 S ribosomal protein L7A (RPL7aB)	At3g62870	77/86 (89%)	protein biosynthesis
2710	PC778-3	<349	unknown protein	At5g64400	42/74 (56%)	biological process unknown
2711	PC779-1	245	ATGCN4	At3g54540	54/60 (90%)	-
2712	PC779-2	246	ATGCN4	At3g54540	72/81 (88%)	-
2719	PC781-1	113	PMZ (see 767-2)	At3g28210	24/33 (72%)	biological process unknown
2720	PC781-2	113	PMZ (see 767-2)	At3g28210	24/33 (72%)	biological process unknown
2721	PC781-4	113	PMZ (see 767-2)	At3g28210	24/33 (72%)	biological process unknown
2726	PC782-4	76	oxidoreductase (see 770-2)	At4g11410	13/20 (65%)	metabolism
2742	PC786-4	356	calmodulin binding (see 787-2)	At2g26190	42/54 (77%)	N-terminal protein myristoylation [pmid 12912986]
2744	PC787-2	358	calmodulin binding (see 278-2)	At2g26190	81/110 (73%)	N-terminal protein myristoylation [pmid 12912986]
2747	PC789-1	476	unknown protein (F9L1_1)	At1g15070	98/155 (63%)	-
2749	PC789-3	71	putative cathepsin B-like cysteine protease	At4g01610	19/22 (86%)	proteolysis
2750	PC789-4	71	putative cathepsin B-like cysteine protease	At4g01610	19/22 (86%)	proteolysis
2751	PC790-1	71	putative cathepsin B-like cysteine protease	At4g01610	19/22 (86%)	proteolysis
2754	PC790-4	71	putative cathepsin B-like cysteine protease	At4g01610	19/22 (86%)	proteolysis
2756	PC791-2	428	unknown protein	At2g44260	75/136 (55%9	-
2757	PC791-3	428	unknown protein	At2g44260	76/136 (55%)	-

2760	PC792-2	243	ATP binding / protein kinase/ protein serine/threonine kinase/ protein-tyr	At4g27290	23/62 (37%)	protein amino acid phosphorylation
2764	PC793-2	229	SHM4 (SERINE HYDROXYMETHYLTRANSFERASE 4)	At4g13930	35/49 (71%)	glycine metabolism; L-serine metabolism
2766	PC793-4	230	F-box protein family (see 347-2)	At4g22030	35/78 (44%)	biological process unknown
2767	PC794-1	224	unknown protein	At1g13570	31/47 (65%)	biological process unknown
2768	PC794-2	227	peroxidase	At1g14550	47/74 (63%)	response to oxidative stress
2769	PC794-3	226	peroxidase	At1g14550	35/58 (60%)	response to oxidative stress
2773	PC796-3	174	expressed protein (see 557-2)	At3g46430	33/48 (68%)	biological process unknown
2774	PC796-4	231	unknown protein (see 793-4)	At4g22030	26/40 (65%)	biological process unknown
2775	PC797-1	412	CPK2 (CALMODULIN-DOMAIN PROTEIN KINASE CDPK ISOFOR	At3g10660	96/136 (70%)	N-terminal protein myristoylation [pmid 12912986]; protein amino ac
2776	PC797-2	408	ATGPAT6/GPAT6; 1-acylglycerol-3-phosphate O-acyltransferase/ acyltr	At2g38110	60/82 (73%)	metabolism
2777	PC797-3	412	CPK2 (CALMODULIN-DOMAIN PROTEIN KINASE CDPK ISOFOR	At3g10660	103/136 (75%)	N-terminal protein myristoylation [pmid 12912986]; protein amino ac
2780	PC798-2	341	CYP94B1; heme binding / iron ion binding / monooxygenase/ oxygen bin	At5g63450	42/60 (70%)	electron transport
2781	PC798-3	341	CYP94B1; heme binding / iron ion binding / monooxygenase/ oxygen bin	At5g63450	39/60 (65%)	electron transport
2786	PC799-4	252	unknown protein	At1g19720	24/41 (58%)	biological process unknown
2787	PC800-1	174	putative disease resistance protein (CC-NBS-LRR class)	At1g33560	25/50 (50%)	-
2789	PC800-3	175	ethylene-response factor 1 (ERF1)	At3g23240	36/41 (87%)	-
2792	PC801-2	114	oxidoreductase family (see pc802-3)	At1g12550	19/29 (65%)	L-serine biosynthesis
2793	PC801-3	114	oxidoreductase family (see pc802-3)	At1g12550	19/29 (65%)	L-serine biosynthesis
2794	PC801-4	116	putative heat shock protein	At3g47940	26/37 (70%)	protein folding
2797	PC802-3	114	oxidoreductase family (see 801-2)	At1g12550	19/29 (65%)	L-serine biosynthesis
2799	PC803-1	114	oxidoreductase family (see 801-2)	At1g12550	19/29 (65%)	L-serine biosynthesis
2800	PC803-2	114	oxidoreductase family (see 801-2)	At1g12550	18/29 (62%)	L-serine biosynthesis
2801	PC803-3	110	unknown protein	At3g43240	34/36 (94%)	-
2820	PC809-1	126	putative protein kinase	At3g22750	34/41 (82%)	-
2821	PC809-2	126	putative protein kinase	At3g22750	39/41 (95%)	-
2823	PC809-4	125	putative protein kinase	At3g22750	27/29 (93%)	-
2824	PC810-1	91	expressed protein	At5g56120	24/30 (80%)	-
2825	PC810-3	72	CYP76C1; heme binding / iron ion binding / monooxygenase	At2g45560	16/23 (69%)	electron transport
2829	PC811-3	140	expressed protein (see 758-1)	At2g01600	34/39 (87%)	N-terminal protein myristoylation [pmid 12912986]
2830	PC811-4	443	transporter	At4g12650	64/104 (61%)	transport
2835	PC813-1	316	unknown protein	At3g15395	29/45 (64%)	biological process unknown
2836	PC813-2	317	ALATS (ALANYL-TRNA SYNTHETASE); ATP binding / alanine-tRN	At1g50200	28/35 (80%)	alanyl-tRNA aminoacylation
2840	PC814-2	232	unknown protein	At5g14310	17/18 (94%)	biological process unknown
2841	PC814-3	230	RNA binding / nucleic acid binding	At3g52120	51/94 (54%)	RNA processing
2842	PC814-4	233	RNA binding / nucleic acid binding	At3g52120	44/63 (69%)	RNA processing
2843	PC815-1	204	putative 2-oxoglutarate-dependent dioxygenase	At1g06650	25/51 (49%)	-
2844	PC815-2	205	putative 2-oxoglutarate-dependent dioxygenase	At1g06650	30/65 (46%)	-
2845	PC815-3	205	putative 2-oxoglutarate-dependent dioxygenase	At1g06650	30/65 (46%)	-
2846	PC815-4	205	putative 2-oxoglutarate-dependent dioxygenase	At1g06650	25/51 (49%)	-
2849	PC816-3	188	expressed protein	At1g13360	20/28 (71%)	-
2851	PC817-1	170	unknown protein	At3g14870	16/25 (64%)	biological process unknown
2852	PC817-2	173	EMB2386 (see 396-2)	At1g02780	24/25 (96%)	protein biosynthesis, ribosome biogenesis
2853	PC817-3	171	EMB2386 (see 396-2)	At1g02780	24/25 (96%)	protein biosynthesis, ribosome biogenesis
2855	PC818-1	122	unknown protein (see 820-4)	At1g18740	19/37 (51%)	biological process unknown
2856	PC818-2	122	unknown protein (see 820-4)	At1g18740	20/37 (54%)	biological process unknown
2857	PC818-3	124	unknown protein (see 820-1)	At1g74450	21/39 (53%)	biological process unknown
2860	PC819-2	117	stress enhanced protein 2 (SEP2)	At2g21970	25/38 (65%)	photosynthesis light harvesting [pmid 10725357]
2861	PC819-3	119	stress enhanced protein 2 (SEP2)	At2g21970	26/31 (83%)	photosynthesis light harvesting [pmid 10725357]
2862	PC819-4	119	stress enhanced protein 2 (SEP2)	At2g21970	26/31 (83%)	photosynthesis light harvesting [pmid 10725357]
2863	PC820-1	120	unknown protein (see 818-3)	At1g74450	18/34 (52%)	biological process unknown
2865	PC820-3	123	unknown protein (see 818-3)	At1g74450	18/40 (43%)	biological process unknown
2866	PC820-4	124	unknown protein (see 818-1)	At1g18740	16/28 (57%)	biological process unknown

2873	PC822-3	566	ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ pro	At5g01850	133/145 (91%)	protein amino acid phosphorylation
2874	PC822-4	564	ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ pro	At5g01850	126/136 (92%)	protein amino acid phosphorylation
2886	PC825-4	243	ATP binding / nucleoside-triphosphatase/ nucleotide binding / transmemb	At5g17970	17/36 (47%)	apoptosis; defense response; defense response to pathogen
2911	PC832-1	276	ATCDPK1; calcium- and calmodulin-dependent protein kinase/ kinase/ p	At1g18890	19/26 (73%)	-abscisic acid mediated signaling [pmid 8943201]; N-terminal protein
2912	PC832-2	277	CPK30; calcium- and calmodulin-dependent protein kinase (see 701-2-1)	At1g74740	19/27 (70%)	abscisic acid mediated signaling [pmid 8943201]; N-terminal protein
2913	PC832-3	278	CPK30; calcium- and calmodulin-dependent protein kinase (see 701-2-1)	At1g74740	19/27 (70%)	abscisic acid mediated signaling [pmid 8943201]; N-terminal protein
2914	PC832-4	276	CPK30; calcium- and calmodulin-dependent protein kinase (see 701-2-1)	At1g74740	23/32 (71%)	abscisic acid mediated signaling [pmid 8943201]; N-terminal protein
2916	PC833-2	276	CPK30; calcium- and calmodulin-dependent protein kinase (see 832-2)	At1g74740	19/30 (63%)	abscisic acid mediated signaling [pmid 8943201]; N-terminal protein
2918	PC833-4	276	CPK30; calcium- and calmodulin-dependent protein kinase (see 832-2)	At1g74740	23/32 (71%)	abscisic acid mediated signaling [pmid 8943201]; N-terminal protein
2919	PC835-1	230	inner mitochondrial membrane protein	At1g72750	45/90 (50%)	-
2921	PC835-3	230	inner mitochondrial membrane protein	At1g72750	49/90 (54%)	-
2926	PC836-3	298	GTP binding	At1g08410	24/45 (53%)	biological process unknown
2929	PC837-3	230	GTP binding (see 735-1, protein level)	At3g62290	63/70 (90%)	N-terminal protein myristoylation [pmid 12912986]

Bemerkung
DEAD/DEAH box helicase, putative
60S ribosomal protein L37 (RPL37A)
expressed protein
integral membrane protein, putative, contains 3 transmembrane domains; contains Pfam PF04535 : Domain of unknown function (DUF588); similar to putative ethylene responsive element binding protein (GI:22135858) (Arabidopsis thaliana)
heat shock cognate 70 kDa protein 1 (HSC70-1) (HSP70-1)
heat shock cognate 70 kDa protein 1 (HSC70-1) (HSP70-1)
heat shock cognate 70 kDa protein 1 (HSC70-1) (HSP70-1)
heat shock cognate 70 kDa protein 1 (HSC70-1) (HSP70-1)
integral membrane protein, putative, contains 3 transmembrane domains; contains Pfam PF04535 : Domain of unknown function (DUF588); similar to putative ethylene responsive element binding protein (GI:22135858) (Arabidopsis thaliana)
integral membrane protein, putative, contains 3 transmembrane domains; contains Pfam PF04535 : Domain of unknown function (DUF588); similar to putative ethylene responsive element binding protein (GI:22135858) (Arabidopsis thaliana)
integral membrane protein, putative, contains 3 transmembrane domains; contains Pfam PF04535 : Domain of unknown function (DUF588); similar to putative ethylene responsive element binding protein (GI:22135858) (Arabidopsis thaliana)
heat shock cognate 70 kDa protein 1 (HSC70-1) (HSP70-1)
putative AVR9 elicitor response protein, galactosyltransferase family protein
dynamin-like protein D (DL1D)
nematode resistance protein Hs1pro-1
nematode resistance protein Hs1pro-1
protein phosphatase 2C family protein
integral membrane protein, putative, contains 3 transmembrane domains; contains Pfam PF04535 : Domain of unknown function (DUF588); similar to putative ethylene responsive element binding protein (GI:22135858) (Arabidopsis thaliana)
integral membrane protein, putative, contains 3 transmembrane domains; contains Pfam PF04535 : Domain of unknown function (DUF588); similar to putative ethylene responsive element binding protein (GI:22135858) (Arabidopsis thaliana)
heat shock cognate 70 kDa protein 1 (HSC70-1) (HSP70-1)
heat shock cognate 70 kDa protein 1 (HSC70-1) (HSP70-1)
heat shock cognate 70 kDa protein 1 (HSC70-1) (HSP70-1)
heat shock cognate 70 kDa protein 1 (HSC70-1) (HSP70-1)
expressed protein
expressed protein
40S ribosomal protein S8 (RPS8A)
integral membrane protein, putative, contains 3 transmembrane domains; contains Pfam PF04535 : Domain of unknown function (DUF588); similar to putative ethylene responsive element binding protein (GI:22135858) (Arabidopsis thaliana)
integral membrane protein, putative, contains 3 transmembrane domains; contains Pfam PF04535 : Domain of unknown function (DUF588); similar to putative ethylene responsive element binding protein (GI:22135858) (Arabidopsis thaliana)
integral membrane protein, putative, contains 3 transmembrane domains; contains Pfam PF04535 : Domain of unknown function (DUF588); similar to putative ethylene responsive element binding protein (GI:22135858) (Arabidopsis thaliana)
integral membrane protein, putative, contains 3 transmembrane domains; contains Pfam PF04535 : Domain of unknown function (DUF588); similar to putative ethylene responsive element binding protein (GI:22135858) (Arabidopsis thaliana)
fringe-related protein
ABC transporter family protein
aspartyl protease family protein
aspartyl protease family protein
heat shock cognate 70 kDa protein 1 (HSC70-1) (HSP70-1)
-
-
phosphoinositide phosphatase family protein
transducin family protein / WD-40 repeat family protein
oxidoreductase, zinc-binding dehydrogenase family protein
putative AVR9 elicitor response protein, galactosyltransferase family protein
pentatricopeptide (PPR) repeat-containing protein
phosphoinositide phosphatase family protein
phosphoinositide phosphatase family protein
amino acid transporter family protein
epoxide hydrolase, putative
epoxide hydrolase, putative
epoxide hydrolase, putative
epoxide hydrolase, putative
expressed protein, GTP-binding regulatory protein beta chain, Dictyostelium discoideum, PIR:A47370
pectinesterase family protein

casein kinase, putative
casein kinase, putative
pectinesterase family protein
aldo/keto reductase, putative
lipoxygenase, putative, similar to lipoxygenase gi:1495804 (Solanum tuberosum)
lipoxygenase, putative, similar to lipoxygenase gi:1495804 (Solanum tuberosum)
lipoxygenase, putative, similar to lipoxygenase gi:1495804 (Solanum tuberosum)
60S ribosomal protein L17 (RPL17B)
60S ribosomal protein L17 (RPL17B)
60S ribosomal protein L17 (RPL17B)
-
expressed protein
protein kinase, putative, similar to protein kinase APK1A (Arabidopsis thaliana) Swiss-Prot:Q06548
protein kinase, putative, similar to protein kinase APK1A (Arabidopsis thaliana) Swiss-Prot:Q06548
protein kinase, putative, similar to protein kinase APK1A (Arabidopsis thaliana) Swiss-Prot:Q06548
kinesin motor protein-related, several kinesin-like proteins
calcium-binding EF hand family protein, contains Pfam profile: PF00036 EF hand
calnexin 1 (CNX1), identical to calnexin homolog 1, Arabidopsis thaliana, EMBL:AT08315 (SP|P29402)
galactosyl transferase GMA12/MNN10 family protein, low similarity to alpha-1,2-galactosyltransferase, Schizosaccharomyces pombe (SP|Q09174)
galactosyltransferase family protein, contains Pfam profile: PF01762 galactosyltransferase ;contains similarity to Avr9 elicitor response protein GI:4138265 from (Nicotiana tabacum)
4-aminobutyrate aminotransferase / gamma-amino-N-butyrate transaminase / GABA transaminase
expressed protein, contains Pfam profile: PF01363 FYVE zinc finger
expressed protein, contains Pfam profile: PF01363 FYVE zinc finger
expressed protein, contains Pfam profile: PF01363 FYVE zinc finger
NAD-dependent epimerase/dehydratase family protein
ripening-responsive protein, putative
midasin-related, similar to Midasin (MIDAS-containing protein) (Swiss-Prot:Q12019) (Saccharomyces cerevisiae)
NAD-dependent epimerase/dehydratase family protein
oxidoreductase, zinc-binding dehydrogenase family protein, contains Pfam profile PF00107: oxidoreductase, zinc-binding dehydrogenase family
ripening-responsive protein, putative
CBL-interacting protein kinase 17 (CIPK17), identical to CBL-interacting protein kinase 17 (Arabidopsis thaliana) gi|14571553|gb|AAK64513
glutamate receptor family protein (GLR2.8) (GLUR9), plant glutamate receptor family, PMID:11379626
transferase family protein, similar to anthranilate N-hydroxycinnamoyl/benzoyltransferase, Dianthus caryophyllus (gi:2239091)
expressed protein
60S ribosomal protein L35a (RPL35aC)
similar to beta-expansin, putative (EXPB4)[Arabidopsis thaliana] (TAIR:At2g45110.1)
glutamate receptor family protein (GLR2.8) (GLUR9), plant glutamate receptor family, PMID:11379626
peptidyl-prolyl cis-trans isomerase / cyclophilin (CYP2) / rotamase, identical to cyclophilin (Arabidopsis thaliana) gi|2443757|gb|AAB71402
MutT/nudix family protein
similar to beta-expansin, putative (EXPB4)[Arabidopsis thaliana] (TAIR:At2g45110.1)
glutamate receptor family protein (GLR2.8) (GLUR9), plant glutamate receptor family, PMID:11379626
MutT/nudix family protein
60S ribosomal protein L17 (RPL17B)
putative CCCH-type zinc finger protein
similar to riboflavin biosynthesis protein, putative [Arabidopsis thaliana] (TAIR:At2g22450.1)
expressed protein
60S ribosomal protein L7A (RPL7aA)
60S ribosomal protein L35a (RPL35aC)
60S ribosomal protein L35a (RPL35aC)
60S ribosomal protein L35a (RPL35aC)
60S ribosomal protein L35a (RPL35aC)
60S ribosomal protein L35a (RPL35aC)

60S ribosomal protein L35a (RPL35aC)
harpin-induced protein-related / HIN1-related / harpin-responsive protein-related, weak similarity to harpin inducing protein (hin1), Nicotiana tabacum, EMBL:AF212183, GI:1619321
peroxidase, putative, similar to peroxidase (Nicotiana tabacum) gi|5381253|dbj|BAA82306
peroxidase, putative, similar to peroxidase (Nicotiana tabacum) gi|5381253|dbj|BAA82306
peroxidase, putative, similar to peroxidase (Nicotiana tabacum) gi|5381253|dbj|BAA82306
peroxidase, putative, similar to peroxidase (Nicotiana tabacum) gi|5381253|dbj|BAA82306
ribose 5-phosphate isomerase-related
cathepsin B-like cysteine protease, putative
cysteine proteinase, putative / AALP protein(AALP), identical to AALP protein GI:7230640 from (Arabidopsis thaliana)
calcineurin-like phosphoesterase family
expressed protein
expressed protein
-
peroxidase, putative, similar to peroxidase (Nicotiana tabacum) gi|5381253|dbj|BAA82306
40S ribosomal protein S20 (RPS20C)
ubiquitin-specific protease 16, putative (UBP16)
ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein
peptidyl-prolyl cis-trans isomerase / cyclophilin (CYP2) / rotamase, identical to cyclophilin (Arabidopsis thaliana) gi|2443757|gb|AAB71402
pfkB-type carbohydrate kinase family protein
pfkB-type carbohydrate kinase family protein
pfkB-type carbohydrate kinase family protein
pfkB-type carbohydrate kinase family protein
peroxidase, putative, similar to peroxidase (Nicotiana tabacum) gi|5381253|dbj|BAA82306
pfkB-type carbohydrate kinase family protein
pfkB-type carbohydrate kinase family protein
laccase, putative / diphenol oxidase, putative, similar to laccase (Populus balsamifera subsp. trichocarpa)(GI:3805960)
expressed protein
band 7 family protein, similar to hypersensitive-induced response protein (Zea mays)
-
mitochondrial import inner membrane translocase subunit TIM44, putative
expressed protein
peroxidase, putative, similar to peroxidase (Nicotiana tabacum) gi|5381253|dbj|BAA82306
peroxidase, putative, similar to peroxidase (Nicotiana tabacum) gi|5381253|dbj|BAA82306
peroxidase, putative, similar to peroxidase (Nicotiana tabacum) gi|5381253|dbj|BAA82306
similar to speckle-type POZ protein-related [Arabidopsis thaliana] (TAIR:At3g06190.1)
splicing factor RSZ33 (RSZ33)
DC 1 domain-containing protein
splicing factor RSZ33 (RSZ33)
splicing factor RSZ33 (RSZ33)
splicing factor RSZ33 (RSZ33)
DC 1 domain-containing protein
similar to PC180-3 (AT3G51550)
splicing factor RSZ33 (RSZ33)
splicing factor RSZ33 (RSZ33)
DC 1 domain-containing protein
serine-rich protein-related
serine-rich protein-related
serine-rich protein-related
-
calreticulin 2 (CRT2)
leucine-rich repeat family protein / extensin family protein, similar to extensin-like protein (Lycopersicon esculentum)
leucine-rich repeat family protein / extensin family protein, similar to extensin-like protein (Lycopersicon esculentum)

tropinone reductase, putative
tropinone reductase, putative
tropinone reductase, putative
peroxidase, putative, similar to peroxidase (Nicotiana tabacum) gi|5381253|dbj|BAA82306
peroxidase, putative, similar to peroxidase (Nicotiana tabacum) gi|5381253|dbj|BAA82306
-
tropinone reductase, putative
tropinone reductase, putative
tropinone reductase, putative
tropinone reductase, putative
putative disease resistance protein (CC-NBS-LRR)
putative disease resistance protein (CC-NBS-LRR)
putative disease resistance protein (CC-NBS-LRR)
putative disease resistance protein (CC-NBS-LRR)
putative disease resistance protein (CC-NBS-LRR class)
putative disease resistance protein (CC-NBS-LRR class)
putative disease resistance protein (CC-NBS-LRR class)
putative disease resistance protein (CC-NBS-LRR class)
CwfJ-like family protein
CwfJ-like family protein
CwfJ-like family protein
-
-
expressed protein
heat shock protein mtHsc 70-2 (Hsc70-5)
chaperonin, putative, similar to SWISS-PROT:P50143- T-complex protein 1, gamma subunit (TCP-1-gamma) (Xenopus laevis)
chaperonin, putative, similar to SWISS-PROT:P50143- T-complex protein 1, gamma subunit (TCP-1-gamma) (Xenopus laevis)
oxidoreductase, zinc-binding dehydrogenase family protein, contains Pfam profile PF00107: oxidoreductase, zinc-binding dehydrogenase family
oxidoreductase, zinc-binding dehydrogenase family protein, contains Pfam profile PF00107: oxidoreductase, zinc-binding dehydrogenase family
oxidoreductase, zinc-binding dehydrogenase family protein, contains Pfam profile PF00107: oxidoreductase, zinc-binding dehydrogenase family
oxidoreductase, zinc-binding dehydrogenase family protein, contains Pfam profile PF00107: oxidoreductase, zinc-binding dehydrogenase family
oxidoreductase, zinc-binding dehydrogenase family protein, contains Pfam profile PF00107: oxidoreductase, zinc-binding dehydrogenase family
oxidoreductase, zinc-binding dehydrogenase family protein, contains Pfam profile PF00107: oxidoreductase, zinc-binding dehydrogenase family
oxidoreductase, zinc-binding dehydrogenase family protein, contains Pfam profile PF00107: oxidoreductase, zinc-binding dehydrogenase family
oxidoreductase, zinc-binding dehydrogenase family protein, contains Pfam profile PF00107: oxidoreductase, zinc-binding dehydrogenase family
oxidoreductase, zinc-binding dehydrogenase family protein, contains Pfam profile PF00107: oxidoreductase, zinc-binding dehydrogenase family
oxidoreductase, zinc-binding dehydrogenase family protein, contains Pfam profile PF00107: oxidoreductase, zinc-binding dehydrogenase family
-
laccase family protein / diphenol oxidase family protein, similar to laccase (Pinus taeda)
Harpin-induced protein 1 (Hin1); pfam07320
galactinol synthase, putative
galactinol synthase, putative
galactinol synthase, putative
expressed protein
protein kinase family protein, contains Pfam PF00069: Protein kinase domain
oxidoreductase, zinc-binding dehydrogenase family protein, contains Pfam profile PF00107: oxidoreductase, zinc-binding dehydrogenase family
senescence-associated protein (SEN1), identical to senescence-associated protein GI:1046270 from (Arabidopsis thaliana)
senescence-associated protein (SEN1), identical to senescence-associated protein GI:1046270 from (Arabidopsis thaliana)
secretory protein, putative, similar to NtPRp27 (Nicotiana tabacum) GI:5360263
U-box domain-containing protein, similar to immediate-early fungal elicitor protein CMPG1 (Petroselinum crispum) GI:14582200
XS domain-containing protein / XS zinc finger domain-containing protein-related
malate dehydrogenase, cytosolic, putative, strong similarity to cytosolic malate dehydrogenase (EC 1.1.1.37) SP|O24047 {Mesembryanthemum crystallinum}

dehydration -induced protein family
purine permease; putative purine permease (or PR1-2 from Pc)
protein kinase family protein
phosphoglycerate/bisphosphoglycerate mutase family protein
FAD-linked oxidoreductase family
60S ribosomal protein L37 (RPL37A)
Harpin-induced protein 1 (Hin1); pfam07320
Harpin-induced protein 1 (Hin1); pfam07320
Harpin-induced protein 1 (Hin1); pfam07320
oxidoreductase, zinc-binding dehydrogenase family protein, contains Pfam profile PF00107: oxidoreductase, zinc-binding dehydrogenase family
secretory protein, putative, similar to NtPRp27 (Nicotiana tabacum) GI:5360263
secretory protein, putative, similar to NtPRp27 (Nicotiana tabacum) GI:5360263
secretory protein, putative, similar to NtPRp27 (Nicotiana tabacum) GI:5360263
Harpin-induced protein 1 (Hin1); pfam07320
secretory protein, putative, similar to NtPRp27 (Nicotiana tabacum) GI:5360263
dual specificity protein phosphatase family protein, contains Pfam profile: PF00782 dual specificity phosphatase, catalytic domain
ATP synthase beta chain 1, mitochondrial, identical to SP|P83483 ATP synthase beta chain 1, mitochondrial precursor (EC 3.6.3.14) {Arabidopsis thaliana}
secretory protein, putative, similar to NtPRp27 (Nicotiana tabacum) GI:5360263
secretory protein, putative, similar to NtPRp27 (Nicotiana tabacum) GI:5360263
phospholipid/glycerol acyltransferase family protein
phospholipid/glycerol acyltransferase family protein
U-box domain-containing protein, similar to immediate-early fungal elicitor protein CMPG1 (Petroselinum crispum) GI:14582200; contains Pfam profile PF04564: U-box domain
U-box domain-containing protein, similar to immediate-early fungal elicitor protein CMPG1 (Petroselinum crispum) GI:14582200; contains Pfam profile PF04564: U-box domain
heat shock protein, putative, strong similarity to SP|P55737 Heat shock protein 81-2 (HSP81-2) {Arabidopsis thaliana}
Harpin-induced protein 1 (Hin1); pfam07320
protein kinase, putative, similar to protein kinase ATN1 (Arabidopsis thaliana) gi|1054633|emb|CAA63387
amino acid transporter family protein
short-chain dehydrogenase/reductase (SDR) family protein, similar to carbonyl reductase GI:1049108 from (Mus musculus)
short-chain dehydrogenase/reductase (SDR) family protein, similar to carbonyl reductase GI:1049108 from (Mus musculus)
short-chain dehydrogenase/reductase (SDR) family protein, similar to carbonyl reductase GI:1049108 from (Mus musculus)
chaperonin, putative, similar to SWISS-PROT:P50143- T-complex protein 1, gamma subunit (TCP-1-gamma) (Xenopus laevis)
40S ribosomal protein S15A (RPS15aA)
Transcription initiation factor IIB (AtTGIIB2)
chaperonin, putative, similar to SWISS-PROT:P50143- T-complex protein 1, gamma subunit (TCP-1-gamma) (Xenopus laevis)
protein kinase family protein
oxidoreductase, zinc-binding dehydrogenase family protein, contains Pfam profile PF00107: oxidoreductase, zinc-binding dehydrogenase family
oxidoreductase, zinc-binding dehydrogenase family protein, contains Pfam profile PF00107: oxidoreductase, zinc-binding dehydrogenase family
AAA-type ATPase family protein
expressed protein
expressed protein
secretory protein, putative, similar to NtPRp27 (Nicotiana tabacum) GI:5360263
peptidase M1 family protein, similar to SP|P04825 Aminopeptidase N (EC 3.4.11.2) (Alpha-aminoacylpeptide hydrolase) {Escherichia coli}
secretory protein, putative, similar to NtPRp27 (Nicotiana tabacum) GI:5360263
secretory protein, putative, similar to NtPRp27 (Nicotiana tabacum) GI:5360263
LEM3 (ligand-effect modulator 3) family protein
LEM3 (ligand-effect modulator 3) family protein
oxidoreductase, zinc-binding dehydrogenase family protein, contains Pfam profile PF00107: oxidoreductase, zinc-binding dehydrogenase family
secretory protein, putative, similar to NtPRp27 (Nicotiana tabacum) GI:5360263
Harpin-induced protein 1 (Hin1); pfam07320
Harpin-induced protein 1 (Hin1); pfam07320
Harpin-induced protein 1 (Hin1); pfam07320
sulfate adenylyltransferase 1 / ATP-sulfurylase 1 (APS1), nearly identical to ATP sulfurylase (APS1) (Arabidopsis thaliana) GI:6606509

sulfate adenylyltransferase 1 / ATP-sulfurylase 1 (APS1), nearly identical to ATP sulfurylase (APS1) (Arabidopsis thaliana) GI:6606509
S-locus protein kinase, putative, similar to receptor protein kinase (Ipomoea trifida)
strong similarity to SP|Q42908 2,3-bisphosphoglycerate-independent phosphoglycerate mutase (EC 5.4.2.1) (Phosphoglyceromutase) {Mesembryanthemum crystallinum}
secretory protein, putative, similar to NtPRp27 (Nicotiana tabacum) GI:5360263
secretory protein, putative, similar to NtPRp27 (Nicotiana tabacum) GI:5360263
putataive 1-aminocyclopropane-1-carboxylate synthase
secretory protein, putative, similar to NtPRp27 (Nicotiana tabacum) GI:5360263
secretory protein, putative, similar to NtPRp27 (Nicotiana tabacum) GI:5360263
secretory protein, putative, similar to NtPRp27 (Nicotiana tabacum) GI:5360263
secretory protein, putative, similar to NtPRp27 (Nicotiana tabacum) GI:5360263
secretory protein, putative, similar to NtPRp27 (Nicotiana tabacum) GI:5360263
secretory protein, putative, similar to NtPRp27 (Nicotiana tabacum) GI:5360263
secretory protein, putative, similar to NtPRp27 (Nicotiana tabacum) GI:5360263
secretory protein, putative, similar to NtPRp27 (Nicotiana tabacum) GI:5360263
in plants expressed in root, inflorescence, stem, rosette leaf
-
putative cinnamoyl-alcohol dehydrogenase
shaggy-related protein kinase alpha / ASK-alpha (ASK1), identical to shaggy-related protein kinase alpha SP:P43288 GI:460832 from (Arabidopsis thaliana)
protein kinase, putative, similar to protein kinase ATN1 (Arabidopsis thaliana) gi|1054633|emb|CAA63387
MD-2-related lipid recognition domain-containing protein
MD-2-related lipid recognition domain-containing protein
MD-2-related lipid recognition domain-containing protein
glycosyl hydrolase family 3 protein
protein kinase family protein
exostosin family protein
SKP1 interacting partner 4 (SKIP4), almost idential to SKP1 interacting partner 4 GI:10716953 from (Arabidopsis thaliana)
SKP1 interacting partner 4 (SKIP4), almost idential to SKP1 interacting partner 4 GI:10716953 from (Arabidopsis thaliana)
stress-responsive protein, putative, similar to cold acclimation WCOR413-like protein gamma form (Hordeum vulgare) gi|18449100|gb|AAL69988
alcohol dehydrogenase, putative, similar to alcohol dehydrogenase from Solanum tuberosum (SP|p14673)
alcohol dehydrogenase, putative, similar to alcohol dehydrogenase from Solanum tuberosum (SP|p14673)
putative P450 cytochrome
phosphatidylinositol-4-phosphate 5-kinase family protein
long-chain acyl-CoA synthetase/AMP binding protein
scarecrow-like transcription factor 5 (SCL5)
respiratory burst oxidase protein D (RbohD) / NADPH oxidase
respiratory burst oxidase protein D (RbohD) / NADPH oxidase
beta-Ig-H3 domain-containing protein / fasciclin domain-containing protein, weak similarity to osteoblast specific factor 2 (Homo sapiens) GI:393319
zinc finger (C3HC4-type RING finger) family protein
-
-
Harpin-induced protein 1 (Hin1); pfam07320
oxidoreductase, zinc-binding dehydrogenase family protein, contains Pfam profile PF00107: oxidoreductase, zinc-binding dehydrogenase family
oxidoreductase, zinc-binding dehydrogenase family protein, contains Pfam profile PF00107: oxidoreductase, zinc-binding dehydrogenase family
GDSL-motif ligase/hydrolase-like protein
Harpin-induced protein 1 (Hin1); pfam07320
putataive 1-aminocyclopropane-1-carboxylate synthase
putataive 1-aminocyclopropane-1-carboxylate synthase
universal stress protein (USP) family protein
zinc finger protein-related
putataive 1-aminocyclopropane-1-carboxylate synthase
putataive 1-aminocyclopropane-1-carboxylate synthase
zinc finger protein-related

leucine-rich repeat family protein
leucine-rich repeat family protein
-
-
putative cinnamoyl-alcohol dehydrogenase
interferon-related developmental regulator family protein
FAD-binding domain-containing protein, similar to SP|P30986 reticuline oxidase precursor (Berberine-bridge-forming enzyme) (BBE)
glutamate receptor family protein (GLR2.8) (GLUR9), plant glutamate receptor family, PMID:11379626
glutamate receptor family protein (GLR2.8) (GLUR9), plant glutamate receptor family, PMID:11379626
expressed protein
expressed protein
expressed protein
L-ascorbate peroxidase 1, cytosolic (APX1)
FAD-binding domain-containing protein, similar to SP|P30986 reticuline oxidase precursor (Berberine-bridge-forming enzyme) (BBE) (Tetrahydroprotoberberine synthase) (Eschscholzia californica); contains PF01565 FAD binding domain
protein kinase family protein
VHS domain-containing protein / GAT domain-containing protein, weak similarity to hepatocyte growth factor-regulated tyrosine kinase substrate (Homo sapiens) GI:2731383
VHS domain-containing protein / GAT domain-containing protein, weak similarity to hepatocyte growth factor-regulated tyrosine kinase substrate (Homo sapiens) GI:2731383
similar to glutamate decarboxylase 1 (GAD 1) [Arabidopsis thaliana] (TAIR:At5g17330.1)
protein kinase family protein, contains protein kinase domain, Pfam:PF00069
UDP-sulfoquinovose:DAG sulfoquinovosyltransferase / sulfolipid synthase (SQD2), identical to GI:20302857
importin alpha-2, putative (IMPA-2), similar to importin alpha 2 (Capsicum annuum) GI:13752562
ubiquitin-specific protease 6, putative (UBP6) similar to GI:11993465
pectate lyase family protein, similar to pectate lyase GI:14289169 from (Salix gilgiana)
sodium/calcium exchanger family protein / calcium-binding EF hand family protein
shepherd protein (SHD) / clavata formation protein, putative, nearly identical to SHEPHERD (Arabidopsis thaliana) GI:19570872
quinolinate phosphoribosyl transferase family protein, contains Pfam profile: PF01729 quinolinate phosphoribosyl transferase, C-terminal domain
leucine-rich repeat transmembrane protein kinase, putative, similar to receptor protein kinase GB:BAA11869 GI:1389566 from (Arabidopsis thaliana)
NL1 interacting factor (NIF) family protein
putative DNA-dirceted RNA polymerase
putative DNA-dirceted RNA polymerase
L-ascorbate oxidase, putative, similar to SP|P14133 L-ascorbate oxidase precursor (EC 1.10.3.3) (Ascorbase) {Cucumis sativus}
Ras-related GTP-binding protein, putative, similar to GTP-binding protein RAB5A GI:1370178 from (Lotus japonicus)
small nuclear ribonucleoprotein E, putative / snRNP-E, putative / Sm protein E, putative
F-box family protein, PF0064: F-box domain
40S ribosomal protein S3 (RPS3C)
protease inhibitor, putative, similar to SP|P19873 Inhibitor of trypsin and hageman factor (CMTI-V) {Cucurbita maxima}
protease inhibitor, putative, similar to SP|P19873 Inhibitor of trypsin and hageman factor (CMTI-V) {Cucurbita maxima}
FAD-binding domain-containing protein (Berberine-bridge-forming enzyme) (BBE)
-
signal recognition particle 54 kDa protein 3 /SRP54 (SRP-54C), identical to SP|P49967 Signal recognition particle 54 kDa protein 3 (SRP54) {Arabidopsis thaliana}
S-locus lectin protein kinase family protein
protein kinase family
putative glutathione peroxidase
armadillo/beta-catenin repeat family protein / F-box family protein, contains similarity to F-box protein FBL2 GI:6010699 from (Rattus norvegicus)
calmodulin-binding family protein
calmodulin-binding family protein
calmodulin-binding family protein
eukaryotic translation initiation factor 2B family protein / eIF-2B family protein, similar to CIG2 (Nicotiana tabacum) GI:15216226
transcription regulatory protein SNF2, putative
transcription regulatory protein SNF2, putative
XS domain-containing protein / XS zinc finger domain-containing protein-related
expressed protein

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expressed protein
cyclic nucleotide-binding transporter 1 / CNBT1 (CNGC20), identical to cyclic nucleotide-binding transporter 1 (CNBT1) GI:8131898 from (Arabidopsis thaliana)
expressed protein
VHS domain-containing protein / GAT domain-containing protein, weak similarity to hepatocyte growth factor-regulated tyrosine kinase substrate (Homo sapiens) GI:2731383
VHS domain-containing protein / GAT domain-containing protein, weak similarity to hepatocyte growth factor-regulated tyrosine kinase substrate (Homo sapiens) GI:2731383
cyclic nucleotide-binding transporter 1 / CNBT1 (CNGC20), identical to cyclic nucleotide-binding transporter 1 (CNBT1) GI:8131898 from (Arabidopsis thaliana)
cyclic nucleotide-binding transporter 1 / CNBT1 (CNGC20), identical to cyclic nucleotide-binding transporter 1 (CNBT1) GI:8131898 from (Arabidopsis thaliana)
serine/threonine protein phosphatase PP2A-2 catalytic subunit (PP2A2), identical to SP|Q07099 Serine/threonine protein phosphatase PP2A-2 catalytic subunit (EC 3.1.3.16) {Arabidopsis thaliana}
expressed protein, MtN19, Medicago truncatula (immer nur ein Primer vorhanden)
actin 7 (ACT7) / actin 2, identical to SP|P53492 Actin 7 (Actin-2) {Arabidopsis thaliana}
zinc finger (C3HC4-type RING finger) family protein
protein phosphatase 2C, putative / PP2C, putative, phosphoprotein phosphatase (EC 3.1.3.16) 1A-alpha - Homo sapiens, PIR:S22423
FAD-binding domain-containing protein, similar to SP|P30986 reticuline oxidase precursor (Berberine-bridge-forming enzyme) (BBE) (Tetrahydroprotoberberine synthase) (Eschscholzia californica); contains PF01565 FAD binding domain
putative cytochrome P450
-
protease inhibitor, putative, similar to SP|P19873 Inhibitor of trypsin and hageman factor (CMTI-V) {Cucurbita maxima}
-
ras-related GTP-binding protein, putative
protease inhibitor, putative, similar to SP|P19873 Inhibitor of trypsin and hageman factor (CMTI-V) {Cucurbita maxima}
zinc finger (C3HC4-type RING finger) family protein (ATL3) or similar to Avr9/Cf-9 rapidly elicited protein 132 (Nicotiana tabacum)
FAD-binding domain-containing protein, similar to SP|P30986 reticuline oxidase precursor (Berberine-bridge-forming enzyme) (BBE)
FAD-binding domain-containing protein, similar to SP|P30986 reticuline oxidase precursor (Berberine-bridge-forming enzyme) (BBE)
delta8 sphingolipid desaturase (EC 1.14.99.)
fructose-bisphosphate aldolase, putative, similar to plastidic aldolase NPALDP1 from Nicotiana paniculata (GI:4827251)
zinc finger (C3HC4-type RING finger) family protein
zinc finger (C3HC4-type RING finger) family protein
zinc finger (C3HC4-type RING finger) family protein
zinc finger (C3HC4-type RING finger) family protein
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-
-
calmodulin-binding family protein
serine protease inhibitor, Kazal-type family protein
XS domain-containing protein / XS zinc finger domain-containing protein-related
-
-
-
-
-
-
expressed protein
expressed protein
putative aconitate hydratase, cytoplasmic
calmodulin-binding family protein
expressed protein
dual specificity protein phosphatase family protein, contains Pfam profile: PF00782 dual specificity phosphatase, catalytic domain
20S proteasome alpha subunit D2 (PRS1) PRC6)
20S proteasome alpha subunit D2 (PRS1) PRC6)
20S proteasome alpha subunit D2 (PRS1) PRC6)
expressed protein
expressed protein

transcriptional adaptor (ADA2a) protein
expressed protein; step II splicing factor-like protein
expressed protein; step II splicing factor-like protein
expressed protein; step II splicing factor-like protein
mitochondrial substrate carrier family protein
zinc finger (C3HC4-type RING finger) family protein
zinc finger (C3HC4-type RING finger) family protein
expressed protein
expressed protein
expressed protein
expressed protein
NC domain-containing protein
enoyl-CoA hydratase/isomerase family protein, low similarity to PhaB (Pseudomonas putida) GI:3253198, SP|P31551 Carnitine racemase {Escherichia coli}
purine permease; putative purine permease (or PR1-2 from Pc)
trehalose-6-phosphate synthase, putative, similar to Alpha,alpha-trehalose-phosphate synthase (UDP-forming) (EC 2.4.1.15)
F-box family protein, PF0064: F-box domain
trehalose-6-phosphate synthase, putative, similar to Alpha,alpha-trehalose-phosphate synthase (UDP-forming) (EC 2.4.1.15)
F-box family protein, PF0064: F-box domain
F-box family protein, PF0064: F-box domain
F-box family protein, PF0064: F-box domain
F-box family protein, PF0064: F-box domain
S-locus protein kinase, putative, similar to S-receptor kinase gi|392557|gb|AAA62232
S-locus protein kinase, putative, similar to S-receptor kinase gi|392557|gb|AAA62232
S-locus protein kinase, putative, similar to S-receptor kinase gi|392557|gb|AAA62232
S-locus protein kinase, putative, similar to S-receptor kinase gi|392557|gb|AAA62232
putative protein kinase
exostosin family protein
inorganic phosphate transporter (PHT5)
leucine-rich repeat family protein
putative ATPase, plasma membrane-type / proton pump
inorganic phosphate transporter (PHT5)
calnexin 1 (CNX1), identical to calnexin homolog 1, Arabidopsis thaliana, EMBL:AT08315 (SP|P29402)
tubulin beta-6 chain (TUB6), nearly identical to SP|P29514 Tubulin beta-6 chain {Arabidopsis thaliana}
tubulin beta-6 chain (TUB6), nearly identical to SP|P29514 Tubulin beta-6 chain {Arabidopsis thaliana}
60 S ribosmal protein L3 (RPL3B)
COP1-interactive protein 1 / CIP1, almost identical to CIP1 (GI:836950) (Arabidopsis thaliana)
polyubiquitin (UBQ3), identical to GI:928809
polyubiquitin (UBQ3), identical to GI:928809
S-locus protein kinase, putative, similar to S-receptor kinase gi|392557|gb|AAA62232
seven transmembrane MLO family protein/MLO-like protein 8 (MLO8)
serine protease inhibitor, Kazal-type family protein
glycyl-tRNA synthetase / glycine--tRNA ligase, identical to SP|O23627 Glycyl-tRNA synthetase (EC 6.1.1.14) (Glycine--tRNA ligase) (GlyRS) {Arabidopsis thaliana}
glycyl-tRNA synthetase / glycine--tRNA ligase, identical to SP|O23627 Glycyl-tRNA synthetase (EC 6.1.1.14) (Glycine--tRNA ligase) (GlyRS) {Arabidopsis thaliana}
glycyl-tRNA synthetase / glycine--tRNA ligase, identical to SP|O23627 Glycyl-tRNA synthetase (EC 6.1.1.14) (Glycine--tRNA ligase) (GlyRS) {Arabidopsis thaliana}
UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase
integral membrane family protein
SKP1 interacting partner 2 (SKIP2), identical to SKP1 interacting partner 2 GI:10716949 from (Arabidopsis thaliana)
FAD-binding domain-containing protein, similar to SP|P30986 reticuline oxidase precursor (Berberine-bridge-forming enzyme) (BBE) (Tetrahydroprotoberberine synthase) (Eschscholzia californica); contains PF01565 FAD binding domain
expressed protein
FAD-binding domain-containing protein, similar to SP|P30986 reticuline oxidase precursor (Berberine-bridge-forming enzyme) (BBE) (Tetrahydroprotoberberine synthase) (Eschscholzia californica); contains PF01565 FAD binding domain
FAD-binding domain-containing protein, similar to SP|P30986 reticuline oxidase precursor (Berberine-bridge-forming enzyme) (BBE) (Tetrahydroprotoberberine synthase) (Eschscholzia californica); contains PF01565 FAD binding domain
FAD-binding domain-containing protein, similar to SP|P30986 reticuline oxidase precursor (Berberine-bridge-forming enzyme) (BBE) (Tetrahydroprotoberberine synthase) (Eschscholzia californica); contains PF01565 FAD binding domain

FAD-binding domain-containing protein, similar to SP|P30986 reticuline oxidase precursor (Berberine-bridge-forming enzyme) (BBE) (Tetrahydroprotoberberine synthase) (Eschscholzia californica); contains PF01565 FAD binding domain
harpin-induced family protein (YLS9) / HIN1 family protein / harpin-responsive family protein, similar to harpin-induced protein hin1 (GI:1619321) (Nicotiana tabacum)
harpin-induced family protein (YLS9) / HIN1 family protein / harpin-responsive family protein, similar to harpin-induced protein hin1 (GI:1619321) (Nicotiana tabacum)
40 S ribosomal protein S6
-
40 S ribosomal protein S6
40 S ribosomal protein S6
40 S ribosomal protein S6
40 S ribosomal protein S6
expressed protein
glycosyl hydrolase family 17 protein
phospholipid/glycerol acyltransferase family protein
aminoacyl-tRNA synthetase family protein
aminoacyl-tRNA synthetase family protein
40 S ribosomal protein S6
expressed protein
FAD-binding domain-containing protein, similar to SP|P30986 reticuline oxidase precursor (Berberine-bridge-forming enzyme) (BBE) (Tetrahydroprotoberberine synthase) (Eschscholzia californica); contains PF01565 FAD binding domain
tetratricopeptide repeat (TPR)-containing protein
60 S ribosmal protein L7 (RPL7C)
laccase family protein / diphenol oxidase family protein, similar to laccase (Pinus taeda)
DNA replication licensing factor (CDC21)
expressed protein
U-box domain-containing protein, similar to immediate-early fungal elicitor protein CMPG1 (Petroselinum crispum) GI:14582200
zinc finger (C3HC4-type RING finger) family protein
ligasetetratricopeptide repeat (TPR)-containing protein
tetratricopeptide repeat (TPR)-containing protein
tetratricopeptide repeat (TPR)-containing protein
tetratricopeptide repeat (TPR)-containing protein
synthaxin SYP124 (in PEN1)
short-chain dehydrogenase/reductase (SDR) family protein, similar to WW-domain oxidoreductase
60S ribosomal protein L19 (RPL19A)
-
-
flavin-containing monooxygenase family protein
leucine-rich repeat protein
ubiquitin fusion degradation UFD1 family protein, similar to SP|P70362 Ubiquitin fusion degradation protein 1 homolog (UB fusion protein 1) {Mus musculus}
pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat
4-alpha glucanotransferase
putative disease resistance protein (TIR-NBS-LRR class)
ubiquitin fusion degradation UFD1 family protein, similar to SP|P70362 Ubiquitin fusion degradation protein 1 homolog (UB fusion protein 1) {Mus musculus}
60S ribosomal protein L23 (RPL23A)
similar to expressed protein [Arabidopsis thaliana] (TAIR:At5g58510.1)
-
-
-
proteinputative Hs1pro-1 homolog
heat shock protein 81-2 (HSP81-2)
long-chain-fatty-acid--CoA ligase (acyl-CoA synthetase)
pyruvate dehydrogenase E1 alpha subunit
pyruvate dehydrogenase E1 alpha subunit
pyruvate dehydrogenase E1 alpha subunit
putative NTF2-containing RNA-binding protein

nucleic acid binding / transcription factor/ zinc ion binding
expressed protein
expressed protein
-
-
-
-
No apical meristem (NAM) protein; pfam02365
No apical meristem (NAM) protein; pfam02365
-
CCR4-NOT transcription complex protein, putative, similar to SWISS-PROT:Q9UFF9 CCR4-NOT transcription complex, subunit 8 (CAF1-like protein, CALIFp) (Homo sapiens)
CCR4-NOT transcription complex protein, putative, similar to SWISS-PROT:Q9UFF9 CCR4-NOT transcription complex, subunit 8 (CAF1-like protein, CALIFp) (Homo sapiens)
CCR4-NOT transcription complex protein, putative, similar to SWISS-PROT:Q9UFF9 CCR4-NOT transcription complex, subunit 8 (CAF1-like protein, CALIFp) (Homo sapiens)
CCR4-NOT transcription complex protein, putative, similar to SWISS-PROT:Q9UFF9 CCR4-NOT transcription complex, subunit 8 (CAF1-like protein, CALIFp) (Homo sapiens)
CCR4-NOT transcription complex protein, putative, similar to SWISS-PROT:Q9UFF9 CCR4-NOT transcription complex, subunit 8 (CAF1-like protein, CALIFp) (Homo sapiens)
oxidoreductase, zinc-binding dehydrogenase family protein, contains Pfam profile PF00107: oxidoreductase, zinc-binding dehydrogenase family
CBL-interacting protein kinase 14 (CIPK14)
expressed protein
expressed protein
expressed protein
expressed protein
expressed protein
AAA-type ATPase family
FAD-binding domain-containing protein, similar to SP|P30986 reticuline oxidase precursor (Berberine-bridge-forming enzyme) (BBE)
tudor domain-containing protein / nuclease family protein, contains Pfam domains PF00567: Tudor domain and PF00565: Staphylococcal nuclease homologue
mitochondrial protein-like
chromodomain-helicase-DNA-binding family protein
lactoylglutathione lyase family protein / glyoxalase I family protein
lactoylglutathione lyase family protein / glyoxalase I family protein
pre-mRNA splicing factor, putative, strong similarity to SP|O22315 Pre-mRNA splicing factor SF2 (SR1 protein) {Arabidopsis thaliana}
pre-mRNA splicing factor, putative, strong similarity to SP|O22315 Pre-mRNA splicing factor SF2 (SR1 protein) {Arabidopsis thaliana}
pre-mRNA splicing factor, putative, strong similarity to SP|O22315 Pre-mRNA splicing factor SF2 (SR1 protein) {Arabidopsis thaliana}
rhodanese-like domain protein
similar to glutamate decarboxylase 1 (GAD 1) [Arabidopsis thaliana] (TAIR:At5g17330.1)
putative DNA-damage-repair/toleration protein (ORT 100)
putative DNA-damage-repair/toleration protein (ORT 100)
putative DNA-damage-repair/toleration protein (ORT 100)
protein kinase family (putative ser/thr protein kinase)
esterase/lipase/thioesterase family protein, similar to late embryogenesis abundant protein
esterase/lipase/thioesterase family protein, similar to late embryogenesis abundant protein
esterase/lipase/thioesterase family protein, similar to late embryogenesis abundant protein
esterase/lipase/thioesterase family protein, similar to late embryogenesis abundant protein
putative polcalein (calcium-binding pollen allergen)
exocyst subunit EXO70 family
exocyst subunit EXO70 family
60S ribosomal protein L7A (RPL7aA)
mitochondrial import receptor subunit TOM20-3 / translocase of outer membrane 20 kDa subunit 3 (TOM20-3)
expressed protein
expressed protein
expressed protein
expressed protein
AAA-type ATPase family protein / vacuolar sorting protein-related

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-
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Harpin-induced protein 1 (Hin1); pfam07320
similar to expressed protein [Arabidopsis thaliana] (TAIR:At4g14290.1)
expressed protein
zinc finger (C3HC4-type RING finger) family protein
far-red impaired responsive protein, putative
putative coatomer protein complex, subunit alpha
Harpin-induced protein 1 (Hin1); pfam07320
Harpin-induced protein 1 (Hin1); pfam07320
Harpin-induced protein 1 (Hin1); pfam07320
Harpin-induced protein 1 (Hin1); pfam07320
Harpin-induced protein 1 (Hin1); pfam07320
Harpin-induced protein 1 (Hin1); pfam07320
U-box domain-containing protein, similar to immediate-early fungal elicitor protein CMPG1 (Petroselinum crispum) GI:14582200; contains Pfam profile PF04564: U-box domain
Harpin-induced protein 1 (Hin1); pfam07320
U-box domain-containing protein, similar to immediate-early fungal elicitor protein CMPG1 (Petroselinum crispum) GI:14582200; contains Pfam profile PF04564: U-box domain
Harpin-induced protein 1 (Hin1); pfam07320
glycosyl hydrolase family 9
short-chain dehydrogenase/reductase family protein
expressed protein
expressed protein
ABC transporter family protein, related to multidrug resistance proteins and P-glycoproteins
leucine rich repeat family protein
-
transcriptional factor B3 family protein, low similarity to FUSCA3 (Arabidopsis thaliana) GI:3582518
F-box protein family (FBX 6)
60S ribosomal protein L27A
expressed protein
UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase
UDP-glucoronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase
esterase/lipase/thioesterase family protein
putative cytochrome P450
DNA helicase (RECQl4A), nearly identical to DNA Helicase (Arabidopsis thaliana) GI:11121449
RabGAP/TBC domain-containing protein
dynamin-like protein 2B (ADL2b)
glycosyl transferase family 8 protein
putative leucine-rich repeat transmembrane protein kinase
putative leucine-rich repeat transmembrane protein kinase
putative leucine-rich repeat transmembrane protein kinase
DNAJ heat shock N-terminal domain-containing protein (J20), identical to DnaJ-like protein GI:6691127
DNAJ heat shock N-terminal domain-containing protein (J20), identical to DnaJ-like protein GI:6691127
DNAJ heat shock N-terminal domain-containing protein (J20), identical to DnaJ-like protein GI:6691127
glycoside hydrolase family 2 protein, similar to beta-galactosidase (lactase) from Alteromonas haloplanktis (SP|P81650)
glycoside hydrolase family 2 protein, similar to beta-galactosidase (lactase) from Alteromonas haloplanktis (SP|P81650)
glycoside hydrolase family 2 protein, similar to beta-galactosidase (lactase) from Alteromonas haloplanktis (SP|P81650)
glycoside hydrolase family 2 protein, similar to beta-galactosidase (lactase) from Alteromonas haloplanktis (SP|P81650)
human Rev interacting-like protein-related / hRIP protein-related
human Rev interacting-like protein-related / hRIP protein-related
human Rev interacting-like protein-related / hRIP protein-related
human Rev interacting-like protein-related / hRIP protein-related

human Rev interacting-like protein-related / hRIP protein-related
human Rev interacting-like protein-related / hRIP protein-related
putative succinate dehydrogenase iron-protein subunit
C2 domain-containing protein
zinc finger (C2H2 type) family protein
zinc finger (CCCH-type) family protein, contains Pfam domain, PF00642: Zinc finger C-x8-C-x5-C-x3-H type (and similar) and Pfam domain, PF00023: Ankyrin repeat
zinc finger (CCCH-type) family protein, contains Pfam domain, PF00642: Zinc finger C-x8-C-x5-C-x3-H type (and similar) and Pfam domain, PF00023: Ankyrin repeat
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zinc finger (CCCH-type) family protein, contains Pfam domain, PF00642: Zinc finger C-x8-C-x5-C-x3-H type (and similar) and Pfam domain, PF00023: Ankyrin repeat
calpain-type cysteine protease family
putative AP2 domain-containing transcription factor
putative AP2 domain-containing transcription factor
putative AP2 domain-containing transcription factor
disease resistance protein (EDS1)
expressed protein
elongation factor 1B-gamma (eEF-1B gamma)
elongation factor 1B-gamma (eEF-1B gamma)
MATE - efflux protein-related
MATE - efflux protein-related
glycosyl transferase family 8
expressed protein
expressed protein
expressed protein
S-locus lectin protein kinase family protein
expressed protein
expressed protein
expressed protein
expressed protein
shaggy-related protein kinase eta / ASK-eta (ASK7)
expressed protein, contains similarity to hedgehog-interacting protein GI:4868122 from (Mus musculus)
similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g66860.1)
similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g66860.1)
zinc finger (CCCH type) helicase family protein
FAD-binding domain-containing protein
expressed protein
zinc finger (C2H2 type) protein family
glucan phosphorylase, putative, similar to alpha-glucan phosphorylase, L isozyme 1 precursor GB:P04045 from (Solanum tuberosum) (J. Biochem. 106 (4), 691-695 (1989))
Harpin-induced protein 1 (Hin1)
Harpin-induced protein 1 (Hin1)
Harpin-induced protein 1 (Hin1)
hydrolase alpha/beta fold family
Glucose-methanol-choline (GMC) oxidoreductase family protein, similar to mandelonitrile lyase from Prunus serotina (SP|P52706, SP|P52707)
putative AP2 domain-containing transcription factor
Glucose-methanol-choline (GMC) oxidoreductase family protein, similar to mandelonitrile lyase from Prunus serotina (SP|P52706, SP|P52707)
-
-
scarecrow-like transcription factor (SCL 8)
scarecrow-like transcription factor (SCL 8)
scarecrow-like transcription factor (SCL 8)
scarecrow-like transcription factor (SCL 8)
F-box protein family
F-box protein family

F-box protein family
F-box protein family
F-box protein family
elongation factor 1B-gamma (eEF-1B gamma)
Type 1 glutamine amidotransferase (GATase1)-like domain found in Human DJ-1; cd03135
potassium channel tetramerisation domain-containing protein, contains Pfam profile PF02214: K+ channel tetramerisation domain
potassium channel tetramerisation domain-containing protein, contains Pfam profile PF02214: K+ channel tetramerisation domain
AAA-type ATPase family protein, contains Pfam profile PF00004: ATPase, AAA family
FAD-linked oxidoreductase family (berberine bridge enzyme)
-
-
-
lipoic acid synthase (LIP1)
putative CCCH-type zinc finger protein
probable gibberllin beta-hydroxylase
(JR3 protein) IAA-Ala hydrolase (IAR3)
(JR3 protein) IAA-Ala hydrolase (IAR3)
expressed protein
(JR3 protein) IAA-Ala hydrolase (IAR3)
(JR3 protein) IAA-Ala hydrolase (IAR3)
(JR3 protein) IAA-Ala hydrolase (IAR3)
expressed protein
disease resistance protein (CC-NBS-LRR class)
disease resistance protein RPS5 (CC-NBS-LRR class)
similar to ser/thr-specific protein kinase NPK15 (Nicotiana tabacum) gi|505146|dbj|BAA06538
similar to ser/thr-specific protein kinase NPK15 (Nicotiana tabacum) gi|505146|dbj|BAA06538
similar to ser/thr-specific protein kinase NPK15 (Nicotiana tabacum) gi|505146|dbj|BAA06538
similar to ser/thr-specific protein kinase NPK15 (Nicotiana tabacum) gi|505146|dbj|BAA06538
-
-
-
-
ser/thr protein phosphatase 2A (regulatory chain)
putative coatomer complex subunit
-
endomembrane protein 70, putative, p76, Homo sapiens, EMBL:HSU81006
protein kinase family
glutathione peroxidase
armadillo/beta-catenin repeat family protein / F-box family protein, contains similarity to F-box protein FBL2 GI:6010699 from (Rattus norvegicus)
protein kinase family protein, contains Pfam domain, PF00069: Protein kinase domain
60S ribosomal protien L7 (RPL7D)
zinc finger (C3HC4-type RING finger) family protein
protein phosphatase 2C, putative / PP2C, putative, phosphoprotein phosphatase (EC 3.1.3.16) 1A-alpha - Homo sapiens, PIR:S22423
putative ATP-citrate synthase (ATP-citrate(pro-S)-lyase/citrate cleavage enzyme)
Vacuolar protein sorting-associated protein [Intracellular trafficking and secretion]; COG5043
expressed protein
galactosyltransferase family protein
EXS family protein/ ERD1/XPR1 (PHO1-like)/SYG1 family protein
expressed protein
expressed protein, non-consensus GA donor splice site at exon 6
expressed protein
expressed protein

expressed protein, non-consensus GA donor splice site at exon 6
expressed protein
putative 1,2-diacylglycerol 3-beta-galactosyltransferase
zinc finger (C3HC4-type RING finger) family protein
expressed protein
putative cinnamoyl-alcohol dehydrogenase
IAA-aminoacid hydrolase I (ILR1)
-
leucine-rich repeat family protein/protein kinase family protein
leucine-rich repeat family protein/protein kinase family protein
polyadenylate-binding protein, putative / PABP, putative, similar to poly(A)-binding protein GB:AAF66825 GI:7673359 from (Nicotiana tabacum)
polyadenylate-binding protein, putative / PABP, putative, similar to poly(A)-binding protein GB:AAF66825 GI:7673359 from (Nicotiana tabacum)
polyadenylate-binding protein, putative / PABP, putative, similar to poly(A)-binding protein GB:AAF66825 GI:7673359 from (Nicotiana tabacum)
exportin 1 (XPO1)
short-chain dehydrogenase/reductase (SDR) family protein
sec34-like family protein (vesicle docking protein)
zinc finger (C3HC4-type RING finger) family protein
expressed protein
nuclear transport factor 2 (NTF2) family protein
cell division cycle protein 48 (CDC 48A)
short-chain dehydrogenase/reductase (SDR) family protein, similar to WW-domain oxidoreductase
oxidoreductase, 2 OG-Fe(II) oxygenase family protein
-
tropinone reductase, putative
Pep3/Vsp18/deep orange family protein
-
root hair defect 3 GTP-binding (RHD3) family protein
expressed protein
expressed protein (putative DNA J protein)
DNAJ heat shock N-terminal domain-containing protein
-
-
-
putative cetromere/kinetochore protein (ZW10)
putative wall-associated kinase
putative wall-associated kinase
putative wall-associated kinase
esterase/lipase/thioesterase family protein
putative wall-associated kinase
putative histone H2A
putative leucine-rich repeat transmembrane protein kinase
putative leucine-rich repeat transmembrane protein kinase
putative leucine-rich repeat transmembrane protein kinase
-
metallopeptidase M24 family protein
metallopeptidase M24 family protein
putative iron-deficiency-responsive protein
2-nitropropane dioxygenase family/NPD family
protein kinase family protein
-
protein kinase family protein
zinc finger (C3HC4-type RING finger) family protein

putative leucine-rich repeat transmembrane protein kinase, similar to brassinosteroid insensitive 1
putative leucine-rich repeat transmembrane protein kinase, similar to brassinosteroid insensitive 1
cytochrome P450 family protein
NC domain-containing protein
NC domain-containing protein
cellulose synthase family protein (CslD3), similar to cellulose synthase catalytic subunit gi:2827143
cellulose synthase family protein (CslD3), similar to cellulose synthase catalytic subunit gi:2827143
cellulose synthase family protein (CslD3), similar to cellulose synthase catalytic subunit gi:2827143
cellulose synthase family protein (CslD3), similar to cellulose synthase catalytic subunit gi:2827143
probable gibberllin beta-hydroxylase
probable gibberllin beta-hydroxylase
zinc finger (C3HC4-type RING finger) family protein
expressed protein
expressed protein
strictosidine synthase family protein
expressed protein
expressed protein
expressed protein
expressed protein
haloacid dehalogenase-like hydrolase family protein
ankyrin repeat family protein, regulator of chromosomal condensation (RCC1) family protein
ankyrin repeat family protein, regulator of chromosomal condensation (RCC1) family protein
diacylglycerol kinase 1 (DGK1)
short-chain dehydrogenase/reductase (SDR) family protein
expressed protein
expressed protein
expressed protein
S-locus protein kinase, putative, similar to S-receptor kinase gi|392557|gb|AAA62232
S-locus protein kinase, putative, similar to S-receptor kinase gi|392557|gb|AAA62232
S-locus protein kinase, putative, similar to S-receptor kinase gi|392557|gb|AAA62232
-
late embryogenesis abundant protein-related
S-locus protein kinase, putative, similar to S-receptor kinase gi|392557|gb|AAA62232
late embryogenesis abundant protein-related
late embryogenesis abundant protein-related
S-locus protein kinase, putative, similar to receptor protein kinase (Ipomoea trifida)
Ku 80 family protein
Ku 80 family protein
Ku 80 family protein
Ku 80 family protein
zinc finger (CCCH-type) family protein
-
phosphoglycerate/bisphosphoglycerate mutase family protein
tRNA synthetase class I (C) family protein
alpha-1,4-glycosyltransferase family protein
protein kinase family protein
protein kinase family protein
oxidoreductase, 2OG-Fe(II) oxygenase family protein
phosphoesterase family protein
ADP-ribosylation factor
similar to MATE efflux family protein
similar to MATE efflux family protein

putative ammonium transporter
oxidoreductase, 2OG-Fe(II) oxygenase family protein
calcium-transporting ATPase 1, endoplasmic reticulum-type (ECA1)
sec23/sec24 treansport protein-related
-
ADP ribosylation factor
-
20S proteasome alpha subunit A2 (PAA2)
20S proteasome alpha subunit A2 (PAA2)
20S proteasome alpha subunit A2 (PAA2)
20S proteasome alpha subunit A2 (PAA2)
20S proteasome alpha subunit A2 (PAA2)
20S proteasome alpha subunit A2 (PAA2)
putative Calcium-transporting ATPase, plasmamembrane-type
RNA polymerase sigma subunit SigF (SigF)
ankyrin repeat family protein (putative RING zinc finger)
ankyrin repeat family protein (putative RING zinc finger)
putative Calcium-dependent protein kinase (CDPK)
RNA recognition motif (RRM)-containing protein
-
putative disease resistance protein (CC-NBS-LRR class)
putative disease resistance protein (CC-NBS-LRR class)
putative disease resistance protein (CC-NBS-LRR class)
FAD-binding domain-containing protein
-
ABC transporter family protein
RNA recognition motif (RRM)-containing protein
oxidoreductase, 2OG-Fe(II) oxygenase family protein
oxidoreductase, 2OG-Fe(II) oxygenase family protein
oxidoreductase, 2OG-Fe(II) oxygenase family protein
oxidoreductase, 2OG-Fe(II) oxygenase family protein
oxidoreductase, 2OG-Fe(II) oxygenase family protein
oxidoreductase, 2OG-Fe(II) oxygenase family protein
AMP-dependent synthetase & ligase family protein
AMP-dependent synthetase & ligase family protein
AMP-dependent synthetase & ligase family protein
FAD-binding domain-containing protein (Berberine-bridge-forming enzyme) (BBE)
AMP-dependent synthetase & ligase family protein
expressed protein
-
-
ankyrin repeat family protein (ankyrin repeats mediate)
putative mannitol transporter
putative mannitol transporter
putative mannitol transporter
putative mannitol transporter
ADP ribosylation factor
oxidoreductase, 2OG-Fe(II) oxygenase family protein
pyruvate dehydrogenase E1 component beta subunit, mitochondrial
pyruvate dehydrogenase E1 component beta subunit, mitochondrial
pyruvate dehydrogenase E1 component beta subunit, mitochondrial
60 S ribosomal protein L26 (RPL26A)

ADP ribosylation factor
ADP ribosylation factor
ADP ribosylation factor
ADP ribosylation factor
ADP ribosylation factor
-
AMP-dependent synthetase & ligase family protein
MutT/nudix family protein
similar to PAL1 or PAL2
aconitase family
aconitase family
-
-
-
-
epsin N-terminal homology (ENTH) domain-containing protein, contains Pfam PF01417: ENTH domain
epsin N-terminal homology (ENTH) domain-containing protein, contains Pfam PF01417: ENTH domain
glycosyl transferase family 48 protein,
alcohol oxidase-related
sec34-like family protein (vesicle docking protein)
similar to glycine-rich protein
expressed protein
zinc finger (AN1-like) family protein, contains Pfam profile: PF01428 AN1-like zinc finger
expressed protein
cytochrome P450 family
short-chain dehydrogenase/reductase family protein
-
-
-
expressed protein
-
-
scarecrow-like transcription factor 21 (SCL21)
EXS family protein / ERD1/XPR1/SYG1 family protein
EXS family protein / ERD1/XPR1/SYG1 family protein
-
expressed protein
ABC transporter family
ABC transporter family
zinc finger (AN1-like) family protein, contains Pfam profile: PF01428 AN1-like zinc finger
zinc finger (AN1-like) family protein, contains Pfam profile: PF01428 AN1-like zinc finger
zinc finger (AN1-like) family protein, contains Pfam profile: PF01428 AN1-like zinc finger
short-chain dehydrogenase/reductase family protein
calmodulin-binding family protein
calmodulin-binding family protein
-
-
-
-
-
expressed protein
expressed protein

S-locus protein kinase, putative, similar to S-receptor kinase gi|392557|gb|AAA62232
glycine hydroxymethyltransferase
F-box family protein, PF0064: F-box domain
F-box family protein
putative anionic peroxidase
putative anionic peroxidase
-
F-box family protein, PF0064: F-box domain
calcium- and calmodulin-dependent protein kinase/ kinase
phospholipid/glycerol acyltransferase family protein
calcium- and calmodulin-dependent protein kinase/ kinase
putative cytochrome P450
putative cytochrome P450
pentatricopeptide (PPR) repeat-containing protein
-
-
oxidoreductase, acting on the CH-OH group of donors, NAD or NADP as acceptor
oxidoreductase, acting on the CH-OH group of donors, NAD or NADP as acceptor
DNAJ heat shock protein, putative, similar to SP|O89114 DnaJ homolog subfamily B member 5 (Heat shock protein Hsp40-3) {Mus musculus}
oxidoreductase, acting on the CH-OH group of donors, NAD or NADP as acceptor
oxidoreductase, acting on the CH-OH group of donors, NAD or NADP as acceptor
oxidoreductase, acting on the CH-OH group of donors, NAD or NADP as acceptor
-
-
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-
-
cytochrome P450
epsin N-terminal homology (ENTH) domain-containing protein, contains Pfam PF01417: ENTH domain
putative endomembrane protein 70, TM4 family
expressed protein
mitochondrial tRNA-Ala synthetase
expressed protein; Esterase/lipase
SWAP (Suppressor-of-White-APricot)/surp domain-containing protein
SWAP (Suppressor-of-White-APricot)/surp domain-containing protein
-
-
-
-
-
expressed protein, similar to expressed protein
60S ribosomal protien L19 (RPL19A)
60S ribosomal protien L19 (RPL19A)
expressed protein, very similar to PC818-3
expressed protein, very similar to PC818-3
expressed protein
-
-
-
expressed protein
expressed protein
expressed protein, very similar to PC818-3

-
-
putative disease resistance protein (TIR-NBS-LRR class)
but very similar to pc832-2 und pc701-2-1
-
-
-
-
-
-
-
GTP-binding family protein
ADP ribosylation factor