

Supplemental Table 1. Accession numbers, annotations and MS identification details of all 242 proteins identified by TPP analysis. Accession numbers, lab annotation, maximum probability based Mowse scores, and Adapted MapMan Bin and simplified functional classifications are listed.

Accession	Lab Annot.	max MOWSE score	MapMan bin	Simplified Functional category
A15g18180.1	glycine-rich protein	71	27 (Regulation) transcription and translation	(Regulation) DNA organization,transcription and translation
A13g03920.1	glycine-rich protein	71	28 (Regulation) transcription and translation	(Regulation) DNA organization,transcription and translation
A14g13010.1	ceQORH - oxidoreductase, Zn binding dehy	112	28 (Regulation) transcription and translation	(Regulation) DNA organization,transcription and translation
A14g24770.1	RNA binding protein CP31	83	28 (Regulation) transcription and translation	(Regulation) DNA organization,transcription and translation
A11g07320.1	50S ribosomal protein L4	337	29.2.1 protein.synthesis.chloroplast - plastid	(Regulation) DNA organization,transcription and translation
A13g27830.1	50S ribosomal protein L12-A	248	29.2.1 protein.synthesis.chloroplast - plastid	(Regulation) DNA organization,transcription and translation
A13g27850.1	50S ribosomal protein L12-C	248	29.2.1 protein.synthesis.chloroplast - plastid	(Regulation) DNA organization,transcription and translation
A13g56010.1	expressed protein CHLOROPLAST 30S RI	59	29.2.1 protein.synthesis.chloroplast - plastid	(Regulation) DNA organization,transcription and translation
A13g63490.1	ribosomal protein L1p family	197	29.2.1 protein.synthesis.chloroplast - plastid	(Regulation) DNA organization,transcription and translation
A13g53470.1	S40 ribosomal protein S25	126	29.2.2 protein.synthesis.misc ribosomal p	(Regulation) DNA organization,transcription and translation
A14g20360.1	elongation factor Tu, chloroplast precursor	604	29.2.3 protein.synthesis.initiation	(Regulation) DNA organization,transcription and translation
A13g16000.1	MFP1 - nucleoid binding	877	31.1 cell.organisation	(Regulation) DNA organization,transcription and translation
A11g32060.1	phosphoribulokinase precursor	248	1.3 PS.calvin cyle	Calvin cycle, photorespiration, minor carbohydrates, starch, OPP, glycolysis
A11g42970.1	glyceraldehyde-3-phosphate dehydrogenase	396	1.3 PS.calvin cyle	Calvin cycle, photorespiration, minor carbohydrates, starch, OPP, glycolysis
A11g67090.1	Rubisco small subunit (RBCS) - very abund	92	1.3 PS.calvin cyle	Calvin cycle, photorespiration, minor carbohydrates, starch, OPP, glycolysis
A11g73110.1	activase -related	332	1.3 PS.calvin cyle	Calvin cycle, photorespiration, minor carbohydrates, starch, OPP, glycolysis
A12g39730.1	Rubisco activase	1131	1.3 PS.calvin cyle	Calvin cycle, photorespiration, minor carbohydrates, starch, OPP, glycolysis
A13g26650.1	glyceraldehyde 3-phosphate dehydrogenase	302	1.3 PS.calvin cyle	Calvin cycle, photorespiration, minor carbohydrates, starch, OPP, glycolysis
ATCG00490	Rubisco large subunit (RBCL)	357	1.3 PS.calvin cyle	Calvin cycle, photorespiration, minor carbohydrates, starch, OPP, glycolysis
A13g04790.1	ribose 5-phosphate isomerase	275	7.2 OPP.non-reductive PP	Calvin cycle, photorespiration, minor carbohydrates, starch, OPP, glycolysis
A13g25760.1	allene oxide cyclase family (ERD12)	238	17.7.1 hormone metabolism.jasmonate.synth	hormone and lipid metabolism
A13g25770.1	allene oxide cyclase family - (ERD12)	486	17.7.1 hormone metabolism.jasmonate.synth	hormone and lipid metabolism
A13g45140.1	lipoygenase AtLOX2	527	17.7.1 hormone metabolism.jasmonate.synth	hormone and lipid metabolism
A15g42650.1	allene oxide synthase	889	17.7.1 hormone metabolism.jasmonate.synth	hormone and lipid metabolism
A15g35630.1	glutamate-ammonia ligase, chloroplast	362	12.2 N-metabolism.ammonia metabolism	N, S, aa and nucleotide metabolism
A15g35170.1	adenylate kinase	45	23.4 nucleotide metabolism.phosphotransfer	N, S, aa and nucleotide metabolism
A13g56690.1	calmodulin-binding protein	37	.3 signalling.calcium	other developmental & signalling functions
A15g22640.1	expressed protein	133	.4 signalling.phosphinositides	other developmental & signalling functions
A11g50020.1	tubulin alpha-6 chain	173	31.1 cell.organisation	other developmental & signalling functions
A11g52410.1	myosin-related, Poly-adenylate binding pro	42	31.1 cell.organisation	other developmental & signalling functions
A13g01500.1	carbonic anhydrase	329	8.3 TCA / org. transformation.carbonic anhy	other metabolic functions
A15g14740.1	carbonic anhydrase 2	196	8.3 TCA / org. transformation.carbonic anhy	other metabolic functions
A12g21160.1	signal sequence receptor, alpha subunit (SS	71	29.3 protein.targeting	protein fate
A12g28800.1	Alb3 (Albino 3)	109	29.3 protein.targeting	protein fate
A12g47450.1	cpSRP43	59	29.3 protein.targeting	protein fate
A14g14870.1	cpSecE	220	29.3 protein.targeting	protein fate
A15g16620.1	Tic40	160	29.3 protein.targeting	protein fate
A15g28750.1	Tha4 TatA/E	108	29.3 protein.targeting	protein fate
A15g52440.1	hcf106 TatB	204	29.3 protein.targeting	protein fate
A11g06430.1	FtsH8 TAT ITP	1033	29.5 protein.degradation	protein fate
A11g07510.1	FtsH10 - mTP predicted	54	29.5 protein.degradation	protein fate
A11g50250.1	FtsH1 (Var1)	1284	29.5 protein.degradation	protein fate
A12g29080.1	FtsH3 - mitochondrial predicted	54	29.5 protein.degradation	protein fate
A12g30950.1	FtsH2 (VAR2 and Pftf)	1542	29.5 protein.degradation	protein fate
A15g05740.1	expressed protein similar to unknown prote	37	29.5 protein.degradation	protein fate
A15g42270.1	FtsH5 (VAR1)	1375	29.5 protein.degradation	protein fate
A15g51540.1	expressed protein	257	29.5 protein.degradation	protein fate
A11g18170.1	Isomerases TAT ITP	186	29.6 protein.(un)folding (includes isomerase	protein fate
A13g01480.1	Tlp-40	1123	29.6 protein.(un)folding (includes isomerase	protein fate
A13g15520.1	Isomerases	71	29.6 protein.(un)folding (includes isomerase	protein fate
A13g62030.1	peptidylprolyl isomerase ROC4	254	29.6 protein.(un)folding (includes isomerase	protein fate
A14g39710.1	Isomerases	250	29.6 protein.(un)folding (includes isomerase	protein fate
A15g13120.1	peptidyl-prolyl isomerase protein - TLP21	188	29.6 protein.(un)folding (includes isomerase	protein fate
A15g13410.1	Isomerases TAT ITP	250	29.6 protein.(un)folding (includes isomerase	protein fate
A15g50920.1	ClpC1	352	29.6 protein.(un)folding (includes isomerase	protein fate
A13g24590.1	TPP-2 lumen	585	29.7 protein. processing	protein fate
A11g54500.1	rubredoxin	492	29.8 protein assembly and cofactor ligation	protein fate
A14g37200.1	HCF164 Fd like	351	29.8 protein assembly and cofactor ligation	protein fate
A15g17170.1	expressed protein Rubredoxin and PDZ dor	314	29.8 protein assembly and cofactor ligation	protein fate
A15g23120.1	HCF136 Tat ltp	222	29.8 protein assembly and cofactor ligation	protein fate
A11g65260.1	Vipp1 - mutant HCF155	459	31.4 cell. vesicle transport	protein fate
A13g18890.1	UOS1	889	11.8 hormone and lipid	hormone and lipid metabolism
A15g47110.1	LiI3.1	115	.2.5 stress abiotic light	redox proteins & oxidative defense & stress response
A14g17600.1	LiI3.2	198	.2.5 stress.abiotic.light	redox proteins & oxidative defense & stress response
A11g77490.1	thylakoid bound APX	231	21.2 redox.ascorbate and glutathione	redox proteins & oxidative defense & stress response
A12g25080.1	glutathione peroxidase putative	70	21.2 redox.ascorbate and glutathione	redox proteins & oxidative defense & stress response
A14g09010.1	Putative Asc-perox lumen Tat ltp	606	21.2 redox.ascorbate and glutathione	redox proteins & oxidative defense & stress response
A15g03880.1	auxin-regulated protein predicted protein, A	148	21.2 redox.ascorbate and glutathione	redox proteins & oxidative defense & stress response
A13g48890.1	cytochrome b5 domain-containing protein (119	21.3 redox.heme	redox proteins & oxidative defense & stress response
A13g26060.1	Peroxioredoxin Q	82	21.5 redox.periredoxins	redox proteins & oxidative defense & stress response
A11g51110.1	fibrillin (similar to PAP2 B. rapa)	103	26.19 misc. fibrillins	redox proteins & oxidative defense & stress response
A12g35490.1	fibrillin	352	26.19 misc. fibrillins	redox proteins & oxidative defense & stress response
A13g23400.1	fibrillin	648	26.19 misc. fibrillins	redox proteins & oxidative defense & stress response
A13g26070.1	fibrillin	306	26.19 misc. fibrillins	redox proteins & oxidative defense & stress response
A13g58010.1	fibrillin	137	26.19 misc. fibrillins	redox proteins & oxidative defense & stress response
A14g04020.1	fibrillin	1005	26.19 misc. fibrillins	redox proteins & oxidative defense & stress response

At4g22240.1	fibrillin	1017	26.19 misc. fibrillins	redox proteins & oxidative defense & stress response
At1g74470.1	geranylgeranyl reductase (GGDR)	414	16.1 secondary metabolism.terpenoids	terpenoids & tetrapyrrole synthesis & degradation
At2g34460.1	flavin reductase-related	250	16.3 secondary metabolism.flavonoids	terpenoids & tetrapyrrole synthesis & degradation
At1g03630.1	PORC- -constitutive expression	275	19 tetrapyrrole synthesis	terpenoids & tetrapyrrole synthesis & degradation
At3g56940.1	CHL27 or Crd1	121	19 tetrapyrrole synthesis	terpenoids & tetrapyrrole synthesis & degradation
At4g27440.1	PORB - constitutive expression - main prot	173	19 tetrapyrrole synthesis	terpenoids & tetrapyrrole synthesis & degradation
At3g14110.1	Flu gene - TPR motif, regulation tetrapyrrol	203	19. tetrapyrrole synthesis	terpenoids & tetrapyrrole synthesis & degradation
At1g20020.1	FNR-2	806	1.1 PS.lightreaction	thylakoid (cyclic) electron transport, ATP synthesis and chlororespiration
At5g66190.1	FNR-1	865	1.1 PS.lightreaction	thylakoid (cyclic) electron transport, ATP synthesis and chlororespiration
At1g03600.1	PSII Lumen Tat ITP	181	1.1.1 PS.lightreaction - Photosystem II	thylakoid (cyclic) electron transport, ATP synthesis and chlororespiration
At1g06680.1	psbP OEC23 Tat ITP	504	1.1.1 PS.lightreaction - Photosystem II	thylakoid (cyclic) electron transport, ATP synthesis and chlororespiration
At1g14150.1	PsbQ domain Tat ITP	181	1.1.1 PS.lightreaction - Photosystem II	thylakoid (cyclic) electron transport, ATP synthesis and chlororespiration
At1g15820.1	LHCII-6 - CP24	525	1.1.1 PS.lightreaction - Photosystem II	thylakoid (cyclic) electron transport, ATP synthesis and chlororespiration
At1g29910.1	LHCII-1.1 - 100% identical to lhcb-1.2,3-r	470	1.1.1 PS.lightreaction - Photosystem II	thylakoid (cyclic) electron transport, ATP synthesis and chlororespiration
At1g29920.1	LHCII-1.2 - 100% identical to lhcb-1.1,3-r	470	1.1.1 PS.lightreaction - Photosystem II	thylakoid (cyclic) electron transport, ATP synthesis and chlororespiration
At1g29930.1	LHCII-1.3 - 100% identical to lhcb-1.1,2 -r	470	1.1.1 PS.lightreaction - Photosystem II	thylakoid (cyclic) electron transport, ATP synthesis and chlororespiration
At1g34000.1	Ohp2	253	1.1.1 PS.lightreaction - Photosystem II	thylakoid (cyclic) electron transport, ATP synthesis and chlororespiration
At1g44575.1	psbS	902	1.1.1 PS.lightreaction - Photosystem II	thylakoid (cyclic) electron transport, ATP synthesis and chlororespiration
At1g79040.1	psbR	171	1.1.1 PS.lightreaction - Photosystem II	thylakoid (cyclic) electron transport, ATP synthesis and chlororespiration
At2g05070.1	LHCII-2.2	431	1.1.1 PS.lightreaction - Photosystem II	thylakoid (cyclic) electron transport, ATP synthesis and chlororespiration
At2g05100.1	LHCII-2.1	345	1.1.1 PS.lightreaction - Photosystem II	thylakoid (cyclic) electron transport, ATP synthesis and chlororespiration
At2g34420.1	LHCII-1.5	438	1.1.1 PS.lightreaction - Photosystem II	thylakoid (cyclic) electron transport, ATP synthesis and chlororespiration
At2g34430.1	LHCII-1.4	334	1.1.1 PS.lightreaction - Photosystem II	thylakoid (cyclic) electron transport, ATP synthesis and chlororespiration
At2g39470.1	OEC23-like Tat ITP	50	1.1.1 PS.lightreaction - Photosystem II	thylakoid (cyclic) electron transport, ATP synthesis and chlororespiration
At2g40100.1	LHCII-4.3 -CP29	178	1.1.1 PS.lightreaction - Photosystem II	thylakoid (cyclic) electron transport, ATP synthesis and chlororespiration
At3g01440.1	PsbQ domain Tat ITP	170	1.1.1 PS.lightreaction - Photosystem II	thylakoid (cyclic) electron transport, ATP synthesis and chlororespiration
At3g08940.1	LHCII-4.2 - CP29	98	1.1.1 PS.lightreaction - Photosystem II	thylakoid (cyclic) electron transport, ATP synthesis and chlororespiration
At3g27690.1	LHCII-2.4	411	1.1.1 PS.lightreaction - Photosystem II	thylakoid (cyclic) electron transport, ATP synthesis and chlororespiration
At3g50820.1	psbO OEC33-like	775	1.1.1 PS.lightreaction - Photosystem II	thylakoid (cyclic) electron transport, ATP synthesis and chlororespiration
At4g05180.1	psbQ OEC16-like Tat ITP	218	1.1.1 PS.lightreaction - Photosystem II	thylakoid (cyclic) electron transport, ATP synthesis and chlororespiration
At4g10340.1	LHCII-5 - CP26	717	1.1.1 PS.lightreaction - Photosystem II	thylakoid (cyclic) electron transport, ATP synthesis and chlororespiration
At4g21280.1	psbQ OEC16 Tat Itp	216	1.1.1 PS.lightreaction - Photosystem II	thylakoid (cyclic) electron transport, ATP synthesis and chlororespiration
At4g28660.1	psbW -like sequencing project	96	1.1.1 PS.lightreaction - Photosystem II	thylakoid (cyclic) electron transport, ATP synthesis and chlororespiration
At5g01530.1	LHCII-4.1-CP29	317	1.1.1 PS.lightreaction - Photosystem II	thylakoid (cyclic) electron transport, ATP synthesis and chlororespiration
At5g11450.1	OEC23-like Tat Itp TP21.5	145	1.1.1 PS.lightreaction - Photosystem II	thylakoid (cyclic) electron transport, ATP synthesis and chlororespiration
At5g54270.1	LHCII-3	295	1.1.1 PS.lightreaction - Photosystem II	thylakoid (cyclic) electron transport, ATP synthesis and chlororespiration
At5g66570.1	psbO OEC33	760	1.1.1 PS.lightreaction - Photosystem II	thylakoid (cyclic) electron transport, ATP synthesis and chlororespiration
ATCG00270	psbD D2	378	1.1.1 PS.lightreaction - Photosystem II	thylakoid (cyclic) electron transport, ATP synthesis and chlororespiration
ATCG00280	psbC CP43	545	1.1.1 PS.lightreaction - Photosystem II	thylakoid (cyclic) electron transport, ATP synthesis and chlororespiration
ATCG00560	psbL	34	1.1.1 PS.lightreaction - Photosystem II	thylakoid (cyclic) electron transport, ATP synthesis and chlororespiration
ATCG00580	psbE cytb559a	116	1.1.1 PS.lightreaction - Photosystem II	thylakoid (cyclic) electron transport, ATP synthesis and chlororespiration
ATCG00680	psbB CP47	566	1.1.1 PS.lightreaction - Photosystem II	thylakoid (cyclic) electron transport, ATP synthesis and chlororespiration
ATCG00710	psbH-phospho	49	1.1.1 PS.lightreaction - Photosystem II	thylakoid (cyclic) electron transport, ATP synthesis and chlororespiration
At1g03130.1	psaD-1 subunit II - stromal side-tight	368	1.1.2 PS.lightreaction - Photosystem I	thylakoid (cyclic) electron transport, ATP synthesis and chlororespiration
At1g03080.1	psaK - subunit X	48	1.1.2 PS.lightreaction - Photosystem I	thylakoid (cyclic) electron transport, ATP synthesis and chlororespiration
At1g31330.1	psaF- subunit III - LTP - hydrophobic	352	1.1.2 PS.lightreaction - Photosystem I	thylakoid (cyclic) electron transport, ATP synthesis and chlororespiration
At1g52230.1	psaH-2 - subunit VI	203	1.1.2 PS.lightreaction - Photosystem I	thylakoid (cyclic) electron transport, ATP synthesis and chlororespiration
At1g55670.1	psaG - subunit V- stromal side	92	1.1.2 PS.lightreaction - Photosystem I	thylakoid (cyclic) electron transport, ATP synthesis and chlororespiration
At1g61520.1	LHCI-3 - LHCI-680A CAB4	340	1.1.2 PS.lightreaction - Photosystem I	thylakoid (cyclic) electron transport, ATP synthesis and chlororespiration
At2g0260.1	psaE-2 subunit IV - stromal side	211	1.1.2 PS.lightreaction - Photosystem I	thylakoid (cyclic) electron transport, ATP synthesis and chlororespiration
At3g16140.1	psaH-1 - subunit VI	183	1.1.2 PS.lightreaction - Photosystem I	thylakoid (cyclic) electron transport, ATP synthesis and chlororespiration
At3g47470.1	LHCI-4 - LHCI-730	465	1.1.2 PS.lightreaction - Photosystem I	thylakoid (cyclic) electron transport, ATP synthesis and chlororespiration
At3g54890.1	LHCI-1-1 - LHCI-730	114	1.1.2 PS.lightreaction - Photosystem I	thylakoid (cyclic) electron transport, ATP synthesis and chlororespiration
At3g61470.1	LHCI-2.1 - LHCI-680B	143	1.1.2 PS.lightreaction - Photosystem I	thylakoid (cyclic) electron transport, ATP synthesis and chlororespiration
At4g02770.1	psaD-2 subunit II - stromal side-tight	675	1.1.2 PS.lightreaction - Photosystem I	thylakoid (cyclic) electron transport, ATP synthesis and chlororespiration
At4g12800.1	psaL - subunit XI (also named V)	184	1.1.2 PS.lightreaction - Photosystem I	thylakoid (cyclic) electron transport, ATP synthesis and chlororespiration
At4g28750.1	psaE-1 subunit IV - stromal side	271	1.1.2 PS.lightreaction - Photosystem I	thylakoid (cyclic) electron transport, ATP synthesis and chlororespiration
At5g64040.1	psaN - TAT LTP	422	1.1.2 PS.lightreaction - Photosystem I	thylakoid (cyclic) electron transport, ATP synthesis and chlororespiration
ATCG00020	psbA D1	315	1.1.2 PS.lightreaction - Photosystem I	thylakoid (cyclic) electron transport, ATP synthesis and chlororespiration
ATCG00340	psaB - subunit Ib	326	1.1.2 PS.lightreaction - Photosystem I	thylakoid (cyclic) electron transport, ATP synthesis and chlororespiration
ATCG00350	psaA - subunit Ia	203	1.1.2 PS.lightreaction - Photosystem I	thylakoid (cyclic) electron transport, ATP synthesis and chlororespiration
ATCG01060	psaC - subunit VII - stromal side	195	1.1.2 PS.lightreaction - Photosystem I	thylakoid (cyclic) electron transport, ATP synthesis and chlororespiration
At2g26500.1	petM - 4 kDa Tat Itp	77	1.1.3 PS.lightreaction - Cytochrome b6f con	thylakoid (cyclic) electron transport, ATP synthesis and chlororespiration
At4g03280.1	petC - Rieske Fe-S protein - LTP	227	1.1.3 PS.lightreaction - Cytochrome b6f con	thylakoid (cyclic) electron transport, ATP synthesis and chlororespiration
ATCG00540	petA - cytochrome f (cleavable ss of 35 aa)	773	1.1.3 PS.lightreaction - Cytochrome b6f con	thylakoid (cyclic) electron transport, ATP synthesis and chlororespiration
ATCG00720	petB - Cytochrome b6	126	1.1.3 PS.lightreaction - Cytochrome b6f con	thylakoid (cyclic) electron transport, ATP synthesis and chlororespiration
ATCG00730	petD - subIV	74	1.1.3 PS.lightreaction - Cytochrome b6f con	thylakoid (cyclic) electron transport, ATP synthesis and chlororespiration
At4g04640.1	CF1y - atpC	572	1.1.4 PS.lightreaction - ATP synthase	thylakoid (cyclic) electron transport, ATP synthesis and chlororespiration
At4g09650.1	CF1d - atpD	576	1.1.4 PS.lightreaction - ATP synthase	thylakoid (cyclic) electron transport, ATP synthesis and chlororespiration
At4g32260.1	CFO-II - atpG	502	1.1.4 PS.lightreaction - ATP synthase	thylakoid (cyclic) electron transport, ATP synthesis and chlororespiration
ATCG00120	CF1a - atpA	777	1.1.4 PS.lightreaction - ATP synthase	thylakoid (cyclic) electron transport, ATP synthesis and chlororespiration
ATCG00130	CFO-I - atpF	406	1.1.4 PS.lightreaction - ATP synthase	thylakoid (cyclic) electron transport, ATP synthesis and chlororespiration
ATCG00140	CFO-III - atpH	58	1.1.4 PS.lightreaction - ATP synthase	thylakoid (cyclic) electron transport, ATP synthesis and chlororespiration
ATCG00150	CFO-IV - atpI	64	1.1.4 PS.lightreaction - ATP synthase	thylakoid (cyclic) electron transport, ATP synthesis and chlororespiration
ATCG00470	CF1e - atpE	333	1.1.4 PS.lightreaction - ATP synthase	thylakoid (cyclic) electron transport, ATP synthesis and chlororespiration
ATCG00480	CF1b - atpB	1459	1.1.4 PS.lightreaction - ATP synthase	thylakoid (cyclic) electron transport, ATP synthesis and chlororespiration
ATCG01110	NDH 7	46	1.4 PS Cyclic electron flow-chlororespiratio	thylakoid (cyclic) electron transport, ATP synthesis and chlororespiration
At5g53560.1	cytochrome b5	55	26.1 misc.misc2	unknown function
At1g75690.1	DnaJ domain family	246	26.14 misc. DnaJ domain with unknown fur	unknown function
At1g80030.1	DnaJ domain family	211	26.14 misc. DnaJ domain with unknown fur	unknown function
At2g22360.1	DnaJ domain family	94	26.14 misc. DnaJ domain with unknown fur	unknown function
At4g13670.1	DnaJ domain family	130	26.14 misc. DnaJ domain with unknown fur	unknown function
At4g39960.1	DnaJ domain family	201	26.14 misc. DnaJ domain with unknown fur	unknown function
At5g21430.1	DnaJ domain family	460	26.14 misc. DnaJ domain with unknown fur	unknown function

At1g12250.1	thylakoid lumen pentapeptide repeat	526	26.15 misc. Pentapeptide repeat (PPR) unkn	unknown function
At2g37230.1	pentatricopeptide (PPR) repeat-containing f	44	26.15 misc. Pentapeptide repeat (PPR) unkn	unknown function
At2g44920.1	thylakoid lumen pentapeptide repeat	141	26.15 misc. Pentapeptide repeat (PPR) unkn	unknown function
At2g42220.1	rhodanese-like domain protein contains rho	114	26.16 misc. Rhodanese domain unknown fu	unknown function
At3g25480.1	rhodanese-like domain	52	26.16 misc. Rhodanese domain unknown fu	unknown function
At4g01050.1	expressed protein ITP? Rhodanese-like don	614	26.16 misc. Rhodanese domain unknown fu	unknown function
At4g27700.1	rhodanese-like domain protein	168	26.16 misc. Rhodanese domain unknown fu	unknown function
At1g22700.1	tetratricopeptide repeat (TPR)-containing p	73	26.17 misc. tetratricopeptide repeat (TPR) u	unknown function
At1g71500.1	Rieske [2Fe-2S] domain	771	26.18 misc. other Ferredoxins and Rieske d	unknown function
At1g14345.1	expressed protein	113	35.2 not assigned. unknown	unknown function
At1g16790.1	expressed protein	52	35.2 not assigned. unknown	unknown function
At1g16880.1	expressed protein	117	35.2 not assigned. unknown	unknown function
At1g18730.1	unknown protein	88	35.2 not assigned. unknown	unknown function
At1g33810.1	expressed protein	230	35.2 not assigned. unknown	unknown function
At1g42960.1	Hp17	69	35.2 not assigned. unknown	unknown function
At1g52220.1	expressed protein	49	35.2 not assigned. unknown	unknown function
At1g55480.1	expressed protein	378	35.2 not assigned. unknown	unknown function
At1g72640.1	expressed protein	73	35.2 not assigned. unknown	unknown function
At1g73885.1	expressed protein	61	35.2 not assigned. unknown	unknown function
At1g74730.1	expressed protein	79	35.2 not assigned. unknown	unknown function
At1g74880.1	expressed protein	99	35.2 not assigned. unknown	unknown function
At1g78915.1	unknown protein	558	35.2 not assigned. unknown	unknown function
At2g01870.1	expressed protein	60	35.2 not assigned. unknown	unknown function
At2g17972.1	expressed protein	105	35.2 not assigned. unknown	unknown function
At2g20890.1	expressed protein sll11414 homologue	129	35.2 not assigned. unknown	unknown function
At2g23670.1	ycf37 Synechocystis -stromal predicted	170	35.2 not assigned. unknown	unknown function
At2g26340.1	stromal predicted??	181	35.2 not assigned. unknown	unknown function
At2g27290.1	expressed protein	157	35.2 not assigned. unknown	unknown function
At2g29180.1	expressed protein	43	35.2 not assigned. unknown	unknown function
At2g36145.1	expressed protein	140	35.2 not assigned. unknown	unknown function
At2g42975.1	expressed protein	67	35.2 not assigned. unknown	unknown function
At2g43630.1	expressed protein	126	35.2 not assigned. unknown	unknown function
At2g46820.1	expressed protein - C/M	148	35.2 not assigned. unknown	unknown function
At3g09050.1	unknown protein	389	35.2 not assigned. unknown	unknown function
At3g15110.1	expressed protein	57	35.2 not assigned. unknown	unknown function
At3g17930.1	expressed protein C/M	64	35.2 not assigned. unknown	unknown function
At3g26580.1	expressed protein	64	35.2 not assigned. unknown	unknown function
At3g46780.1	expressed protein	270	35.2 not assigned. unknown	unknown function
At3g47860.1	expressed protein	304	35.2 not assigned. unknown	unknown function
At3g49720.1	expressed protein	42	35.2 not assigned. unknown	unknown function
At3g51510.1	expressed protein - C/M	130	35.2 not assigned. unknown	unknown function
At3g63160.1	OEP6	38	35.2 not assigned. unknown	unknown function
At4g01150.1	expressed protein C/M	193	35.2 not assigned. unknown	unknown function
At4g11960.1	expressed protein	312	35.2 not assigned. unknown	unknown function
At4g13200.1	expressed protein ITP? C/M	436	35.2 not assigned. unknown	unknown function
At4g22890.1	expressed protein TPP/C/M	731	35.2 not assigned. unknown	unknown function
At4g23890.1	expressed protein hypothetical protein, Syn	230	35.2 not assigned. unknown	unknown function
At4g28025.1	expressed protein	41	35.2 not assigned. unknown	unknown function
At4g37920.1	expressed protein	240	35.2 not assigned. unknown	unknown function
At4g38100.1	expressed protein	214	35.2 not assigned. unknown	unknown function
At5g02160.1	expressed protein	132	35.2 not assigned. unknown	unknown function
At5g08050.1	expressed protein	106	35.2 not assigned. unknown	unknown function
At5g08540.1	expressed protein	74	35.2 not assigned. unknown	unknown function
At5g23060.1	expressed protein - C/M	359	35.2 not assigned. unknown	unknown function
At5g37360.1	expressed protein	58	35.2 not assigned. unknown	unknown function
At5g38660.1	expressed protein similar to unknown prote	59	35.2 not assigned. unknown	unknown function
At5g42070.1	expressed protein	129	35.2 not assigned. unknown	unknown function
At5g43750.1	expressed protein	256	35.2 not assigned. unknown	unknown function
At5g44650.1	expressed protein TMs in PPDB	262	35.2 not assigned. unknown	unknown function
At5g52780.1	expressed protein	112	35.2 not assigned. unknown	unknown function
At1g06690.1	aldo/keto reductase family	54	35.2 not assigned. unknown	unknown function
At1g54780.1	thylakoid lumen 18.3 kDa	689	35.2 not assigned. unknown	unknown function
At1g71480.1	expressed protein	49	35.2 not assigned. unknown	unknown function
At1g74640.1	expressed protein contains Pfam profile: PF	67	35.2 not assigned. unknown	unknown function
At2g10940.1	protease inhibitor/seed storage/lipid transfe	69	35.2 not assigned. unknown	unknown function
At2g21530.1	unknown protein	339	35.2 not assigned. unknown	unknown function
At2g24020.1	expressed protein	228	35.2 not assigned. unknown	unknown function
At2g45180.1	protease inhibitor/seed storage/lipid transfe	99	35.2 not assigned. unknown	unknown function
At3g10130.1	expressed protein	156	35.2 not assigned. unknown	unknown function
At3g47070.1	phosphoprotein -peripheral thylakoid	176	35.2 not assigned. unknown	unknown function
At3g52230.1	OM24 orthologue	211	35.2 not assigned. unknown	unknown function
At3g53560.1	chloroplast lumen common protein family	76	35.2 not assigned. unknown	unknown function
At4g02530.1	thylakoid lumen protein TL16.5	452	35.2 not assigned. unknown	unknown function
At4g39730.1	expressed protein	38	35.2 not assigned. unknown	unknown function
At5g04740.1	ACT domain-containing protein	207	35.2 not assigned. unknown	unknown function
At5g07020.1	proline-rich protein family	251	35.2 not assigned. unknown	unknown function
At5g19390.2	expressed protein	33	35.2 not assigned. unknown	unknown function
At5g20140.1	expressed protein	236	35.2 not assigned. unknown	unknown function
At5g23890.1	expressed protein	305	35.2 not assigned. unknown	unknown function