

Accession	pgID	Master Protein	Description (curated)	Length	Localization (curated)	Calculated Pi PPDB	Calculated MW PPDB	Function (putative)	MapManBin (PPDB)	Localization (TAIR)	ChloroP	TargetP	Curated localization (PPDB)	Aramemnon
AT1G01080	1	AT1G01080.1	33 kDa ribonucleoprotein, chloroplast, putative / RNA-binding protein cp33, putative	293	Ch/S	9.0	32.5699997	RNA binding ?	27.4 RNA.RNA binding		plastid	plastid	plastid stroma	
AT1G01090	2	AT1G01090.1	PDH-E1 ALPHA (PYRUVATE DEHYDROGENASE E1 ALPHA); pyruvate dehydrogenase (acetyl-transferring)	428	Ch/E & Ch/S	7.15999985	47.1699982	metabolism lipid	11.1.31 lipid metabolism. FA synthesis and FA elongation.p yruvate DH		plastid	plastid	envelope-inner-peripheral-stromal-side	
AT1G01620	3	AT1G01620.1	PIP1C (PLASMA MEMBRANE INTRINSIC PROTEIN 1;3); water channel	286	other	9.01000023	30.6299992	transporter aquaporin	34.19.1 transport.Major Intrinsic Proteins.PIP	other (e.g. cytoplasm)			plasma membrane	6.0
AT1G01790	4	AT1G01790.1	KEA1 (K EFFLUX ANTIporter 1); potassium:hydrogen antiporter	618	Ch/E/IM	6.0999999	64.9800034	transporter K	34.8 transport.metabolite transporters at the envelope membrane	cellular component unknown	plastid		envelope-inner-integral	13.0
AT1G02150	5	AT1G02150.1	pentatricopeptide (PPR) repeat-containing protein	524	Ch/S	8.22999954	59.8800011	unknown	27.7* RNA.misc.pentatricopeptide (PPR) repeat-containing protein		plastid	mitochondrion	plastid	
AT1G02280	6	AT1G02280.1	TOC33 (PLASTID PROTEIN IMPORT 1); GTP binding	297	Ch/E/OM	9.10000038	32.9199982	protein targeting Toc	29.3.3 protein.targeting.chloroplast				envelope-outer-integral	
AT1G02560	7	AT1G02560.1	CLPP5 (NUCLEAR ENCODED CLP PROTEASE 1); endopeptidase Clp	298	Ch/S & Ch/E	8.34000015	32.3499985	chaperone and protease	29.5.5 protein.degradation.serine protease	chloroplastic endopeptidase Clp complex & chloroplast stroma & thylakoid (sensu Viridiplantae)	plastid	plastid	plastid stroma	

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AT1G02910	8	AT1G02910.1	LPA1 (LOW PSII ACCUMULATION1); binding	453	Ch/Th	9.36999989	50.7400017	chaperone and protease PSII D1	29.8 protein assembly and cofactor ligation		plastid	plastid	thylakoid-integral	2.0
AT1G03130	9	AT1G03130.1	PSAD-2 (photosystem I subunit D-2)	204	Ch/Th	9.77999973	22.2999992	PS PSI	1.1.2.2 PS.lightreaction.photosystem I.PSI polypeptide subunits	chloroplast	Y	C	thylakoid-peripheral-stromal-side	
AT1G03310	10	AT1G03310.1	ATISA2/BE2/DBE1/ISA2 (DEBRANCHING ENZYME 1); alpha-amylase/isoamylase	882		5.63999987	98.8799973		2.1.2.4 major CHO metabolism.synthesis.starch.debranching	chloroplast	Y	C	plastid	
AT1G03475	11	AT1G03475.1	LIN2 (LESION INITIATION 2); coproporphyrinogen oxidase	362	Ch/S	7.65999985	40.7599983	metabolism vitamin and pigment	19.8 tetrapyrrole synthesis.coproporphyrinogen III oxidase	plastid	plastid	plastid	plastid stroma	
AT1G03600	12	AT1G03600.1	photosystem II family protein	174	Ch/Th	9.88000011	18.8299999	PS PSII	1.1.1.2 PS.lightreaction.photosystem II.PSII polypeptide subunits	thylakoid membrane (sensu Viridiplantae) & thylakoid lumen (sensu Viridiplantae)	plastid	plastid	thylakoid-peripheral-lumenal-side	
AT1G03630	13	AT1G03630.1	POR C (PROTOCHLOROPHYLLIDE OXIDOREDUCTASE); NADPH dehydrogenase/oxidoreductase/protochlorophyllide reductase	401	Ch/E & Ch/Th	9.18000031	43.8800011	metabolism vitamin and pigment	19.14 tetrapyrrole synthesis.protochlorophyllide reductase	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	thylakoid-peripheral-stromal-side	

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AT1G03680	14	AT1G03680.1	ATHM1 (Arabidopsis thioredoxin M-type 1); thiol-disulfide exchange intermediate	179	Ch/S & Ch/E	9.13000011	19.6599998	redox	21.1 redox.thioredoxin		plastid	plastid	thylakoid-peripheral-stromal-side	
AT1G03830	15	AT1G03830.1	guanylate-binding family protein	991		5.57000017	112.5		35.1 not assigned.no ontology	other (e.g. cytoplasm)			-	
AT1G04270	16	AT1G04270.1	RPS15 (CYTOSOLIC RIBOSOMAL PROTEIN S15); structural constituent of ribosome	152	Ch/E & other	10.3400002	17.1299992	translation cytosol	29.2.1.2.1.15 protein.synthesis.ribosomal protein.eukaryotic.40S subunit.S15	other (e.g. cytoplasm)			cytosol	
AT1G04410	17	AT1G04410.1	malate dehydrogenase, cytosolic, putative	332		6.0999999	35.5699997		8.2.9 TCA / org.transformation.other organic acid transformations.cyt MDH	undefined			cytosol	
AT1G04420	18	AT1G04420.1	aldo/keto reductase family protein	412	Ch/S	8.68999958	46.4199982	redox ?	3.5 minor CHO metabolism.others		plastid	plastid	plastid stroma	
AT1G04620	19	AT1G04620.1	coenzyme F420 hydrogenase family / dehydrogenase, beta subunit family	462	Ch/Th & Ch/E	8.35999966	51.6599998	metabolism vitamin and pigment	19.50* tetrapyrrole degradation		plastid	plastid	plastid	
AT1G04820	20	AT1G04820.1	TUA4 (tubulin alpha-4 chain)	450		4.92000008	49.5400009		31.1 cell.organisation	undefined			-	
AT1G05140	21	AT1G05140.1	membrane-associated zinc metalloprotease, putative	441	Ch/Th	9.06000042	47.7700005	chaperone and protease ?	29.5.7 protein.degradation.metall protease		plastid	plastid	plastid	4.0

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AT1G05190	22	AT1G05190.1	EMB2394 (EMBRYO DEFECTIVE 2394); structural constituent of ribosome	223	Ch/S & Ch/E	9.89000034	24.7000008	translation stroma	29.2.1.1.1.2.6 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.50S subunit.L6		plastid	plastid	plastid ribosome	
AT1G06230	23	AT1G06230.1	GTE4 (GLOBAL TRANSCRIPTION FACTOR GROUP E 4); DNA binding	766		5.23000002	84.0899963		27.3.52 RNA.regulation of transcription. Global transcription factor group	other (e.g. cytoplasm)			-	
AT1G06430	24	AT1G06430.1	FTSH8 (FtsH protease 8); ATP-dependent peptidase/ATPase/metallopeptidase/ zinc ion binding	685	Ch/Th	5.71000004	73.1900024	chaperone and protease	29.5.7 protein.degradation.metalloprotease	thylakoid membrane (sensu Viridiplantae) & chloroplast	plastid	plastid	thylakoid-integral	1.0
AT1G06680	25	AT1G06680.1	PSBP-1 (OXYGEN-EVOLVING ENHANCER PROTEIN 2); poly(U) binding	263	Ch/Th & Ch/S	6.9000001	28.0900002	PS PSII OEE	1.1.1.2 PS.lightreaction.photosystem II.PSII polypeptide subunits		plastid	plastid	thylakoid-peripheral-lumenal-side	
AT1G06690	26	AT1G06690.1	aldo/keto reductase family protein	377	Ch/E/IM	8.85000038	41.4900017	redox ?	35.1 not assigned.no ontology	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	plastoglobules	
AT1G06820	27	AT1G06820.1	CRTISO (CAROTENOID ISOMERASE); carotenoid isomerase	595	Ch/E/IM	8.32999992	65.4199982	metabolism vitamin and pigment	16.1.4 secondary metabolism.isoprenoids.carotenoids	chloroplast	plastid		plastid	

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AT1G06950	28	AT1G06950.1	ATTIC110/TIC110 (TRANSLOCATION AT THE INNER ENVELOPE MEMBRANE OF CHLOROPLASTS 110)	1016	Ch/E/IM	5.71999979	112.120003	protein targeting Tic	29.3.3 protein.targeting.chloroplast	chloroplast	plastid	plastid	envelope-inner-integral	2.0
AT1G07040	29	AT1G07040.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G27030.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO41035.1)	371		8.84000015	40.6300011		35.2 not assigned.unknown	chloroplast	Y	C	-	
AT1G07140	30	AT1G07140.1	SIRANBP (Ran-binding protein 1a); Ran GTPase binding	228		4.9000001	25.6000004		27.4 RNA.RNA binding	other (e.g. cytoplasm)			-	
AT1G07320	31	AT1G07320.3	RPL4 (ribosomal protein L4); poly(U) binding / structural constituent of ribosome	282	Ch/S & Ch/E	8.92000008	30.5499992	translation stroma	29.2.1.1.1.2.4 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.50S subunit.L4	thylakoid membrane (sensu Viridiplantae) & plastid large ribosomal subunit	plastid	plastid	plastid ribosome	
AT1G07640	32	AT1G07640.1	OBP2 (OBF BINDING PROTEIN 2); DNA binding / transcription factor	275		9.52999973	29.5300007		27.3.8 RNA.regulation of transcription.C2C2(Zn) DOF zinc finger family	undefined			-	
AT1G07660	33	AT1G07660.1	histone H4	103	other	11.4700003	11.4099998	DNA binding	28.1.3 DNA.synthesis/chromatin structure.histone	undefined			nucleus	

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AT1G07780	34	AT1G07780.1	PAI1 (PHOSPHO RIBOSYLANTHRANILATE ISOMERASE 1); phosphoribosylanthranilate isomerase	275		8.6300011	29.6299992		13.1.6.5.3 amino acid metabolism.synthesis.aromatic aa.tryptophan.phosphoribosylanthranilate isomerase	chloroplast	Y	C	plastid stroma	
AT1G07920	35	AT1G07920.1	elongation factor 1-alpha / EF-1-alpha	449	Ch/E & other	9.18999958	49.5	translation cytosol		mitochondrion	-	-	mitochondria	
AT1G08110	36	AT1G08110.1	lactoylglutathione lyase, putative / glyoxalase I, putative	185		5.13999987	20.8400002		13.2.3.2 amino acid metabolism.degradation.aspartate family.threonine	chloroplast			not plastid	
AT1G08380	37	AT1G08380.1	PSAO (photosystem I subunit O)	140	Ch/Th	9.77000046	15.1400003	PS PSI	1.1.2.2 PS.lightreaction.photosystem I.PSI polypeptide subunits		plastid	plastid	thylakoid-integral	2.0
AT1G08490	38	AT1G08490.1	ATCPNIFS/ATNFS2/ATNFS/CPNIFS/SUFS (CHLOROPLASTIC NIFS-LIKE CYSTEINE DESULFURASE); cysteine desulfurase/selenocysteine lyase/transaminase	463		6.21999979	50.4799995		14 S-assimilation	chloroplast	Y	C	plastid stroma	

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AT1G08520	39	AT1G08520.1	CHLD/PDE166 (PIGMENT DEFECTIVE 166); magnesium chelatase/nucleoside-triphosphatase/nucleotide binding	760	Ch/Th & Ch/S	5.26000023	83.2799988	metabolism vitamin and pigment	19.10 tetrapyrrole synthesis.magnesium chelatase	magnesium chelatase complex	plastid	plastid	plastid	
AT1G08530	40	AT1G08530.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G09995.3); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G09995.2); similar to unnamed protein product [Vitis vinifera] (GB:CAO70794.1)	257	Ch/E/IM	7.71999979	27.0100002	unknown	35.2 not assigned.unknown		plastid	plastid		1.0
AT1G08550	41	AT1G08550.1	NPQ1 (NON-PHOTOCHEMICAL QUENCHING 1)	462	Ch/Th	5.17999983	52.0099983	metabolism vitamin and pigment carotenoids	16.1.4.21 secondary metabolism.isoprenoids.carotenoids.violaxanthin de-epoxidase	thylakoid lumen (sensu Viridiplantae) & photosystem II (sensu Viridiplantae)			thylakoid-peripheral-lumenal-side	
AT1G08640	42	AT1G08640.1	heat shock protein binding	294	Ch/E/IM	9.81999969	32.9000015	chaperone and protease	26.29* misc.DnaJ domain with unknown function		plastid	plastid	envelope-inner-integral	3.0
AT1G09130	43	AT1G09130.1	ATP-dependent Clp protease proteolytic subunit, putative	330	Ch/E & Ch/S	8.63000011	36.2999992	chaperone and protease	29.5.5 protein.degradation.serine protease	mitochondrion & chloroplast stroma	plastid	plastid	plastid stroma	

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AT1G09200	44	AT1G09200.1	histone H3	136		11.29	15.2600002		28.1.3 DNA.synthesis/chromatin structure.hist one	chloroplast	Y	C	nucleus	
AT1G09310	45	AT1G09310.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G56580.1); similar to unknown [Populus trichocarpa] (GB:ABK94207.1); contains InterPro domain Protein of unknown function DUF538 (InterPro:IPR007493)	179		5.36000013	19.9400005		35.2 not assigned.unk nown	other (e.g. cytoplasm)			-	
AT1G09340	46	AT1G09340.1	CRB; binding / catalytic/ coenzyme binding	378	Ch/S ?? & Ch/Th ?? & Ch/E ??	8.18000031	42.6199989	RNA Binding	27 RNA				cytosol; plastid stroma	
AT1G09780	47	AT1G09780.1	2,3-biphosphoglycerate-independent phosphoglycerate mutase, putative / phosphoglyceromutase, putative	557		5.30999994	60.5800018		4.11 glycolysis.phosphoglycerate mutase	other (e.g. cytoplasm)			cytosol	
AT1G09795	48	AT1G09795.1	ATATP-PRT2 (ATP PHOSPHORIBOSYLTRANSFERASE 2); ATP phosphoribosyltransferase	413	Ch/S	6.34000015	44.75	metabolism amino acids Histidine	13.1.7.1 amino acid metabolism.synthesis.histidine.ATP phosphoribosyltransferase		plastid	plastid	plastid stroma	

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AT1G09830	49	AT1G09830.1	phosphoribosylamine--glycine ligase (PUR2)	532		5.5	56.4700012		23.1.2.2 nucleotide metabolism.synthesis.purine.GAR Synthetase	chloroplast	Y	C	plastid stroma		
AT1G10510	50	AT1G10510.1	EMB2004 (EMBRYO DEFECTIVE 2004); protein binding	605	Ch/E/IM	7.17999983	64.7200012	RNA metabolism?	33.99 development.unspecified	chloroplast envelope		plastid	plastid	plastid	1.0
AT1G10630	51	AT1G10630.1	ATARFA1F; GTP binding / phospholipase activator/protein binding	181	Ch/E ?	6.42000008	20.6200008	vesicular trafficking ?	29.3.4.99 protein.targeting.secretory pathway.unspecified	undefined		M	-		
AT1G10760	52	AT1G10760.1	SEX1 (STARCH EXCESS 1)	1399	Ch/S	5.6500001	156.580002	metabolism carbon	2.2.2.3 major CHO metabolism.degradation.starch.glucan water dikinase	mitochondrion		plastid	plastid stroma		
AT1G11320	53	AT1G11320.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO60944.1)	424	Ch/E ?	6.53999996	46.8899994	unknown	35.2 not assigned.unknown	undefined			-		
AT1G11430	54	AT1G11430.1	plastid developmental protein DAG, putative	232	Ch/S & Ch/Th	8.98999977	26.2000008	RNA editing	27.1.5* RNA.editing			plastid	plastid	plastid stroma	
AT1G11720	55	AT1G11720.1	ATSS3 (STARCH SYNTHASE 3); starch synthase/transferase, transferring glycosyl groups	1025	Ch/S	5.94999981	116.410004	starch biosynthesis	2.1.2.2 major CHO metabolism.synthesis.starch.starch synthase			plastid	mitochondrion	plastid stroma	
AT1G11750	56	AT1G11750.1	CLPP6 (Clp protease proteolytic subunit 6); endopeptidase Clp	271	Ch/S & Ch/E	9.36999989	29.3799992	chaperone and protease	29.5.5 protein.degradation.serine protease			plastid	plastid	plastid stroma	

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AT1G11860	57	AT1G11860.1	aminomethyl transferase, putative	408	Ch/Th & Ch/S	8.55000019	44.4399986	unknown	13.2.5.2 amino acid metabolism. degradation. serine-glycine-cysteine group.glycine				mitochondrion	not plastid	
AT1G11870	58	AT1G11870.1	AtSRS (OVULE ABORTION 7); serine-tRNA ligase	512		6.48999977	57.1800003		29.1.11 protein.aa activation.serine-tRNA ligase	undefined	Y	M	mitochondria ; plastid stroma		
AT1G11930	59	AT1G11930.1	alanine racemase family protein	257		5.11000013	28.0		35.1 not assigned.no ontology	other (e.g. cytoplasm)			not plastid		
AT1G12230	60	AT1G12230.1	transaldolase, putative	405	Ch/E & Ch/S & Ch/Th	6.40999985	43.9900017	metabolism carbon	7.2.2 OPP.non-reductive PP.transaldolase		plastid	plastid	plastid stroma		
AT1G12250	61	AT1G12250.1	thylakoid luminal protein-related	280	Ch/Th	8.72000027	30.0599995	RNA Binding ?	27.7* RNA.misc.pentatricopeptide (PPR) repeat-containing protein		plastid	plastid	thylakoid-peripheral-luminal-side		
AT1G12410	62	AT1G12410.1	CLPR2 (Clp protease proteolytic subunit 2); endopeptidase Clp	279	Ch/S & Ch/E	9.18999958	31.2000008	chaperone and protease	29.5.5 protein.degradation.serine protease	chloroplastic endopeptidase Clp complex & chloroplast stroma & thylakoid (sensu Viridiplantae)	plastid	plastid	plastid stroma		
AT1G12520	63	AT1G12520.1	CCS1 (copper chaperone for superoxide dismutase 1); superoxide dismutase copper chaperone	320		4.92999983	27.1900005		15.2 metal handling.binding, chelation and storage	chloroplast	Y		plastid stroma		

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AT1G12770	64	AT1G12770.1	EMB1586 (EMBRYO DEFECTIVE 1586)	551		9.28999996	60.7099991		27.5* RNA.DEAD/DEAH BOX helicase	undefined		M	-	
AT1G12800	65	AT1G12800.1	S1 RNA-binding domain-containing protein	767	Ch/S & Ch/Th	5.30000019	85.6600037	RNA Binding ?	27.3.23 RNA.regulation of transcription. HSF,Heat-shock transcription factor family		plastid	plastid	plastid stroma	
AT1G12840	66	AT1G12840.1	DET3 (DE-ETIOLATED 3)	375	na	5.4000001	42.6199989	transporter ATPase	34.1 transport.p-and v-ATPases	plasma membrane & hydrogen-transporting ATPase V1 domain		mitochondrion	vacuole	
AT1G12900	67	AT1G12900.1	GAPA-2; glyceraldehyde-3-phosphate dehydrogenase	399	Ch/S & Ch/E	8.14999962	42.8400002	metabolism carbon Calvin cycle	1.3.4 PS.calvin cycle.GAP		plastid	plastid	plastid stroma	
AT1G13270	68	AT1G13270.1	MAP1C (METHIONINE AMINOPEPTIDASE 1B); metalloexopeptidase	369	Ch/Th	7.13999987	40.4199982	chaperone and protease ?	29.5.7 protein.degradation.metall oprotease	mitochondrion & chloroplast	plastid	plastid	mitochondria ; plastid stroma	
AT1G13280	69	AT1G13280.1	AOC4 (ALLENE OXIDE CYCLASE 4)	254		9.14999962	27.8099995		17.7.1.4 hormone metabolism.j asmonate.synthesis-degradation. allene oxidase cyclase	chloroplast	Y	C	plastid stroma	
AT1G13440	70	AT1G13440.1	GAPC-2; glyceraldehyde-3-phosphate dehydrogenase	338		6.67000008	36.9099998		4.9 glycolysis.gly ceraldehyde 3-phosphate dehydrogenase	undefined			not plastid	

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AT1G13930	71	AT1G13930.1	similar to nodulin-related [Arabidopsis thaliana] (TAIR:AT2G03440.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN63832.1)	155	Ch & other	4.8200017	16.1599998	unknown	20.2.3 stress.abiotic.drought/salt	undefined			-	
AT1G14030	72	AT1G14030.1	ribulose-1,5 bisphosphate carboxylase oxygenase large subunit N-methyltransferase, putative	482	Ch/S	5.0100023	54.6100006	metabolism carbon Calvin cycle	1.3.13 PS.calvin cycle.rubisco interacting		plastid	plastid	plastid stroma	
AT1G14150	73	AT1G14150.1	oxygen evolving enhancer 3 (PsbQ) family protein	190	Ch/Th	8.7899996	22.1499996	PS PSII OEE or NDH ?	1.1.6 PS.lightreaction.NADH DH	thylakoid membrane (sensu Viridiplantae) & thylakoid lumen (sensu Viridiplantae)	plastid	plastid	thylakoid-peripheral-lumenal-side	
AT1G14345	74	AT1G14345.1	oxidoreductase	196	Ch/Th	9.8100042	21.2199993	redox ?	35.2 not assigned.unknown	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	thylakoid-integral	1.0
AT1G14410	75	AT1G14410.1	ATWHY1/PTAC1 (A. THALIANA WHIRLY 1); DNA binding / telomeric DNA binding	263	Ch/S	9.3800011	29.0499992	DNA Binding	27.3.67 RNA.regulation of transcription.putative transcription regulator	plastid chromosome & chloroplast	plastid	plastid	plastid stroma	1.0
AT1G14810	76	AT1G14810.1	semialdehyde dehydrogenase family protein	375	Ch/S	6.5199998	40.7400017	metabolism aa Asp	13.1.3.6.1.2 amino acid metabolism.synthesis.aspartate family.misc.homoserine.aspartate semialdehyde dehydrogenase	mitochondrion	plastid	plastid	plastid stroma	

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AT1G15140	77	AT1G15140.1	oxidoreductase NAD-binding domain-containing protein	295	Ch/S	7.78999996	31.9200001	redox	26.7 misc.oxidases - copper, flavone etc.		plastid	plastid	plastid stroma		
AT1G15390	78	AT1G15390.1	PDF1A (PEPTIDE DEFORMYLASE 1A); peptide deformylase	269		8.60000038	29.9899998		29.4 protein.posttranslational modification	undefined	Y	C	plastid; mitochondria		
AT1G15500	79	AT1G15500.1	ATNTT2; ATP:ADP antiporter	618	Ch/E/IM	9.51000023	67.5299988	transporter ATP/ADP	34.8 transport.metabolite transporters at the envelope membrane	cytoplasm	plastid	mitochondrion	envelope-inner-integral	11.0	
AT1G15690	80	AT1G15690.1	AVP1 (vacuolar-type H ⁺ -pumping pyrophosphatase 1); ATPase	770	na	5.11999989	80.8199997	transporter ATPase	23.4.99 nucleotide metabolism.phosphotransfer and pyrophosphatases.misc				extracellular, endoplasmic reticulum, golgi	plasma membrane; vacuole-tonoplast	
AT1G15730	81	AT1G15730.1	PRLI-interacting factor L, putative	448		5.25	50.25		31.1 cell.organisation	undefined	Y	C	plastid		
AT1G15820	82	AT1G15820.1	LHCB6 (LIGHT HARVESTING COMPLEX PSII); chlorophyll binding	258	Ch/Th	6.75	27.5200005	PS LHCII	1.1.1.1 PS.lightreaction.photosystem II.LHC-II	thylakoid membrane (sensu Viridiplantae)	plastid	mitochondrion	thylakoid-integral	2.0	

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AT1G15980	83	AT1G15980.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO49411.1); contains domain G3DSA:3.40.50.2000 (G3DSA:3.40.50.2000); contains domain SSF53756 (SSF53756)	461	Ch/Th	6.48999977	51.0200005	NDH	1.1.6 PS.lightreaction.NADH DH		plastid	plastid	thylakoid	
AT1G16080	84	AT1G16080.1	similar to unknown [Populus trichocarpa] (GB:ABK94042.1)	313	Ch/S	6.38000011	34.1300011	unknown	35.2 not assigned.unknown		plastid	plastid	plastoglobules	
AT1G16720	85	AT1G16720.1	HCF173 (HIGH CHLOROPHYLL FLUORESCENCE PHENOTYPE 173); binding / catalytic/ oxidoreductase/ transcription repressor	598	Ch/S	9.14000034	65.6999969	chaperone and protease or translation PSII ?	29.2.99 protein.synthesis.misc		plastid	plastid	plastid	
AT1G16790	86	AT1G16790.1	ribosomal protein-related	144	Ch/E ??	9.55000019	15.4499998	translation stroma	29.2.1.99.99 protein.synthesis.ribosomal protein.unknown	thylakoid membrane (sensu Viridiplantae)			plastid	
AT1G16880	87	AT1G16880.1	uridylyltransferase-related	290	Ch/S & Ch/E	4.96999979	31.2900009	metabolism carbon	3.8.3 minor CHO metabolism.galactose.galactose-1-phosphate uridylyl transferases	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	plastid stroma; thylakoid-peripheral-stromal-side	

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AT1G17050	88	AT1G17050.1	SPS2 (SOLANESYL DIPHOSPHATE SYNTHASE 2); dimethylallyl transferase/ trans-octaprenyl transferase	417		5.4400006	46.0400009		16.1.1 secondary metabolism. isoprenoids. non-mevalonate pathway	undefined	Y	C	plastid stroma	
AT1G17160	89	AT1G17160.1	pfkB-type carbohydrate kinase family protein	379		6.1100013	40.1899986		3.5 minor CHO metabolism. others	chloroplast	Y	C	-	
AT1G17220	90	AT1G17220.1	FUG1 (FUGAERI1); translation initiation factor	1026	Ch/S	7.1399987	109.739998	translation stroma	29.2.3 protein synthesis. initiation		plastid	plastid	plastid stroma	
AT1G17580	91	AT1G17580.1	MYA1 (ARABIDOPSIS MYOSIN); motor/protein binding	1520	Ch/E ?	8.5600042	172.910004	plastid positioning ?	31.1 cell organization	undefined			-	
AT1G17650	92	AT1G17650.1	phosphoglucuronate dehydrogenase (decarboxylating)	358	Ch/S	8.6800031	37.7799988	metabolism carbon	7.1.3 OPP. oxidative PP. 6-phosphoglucuronate dehydrogenase		plastid	plastid	plastid stroma	
AT1G17745	93	AT1G17745.1	PGDH (3-PHOSPHOGLYCERATE DEHYDROGENASE); phosphoglycerate dehydrogenase	624	Ch/S	5.8000019	66.4499969	metabolism aa serine	13.1.5.1.1 amino acid metabolism. synthesis. serine-glycine-cysteine group. serine. phosphoglycerate dehydrogenase		plastid	plastid	plastid stroma	

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AT1G18060	94	AT1G18060.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO68142.1)	226	Ch/Th ?	9.67000008	25.1900005	unknown	35.2 not assigned.unkn own		plastid	plastid	thylakoid-peripheral-stromal-side	
AT1G18170	95	AT1G18170.1	immunophilin / FKBP-type peptidyl-prolyl cis-trans isomerase family protein	247	Ch/Th	8.96000004	26.5300007	chaperone and protease	29.6 protein.foldin g	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	thylakoid-lumenal-side	1.0
AT1G18360	96	AT1G18360.1	hydrolase, alpha/beta fold family protein	382	Ch/E/IM	9.60999966	41.9599991	metabolism lipid	35.1 not assigned.no ontology	chloroplast	Y	C	-	
AT1G18500	97	AT1G18500.1	IPMS1/MAM L-4 (METHYLTH IOALKYLMALATE SYNTHASE-LIKE 4); 2-isopropylmalate synthase	631	Ch/S	6.1500001	68.6699982	metabolism amino acids branched chain	13.1.4.4.1 amino acid metabolism.s ynthesis.bra nched chain group.leucin e specific.2-isopropylmalate synthase		plastid	plastid	plastid stroma	
AT1G18640	98	AT1G18640.1	PSP (3-PHOSPHOS ERINE PHOSPHAT ASE)	295	Ch/S	6.03999996	32.3100014	metabolism aa serine	13.1.5.1.3 amino acid metabolism.s ynthesis.serine-glycine-cysteine group.serine.phosphoseri ne phosphatase	chloroplast		plastid	plastid	
AT1G19740	99	AT1G19740.1	ATP-dependent protease La (LON) domain-containing protein	278		8.28999996	31.3700008		29.5.5 protein.degra dation.serine protease	chloroplast	Y	C	-	
AT1G19800	100	AT1G19800.1	TGD1 (TRIGALAC TOSYLDIAC YLGLYCER OL 1)	350	Ch/E/IM	9.0	37.9000015	transporter lipids	11.15* lipid metabolism.t ransport	chloroplast outer membrane & chloroplast envelope & chloroplast inner membrane			envelope-inner-integral	5.0

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AT1G19910	101	AT1G19910.1	AVA-P2 (vacuolar-H ⁺ -pumping ATPase 16 kDa proteolipid subunit 2); ATPase	165	other	8.60999966	16.6399994	transporter ATPase	34.1.1 transport.p- and v-ATPases.H ⁺ -transporting two-sector ATPase	secreted	Y	S	-	3.0
AT1G19920	102	AT1G19920.1	APS2 (ATP SULFURYLASE PRECURSOR)	476		6.13999987	53.6300011		14.1 S-assimilation. APS	chloroplast	Y	C	-	
AT1G20010	103	AT1G20010.1	TUB5 (tubulin beta-5 chain)	449		4.65999985	50.3400002		31.1 cell.organisation	other (e.g. cytoplasm)			-	
AT1G20020	104	AT1G20020.1	ATLFNR2 (LEAF FNR 2); NADPH dehydrogenase/oxidoreductase/ poly(U) binding	369	Ch/S & Ch/Th	8.5	41.1599998	redox	1.1.7 PS.lightreaction.ferredoxin reductase	thylakoid membrane (sensu Viridiplantae) & chloroplast stroma	plastid	plastid	thylakoid-peripheral-stromal-side	
AT1G20340	105	AT1G20340.1	DRT112 (DNA-damage-repair/tolerance protein 112); copper ion binding / electron carrier	167	Ch/Th & Ch/S & Ch/E	5.05999994	16.9799995	PS b6/f PSI electron transfer	1.1.5.1 PS.lightreaction.other electron carrier (ox/red).plastocyanin	thylakoid lumen (sensu Viridiplantae)	plastid	plastid	thylakoid-peripheral-lumenal-side	1.0
AT1G20440	106	AT1G20440.1	COR47 (cold regulated 47)	265		4.75	29.8899994		20.2.99 stress.abiotic.unspecified	other (e.g. cytoplasm)			-	
AT1G20450	107	AT1G20450.1	ERD10/LTI45 (EARLY RESPONSIVE TO DEHYDRATION 10)	260		5.11000013	29.5400009		20.2.99 stress.abiotic.unspecified	other (e.g. cytoplasm)			-	
AT1G20620	108	AT1G20620.1	CAT3 (CATALASE 3); catalase	492	na	7.30999994	56.6899986	stress oxidative	21.6 redox.dismutases and catalases	mitochondrion & peroxisome			peroxisome	

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AT1G20816	109	AT1G20816.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G76405.2); similar to unnamed protein product [Vitis vinifera] (GB:CAO66270.1)	167	Ch/E/OM	9.51000023	19.7800007	transporter ion channel	35.2 not assigned.unknown					
AT1G20830	110	AT1G20830.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO66272.1)	349	Ch/E/IM	9.09000015	39.4099998	unknown	31.2.5 cell.division.plastid; 35.2 not assigned.unknown	chloroplast	Y	C	envelope-inner	1.0
AT1G21200	111	AT1G21200.1	transcription factor	443		5.88000011	50.9300003		27.3.30 RNA.regulation of transcription. Trihelix, Triple-Helix transcription factor family	undefined			-	
AT1G21440	112	AT1G21440.1	mutase family protein	336	Ch/S	6.67000008	36.2999992	metabolism carbon ?	35.2 not assigned.unknown		plastid	plastid	plastid stroma	

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AT1G21500	113	AT1G21500.1	similar to hypothetical protein Osl_030994 [Oryza sativa (indica cultivar-group)] (GB:EAZ09762.1); similar to Os09g0517000 [Oryza sativa (japonica cultivar-group)] (GB:NP_001063677.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)]	126	Ch/E ?	10.6499996	13.25	unknown	35.2 not assigned.unknown	chloroplast	Y	C	-	
AT1G21650	114	AT1G21650.1	ATP binding	1579	Ch/E ?	5.38999987	177.639999	protein targeting ?	29.3.3 protein.targeting.chloroplast	chloroplast			-	
AT1G22700	115	AT1G22700.1	tetratricopeptide repeat (TPR)-containing protein	301	Ch/Th	9.40999985	33.6599998	chaperone and protease ?	29.8 protein assembly and cofactor ligation			plastid	thylakoid-integral	
AT1G22740	116	AT1G22740.1	RAB7 (Ras-related protein 7); GTP binding	203	Ch/E ?	5.28000021	22.9400005	signalling / SNARE effector	30.5 signalling.G-proteins	undefined		M	-	
AT1G22780	117	AT1G22780.1	PFL (POINTED FIRST LEAVES); structural constituent of ribosome	152	Ch/E & other	10.5299997	17.5400009	translation cytosol	29.2.1.2.1.18 protein.synthesis.ribosomal protein.eukaryotic.40S subunit.S18	undefined			cytosol	

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AT1G22940	118	AT1G22940.1	TH1 (THIAMINE REQUIRING 1); catalytic/ phosphomet hylpyrimidine kinase/ thiamin- phosphate diphosphoryl ase	522		6.0999999	55.8100014		18.2.2 Co- factor and vitamine metabolism.t hiamine.hydr oxymethylpyr imidine kinase	undefined	Y	M	-	
AT1G23180	119	AT1G23180.1	armadillo/bet a-catenin repeat family protein	834		5.32999992	91.6900024		35.1.3 not assigned.no ontology.arm adillo/beta- catenin repeat family protein	undefined		C	plastid	
AT1G23190	120	AT1G23190.1	phosphogluc omutase, cytoplasmic, putative / glucose phosphomut ase, putative	583		5.90999985	63.1699982		4.2 glycolysis.P GM	other (e.g. cytoplasm)	Y		-	
AT1G23310	121	AT1G23310.1	GGT1 (ALANINE-2- OXOGLUTA RATE AMINOTRA NSFERASE 1)	481		6.48999977	53.2999992		1.2.3 PS.aminotra nsferases peroxisomal	other (e.g. cytoplasm)			peroxisome	
AT1G23730	122	AT1G23730.1	carbonic anhydrase, putative / carbonate dehydratase, putative	258	other	6.53000021	28.8199997	metabolism carbon	8.3 TCA / org.transfor mation.carbo nic anhydrases	other (e.g. cytoplasm)			cytosol	
AT1G23740	123	AT1G23740.1	oxidoreducta se, zinc- binding dehydrogena se family protein	386	Ch/S	8.46000004	40.9799995	redox ?	26.7 misc.oxidase s - copper, flavone etc.		plastid	plastid	plastid stroma	
AT1G24040	124	AT1G24040.1	GCN5- related N- acetyltransfe rase (GNAT) family protein	319	Ch/E	6.46999979	36.0200005	unknown	26.24 misc.GCN5- related N- acetyltransfe rase		plastid	plastid		

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AT1G24360	125	AT1G24360.1	3-oxoacyl-(acyl-carrier protein) reductase, chloroplast / 3-ketoacyl-acyl carrier protein reductase	319	Ch/S & Ch/Th & Ch/E	9.4499981	33.5400009	metabolism lipid	11.1.4 lipid metabolism. FA synthesis and FA elongation. ACP oxoacyl reductase		plastid	plastid	plastid stroma	
AT1G25290	126	AT1G25290.1	rhomboid family protein	343	Ch/E/IM	10.79	38.2200012	chaperone and protease	29.5.5 protein.degradation.serine protease	undefined		C	golgi	3.0
AT1G25375	127	AT1G25375.1	metallo-beta-lactamase family protein	524	Ch/E	6.5199998	58.0600014	hydrolase ?	35.1 not assigned.no ontology	other (e.g. cytoplasm)			-	1.0
AT1G26230	128	AT1G26230.1	chaperonin, putative	611	Ch/E ?	9.22000027	66.7900009	chaperone and protease	29.6 protein.foldin g	chloroplast	Y	C	plastid	
AT1G26340	129	AT1G26340.1	B5 #6 (cytochrome b5 family protein #6); heme binding / transition metal ion binding	135	Ch/E & other	4.48999977	15.2200003	metabolism lipid	21.3 redox.heme	other (e.g. cytoplasm)			envelope	1.0
AT1G26630	130	AT1G26630.1	FBR12 (FUMONISIN B1-RESISTANT 12); translation initiation factor	159	Ch/Th	5.53999996	17.1399994	translation	29.2.3 protein.synthesis.initiation				not plastid	
AT1G27400	131	AT1G27400.1	60S ribosomal protein L17 (RPL17A)	176	Ch/E & other	10.1099997	19.8899994	translation cytosol	29.2.1.2.2.17 protein.synthesis.ribosomal protein.eukaryotic.60S subunit.L17	other (e.g. cytoplasm)			cytosol	
AT1G27450	132	AT1G27450.1	APT1; adenine phosphoribosyltransferase	243	Ch/S	8.64999962	26.3899994	metabolism nucleotide	23.3.1.1 nucleotide metabolism.s alvage.phosphoribosyltransferases.aprt	cytosol & cell wall (sensu Magnoliophyta)	plastid	plastid	cytosol	

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AT1G27900	133	AT1G27900.1	RNA helicase, putative	700		8.18999958	78.3700027		27.1.2 RNA.processing.RNA helicase	undefined			-	
AT1G28140	134	AT1G28140.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO68697.1)	280	Ch/Th	8.51000023	30.2700005	unknown	35.2 not assigned.unknown		plastid	mitochondrion	plastid	6.0
AT1G28530	135	AT1G28530.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO66376.1)	614	Ch/E/IM	7.98999977	68.4499969	transporter ABC ?	35.2 not assigned.unknown	chloroplast	Y	C	-	1.0
AT1G29670	136	AT1G29670.1	GDSL-motif lipase/hydrolase family protein	363	Ch/Th	8.84000015	39.8699989	unknown	26.28 misc.GDSL-motif lipase			extracellular, endoplasmic reticulum, golgi	not plastid	
AT1G29700	137	AT1G29700.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO42101.1); contains domain SSF56281 (SSF56281)	350	Ch/E & Ch/S	5.82999992	38.1500015	unknown	35.2 not assigned.unknown		plastid	plastid	plastid	
AT1G29840	138	AT1G29840.1	esterase/lipase/thioesterase family protein	263		5.86999989	29.5599995		35.1 not assigned.no ontology	undefined			-	
AT1G29900	139	AT1G29900.1	CARB (CARBAMOYL PHOSPHATE SYNTHETASE B); ATP binding / carbamoyl-phosphate synthase	1187		5.53000021	129.949997				Y	C	plastid stroma	

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AT1G29910	140	AT1G29910.1	CAB3 (CHLOROPHYLL A/B BINDING PROTEIN 3); chlorophyll binding	267	Ch/Th & other	5.28000021	28.2199993	PS LHC	1.1.1.1 PS.lightreaction.photosystem II.LHC-II	chloroplast	Y	C	thylakoid-integral	2.0
AT1G29930	141	AT1G29930.1	CAB1 (CHLOROPHYLL A/B BINDING PROTEIN 1); chlorophyll binding	267	Ch/Th	5.46000004	28.2399998	PS LHCII	1.1.1.1 PS.lightreaction.photosystem II.LHC-II	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	thylakoid-integral	2.0
AT1G30120	142	AT1G30120.1	PDH-E1 BETA (PYRUVATE DEHYDROGENASE E1 BETA); pyruvate dehydrogenase (acetyl-transferring)	406	Ch/E/IM	5.90999985	44.2400017	metabolism lipid	11.1.31 lipid metabolism. FA synthesis and FA elongation.pyruvate DH	chloroplast	Y	C	-	
AT1G30380	143	AT1G30380.1	PSAK (PHOTOSYSTEM I SUBUNIT K)	130	Ch/Th	10.5100002	13.1999998	PS PSI	1.1.2.2 PS.lightreaction.photosystem I.PSI polypeptide subunits	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	thylakoid-integral	2.0
AT1G30410	144	AT1G30410.1	ATMRP13 (Arabidopsis thaliana multidrug resistance-associated protein 13)	1495		8.39999962	167.949997		34.16 transport.ABC transporters and multidrug resistance systems	other (e.g. cytoplasm)			-	13.0
AT1G30510	145	AT1G30510.3	ATRFNR2 (ROOT FNR 2); oxidoreductase	381		8.77000046	42.6599998		7.3 OPP.electron transfer	chloroplast	Y	C	-	
AT1G31160	146	AT1G31160.1	zinc-binding protein, putative / protein kinase C inhibitor, putative	187		9.22000027	20.3999996		29.4.2* protein.posttranslational modification. kinase inhibitor	undefined	Y	C	-	

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AT1G31180	147	AT1G31180.1	3-isopropylmalate dehydrogenase, chloroplast, putative	404	Ch/S	5.5999999	43.8400002	metabolism amino acids branched chain	13.1.4.4.3 amino acid metabolism.synthesis.branched chain group.leucine specific.3-isopropylmalate dehydrogenase			mitochondrion	plastid stroma	
AT1G31190	148	AT1G31190.1	inositol monophosphatase family protein	371		6.76000023	40.4399986		3.4.5 minor CHO metabolism.myo-inositol.inositol phosphatase	chloroplast	Y	C	plastid stroma	
AT1G31220	149	AT1G31220.1	phosphoribosylglycinamide formyltransferase	292		8.92000008	32.1699982		23.1.2.3 nucleotide metabolism.synthesis.purine.GAR transformylase	chloroplast	Y	C	-	
AT1G31230	150	AT1G31230.1	AK-HSDH/AK-HSDH I (ASPARTATE KINASE-HOMOSERINE DEHYDROGENASE I); aspartate kinase/homoserine dehydrogenase	911		6.32999992	99.4000015				Y	C	plastid stroma	
AT1G31330	151	AT1G31330.1	PSAF (photosystem I subunit F)	221	Ch/Th & Ch/E	9.56999969	24.1700001	PS PSI	1.1.2.2 PS.lightreaction.photosystem I.PSI polypeptide subunits	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	thylakoid-integral	2.0
AT1G31410	152	AT1G31410.1	putrescine-binding periplasmic protein-related	524	Ch/E/IM	9.19999981	58.2900009	transporter solute binding ?	35.1 not assigned.no ontology	chloroplast		C	-	

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AT1G31800	153	AT1G31800.1	CYP97A3/LUT5 (CYTOCHROME P450-TYPE MONOOXYGENASE 97A3); carotene beta-ring hydroxylase/oxygen binding	595	Ch/E/IM	5.80999994	66.8399963	cytochrome P450	26.10 misc.cytochrome P450		plastid	plastid	plastid	
AT1G31860	154	AT1G31860.1	AT-IE (Arabidopsis thaliana bifunctional HisI-HisE protein)	281		5.88999987	31.6599998		13.1.7.2 amino acid metabolism.synthesis.histidine.phosphoribosyl-ATP diphosphatase	undefined	Y	M	plastid stroma	
AT1G32060	155	AT1G32060.1	PRK (PHOSPHORIBULOKINASE); ATP binding / phosphoribulokinase/protein binding	395	Ch/S	5.69999981	44.4599991	metabolism carbon Calvin cycle	1.3.12 PS.calvin cycle.PRK	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	plastid stroma	
AT1G32080	156	AT1G32080.1	membrane protein, putative	512	Ch/E/IM	9.63000011	54.0099983	transporter ?	34.8 transport.metabolite transporters at the envelope membrane	chloroplast inner membrane	plastid	plastid	envelope-inner-integral	12.0

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AT1G32160	157	AT1G32160.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G17800.1); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G17800.2); similar to unnamed protein product [Vitis vinifera] (GB:CAO63331.1); contains InterPro domain Protein of unkno	406		5.53000021	45.8600006		35.2 not assigned.unknown	chloroplast	Y	C	-	
AT1G32200	158	AT1G32200.1	ATS1 (ACYLTRANSFERASE 1)	459		6.11000013	50.4199982		11.3.1 lipid metabolism. Phospholipid synthesis.1-acylglycerol-3-phosphate O-acyltransferase	undefined	Y	C	plastid stroma	
AT1G32220	159	AT1G32220.1	binding / catalytic/coenzyme binding	296	Ch/S	5.55999994	31.9699993	unknown	35.2 not assigned.unknown		plastid	plastid	plastoglobules	
AT1G32500	160	AT1G32500.1	ATNAP6 (NON-INTRINSIC ABC PROTEIN 6); protein binding	475		5.65999985	52.8199997		14 S-assimilation	chloroplast	Y	C	plastid stroma	
AT1G32550	161	AT1G32550.1	ferredoxin family protein	181	Ch/E & Ch/S	5.57000017	20.3700008	PS redox	1.1.5.2 PS.lightreaction.other electron carrier (ox/red).ferredoxin		plastid	plastid	plastid	

Accession	pgID	Master Protein	Description (curated)	Length	Localization (curated)	Calculated Pi PPDB	Calculated MW PPDB	Function (putative)	MapManBin (PPDB)	Localization (TAIR)	ChloroP	TargetP	Curated localization (PPDB)	Aramemnon
AT1G32900	162	AT1G32900.1	starch synthase, putative	610	Ch/Th	8.7600023	66.8799973	metabolism starch	2.1.2.2 major CHO metabolism.synthesis.starch.starch synthase		plastid	plastid	plastid stroma	
AT1G32990	163	AT1G32990.1	PRPL11 (PLASTID RIBOSOMAL PROTEIN L11); structural constituent of ribosome	222	Ch/S & Ch/Th & Ch/E	9.6800031	23.1399994	translation stroma	29.2.1.1.1.2.11 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.50S subunit.L11	cytosolic ribosome (sensu Eukaryota)	plastid	plastid	plastid ribosome	
AT1G33780	164	AT1G33780.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G29240.2); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G29240.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN64828.1); contains InterPro domain Protein of unknown	325		6.61999989	36.3899994		35.1 not assigned.no ontology	chloroplast	Y	C	-	
AT1G33810	165	AT1G33810.1	similar to unknown [Populus trichocarpa] (GB:ABK94119.1)	138	Ch/E ?? & Ch/Th ??	8.81999969	15.6899996	unknown	35.2 not assigned.unknown	thylakoid membrane (sensu Viridiplantae)			thylakoid	
AT1G34000	166	AT1G34000.1	OHP2 (ONE-HELIX PROTEIN 2)	172	Ch/Th	9.43000031	18.6599998	PS PSII stress oxidative	1.1.8* light stress chlorophyll binding	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	thylakoid-integral	

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AT1G34430	167	AT1G34430.1	EMB3003 (EMBRYO DEFECTIVE 3003); dihydrolipoyl lysine-residue acetyltransferase	465	Ch/E & Ch/Th & Ch/S	8.80000019	48.2999992	metabolism lipid	11.1.31 lipid metabolism. FA synthesis and FA elongation.p yruvate DH		plastid	plastid	envelope-inner-peripheral-stromal-side	
AT1G35340	168	AT1G35340.1	ATP-dependent protease La (LON) domain-containing protein	316		8.53999996	32.8199997		29.5 protein.degradation	chloroplast	Y	C	-	
AT1G35420	169	AT1G35420.1	dienelactone hydrolase family protein	310		5.26999998	34.1599998		35.2 not assigned.unkn own	chloroplast	Y	C	plastid stroma	
AT1G35680	170	AT1G35680.1	50S ribosomal protein L21, chloroplast / CL21 (RPL21)	220	Ch/S & Ch/E	9.31000042	24.0300007	translation stroma	29.2.1.1.1.2.21 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.50S subunit.L21		plastid	plastid	plastid ribosome	
AT1G35720	171	AT1G35720.1	ANNAT1 (ANNEXIN ARABIDOPSIS 1); calcium ion binding / calcium-dependent phospholipid binding	317		5.21000004	36.2000008		31.1 cell.organisation	other (e.g. cytoplasm)			plastid	
AT1G35730	172	AT1G35730.1	APUM9 (ARABIDOPSIS PUMILIO 9); RNA binding	564		8.28999996	63.25		35.1.12 not assigned.no ontology.pumilio/Puf RNA-binding domain-containing protein	other (e.g. cytoplasm)			-	
AT1G36280	173	AT1G36280.1	adenylosuccinate lyase, putative / adenylosuccinase, putative	527		7.0	58.8100014		23.1.2.8 nucleotide metabolism.synthesis.purine.SAICAR lyase	chloroplast	Y	C	plastid stroma	

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AT1G36390	174	AT1G36390.1	co-chaperone grpE family protein	279		9.43000031	31.2199993		29.6 protein.folding	chloroplast	Y	C	plastid stroma	
AT1G42960	175	AT1G42960.1	expressed protein localized to the inner membrane of the chloroplast.	168	Ch/E/IM	8.53999996	17.8199997	unknown	35.2 not assigned.unknown	thylakoid membrane (sensu Viridiplantae) & chloroplast inner membrane	plastid	plastid	thylakoid	1.0
AT1G42970	176	AT1G42970.1	GAPB (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE B SUBUNIT); glyceraldehyde-3-phosphate dehydrogenase	447	Ch/S & Ch/E	6.32999992	47.6599998	metabolism carbon Calvin cycle	1.3.4 PS.calvin cycle.GAP	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	plastid stroma	
AT1G43560	177	AT1G43560.1	ATY2 (Arabidopsis thioredoxin y2); thiol-disulfide exchange intermediate	167		8.43999958	18.5900002		21.1 redox.thioredoxin	chloroplast	Y	C	plastid stroma	
AT1G43670	178	AT1G43670.1	fructose-1,6-bisphosphatase, putative / D-fructose-1,6-bisphosphate 1-phosphohydrolase, putative / FBPase, putative	341		5.26999998	37.2799988		2.1.1.3 major CHO metabolism.synthesis.sucrose.FBPase	other (e.g. cytoplasm)			-	
AT1G44318	179	AT1G44318.1	HEMB2; porphobilinogen synthase	406		8.38000011	44.8699989		19.4 tetrapyrrole synthesis.AL A dehydratase	undefined	Y		-	

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AT1G44575	180	AT1G44575.1	NPQ4 (NONPHOTOCHEMICAL QUENCHING)	265	Ch/Th	9.23999977	28.0	PS PSII NPQ	1.1.1.2 PS.lightreaction.photosystem II.PSII polypeptide subunits	thylakoid membrane (sensu Viridiplantae) & PSII associated light-harvesting complex II	plastid	plastid	thylakoid-integral	4.0
AT1G44920	181	AT1G44920.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO61509.1)	258	Ch/E/IM	10.0299997	27.7099991	unknown	35.2 not assigned.unknown		plastid	plastid	plastid	4.0
AT1G45474	182	AT1G45474.1	LHCA5 (Photosystem I light harvesting complex gene 5)	256	Ch/Th	6.6500001	27.7999992	PS LHCI	1.1.2.1 PS.lightreaction.photosystem I.LHC-I	photosystem I antenna complex		mitochondrion	thylakoid-integral	
AT1G47900	183	AT1G47900.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G19835.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO48232.1); similar to hypothetical protein Osl_010472 [Oryza sativa (indica cultivar-group)] (GB:EAY89239.1); similar to h	1054		4.88999987	118.540001		35.2 not assigned.unknown	undefined			-	

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AT1G48030	184	AT1G48030.1	dihydrolipoamide dehydrogenase 1, mitochondrial / lipoamide dehydrogenase 1 (MTLPD1)	507		6.9499981	53.9799995		8.1.1.3 TCA / org.transformation.TCA.pyruvate DH.E3	mitochondrion	Y	M	mitochondria	
AT1G48350	185	AT1G48350.1	ribosomal protein L18 family protein	170	Ch/S	9.9200008	18.7199993	translation stroma	29.2.1.1.1.2.18 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.50S subunit.L18		plastid	plastid	plastid ribosome	
AT1G48420	186	AT1G48420.1	D-CDES (D-CYSTEINE DESULFHYDRASE); 1-aminocyclopropane-1-carboxylate deaminase/ D-cysteine desulfhydrase/ catalytic	401		6.8699989	43.9000015		17.5.1 hormone metabolism. ethylene.synthesis-degradation	undefined		M	plastid	
AT1G48460	187	AT1G48460.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G63040.2); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G63040.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO61244.1)	340	Ch/E/IM	9.6800031	38.0699997	transporter ion channel ?	35.2 not assigned.unknown		plastid	plastid	envelope	5.0

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AT1G48520	188	AT1G48520.1	GATB (GLU-ADT SUBUNIT B); glutamyl-tRNA synthase (glutamine-hydrolyzing)	550		7.5100023	60.9399986		29.1.50* protein.aa activation.glutamate-tRNA amidotransferase	mitochondrion	Y	M	mitochondria ; plastid stroma	
AT1G48850	189	AT1G48850.1	EMB1144 (EMBRYO DEFECTIVE 1144); chorismate synthase	436		8.3599966	47.3100014		13.1.6.1.7 amino acid metabolism.synthesis.aromatic aa.chorismate.chorismate synthase	chloroplast	Y	C	plastid	
AT1G49240	190	AT1G49240.1	ACT8 (ACTIN 8); structural constituent of cytoskeleton	377	Ch/E & other	5.3600013	41.8600006	plastid positioning ?	31.1 cell.organisation	other (e.g. cytoplasm)			-	
AT1G49510	191	AT1G49510.1	EMB1273 (EMBRYO DEFECTIVE 1273)	240	Ch/E/IM	9.7299954	27.3799992	unknown	33.99 development.unspecified		plastid	plastid		4.0
AT1G49650	192	AT1G49650.1	cell death associated protein-related	374		6.5	41.6899986		35.1 not assigned.no ontology	undefined	Y	M	-	
AT1G49970	193	AT1G49970.1	CLPR1 (Clp protease proteolytic subunit 5); endopeptidase Clp	387	Ch/S & Ch/E	8.8100042	42.6199989	chaperone and protease	29.5.5 protein.degradation.serine protease	chloroplastic endopeptidase Clp complex & chloroplast stroma & thylakoid (sensu Viridiplantae)	plastid	plastid	plastid stroma	
AT1G50250	194	AT1G50250.1	FTSH1 (FtsH protease 1); ATP-dependent peptidase/ATPase/metallopeptidase	716	Ch/Th & Ch/E	5.6300011	76.7600021	chaperone and protease	29.5.7 protein.degradation.metalloprotease	thylakoid membrane (sensu Viridiplantae) & chloroplast	plastid	plastid	thylakoid-integral	2.0

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AT1G50320	195	AT1G50320.1	ATHX (THIOREDOXIN X); thiol-disulfide exchange intermediate	182		9.0600042	19.6399994		21.1 redox.thioredoxin	chloroplast	Y	C	plastid stroma	
AT1G50450	196	AT1G50450.1	binding / catalytic	428	Ch/Th ?? & Ch/E ??	8.1800031	46.5600014	unknown	35.2 not assigned.unknown			mitochondrion	plastid	
AT1G50730	197	AT1G50730.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO38919.1); contains domain PTHR13673 (PTHR13673)	1013		5.2300002	113.889999		35.2 not assigned.unknown	undefined		M	-	2.0
AT1G51060	198	AT1G51060.1	HTA10; DNA binding	132	other	10.0900002	13.9300003	DNA binding	28.1.3 DNA.synthesis/chromatin structure.histone	undefined	Y	M	-	
AT1G51100	199	AT1G51100.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO39038.1)	211		9.35999966	24.1599998		35.2 not assigned.unknown	chloroplast	Y	C	plastid stroma	
AT1G51110	200	AT1G51110.1	plastid-lipid associated protein PAP / fibrillin family protein	409	Ch/Th & Ch/E	8.10000038	45.7599983	PAP_fibrillin	26.31* misc.fibrillins	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	thylakoid-peripheral-stromal-side	

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AT1G51900	201	AT1G51900.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G14830.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO24094.1); contains InterPro domain Protein of unknown function DUF292, eukaryotic (InterPro:IPR005061)	774		5.25	92.1900024		35.2 not assigned.unknown	mitochondrion	Y	M	-	
AT1G51965	202	AT1G51965.1	pentatricopeptide (PPR) repeat-containing protein	650		8.64999962	73.8799973		26.54* misc.pentatricopeptide (PPR) repeat-containing protein	undefined	Y	M	-	

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AT1G52220	203	AT1G52220.1	similar to PSAP/PSI-P/PTAC8/TM P14 (THYLAKOID MEMBRANE PHOSPHOPROTEIN OF 14 KDA) [Arabidopsis thaliana] (TAIR:AT2G46820.2); similar to PSAP/PSI-P/PTAC8/TM P14 (THYLAKOID MEMBRANE PHOSPHOPROTEIN OF 14 KDA), DNA binding [Arabidopsis thaliana] (TAIR:AT2G4	156	Ch/Th	9.0	16.9400005	PS PSI ?	1.1.2.2 PS.lightreaction.photosystem I.PSI polypeptide subunits	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	thylakoid	2.0
AT1G52230	204	AT1G52230.1	PSAH-2/PSAH2/PSI-H (PHOTOSYSTEM I SUBUNIT H-2)	145	Ch/Th	9.89000034	15.2700005	PS PSI	1.1.2.2 PS.lightreaction.photosystem I.PSI polypeptide subunits	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	thylakoid-integral	
AT1G52400	205	AT1G52400.1	BGL1 (BETA-GLUCOSIDASE HOMOLOG 1); hydrolase, hydrolyzing O-glycosyl compounds	528	Ch/E ?	6.73999977	60.4599991	metabolism hormone ?	26.3 misc.gluco-, galacto- and mannosidases	secreted		S	-	
AT1G52510	206	AT1G52510.1	hydrolase, alpha/beta fold family protein	380	Ch/S & Ch/E	6.55000019	41.8400002	hydrolase ?	35.2 not assigned.unknown		plastid	plastid	plastid stroma	

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AT1G52670	207	AT1G52670.1	biotin/lipoyl attachment domain-containing protein	274		8.59000015	29.5699997		35.1 not assigned.no ontology	undefined	Y	C	plastid	
AT1G52740	208	AT1G52740.1	HTA9; DNA binding	134	other	10.2799997	14.2700005	DNA binding	28.1.3 DNA.synthesis/chromatin structure.hist one	undefined	Y		nucleus	
AT1G53180	209	AT1G53180.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G15115.1)	358		9.60999966	40.4199982		35.2 not assigned.unknown	undefined			-	
AT1G53240	210	AT1G53240.1	malate dehydrogenase (NAD), mitochondria	341	other	8.52999973	35.7999992	metabolism carbon	8.1.9 TCA / org.transformation.TCA.malate DH	undefined	Y	M	mitochondria	
AT1G53280	211	AT1G53280.1	DJ-1 family protein	438	Ch/S	7.98000002	46.9900017	unknown	35.1 not assigned.no ontology		plastid	plastid	plastid	
AT1G53520	212	AT1G53520.1	chalcone-flavanone isomerase-related	287	Ch/S	8.63000011	30.7199993	metabolism flavonoids	16.8.2 secondary metabolism.flavonoids.chalcones			plastid	plastid	
AT1G54040	213	AT1G54040.1	ESP (EPITHIOSPERMATEIN)	261		5.09000015	28.5200005		17.7.3 hormone metabolism.jasmonate.induced-regulated-responsive-activated	undefined			-	
AT1G54270	214	AT1G54270.1	EIF4A-2 (eukaryotic translation initiation factor 4A-2); ATP-dependent helicase	412		5.44999981	46.7599983		29.2.3 protein.synthesis.initiation	other (e.g. cytoplasm)			-	
AT1G54500	215	AT1G54500.1	rubredoxin family protein	195	Ch/E & Ch/Th	6.28000021	21.8700008	redox ?	29.8 protein assembly and cofactor ligation	thylakoid membrane (sensu Viridiplantae)		plastid	thylakoid-integral	1.0

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AT1G54520	216	AT1G54520.1	similar to unknown [Populus trichocarpa x Populus deltoides] (GB:ABK96363.1); contains InterPro domain Protein of unknown function DUF1517 (InterPro:IPR010903)	391	Ch/E/IM	9.22000027	42.8400002	unknown	35.2 not assigned.unknown		plastid	plastid	plastid	2.0
AT1G54580	217	AT1G54580.1	ACP2 (ACYL CARRIER PROTEIN 2)	136		5.28000021	14.5200005		11.1.12 lipid metabolism. FA synthesis and FA elongation.A CP protein	chloroplast	Y	C	plastid	
AT1G54630	218	AT1G54630.1	ACP3 (ACYL CARRIER PROTEIN 3)	136		5.28000021	14.6499996		11.1.12 lipid metabolism. FA synthesis and FA elongation.A CP protein	chloroplast	Y	C	plastid	
AT1G54780	219	AT1G54780.1	thylakoid lumen 18.3 kDa protein	285	Ch/Th	8.81000042	31.1299992	unknown	35.2 not assigned.unknown	thylakoid membrane (sensu Viridiplantae) & thylakoid lumen (sensu Viridiplantae)	plastid	plastid	thylakoid-peripheral-lumenal-side	2.0
AT1G55450	220	AT1G55450.1	embryo-abundant protein-related	311	Ch/E ?	6.75	34.4700012	unknown	27.3.99 RNA.regulation of transcription.unclassified	undefined			-	1.0
AT1G55480	221	AT1G55480.1	binding / protein binding	335	Ch/Th & Ch/E	8.18000031	37.4099998	RNA Binding ?	35.2 not assigned.unknown	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	thylakoid-peripheral-stromal-side	

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AT1G55490	222	AT1G55490.1	CPN60B (CHAPERONIN 60 BETA); ATP binding / protein binding / unfolded protein binding	600	Ch/S	6.19999981	63.8100014	chaperone and protease	29.6 protein.folding		plastid	plastid	plastid stroma	
AT1G55670	223	AT1G55670.1	PSAG	160	Ch/Th	9.56000042	17.0799999	PS PSI	1.1.2.2 PS.lightreaction.photosystem I.PSI polypeptide subunits	thylakoid membrane (sensu Viridiplantae) & photosystem I (sensu Viridiplantae)	plastid	plastid	thylakoid-integral	2.0
AT1G55930	224	AT1G55930.1	CBS domain-containing protein / transporter associated domain-containing protein	653	Ch/E/IM	5.46000004	72.9300003	transporter Mg & Co ?	35.1 not assigned.no ontology		plastid	plastid		5.0
AT1G56050	225	AT1G56050.1	GTP-binding protein-related	421	Ch/S	5.71999979	45.6199989	signaling G-proteins	30.5 signalling.G-proteins		plastid	plastid	plastid stroma	
AT1G56070	226	AT1G56070.1	LOS1 (Low expression of osmotically responsive genes 1); translation elongation factor/ translation factor, nucleic acid binding	843	na	5.88999987	93.8899994	translation cytosol	29.2.4 protein.synthesis.elongation				not plastid	
AT1G56190	227	AT1G56190.1	phosphoglycerate kinase, putative	478	Ch/S	8.27000046	49.9300003	metabolism carbon Calvin cycle	1.3.3 PS.calvin cycle.phosphoglycerate kinase	mitochondrion	plastid	plastid	plastid stroma	
AT1G56200	228	AT1G56200.1	EMB1303 (EMBRYO DEFECTIVE 1303)	154	Ch/E/IM	9.32999992	15.9799995	unknown	33.99 development .unspecified	chloroplast	Y	C	plastid	1.0

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AT1G56500	229	AT1G56500.1	haloacid dehalogenase-like hydrolase family protein	1055	Ch/Th & Ch/S	5.42000008	114.400002	unknown	3.2 minor CHO metabolism.t rehalose		plastid	plastid	plastid stroma	
AT1G57770	230	AT1G57770.1	amine oxidase family	574	Ch/E	6.51000023	61.7200012	metabolism vitamin and pigment ?	16.1.4 secondary metabolism.i soprenoids.c arotenoids		plastid	plastid	plastid	
AT1G58080	231	AT1G58080.1	ATATP-PRT1 (ATP PHOSPHORIBOSYL TRANSFERASE)	411		6.03000021	44.5499992		13.1.7.1 amino acid metabolism.s synthesis.histi dine.ATP phosphoribosyl transferase	chloroplast	Y	C	-	
AT1G58200	232	AT1G58200.1	MSL3 (MSCS-LIKE 3)	678	Ch/E	8.57999992	74.1900024	transporter ion channel	31.2.5 cell.division. plastid	undefined			envelope	4.0
AT1G58848	233	AT1G58848.1	ATP binding / protein binding	1049		6.8499999	121.040001		20.1 stress.biotic	undefined			-	2.0
AT1G60000	234	AT1G60000.1	29 kDa ribonucleoprotein, chloroplast, putative / RNA-binding protein cp29, putative	258		5.3499999	28.4899998		27.4 RNA.RNA binding	chloroplast	Y	C	plastid stroma	
AT1G61520	235	AT1G61520.1	LHCA3 (Photosystem I light harvesting complex gene 3); chlorophyll binding	273	Ch/Th	8.60999966	29.1800003	PS LHCI	1.1.2.1 PS.lightreaction.photosystem I.LHC-I		plastid	plastid	thylakoid-integral	
AT1G62180	236	AT1G62180.1	APR2 (5'ADENYLYLPHOSPHOSULFATE REDUCTASE 2)	454		6.44999981	50.6500015		14.2 S-assimilation. APR	chloroplast	Y	C	plastid stroma	

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AT1G62640	237	AT1G62640.1	KAS III (3-KETOACYL-ACYL CARRIER PROTEIN SYNTHASE III); 3-oxoacyl-[acyl-carrier-protein] synthase	404	Ch/S	7.05000019	42.8400002	metabolism lipid	11.1.3 lipid metabolism. FA synthesis and FA elongation.k etoacyl ACP synthase		plastid	plastid	plastid stroma	
AT1G62750	238	AT1G62750.1	ATSCO1/ATSCO1/CPEF-G/SCO1 (SNOWY COTYLEDON1); translation elongation factor/ translation factor, nucleic acid binding	783	Ch/S	5.42999983	86.0500031	translation stroma	29.2.4 protein.synthesis.elongation	chloroplast	plastid	plastid	plastid stroma	
AT1G62780	239	AT1G62780.1	similar to hypothetical protein [Vitis vinifera] (GB:CAN83165.1)	237	Ch/S	5.76999998	27.2099991	unknown	35.2 not assigned.unknown			plastid	plastid stroma	
AT1G63610	240	AT1G63610.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G14910.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO62022.1); similar to unknown [Populus trichocarpa] (GB:ABK95713.1)	340		6.26000023	37.9500008		35.2 not assigned.unknown	chloroplast	Y	C	-	

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AT1G63680	241	AT1G63680.1	ATMURE/PDE316 (PIGMENT DEFECTIVE EMBRYO); ATP binding / ligase	767	Ch/S	4.55000019	85.0199966	unknown	28.3* DNA.plastid nucleoid interacting		plastid	plastid	plastid	1.0
AT1G63770	242	AT1G63770.2	peptidase M1 family protein	945		6.11000013	106.099998		29.5 protein.degradation	chloroplast	Y	C	plastid stroma	
AT1G63940	243	AT1G63940.1	monodehydroascorbate reductase, putative	486	Ch/S	7.05000019	52.5	redox	21.2.1 redox.ascorbate and glutathione.ascorbate	mitochondrion	plastid	plastid	mitochondria ; plastid stroma	
AT1G63970	244	AT1G63970.1	ISPF (Homolog of E. coli ispF (isoprenoids F)); 2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	231		8.93999958	24.8099995		16.1.1.5 secondary metabolism.isoprenoids.non-mevalonate pathway.MCS	chloroplast	Y	C	plastid stroma	
AT1G64190	245	AT1G64190.1	6-phosphoglucuronate dehydrogenase family protein	487	Ch/S	5.32999992	53.3699989	metabolism carbon	7.1.3 OPP.oxidative PP.6-phosphoglucuronate dehydrogenase			extracellular, endoplasmic reticulum, golgi	plastid	
AT1G64510	246	AT1G64510.1	ribosomal protein S6 family protein	207	Ch/S	5.92000008	22.7600002	translation stroma	29.2.1.1.1.1.6 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.30S subunit.S6		plastid	plastid	plastid ribosome	

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AT1G64680	247	AT1G64680.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G03055.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO62908.1)	250	Ch/E ?? & Ch/Th ??	8.52000046	28.1599998	unknown	35.2 not assigned.unkn own			mitochondrion		
AT1G64770	248	AT1G64770.1	carbohydrate binding / catalytic	348	Ch/Th	6.38000011	38.0	NDH	1.1.6 PS.lightreaction.NADH DH			plastid	thylakoid	
AT1G64850	249	AT1G64850.1	calcium-binding EF hand family protein	162	Ch/E	6.11000013	18.0900002	signalling calcium ?	30.3 signalling.calcium	undefined			-	2.0
AT1G64970	250	AT1G64970.1	G-TMT (GAMMA-TOCOPHEROL METHYLTRANSFERASE)	348	Ch/E/IM	6.71000004	38.0699997	metabolism vitamin and pigment	16.1.3.5 secondary metabolism.isoprenoids.tocopherol biosynthesis.tocopherol methyltransferase		plastid	plastid	plastid	
AT1G65130	251	AT1G65130.1	ubiquitin carboxyl-terminal hydrolase-related	1086		5.5999999	124.650002				-	-		
AT1G65260	252	AT1G65260.1	PTAC4 (PLASTID TRANSCRIPTIONALLY ACTIVE4)	330	Ch/E & Ch/S	9.17000008	36.3899994	vesicle formation	29.3.3 protein.targeting.chloroplast	thylakoid membrane (sensu Viridiplantae) & plastid chromosome & chloroplast envelope & thylakoid (sensu Viridiplantae)	plastid	plastid	envelope-intermembrane space; plastid stroma; thylakoid-peripheral-stromal-side	

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AT1G65410	253	AT1G65410.1	ATNAP11 (ARABIDOPSIS THALIANA NON-INTRINSIC ABC PROTEIN 11)	345	Ch/E/IM	7.63000011	37.5099983	transporter ABC lipids	11.15* lipid metabolism.t ransport		plastid	plastid	envelope-inner-peripheral-stromal-side	
AT1G65930	254	AT1G65930.1	isocitrate dehydrogenase, putative / NADP+ isocitrate dehydrogenase, putative	410		6.13000011	45.7400017		8.1.4 TCA / org.transformation.TCA.I DH	other (e.g. cytoplasm)			-	
AT1G66200	255	AT1G66200.1	ATGSR2 (Arabidopsis thaliana glutamine synthase clone R2); glutamate-ammonia ligase	356		5.13000011	39.2000008		12.2.2 N-metabolism. ammonia metabolism. glutamine synthase	other (e.g. cytoplasm)			-	
AT1G66430	256	AT1G66430.1	pfkB-type carbohydrate kinase family protein	384		5.53999996	41.4700012		2.2.1.1 major CHO metabolism. degradation. sucrose.fructokinase	chloroplast	Y	C	plastid stroma	
AT1G66670	257	AT1G66670.1	CLPP3 (Clp protease proteolytic subunit 3); endopeptidase Clp	309	Ch/S & Ch/E	7.59000015	33.9199982	chaperone and protease	29.5.5 protein.degradation.serine protease	chloroplastic endopeptidase Clp complex & chloroplast stroma & thylakoid (sensu Viridiplantae)	plastid	plastid	plastid stroma	
AT1G66820	258	AT1G66820.1	glycine-rich protein	109	CH/E ?	7.76999998	11.04	unknown	35.1.40 not assigned.no ontology.glycine rich proteins	undefined			-	2.0

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AT1G67080	259	AT1G67080.1	ABA4 (ABSCISIC ACID (ABA)-DEFICIENT 4); intramolecular oxidoreductase	220	Ch/E	9.43999958	24.6200008	unknown	16.1.4 secondary metabolism.i soprenoids.c arotenoids	chloroplast	Y	C	plastid	4.0
AT1G67090	260	AT1G67090.1	RBCS1A; ribulose-bisphosphate carboxylase	180	Ch/S & Ch/E	7.57999992	20.2099991	metabolism carbon Calvin cycle	1.3.2 PS.calvin cyle.rubisco small subunit	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	plastid stroma	
AT1G67120	261	AT1G67120.1	midasin-related	1700		5.11999989	604.090027		35.1 not assigned.no ontology	secreted		S	-	
AT1G67280	262	AT1G67280.1	lactoylglutathione lyase, putative / glyoxalase I, putative	350	Ch/S	6.96000004	39.1599998	unknown	13.2.3.2 amino acid metabolism.degradation.aspartate family.threonine		plastid	plastid	plastid stroma; thylakoid-peripheral-stromal-side	
AT1G67700	263	AT1G67700.1	similar to unknown [Populus trichocarpa] (GB:ABK95743.1); contains domain PTHR11804:SF2 (PTHR11804:SF2); contains domain PTHR11804 (PTHR11804)	230	Ch/E ?? & Ch/Th ??	9.56999969	26.0100002	unknown	35.1 not assigned.no ontology			mitochondrion	plastid	
AT1G67740	264	AT1G67740.1	PSBY (photosystem II BY)	189		9.56000042	19.4599991		1.1.1.2 PS.lightreaction.photosystem II.PSII polypeptide subunits	chloroplast	Y	C	thylakoid-integral	4.0

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AT1G68010	265	AT1G68010.1	HPR (HYDROXY PYRUVATE REDUCTASE); glycerate dehydrogenase/ poly(U) binding	386	Ch/Th & Ch/S	6.67000008	42.2400017	metabolism carbon	1.2.6 PS.photosynthesis.pyr.oxypyruvate reductase	peroxisome			peroxisome	
AT1G68590	266	AT1G68590.1	plastid-specific 30S ribosomal protein 3, putative / PSRP-3, putative	166	Ch/S	9.26000023	18.4699993	translation stroma	29.2.1.1.1.1.83 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.30S subunit.PSRP3		plastid	plastid	plastid ribosome	
AT1G68660	267	AT1G68660.1	similar to unknown [Populus trichocarpa] (GB:ABK92624.1); contains InterPro domain Ribosomal protein L7/L12, C-terminal/adaptor protein ClpS-like (InterPro:IPR014719); contains InterPro domain Adaptor protein ClpS, core (InterPro:IPR003769)	159		8.63000011	17.0		29.5.5 protein.degradation.serine protease	undefined	Y	C	plastid stroma	
AT1G69160	268	AT1G69160.1	unknown protein	321		8.39000034	36.3199997		35.2 not assigned.unknown	undefined			-	
AT1G69200	269	AT1G69200.1	kinase	614	Ch/S	5.13000011	68.9800034	kinase	29.4.1 protein.posttranslational modification.kinase		plastid	extracellular, endoplasmic reticulum, golgi	plastid	

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AT1G69390	270	AT1G69390.1	ATMINE1 (ARABIDOPSIS HOMOLOGUE OF BACTERIAL MINE 1); protein binding	229	Ch/E/IM	6.32000017	25.7399998	plastid division	31.2.5 cell.division.plastid	chloroplast	Y	C	envelope-inner; plastid stroma	
AT1G69740	271	AT1G69740.1	HEMB1; porphobilinogen synthase	430	Ch/S	6.94999981	46.6899986	metabolism vitamin and pigment	19.4 tetrapyrrole synthesis.AL A dehydratase		plastid	plastid	plastid stroma	
AT1G69830	272	AT1G69830.1	AMY3/ATAMY3 (ALPHA-AMYLASE-LIKE 3); alpha-amylase	887	Ch/S	5.71999979	99.8399963	starch degradation	2.2.2.1 major CHO metabolism.degradation.starch.starch cleavage	chloroplast	plastid	plastid	plastid stroma	
AT1G70570	273	AT1G70570.1	anthranilate phosphoribosyltransferase, putative	595		6.42999983	65.2200012		13.1.6.5.2 amino acid metabolism.synthesis.aromatic aa.tryptophan.anthranilate phosphoribosyltransferase	chloroplast	Y	C	-	
AT1G70610	274	AT1G70610.1	ATTAP1 (Arabidopsis thaliana transporter associated with antigen processing protein 1); ATPase, coupled to transmembrane movement of substances	700	Ch/E/IM	8.67000008	78.0400009	transporter ABC	34.8 transport.metabolite transporters at the envelope membrane	chloroplast	Y	C	envelope	4.0

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AT1G70710	275	AT1G70710.1	AtGH9B1 (ARABIDOPSIS THALIANA GLYCOSYL HYDROLASE 9B1); hydrolase, hydrolyzing O-glycosyl compounds	492	Ch/Th	9.32999992	54.6100006	unknown	10.6.1 cell wall.degradation.cellulases and beta - 1,4-glucanases			extracellular, endoplasmic reticulum, golgi		
AT1G70730	276	AT1G70730.1	phosphoglucosyltransferase, cytoplasmic, putative / glucose phosphomutase, putative	585		5.55999994	63.4799995		4.2 glycolysis.PGM	undefined	Y		-	
AT1G70820	277	AT1G70820.1	phosphoglucosyltransferase, putative / glucose phosphomutase, putative	615	Ch/S	5.61000013	67.3099976	unknown	4.2 glycolysis.PGM		plastid	plastid	plastid stroma	
AT1G71240	278	AT1G71240.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G48840.1); similar to Os01g0869000 [Oryza sativa (japonica cultivar-group)] (GB:NP_001044923.1); similar to hypothetical protein OsJ_004118 [Oryza sativa (japonica cultivar-group)] (GB:EAZ142	824	Ch/E/IM	9.39999962	92.8700027	unknown	35.2 not assigned.unknown		plastid	mitochondrion	plastid nucleoid	2.0
AT1G71500	279	AT1G71500.1	Rieske (2Fe-2S) domain-containing protein	287	Ch/Th & Ch/E	8.88000011	31.7199993	redox ? PSII ? NPQ ?	26.30 misc.other Ferredoxins and Rieske domain	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	thylakoid	

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AT1G71920	280	AT1G71920.1	histidinol-phosphate aminotransferase, putative	415		5.98000002	46.3600006		13.1.7.6 amino acid metabolism.synthesis.histidine.histidinol-phosphate aminotransferase	chloroplast	Y	C	-	
AT1G72150	281	AT1G72150.1	PATL1 (PATELLIN 1); transporter	573	Ch/E & other	4.82000017	64.0400009	vesicular trafficking ?			-	-		
AT1G72250	282	AT1G72250.1	kinesin motor protein-related	1195	Ch/E	6.13000011	133.380005	plastid positioning ?	31.1 cell.organisation					
AT1G72640	283	AT1G72640.1	binding / catalytic	312	Ch/Th & Ch/E	5.55000019	33.6300011	protein targeting Tic ?	35.2 not assigned.unknown	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	plastid	
AT1G72810	284	AT1G72810.1	threonine synthase, putative	516		8.22999954	56.9199982				Y	C		
AT1G73060	285	AT1G73060.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G48790.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO49401.1)	358	Ch/Th	5.11999989	40.0299988	PS PSII ?	35.2 not assigned.unknown		plastid	plastid	thylakoid-peripheral-stromal-side	
AT1G73110	286	AT1G73110.1	ribulose bisphosphate carboxylase/oxygenase activase, putative / RuBisCO activase, putative	432	Ch/Th & Ch/S	6.80999994	48.3199997	metabolism carbon Calvin cycle chaperone and protease	1.3.13 PS.calvin cycle.rubisco interacting	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	plastid	

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AT1G73990	287	AT1G73990.1	SPPA (signal peptide peptidase); protease IV/serine-type endopeptidase	677	Ch/E & Ch/Th	9.18000031	75.0899963	chaperone and protease	29.5 protein.degradation	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	thylakoid-integral	
AT1G74030	288	AT1G74030.1	enolase, putative	477		5.78000021	51.4700012		4.12 glycolysis.enolase	chloroplast	Y	C	plastid	
AT1G74070	289	AT1G74070.1	peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein	317	Ch/Th	9.51000023	34.3699989	chaperone and protease	29.6 protein.folding		plastid	plastid	plastid	
AT1G74260	290	AT1G74260.1	catalytic	1387		5.15999985	151.779999		23.1.2.4 nucleotide metabolism.synthesis.purine.FGAR amidotransferase	chloroplast	Y	M	mitochondria ; plastid stroma	
AT1G74310	291	AT1G74310.1	ATHSP101 (HEAT SHOCK PROTEIN 101); ATP binding / ATPase	911	Ch/E ?	5.80000019	101.290001	chaperone and protease	20.2.1 stress.abiotic.heat	other (e.g. cytoplasm)			-	
AT1G74470	292	AT1G74470.1	geranylgeranyl reductase	467	Ch/Th	9.02999973	51.8300018	metabolism vitamin and pigment	16.1.1 secondary metabolism.isoprenoids.non-mevalonate pathway	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	thylakoid	

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AT1G74640	293	AT1G74640.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO64553.1); contains domain SSF53474 (SSF53474); contains domain G3DSA:3.40.50.1820 (G3DSA:3.40.50.1820)	370	Ch/E/IM	8.30000019	41.0499992	unknown	35.2 not assigned.unknown	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	plastid	
AT1G74730	294	AT1G74730.1	similar to unknown [Populus trichocarpa x Populus deltoides] (GB:ABK96654.1); contains InterPro domain Protein of unknown function DUF1118 (InterPro:IPR009500)	198	Ch/Th	9.30000019	20.7299995	unknown	35.2 not assigned.unknown	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	thylakoid	2.0
AT1G74850	295	AT1G74850.1	PTAC2 (PLASTID TRANSCRIPTIONALLY ACTIVE2)	862	Ch/S	5.67000008	96.3199997	RNA binding ?	27.7* RNA.misc.pentatricopeptide (PPR) repeat-containing protein	plastid chromosome	plastid	plastid	plastid nucleoid	
AT1G74880	296	AT1G74880.1	NDH-O (NAD(P)H:PLASTOQUINONE DEHYDROGENASE COMPLEX SUBUNIT O)	158	Ch/Th & Ch/S	9.22999954	17.6499996	NDH	1.1.6 PS.lightreaction.NADH DH	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	thylakoid	

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AT1G74960	297	AT1G74960.1	FAB1 (FATTY ACID BIOSYNTHESIS 1); fatty-acid synthase	541	Ch/S	8.10000038	57.5999985	metabolism lipid	11.1.3 lipid metabolism. FA synthesis and FA elongation. ketoacyl ACP synthase		plastid	plastid	plastid	
AT1G74970	298	AT1G74970.1	RPS9 (RIBOSOMAL PROTEIN S9); structural constituent of ribosome	208	Ch/S & Ch/E	10.46	22.5699997	translation stroma	29.2.1.1.1.1.9 protein synthesis. ribosomal protein. prokaryotic. chloroplast. 30S subunit. S9	plastid small ribosomal subunit	plastid	plastid	plastid ribosome	
AT1G75330	299	AT1G75330.1	OTC (ORNITHINE CARBAMOYLTRANSFERASE); amino acid binding / carboxyl- or carbamoyltransferase	375	Ch/S	7.17000008	41.0	unknown	13.1.2.3.21 amino acid metabolism. synthesis. glutamate family. arginine. ornithine carbamoyltransferase		plastid	plastid	plastid stroma	
AT1G75350	300	AT1G75350.1	EMB2184 (EMBRYO DEFECTIVE 2184); structural constituent of ribosome	144	Ch/S & Ch/Th & Ch/E	9.81000042	16.0300007	translation stroma	29.2.1.1.1.2.31 protein synthesis. ribosomal protein. prokaryotic. chloroplast. 50S subunit. L31		plastid	plastid	plastid ribosome	
AT1G75460	301	AT1G75460.1	ATP-dependent protease La (LON) domain-containing protein	278		8.64999962	31.3299999		29.5 protein degradation	chloroplast	Y	C	plastid	
AT1G76030	302	AT1G76030.1	(VACUOLAR ATP SYNTHASE SUBUNIT B1); hydrogen ion transporting ATP synthase, rotational mechanism	486	na	4.98000002	54.0999985	transporter ATPase	34.1.1 transport. p- and v-ATPases. H ⁺ -transporting two-sector ATPase				vacuole	

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AT1G76080	303	AT1G76080.1	ATCDSP32/CDSP32 (CHLOROPLASTIC DROUGHT-INDUCED STRESS PROTEIN OF 32 KD); thiol-disulfide exchange intermediate	302	Ch/S	8.64999962	33.6800003	redox	21.1 redox.thioredoxin		plastid	plastid	plastid stroma	
AT1G76100	304	AT1G76100.1	plastocyanin	171	Ch/Th	5.65999985	17.5799999	PS b6/f PSI electron transfer	1.1.5.1 PS.lightreaction.other electron carrier (ox/red).plastocyanin	thylakoid lumen (sensu Viridiplantae)	plastid	plastid	thylakoid-peripheral-lumenal-side	1.0
AT1G76140	305	AT1G76140.1	prolyl oligopeptidase	795		5.51999998	89.4000015		29.5 protein.degradation	chloroplast	Y	C	-	
AT1G76180	306	AT1G76180.1	ERD14 (EARLY RESPONSE TO DEHYDRATION 14)	185	Ch/E & Ch/S	5.40999985	20.7800007	stress dehydration	20.2.99 stress.abiotic.unspecified				peroxisome	
AT1G76405	307	AT1G76405.2	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G20816.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO66270.1)	167	Ch/E/OM	9.48999977	19.4500008	transporter ion channel	34.8 transport.metabolite transporters at the envelope membrane	chloroplast envelope			envelope-outer	
AT1G76760	308	AT1G76760.1	ATY1 (Arabidopsis thioredoxin y1); thiol-disulfide exchange intermediate	172		9.02000046	19.25		21.1 redox.thioredoxin	chloroplast	Y	C	plastid stroma	

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AT1G77060	309	AT1G77060.1	mutase family protein	339		6.4000001	36.5600014		27.3.99 RNA.regulation of transcription.unclassified	undefined	Y	C	plastid stroma	
AT1G77090	310	AT1G77090.1	thylakoid lumenal 29.8 kDa protein	260	Ch/Th & Ch/S	7.01999998	28.5	PS PSII OEE ?	1.1.1.2 PS.lightreaction.photosystem II.PSII polypeptide subunits	thylakoid lumen (sensu Viridiplantae)		plastid	thylakoid-peripheral-lumenal-side	
AT1G77490	311	AT1G77490.1	TAPX; L-ascorbate peroxidase	426	Ch/Th & Ch/E	6.80000019	46.0900002	stress oxidative	21.2.1 redox.ascorbate and glutathione.ascorbate	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	thylakoid-integral	1.0
AT1G77590	312	AT1G77590.1	LACS9 (LONG CHAIN ACYL-COA SYNTHETASE 9); long-chain-fatty-acid-CoA ligase	691	Ch/E/IM	6.53000021	76.1699982	metabolism lipid	11.1.9 lipid metabolism.FA synthesis and FA elongation.long chain fatty acid CoA ligase	chloroplast		plastid	envelope-outer	
AT1G77670	313	AT1G77670.1	aminotransferase class I and II family protein	440		7.63000011	48.7099991		16.2 secondary metabolism.phenylpropenoids	undefined	Y	M	-	
AT1G78010	314	AT1G78010.1	tRNA modification GTPase, putative	560		5.19000006	61.1199989		30.5 signalling.G-proteins	undefined	Y	M	-	
AT1G78180	315	AT1G78180.1	binding	418	Ch/E/IM	9.85999966	37.5400009	transporter ATP/ADP ?	34.9 transport.metabolite transporters at the mitochondria l membrane		plastid	plastid		2.0
AT1G78370	316	AT1G78370.1	ATGSTU20 (Arabidopsis thaliana Glutathione S-transferase (class tau) 20); glutathione transferase	217		5.61999989	25.0		26.9 misc.glutathione S transferases	undefined		M	not plastid	

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AT1G78380	317	AT1G78380.1	ATGSTU19 (GLUTATHIONE TRANSFERASE 8); glutathione transferase	219		5.78999996	25.6499996		26.9 misc.glutathione S transferases	undefined			not plastid	
AT1G78560	318	AT1G78560.1	bile acid:sodium symporter family protein	401	Ch/E/IM	9.55000019	42.7400017	transporter Na/X ?	34.14 transport.unspecified cations		plastid	plastid	envelope	9.0
AT1G78620	319	AT1G78620.1	integral membrane family protein	333	Ch/E/IM	9.82999992	34.8699989	unknown	35.2 not assigned.unknown	chloroplast inner membrane	plastid	plastid	envelope-inner-integral	
AT1G78630	320	AT1G78630.1	EMB1473 (EMBRYO DEFECTIVE 1473); structural constituent of ribosome	241	Ch/S & Ch/E	9.93000031	26.7800007	translation stroma	29.2.1.1.1.2.13 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.50S subunit.L13		plastid	plastid	plastid ribosome	
AT1G78900	321	AT1G78900.1	VHA-A; ATP binding / hydrogen ion transporting ATP synthase, rotational mechanism	623	na	5.11000013	68.8099976	transporter ATPase	34.1 transport.p-and v-ATPases				vacuole	
AT1G78915	322	AT1G78915.1	binding	385	Ch/Th	7.65999985	42.5800018	RNA Binding ?	26.33* misc.tetratricopeptide repeat (TPR) unknown function		plastid	plastid	thylakoid	
AT1G78995	323	AT1G78995.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO41778.1)	159		9.19999981	17.1499996		35.2 not assigned.unknown	undefined	Y	C	-	1.0
AT1G79040	324	AT1G79040.1	PSBR (photosystem II subunit R)	140	Ch/Th	9.61999989	14.5799999	PS PSII	1.1.1.2 PS.lightreaction.photosystem II.PSII polypeptide subunits	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	thylakoid-integral	1.0

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AT1G79230	325	AT1G79230.1	ST1 (MERCAPTOPYRUVATE SULFURTRANSFERASE 1); thiosulfate sulfurtransferase	379		5.94000006	41.8899994		13.2.5.3 amino acid metabolism.degradation.serine-glycine-cysteine group.cysteine	undefined	Y	C	mitochondria	
AT1G79440	326	AT1G79440.1	ALDH5F1 (SUCCINIC SEMIALDEHYDE DEHYDROGENASE); 3-chloroallyl aldehyde dehydrogenase/succinate-semialdehyde dehydrogenase	528		6.51000023	56.5600014		13.1.1.1.3 amino acid metabolism.synthesis.central amino acid metabolism.GABA.SSADH	undefined	Y	M	-	
AT1G79550	327	AT1G79550.1	PGK (PHOSPHOGLYCERATE KINASE)	401	Ch/E ?	5.48000002	42.1300011	metabolism carbon	4.10 glycolysis.phosphoglycerate kinase	other (e.g. cytoplasm)			-	
AT1G79560	328	AT1G79560.1	EMB1047/FTSH12 (EMBRYO DEFECTIVE 1047); ATP-dependent peptidase/ATPase/metallopeptidase	1008	Ch/E/IM	6.48000002	115.099998	chaperone and protease	29.5.7 protein.degradation.metall oprotease	chloroplast	plastid	plastid	plastid	2.0
AT1G79600	329	AT1G79600.1	ABC1 family protein	711	Ch/Th	6.3499999	79.0199966	kinase	26.56* misc.ABC1k family		plastid	plastid	plastoglobules	
AT1G79790	330	AT1G79790.1	haloacid dehalogenase-like hydrolase family protein	245		4.76000023	27.6900005		35.1 not assigned.no ontology	chloroplast		C	plastid stroma	

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AT1G79850	331	AT1G79850.1	RPS17 (ribosomal protein S17); structural constituent of ribosome	149	Ch/S & Ch/Th & Ch/E	10.5699997	16.2800007	translation stroma	29.2.1.1.1.1.17 protein.synthesis.ribosomal.protein.prokaryotic.chloroplast.30S.subunit.S17		plastid	plastid	plastid ribosome	
AT1G79870	332	AT1G79870.1	oxidoreductase family protein	313		5.61999989	34.1599998		26.1 misc.misc2	undefined			-	
AT1G80030	333	AT1G80030.1	DNAJ heat shock protein, putative	500	Ch/E/IM	7.48000002	53.8199997	chaperone and protease	26.29* misc.DnaJ domain with unknown function	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	thylakoid	
AT1G80300	334	AT1G80300.1	ATNTT1; ATP:ADP antiporter	624	Ch/E/IM	9.39000034	68.1299973	transporter ATP/ADP	34.8 transport.metabolite transporters at the envelope membrane		plastid	plastid	envelope-inner-integral	11.0
AT1G80380	335	AT1G80380.2	phosphoribulokinase/uridine kinase-related	456	Ch/S	6.71000004	51.0099983	metabolism carbon	1.2.7 PS.photosynthesis.glycerate kinase		plastid	plastid	plastid stroma	
AT1G80480	336	AT1G80480.1	PTAC17 (PLASTID TRANSCRIPTIONALLY ACTIVE17)	444	Ch/S	5.67000008	49.4799995	DNA Binding ?	28.3* DNA.plastid nucleoid interacting	plastid chromosome	plastid	plastid	plastid stroma	
AT1G80560	337	AT1G80560.1	3-isopropylmalate dehydrogenase, chloroplast, putative	405		5.78999996	43.3699989		13.1.4.4.3 amino acid metabolism.synthesis.branded chain group.leucine specific.3-isopropylmalate dehydrogenase	undefined	Y	C	plastid stroma	

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AT1G80600	338	AT1G80600.1	acetylornithine aminotransferase, mitochondrial, putative / acetylornithine transaminase, putative / AOTA, putative / ACOAT, putative	457		6.3600013	48.8199997		13.1.2.3.4 amino acid metabolism.synthesis.glutamate family.arginine.acetylornithine aminotransferase	undefined		C	plastid stroma	
AT2G01140	339	AT2G01140.1	fructose-bisphosphate aldolase, putative	391	Ch/S & Ch/Th & Ch/E	8.18999958	42.3199997	metabolism carbon Calvin cycle	1.3.6 PS.calvin cycle.aldolase	mitochondrion	plastid	plastid	plastid	
AT2G01320	340	AT2G01320.1	ABC transporter family protein	725	Ch/E ??	5.71000004	78.9000015	transporter ABC ?	34.16 transport.ABC transporters and multidrug resistance systems				plastid	4.0
AT2G01350	341	AT2G01350.1	QPT (QUINOLINATE PHOSPHORIBOSYLTRANSFERASE) ; nicotinate-nucleotide diphosphorylase (carboxylating)	348		5.88999987	37.9500008		35.1 not assigned.no ontology	undefined		M	-	
AT2G02500	342	AT2G02500.1	ISPD (2-C-METHYL-D-ERYTHRITOL 4-PHOSPHATE CYTIDYLTRANSFERASE)	302		5.9000001	33.9300003		16.1.1.3 secondary metabolism.isoprenoids.non-mevalonate pathway.CMS	undefined	Y	M	plastid stroma	

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AT2G02590	343	AT2G02590.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO41025.1); contains InterPro domain Putative small multi-drug export (InterPro:IPR009577)	324	Ch/E/IM	10.04	35.5200005	transporter multidrug ?	34 transport	chloroplast	Y	C	-	6.0
AT2G02740	344	AT2G02740.1	ATWHY3/PTAC11 (A. THALIANA WHIRLY 3); DNA binding	268	Ch/S	9.52999973	29.7199993	DNA Binding	27.3.82 RNA.regulation of transcription. plant TF (pbf2)		plastid	plastid	plastid nucleoid	
AT2G03420	345	AT2G03420.1	similar to expressed protein [Oryza sativa (japonica cultivar-group)] (GB:ABF94594.1); similar to hypothetical protein Osl_010237 [Oryza sativa (indica cultivar-group)] (GB:EAY89004.1)	170	Ch/Th	8.63000011	19.0200005	unknown	35.2 not assigned.unknown		plastid	plastid		
AT2G04030	346	AT2G04030.1	CR88 (EMBRYO DEFECTIVE 1956); ATP binding	780	Ch/S	4.92999983	88.6600037	chaperone and protease	29.6 protein.folding	mitochondrion & chloroplast stroma	plastid	plastid	plastid stroma	
AT2G04039	347	AT2G04039.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO41070.1)	199	Ch/Th ?	6.1500001	21.4099998	unknown	35.2 not assigned.unknown		plastid	plastid	plastid	

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AT2G04350	348	AT2G04350.1	long-chain-fatty-acid--CoA ligase family protein / long-chain acyl-CoA synthetase family protein (LACS8)	720	Ch/E ?	7.5	78.3399963	metabolism lipid	11.1.9 lipid metabolism. FA synthesis and FA elongation. long chain fatty acid CoA ligase	other (e.g. cytoplasm)			-	1.0
AT2G04400	349	AT2G04400.1	indole-3-glycerol phosphate synthase (IGPS)	402	Ch/S	6.98000002	44.5699997	metabolism amino acids Tryptophan	13.1.6.5.4 amino acid metabolism. synthesis. aromatic aa. tryptophan. indole-3-glycerol phosphate synthase		plastid	plastid	plastid stroma	
AT2G04700	350	AT2G04700.1	ferredoxin thioredoxin reductase catalytic beta chain family protein	146	Ch/E ?	8.10999966	16.4300003	redox	21.1 redox. thioredoxin	chloroplast	Y	C	-	
AT2G04842	351	AT2G04842.1	EMB2761 (EMBRYO DEFECTIVE 2761); threonine-tRNA ligase	650	Ch/S	6.46999979	74.7799988	unknown	29.1.3 protein. aa activation. threonine-tRNA ligase	mitochondrion & chloroplast	plastid	plastid	mitochondria ; plastid stroma	
AT2G05070	352	AT2G05070.1	LHCB2.2 (Photosystem II light harvesting complex gene 2.2); chlorophyll binding	265	Ch/Th	5.28000021	28.6200008	PS LHCII	1.1.1.1 PS. light reaction. photosystem II. LHC-II	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	thylakoid-integral	2.0
AT2G05620	353	AT2G05620.1	PGR5 (PROTON GRADIENT REGULATION 5)	133	Ch/Th & Ch/E	10.6499996	14.29	PS cyclic electron flows	1.1.40 PS. light reaction. cyclic electron flow-chlororespiration	thylakoid (sensu Viridiplantae)	plastid		thylakoid-peripheral-stromal-side	

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AT2G05710	354	AT2G05710.1	aconitate hydratase, cytoplasmic, putative / citrate hydrolyase/aconitase, putative	990		6.71999979	108.199997		8.2.3 TCA / org.transformation.other organic acid transformaitons.aconitase	chloroplast	Y	C	plastid stroma	
AT2G05990	355	AT2G05990.1	MOD1 (MOSAIC DEATH 1); enoyl-[acyl-carrier-protein] reductase (NADH)/oxidoreductase	390	Ch/S	9.09000015	41.2099991	metabolism lipid	11.1.6 lipid metabolism. FA synthesis and FA elongation.enoyl ACP reductase	fatty acid synthase complex	plastid	plastid	plastid stroma	2.0
AT2G07698	356	AT2G07698.1	ATP synthase alpha chain, mitochondrial, putative	777	na	5.42999983	85.9300003	Mito ATPase	9.9 mitochondria l electron transport / ATP synthesis.F1-ATPase	mitochondrion	plastid	extracellular, endoplasmic reticulum, golgi	not plastid	3.0
AT2G12550	357	AT2G12550.1	ubiquitin-associated (UBA)/TS-N domain-containing protein	562	Ch/Th ??	4.9000001	62.0800018	protein degradation ubiquitin	29.5.11 protein.degradation.ubiquitin					
AT2G13360	358	AT2G13360.1	AGT (ALANINE:GLYOXYLATE AMINOTRANSFERASE)	401	Ch/S	7.67999983	44.2000008	unknown	1.2.3 PS.aminotransferases peroxisomal	peroxisome			peroxisome	
AT2G14880	359	AT2G14880.1	SWIB complex BAF60b domain-containing protein	141		9.86999989	15.8999996		35.1 not assigned.no ontology	chloroplast	Y	C	-	

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AT2G15290	360	AT2G15290.1	ATTIC21/CIA5/PIC1/TIC21 (CHLOROPLAST IMPORT APPARATUS 5); copper uptake transmembrane transporter/iron ion transmembrane transporter/protein homodimerization	296	Ch/E/IM	10.2299995	31.2700005	protein targeting Tic ? Transporter Iron ?	34.12 transport.met.al		plastid	plastid	envelope-inner-integral	4.0
AT2G15620	361	AT2G15620.1	NIR1 (NITRITE REDUCTASE); ferredoxin-nitrate reductase	586	Ch/S	5.9499981	65.5	redox	12.1.2 N-metabolism.nitrate metabolism.nitrite reductase	mitochondrion	plastid	plastid	plastid stroma	
AT2G16070	362	AT2G16070.2	PDV2 (PLASTID DIVISION2)	224	Ch/E/OM	9.1599985	24.7700005	plastid division	31.2.5 cell.division.plastid			mitochondrion	envelope-outer	
AT2G16640	363	AT2G16640.1	ATTOC132/TOC132 (MULTIMERIC TRANSLOCATION COMPLEX IN THE OUTER ENVELOPE MEMBRANE 132); transmembrane receptor	1206	Ch/E/OM	4.75	132.270004	protein targeting Toc	29.3.3 protein.targeting.chloroplast	other (e.g. cytoplasm)			envelope-outer	
AT2G17265	364	AT2G17265.1	HSK (HOMOSERINE KINASE); homoserine kinase	370	Ch/S	8.5100023	38.5200005	metabolism aa Asp	13.1.3.6.1.4 amino acid metabolism.synthesis.aspartate family.misc.homoserine.homoserine kinase	chloroplast stroma	plastid	plastid	plastid	

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AT2G17390	365	AT2G17390.1	AKR2B; protein binding / transcription regulator	344		4.36999989	36.8899994		27.3.39 RNA.regulation of transcription. AtSR Transcription Factor family	undefined			-	
AT2G17630	366	AT2G17630.1	phosphoserine aminotransferase, putative	422		8.26000023	46.6300011		13.1.5.1.2 amino acid metabolism.synthesis.serine-glycine-cysteine group.serine.phosphoserine aminotransferase	chloroplast	Y	C	-	
AT2G17695	367	AT2G17695.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO40657.1)	205	Ch/E ??	9.19999981	23.2399998	unknown	35.2 not assigned.unknown			mitochondrion	envelope	
AT2G18020	368	AT2G18020.1	EMB2296 (EMBRYO DEFECTIVE 2296); structural constituent of ribosome	258	na	10.9099998	27.8600006	translation cytosol	29.2.1.2.2.8 Protein.synthesis.ribosomal protein.eukaryotic.60S subunit.L8	cytosolic ribosome (sensu Eukaryota)		mitochondrion	cytosol	
AT2G18710	369	AT2G18710.1	SCY1 (SECY HOMOLOG 1); P-P-bond-hydrolysis-driven protein transmembrane transporter	551	Ch/Th	9.48999977	59.4900017	protein targeting	29.3.3 protein.targeting.chloroplast		plastid	plastid	thylakoid-integral	10.0
AT2G19940	370	AT2G19940.1	semialdehyde dehydrogenase family protein	359	Ch/S	6.5	39.5999985	unknown	13.1.2.3 amino acid metabolism.synthesis.glutamate family.arginine		plastid	plastid	plastid stroma	

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AT2G20260	371	AT2G20260.1	PSAE-2 (photosystem I subunit E-2); catalytic	145	Ch/Th & Ch/E	9.93999958	15.1800003	PS PSI	1.1.2.2 PS.lightreaction.photosystem I.PSI polypeptide subunits	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	thylakoid-peripheral-stromal-side	
AT2G20270	372	AT2G20270.1	glutaredoxin family protein	179		8.35999966	19.1200008		21.4 redox.glutaredoxins	chloroplast	Y	C	plastid stroma	
AT2G20690	373	AT2G20690.1	lumazine-binding family protein	271		7.61999989	29.6399994		18.3.2 Co-factor and vitamine metabolism.riboflavin.riboflavin synthase	chloroplast	Y	C	plastid	
AT2G20890	374	AT2G20890.1	PSB29 (THYLAKOID FORMATION1)	300	Ch/Th & Ch/E	9.19999981	33.7900009	vesicle formation	29.3.3 protein.targeting.chloroplast	thylakoid membrane (sensu Viridiplantae) & plastid stroma & chloroplast & plastid outer membrane & plastid inner membrane	plastid	plastid	envelope-inner-peripheral-stromal-side; thylakoid-peripheral-stromal-side	
AT2G21170	375	AT2G21170.1	TIM (TRIOSEPHOSPHATE ISOMERASE); triose-phosphate isomerase	315	Ch/S	7.67000008	33.3400002	metabolism carbon	1.3.5 PS.calvin cycle.TPI	mitochondrion	plastid	plastid	plastid stroma	
AT2G21195	376	AT2G21195.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO44591.1)	93	CH/E ?	8.93000031	10.3599997	unknown	35.2 not assigned.unknown	other (e.g. cytoplasm)			-	
AT2G21280	377	AT2G21280.1	GC1 (GIANT CHLOROPLAST 1); binding / catalytic/coenzyme binding	347	Ch/E & Ch/Th	9.31000042	37.7400017	plastid division	31.2.5 cell.division.plastid	plastid	plastid	plastid	envelope-inner-peripheral-stromal-side	
AT2G21330	378	AT2G21330.1	fructose-bisphosphate aldolase, putative	399	Ch/S & Ch/Th & Ch/E	6.17000008	42.9300003	metabolism carbon Calvin cycle	1.3.6 PS.calvin cycle.aldolase	chloroplast stroma	plastid	plastid	plastid stroma	

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AT2G21340	379	AT2G21340.1	enhanced disease susceptibility protein, putative / salicylic acid induction deficient protein, putative	555	Ch/E/IM	7.48999977	59.7400017	transporter multidrug ?	34 transport		plastid	plastid	envelope	9.0
AT2G21370	380	AT2G21370.1	xylulose kinase, putative	478		6.36000013	52.4599991			cytoplasm	Y	M	plastid	
AT2G21385	381	AT2G21385.1	similar to Os09g0531100 [Oryza sativa (japonica cultivar-group)] (GB:NP_001063753.1); similar to unknown [Picea sitchensis] (GB:ABK27019.1)	330	Ch/S	7.01999998	37.5499992	unknown	35.2 not assigned.unknown		plastid	plastid	plastid stroma	
AT2G21530	382	AT2G21530.1	forkhead-associated domain-containing protein / FHA domain-containing protein	209	Ch/S	7.73000002	22.6700001	unknown	35.1 not assigned.no ontology	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	plastid stroma; thylakoid-peripheral-stromal-side	
AT2G21660	383	AT2G21660.1	ATGRP7 (COLD, CIRCADIAN RHYTHM, AND RNA BINDING 2); RNA binding / double-stranded DNA binding / single-stranded DNA binding	176	na	5.8499999	16.8899994	RNA Binding	27.4 RNA.RNA binding				cytosol; nucleus	

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AT2G21960	384	AT2G21960.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G56180.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO71767.1)	332	Ch/Th	8.82999992	35.7999992	unknown	35.2 not assigned.unknown		plastid	plastid	plastid	3.0
AT2G22230	385	AT2G22230.1	beta-hydroxyacyl-ACP dehydratase, putative	220	Ch/Th	8.60000038	24.2399998	metabolism lipid	11.1.5 lipid metabolism. FA synthesis and FA elongation.beta hydroxyacyl ACP dehydratase		plastid	plastid	plastid	
AT2G22250	386	AT2G22250.1	AAT/ATAAT/MEE17 (maternal effect embryo arrest 17); aspartate transaminase	428		6.17999983	46.0299998		13.1.1.2.1 amino acid metabolism.synthesis.central amino acid metabolism.aspartate.aspartate aminotransferase	chloroplast	Y	C	plastid	
AT2G22360	387	AT2G22360.1	DNAJ heat shock family protein	442	Ch/E & Ch/S	9.23999977	47.7599983	chaperone and protease	26.29* misc.DnaJ domain with unknown function	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	thylakoid	
AT2G22450	388	AT2G22450.1	riboflavin biosynthesis protein, putative	476		5.80000019	52.2000008		18.3.1 Co-factor and vitamin metabolism.riboflavin.GTP cyclohydrolase II	undefined	Y		plastid	
AT2G22560	389	AT2G22560.1	kinase interacting protein-related	891		4.96000004	101.459999		29.4.1 protein.posttranslational modification.kinase	undefined			-	

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AT2G22910	390	AT2G22910.1	GCN5-related N-acetyltransferase (GNAT) family protein / amino acid kinase family protein	609		7.11000013	67.1800003		26.24 misc.GCN5-related N-acetyltransferase	undefined			-	
AT2G23670	391	AT2G23670.1	YCF37 (Arabidopsis homolog of Synechocystis YCF37)	167	Ch/Th	6.75	17.0699997	unknown	35.2 not assigned.unknown	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	thylakoid	1.0
AT2G23820	392	AT2G23820.1	metal-dependent phosphohydrolase HD domain-containing protein	245		5.80000019	26.9300003		35.1 not assigned.no ontology	undefined	Y	M	-	
AT2G24020	393	AT2G24020.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G30620.1); similar to unknown [Picea sitchensis] (GB:ABK26000.1); similar to Os02g0180200 [Oryza sativa (japonica cultivar-group)] (GB:NP_001046090.1); contains InterPro domain Conserved hypo	182	Ch/S & Ch/E	9.13000011	19.8099995	unknown	35.2 not assigned.unknown	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	plastid stroma	
AT2G24060	394	AT2G24060.1	translation initiation factor 3 (IF-3) family protein	312	Ch/Th	5.76999998	35.1399994	translation stroma	29.2.3 protein.synthesis.initiation		plastid	plastid	plastid	

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AT2G24090	395	AT2G24090.1	ribosomal protein L35 family protein	145	Ch/S	11.8299999	16.0799999	translation stroma	29.2.1.1.1.2 protein.synthesis.ribosomal.prokaryotic.chloroplast.50S subunit		plastid	plastid	plastid ribosome	
AT2G24200	396	AT2G24200.1	cytosol aminopeptidase	520		5.6500001	54.5099983		29.5 protein.degradation	other (e.g. cytoplasm)			not plastid	
AT2G24270	397	AT2G24270.1	ALDH11A3 (Aldehyde dehydrogenase 11A3); 3-chloroallyl aldehyde dehydrogenase/ glyceraldehyde-3-phosphate dehydrogenase (NADP+)	496		6.21999979	53.0600014		1.3.4 PS.calvin cycle.GAP	other (e.g. cytoplasm)			cytosol	
AT2G24820	398	AT2G24820.1	TIC55 (TRANSLOCATION AT THE INNER ENVELOPE MEMBRANE OF CHLOROPLASTS 55); oxidoreductase	539	Ch/E/IM	8.93999958	60.5999985	protein targeting Tic	29.3.3 protein.targeting.chloroplast		plastid	plastid	envelope-inner-integral	2.0
AT2G25080	399	AT2G25080.1	ATGPX1 (GLUTATHIONE PEROXIDASE 1); glutathione peroxidase	236	Ch/E & Ch/S & Ch/Th	9.40999985	26.0100002	stress oxidative	21.2.2 redox.ascorbate and glutathione.glutathione	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	plastid stroma	
AT2G25140	400	AT2G25140.1	CLPB-M/CLPB4/HSP98.7 (HEAT SHOCK PROTEIN 98.7); ATP binding / ATPase	964	Ch/E/IM	6.53000021	108.660004	chaperone and protease	29.6 protein.folding	undefined	Y	M	-	

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AT2G25730	401	AT2G25730.1	binding / heme binding	2464		5.6500001	274.769989		26.33* misc.tetratricopeptide repeat (TPR) unknown function	undefined			-	2.0
AT2G25840	402	AT2G25840.1	OVA4 (OVULE ABORTION 4); ATP binding / aminoacyl-tRNA ligase	408	Ch/S	8.27999973	45.2999992	unknown	29.1 protein.aa activation	mitochondrion & chloroplast	plastid	plastid	mitochondria ; plastid stroma	
AT2G26340	403	AT2G26340.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO43885.1)	253	Ch/Th	6.73999977	25.3400002	unknown	35.2 not assigned.unknown	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	thylakoid	
AT2G26540	404	AT2G26540.1	HEMD; uroporphyrinogen-III synthase	321	??	7.80000019	34.2200012	metabolism vitamin and pigment	19.6 tetrapyrrole synthesis.uroporphyrinogen III synthase		plastid	plastid	plastid	
AT2G26670	405	AT2G26670.1	HY1 (HEME OXYGENASE 1)	282		6.5	32.6899986		19.21 tetrapyrrole synthesis.heme oxygenase	chloroplast	Y	C	plastid	
AT2G26900	406	AT2G26900.1	bile acid:sodium symporter family protein	409	Ch/E & Ch/Th	8.94999981	43.5999985	transporter Na/X ?	34.8 transport.metabolite transporters at the envelope membrane		plastid	plastid	envelope-inner-integral	9.0
AT2G26930	407	AT2G26930.1	ATCDPMEK (PIGMENT DEFECTIVE 277); 4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol kinase	383	Ch/S	6.55000019	42.0400009	metabolism isoprenoids	16.1.1.4 secondary metabolism.isoprenoids.non-mevalonate pathway.CMK		plastid	plastid	plastid	

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AT2G27290	408	AT2G27290.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO48682.1); contains InterPro domain Protein of unknown function DUF1279 (InterPro:IPR009688)	201	Ch/Th	9.18999958	21.7600002	unknown	35.2 not assigned.unknown	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	plastid	1.0
AT2G27490	409	AT2G27490.1	ATCOAE; ATP binding / dephospho-CoA kinase	232	Ch/E ?	9.53999996	25.7399998	coenzyme A biosynthesis	35.1 not assigned.no ontology	undefined			-	
AT2G27680	410	AT2G27680.1	aldo/keto reductase family protein	384	Ch/Th & Ch/S & Ch/E	8.19999981	43.1500015	redox ?	3.5 minor CHO metabolism.others		plastid	plastid	plastid stroma	
AT2G27710	411	AT2G27710.1	60S acidic ribosomal protein P2 (RPP2B)	115	Ch/E & other	4.65999985	11.4399996	translation cytosol	29.2.1.2.2.82 protein.synthesis.ribosomal protein.eukaryotic.60S subunit.P2	secreted		S	cytosol	
AT2G28000	412	AT2G28000.1	CPN60A (chloroplast / 60 kDa chaperonin alpha subunit); ATP binding / protein binding / unfolded protein binding	586	Ch/S & Ch/E	5.07999992	62.0699997	chaperone and protease	29.6 protein.folding	mitochondrion & chloroplast	plastid	plastid	plastid stroma	
AT2G28050	413	AT2G28050.1	pentatricopeptide (PPR) repeat-containing protein	462		5.44000006	52.9300003		35.1.5 not assigned.no ontology.pentatricopeptide (PPR) repeat-containing protein	undefined	Y		-	1.0

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AT2G28190	414	AT2G28190.1	CSD2 (COPPER/ZINC SUPEROXIDE DISMUTASE 2); copper, zinc superoxide dismutase	216	Ch/S	6.48000002	22.2399998	stress oxidative	21.6 redox.dismutases and catalases	chloroplast	plastid	plastid	plastid stroma; thylakoid-peripheral-stromal-side	
AT2G28800	415	AT2G28800.1	ALB3 (ALBINO 3); P-P-bond-hydrolysis-driven protein transmembrane transporter	462	Ch/Th	9.07999992	50.2400017	protein targeting	29.3.3 protein.targeting.chloroplast	thylakoid membrane (sensu Viridiplantae) & chloroplast	plastid	plastid	thylakoid-integral	4.0
AT2G28900	416	AT2G28900.1	OEP16 (OUTER ENVELOPE PROTEIN 16); P-P-bond-hydrolysis-driven protein transmembrane transporter	148	Ch/E & Ch/Th	9.15999985	15.4799995	aa channel / protein targeting ?	34.8 transport.metabolite transporters at the envelope membrane				envelope-outer	
AT2G29630	417	AT2G29630.1	thiamine biosynthesis family protein / thiC family protein	644		5.98999977	71.9800034		18.2 Co-factor and vitamine metabolism.thiamine	chloroplast	Y	C	plastid stroma	
AT2G29650	418	AT2G29650.1	inorganic phosphate transporter, putative	512	Ch/E/IM	9.0	56.4900017	transporter Pi ?	34.7 transport.phosphate		plastid	plastid	envelope-inner-integral; thylakoid-integral	
AT2G29690	419	AT2G29690.1	ASA2 (anthranilate synthase 2); anthranilate synthase	621		6.25	69.8099976		13.1.6.5.1 amino acid metabolism.synthesis.aromatic aa.tryptophan.anthranilate synthase	chloroplast	Y	C	plastid stroma	
AT2G29720	420	AT2G29720.1	CTF2B; monooxygenase	427	CH/E ?	9.52000046	46.8800011	redox ?			-	M		

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AT2G30170	421	AT2G30170.1	catalytic	298		5.11000013	32.2799988		35.2 not assigned.unknown	undefined		C	plastid; plastid	
AT2G30200	422	AT2G30200.1	[acyl-carrier-protein] S-malonyltransferase/ binding / catalytic/ transferase	393	Ch/E & Ch/S	8.72000027	41.5200005	metabolism lipid	11.1.2 lipid metabolism. FA synthesis and FA elongation. Acetyl CoA Transacylase	chloroplast	Y	C	plastid stroma	
AT2G30390	423	AT2G30390.1	ferrochelatase II	512	Ch/Th	5.21000004	56.6199989	metabolism vitamin and pigment	19.20 tetrapyrrole synthesis. ferrochelatase		plastid	plastid	plastid	
AT2G30695	424	AT2G30695.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO46271.1); contains InterPro domain Trigger factor, ribosome-binding, bacterial; (InterPro:IPR008881)	199	Ch/S	6.32000017	22.2600002	unknown	29.6 protein.folding		plastid	plastid	plastid stroma	
AT2G30790	425	AT2G30790.1	PSBP-2 (photosystem II subunit P-2); calcium ion binding	261	Ch/Th/Lum	9.0	28.1800003	PS PSII OEE	1.1.1.2 PS.lightreaction.photosystem II.PSII polypeptide subunits	chloroplast	Y	C	thylakoid-peripheral-lumenal-side	
AT2G30860	426	AT2G30860.1	ATGSTF9 (Arabidopsis thaliana Glutathione S-transferase (class phi) 9); glutathione transferase	215		6.15999985	24.1399994		26.9 misc.glutathione S transferases	undefined			not plastid	

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AT2G30930	427	AT2G30930.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G06540.1)	164	Ch/E & other	4.92000008	16.93000003	unknown	35.2 not assigned.unknown	undefined		C	-	
AT2G30950	428	AT2G30950.1	VAR2 (VARIEGATED 2); ATP-dependent peptidase/ATPase/metallopeptidase/ zinc ion binding	695	Ch/Th & Ch/E	5.98999977	74.1500015	chaperone and protease	29.5.7 protein.degradation.metall oprotease	thylakoid membrane (sensu Viridiplantae) & chloroplast	plastid	plastid	thylakoid-integral	1.0
AT2G31040	429	AT2G31040.1	ATP synthase protein I - related	350	Ch/Th	9.27000046	38.6100006	unknown	35.2 not assigned.unknown			plastid		2.0
AT2G31170	430	AT2G31170.1	tRNA synthetase class I (C) family protein	563		6.75	63.9099998		29.1.16 protein.aa activation.cy steine-tRNA ligase	chloroplast	Y	C	mitochondria ; plastid stroma	
AT2G31190	431	AT2G31190.1	similar to EMB1879 (EMBRYO DEFECTIVE 1879) [Arabidopsis thaliana] (TAIR:AT5G49820.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO40639.1); contains InterPro domain Protein of unknown function DUF647 (InterPro:IPR006968)	433	CH/E ?	7.69999981	48.25	unknown	35.2 not assigned.unknown	other (e.g. cytoplasm)			-	2.0

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AT2G31610	432	AT2G31610.1	40S ribosomal protein S3 (RPS3A)	250	na	9.56000042	27.5200005	translation cytosol	29.2.1.2.1.3 protein.synthesis.ribosomal protein.eukaryotic.40S subunit.S3	cytosolic ribosome (sensu Eukaryota)			cytosol	
AT2G31670	433	AT2G31670.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G51360.1); similar to unknown [Populus trichocarpa] (GB:ABK93857.1); contains InterPro domain Dimeric alpha-beta barrel (InterPro:IPR011008); contains InterPro domain Stress responsive alpha-	263		6.44000006	28.8600006		35.2 not assigned.unknown	undefined	Y	M	plastid stroma	
AT2G31810	434	AT2G31810.1	acetolactate synthase small subunit, putative	491	Ch/S	9.06999969	53.8699989	metabolism amino acids branched chain	13.1.4.1.1 amino acid metabolism.synthesis.branched chain group.common.acetolactate synthase		plastid	plastid	plastid	
AT2G32290	435	AT2G32290.1	BAM6/BMY5 (BETA-AMYLASE 6); beta-amylase	577	Ch/E	6.32000017	66.5599976	metabolism carbon	2.2.2.1 major CHO metabolism.degradation.starch.starch cleavage					

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AT2G32760	436	AT2G32760.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO50091.1); contains domain PTHR15157 (PTHR15157); contains domain PTHR15157:SF2 (PTHR15157:SF2)	352		8.5600042	39.9099998		35.2 not assigned.unknown	undefined			-	
AT2G33210	437	AT2G33210.1	chaperonin, putative	585	Ch/E & other	6.36999989	61.9700012	chaperone and protease	29.6 protein.foldin g	undefined		M	mitochondria	
AT2G33430	438	AT2G33430.1	plastid developmental protein DAG, putative	219		8.51000023	24.7099991		29.2.7* protein.synthesis.ribosome biogenesis	undefined	Y	M	plastid	
AT2G33450	439	AT2G33450.1	50S ribosomal protein L28, chloroplast (CL28)	143	Ch/S & Ch/E	11.1700001	16.0300007	translation stroma	29.2.1.1.1.2.28 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.50S subunit.L28		plastid	plastid	plastid ribosome	
AT2G33800	440	AT2G33800.1	ribosomal protein S5 family protein	303	Ch/S & Ch/E & Ch/Th	8.98999977	32.6399994	translation stroma	29.2.1.1.1.1.5 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.30S subunit.S5		plastid	plastid	plastid ribosome	
AT2G34420	441	AT2G34420.1	LHB1B2 (Photosystem II light harvesting complex gene 1.5); chlorophyll binding	265	Ch/Th	5.28000021	28.0499992	PS LHCII	1.1.1.1 PS.lightreaction.photosystem II.LHC-II	thylakoid membrane (sensu Viridiplantae) & thylakoid membrane	plastid	plastid	thylakoid-integral	2.0

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AT2G34430	442	AT2G34430.1	LHB1B1 (Photosystem II light harvesting complex gene 1.4); chlorophyll binding	266	Ch/Th	5.1500001	28.1700001	PS LHCII	1.1.1.1 PS.lightreaction.photosystem II.LHC-II	thylakoid membrane (sensu Viridiplantae) & thylakoid membrane	plastid	plastid	thylakoid-integral	2.0
AT2G34460	443	AT2G34460.1	flavin reductase-related	280	Ch/E & Ch/Th	9.02999973	30.4699993	protein targeting Tic ?	35.1 not assigned.no ontology	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	plastoglobules	
AT2G34585	444	AT2G34585.1	similar to unknown [Populus trichocarpa] (GB:ABK92885.1)	81	Ch/E & other	4.03000021	8.56999969	unknown	35.2 not assigned.unknown	secreted		S	-	
AT2G35040	445	AT2G35040.1	AICARFT/IMPC Hase bienzyme family protein	596	Ch/S	6.44999981	64.9000015	metabolism nucleotide	23.1.2.9 nucleotide metabolism.synthesis.purine.AICAR transformylase and IMP synthase		plastid	plastid	plastid stroma	
AT2G35410	446	AT2G35410.1	33 kDa ribonucleoprotein, chloroplast, putative / RNA-binding protein cp33, putative	308	Ch/S	5.55000019	33.7799988	RNA binding ?	27.4 RNA.RNA binding		plastid	plastid	plastid stroma	
AT2G35490	447	AT2G35490.1	plastid-lipid associated protein PAP, putative	376	Ch/Th	4.44999981	40.5	PAP_fibrillin	26.31* misc.fibrillins	thylakoid membrane (sensu Viridiplantae)		plastid	plastoglobules	
AT2G35500	448	AT2G35500.1	shikimate kinase-related	387		5.88999987	42.6800003		13.1.6.1.5 amino acid metabolism.synthesis.aromatic aa.chorismate.shikimate kinase	chloroplast	Y	C	plastid stroma	
AT2G35800	449	AT2G35800.1	mitochondrial substrate carrier family protein	823	Ch/E ??	8.94999981	90.6200027	unknown	34.8 transport.metabolite transporters at the envelope membrane				envelope	2.0

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AT2G36145	450	AT2G36145.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO15876.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN74693.1)	186	Ch/S	9.31999969	19.8999996	unknown	35.2 not assigned.unknown	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	thylakoid	
AT2G36160	451	AT2G36160.1	40S ribosomal protein S14 (RPS14A)	150	na	10.6000004	16.25	translation cytosol	29.2.1.2.1.14 protein.synthesis.ribosomal protein.eukaryotic.40S subunit.S14				cytosol	
AT2G36230	452	AT2G36230.1	APG10 (ALBINO AND PALE GREEN 10); 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase	304		6.55000019	33.3600006		13.1.7.4 amino acid metabolism.synthesis.histidine.N-5-phosphoribosyl-formimino-5-aminoimidazole-4-carboxamide ribonucleotide isomerase	undefined	Y	M	-	
AT2G36250	453	AT2G36250.1	FTSZ2-1 (FtsZ homolog 2-1); structural molecule	478	Ch/Th & Ch/S	5.55000019	50.7200012	plastid division	31.2.5 cell.division.plastid	chloroplast stroma & chloroplast		plastid	plastid stroma	
AT2G36390	454	AT2G36390.1	SBE2.1 (STARCH BRANCHING ENZYME 2.1); 1,4-alpha-glucan branching enzyme	858		5.34000015	97.6600037		2.1.2.3 major CHO metabolism.synthesis.starch.starch branching	chloroplast	Y	C	plastid stroma	
AT2G36460	455	AT2G36460.1	fructose-bisphosphate aldolase, putative	358		7.01000023	38.3800011		4.7 glycolysis.aldolase	undefined			cytosol	

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AT2G36530	456	AT2G36530.1	LOS2 (Low expression of osmotically responsive genes 1); phosphopyruvate hydratase	444		5.53999996	47.7200012		4.12 glycolysis.enolase	undefined			cytosol	1.0
AT2G36830	457	AT2G36830.1	GAMMA-TIP (Tonoplast intrinsic protein (TIP) gamma); water channel	251	Ch/E & other	6.01999998	25.6200008	transporter aquaporin	34.19.2 transport.Major Intrinsic Proteins.TIP	undefined			-	7.0
AT2G36835	458	AT2G36835.1	similar to hypothetical protein [Vitis vinifera] (GB:CAN81061.1)	124	Ch/E/IM	7.84000015	13.3800001	unknown	35.2 not assigned.unknown	undefined		C	-	
AT2G36885	459	AT2G36885.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO63025.1)	256	Ch/Th	6.36999989	27.4899998	unknown	35.2 not assigned.unknown		plastid	plastid		5.0
AT2G37020	460	AT2G37020.1	DNA binding	238		5.3499999	27.3199997		35.1 not assigned.no ontology	chloroplast			-	
AT2G37080	461	AT2G37080.1	myosin heavy chain-related	583		5.17000008	65.8499985		31.1 cell.organisation	chloroplast	Y	C	-	
AT2G37190	462	AT2G37190.1	60S ribosomal protein L12 (RPL12A)	166	Ch/E & other	9.05000019	17.9400005	translation cytosol	29.2.1.2.2.12 protein.synthesis.ribosomal protein.eukaryotic.60S subunit.L12	undefined			cytosol	
AT2G37220	463	AT2G37220.1	29 kDa ribonucleoprotein, chloroplast, putative / RNA-binding protein cp29, putative	289	Ch/S & Ch/Th & Ch/E	5.05000019	30.7099991	RNA Binding	27.4 RNA.RNA binding		plastid	plastid	plastid stroma	

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AT2G37230	464	AT2G37230.1	pentatricopeptide (PPR) repeat-containing protein	757	Ch/Th	8.89000034	85.6999969	RNA Binding ?	27.7* RNA.misc.pentatricopeptide (PPR) repeat-containing protein	thylakoid membrane (sensu Viridiplantae)	plastid	mitochondrion		
AT2G37400	465	AT2G37400.1	chloroplast lumen common family protein	333	Ch/E/IM	6.69999981	38.1500015	unknown	35.1 not assigned.no ontology		plastid	plastid	plastid	
AT2G37500	466	AT2G37500.1	arginine biosynthesis protein ArgJ family	468		6.21000004	48.7099991				Y	C	plastid stroma	
AT2G37660	467	AT2G37660.1	binding / catalytic/ coenzyme binding	325	Ch/S	8.36999989	34.8800011	protein targeting Tic ?	35.2 not assigned.unknown		plastid	plastid	plastid stroma	
AT2G37690	468	AT2G37690.1	phosphoribosylaminoimidazole carboxylase, putative / AIR carboxylase, putative	642		6.51999998	69.75		23.1.2.6 nucleotide metabolism.synthesis.purine.AIR carboxylase	undefined	Y	C	plastid	
AT2G37860	469	AT2G37860.3	LCD1 (LOWER CELL DENSITY 1)	347	Ch/E/IM	5.57000017	37.3499985	unknown	33.99 development.unspecified		plastid	plastid	plastid	

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AT2G38025	470	AT2G38025.1	similar to OTU-like cysteine protease family protein [Arabidopsis thaliana] (TAIR:AT3G57810.1); similar to OTU-like cysteine protease family protein [Arabidopsis thaliana] (TAIR:AT3G57810.3); similar to OTU-like cysteine protease family protein [Arab	234	Ch/E/IM	9.4700027	26.2700005	chaperone and protease	35.2 not assigned.unkn	chloroplast	Y	C	-	
AT2G38040	471	AT2G38040.1	CAC3 (acetyl co-enzyme A carboxylase carboxyltransferase alpha subunit); acetyl-CoA carboxylase	769	Ch/E	5.6100013	85.3000031	metabolism lipid	11.1.1 lipid metabolism. FA synthesis and FA elongation. Acetyl CoA Carboxylation		plastid	plastid	envelope-inner-peripheral-stromal-side	
AT2G38140	472	AT2G38140.1	PSRP4 (PLASTID-SPECIFIC RIBOSOMAL PROTEIN 4); structural constituent of ribosome	118	Ch/S & Ch/E	10.1700001	12.7799997	translation stroma	29.2.1.1.1.1.31 protein. synthesis. ribosomal protein. prokaryotic. chloroplast. 30S subunit. S31		plastid	plastid	plastid ribosome	
AT2G38270	473	AT2G38270.1	CXIP2 (CAX-INTERACTING PROTEIN 2); electron carrier/protein disulfide oxidoreductase	293	Ch/S	7.71999979	32.2000008	redox	34.21 transport. calcium		plastid	plastid	plastid stroma	

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AT2G38530	474	AT2G38530.1	LTP2 (LIPID TRANSFER PROTEIN 2); lipid binding	118		9.31999969	11.9300003		11.6 lipid metabolism.lipid transfer proteins etc	secreted		S	-	
AT2G38540	475	AT2G38540.1	LP1 (nonspecific lipid transfer protein 1)	118	Ch/Th	9.30000019	11.75	metabolism lipid ?	11.6 lipid metabolism.lipid transfer proteins etc	cell wall (sensu Magnoliophyta)		extracellular, endoplasmic reticulum, golgi	cytosol; plasma membrane	
AT2G38550	476	AT2G38550.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G57280.1); similar to non-green plastid inner envelope membrane protein precursor (GB:AAA84891.1); contains InterPro domain Protein of unknown function UPF0136, Transmembrane; (InterPro:IPR00	335	Ch/E/IM	6.98999977	36.7000008	unknown	35.2 not assigned.unknown	chloroplast inner membrane	plastid	plastid	envelope-inner-integral	4.0
AT2G38810	477	AT2G38810.1	HTA8; DNA binding	136	other	10.4700003	14.3699999	DNA binding	28.1.3 DNA.synthesis/chromatin structure.histone	undefined	Y	C	-	
AT2G39080	478	AT2G39080.1	binding / catalytic	351		7.6500001	38.25		35.2 not assigned.unknown	chloroplast	Y	C	plastid stroma	

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AT2G39290	479	AT2G39290.1	PGP1/PGPS1/PGS1 (PHOSPHATIDYLGLYCEROLPHOSPHATE SYNTHASE 1); CDP-alcohol phosphatidyltransferase/CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase	296	Ch/E/IM	10.3000002	32.1500015	metabolism lipid	11.10 lipid metabolism.glycolipid synthesis	mitochondrion & chloroplast	plastid	plastid	mitochondria ; plastid	2.0
AT2G39470	480	AT2G39470.1	PPL2 (PSBP-LIKE PROTEIN 2); calcium ion binding	238	Ch/Th	8.89000034	26.9599991	PS PSII or NDH ?	1.1.6 PS.lightreaction.NADH DH	thylakoid membrane (sensu Viridiplantae) & thylakoid lumen (sensu Viridiplantae)		plastid	thylakoid-peripheral-lumenal-side	
AT2G39730	481	AT2G39730.1	RCA (RUBISCO ACTIVASE)	446	Ch & other	7.53999996	49.0999985	chaperone and protease	1.3.13 PS.calvin cycle.rubisco interacting	chloroplast	Y	C	plastid stroma	
AT2G39730	482	AT2G39730.2	RCA (RUBISCO ACTIVASE)	446	Ch/S & Ch/E	7.53999996	49.0999985	metabolism carbon Calvin cycle chaperone and protease	1.3.13 PS.calvin cycle.rubisco interacting	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	plastid stroma	
AT2G39930	483	AT2G39930.1	ATISA1/ISA1 (ISOAMYLASE 1); alpha-amylase/isoamylase	783		5.76999998	89.4800034		2.1.2.4 major CHO metabolism.synthesis.starch.debranching	undefined	Y	C	plastid	
AT2G40010	484	AT2G40010.1	60S acidic ribosomal protein P0 (RPP0A)	317	Ch/E & other	5.17999983	33.6599998	translation cytosol	29.2.1.2.2.80 protein.synthesis.ribosomal protein.eukaryotic.60S subunit.P0	secreted		S	cytosol	

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AT2G40030	485	AT2G40030.1	NRPD1b (nuclear RNA polymerase D 1b); DNA binding / DNA-directed RNA polymerase	501		5.8800011	218.220001		27.2 RNA.transcription	undefined			-	
AT2G40100	486	AT2G40100.1	LHCB4.3 (LIGHT HARVESTING COMPLEX PSII); chlorophyll binding	276	Ch/Th	5.2199979	30.2099991	PS LHCII	1.1.1.1 PS.lightreaction.photosystem II.LHC-II	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	thylakoid-integral	3.0
AT2G40300	487	AT2G40300.1	ATFER4 (FERRITIN 4); ferric iron binding	259		6.1500001	29.0200005		15.2 metal handling.binding, chelation and storage	chloroplast	Y	C	plastid stroma	
AT2G40490	488	AT2G40490.1	HEME2; uroporphyrinogen decarboxylase	394	Ch/S	8.2799973	43.5800018	metabolism vitamin and pigment	19.7 tetrapyrrole synthesis.uroporphyrinogen decarboxylase		plastid	plastid	plastid stroma	
AT2G40510	489	AT2G40510.1	40S ribosomal protein S26 (RPS26A)	133	Ch & other	11.0900002	14.8400002	translation cytosol	29.2.1.2.1.26 protein.synthesis.ribosomal protein.eukaryotic.40S subunit.S26	undefined			-	
AT2G40690	490	AT2G40690.1	GLY1 (SUPPRESSOR OF FATTY ACID DESATURASE DEFICIENCY 1); glycerol-3-phosphate dehydrogenase (NAD+)	300	Ch/E/IM	8.75	45.0900002	metabolism lipid ?	11.5.2 lipid metabolism.glycerol metabolism.Glycerol-3-phosphate dehydrogenase (NAD+)				plastid	

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AT2G41680	491	AT2G41680.1	thioredoxin reductase, putative / NADPH-dependent thioredoxin reductase, putative	529	Ch/S	6.30000019	57.9500008	redox	21.1 redox.thioredoxin		plastid	plastid	plastid stroma	
AT2G41950	492	AT2G41950.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO23423.1); contains domain S-adenosyl-L-methionine-dependent methyltransferases (SSF53335)	266		5.53999996	30.0200005		35.2 not assigned.unknown	chloroplast	Y	C	plastid stroma	
AT2G42130	493	AT2G42130.4	Identical to Probable plastid-lipid-associated protein 13, chloroplast precursor (PAP13) [Arabidopsis thaliana] (GB:Q8S9M1;GB:O48521;GB:Q84X37;GB:Q84X38;GB:Q84X39;GB:Q8GY49); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G58010.1); simi	299	Ch/Th & Ch/S	4.84000015	27.6599998	PAP_fibrillin	26.31* misc.fibrillins		plastid	plastid	plastoglobules	
AT2G42220	494	AT2G42220.1	rhodanese-like domain-containing protein	234	Ch/Th & Ch/E	8.85999966	25.5100002	chaperone and protease ?	26.23 misc.rhodanese	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	thylakoid	1.0
AT2G42530	495	AT2G42530.1	COR15B	141		6.61999989	14.96		20.2.2 stress.abiotic.cold	undefined	Y	C	plastid stroma	

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AT2G42540	496	AT2G42540.1	COR15A (COLD-REGULATED 15A)	127		6.61000013	13.4499998		20.2.2 stress.abiotic.cold	undefined	Y	M	plastid stroma	
AT2G42740	497	AT2G42740.1	RPL16A (ribosomal protein large subunit 16A); structural constituent of ribosome	182	Ch/E & other	9.93000031	20.8299999	translation cytosol	29.2.1.2.2.11 protein.synthesis.ribosomal protein.eukaryotic.60S subunit.L11	undefined			-	
AT2G42770	498	AT2G42770.1	peroxisomal membrane 22 kDa family protein	232	Ch/E/IM	9.81000042	25.9099998	transporter ?	35.1 not assigned.no ontology		plastid		envelope-inner-integral	2.0
AT2G43030	499	AT2G43030.1	ribosomal protein L3 family protein	271	Ch/S & Ch/E	10.4300003	29.3600006	translation stroma	29.2.1.1.1.2.3 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.50S subunit.L3		plastid	plastid	plastid ribosome	
AT2G43090	500	AT2G43090.1	aconitase C-terminal domain-containing protein	251		6.32999992	26.7900009		13.1.4.4 amino acid metabolism.synthesis.branched chain group.leucine specific	chloroplast	Y	C	-	
AT2G43240	501	AT2G43240.1	nucleotide-sugar transmembrane transporter	406	Ch/E ?	8.92000008	86.9499969	unknown	34.2 transport.sugars	undefined			-	8.0
AT2G43560	502	AT2G43560.1	immunophilin / FKBP-type peptidyl-prolyl cis-trans isomerase family protein	223	Ch/Th & Ch/S & Ch/E	8.39999962	23.5599995	chaperone and protease	29.6 protein.folding	thylakoid lumen (sensu Viridiplantae)	plastid	plastid	thylakoid-peripheral-lumenal-side	

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AT2G43630	503	AT2G43630.1	similar to glycine-rich protein [Arabidopsis thaliana] (TAIR:AT3G59640.2); similar to glycine-rich protein [Arabidopsis thaliana] (TAIR:AT3G59640.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO46269.1)	274	Ch/E/IM	8.28999996	30.7000008	unknown	35.2 not assigned.unknown	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	plastid	1.0
AT2G43710	504	AT2G43710.1	SSI2 (fatty acid biosynthesis 2); acyl-[acyl-carrier-protein] desaturase	401	Ch/Th & Ch/S	6.05000019	45.6899986	metabolism lipid	11.1.15 lipid metabolism. FA synthesis and FA elongation.ACP desaturase		plastid	plastid	plastid stroma	
AT2G43750	505	AT2G43750.1	OASB (O-ACETYLSERINE (THIOL) LYASE B); cysteine synthase	392	Ch/S	8.13000011	41.6500015	metabolism aa Cys	13.1.5.3.1 amino acid metabolism.serine-glycine-cysteine group.cysteine.OASTL		plastid	plastid	plastid stroma	

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AT2G43945	506	AT2G43945.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G59870.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN60471.1); contains InterPro domain Gamma thionin; (InterPro:IPR008176)	289	Ch/S	6.25	32.1599998	unknown	35.2 not assigned.unknown		plastid	plastid	plastid stroma	
AT2G43950	507	AT2G43950.1	OEP37; ion channel	343	Ch/E/OM	9.15999985	38.8300018	transporter ion channel	34.8 transport.metabolite transporters at the envelope membrane	chloroplast & chloroplast inner membrane	plastid	plastid	envelope-outer	
AT2G44040	508	AT2G44040.1	dihydrodipicolinate reductase family protein	347	Ch/S	6.01000023	37.5499992	metabolism amino acids lysine	13.1.3.5.2 amino acid metabolism.synthesis.aspartate family.lysine.dihydrodipicolinate reductase		plastid	plastid	plastid stroma	
AT2G44050	509	AT2G44050.1	COS1 (COI1 SUPPRESSOR1); 6,7-dimethyl-8-ribityllumazine synthase	227	Ch/S	8.61999989	24.0200005	unknown	18.3.2 Co-factor and vitamine metabolism.riboflavin.riboflavin synthase		plastid	plastid	plastid	
AT2G44530	510	AT2G44530.1	ribose-phosphate pyrophosphokinase, putative / phosphoribosyl diphosphate synthetase, putative	394	Ch/S	6.71000004	42.6199989	metabolism nucleotide	23.1.3 nucleotide metabolism.synthesis.PRS-PP		plastid	plastid	plastid stroma	

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AT2G44610	511	AT2G44610.1	RAB6; GTP binding	208	Ch/E ?	7.67000008	23.1299992	signalling / SNARE effector	30.5 signalling.G-proteins	undefined			-	
AT2G44640	512	AT2G44640.1	similar to PDE320 (PIGMENT DEFECTIVE 320) [Arabidopsis thaliana] (TAIR:AT3G06960.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO70456.1)	451	Ch/E ?	8.80000019	49.8300018	transporter lipids	35.2 not assigned.unknown	chloroplast envelope		plastid	envelope	
AT2G44650	513	AT2G44650.1	CHL-CPN10 (chloroplast chaperonin 10)	139	Ch/S	8.73999977	15.0500002	chaperone and protease	29.6 protein.folding	chloroplast	Y	C	plastid stroma	
AT2G44870	514	AT2G44870.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO62235.1); contains domain Zinc beta-ribbon (SSF57783)	248	Ch/E/IM	9.93000031	28.0699997	RNA transcription ?	35.2 not assigned.unknown		plastid	mitochondrion		2.0
AT2G44920	515	AT2G44920.2	thylakoid lumenal 15 kDa protein, chloroplast	224	Ch/Th	7.55000019	23.7700005	RNA Binding ?	27.7* RNA.misc.peptidicopeptide (PPR) repeat-containing protein	thylakoid membrane (sensu Viridiplantae) & thylakoid lumen (sensu Viridiplantae)	plastid	plastid	thylakoid-peripheral-lumenal-side	
AT2G45290	516	AT2G45290.1	transketolase, putative	741	Ch/S	6.11999989	79.9199982	metabolism carbon	1.3.8 PS.calvin cycle.transketolase	chloroplast	Y	C	-	

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AT2G45300	517	AT2G45300.1	3-phosphoshikimate 1-carboxyvinyltransferase / 5-enolpyruvylshikimate-3-phosphate / EPSP synthase	520		6.28999996	55.7299995		13.1.6.1.6 amino acid metabolism.synthesis.aromatic aa.chorismate.e.5-enolpyruvylshikimate-3-phosphate synthase	chloroplast	Y	C	-	
AT2G45440	518	AT2G45440.1	DHDPS2 (DIHYDRODIPICOLINATE SYNTHASE); dihydrodipicolinate synthase	365		7.17000008	40.2900009		13.1.3.5.1 amino acid metabolism.synthesis.aspartate family.lysine.dihydrodipicolinate synthase	undefined	Y	C	-	
AT2G45540	519	AT2G45540.1	WD-40 repeat family protein / beige-related	2946		5.55999994	321.929993		35.1 not assigned.no ontology	other (e.g. cytoplasm)			-	2.0
AT2G45740	520	AT2G45740.1	PEX11D	236	na	9.97999954	25.9400005	unknown	35.1 not assigned.no ontology			extracellular, endoplasmic reticulum, golgi	peroxisome	2.0
AT2G45770	521	AT2G45770.1	CPFTSY (ferric reductase deficient 4); GTP binding	366	Ch/E & Ch/Th & Ch/S	7.59000015	39.6699982	protein targeting	29.3.3 protein.targeting.chloroplast		plastid	plastid	thylakoid-peripheral-stromal-side	
AT2G45990	522	AT2G45990.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO39632.1); contains domain HAD-like (SSF56784)	268		5.05000019	30.1100006		35.2 not assigned.unknown	undefined			plastid stroma	

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AT2G46100	523	AT2G46100.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G04890.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO39659.1); contains domain SSF54427 (SSF54427)	240	Ch/E/IM	8.85999966	26.8400002	unknown	35.2 not assigned.unkn own	chloroplast	Y	C	-	
AT2G46820	524	AT2G46820.1	PSAP/PSI-P/PTAC8/TMP14 (THYLAKOID MEMBRANE PHOSPHOPROTEIN OF 14 KDA); DNA binding	174	Ch/Th	7.71999979	18.4799995	PS PSI	1.1.2.2 PS.lightreacti on.photosyst em I.PSI polypeptide subunits	thylakoid membrane (sensu Viridiplantae) & photosystem I (sensu Viridiplantae) & plastid chromosome	plastid	plastid	thylakoid	
AT2G46910	525	AT2G46910.1	plastid-lipid associated protein PAP / fibrillin family protein	284	Ch/S	8.34000015	31.5799999	PAP_fibrillin	26.31* misc.fibrillins		plastid	plastid	plastoglobules	
AT2G47220	526	AT2G47220.1	3' exoribonuclease family domain 1 protein-related	469		5.42000008	52.4000015		27.1.19 RNA.process ing.ribonucle ases	undefined			-	
AT2G47390	527	AT2G47390.1	serine-type endopeptidase/ serine-type peptidase	961		5.98999977	106.260002		29.5.5 protein.degra dation.serine protease	chloroplast	Y	C	plastid stroma	
AT2G47400	528	AT2G47400.1	CP12-1 (CP12 domain-containing protein 1)	124	Ch/E ?	4.8499999	13.4799995	metabolism carbon	1.3.14* PS.calvin cycle regulation CP12	undefined	Y	C	-	
AT2G47450	529	AT2G47450.1	CAO (CHAOS); chromatin binding	373		4.51999998	41.2700005		29.3.3 protein.target ing.chloropla st	chloroplast	Y	C	plastid stroma	

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AT2G47730	530	AT2G47730.1	ATGSTF8 (GLUTATHIONE S-TRANSFERASE 8); glutathione transferase	263		8.48999977	29.2299995		26.9 misc.glutathione S transferases	chloroplast	Y	C	-	
AT2G47840	531	AT2G47840.1	tic20 protein-related	208	Ch/E/IM	10.2799997	22.9099998	protein targeting Tic ?	29.3.3 protein.targeting.chloroplast		plastid	plastid	envelope-inner-integral	4.0
AT2G47910	532	AT2G47910.1	CRR6 (CHLOROPHYLL REDUCTASE 6)	246		5.34000015	28.0200005		1.1.6.1* PS.lightreaction.NADH DH.assembly	undefined		M	plastid stroma	
AT2G47940	533	AT2G47940.1	DEGP2 (DEGP PROTEASE 2); serine-type peptidase/trypsin	607	Ch/S & Ch/E	5.69999981	66.8000031	chaperone and protease	29.5.5 protein.degradation.serine protease	thylakoid membrane (sensu Viridiplantae) & chloroplast stromal thylakoid	plastid	plastid	plastid stroma	
AT3G01120	534	AT3G01120.1	MTO1 (METHIONINE OVERACCUMULATION 1)	563		6.4000001	59.9099998		13.1.3.4.1 amino acid metabolism.synthesis.aspartate family.methionine.cystathionine.gamma-synthase	chloroplast	Y	C	-	1.0
AT3G01390	535	AT3G01390.1	VMA10 (VACUOLAR MEMBRANE ATPASE 10)	110	other	5.76000023	12.3900003	transporter ATPase	34.1 transport.p-and v-ATPases	undefined			-	
AT3G01440	536	AT3G01440.1	oxygen evolving enhancer 3 (PsbQ) family protein	220	Ch/Th	7.67000008	24.7800007	PS PSII OEE or NDH ?	1.1.6 PS.lightreaction.NADH DH	thylakoid membrane (sensu Viridiplantae) & thylakoid lumen (sensu Viridiplantae) & oxygen evolving complex	plastid	plastid	thylakoid-peripheral-lumenal-side	

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AT3G01480	537	AT3G01480.1	CYP38 (CYCLOPHILIN 38); peptidyl-prolyl cis-trans isomerase	437	Ch/Th	5.05000019	47.9799995	chaperone and protease	29.6 protein.folding	thylakoid membrane (sensu Viridiplantae) & thylakoid lumen (sensu Viridiplantae)	plastid	plastid	thylakoid-peripheral-lumenal-side	1.0
AT3G01500	538	AT3G01500.1	CA1 (CARBONIC ANHYDRASE 1); carbonate dehydratase/zinc ion binding	270	Ch	5.53000021	29.5	metabolism carbon	8.3 TCA / org.transformation.carbonic anhydrases	chloroplast			plastid stroma	
AT3G01500	539	AT3G01500.3	CA1 (CARBONIC ANHYDRASE 1); carbonate dehydratase/zinc ion binding	270	Ch/E & Ch/S	5.53000021	29.5	metabolism carbon	8.3 TCA / org.transformation.carbonic anhydrases	thylakoid membrane (sensu Viridiplantae)			plastid stroma	
AT3G02360	540	AT3G02360.1	6-phosphogluc onate dehydrogenase family protein	486		7.01999998	53.5699997		7.1.3 OPP.oxidative PP.6-phosphogluc onate dehydrogenase	secreted		S	-	
AT3G02450	541	AT3G02450.1	cell division protein ftsH, putative	622	Ch/E/IM	9.67000008	69.4100037	chaperone and protease	29.5.7 protein.degradation.metall oprotease	chloroplast	Y	C	-	3.0
AT3G02660	542	AT3G02660.1	EMB2768 (EMBRYO DEFECTIVE 2768); ATP binding / aminoacyl-tRNA ligase	511	Ch/S	6.01000023	56.6100006	unknown	29.1.1 protein.aa activation.tyrosine-tRNA ligase	mitochondrion & chloroplast	plastid	plastid	mitochondria ; plastid stroma	
AT3G02730	543	AT3G02730.1	ATF1/TRXF1 (THIOREDOXIN F-TYPE 1); thiol-disulfide exchange intermediate	178		9.11999989	19.3199997		21.1 redox.thioredoxin	chloroplast	Y	C	plastid stroma; thylakoid-peripheral-stromal-side	

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AT3G02780	544	AT3G02780.1	IDI2/IPIAT1/PP2 (ISOPENTE NYL DIPHOSPHATE ISOMERASE 2, ISOPENTENYL PYROPHOSPHATE:DIMETHYLLALLYL PYROPHOSPHATE ISOMERASE 2); isopentenyl-diphosphate delta-isomerase	284	Ch/E ?	6.09000015	32.5999985	metabolism vitamin and pigment	16.1.2.7 secondary metabolism.i soprenoids. mevalonate pathway.isop entenyl pyrophosphate:dimethyl lal yl pyrophosphate isomerase	chloroplast	Y	C	cytosol; mitochondria	
AT3G02900	545	AT3G02900.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G16660.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO62132.1)	162	Ch/E/IM	9.51000023	17.3199997	unknown	35.2 not assigned.unk nown		plastid	plastid	plastid	1.0
AT3G03710	546	AT3G03710.1	RIF10 (RESISTANT TO INHIBITION WITH FSM 10); 3'-5'-exoribonuclease/ RNA binding / nucleic acid binding	922	Ch/S	5.4000001	99.5599976	unknown	27.1.19 RNA.process ing.ribonucle ases		plastid	plastid	plastid stroma	
AT3G04260	547	AT3G04260.1	PTAC3 (PLASTID TRANSCRIPTIONALLY ACTIVE3); DNA binding	913	Ch/S	4.94000006	103.120003	DNA Binding ?	28.3* DNA.plastid nucleoid interacting	plastid chromosome	plastid	plastid	plastid	

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AT3G04340	548	AT3G04340.1	EMB2458 (EMBRYO DEFECTIVE 2458); ATPase	960	Ch/E/IM	8.01000023	111.010002	chaperone and protease	29.5.7 protein.degradation.metall oprotease	chloroplast			plastid	
AT3G04550	549	AT3G04550.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G28500.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO65032.1)	449		5.76999998	50.2000008		35.2 not assigned.unk nown	chloroplast	Y	C	plastid stroma	
AT3G04790	550	AT3G04790.1	ribose 5-phosphate isomerase-related	276	Ch/S	5.71999979	29.2999992	metabolism carbon Calvin cycle	1.3.10 PS.calvin cyle.Rib5P Isomerase	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	plastid stroma; thylakoid-peripheral-stromal-side	
AT3G04840	551	AT3G04840.1	40S ribosomal protein S3A (RPS3aA)	262	Ch/E & other	9.77000046	29.8500004	translation cytosol	29.2.1.2.1.53 protein.synthesis.ribosomal protein.eukaryotic.40S subunit.S3A	other (e.g. cytoplasm)			cytosol	
AT3G04870	552	AT3G04870.1	ZDS (ZETA-CAROTENE DESATURASE); carotene 7,8-desaturase	558	Ch/E & Ch/S	7.03000021	61.6300011	metabolism vitamin and pigment	16.1.4.3 secondary metabolism.isoprenoids.carotenoids.z eta-carotene desaturase		plastid	plastid	plastid	

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AT3G04890	553	AT3G04890.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G46100.1); similar to unknown [Picea sitchensis] (GB:ABK21558.1); contains domain SSF54427 (SSF54427)	216	Ch/E/IM	6.6100013	24.4300003	unknown	35.2 not assigned.unknown		plastid	plastid	plastid	
AT3G04940	554	AT3G04940.1	ATCYSD1 (Arabidopsis thaliana cysteine synthase D1); cysteine synthase	324		5.23000002	34.2900009		13.1.5.3.1 amino acid metabolism.synthesis.serine-glycine-cysteine group.cysteine.OASTL	other (e.g. cytoplasm)			-	
AT3G05350	555	AT3G05350.1	aminopeptidase	548		5.32000017	60.8499985		29.5 protein.degradation	undefined			plastid stroma	
AT3G05625	556	AT3G05625.1	binding	257		6.94999981	28.9500008		26.33* misc.tetratricopeptide repeat (TPR) unknown function	chloroplast	Y	C	plastid	
AT3G06030	557	AT3G06030.1	ANP3 (Arabidopsis NPK1-related protein kinase 3); kinase	651		8.40999985	71.6500015		29.4 protein.posttranslational modification	undefined	Y		-	

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AT3G06350	558	AT3G06350.1	EMB3004/ME32 (EMBRYO DEFECTIVE 3004); 3-dehydroquinase dehydratase/NADP binding / binding / catalytic/shikimate 5-dehydrogenase	603	Ch/S	6.4000001	65.7900009	metabolism aminoacids aromatic	13.1.6.1.10 amino acid metabolism.synthesis.aromatic aa.chorismate.dehydroquinase/shikimate dehydrogenase		plastid	plastid	plastid	
AT3G06510	559	AT3G06510.1	SFR2 (SENSITIVE TO FREEZING 2); hydrolase, hydrolyzing O-glycosyl compounds	622	Ch/E/OM	8.78999996	70.7699966	stress freezing	11.10 lipid metabolism.glycolipid synthesis			extracellular, endoplasmic reticulum, golgi	envelope-outer	1.0
AT3G06730	560	AT3G06730.1	thioredoxin family protein	183	Ch/S	5.63999987	20.6700001	redox	21.1 redox.thioredoxin		plastid	plastid	plastid	
AT3G06960	561	AT3G06960.1	PDE320 (PIGMENT DEFECTIVE 320)	479	Ch/E/OM ?	6.36000013	52.8199997	unknown	11.15* lipid metabolism.t transport				envelope-outer	
AT3G07430	562	AT3G07430.1	EMB1990 (EMBRYO DEFECTIVE 1990)	232	Ch/E/IM	10.6599998	24.9200001	cytochrome biogenesis ?	35.1 not assigned.no ontology		plastid	plastid	plastid ribosome	
AT3G07440	563	AT3G07440.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G48530.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN82702.1)	235		9.35000038	28.5400009		35.2 not assigned.unknown	undefined		M	-	

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AT3G07630	564	AT3G07630.1	ADT2 (AROGENATE DEHYDRATASE 2); arogenate dehydratase/prephenate dehydratase	381		7.6700008	42.1100006		13.1.6.3.1 amino acid metabolism.synthesis.aromatic aa.phenylalanine.arogenate dehydratase / prephenate dehydratase	undefined	Y	C	plastid stroma	
AT3G07770	565	AT3G07770.1	ATP binding	799		5.25	90.9499969		20.2.1 stress.abiotic.heat	mitochondrion	Y	M	-	
AT3G08010	566	AT3G08010.1	ATAB2; RNA binding	374	Ch/S	5.0	41.9099998	RNA binding ?	27.4 RNA.RNA binding		plastid	plastid	plastid	
AT3G08580	567	AT3G08580.1	AAC1 (ADP/ATP CARRIER 1); ATP:ADP antiporter/binding	381	na	9.8299992	41.4700012	Mito transporter ATP/ADP	34.9 transport.metabolite transporters at the mitochondrial membrane	mitochondrial envelope & mitochondrion	plastid		mitochondria	3.0
AT3G08640	568	AT3G08640.1	alphavirus core protein family	337	Ch/E/IM	9.0	35.25	unknown	35.1 not assigned.no ontology	chloroplast envelope	plastid	plastid	envelope	3.0
AT3G08740	569	AT3G08740.1	elongation factor P (EF-P) family protein	236	Ch/S	8.60999966	26.2199993	translation stroma	29.2.4 protein.synthesis.elongation		plastid	plastid	plastid stroma	
AT3G08920	570	AT3G08920.1	rhodanese-like domain-containing protein	214	Ch/Th ?? & Ch/E ??	9.31999969	23.7800007	unknown	26.23 misc.rhodanese			mitochondrion	thylakoid	1.0
AT3G08940	571	AT3G08940.2	LHCB4.2 (LIGHT HARVESTING COMPLEX PSII); chlorophyll binding	287	Ch/Th	5.8499999	31.1900005	PS LHCII	1.1.1.1 PS.lightreaction.photosystem II.LHC-II	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	thylakoid-integral	
AT3G09440	572	AT3G09440.1	heat shock cognate 70 kDa protein 3 (HSC70-3) (HSP70-3)	649	Ch/E & Ch/S	4.96999979	71.1399994	chaperone and protease	20.2.1 stress.abiotic.heat				not plastid	

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AT3G09580	573	AT3G09580.1	amine oxidase family protein	477	Ch/E/IM	7.01999998	52.25	metabolism vitamin and pigment ?	16.1.4 secondary metabolism.i soprenoids.c arotenoids		plastid	plastid	plastid	
AT3G10050	574	AT3G10050.1	OMR1 (L-O-METHYLTHREONINE RESISTANT 1); L-threonine ammonia-lyase	592		7.19999981	64.6299973		13.1.4.5.1 amino acid metabolism.s ynthesis.branched chain group.isoleucine specific.threonine ammonia-lyase	chloroplast	Y	C	-	1.0
AT3G10060	575	AT3G10060.1	immunophilin , putative / FKBP-type peptidyl-prolyl cis-trans isomerase, putative	230	Ch/Th	9.65999985	24.5	chaperone and protease	29.6 protein.foldin g	thylakoid lumen (sensu Viridiplantae)	plastid	plastid	thylakoid-peripheral-lumenal-side	
AT3G10230	576	AT3G10230.1	LYC (LYCOPENE CYCLASE); lycopene beta cyclase	501	Ch/E ?	7.5999999	56.1699982	metabolism vitamin and pigment	16.1.4.5 secondary metabolism.i soprenoids.c arotenoids.ly copene beta cyclase	undefined			-	
AT3G10350	577	AT3G10350.1	anion-transporting ATPase family protein	411	Ch/S	7.63000011	44.75	transporter anion ?	34.18.1 transport.uns pecified anions.arsen ite-transporting ATPase		plastid	plastid	plastid	
AT3G10670	578	AT3G10670.1	ATNAP7 (Arabidopsis thaliana non-intrinsic ABC protein 7)	338	Ch/S	6.61000013	36.9300003	transporter ABC	14 S-assimilation	chloroplast	plastid	plastid	plastid stroma	
AT3G10680	579	AT3G10680.1	heat shock protein-related	490	Ch/E/IM	8.94999981	54.1899986	chaperone and protease	20.2.1 stress.abiotic .heat	undefined	Y	C	-	1.0
AT3G10690	580	AT3G10690.1	DNA gyrase subunit A family protein	950	Ch/Th	6.46000004	104.529999	DNA Binding	28.2 DNA.repair	mitochondrion	plastid	plastid	mitochondria ; plastid	

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AT3G10840	581	AT3G10840.1	hydrolase, alpha/beta fold family protein	466	Ch/E/IM	8.59000015	50.8800011	metabolism lipid ?	11.9.2 lipid metabolism.lipid degradation.lipases		plastid	plastid	plastid	
AT3G10920	582	AT3G10920.1	MSD1 (MANGANESE SUPEROXIDE DISMUTASE 1); manganese superoxide dismutase	231		8.46000004	25.4400005		21.6 redox.dismutases and catalases	undefined		M	mitochondria	
AT3G11170	583	AT3G11170.1	FAD7 (FATTY ACID DESATURASE 7); omega-3 fatty acid desaturase	446	Ch/E/IM	8.14000034	51.1699982	metabolism lipid	11.2.3 lipid metabolism.FA desaturation.omega 3 desaturase	plastid membrane		plastid	envelope-inner-integral	4.0
AT3G11510	584	AT3G11510.1	40S ribosomal protein S14 (RPS14B)	150	Ch/E & other	10.6000004	16.2700005	translation cytosol	29.2.1.2.1.14 protein.synthesis.ribosomal protein.eukaryotic.40S subunit.S14	other (e.g. cytoplasm)			cytosol	
AT3G11560	585	AT3G11560.2	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G06220.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO15863.1)	619	Ch/E/IM	8.31999969	69.6800003	transporter K+/H+?	35.2 not assigned.unknown		plastid	plastid	envelope	
AT3G11630	586	AT3G11630.1	2-cys peroxiredoxin, chloroplast (BAS1)	266	Ch/S	6.90999985	29.0900002	redox	21.5 redox.peroxi		plastid	plastid	plastid stroma; thylakoid-peripheral-stromal-side	

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AT3G11940	587	AT3G11940.1	ATRPS5A (RIBOSOMAL PROTEIN 5A); structural constituent of ribosome	207	Ch & other	9.6499962	22.9200001	translation cytosol	29.2.1.2.1.5 protein.synthesis.ribosomal.protein.eukaryotic.40S.subunit.S5	undefined			-	
AT3G11950	588	AT3G11950.1	homogentisate farnesyltransferase/homogentisate geranylgeranyltransferase / homogentisate solanesyltransferase/prenyltransferase	572	Ch/E/IM	5.1500001	106.650002	metabolism isoprenoids	16.1 secondary.metabolism.isoprenoids	other (e.g. cytoplasm)			-	7.0
AT3G12080	589	AT3G12080.1	EMB2738 (EMBRYO DEFECTIVE 2738); GTP binding	663	Ch/S	6.1399987	73.1200027	unknown	29.2.7* protein.synthesis.ribosome biogenesis		plastid	plastid	plastid	
AT3G12110	590	AT3G12110.1	ACT11 (ACTIN-11); structural constituent of cytoskeleton	377	Ch/E & other	5.2199979	41.6699982	plastid positioning ?	31.1 cell.organisation	other (e.g. cytoplasm)			-	
AT3G12780	591	AT3G12780.1	PGK1 (PHOSPHOGLYCERATE KINASE 1); phosphoglycerate kinase	481	Ch/S	5.9099985	50.1100006	metabolism carbon Calvin cycle	1.3.3 PS.calvin cycle.phosphoglycerate kinase	mitochondrion & cytoplasm	plastid	plastid	plastid stroma	
AT3G13070	592	AT3G13070.1	CBS domain-containing protein / transporter associated domain-containing protein	661	Ch/E/IM	5.0	73.75	transporter Mg & Co ?	35.1 not assigned.no ontology		plastid	plastid	plastid	5.0

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AT3G13120	593	AT3G13120.1	30S ribosomal protein S10, chloroplast, putative	191	Ch/S	8.98999977	20.8299999	translation stroma	29.2.1.1.1.1.1.10 protein.synthesis.ribosomal.protein.prokaryotic.chloroplast.30S.subunit.S10		plastid	plastid	plastid ribosome	
AT3G13180	594	AT3G13180.1	NOL1/NOP2/sun family protein / antitermination NusB domain-containing protein	523	Ch/S	9.10999966	58.3400002	nd	35.1 not assigned.no ontology		plastid	plastid	plastid	
AT3G13470	595	AT3G13470.1	chaperonin, putative	596	Ch/S & Ch/E	5.59000015	63.3400002	chaperone and protease	29.6 protein.folding	mitochondrion	plastid	plastid	plastid stroma	
AT3G13490	596	AT3G13490.1	OVA5 (OVULE ABORTION 5); ATP binding / aminoacyl-tRNA ligase	602		5.73000002	67.5800018		29.1.6 protein.aa.activation.lysine-tRNA ligase	undefined	Y	M	mitochondria ; plastid stroma	
AT3G13800	597	AT3G13800.1	metallo-beta-lactamase family protein	361		7.21000004	40.3800011		35.1 not assigned.no ontology	chloroplast	Y	C	-	
AT3G14110	598	AT3G14110.1	FLU (FLUORESCENT IN BLUE LIGHT); binding	316	Ch/Th & Ch/E	9.09000015	34.5800018	metabolism vitamin and pigment	19.40 tetrapyrrole synthesis.regulation			plastid	envelope-inner; thylakoid	
AT3G14270	599	AT3G14270.1	phosphatidylinositol-4-phosphate 5-kinase family protein	1791		5.61999989	200.830002		30.4.1 signalling.phosphoinositids.phosphatidylinositol-4-phosphate 5-kinase	undefined			-	

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AT3G14390	600	AT3G14390.1	diaminopimelate decarboxylase, putative / DAP carboxylase, putative	484		6.51000023	53.5499992		13.1.3.5.5 amino acid metabolism.synthesis.aspartate family.lysine.diaminopimelate decarboxylase	chloroplast	Y	C	-	
AT3G14415	601	AT3G14415.1	(S)-2-hydroxy-acid oxidase, peroxisomal, putative / glycolate oxidase, putative / short chain alpha-hydroxy acid oxidase, putative	367	Ch/S	8.98999977	40.2999992	stress oxidative	1.2.2 PS.photosynthesis.pigment.glycolate oxidase				peroxisome	
AT3G14420	602	AT3G14420.1	(S)-2-hydroxy-acid oxidase, peroxisomal, putative / glycolate oxidase, putative / short chain alpha-hydroxy acid oxidase, putative	367	Ch/S & Ch/E & Ch/Th	9.14999962	40.3400002	stress oxidative	1.2.2 PS.photosynthesis.pigment.glycolate oxidase				peroxisome; plastid	
AT3G14930	603	AT3G14930.1	HEME1; uroporphyrinogen decarboxylase	418		6.63999987	46.25		19.7 tetrapyrrole synthesis.uroporphyrinogen decarboxylase	undefined	Y	C	plastid stroma	
AT3G15110	604	AT3G15110.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO39343.1)	266	Ch/Th	6.17999983	28.6100006	unknown	35.2 not assigned.unknown	thylakoid membrane (sensu Viridiplantae)		mitochondrion	plastid	3.0

Accession	pgID	Master Protein	Description (curated)	Length	Localization (curated)	Calculated Pi PPDB	Calculated MW PPDB	Function (putative)	MapManBin (PPDB)	Localization (TAIR)	ChloroP	TargetP	Curated localization (PPDB)	Aramemnon
AT3G15190	605	AT3G15190.1	chloroplast 30S ribosomal protein S20, putative	202	Ch/S & Ch/E	10.1400003	21.8199997	translation stroma	29.2.1.1.1.1.20 protein.synthesis.ribosomal.prokaryotic.chloroplast.30S.subunit.S20		plastid	plastid	plastid ribosome	
AT3G15356	606	AT3G15356.1	legume lectin family protein	271		8.89999962	29.75		26.16 misc.myosinases-lectin-jacalin	secreted		S	-	
AT3G15360	607	AT3G15360.1	ATHM4 (Arabidopsis thioredoxin M-type 4); thiol-disulfide exchange intermediate	193	Ch/S & Ch/E & Ch/Th	9.60999966	21.1700001	redox	21.1 redox.thioredoxin		plastid	plastid	plastid stroma; thylakoid-peripheral-stromal-side	
AT3G15520	608	AT3G15520.1	peptidyl-prolyl cis-trans isomerase TLP38, chloroplast / thylakoid lumen PPIase of 38 kDa / cyclophilin / rotamase	466	Ch/Th	6.55999994	50.4799995	chaperone and protease	29.6 protein.folding	thylakoid membrane (sensu Viridiplantae) & thylakoid lumen (sensu Viridiplantae)	plastid	plastid	thylakoid-peripheral-lumenal-side	
AT3G15840	609	AT3G15840.1	PIFI (POST-ILLUMINATION CHLOROPHYLL FLUORESCENCE INCREASE)	268	Ch/S	5.82999992	29.6900005	PS CEF cyclic electron flow ?	1.1.40 PS.lightreaction.cyclic electron flow-chlororespiration		plastid	plastid	plastid	
AT3G15850	610	AT3G15850.1	FAD5 (FATTY ACID DESATURASE 5); oxidoreductase	371	Ch/E/IM	9.27000046	42.5800018	metabolism lipid	11.2.1 lipid metabolism.FA desaturation.desaturase	chloroplast	Y	C	-	3.0
AT3G15900	611	AT3G15900.1	similar to unknown [Populus trichocarpa] (GB:ABK95820.1)	141		10.1599998	15.0100002		35.2 not assigned.unknown	chloroplast	Y	C	-	2.0

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AT3G16000	612	AT3G16000.1	MFP1 (MARBINDING FILAMENT-LIKE PROTEIN 1)	726	Ch/Th	5.38000011	81.9700012	DNA Binding	28.3* DNA.plastid nucleoid interacting	thylakoid membrane (sensu Viridiplantae) & plastid nucleoid	plastid	plastid	plastid nucleoid	
AT3G16140	613	AT3G16140.1	PSAH-1 (photosystem I subunit H-1)	145	Ch/Th	9.94999981	15.21	PS PSI	1.1.2.2 PS.lightreaction.photosystem I.PSI polypeptide subunits	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	thylakoid-integral	
AT3G16240	614	AT3G16240.1	DELTA-TIP (delta tonoplast integral protein); water channel	250	na	5.30000019	25.0200005	transporter aquaporin	34.19.2 transport.Major Intrinsic Proteins.TIP	cell wall (sensu Magnoliophyta) & vacuolar membrane (sensu Magnoliophyta)		extracellular, endoplasmic reticulum, golgi	vacuole-tonoplast	6.0
AT3G16290	615	AT3G16290.1	EMB2083 (EMBRYO DEFECTIVE 2083); ATPase/metallopeptidase	876	Ch/E/IM	9.27000046	99.8600006	chaperone and protease	29.5.7 protein.degradation.metall oprotease			plastid	plastid	2.0
AT3G16950	616	AT3G16950.1	LPD1 (LIPOAMIDE DEHYDROGENASE 1)	570	Ch/E & Ch/S	8.13000011	60.75	metabolism lipid	11.1 lipid metabolism. FA synthesis and FA elongation		plastid	plastid	plastid	
AT3G17810	617	AT3G17810.1	dihydroorotate dehydrogenase family protein / dihydroorotate oxidase family protein	426	Ch/S	6.36999989	46.8400002	metabolism nucleotide	23.2 nucleotide metabolism. degradation		plastid	plastid	plastid	
AT3G17830	618	AT3G17830.1	DNAJ heat shock family protein	517	Ch/E/IM	9.48999977	57.2599983	chaperone and protease	20.2.1 stress.abiotic .heat	chloroplast	Y	C	-	1.0

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AT3G17970	619	AT3G17970.1	ATTOC64-III (ARABIDOPSIS THALIANA TRANSLOCATION AT THE OUTER MEMBRANE OF CHLOROPLASTS 64-III); binding / carbon-nitrogen ligase, with glutamine as amido-N-donor	589	Ch/E/OM	8.60999966	64.0199966	protein targeting Toc	26.33* misc.tetratricopeptide repeat (TPR) unknown function			extracellular, endoplasmic reticulum, golgi	envelope-outer	
AT3G18420	620	AT3G18420.1	tetratricopeptide repeat (TPR)-containing protein	316	Ch/E/IM	5.23999977	35.6300011	RNA binding ?	26.33* misc.tetratricopeptide repeat (TPR) unknown function	chloroplast envelope	plastid	plastid	plastid	
AT3G18890	621	AT3G18890.1	binding / catalytic/ coenzyme binding	641	Ch/Th & Ch/E	8.27000046	68.3399963	protein targeting Tic	29.3.3 protein.targeting.chloroplast	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	envelope-inner-peripheral-stromal-side; thylakoid	
AT3G18970	622	AT3G18970.1	pentatricopeptide (PPR) repeat-containing protein	472		9.02999973	52.5499992		35.1.5 not assigned.no ontology.pentatricopeptide (PPR) repeat-containing protein	undefined		M	-	
AT3G19170	623	AT3G19170.1	ATPREP1/A TZNMP (PRESEQUENCE PROTEASE 1); metalloendopeptidase	1080	Ch/S	5.46999979	121.010002	chaperone and protease	29.5.7 protein.degradation.metallprotease	mitochondrion & chloroplast	plastid	plastid	mitochondria; plastid stroma	

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AT3G19480	624	AT3G19480.1	D-3-phosphoglycerate dehydrogenase, putative / 3-PGDH, putative	588	Ch/S	8.4099985	62.1199989	metabolism aa Ser	13.1.5.1.1 amino acid metabolism.synthesis.serine-glycine-cysteine group.serine.phosphoglycerate dehydrogenase	mitochondrion	plastid	plastid	plastid stroma	
AT3G19820	625	AT3G19820.1	DWF1 (DIMINUTO 1); catalytic	561	other	7.9800002	65.3899994	metabolism hormone	17.3.1.2.8 hormone metabolism.brassinosteroid.synthesis-degradation.sterols.DWF1	undefined		M	-	1.0
AT3G20230	626	AT3G20230.1	50S ribosomal protein L18 family	187		10.2399998	21.1200008		29.2.1.1.3.2.18 protein.synthesis.ribosomal protein.prokaryotic.unknown organellar.50S subunit.L18	chloroplast	Y	C	plastid ribosome	
AT3G20320	627	AT3G20320.1	TGD2 (TRIGALACTOSYLDIACYLGLYCEROL2)	381	Ch/E/IM	8.8999962	41.6300011	transporter ABC lipids	11.15* lipid metabolism.t transport	chloroplast inner membrane & chloroplast envelope	plastid	plastid	envelope-inner	1.0
AT3G20330	628	AT3G20330.1	aspartate carbamoyltransferase, chloroplast / aspartate transcarbamylase / ATCase (PYRB)	390	Ch/S	6.1999981	43.1599998	metabolism nucleotide	23.1.1.2 nucleotide metabolism.synthesis.pyrimidine.aspartate transcarbamoylase		plastid	plastid	plastid stroma	
AT3G20390	629	AT3G20390.1	endoribonuclease L-PSP family protein	187	Ch/E & Ch/S	8.5200046	19.8099995	RNA metabolism?	27.1 RNA.processing		plastid	plastid	plastid stroma; thylakoid-peripheral-stromal-side	

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AT3G21110	630	AT3G21110.1	PUR7 (PURIN 7); phosphoribosylaminoimidazole succinocarboxamide synthase	411		6.05999994	46.0600014		23.1.2.7 nucleotide metabolism.synthesis.purine.SAICAR synthetase	undefined	Y	C	plastid stroma	
AT3G21200	631	AT3G21200.1	similar to hypothetical protein [Vitis vinifera] (GB:CAN79599.1); contains InterPro domain FMN-binding split barrel, related (InterPro:IPR009002)	317	Ch/S	5.6500001	35.4599991	PS PSI cyclic electron flow	19 tetrapyrrole synthesis		plastid	plastid	thylakoid-peripheral-stromal-side	
AT3G21580	632	AT3G21580.2	cobalt ion transmembrane transporter	205	Ch/E/IM	9.71000004	22.8700008	transporter ABC Co ?	34.12 transport.metal	chloroplast	Y	M	-	6.0
AT3G22150	633	AT3G22150.1	pentatricopeptide (PPR) repeat-containing protein	820	Ch/E ?	6.94000006	91.8499985	RNA Binding ?	26.54* misc.pentatricopeptide (PPR) repeat-containing protein	chloroplast	Y	C	-	
AT3G22890	634	AT3G22890.1	APS1 (ATP sulfurylase 3)	463	Ch/S	6.32999992	51.4599991	sulfate assimilation	14.1 S-assimilation. APS	chloroplast	plastid	plastid	plastid stroma	
AT3G22960	635	AT3G22960.1	PKP-ALPHA/PKP1 (PLASTIDIAL PYRUVATE KINASE 1); pyruvate kinase	596	Ch/S	5.63999987	65.1299973	metabolism lipid	11.1.30 lipid metabolism. FA synthesis and FA elongation.pyruvate kinase		plastid	plastid	plastid stroma	
AT3G23400	636	AT3G23400.1	plastid-lipid associated protein PAP / fibrillin family protein	284	Ch/Th & Ch/E	5.82000017	30.4500008	PAP_fibrillin	26.31* misc.fibrillins	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	plastoglobules	

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AT3G23700	637	AT3G23700.1	S1 RNA-binding domain-containing protein	392	Ch/S	5.38999987	42.75	translation stroma ?	35.1.14 not assigned.no ontology.S RNA-binding domain-containing protein		plastid	plastid	plastid stroma	
AT3G23710	638	AT3G23710.1	chloroplast inner membrane import protein Tic22, putative	313	Ch/E/IM	8.43000031	34.5699997	protein targeting Tic	29.3.3 protein.targeting.chloroplast	chloroplast	Y	C	-	
AT3G23790	639	AT3G23790.1	AMP-binding protein, putative	722	Ch/E/IM	8.72999954	81.1399994	metabolism lipid	11.1.8 lipid metabolism.FA synthesis and FA elongation.a cyl coa ligase	chloroplast	Y	C	-	
AT3G23940	640	AT3G23940.1	dehydratase family	608		5.8499999	64.9100037		35.1 not assigned.no ontology	chloroplast	Y	C	plastid stroma	
AT3G24430	641	AT3G24430.1	HCF101 (HIGH-CHLOROPHYLL-FLUORESCENCE 101); ATP binding	532	Ch/S	5.90999985	57.7599983	chaperone and protease ?	29.8 protein assembly and cofactor ligation		plastid	plastid	plastid stroma	
AT3G24590	642	AT3G24590.1	signal peptidase I family protein	291	Ch/Th	5.73000002	32.5499992	chaperone and protease	29.9* protein.processing	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	thylakoid-peripheral-lumenal-side	1.0
AT3G25660	643	AT3G25660.1	glutamyl-tRNA(Gln) amidotransferase, putative	537	Ch/S	6.15999985	57.1800003	unknown	29.1.50* protein.aa activation.glutamate-tRNA amidotransferase		plastid	plastid	mitochondria ; plastid stroma	

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AT3G25680	644	AT3G25680.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G23890.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO42077.1); contains InterPro domain S-layer homology region (InterPro:IPR001119)	558	Ch/E/IM	5.1799983	63.0499992	unknown	35.2 not assigned.unknown		plastid	plastid	plastid	1.0
AT3G25690	645	AT3G25690.1	CHUP1 (CHLOROPLAST UNUSUAL POSITIONING 1)	1004	Ch/E	5.4299983	111.910004	plastid positioning	35.1.41 not assigned.no ontology.hydroxyproline rich proteins			extracellular, endoplasmic reticulum, golgi	envelope-outer	
AT3G25760	646	AT3G25760.1	AOC1 (ALLENE OXIDE CYCLASE 1)	254	Ch/E/IM	9.1099966	27.7999992	metabolism hormone jasmonate	17.7.1.3 hormone metabolism.jasmonate.synthesis-degradation.allene oxidase synthase	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	plastid	
AT3G25770	647	AT3G25770.1	AOC2 (ALLENE OXIDE CYCLASE 2)	253	Ch/E & Ch/Th	6.9000001	27.6299992	metabolism hormone jasmonate	17.7.1.4 hormone metabolism.jasmonate.synthesis-degradation.allene oxidase cyclase	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	thylakoid-peripheral-stromal-side	

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AT3G25780	648	AT3G25780.1	AOC3 (ALLEN OXIDE CYCLASE 3)	258	Ch/E/IM	9.18999958	28.3899994	metabolism hormone jasmonate	17.7.1.4 hormone metabolism.jasmonate.synthesis-degradation.allene oxidase cyclase	chloroplast	Y	C	plastid	
AT3G25860	649	AT3G25860.1	LTA2 (PLASTID E2 SUBUNIT OF PYRUVATE DECARBOXYLASE); dihydrolipoyllysine-residue acetyltransferase	480	Ch/E & Ch/Th & Ch/S	8.32999992	50.0800018	metabolism lipid	11.1.31 lipid metabolism.FA synthesis and FA elongation.pyruvate DH	chloroplast stroma	plastid	plastid	plastid	
AT3G25920	650	AT3G25920.1	RPL15 (ribosomal protein L15)	277	Ch/S & Ch/E	10.7700005	29.7000008	translation stroma	29.2.1.1.1.2.15 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.50S subunit.L15	plastid large ribosomal subunit	plastid	plastid	plastid ribosome	
AT3G26060	651	AT3G26060.1	ATPRX Q; antioxidant/peroxiredoxin	216	Ch/Th & Ch/E	9.52999973	23.6700001	redox	21.5 redox.periredoxins	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	plastid	
AT3G26070	652	AT3G26070.1	plastid-lipid associated protein PAP / fibrillin family protein	242	Ch/Th & Ch/E	9.69999981	27.1599998	PAP_fibrillin	26.31* misc.fibrillins	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	thylakoid-peripheral-stromal-side	
AT3G26520	653	AT3G26520.1	TIP2 (TONOPLAST INTRINSIC PROTEIN 2); water channel	253	other	4.90999985	25.8400002	transporter aquaporin	34.19.2 transport.Major Intrinsic Proteins.TIP	undefined			-	6.0
AT3G26570	654	AT3G26570.1	PHT2;1 (phosphate transporter 2;1)	613	Ch/E/IM	9.26000023	64.7799988	transporter Pi	34.7 transport.phosphate	chloroplast envelope	plastid		envelope-inner-integral	

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AT3G26650	655	AT3G26650.1	GAPA (GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A SUBUNIT); glyceraldehyde-3-phosphate dehydrogenase	396	Ch/S & Ch/E	7.61000013	42.4900017	metabolism carbon Calvin cycle	1.3.4 PS.calvin cycle.GAP	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	plastid stroma	
AT3G26710	656	AT3G26710.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO49107.1)	267	Ch/Th	9.78999996	30.1000004	chaperone and protease PS b6f	29.8 protein assembly and cofactor ligation		plastid	plastid	thylakoid	3.0
AT3G26900	657	AT3G26900.1	shikimate kinase family protein	280	Ch/S	5.03999996	30.4699993	metabolism aminoacids aromatic	13.1.6.1.5 amino acid metabolism.synthesis.aromatic aa.chorismate.shikimate kinase		plastid	plastid	plastid stroma	
AT3G27160	658	AT3G27160.1	GHS1 (GLUCOSE HYPERSENSITIVE 1); structural constituent of ribosome	183	Ch/S	9.43999958	20.9099998	translation stroma	29.2.1.1.3.1.21 protein.synthesis.ribosomal protein.prokaryotic.unknown organellar.30S subunit.S21		plastid	plastid	plastid ribosome	
AT3G27740	659	AT3G27740.1	CARA (CARBAMOYL PHOSPHATE SYNTHETASE A); carbamoyl-phosphate synthase (glutamine-hydrolyzing)	430		5.67999983	47.0499992		23.1.1.1 nucleotide metabolism.synthesis.pyrimidine.carbamoyl phosphate synthetase	chloroplast	Y	C	plastid stroma	

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AT3G27830	660	AT3G27830.1	RPL12-A (RIBOSOMAL PROTEIN L12-A); structural constituent of ribosome	191	Ch/S & Ch/Th	5.5	20.0699997	translation stroma		thylakoid membrane (sensu Viridiplantae)	Y	C	plastid ribosome	
AT3G27890	661	AT3G27890.1	NQR (NADPH:QUINONE OXIDOREDUCTASE); FMN reductase	196	Ch/S	6.84000015	21.5499992	unknown	35.1 not assigned.no ontology			mitochondrion	not plastid	
AT3G27925	662	AT3G27925.1	DEGP1 (DEGP PROTEASE 1); serine-type peptidase	439	Ch/Th & Ch/S	5.98999977	46.6699982	chaperone and protease	29.5.5 protein.degradation.serine protease	thylakoid membrane (sensu Viridiplantae) & thylakoid lumen (sensu Viridiplantae) & thylakoid (sensu Viridiplantae)	plastid	plastid	thylakoid-peripheral-lumenal-side	1.0
AT3G28220	663	AT3G28220.1	meprip and TRAF homology domain-containing protein / MATH domain-containing protein	370	Ch/E	8.59000015	42.8800011	chaperone and protease ?	35.2 not assigned.unknown				plastid	1.0
AT3G28345	664	AT3G28345.1	ABC transporter family protein	1240		8.21000004	135.639999		34.16 transport.ABC transporters and multidrug resistance systems	other (e.g. cytoplasm)			-	11.0
AT3G28710	665	AT3G28710.1	H ⁺ -transporting two-sector ATPase, putative	351	other	5.03999996	40.7900009	transporter ATPase	34.1.1 transport.p-and v-ATPases.H ⁺ -transporting two-sector ATPase	undefined			-	

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AT3G28760	666	AT3G28760.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO14940.1); contains InterPro domain 3-dehydroquinase synthase, prokaryotic-type (InterPro:IPR002812)	422		6.6900006	47.0499992		13.1.6.1 amino acid metabolism.synthesis. aromatic.aa.chorismate	undefined	Y	C	-	
AT3G29185	667	AT3G29185.1	similar to hypothetical protein MtrDRAFT_AC147482g2.v2 [Medicago truncatula] (GB:ABD32485.1)	396		5.23999977	44.6699982		35.2 not assigned.unknown	chloroplast	Y	C	-	1.0
AT3G29320	668	AT3G29320.1	glucan phosphorylase, putative	962	Ch/S	5.3499999	108.580002	metabolism carbon	2.2.2.2 major CHO metabolism.degradation.starch.starch phosphorylase		plastid	plastid	plastid stroma	
AT3G32930	669	AT3G32930.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO22035.1)	249	Ch/E/IM	9.60000038	27.4300003	unknown	35.2 not assigned.unknown	chloroplast envelope	plastid	plastid	not plastid	
AT3G42050	670	AT3G42050.1	vacuolar ATP synthase subunit H family protein	441	other	6.57000017	50.2799988	transporter ATPase	34.1.1 transport.p-and v-ATPases.H+-transporting two-sector ATPase	other (e.g. cytoplasm)			-	

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AT3G43520	671	AT3G43520.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G26240.1); similar to predicted protein [Physcomitrella patens subsp. patens] (GB:EDQ63811.1); contains InterPro domain Protein of unknown function UPF0136, Transmembrane; (InterPro:IPR005349	240	Ch/E/IM	9.13000011	24.7600002	unknown	35.1.40 not assigned.no ontology.glycine rich proteins		plastid	plastid	plastid	4.0
AT3G44880	672	AT3G44880.1	ACD1 (ACCELERATED CELL DEATH 1)	537	Ch/E & Ch/Th	7.19000006	60.75	metabolism vitamin and pigment	19.50* tetrapyrrole degradation	chloroplast inner membrane	plastid	plastid	thylakoid	
AT3G44890	673	AT3G44890.1	RPL9 (ribosomal protein L9); structural constituent of ribosome	197	Ch/S & Ch/E & Ch/S	9.68000031	22.1299992	translation stroma	29.2.1.1.1.2.9 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.50S subunit.L9	plastid large ribosomal subunit	plastid	plastid	plastid ribosome	
AT3G45140	674	AT3G45140.1	LOX2 (LIPOXYGENASE 2)	896	Ch/S	5.42000008	102.040001	metabolism lipid	17.7.1.2 hormone metabolism.jasmonate.synthesis-degradation.lipoxygenase	thylakoid membrane (sensu Viridiplantae) & chloroplast	plastid	plastid	plastid stroma	
AT3G45450	675	AT3G45450.1	Clp amino terminal domain-containing protein	341	Ch	8.72999954	37.3400002	chaperone and protease	29.3.99 protein.targeting.unknown	undefined			-	

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AT3G45890	676	AT3G45890.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G13770.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO23851.1); contains InterPro domain Protein of unknown function DUF647 (InterPro:IPR006968)	608	Ch/E/IM	6.4000001	66.3799973	unknown	35.2 not assigned.unkn own	chloroplast	Y	C	-	3.0
AT3G45980	677	AT3G45980.1	HTB9; DNA binding	150		10.0200005	16.4300003		28.1.3 DNA.synthesis/chromatin structure.hist one	other (e.g. cytoplasm)			nucleus	
AT3G46060	678	AT3G46060.1	ARA3; GTP binding	216	Ch/E ?	7.63999987	23.8299999	signalling / SNARE effector	30.5 signalling.G-proteins	undefined			plasma membrane	
AT3G46520	679	AT3G46520.1	ACT12 (ACTIN-12); structural constituent of cytoskeleton	377	Ch/E & other	5.36999989	41.7900009	plastid positioning ?	31.1 cell.organisation	other (e.g. cytoplasm)			-	
AT3G46740	680	AT3G46740.1	TOC75-III (translocon outer membrane complex 75-III); P-P-bond-hydrolysis-driven protein transmembrane transporter	818	Ch/E/OM	8.93000031	89.1900024	protein targeting Toc	29.3.3 protein.targeting.chloroplast	integral to chloroplast outer membrane	plastid	plastid	envelope-outer	

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AT3G46780	681	AT3G46780.1	PTAC16 (PLASTID TRANSCRIPTIONALLY ACTIVE18); binding / catalytic	510	Ch/Th & Ch/E	8.8999962	54.3499985	protein targeting Tic ?	28.3* DNA.plastid nucleoid interacting	thylakoid membrane (sensu Viridiplantae) & plastid chromosome	plastid	plastid	thylakoid	
AT3G46980	682	AT3G46980.1	transporter-related	533	Ch/E/IM	9.7899996	58.2400017	transporter Pi ?	34.7 transport.phosphate	undefined			plastid	12.0
AT3G47010	683	AT3G47010.1	hydrolase, hydrolyzing O-glycosyl compounds	609	Ch/E ?	5.2699998	63.0	hydrolase ?	10.6.1 cell wall.degradation.cellulases and beta - 1,4-glucanases	other (e.g. cytoplasm)			-	
AT3G47060	684	AT3G47060.1	FTSH7 (FtsH protease 7); ATP-dependent peptidase/ATPase/metallopeptidase	802	Ch/E/IM	8.30000019	87.8000031	chaperone and protease	29.5.7 protein.degradation.metalloprotease	undefined	Y	C	-	2.0
AT3G47070	685	AT3G47070.1	similar to unknown [Populus trichocarpa] (GB:ABK95428.1)	100	Ch/Th	9.73999977	10.5299997	PS State transition ?	1.1.30 PS.lightreaction.state transition	thylakoid membrane (sensu Viridiplantae)			thylakoid-peripheral-stromal-side	
AT3G47470	686	AT3G47470.1	LHCA4 (Photosystem I light harvesting complex gene 4); chlorophyll binding	251	Ch/Th	6.21000004	27.7299995	PS LHCI	1.1.2.1 PS.lightreaction.photosystem I.LHC-I	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	thylakoid-integral	
AT3G47520	687	AT3G47520.1	MDH (MALATE DEHYDROGENASE); malate dehydrogenase	403	Ch/E & Ch/S & Ch/Th	8.65999985	42.4000015	metabolism carbon	8.2.99 TCA / org.transformation.other organic acid transformations.misc	mitochondrion & chloroplast	plastid	plastid	plastid stroma	
AT3G47590	688	AT3G47590.1	esterase/lipase/thioesterase family protein	309		7.73000002	35.0400009		35.1 not assigned.no ontology	undefined	Y		-	

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AT3G47650	689	AT3G47650.1	bundle-sheath defective protein 2 family / bsd2 family	136		8.0	14.54		33.99 development .unspecified	chloroplast	Y	C	plastid stroma	
AT3G47860	690	AT3G47860.1	apolipoprotein D-related	353	Ch/Th	6.36000013	39.1100006	Stress light	11.6 lipid metabolism.lipid transfer proteins etc	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	thylakoid	
AT3G48110	691	AT3G48110.1	EDD1 (EMBRYO-DEFECTIVE - DEVELOPMENT 1)	1067	Ch/S	5.69000006	119.769997	translation stroma	29.1.14 protein.aa activation.glycine-tRNA ligase	mitochondrion & chloroplast	plastid	plastid	mitochondria ; plastid stroma	
AT3G48420	692	AT3G48420.1	haloacid dehalogenase-like hydrolase family protein	319	Ch/S	8.30000019	34.2400017	unknown	35.1 not assigned.no ontology		plastid	plastid	plastid stroma	
AT3G48500	693	AT3G48500.1	PDE312/PTAC10 (PIGMENT DEFECTIVE 312); RNA binding / unfolded protein binding	668	Ch/S	4.96000004	78.8099976	DNA Binding ?	28.3* DNA.plastid nucleoid interacting		plastid	plastid	plastid nucleoid	
AT3G48560	694	AT3G48560.1	CSR1 (CHLORSULFURON/IMIDAZOLINONE RESISTANT 1)	670		6.19000006	72.5800018		13.1.4.1.1 amino acid metabolism.synthesis.branched chain group.common.acetolactate synthase	chloroplast	Y	C	plastid stroma	
AT3G48730	695	AT3G48730.1	GSA2 (GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOMUTASE 2); glutamate-1-semialdehyde 2,1-aminomutase	472	Ch/S	7.01000023	50.1399994	metabolism vitamin and pigment	19.3 tetrapyrrole synthesis.GSA		plastid	plastid	plastid stroma	

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AT3G48870	696	AT3G48870.1	ATCLPC (CASEINOLYTIC PROTEASE C); ATP binding / ATPase	952	Ch/E & Ch/S	6.05999994	105.769997	chaperone and protease	29.5.5 protein.degradation.serine protease	mitochondrion & chloroplast stroma & chloroplast		plastid	plastid stroma	
AT3G48990	697	AT3G48990.1	AMP-dependent synthetase and ligase family protein	514		6.07999992	55.5400009		11.1.8 lipid metabolism. FA synthesis and FA elongation.acyl coa ligase	undefined			-	2.0
AT3G49140	698	AT3G49140.1	binding	1215		4.94000006	135.910004		26.54* misc.pentatricopeptide (PPR) repeat-containing protein	undefined		M	-	
AT3G49560	699	AT3G49560.1	mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein	261	Ch/E/OM	9.48999977	27.9799995	protein targeting / aa channel	34.8 transport.metabolite transporters at the envelope membrane				envelope	3.0
AT3G49680	700	AT3G49680.1	ATBCAT-3/BCAT3 (BRANCHE D-CHAIN AMINOTRANSFERASE 3); branched-chain-amino-acid transaminase/ catalytic	413		8.31999969	44.9700012		13.1.4.1.4 amino acid metabolism.synthesis.branched chain group.common.branched-chain amino acid aminotransferase	chloroplast	Y	C	plastid stroma	
AT3G50820	701	AT3G50820.1	PSBO-2/PSBO2 (PHOTOSYSTEM II SUBUNIT O-2); oxygen evolving/poly(U) binding	331	Ch/Th	5.92000008	35.0099983	PS PSII OEE	1.1.1.2 PS.lightreaction.photosystem II.PSII polypeptide subunits	thylakoid membrane (sensu Viridiplantae) & thylakoid lumen (sensu Viridiplantae)	plastid	plastid	thylakoid-peripheral-lumenal-side	

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AT3G51140	702	AT3G51140.1	heat shock protein binding	278	Ch/E/IM	10.6599998	31.5300007	signalling ?	35.2 not assigned.unknown	chloroplast inner membrane	plastid	plastid	plastid	4.0
AT3G51510	703	AT3G51510.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO14460.1)	181	Ch/Th	6.19999981	19.8400002	unknown	35.2 not assigned.unknown	thylakoid membrane (sensu Viridiplantae)		plastid	thylakoid	2.0
AT3G51600	704	AT3G51600.1	LTP5 (LIPID TRANSFER PROTEIN 5); lipid transporter	118		10.4300003	12.4899998		11.6 lipid metabolism.lipid transfer proteins etc	secreted		S	-	
AT3G51800	705	AT3G51800.1	ATG2 (G2p-related protein); metalloexopeptidase	392		6.3499999	42.9799995		29.5.7 protein.degradation.metalloprotease	other (e.g. cytoplasm)			-	
AT3G51820	706	AT3G51820.1	ATG4/CHLG/G4 (CHLOROPHYLL SYNTHASE); chlorophyll synthetase	387	Ch/Th	8.52000046	41.8800011	metabolism vitamin and pigment	19.15 tetrapyrrole synthesis.chlorophyll synthase	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	thylakoid	8.0
AT3G51870	707	AT3G51870.1	mitochondrial substrate carrier family protein	381	Ch/E/IM	9.75	41.8100014	transporter MCF Ca/X ?	34.99 transport.misc	undefined	Y	C	-	2.0
AT3G52150	708	AT3G52150.1	RNA recognition motif (RRM)-containing protein	253	Ch/S & Ch/E	8.93999958	27.7399998	translation stroma ?	29.2.1.1.1.1 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.30S subunit		plastid	plastid	plastid ribosome	
AT3G52180	709	AT3G52180.1	ATPTPKIS1/DSP4/SEX4 (STARCH-EXCESS 4); polysaccharide binding / protein tyrosine/serine/threonine phosphatase	379	Ch/S	6.11000013	42.6199989	starch degradation	2.2.2.2 major CHO metabolism.degradation.starch.starch phosphorylase	chloroplast	plastid	plastid	plastid stroma	

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AT3G52230	710	AT3G52230.1	similar to unknown [Populus trichocarpa] (GB:ABK93315.1)	145	Ch/E/OM	4.5100023	16.1200008	transporter ion channel	35.2 not assigned.unknown	chloroplast outer membrane & thylakoid membrane (sensu Viridiplantae)			envelope-outer	
AT3G52380	711	AT3G52380.1	CP33 (PIGMENT DEFECTIVE 322); RNA binding	329	Ch/E & Ch/S	4.6100013	35.7400017	RNA Binding ?	27.4 RNA.RNA binding	chloroplast	Y	C	plastid stroma	
AT3G52750	712	AT3G52750.1	FTSZ2-2 (FtsZ2-2); structural molecule	473	Ch/S & Ch/Th	5.6700008	50.3100014	plastid division	31.2.5 cell.division.plastid	chloroplast stroma & chloroplast			plastid stroma	
AT3G52880	713	AT3G52880.1	ATMDAR1 (MONODEHYDROASCORBATE REDUCTASE 1); monodehydroascorbate reductase (NADH)	434		6.40999985	46.4799995		21.2.1 redox.ascorbate and glutathione.ascorbate	secreted			peroxisome	
AT3G52930	714	AT3G52930.1	fructose-bisphosphate aldolase, putative	358		6.03999996	38.5400009		4.7 glycolysis.aldolase	undefined			cytosol	
AT3G52960	715	AT3G52960.1	peroxiredoxin type 2, putative	234	Ch/S & Ch/E	9.10999966	24.6800003	redox	21.5 redox.peroxidoxins		plastid	plastid	plastid stroma	
AT3G53130	716	AT3G53130.1	LUT1 (LUTEIN DEFICIENT 1); oxygen binding	539	Ch/E/IM	6.03999996	60.5499992	metabolism vitamin and pigment	16.1.4 secondary metabolism.isoprenoids.carotenoids	chloroplast	plastid	plastid	plastid	
AT3G53220	717	AT3G53220.1	thioredoxin family protein	126	Ch/E ?	5.9000001	14.4099998	redox	21.1 redox.thioredoxin	other (e.g. cytoplasm)			-	
AT3G53460	718	AT3G53460.1	CP29 (chloroplast 29 kDa ribonucleoprotein); RNA binding / poly(U) binding	342	Ch/Th & Ch/S	5.23999977	36.0	RNA Binding	27.4 RNA.RNA binding		plastid	plastid	plastid stroma	

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AT3G53560	719	AT3G53560.1	chloroplast lumen common family protein	340	Ch/E & Ch/Th	6.57999992	38.6599998	unknown	35.1 not assigned.no ontology	undefined	Y	C	plastid	
AT3G53580	720	AT3G53580.1	diaminopimelate epimerase family protein	362	Ch/S	5.44999981	38.9799995	metabolism aa Asp	13.1.3.5.4 amino acid metabolism.synthesis.aspartate family.lysine.diaminopimelate epimerase		plastid	plastid	plastid stroma	
AT3G53900	721	AT3G53900.1	uracil phosphoribosyltransferase, putative / UMP pyrophosphorylase, putative / UPRTase, putative	231		6.30999994	25.1599998		23.3.1.3 nucleotide metabolism.salvage.phosphoribosyltransferases.upp	chloroplast		C	plastid stroma	
AT3G54050	722	AT3G54050.1	fructose-1,6-bisphosphatase, putative / D-fructose-1,6-bisphosphate 1-phosphohydrolase, putative / FBPase, putative	417	Ch/S	5.23999977	45.1599998	metabolism carbon Calvin cycle	1.3.7 PS.calvin cycle.FBPase		plastid	plastid	plastid stroma	
AT3G54090	723	AT3G54090.1	pfkB-type carbohydrate kinase family protein	471	Ch/S	5.76000023	53.7799988	Kinase	29.4.1 protein.posttranslational modification.kinase	nucleus & cytoplasm	plastid	plastid	cytosol; nucleus; plastid nucleoid	
AT3G54170	724	AT3G54170.1	ATFIP37 (ARABIDOPSIS THALIANA FKBP12 INTERACTING PROTEIN 37)	330		4.92999983	37.2099991		31.1 cell.organisation	other (e.g. cytoplasm)			-	

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AT3G54210	725	AT3G54210.1	ribosomal protein L17 family protein	211	Ch/E & Ch/S	11.3800001	23.4799995	translation stroma	29.2.1.1.1.2.17 protein.synthesis.ribosomal.protein.prokaryotic.chloroplast.50S.subunit.L17		plastid	plastid	plastid ribosome	
AT3G54400	726	AT3G54400.1	aspartyl protease family protein	425	Ch/Th	9.30000019	45.4700012	DNA binding ?	27.3.99 RNA.regulation.of.transcription.unclassified			extracellular, endoplasmic reticulum, golgi	not plastid	
AT3G54640	727	AT3G54640.1	TSA1 (TRYPTOPHAN SYNTHASE ALPHA CHAIN); tryptophan synthase	312		6.76000023	33.2000008		13.1.6.5.5 amino acid metabolism.synthesis.aromatic.aa.tryptophan.tryptophan synthase	chloroplast	Y	C	plastid stroma	
AT3G54660	728	AT3G54660.1	GR (GLUTATHIONE REDUCTASE); glutathione-disulfide reductase	565	Ch & other	7.96000004	60.8499985	redox	21.2.2 redox.ascorbate and glutathione.glutathione	chloroplast	Y	C	plastid stroma	
AT3G54890	729	AT3G54890.1	LHCA1; chlorophyll binding	241	Ch/Th	6.21000004	25.9899998	PS LHCI	1.1.2.1 PS.lightreaction.photosystem I.LHC-I		plastid	plastid	thylakoid-integral	
AT3G54900	730	AT3G54900.1	CXIP1 (CAX INTERACTING PROTEIN 1)	173	Ch/S & Ch/E	8.65999985	19.3099995	redox	21.5 redox.periredoxins		plastid	plastid	plastid	
AT3G55010	731	AT3G55010.1	ATPURM/PUR5; phosphoribosylformylglycinamide cyclase	389		5.30999994	41.5		23.1.2.5 nucleotide metabolism.synthesis.purine.AIR synthase	chloroplast	Y	C	plastid stroma	

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AT3G55030	732	AT3G55030.1	PGPS2 (phosphatidylglycerolphosphate synthase 2); CDP-alcohol phosphatidyltransferase/CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase	233	Ch/E/IM	9.60999966	25.2199993	metabolism lipid	11.3.3 lipid metabolism. Phospholipid synthesis.phosphatidate cytidyltransferase	microsome	plastid			4.0
AT3G55040	733	AT3G55040.1	In2-1 protein, putative	292		6.76999998	33.0499992		26.9 misc.glutathione S transferases	chloroplast	Y	C	plastid stroma	
AT3G55250	734	AT3G55250.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO14780.1)	277	Ch/E & Ch/S	5.8499999	31.2399998	signalling Calcium ?	35.2 not assigned.unknown	mitochondrion	plastid	plastid	plastid	1.0
AT3G55330	735	AT3G55330.1	PPL1 (PSBP-LIKE PROTEIN 1); calcium ion binding	230	Ch/Th	9.35999966	25.6200008	PS PSII OEE ?	1.1.1.2 PS.lightreaction.photosystem II.PSII polypeptide subunits	thylakoid lumen (sensu Viridiplantae)	plastid	plastid	thylakoid-peripheral-lumenal-side	
AT3G55400	736	AT3G55400.1	OVA1 (OVULE ABORTION 1); ATP binding / aminoacyl-tRNA ligase	616		6.1500001	69.2699966		29.1.10 protein.aa activation.methionine-tRNA ligase	chloroplast	Y	C	mitochondria ; plastid stroma	
AT3G55440	737	AT3G55440.1	ATCTIMC (CYTOSOLIC TRIOSE PHOSPHATE ISOMERASE); triose-phosphate isomerase	254		5.38999987	27.1599998		4.8 glycolysis.TP	undefined			not plastid	

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AT3G55610	738	AT3G55610.1	P5CS2 (DELTA 1-PYRROLINE-5-CARBOXYLATE SYNTHASE 2); catalytic/ glutamate 5-kinase/ glutamate-5-semialdehyde dehydrogenase/ oxidoreductase	726		6.34000015	78.8700027		13.1.2.2.1 amino acid metabolism.synthesis.glutamate family.proline .delta 1-pyrroline-5-carboxylate synthetase	undefined			-	
AT3G55760	739	AT3G55760.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G42430.1); similar to hypothetical protein [Trifolium pratense] (GB:BAE71279.1)	578	Ch/S	5.30999994	65.5699997	unknown	35.2 not assigned.unknown		plastid	plastid	plastid	
AT3G55800	740	AT3G55800.1	SBPASE (SEDOHEPTULOSE-BISPHOSPHATASE); phosphoric ester hydrolase/ sedoheptulose-bisphosphatase	393	Ch/S	6.17000008	42.4099998	metabolism carbon Calvin cycle	1.3.9 PS.calvin cycle.seduheptulose bisphosphatase		plastid	plastid	plastid stroma	
AT3G56090	741	AT3G56090.1	ATFER3 (FERRITIN 3); ferric iron binding	259		5.53999996	28.8299999		15.2 metal handling.binding, chelation and storage	chloroplast	Y	C	plastid stroma	

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AT3G56130	742	AT3G56130.1	biotin/lipoyl attachment domain-containing protein	281		8.85999966	29.5699997		11.1.1 lipid metabolism. FA synthesis and FA elongation. Acetyl CoA Carboxylation	chloroplast	Y	C	plastid	
AT3G56160	743	AT3G56160.1	bile acid:sodium symporter	436	Ch/E/IM	9.90999985	46.5299988	transporter Na/X ?	34.8 transport.metabolite transporters at the envelope membrane		plastid	plastid	envelope-inner-integral	7.0
AT3G56650	744	AT3G56650.1	thylakoid lumenal 20 kDa protein	262	Ch/Th & Ch/S	9.28999996	28.6299992	PS PSII OEE ?	1.1.1.2 PS.lightreaction.photosystem II.PSII polypeptide subunits	thylakoid lumen (sensu Viridiplantae)	plastid	plastid	thylakoid-peripheral-lumenal-side	
AT3G56690	745	AT3G56690.1	CIP111 (CAM INTERACTING PROTEIN 111); ATPase/calmodulin binding	1022	Ch/E & Ch/Th	6.05000019	111.519997	signalling Calcium ?	30.3 signalling.calcium	undefined	Y	C	-	
AT3G56910	746	AT3G56910.1	PSRP5 (PLASTID-SPECIFIC 50S RIBOSOMAL PROTEIN 5)	148	Ch/E & Ch/S	10.8500004	16.3600006	translation stroma	29.2.1.1.1.2.85 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.50S subunit.PSRP5		plastid	plastid	plastid ribosome	
AT3G56940	747	AT3G56940.1	AT103 (DICARBOXYLATE DIIRON 1)	409	Ch/E & Ch/Th	8.55000019	47.6300011	metabolism vitamin and pigment	19.12 tetrapyrrole synthesis.magnesium-protoporphyrin IX monomethyl ester (oxidative) cyclase	thylakoid membrane (sensu Viridiplantae) & chloroplast inner membrane	plastid	plastid	envelope-inner-peripheral-stromal-side; thylakoid-peripheral-stromal-side	

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AT3G57050	748	AT3G57050.1	CBL (CYSTATHIONINE BETA-LYASE)	464		6.9000001	50.4300003		13.1.3.4.2 amino acid metabolism.synthesis.asp artate family.methionine.cystathionine beta-lyase	chloroplast	Y	C	plastid	
AT3G57090	749	AT3G57090.1	BIGYIN; binding	170	Ch/E/OM ??	5.53999996	18.6900005	RNA binding ?	26.33* misc.tetratricopeptide repeat (TPR) unknown function				mitochondria ; peroxisome; plastid	1.0
AT3G57280	750	AT3G57280.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G20510.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO23643.1); contains InterPro domain Protein of unknown function UPF0136, Transmembrane; (InterPro:IPR005349)	226	Ch/E/IM	9.17000008	24.3400002	unknown	35.2 not assigned.unknown	chloroplast inner membrane	plastid	plastid	envelope	4.0
AT3G57560	751	AT3G57560.1	aspartate/glutamate/uridylate kinase family protein	347	Ch/Th	9.03999996	36.5900002	unknown	13.1.2.3.2 amino acid metabolism.synthesis.glutamate family.arginine.acetylglutamate kinase	chloroplast	plastid	plastid	plastid stroma	

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AT3G57610	752	AT3G57610.1	ATPURA; adenylsuccinate synthase	490	Ch/S	6.67000008	52.9599991	metabolism nucleotide	23.1.2.20 nucleotide metabolism.synthesis.purine.adenyosuccinate synthase		plastid	plastid	plastid stroma	
AT3G58010	753	AT3G58010.1	Identical to Probable plastid-lipid-associated protein 9, chloroplast precursor (PAP9) [Arabidopsis Thaliana] (GB:Q9M2P7); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G42130.4); similar to unknown [Populus trichocarpa] (GB:ABK96151.1)	308	Ch/Th ?	5.36000013	34.0900002	PAP_fibrillin	26.31* misc.fibrillins	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	plastoglobules	
AT3G58140	754	AT3G58140.1	phenylalanyl-tRNA synthetase class IIc family protein	429	Ch/S	5.98000002	49.25	translation stroma	29.1.20 protein.aa activation.phenylalanine-tRNA ligase	mitochondrion & chloroplast	plastid	plastid	mitochondria ; plastid stroma	
AT3G58160	755	AT3G58160.1	XIJ (Myosin-like protein XIJ)	1242		5.73999977	141.410004		31.1 cell.organisation	other (e.g. cytoplasm)			-	
AT3G58610	756	AT3G58610.1	ketol-acid reductoisomerase	591	Ch/S	6.3499999	63.8100014	metabolism amino acids branched chain	13.1.4.1.2 amino acid metabolism.synthesis.branched chain group.common.ketol-acid reductoisomerase	mitochondrion	plastid	plastid	plastid stroma	2.0

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AT3G58730	757	AT3G58730.1	(VACUOLAR ATP SYNTHASE SUBUNIT D); ATPase, coupled to transmembrane movement of substances / hydrogen ion transporting ATPase, rotational mechanism	261	other	9.51000023	29.0499992	transporter ATPase	34.1.1 transport.p-and v-ATPases.H+-transporting two-sector ATPase	undefined		M	-	
AT3G59760	758	AT3G59760.1	OASC (O-ACETYLSE RINE (THIOL) LYASE ISOFORM C); cysteine synthase	433	Ch/S	8.57999992	46.1100006	metabolism aa cysteine	13.1.5.3.1 amino acid metabolism.s ynthesis.seri ne-glycine-cysteine group.cystei ne.OASTL	mitochondrion	plastid	plastid	mitochondria	
AT3G59780	759	AT3G59780.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G23060.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO46311.1); contains InterPro domain Rhodanese-like (InterPro:IPR001763)	610	Ch/Th	4.55000019	65.3300018	unknown	35.2 not assigned.unkn own			mitochondrion	thylakoid	3.0
AT3G59840	760	AT3G59840.1	similar to hypothetical protein [Vitis vinifera] (GB:CAN83312.1)	97	Ch/E/IM	4.63999987	10.5	redox ?	35.2 not assigned.unkn own	chloroplast		C	-	

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AT3G59870	761	AT3G59870.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G43945.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN60471.1)	288		6.94999981	32.4099998		35.2 not assigned.unknown	chloroplast	Y	C	plastid stroma	
AT3G60590	762	AT3G60590.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G48460.1); similar to unknown [Populus trichocarpa x Populus deltoides] (GB:ABK96523.1)	236	Ch/E/IM	9.60000038	26.2700005	transporter aa ?	35.2 not assigned.unknown	chloroplast inner membrane	plastid	mitochondrion		
AT3G60620	763	AT3G60620.1	phosphatidate cytidyltransferase family protein	399	Ch/E/IM	9.30000019	43.25	metabolism lipid	11.3.3 lipid metabolism. Phospholipid synthesis.phosphatidate cytidyltransferase			plastid	plastid	7.0
AT3G60750	764	AT3G60750.1	transketolase, putative	741	Ch/S	5.92999983	79.9599991	metabolism carbon Calvin cycle	1.3.8 PS.calvin cycle.transketolase		plastid	plastid	plastid stroma	
AT3G61080	765	AT3G61080.1	fructosamine kinase family protein	326	Ch/S	6.51000023	36.4700012	kinase	29.4.1 protein.posttranslational modification.kinase	mitochondrion		plastid	plastid stroma	
AT3G61470	766	AT3G61470.1	LHCA2 (Photosystem I light harvesting complex gene 2); chlorophyll binding	257	Ch/Th	6.9000001	27.7800007	PS LHCI	1.1.2.1 PS.lightreaction.photosystem I.LHC-I	thylakoid membrane (sensu Viridiplantae) & photosystem I antenna complex	plastid	plastid	thylakoid-integral	

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AT3G61540	767	AT3G61540.1	peptidase family protein	515		6.86999989	57.5800018		29.5 protein.degradation	undefined	Y	C	-	
AT3G61770	768	AT3G61770.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G67600.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO14376.1); contains InterPro domain Acid phosphatase /vanadium-dependent haloperoxidase related (InterPro:IPR003832)	284	Ch/E/IM	9.42000008	31.0799999	unknown	35.2 not assigned.unknown	chloroplast	Y	C	-	4.0
AT3G61870	769	AT3G61870.1	similar to unknown [Populus trichocarpa] (GB:ABK95718.1)	272	Ch/Th & Ch/E	9.34000015	29.5799999	unknown	35.2 not assigned.unknown	chloroplast inner membrane	plastid	plastid	plastid	4.0
AT3G62030	770	AT3G62030.1	ROC4 (ROTAMASE CYP 4); peptidyl-prolyl cis-trans isomerase	260	Ch/S & Ch/E	8.82999992	28.2000008	chaperone and protease	29.6 protein.folding		plastid	plastid	plastid stroma	
AT3G62410	771	AT3G62410.1	CP12-2	131		4.80999994	14.1599998		1.3 PS.calvin cycle	undefined		C	plastid stroma	
AT3G62530	772	AT3G62530.1	PBS lyase HEAT-like repeat-containing protein	221		6.13999987	24.5		35.1 not assigned.no ontology	undefined		M	-	

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AT3G62910	773	AT3G62910.1	APG3 (ALBINO AND PALE GREEN); translation release factor	422	Ch/Th & Ch/S	7.57999992	47.5299988	unknown	29.2.5 protein.synthesis.release		plastid	plastid	plastid	
AT3G63140	774	AT3G63140.1	mRNA-binding protein, putative	406	Ch/S & Ch/Th & Ch/E	8.53999996	43.9300003	RNA Binding	27.3.99 RNA.regulation of transcription.unclassified		plastid	plastid	plastid stroma	
AT3G63160	775	AT3G63160.1	unknown protein	69	Ch/E & Ch/Th	9.03999996	7.25	unknown	35.2 not assigned.unknown	chloroplast outer membrane & thylakoid membrane (sensu Viridiplantae)			envelope-outer-integral	1.0
AT3G63170	776	AT3G63170.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G26310.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO22529.1); contains InterPro domain Chalcone isomerase-like (InterPro:IPR016087)	279	Ch/E	6.96999979	30.3899994	metabolism flavonoids ?	11.1 lipid metabolism. FA synthesis and FA elongation		plastid	plastid	plastid stroma	
AT3G63190	777	AT3G63190.1	RRF (RIBOSOME RECYCLING FACTOR, CHLOROPLAST PRECURSOR)	275	Ch/S & Ch/Th	9.44999981	30.4200001	translation stroma	29.2.9* protein.synthesis.ribosome recycling		plastid	plastid	plastid stroma	

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AT3G63390	778	AT3G63390.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO22605.1)	175	Ch/E ?	5.57999992	19.1599998	unknown	35.2 not assigned.unknown	other (e.g. cytoplasm)			-	
AT3G63410	779	AT3G63410.1	APG1 (ALBINO OR PALE GREEN MUTANT 1); methyltransferase	338	Ch/E/IM	9.18000031	37.9199982	metabolism vitamin and pigment	16.1.3.3 secondary metabolism.i soprenoids.t ocopherol biosynthesis. MPBQ/MSB Q methyltransferase	chloroplast	plastid	plastid	envelope-inner-integral	1.0
AT3G63490	780	AT3G63490.1	ribosomal protein L1 family protein	346	Ch/S & Ch/E	9.28999996	37.6300011	translation stroma	29.2.1.1.1.2.1 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.50S subunit.L1	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	plastid ribosome	
AT3G63520	781	AT3G63520.1	CCD1 (CAROTENOID CLEAVAGE DIOXYGENASE 1)	538	Ch/E & other	6.03999996	60.9000015	metabolism hormone ABA	16.1.4.10 secondary metabolism.i soprenoids.c arotenoids.c arotenoid cleavage dioxygenase	undefined			cytosol	
AT4G00290	782	AT4G00290.1	mechanosensitive ion channel domain-containing protein / MS ion channel domain-containing protein	497	Ch/E/IM	9.06000042	53.8800011	transporter ion channel	35.1 not assigned.no ontology	undefined	Y	M	-	5.0
AT4G00370	783	AT4G00370.1	ANTR2 (anion transporter 2); organic anion transmembrane transporter	541	Ch/E/IM	9.25	59.6100006	transporter Pi ?	34.7 transport.phosphate			plastid	envelope-inner-integral	10.0

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AT4G00490	784	AT4G00490.1	BAM2/BMY9 (BETA-AMYLASE 2); beta-amylase	542	Ch/S	4.84000015	62.6399994	metabolism carbon	2.2.2.1 major CHO metabolism. degradation. starch.starch cleavage		plastid	plastid	plastid stroma	1.0
AT4G00620	785	AT4G00620.1	tetrahydrofolate dehydrogenase/cyclohydrolase, putative	360		8.56999969	38.7400017		25.5 C1-metabolism. Methylenetetrahydrofolate dehydrogenase & Methenyltetrahydrofolate cyclohydrolase	chloroplast	Y	C	plastid stroma	
AT4G00630	786	AT4G00630.1	KEA2 (K+ efflux antiporter); potassium:hydrogen antiporter	627	Ch/E/IM	7.07000017	66.4100037	transporter K	34.15 transport.potassium				envelope	
AT4G00640	787	AT4G00640.1	-	467	Ch/E	4.82000017	51.4099998	transporter K	-	undefined			-	1.0
AT4G00860	788	AT4G00860.1	ATOZ11 (ARABIDOPSIS THALIANA OZONE-INDUCED PROTEIN 1)	80		8.97000027	8.60000038		20 stress	secreted		S	-	
AT4G01050	789	AT4G01050.1	hydroxyproline-rich glycoprotein family protein	466	Ch/Th	5.21000004	49.3800011	chaperone and protease ?	26.23 misc.rhodanese	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	thylakoid	2.0

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AT4G01150	790	AT4G01150.1	Identical to Uncharacterized protein At4g01150, chloroplast precursor [Arabidopsis Thaliana] (GB:O04616; GB:Q38835); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G38100.1); similar to unknown [Populus trichocarpa] (GB:ABK95729.1)	164	Ch/Th	9.21000004	17.6900005	PS PSI ?	35.2 not assigned.unknown	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	thylakoid-integral	2.0
AT4G01310	791	AT4G01310.1	ribosomal protein L5 family protein	262	Ch/S & Ch/E	10.0	28.3400002	translation stroma	29.2.1.1.1.2.5 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.50S subunit.L5	cytosolic ribosome (sensu Eukaryota)	plastid	plastid	plastid ribosome	
AT4G01690	792	AT4G01690.1	PPOX (PROTOPORPHYRINOGEN OXIDASE); protoporphyrinogen oxidase	537	Ch/E & Ch/Th	9.13000011	57.6899986	metabolism vitamin and pigment	19.9 tetrapyrrole synthesis.protoporphyrin IX oxidase		plastid	mitochondrion	plastid	1.0
AT4G01800	793	AT4G01800.1	preprotein translocase secA subunit, putative	1022	Ch/S	6.07000017	115.18	protein targeting	29.3.3 protein.targeting.chloroplast		plastid	plastid	plastid stroma; thylakoid-peripheral-stromal-side	

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AT4G01883	794	AT4G01883.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G02475.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO40177.1); contains InterPro domain Streptomycetocyclase/dehydrase (InterPro:IPR005031)	224	Ch/S	9.8599966	25.2800007	unknown	35.2 not assigned.unknown		plastid	plastid	plastid	
AT4G01900	795	AT4G01900.1	GLB1 (glutamine synthetase B1)	196	Ch/Th	9.1700008	21.2700005	unknown	30.1.1 signalling.in sugar and nutrient physiology	chloroplast	plastid	plastid	plastid stroma	
AT4G02510	796	AT4G02510.1	TOC159 (PLASMID PROTEIN IMPORT 2)	1503	Ch/E/OM	4.4200008	160.820007	protein targeting Toc	29.3.3 protein.targeting.chloroplast	chloroplast outer membrane			envelope-outer	
AT4G02520	797	AT4G02520.1	ATGSTF2 (Arabidopsis thaliana Glutathione S-transferase (class phi) 2); glutathione transferase	212		5.9200008	24.1200008		26.9 misc.glutathione S transferases	undefined			not plastid	
AT4G02530	798	AT4G02530.1	chloroplast thylakoid lumen protein	216	Ch/Th & Ch/E	8.53999996	23.6599998	unknown	35.2 not assigned.unknown	thylakoid membrane (sensu Viridiplantae) & thylakoid lumen (sensu Viridiplantae)	plastid	plastid	thylakoid-peripheral-lumenal-side	

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AT4G02620	799	AT4G02620.1	(VACUOLAR ATPASE SUBUNIT F); hydrogen ion transporting ATP synthase, rotational mechanism / hydrogen ion transporting ATPase, rotational mechanism	128	other	6.0700017	14.2600002	transporter ATPase	34.1.1 transport.p-and v-ATPases.H+-transporting two-sector ATPase	undefined			vacuole	
AT4G02725	800	AT4G02725.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO22536.1)	165	Ch/Th	8.8800011	18.7900009	unknown	35.2 not assigned.unknown		plastid	plastid		
AT4G02770	801	AT4G02770.1	PSAD-1 (photosystem I subunit D-1)	208	Ch/Th & Ch/E	9.77999973	22.5900002	PS PSI	1.1.2.2 PS.lightreaction.photosystem I.PSI polypeptide subunits	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	thylakoid-peripheral-stromal-side	
AT4G02990	802	AT4G02990.1	mitochondrial transcription termination factor family protein / mTERF family protein	541		6.32999992	61.5499992		27.3.99 RNA.regulation of transcription.unclassified	undefined	Y	M	plastid	
AT4G03080	803	AT4G03080.1	kelch repeat-containing serine/threonine phosphoesterase family protein	881		5.90999985	96.1399994		29.4 protein.posttranslational modification	other (e.g. cytoplasm)			-	
AT4G03200	804	AT4G03200.1	catalytic	818		5.92000008	91.8300018		35.2 not assigned.unknown	undefined	Y	C	plastid	
AT4G03205	805	AT4G03205.1	HEMF2; coproporphyrinogen oxidase	233		7.09000015	26.1299992		19.8 tetrapyrrole synthesis.coproporphyrinogen III oxidase	chloroplast	Y	C	-	

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AT4G03280	806	AT4G03280.1	PETC (PHOTOSYNTHETIC ELECTRON TRANSFER C)	229	Ch/Th	8.8000019	24.3600006	PS b6-f	1.1.3 PS.lightreaction.cytochrome b6/f	thylakoid membrane (sensu Viridiplantae) & cytochrome b6f complex	plastid	plastid	thylakoid-peripheral-lumenal-side	
AT4G03430	807	AT4G03430.1	EMB2770/STA1 (STABILIZED1); RNA splicing factor, transesterification mechanism	1029		6.8499999	115.57		27.1.1 RNA.processing.splicing	undefined	Y		-	
AT4G03520	808	AT4G03520.1	ATHM2 (Arabidopsis thioredoxin M-type 2); thiol-disulfide exchange intermediate	186	Ch/S	9.3500038	20.3099995	redox	21.1 redox.thioredoxin		plastid	plastid	plastid stroma; thylakoid-peripheral-stromal-side	
AT4G04020	809	AT4G04020.1	FIB (FIBRILLIN); structural molecule	318	Ch/Th	5.4400006	34.9399986	PAP_fibrillin	26.31* misc.fibrillins	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	plastoglobules	
AT4G04350	810	AT4G04350.1	EMB2369 (EMBRYO DEFECTIVE 2369); ATP binding / aminoacyl-tRNA ligase	973		5.9099985	111.029999		29.1.4 protein.aa activation.leucine-tRNA ligase	chloroplast	Y	C	plastid stroma	
AT4G04640	811	AT4G04640.1	ATPC1 (ATP synthase gamma chain 1)	373	Ch/Th & Ch/E	8.1300011	40.9099998	PS ATPase	1.1.4 PS.lightreaction.ATP synthase	thylakoid membrane (sensu Viridiplantae) & chloroplast ATP synthase complex & chloroplast	plastid	plastid	thylakoid-peripheral-stromal-side	
AT4G04770	812	AT4G04770.1	ATABC1 (ARABIDOPSIS THALIANA NUCLEOSOME ASSEMBLY PROTEIN 1)	557		6.4400006	61.8600006		14 S-assimilation	chloroplast	Y	C	plastid	

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AT4G05180	813	AT4G05180.1	PSBQ/PSBQ-2/PSII-Q (PHOTOSYSTEM II SUBUNIT Q-2); calcium ion binding	230	Ch/Th	9.72000027	24.6399994	PS PSII OEE	1.1.1.2 PS.lightreaction.photosystem II.PSII polypeptide subunits	thylakoid membrane (sensu Viridiplantae) & thylakoid lumen (sensu Viridiplantae)	plastid	plastid	thylakoid-peripheral-lumenal-side	
AT4G05390	814	AT4G05390.1	ATRFNR1 (ROOT FNR 1); oxidoreductase	378		8.77000046	42.3899994		7.3 OPP.electron transfer	chloroplast	Y	C	-	
AT4G08390	815	AT4G08390.1	SAPX; L-ascorbate peroxidase	372		8.30000019	40.4000015		21.2.1 redox.ascorbate and glutathione.ascorbate	chloroplast	Y	C	mitochondria ; plastid stroma	
AT4G09000	816	AT4G09000.1	GRF1 (GENERAL REGULATORY FACTOR 1); protein phosphorylated amino acid binding	267		4.67999983	29.9300003		30.7 signalling.14-3-3 proteins	undefined			-	
AT4G09010	817	AT4G09010.1	APX4 (ASCORBATE PEROXIDASE 4); peroxidase	349	Ch/Th	8.57999992	37.9300003	stress oxidative or redox	35.2 not assigned.unknown	thylakoid membrane (sensu Viridiplantae) & thylakoid lumen (sensu Viridiplantae) & nucleus & cytoplasm	plastid	plastid	thylakoid-peripheral-lumenal-side	
AT4G09020	818	AT4G09020.1	ATISA3/ISA3 (ISOAMYLASE 3); alpha-amylase	764		5.6500001	86.3199997		2.1.2.4 major CHO metabolism.synthesis.starch.debranching	chloroplast	Y	C	plastid stroma	
AT4G09040	819	AT4G09040.1	RNA recognition motif (RRM)-containing protein	304	Ch/S	7.11000013	34.0299988	RNA binding ?	27.4 RNA.RNA binding		plastid	plastid	plastid stroma	

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AT4G09320	820	AT4G09320.1	NDPK1 (nucleoside diphosphate kinase 1); ATP binding / nucleoside diphosphate kinase	169	Ch/S & other	8.42000008	18.8099995	metabolism nucleotide	23.4.10 nucleotide metabolism. phosphotransfer and pyrophosphatases.nucleoside diphosphate kinase	undefined			-	
AT4G09430	821	AT4G09430.1	disease resistance protein (TIR-NBS-LRR class), putative	1039		7.55000019	118.370003		20.1.7 stress.biotic. PR-proteins	undefined			-	
AT4G09650	822	AT4G09650.1	ATP synthase delta chain, chloroplast, putative / H(+)-transporting two-sector ATPase, delta (OSCP) subunit, putative	234	Ch/Th & Ch/E	9.03999996	25.6599998	PS ATPase	1.1.4 PS.lightreaction.ATP synthase	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	thylakoid-peripheral-stromal-side	
AT4G10000	823	AT4G10000.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G03880.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO16313.1); contains InterPro domain Thioredoxin-like fold (InterPro:IPR012336); contains InterPro domain Thioredoxin fold	333	Ch/Th	8.93999958	37.0499992	redox ?	21.4 redox.glutaredoxins		plastid	plastid	plastid	

Accession	pgID	Master Protein	Description (curated)	Length	Localization (curated)	Calculated Pi PPDB	Calculated MW PPDB	Function (putative)	MapManBin (PPDB)	Localization (TAIR)	ChloroP	TargetP	Curated localization (PPDB)	Aramemnon	
AT4G10300	824	AT4G10300.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G04300.1); similar to unknown [Populus trichocarpa] (GB:ABK95374.1); contains InterPro domain RmIC-like jelly roll fold (InterPro:IPR014710); contains InterPro domain Protein of unknown funct	134		8.89000034	14.93000003			35.2 not assigned.unknown	chloroplast	Y	C	plastid	
AT4G10340	825	AT4G10340.1	LHCB5 (LIGHT HARVESTING COMPLEX OF PHOTOSYSTEM II 5); chlorophyll binding	280	Ch/Th	5.98999977	30.1499996	PS LHCII	1.1.1.1 PS.lightreaction.photosystem II.LHC-II	thylakoid membrane (sensu Viridiplantae) & chloroplast stromal thylakoid & PSII associated light-harvesting complex II	plastid	plastid	thylakoid-integral	2.0	
AT4G10750	826	AT4G10750.1	HpcH/Hpal aldolase family protein	358	Ch/S	5.69000006	38.4000015	metabolism carbon ?		35.1 not assigned.no ontology	mitochondrion	plastid	plastid	plastid stroma	
AT4G11150	827	AT4G11150.1	TUF (VACUOLAR ATP SYNTHASE SUBUNIT E1)	230	other	6.03999996	26.0599995	transporter ATPase		34.1.1 transport.p-and v-ATPases.H+-transporting two-sector ATPase	undefined			vacuole	
AT4G11175	828	AT4G11175.1	translation initiation factor IF-1, chloroplast, putative	141		10.1499996	15.7299995			29.2.3 protein.synthesis.initiation	undefined	Y	M	plastid stroma	

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AT4G11960	829	AT4G11960.1	PGRL1B (PGR5-LIKE B)	313	Ch/Th	5.05000019	34.9099998	PS cyclic electron flows	1.1.40 PS.lightreaction.cyclic electron flow-chlororespiration	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	thylakoid-integral	2.0
AT4G11980	830	AT4G11980.1	ATNUDT14 (Arabidopsis thaliana Nudix hydrolase homolog 14); hydrolase	309		6.98000002	34.25		26.13 misc.acid and other phosphatases	undefined	Y	M	plastid	
AT4G12060	831	AT4G12060.1	Clp amino terminal domain-containing protein	241	Ch/E & Ch/S	8.85000038	26.5599995	chaperone and protease	29.5.5 protein.degradation.serine protease		plastid	plastid	plastid stroma	
AT4G12770	832	AT4G12770.1	heat shock protein binding	891		6.57999992	100.300003		31.4 cell.vesicle transport	undefined	Y		-	
AT4G12800	833	AT4G12800.1	PSAL (photosystem I subunit L)	219	Ch/Th	9.85000038	23.0499992	PS PSI	1.1.2.2 PS.lightreaction.photosystem I.PSI polypeptide subunits	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	thylakoid-integral	2.0
AT4G12830	834	AT4G12830.1	hydrolase, alpha/beta fold family protein	393	Ch/E/IM	8.59000015	43.7599983	hydrolase ?	35.1 not assigned.no ontology		plastid	mitochondrion	plastid	
AT4G13010	835	AT4G13010.1	oxidoreductase, zinc-binding dehydrogenase family protein	329	Ch/E/IM	9.03999996	34.4300003	redox ?	26.7 misc.oxidases - copper, flavone etc.	thylakoid membrane (sensu Viridiplantae)			envelope-inner-peripheral-stromal-side	
AT4G13140	836	AT4G13140.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO46123.1)	137	Ch/E ?	9.38000011	14.79	unknown	35.2 not assigned.unknown	undefined			-	2.0
AT4G13150	837	AT4G13150.1	unknown protein	119	Ch/E ?	9.15999985	12.7700005	unknown	35.2 not assigned.unknown	undefined			-	

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AT4G13200	838	AT4G13200.1	Identical to Uncharacterized protein At4g13200, chloroplast precursor [Arabidopsis Thaliana] (GB:Q8LDV3;GB:Q9SVQ7); similar to unknown [Picea sitchensis] (GB:ABK25970.1); similar to unknown [Picea sitchensis] (GB:ABK22042.1)	185	Ch/Th	5.26000023	20.4300003	unknown	35.2 not assigned.unknown	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	thylakoid	
AT4G13430	839	AT4G13430.1	aconitase family protein / aconitate hydratase family protein	509	Ch/S	8.06999969	55.0099983	metabolism amino acids branched chain	13.1.4.4 amino acid metabolism.synthesis.branched chain group.leucine specific		plastid	plastid	plastid stroma	
AT4G13500	840	AT4G13500.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G05310.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO41162.1)	125	Ch/Th	9.06000042	13.8100004	unknown	35.2 not assigned.unknown		plastid	plastid	plastid	1.0

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AT4G13590	841	AT4G13590.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G64150.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO71558.1); contains InterPro domain Protein of unknown function UPF0016; (InterPro:IPR001727)	359	Ch/E/IM	8.81999969	37.9300003	translation stroma ?	35.2 not assigned.unknown	chloroplast inner membrane	plastid	plastid		6.0
AT4G13670	842	AT4G13670.1	PTAC5 (PLASTID TRANSCRIPTIONALLY ACTIVE5); heat shock protein binding / unfolded protein binding	387	Ch/E & Ch/Th	4.84000015	44.0200005	unknown	26.29* misc.DnaJ domain with unknown function	thylakoid membrane (sensu Viridiplantae) & plastid chromosome	plastid	plastid	plastid nucleoid	
AT4G13940	843	AT4G13940.1	HOG1 (HOMOLOG Y-DEPENDENT GENE SILENCING 1); adenosylhomocysteine	485		5.65999985	53.3699989		13.2.3.4 amino acid metabolism. degradation. aspartate family.methionine	other (e.g. cytoplasm)			-	
AT4G14070	844	AT4G14070.1	AAE15 (ACYL-ACTIVATING ENZYME 15); long-chain-fatty-acid-[acyl-carrier-protein] ligase	727	Ch/E/IM	8.89000034	81.4599991	metabolism lipid	11.1.8 lipid metabolism. FA synthesis and FA elongation.acyl coa ligase	plastid	plastid	plastid	envelope-inner-peripheral-stromal-side	

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AT4G14210	845	AT4G14210.1	PDS3 (PHYTOENE DESATURASE)	566	Ch/E & Ch/Th	6.07000017	62.9599991	metabolism vitamin and pigment	16.1.4.2 secondary metabolism.i soprenoids.c arotenoids.p hytoene dehydrogenase	chloroplast	plastid	plastid	plastid	
AT4G14880	846	AT4G14880.1	OASA1 (O-ACETYLSE RINE (THIOL) LYASE (OAS-TL) ISOFORM A1)	322		5.9000001	33.7999992		13.1.5.3.1 amino acid metabolism.s ynthesis.serine-glycine-cysteine group.cysteine.OASTL	undefined			-	
AT4G14890	847	AT4G14890.1	ferredoxin family protein	154		4.73999977	16.7299995		26.30 misc.other Ferredoxins and Rieske domain	chloroplast	Y	C	-	
AT4G15110	848	AT4G15110.1	CYP97B3 (cytochrome P450, family 97, subfamily B, polypeptide 3); oxygen binding	580	Ch/E/IM	6.38999987	65.1699982	cytochrome P450	26.10 misc.cytochrome P450		plastid	mitochondrion	plastid	
AT4G15510	849	AT4G15510.1	photosystem II reaction center PsbP family protein	287	Ch/Th	8.92000008	32.2599983	PS PSII	1.1.1.2 PS.lightreaction.photosystem II.PSII polypeptide subunits	thylakoid lumen (sensu Viridiplantae)	plastid	plastid	thylakoid-peripheral-lumenal-side	
AT4G15530	850	AT4G15530.1	PPDK (PYRUVATE ORTHOPHOSPHATE DIKINASE); kinase/ pyruvate, phosphate dikinase	956	Ch/S	5.82000017	104.199997	unknown	4.4 glycolysis.PPFK				plastid stroma	
AT4G15560	851	AT4G15560.1	CLA1 (CLOROPLASTOS ALTERADOS 1)	717		7.03999996	76.8300018		16.1.1.1 secondary metabolism.i soprenoids.non-mevalonate pathway.DXS	chloroplast	Y	C	plastid stroma	

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AT4G15820	852	AT4G15820.1	wound-responsive protein-related	460	CH/E/IM	5.1500001	51.2099991	unknown	20.2.4 stress.abiotic.touch/wounding	undefined	Y	M	-	1.0
AT4G16060	853	AT4G16060.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO44835.1)	289		5.3099994	27.0200005		35.2 not assigned.unknown	chloroplast	Y		plastid	
AT4G16155	854	AT4G16155.1	dihydrolipoamide dehydrogenase 2, plastidic / lipoamide dehydrogenase 2 (PTLPD2)	567	Ch/E & Ch/S	7.2899996	60.1399994	metabolism lipid	11.1.31 lipid metabolism. FA synthesis and FA elongation.pyruvate DH				plastid	
AT4G16390	855	AT4G16390.1	chloroplastic RNA-binding protein P67, putative	688	Ch/S	5.8200017	76.6299973	RNA binding ?	27.4 RNA.RNA binding		plastid	plastid	plastid stroma	
AT4G17040	856	AT4G17040.1	ATP-dependent Clp protease proteolytic subunit, putative	305	Ch/S & Ch/E	9.3299992	33.4399986	chaperone and protease	29.5.5 protein.degradation.serine protease	chloroplast stroma	plastid	plastid	plastid stroma	
AT4G17170	857	AT4G17170.1	AT-RAB2 (Arabidopsis Rab GTPase homolog B1c); GTP binding	211	na	6.9499981	23.1599998	signalling / SNARE effector	30.5 signalling.G-proteins					
AT4G17300	858	AT4G17300.1	NS1 (OVULE ABORTION 8)	567		5.7899996	63.6899986		29.1.22 protein.aa activation.asparagine-tRNA ligase	chloroplast	Y	C	mitochondria ; plastid stroma	
AT4G17530	859	AT4G17530.1	RAB1C; GTP binding	202	na	5.2699998	22.3099995	signalling / SNARE effector	30.5 signalling.G-proteins			extracellular, endoplasmic reticulum, golgi	nucleus	

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AT4G17540	860	AT4G17540.1	similar to hypothetical protein Osl_033497 [Oryza sativa (indica cultivar-group)] (GB:EAY79538.1); similar to Os10g0563400 [Oryza sativa (japonica cultivar-group)] (GB:NP_001065401.1)	294	Ch/E ?	9.5600042	31.75	unknown	35.2 not assigned.unknown	other (e.g. cytoplasm)			-	2.0
AT4G17560	861	AT4G17560.1	ribosomal protein L19 family protein	225	Ch/S & Ch/E	10.0299997	25.5100002	translation stroma	29.2.1.1.1.2.19 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.50S subunit.L19		plastid	plastid	plastid ribosome; plastid ribosome	
AT4G17600	862	AT4G17600.1	LIL3:1; transcription factor	262	Ch/Th	4.94000006	29.3999996	Stress light	1.1.8* light stress chlorophyll binding	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	thylakoid-integral	2.0
AT4G17740	863	AT4G17740.1	C-terminal processing protease, putative	515	Ch/Th	8.97000027	55.7599983	chaperone and protease PSII	29.9* protein.processing	thylakoid lumen (sensu Viridiplantae) & mitochondrion	plastid	plastid	thylakoid-peripheral-lumenal-side	
AT4G18370	864	AT4G18370.1	DEG5/DEGP5/HHOA (DEGP PROTEASE 5); serine-type peptidase/trypsin	323	Ch/Th	5.19000006	34.9199982	chaperone and protease PS PSII	29.5.5 protein.degradation.serine protease	thylakoid lumen (sensu Viridiplantae)	plastid	plastid	thylakoid-peripheral-lumenal-side	
AT4G18440	865	AT4G18440.1	adenylosuccinate lyase, putative / adenylosuccinase, putative	536	Ch/S	5.88000011	59.75	metabolism nucleotide	23.1.2.8 nucleotide metabolism.synthesis.purine.SAICAR lyase		plastid	plastid	plastid stroma	

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AT4G18480	866	AT4G18480.1	CHLI1 (CHLORINA 42); magnesium chelatase	424	Ch/S	6.07999992	46.2700005	metabolism vitamin and pigment	19.10 tetrapyrrole synthesis.magnesium chelatase	magnesium chelatase complex & chloroplast & chloroplast stroma	plastid	plastid	plastid stroma	
AT4G18810	867	AT4G18810.1	binding / catalytic/transcription repressor	596	Ch/S & Ch/E	8.15999985	65.4599991	protein targeting ? Stress ?	20.2.99 stress.abiotic .unspecified		plastid	plastid	plastid stroma	
AT4G19100	868	AT4G19100.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G52780.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN79943.1)	214	Ch/Th	8.68999958	24.2099991	PS PSII biogenesis	29.8 protein assembly and cofactor ligation		plastid	plastid	plastid	
AT4G19390	869	AT4G19390.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G13720.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO63752.1); contains InterPro domain Uncharacterised conserved protein UCP022348 (InterPro:IPR016804); contains InterPro do	273	Ch/E/IM	9.28999996	30.0400009	unknown	35.2 not assigned.unknown	chloroplast	Y	C	-	4.0

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AT4G19710	870	AT4G19710.2	AK-HSDH/AK-HSDH II; aspartate kinase/homoserine dehydrogenase	859		6.3499999	94.4199982		13.1.3.6.1.10 amino acid metabolism.synthesis.aspartate family.misc.homoserine.bifunctional aspartate kinase/homoserine dehydrogenase	chloroplast	Y	C	plastid	
AT4G20260	871	AT4G20260.1	DREPP plasma membrane polypeptide family protein	225	Ch/E ?	4.98999977	24.5799999	stress ?			-	-		
AT4G20360	872	AT4G20360.1	AtRABE1b/AtRab8D (Arabidopsis Rab GTPase homolog E1b); translation elongation factor	476	Ch/S & Ch/Th	5.82999992	51.6300011	translation stroma / signalling / SNARE effector	29.2.4 protein.synthesis.elongation	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	plastid stroma	
AT4G20850	873	AT4G20850.1	TPP2 (TRIPEPTIDYL PEPTIDASE II); subtilase	1380	Ch/S	5.76000023	152.360001	unknown	29.5.1 protein.degradation.subtilases	cytoplasm	plastid	plastid	plastid stroma	
AT4G20960	874	AT4G20960.1	cytidine/deoxycytidylate deaminase family protein	426	Ch/S	6.03999996	46.6699982	unknown	23.5.3 nucleotide metabolism.deoxynucleotide metabolism.cytosine deaminase		plastid	plastid	plastid	
AT4G21210	875	AT4G21210.1	phosphoprotein phosphatase / protein kinase	403	Ch/S	6.92999983	43.6800003	unknown	35.2 not assigned.unknown		plastid	plastid	plastid stroma	

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AT4G21280	876	AT4G21280.1	PSBQ/PSBQ-1/PSBQA; calcium ion binding	223	Ch/Th	9.64000034	23.7900009	PS PSII OEE	1.1.1.2 PS.lightreaction.photosystem II.PSII polypeptide subunits	thylakoid membrane (sensu Viridiplantae) & thylakoid lumen (sensu Viridiplantae)	plastid	plastid	thylakoid-peripheral-lumenal-side	
AT4G21445	877	AT4G21445.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO42770.1)	154		6.59000015	17.6100006		35.2 not assigned.unknown	undefined	Y	C	plastid stroma	
AT4G21670	878	AT4G21670.1	CPL1 (FIERY 2); double-stranded RNA binding	967		5.80999994	108.419998		27.4 RNA.RNA binding	other (e.g. cytoplasm)			-	2.0
AT4G22130	879	AT4G22130.1	SRF8 (STRUBBELIG-RECEPTOR FAMILY 8); kinase	703		6.92000008	76.0800018		29.4.1.57 protein.posttranslational modification.kinase.receptor like cytoplasmatic kinase VII; 30.2.5 signalling.receptor kinases.leucine rich repeat V	secreted		S	-	
AT4G22240	880	AT4G22240.1	plastid-lipid associated protein PAP, putative	310	Ch/Th	5.67000008	33.6500015	PAP_fibrillin	26.31* misc.fibrillins	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	plastoglobules	
AT4G22570	881	AT4G22570.1	APT3 (ADENINE PHOSPHORIBOSYLTRANSFERASE 3); adenine phosphoribosyltransferase	183		5.82999992	20.3500004		23.3.1.1 nucleotide metabolism.salvage.phosphoribosyltransferases.aprt	other (e.g. cytoplasm)			cytosol	

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AT4G22890	882	AT4G22890.1	PGR5-LIKE A	324	Ch/Th	5.1999981	35.7200012	PS cyclic electron flows	1.1.40 PS.lightreaction.cyclic electron flow-chlororespiration	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	thylakoid-integral	
AT4G22930	883	AT4G22930.1	PYR4 (PYRIMIDIN 4); dihydroorotase	377		8.6300011	41.9500008		23.1.1.3 nucleotide metabolism.synthesis.pyrimidine.dihydroorotase	undefined			plastid	
AT4G23100	884	AT4G23100.1	RML1 (ROOT MERISTEMLESS 1); glutamate-cysteine ligase	522	Ch/S	6.1599985	58.5600014	unknown	21.2.2 redox.ascorbate and glutathione.glutathione	chloroplast	plastid	plastid	plastid stroma	
AT4G23430	885	AT4G23430.1	short-chain dehydrogenase/reductase (SDR) family protein	320	Ch/E/IM	8.9499981	34.4900017	protein targeting Tic		chloroplast inner membrane	-	-		
AT4G23890	886	AT4G23890.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO69542.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN73381.1)	250	Ch/Th	8.3100042	27.7199993	NDH	1.1.6 PS.lightreaction.NADH DH	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	thylakoid	
AT4G23940	887	AT4G23940.1	FtsH protease, putative	946	Ch/E/IM	7.6399987	105.540001	chaperone and protease	29.5.7 protein.degradation.metall otease		plastid	plastid	envelope-inner	3.0
AT4G24280	888	AT4G24280.1	CPHSC70-1 (chloroplast heat shock protein 70-1); ATP binding / unfolded protein binding	718	Ch/S	5.0599994	76.5	chaperone and protease	29.6 protein.foldin g	plastid stroma	plastid	plastid	plastid stroma	

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AT4G24460	889	AT4G24460.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G19380.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO61583.1); contains domain Multidrug resistance efflux transporter EmrE (SSF103481)	431	Ch/E/IM	9.93000031	46.6800003	transporter ?	35.2 not assigned.unkn own	chloroplast	Y	C	-	10.0
AT4G24620	890	AT4G24620.1	PGI1 (CHLOROPLASTIC PHOSPHOGLUCOSE ISOMERASE)	613	Ch/S	5.46000004	67.0400009	metabolism carbon	4.3 glycolysis.G6P isomerase		plastid	plastid	plastid stroma	
AT4G24770	891	AT4G24770.1	RBP31 (31-KDA RNA BINDING PROTEIN); RNA binding / poly(U) binding	329	Ch/S & Ch/E	4.57999992	35.7799988	RNA Binding	27.1.5* RNA editing	thylakoid membrane (sensu Viridiplantae) & chloroplast	plastid	plastid	plastid stroma	
AT4G24830	892	AT4G24830.1	arginosuccinate synthase family	494	Ch/S	6.25	53.8400002	metabolism amino acids	13.1.2.3.22 amino acid metabolism.synthesis.glutamate family.arginine.arginosuccinate synthase		plastid	plastid	plastid stroma	
AT4G24930	893	AT4G24930.1	thylakoid lumenal 17.9 kDa protein, chloroplast	225	Ch/Th	6.38999987	24.6900005	unknown	35.2 not assigned.unkn own	thylakoid lumen (sensu Viridiplantae)	plastid	plastid	thylakoid-peripheral-lumenal-side	

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AT4G25050	894	AT4G25050.1	ACP4 (ACYL CARRIER PROTEIN 4)	137	Ch/E/IM	4.73000002	14.54	metabolism lipid	11.1.12 lipid metabolism. FA synthesis and FA elongation.A CP protein	chloroplast	Y	C	plastid stroma	
AT4G25080	895	AT4G25080.1	CHLM (MAGNESIUM-PROTOPORPHYRIN IX METHYLTRANSFERASE); magnesium protoporphyrin IX methyltransferase	312	Ch/E & Ch/Th	7.67999983	33.7900009	metabolism vitamin and pigment	19.11 tetrapyrrole synthesis.magnesium protoporphyrin IX methyltransferase	thylakoid membrane (sensu Viridiplantae) & chloroplast envelope	plastid	plastid	plastid	
AT4G25100	896	AT4G25100.1	FSD1 (FERRIC SUPEROXIDE DISMUTASE 1); iron superoxide dismutase	212		6.05000019	23.7900009		21.6 redox.dismutases and catalases	undefined			cytosol; plastid stroma	
AT4G25130	897	AT4G25130.1	peptide methionine sulfoxide reductase, putative	258	Ch/S & Ch/E	8.94999981	28.6399994	protein modification stress oxidative	29.11* protein.methionine sulfoxide reductases		plastid	plastid	plastid stroma	
AT4G25370	898	AT4G25370.1	Clp amino terminal domain-containing protein	238	Ch	9.23999977	26.0499992	chaperone and protease	29.5.5 protein.degradation.serine protease	chloroplast	Y	C	plastid stroma; thylakoid-peripheral-stromal-side	
AT4G25450	899	AT4G25450.1	ATNAP8 (Arabidopsis thaliana non-intrinsic ABC protein 8); ATPase, coupled to transmembrane movement of substances	714	Ch/E/IM	9.11999989	77.9199982	transporter ABC	34.8 transport.metabolite transporters at the envelope membrane		plastid	mitochondrion	envelope-inner-integral	
AT4G25650	900	AT4G25650.1	ACD1-LIKE; electron carrier	536	Ch/E/IM	8.89999962	61.2599983	protein targeting Tic ?	29.3.3 protein.targeting.chloroplast		plastid	plastid	envelope-inner	2.0

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AT4G25900	901	AT4G25900.1	aldose 1-epimerase family protein	318		9.64999962	36.25		3.5 minor CHO metabolism. others	secreted		S	-	
AT4G25910	902	AT4G25910.1	NFU3 (NFU domain protein 3)	236		6.44999981	25.6499996		29.8.1* protein assembly and cofactor ligation.Fe-S assembly	chloroplast	Y	C	plastid	
AT4G26300	903	AT4G26300.1	EMB1027 (EMBRYO DEFECTIVE 1027); ATP binding / arginine-tRNA ligase	642		6.73000002	72.3799973		29.1.19 protein.aa activation.arginine-tRNA ligase	undefined			plastid stroma	
AT4G26530	904	AT4G26530.1	fructose-bisphosphate aldolase, putative	358		5.63999987	38.2900009		4.7 glycolysis.aldolase	undefined			cytosol	
AT4G26670	905	AT4G26670.1	mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein	210	Ch/E/OM	7.61999989	21.8099995	protein targeting / aa channel	34.8 transport.metabolite transporters at the envelope membrane				envelope-inner-integral	2.0
AT4G26900	906	AT4G26900.1	AT-HF (ARABIDOPSIS THALIANA HISF PROTEIN)	592		6.30000019	64.1900024		13.1.7.10 amino acid metabolism.synthesis.histidine.Imidazole glycerol phosphate synthase	chloroplast	Y	C	plastid stroma	
AT4G27070	907	AT4G27070.1	TSB2 (TRYPTOPHAN SYNTHASE BETA-SUBUNIT); tryptophan synthase	475	Ch/E ?	6.19999981	51.5999985	metabolism amino acid Trp	13.1.6.5.5 amino acid metabolism.synthesis.aromatic aa.tryptophan.tryptophan synthase	chloroplast	Y	C	-	

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AT4G27440	908	AT4G27440.1	PORB (PROTOCHLOROPHYLLIDE OXIDOREDUCTASE B); oxidoreductase/ protochlorophyllide reductase	401	Ch/E & Ch/Th	9.22000027	43.3600006	metabolism vitamin and pigment	19.14 tetrapyrrole synthesis.protochlorophyllide reductase	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	thylakoid-peripheral-stromal-side	
AT4G27700	909	AT4G27700.1	rhodanese-like domain-containing protein	224	Ch/E & Ch/Th	8.77999973	24.8700008	unknown	26.23 misc.rhodanese	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	thylakoid	
AT4G27990	910	AT4G27990.1	YGGT family protein	218	Ch/E/IM	11.2799997	23.7000008	cytochrome biogenesis ?	35.1 not assigned.no ontology	chloroplast envelope	plastid	plastid	plastid	3.0
AT4G28025	911	AT4G28025.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO66511.1); contains domain Chlorophyll a-b binding protein (SSF103511)	157	Ch/Th	10.5900002	16.9500008	unknown	35.2 not assigned.unknown		plastid	plastid	plastid	
AT4G28210	912	AT4G28210.1	EMB1923 (EMBRYO DEFECTIVE 1923)	348	Ch/E/IM	9.76000023	38.3400002	transporter aa ?	35.2 not assigned.unknown		plastid	plastid	plastid	7.0
AT4G28440	913	AT4G28440.1	DNA-binding protein-related	153	Ch/E/IM	9.46000004	16.4500008	DNA binding ?	28.99 DNA.unspecified	undefined	Y	C	-	
AT4G28660	914	AT4G28660.1	PSB28 (PHOTOSYSTEM II REACTION CENTER PSB28 PROTEIN)	183	Ch/S & Ch/Th	9.46000004	20.1900005	PS PSII	1.1.1.2 PS.lightreaction.photosystem II.PSII polypeptide subunits		plastid	plastid	thylakoid-peripheral-lumenal-side	
AT4G28706	915	AT4G28706.1	pfkB-type carbohydrate kinase family protein	401		5.92999983	43.0800018		3.5 minor CHO metabolism.others	undefined	Y	C	plastid stroma	

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AT4G28750	916	AT4G28750.1	PSAE-1 (PSA E1 KNOCKOUT); catalytic	143	Ch/Th & Ch/E	9.92000008	14.96	PS PSI	1.1.2.2 PS.lightreaction.photosystem I.PSI polypeptide subunits	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	thylakoid-peripheral-stromal-side	
AT4G29060	917	AT4G29060.1	EMB2726 (EMBRYO DEFECTIVE 2726); translation elongation factor	953	Ch/S	4.94999981	103.779999	translation stroma	29.2.4 protein.synthesis.elongation		plastid	plastid	plastid ribosome	
AT4G29130	918	AT4G29130.1	ATHXK1 (GLUCOSE INSENSITIVE 2); ATP binding / hexokinase	496	Ch/E/OM	5.75	53.7000008	metabolism carbon	2.2.1.4 major CHO metabolism.degradation.sucrose.hexokinase	mitochondrion		extracellular, endoplasmic reticulum, golgi	mitochondria	
AT4G29590	919	AT4G29590.1	methyltransferase	317	Ch/S	6.96999979	35.3699989	unknown	29.4 protein.postranslational modification		plastid	plastid	plastid	
AT4G29670	920	AT4G29670.1	thioredoxin family protein	235	Ch/S	9.05000019	25.8400002	redox	21.1 redox.thioredoxin		plastid	plastid	plastid stroma	
AT4G29840	921	AT4G29840.1	MTO2 (METHIONINE OVER-ACCUMULATOR); threonine synthase	526	Ch/S	7.11000013	57.7700005	metabolism amino acids Arginine	13.1.3.2.1 amino acid metabolism.synthesis.aspartate family.threonine.threonine synthase		plastid	plastid	plastid stroma	
AT4G30580	922	AT4G30580.1	ATS2 (EMBRYO DEFECTIVE 1995); 1-acylglycerol-3-phosphate O-acyltransferase/acyltransferase	356	Ch/E/IM	9.86999989	39.3899994	metabolism lipid	11.10 lipid metabolism.glycolipid synthesis	undefined	Y	C	envelope-inner-integral	3.0

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AT4G30620	923	AT4G30620.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G24020.1); similar to unknown [Picea sitchensis] (GB:ABK26000.1); similar to Os02g0180200 [Oryza sativa (japonica cultivar-group)] (GB:NP_001046090.1); contains InterPro domain Conserved hypo	180	Ch/E ?	9.18000031	19.5799999	unknown	35.2 not assigned.unknown	chloroplast	Y	C	-	
AT4G30690	924	AT4G30690.1	translation initiation factor 3 (IF-3) family protein	281	Ch/Th & Ch/S	9.53999996	31.8199997	translation stroma	29.2.3 protein.synthesis.initiation		plastid	plastid	plastid stroma	
AT4G30910	925	AT4G30910.1	cytosol aminopeptidase family protein	581		6.25	61.2900009		29.5 protein.degradation	chloroplast	Y	C	plastid stroma	
AT4G30920	926	AT4G30920.1	cytosol aminopeptidase family protein	583	Ch/S	6.61000013	61.2999992	chaperone and protease	29.5 protein.degradation		plastid	plastid	plastid	
AT4G30950	927	AT4G30950.1	FAD6 (FATTY ACID DESATURASE 6); omega-6 fatty acid desaturase	448	Ch/E/IM	9.01000023	51.2200012	metabolism lipid	11.2.4 lipid metabolism.FA desaturation.omega 6 desaturase		plastid	plastid	envelope-inner-integral	3.0

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AT4G31780	928	AT4G31780.2	MGD1 (MONOGALACTOSYLDIACYLGLYCEROL SYNTHASE 1, MONOGALACTOSYLDIACYLGLYCEROL SYNTHASE A); 1,2-diacylglycerol 3-beta-galactosyltransferase/transferase, transferring glycosyl groups	504	Ch/E/IM	9.02999973	55.4300003	metabolism lipid	11.10.1 lipid metabolism.glycolipid synthesis.MGDG synthase	chloroplast inner membrane	plastid	plastid	envelope-inner	
AT4G31990	929	AT4G31990.1	ASP5 (ASPARTATE AMINOTRANSFERASE 5)	453	Ch/S	8.18000031	49.8300018	metabolism aa Asp	13.1.1.2.1 amino acid metabolism.synthesis.central amino acid metabolism.aspartate.aspartate aminotransferase	chloroplast & plastid	plastid	plastid	plastid stroma	
AT4G32250	930	AT4G32250.1	protein kinase family protein	611	Ch/E	7.94000006	68.1500015	kinase	29.4.1 protein.posttranslational modification.kinase				plastid	
AT4G32260	931	AT4G32260.1	ATP synthase family	219	Ch/Th & Ch/E	5.78999996	23.9099998	PS ATPase	1.1.4 PS.lightreaction.ATP synthase	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	thylakoid-integral	1.0
AT4G32400	932	AT4G32400.1	SHS1 (SODIUM HYPERSENSITIVE 1); binding / transporter	392	Ch/E/IM	9.40999985	42.5699997	transporter MCF ATP/ADP ?	34.8 transport.metabolite transporters at the envelope membrane		plastid		envelope-inner-integral; mitochondria	

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AT4G32520	933	AT4G32520.1	SHM3 (SERINE HYDROXYMETHYLTRANSFERASE 3); glycine hydroxymethyltransferase	529	Ch/S	9.02999973	57.9799995	unknown	1.2.5 PS.photorepiration.serine hydroxymethyltransferase		plastid	plastid	plastid	
AT4G32590	934	AT4G32590.1	ferredoxin-related	173		9.25	18.6599998		1.1.5.2 PS.lightreaction.other electron carrier (ox/red).ferredoxin	chloroplast	Y	C	-	
AT4G32770	935	AT4G32770.1	VTE1 (VITAMIN E DEFICIENT 1)	488	Ch/E & Ch/Th	5.94000006	54.7200012	metabolism vitamin and pigment	16.1.3.4 secondary metabolism.isoprenoids.tocopherol biosynthesis.tocopherol cyclase	chloroplast inner membrane	plastid	plastid	plastoglobules	
AT4G33010	936	AT4G33010.1	ATGLDP1 (ARABIDOPSIS THALIANA GLYCINE DECARBOXYLASE P-PROTEIN 1); glycine dehydrogenase (decarboxylating)	1037		6.5	112.919998		13.2.5.2 amino acid metabolism.degradation.serine-glycine-cysteine group.glycine	undefined		M	mitochondria	
AT4G33030	937	AT4G33030.1	SQD1 (sulfoquinovosyl diacylglycerol 1); UDPsulfoquinovose synthase	477		8.40999985	53.1100006		11.10.3 lipid metabolism.glycolipid synthesis.UDP-sulfoquinovose synthase	chloroplast	Y	C	-	
AT4G33090	938	AT4G33090.1	APM1 (AMINOPEPTIDASE M1)	879		5.32999992	98.1800003		29.5 protein.degradation	undefined			-	
AT4G33350	939	AT4G33350.1	chloroplast inner membrane import protein Tic22, putative	268	Ch/E/IM	9.31000042	30.1000004	protein targeting Tic	29.3.3 protein.targeting.chloroplast		plastid	plastid	envelope-outer	

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AT4G33460	940	AT4G33460.1	ATNAP13 (EMBRYO DEFECTIVE 2751)	271	Ch/E/IM	8.68000031	29.6200008	transporter ABC	34.16 transport.ABC transporters and multidrug resistance systems		plastid	plastid	envelope	
AT4G33510	941	AT4G33510.1	DHS2 (3-DEOXY-D-ARABINO-HEPTULOSONATE 7-PHOSPHATE SYNTHASE); 3-deoxy-7-phosphoheptulonate synthase	507	Ch/Th	8.93000031	56.1500015	metabolism aa	13.1.6.1.1 amino acid metabolism.synthesis.aromatic aa.chorismate.3-deoxy-D-arabino-heptulosonate 7-phosphate synthase	chloroplast	plastid	plastid	plastid	
AT4G33520	942	AT4G33520.2	PAA1 (metal-transporting P-type ATPase 1); ATPase, coupled to transmembrane movement of ions, phosphorylative mechanism	949	Ch/E & Ch/S	8.97000027	99.9899979	transporter ATPase Cu	34.12 transport.metabolism	chloroplast	Y	C	envelope- inner	
AT4G33680	943	AT4G33680.1	AGD2 (ABERRANT GROWTH AND DEATH 2); transaminase	461	Ch/S	7.01999998	50.3899994	metabolism aa Asp	13.1.3.5.3 amino acid metabolism.synthesis.aspartate family.lysine.LL-diaminopimelic acid aminotransferase	chloroplast stroma & chloroplast	plastid	plastid	plastid stroma	
AT4G33760	944	AT4G33760.1	tRNA synthetase class II (D, K and N) family protein	664		6.73000002	74.5100021		29.1.12 protein.aa activation.aspartate-tRNA ligase	undefined	Y	C	mitochondria ; plastid stroma	

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AT4G34090	945	AT4G34090.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G23370.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO47838.1)	330	Ch/S	5.6500001	36.9099998	unknown	35.2 not assigned.unknown				plastid	plastid stroma	
AT4G34120	946	AT4G34120.1	LEJ1 (LOSS OF THE TIMING OF ET AND JA BIOSYNTHE SIS 1)	238		7.92999983	25.9500008				Y	C	plastid stroma		
AT4G34200	947	AT4G34200.1	EDA9 (embryo sac development arrest 9); NAD binding / amino acid binding / binding / catalytic/ cofactor binding / oxidoreductase, acting on the CH-OH group of donors, NAD or NADP as acceptor / phosphoglycerate dehydrogenase	603	Ch/S	6.15999985	63.3199997	metabolism aa Ser	13.1.5.1.1 amino acid metabolism.synthesis.serine-glycine-cysteine group.serine.phosphoglycerate dehydrogenase	mitochondrion	plastid	plastid	plastid		
AT4G34240	948	AT4G34240.1	ALDH311 (Aldehyde dehydrogenase 311); 3-chloroallyl aldehyde dehydrogenase/ aldehyde dehydrogenase (NAD)	550	Ch/E/IM	8.72999954	60.1699982	metabolism carbon	5.10 fermentation.aldehyde dehydrogenase		plastid		plastid	2.0	

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AT4G34290	949	AT4G34290.1	SWIB complex BAF60b domain-containing protein	144	Ch/Th & Ch/S	9.78999996	15.9899998	unknown	35.1 not assigned.no ontology		plastid	plastid		
AT4G34350	950	AT4G34350.1	CLB6 (CHLOROPLAST BIOGENESIS 6); 4-hydroxy-3-methylbut-2-en-1-yl diphosphate reductase	466	Ch/S	5.76000023	52.7799988	metabolism isoprenoids	16.1.1.7 secondary metabolism.isoprenoids.non-mevalonate pathway.HDR	chloroplast stroma	plastid	plastid	plastid stroma	
AT4G34620	951	AT4G34620.1	SSR16 (ribosomal protein S16); structural constituent of ribosome	113	Ch/S & Ch/E & Ch/S	9.80000019	12.6899996	translation stroma	29.2.1.1.3.1.16 protein.synthesis.ribosomal protein.prokaryotic.unknown organellar.30S subunit.S16	ribosome		mitochondrion	mitochondria; plastid ribosome	
AT4G34740	952	AT4G34740.1	ATASE2 (GLN PHOSPHORIBOSYL PYROPHOSPHATE AMIDOTRANSFERASE 2); amidophosphoribosyltransferase	561	Ch/S	6.28999996	61.0299988	metabolism nucleotide	23.1.2.1 nucleotide metabolism.synthesis.purine.amidophosphoribosyltransferase		plastid	plastid	plastid	
AT4G34820	953	AT4G34820.1	-	1089	CH/E ?	9.22000027	35.7200012	unknown	-	undefined	Y		-	
AT4G35000	954	AT4G35000.1	APX3 (ASCORBATE PEROXIDASE 3); L-ascorbate peroxidase	287	na	6.46000004	31.5699997	stress oxidative or redox ?	21.2.1 redox.ascorbate and glutathione.ascorbate				peroxisome	1.0
AT4G35090	955	AT4G35090.1	CAT2 (CATALASE 2); catalase	492	other	6.61999989	56.9300003	stress oxidative	21.6 redox.dismutases and catalases	undefined	Y		peroxisome	

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AT4G35100	956	AT4G35100.1	PIP3 (PLASMA MEMBRANE INTRINSIC PROTEIN 3); water channel	280	other	8.9700027	29.7399998	transporter aquaporin	34.19.1 transport.Maj or Intrinsic Proteins.PIP	other (e.g. cytoplasm)			plasma membrane	6.0
AT4G35250	957	AT4G35250.1	vestitone reductase-related	395	Ch/Th	8.6999981	43.7200012	protein targeting ?	35.1 not assigned.no ontology		plastid	plastid	thylakoid	
AT4G35630	958	AT4G35630.1	PSAT (phosphoserine aminotransferase); phosphoserine transaminase	430	Ch/S	8.25	47.3600006	metabolism aa serine	13.1.5.1.2 amino acid metabolism.s ynthesis.serine-glycine-cysteine group.serine.phosphoserine aminotransferase	chloroplast	plastid	plastid	plastid stroma	
AT4G36150	959	AT4G36150.1	disease resistance protein (TIR-NBS-LRR class), putative	1179		7.38000011	134.070007		20.1.7 stress.biotic. PR-proteins	chloroplast	Y	C	-	1.0
AT4G36530	960	AT4G36530.1	hydrolase, alpha/beta fold family protein	321	Ch/E ?? & Ch/Th ??	5.6999981	35.7700005	hydrolase ?	35.1 not assigned.no ontology				plastid	
AT4G36810	961	AT4G36810.1	GGPS1 (GERANYLGERANYL PYROPHOSPHATE SYNTHASE 1); farnesyltransferase	371	Ch/S	6.1599985	40.1699982	metabolism isoprenoids non-mevalonate pathway	16.1.1.10 secondary metabolism.i soprenoids.mevalonate pathway.ger anylgeranyl pyrophosphate synthase	etioplast & chloroplast	plastid	plastid	plastid stroma	
AT4G37000	962	AT4G37000.1	ACD2 (ACCELERATED CELL DEATH 2)	319		5.71000004	36.4399986		19.50* tetrapyrrole degradation	chloroplast	Y	C	mitochondria ; plastid stroma	
AT4G37200	963	AT4G37200.1	HCF164 (High chlorophyll fluorescence 164); thiol-disulfide exchange intermediate	261	Ch/Th	5.26000023	28.7399998	redox ?	29.8 protein assembly and cofactor ligation	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	thylakoid-peripheral-stromal-side	

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AT4G37270	964	AT4G37270.1	HMA1 (Heavy metal ATPase 1); copper-exporting ATPase	819	Ch/E/IM	8.05000019	88.1900024	transporter ATPase Cu	34.12 transport.met al	chloroplast envelope	plastid	mitochondrion	envelope	6.0
AT4G37930	965	AT4G37930.1	SHM1 (SERINE HYDROXYMETHYLTRANSFERASE 1); glycine hydroxymethyltransferase / poly(U) binding	517	Ch/Th & Ch/S	8.11999989	57.4000015	unknown	25.1 C1-metabolism.glycine hydroxymethyltransferase	mitochondrion		mitochondrion	mitochondria	
AT4G38460	966	AT4G38460.1	GGR (GERANYLGERANYL REDUCTASE); farnesyltransferase	326	Ch/S	5.73000002	35.1800003	metabolism isoprenoids non-mevalonate pathway	16.1.1.10 secondary metabolism.isoprenoids.mevalonate pathway.geranylgeranyl pyrophosphate synthase		plastid	plastid	plastid stroma	
AT4G38510	967	AT4G38510.1	(VACUOLAR ATP SYNTHASE SUBUNIT B2); hydrogen ion transporting ATP synthase, rotational mechanism	487	Ch/E & other	5.03000021	54.2999992	transporter ATPase	34.1.1 transport.p-and v-ATPases.H+-transporting two-sector ATPase	other (e.g. cytoplasm)			-	
AT4G38950	968	AT4G38950.1	kinesin motor family protein	836		7.23000002	94.4599991		31.1 cell.organisation	undefined			-	
AT4G38970	969	AT4G38970.1	fructose-bisphosphate aldolase, putative	398	Ch/S & Ch/E & Ch/Th	6.78000021	42.9799995	metabolism carbon Calvin cycle	1.3.6 PS.calvin cycle.aldolase	chloroplast stroma	plastid	plastid	plastid stroma; plastoglobules	
AT4G39080	970	AT4G39080.1	VHA-A3 (VACUOLAR PROTON ATPASE A3); ATPase	821	other	5.6500001	92.8300018	transporter ATPase	34.1 transport.p-and v-ATPases	undefined			-	6.0

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AT4G39120	971	AT4G39120.1	inositol monophosphatase family protein	346		6.01999998	38.2299995		3.4.5 minor CHO metabolism. myo-inositol.inositol phosphatase	chloroplast	Y	C	plastid	
AT4G39260	972	AT4G39260.1	ATGRP8/GR-RBP8 (COLD, CIRCADIAN RHYTHM, AND RNA BINDING 1, GLYCINE-RICH PROTEIN 8); RNA binding	169	Ch/Th	5.57000017	16.5699997	RNA Binding	27.3.75 RNA.regulation of transcription. GRP				nucleus	
AT4G39460	973	AT4G39460.1	SAMC1/SAMT1 (S-ADENOSYL METHIONINE CARRIER 1); S-adenosylmethionine transmembrane transporter/binding	325	Ch/E/IM	9.68000031	34.8600006	transporter MCF SAM	34.8 transport.metabolite transporters at the envelope membrane		plastid	plastid	envelope-inner-integral	
AT4G39710	974	AT4G39710.1	immunophilin, putative / FKBP-type peptidyl-prolyl cis-trans isomerase, putative	217	Ch/Th	8.43999958	23.2600002	NDH	29.8 protein assembly and cofactor ligation		plastid	plastid	thylakoid-peripheral-lumenal-side	
AT4G39960	975	AT4G39960.1	DNAJ heat shock family protein	447	Ch/E & Ch/S	9.22000027	48.0299988	chaperone and protease	26.29* misc.DnaJ domain with unknown function	thylakoid membrane (sensu Viridiplantae)	plastid	mitochondrion	thylakoid	
AT4G39970	976	AT4G39970.1	haloacid dehalogenase-like hydrolase family protein	316	Ch/S	5.38999987	34.6500015	unknown	3.2 minor CHO metabolism.trehalose		plastid	plastid	plastid stroma	

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AT5G01220	977	AT5G01220.1	SQD2 (SULFOQUI NOVOSYLDI ACYLGLYCEROL 2); UDP-sulfoquinovose:DAG sulfoquinovosyltransferase/transferase, transferring glycosyl groups	510	Ch/E/IM	8.60999966	56.6300011	metabolism lipid	11.10.4 lipid metabolism.glycolipid synthesis.sulfolipid synthase		plastid	plastid	envelope	1.0
AT5G01500	978	AT5G01500.1	mitochondrial substrate carrier family protein	415	Ch/E/IM	9.81000042	45.0900002	transporter MCF ATP/ADP ?	34.8 transport.metabolite transporters at the envelope membrane		plastid	plastid	thylakoid	3.0
AT5G01530	979	AT5G01530.1	chlorophyll A-B binding protein CP29 (LHCB4)	290	Ch/Th	5.76000023	31.1399994	PS LHCII	1.1.1.1 PS.lightreaction.photosystem II.LHC-II	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	thylakoid-integral	2.0
AT5G01590	980	AT5G01590.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO63840.1)	424	Ch/E/IM	6.38000011	48.8699989	unknown	35.2 not assigned.unknown	chloroplast envelope	plastid	plastid	plastid	
AT5G01600	981	AT5G01600.1	ATFER1 (FERRETIN 1); ferric iron binding	255	Ch/S	5.73000002	28.1700001	Iron binding	15.2 metal handling.binding, chelation and storage		plastid	plastid	plastid stroma	
AT5G01920	982	AT5G01920.1	STN8 (state transition 8); kinase	495	Ch/Th	9.42000008	54.9700012	PS State transition ?	1.1.30 PS.lightreaction.state transition	thylakoid	plastid	plastid	thylakoid-integral	
AT5G02120	983	AT5G02120.1	OHP (ONE HELIX PROTEIN)	110	Ch/Th	9.56000042	12.0100002	stress light	1.1.8* light stress chlorophyll binding	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	thylakoid-integral	1.0
AT5G02240	984	AT5G02240.1	binding / catalytic/coenzyme binding	253		6.19000006	27.1000004		35.2 not assigned.unknown	undefined			-	

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AT5G02490	985	AT5G02490.1	heat shock cognate 70 kDa protein 2 (HSC70-2) (HSP70-2)	653	Ch/E & other	5.03000021	71.3799973	chaperone and protease	29.6 protein.foldin g	other (e.g. cytoplasm)			-	
AT5G02500	986	AT5G02500.1	HSC70-1 (heat shock cognate 70 kDa protein 1); ATP binding	651	Ch/E & other	5.01999998	71.3499985	chaperone and protease	29.6 protein.foldin g	other (e.g. cytoplasm)			cytosol	
AT5G02940	987	AT5G02940.1	similar to phosphotransferase-related [Arabidopsis thaliana] (TAIR:AT5G43745.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO71282.1); similar to hypothetical protein Osl_009890 [Oryza sativa (indica cultivar-group)] (GB:EAY88657.1); s	813	Ch/E ??	7.53000021	92.1299973	transporter ion channel ?	35.2 not assigned.unknown			mitochondrion	envelope	3.0
AT5G03300	988	AT5G03300.1	ADK2 (ADENOSINE KINASE 2); kinase	345		5.13999987	37.8400002		23.3.2.1 nucleotide metabolism.s alvage.nucleoside kinases.adenosine kinase	undefined			-	
AT5G03630	989	AT5G03630.1	ATMDAR2; monodehydroascorbate reductase (NADH)	435		5.23999977	47.4799995		21.2.1 redox.ascorbate and glutathione.ascorbate	undefined			-	

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AT5G03650	990	AT5G03650.1	SBE2.2 (STARCH BRANCHING ENZYME 2.2); 1,4-alpha-glucan branching enzyme	716		5.44999981	82.8300018		2.1.2.3 major CHO metabolism.synthesis.star ch.starch branching	undefined			plastid stroma	
AT5G03880	991	AT5G03880.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G10000.2); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G10000.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO15903.1); contains InterPro domain Thioredoxin-like	339	Ch/E & Ch/Th	9.01000023	37.0400009	redox ?	21.4 redox.glutare doxins	thylakoid membrane (sensu Viridiplantae)		plastid	thylakoid	2.0

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AT5G03900	992	AT5G03900.2	Identical to Uncharacterized protein At5g03900 precursor [Arabidopsis Thaliana] (GB:Q8GW20;GB:Q8L632;GB:Q8LG15;GB:Q9FFM9;GB:Q9LZB9); similar to unnamed protein product [Vitis vinifera] (GB:CAO15906.1); contains InterPro domain HesB/YadR/YfhF-like (In	429	Ch/E/IM	8.88000011	48.1699982	unknown	35.2 not assigned.unknown		plastid	plastid	plastid	
AT5G03910	993	AT5G03910.1	ATATH12 (Arabidopsis ABC transporter homolog 12); ATPase, coupled to transmembrane movement of substances	634	Ch/E/IM	9.05000019	69.1900024	transporter ABC	34.16 transport.ABC transporters and multidrug resistance systems		plastid	plastid	envelope	6.0
AT5G03940	994	AT5G03940.1	FFC (FIFTY-FOUR CHLOROPLAST HOMOLOGUE); 7S RNA binding / GTP binding / mRNA binding	564	Ch/S	9.47000027	61.2299995	protein targeting	29.3.3 protein.targeting.chloroplast	chloroplast stroma	plastid	plastid	plastid stroma	

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AT5G04140	995	AT5G04140.1	GLS1/GLU1/GLUS (FERREDOXIN-DEPENDENT GLUTAMATE SYNTHASE 1); glutamate synthase (ferredoxin)	1622	Ch/S	5.92999983	176.75	metabolism carbon	12.2.1.1 N-metabolism.ammonia metabolism.glutamate synthase.ferredoxin dependent		plastid	plastid	plastid stroma	
AT5G04360	996	AT5G04360.1	ATLDA/ATP U1 (PULLULANASE 1); alpha-amylase/limit dextrinase	965		5.92999983	107.059998		2.1.2.4 major CHO metabolism.synthesis.starch.debranching	chloroplast	Y	C	plastid	
AT5G04590	997	AT5G04590.1	SIR (sulfite reductase); sulfite reductase (ferredoxin)	642	Ch/S	8.5	71.9499969	metabolism aa Cys	14.3 S-assimilation.sulfite redox	plastid	plastid	plastid	plastid stroma	
AT5G04710	998	AT5G04710.1	aspartyl aminopeptidase, putative	526		6.48999977	57.8600006		29.5.4 protein.degradation.aspartate protease	chloroplast	Y	C	-	
AT5G04740	999	AT5G04740.1	ACT domain-containing protein	301	Ch/S	5.26000023	33.2400017	unknown	13 amino acid metabolism	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	plastid stroma	
AT5G04830	1000	AT5G04830.1	similar to unknown [Populus trichocarpa x Populus deltoides] (GB:ABK96633.1); contains domain SSF54427 (SSF54427)	178	CH/E ?	8.43000031	20.2900009	unknown	35.2 not assigned.unknown	other (e.g. cytoplasm)			-	
AT5G04900	1001	AT5G04900.1	short-chain dehydrogenase/reductase (SDR) family protein	348	Ch/E/IM	9.48999977	38.1399994	metabolism vitamin and pigment	19.50* tetrapyrrole degradation		plastid	plastid	thylakoid	

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AT5G05000	1002	AT5G05000.1	ATTOC34/OEP34 (Translocase of chloroplast 34)	313	Ch/E/OM	9.42000008	34.7000008	protein targeting Toc	29.3.3 protein.targeting.chloroplast	chloroplast outer membrane			envelope-outer-integral	
AT5G05570	1003	AT5G05570.1	transducin family protein / WD-40 repeat family protein	1124		5.46999979	122.660004		35.1 not assigned.no ontology	undefined		M	-	
AT5G05730	1004	AT5G05730.1	ASA1 (ANTHRANILATE SYNTHASE ALPHA SUBUNIT 1); anthranilate synthase	595	Ch/S	6.07999992	66.3099976	metabolism aa tryptophan	13.1.6.5.1 amino acid metabolism.synthesis.aromatic aa.tryptophan.anthranilate synthase	chloroplast		plastid	plastid	
AT5G05740	1005	AT5G05740.1	ATEGY2; metalloendopeptidase	556	Ch/Th	4.98000002	60.0600014	chaperone and protease	29.5.7 protein.degradation.metall opeptase			plastid	thylakoid	
AT5G06130	1006	AT5G06130.1	chaperone protein dnaJ-related	231	Ch/Th ??	8.68000031	25.4400005	chaperone and protease ?	26.29* misc.DnaJ domain with unknown function				plastid	2.0
AT5G06220	1007	AT5G06220.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G11560.3); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G11560.2); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G11560.4); similar to Os08g0482100 [Oryza sativa] (j	813	Ch/E	5.46999979	90.3099976	transporter K+/H+?	35.2 not assigned.unknown			mitochondrion	plastid	3.0

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AT5G06290	1008	AT5G06290.1	2-cys peroxiredoxin, chloroplast, putative	273	Ch/S	5.53999996	29.7800007	redox	21.5 redox.peroxiredoxins		plastid	plastid	plastid stroma	
AT5G06430	1009	AT5G06430.1	thioredoxin-related	194	Ch/E & Ch/S	9.39999962	21.75	redox ?	21.1 redox.thioredoxin	undefined	Y	C	-	
AT5G06670	1010	AT5G06670.1	kinesin motor protein-related	992		5.73999977	110.709999		31.1 cell.organisation	chloroplast	Y	C	-	
AT5G07020	1011	AT5G07020.1	proline-rich family protein	235	Ch/Th	4.71000004	24.3899994	unknown	35.1.42 not assigned.no ontology.proline rich family	thylakoid membrane (sensu Viridiplantae)	plastid		thylakoid	1.0
AT5G07760	1012	AT5G07760.1	formin homology 2 domain-containing protein / FH2 domain-containing protein	853		7.42000008	95.5400009		35.1.20 not assigned.no ontology.for min homology 2 domain-containing protein	chloroplast	Y	C	-	
AT5G08050	1013	AT5G08050.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO62462.1); similar to unknown [Populus trichocarpa] (GB:ABK95457.1); contains InterPro domain Protein of unknown function DUF1118 (InterPro:IPR009500); contains InterPro domain Uncharacterised	158	Ch/Th	9.30000019	16.5799999	unknown	35.2 not assigned.unknown	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	thylakoid	2.0

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AT5G08280	1014	AT5G08280.1	HEMC (HYDROXY METHYLBILANE SYNTHASE) ; hydroxymethylbilane synthase	382	Ch/S	8.75	41.0400009	metabolism vitamin and pigment	19.5 tetrapyrrole synthesis.porphobilinogen deaminase	chloroplast	plastid	plastid	plastid stroma	
AT5G08540	1015	AT5G08540.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO65975.1)	346	Ch/E/IM	5.67000008	38.6500015	unknown	35.2 not assigned.unknown	thylakoid membrane (sensu Viridiplantae) & chloroplast envelope		plastid	envelope-inner	1.0
AT5G08650	1016	AT5G08650.1	GTP-binding protein LepA, putative	681	Ch/S & Ch/Th	6.28999996	75.4300003	translation stroma	29.2.4 protein.synthesis.elongation			plastid	plastid stroma	
AT5G08680	1017	AT5G08680.1	ATP synthase beta chain, mitochondrial, putative	559	other	6.05999994	59.8600006	transporter ATPase	9.9 mitochondrial electron transport / ATP synthesis.F1-ATPase	undefined	Y	M	mitochondria	
AT5G08740	1018	AT5G08740.1	NDC1 (NAD(P)H DEHYDROGENASE C1); NADH dehydrogenase	519	Ch/Th & Ch/E	6.51000023	56.8499985	redox ? metabolism nucleotide ?	21 redox	intrinsic to mitochondrial inner membrane		plastid	mitochondria ; plastoglobules	
AT5G09650	1019	AT5G09650.1	ATPPA6 (ARABIDOPSIS THALIANA PYROPHOSPHORYLASE 6); inorganic diphosphatase/pyrophosphatase	300	Ch/S	5.71000004	33.3800011	metabolism Pi	23.4.99 nucleotide metabolism.phosphotransfer and pyrophosphatases.misc		plastid	plastid	plastid stroma; thylakoid-peripheral-stromal-side	

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AT5G09660	1020	AT5G09660.1	PMDH2 (PEROXISOMAL NAD-MALATE DEHYDROGENASE 2); malate dehydrogenase	354	na	8.14000034	37.3699989	metabolism carbon	6.3 gluconeogenesis.Malate DH				peroxisome	
AT5G09810	1021	AT5G09810.1	ACT7 (actin 7)	377	Ch/E & other	5.30000019	41.7299995	plastid positioning ?	31.1 cell.organisation	other (e.g. cytoplasm)			-	
AT5G09995	1022	AT5G09995.2	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G08530.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN81396.1)	205	Ch/E/IM	9.5	22.4400005	unknown	35.2 not assigned.unknown		plastid	plastid		
AT5G10160	1023	AT5G10160.1	beta-hydroxyacyl-ACP dehydratase, putative	219	Ch/Th & Ch/E	9.31999969	24.1200008	metabolism lipid	11.1.5 lipid metabolism. FA synthesis and FA elongation.beta hydroxyacyl ACP dehydratase		plastid	plastid	plastid stroma	
AT5G10450	1024	AT5G10450.1	GRF6 (G-BOX REGULATING FACTOR 6); protein phosphorylated amino acid binding	248		4.76000023	27.9699993		30.7 signalling.14-3-3 proteins	undefined			-	
AT5G10490	1025	AT5G10490.1	MSL2 (MSCS-LIKE 2)	673	Ch/E/IM	9.56999969	74.4199982	transporter ion channel	31.2.5 cell.division.plastid	chloroplast	Y	C	envelope	2.0
AT5G10920	1026	AT5G10920.1	argininosuccinate lyase, putative / arginosuccinase, putative	517		5.59000015	57.5099983		13.1.2.3.23 amino acid metabolism.synthesis.glutamate family.arginine.argininosuccinate lyase	chloroplast	Y	C	-	

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AT5G11520	1027	AT5G11520.1	ASP3 (ASPARTATE AMINOTRANSFERASE 3)	449		9.34000015	48.9500008		13.1.1.2.1 amino acid metabolism.synthesis.central amino acid metabolism.aspartate.aspartate aminotransferase	undefined	Y	C	peroxisome	
AT5G11880	1028	AT5G11880.1	diaminopimelate decarboxylase, putative / DAP carboxylase, putative	489		6.21000004	54.1599998		13.1.3.5.5 amino acid metabolism.synthesis.aspartate family.lysine.diaminopimelate decarboxylase	chloroplast	Y	C	plastid	
AT5G12040	1029	AT5G12040.1	carbon-nitrogen hydrolase family protein	369		8.77999973	40.3300018		35.1 not assigned.no ontology	chloroplast	Y	C	plastid stroma	
AT5G12470	1030	AT5G12470.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G40400.2); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G40400.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO21888.1)	386	Ch/E/IM	7.01000023	41.3199997	unknown	34.8 transport.metabolite transporters at the envelope membrane	chloroplast inner membrane	plastid	plastid	envelope-inner-integral	4.0

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AT5G12860	1031	AT5G12860.1	DIT1 (DICARBOXYLATE TRANSPORTER 1); oxoglutarate: malate antiporter	557	Ch/E & Ch/Th	9.75	59.2099991	transporter oxoglut/mal	34.8 transport.metabolite transporters at the envelope membrane		plastid	plastid	envelope-inner-integral	
AT5G13030	1032	AT5G13030.1	similar to hypothetical protein Osl_021963 [Oryza sativa (indica cultivar-group)] (GB:EAZ00731.1); similar to Os06g0320700 [Oryza sativa (japonica cultivar-group)] (GB:NP_001057514.1); similar to predicted protein [Physcomitrella patens subsp. patens	633		6.26999998	71.0899963		35.2 not assigned.unknown	undefined	Y	C	plastid stroma	
AT5G13110	1033	AT5G13110.1	G6PD2 (GLUCOSE-6-PHOSPHATE DEHYDROGENASE 2); glucose-6-phosphate dehydrogenase	596		8.44999981	67.1600037		7.1.1 OPP.oxidative PP.G6PD	chloroplast	Y	C	-	
AT5G13120	1034	AT5G13120.1	peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein	259	Ch/Th & Ch/S	9.38000011	28.2999992	NDH	29.8 protein assembly and cofactor ligation		plastid	plastid	thylakoid-peripheral-lumenal-side	

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AT5G13280	1035	AT5G13280.1	AK-LYS1 (ASPARTATE KINASE 1)	569	Ch/S	6.36999989	62.2900009	metabolism aa Asp	13.1.3.6.1.1 amino acid metabolism.synthesis.aspartate family.misc.homoserine.aspartate kinase		plastid	plastid	plastid	
AT5G13410	1036	AT5G13410.1	immunophilin / FKBP-type peptidyl-prolyl cis-trans isomerase family protein	256	Ch/Th ?	7.53999996	27.7700005	chaperone and protease	29.6 protein.folding	thylakoid membrane (sensu Viridiplantae) & thylakoid lumen (sensu Viridiplantae)	plastid	plastid	thylakoid-peripheral-lumenal-side	
AT5G13420	1037	AT5G13420.1	transaldolase, putative	438	Ch/S	6.07000017	47.6899986	metabolism carbon	7.2.2 OPP.non-reductive PP.transaldolase	mitochondrion	plastid	plastid	plastid stroma	1.0
AT5G13490	1038	AT5G13490.1	AAC2 (ADP/ATP CARRIER 2); ATP:ADP antiporter/binding	385	na	9.78999996	41.7400017	Mito transporter ATP/ADP	34.14 transport.unspecified cations	mitochondrial envelope & mitochondrion			mitochondria	
AT5G13510	1039	AT5G13510.1	ribosomal protein L10 family protein	220	Ch/S & Ch/E & Ch/S	9.35999966	24.7299995	translation stroma	29.2.1.1.1.2.10 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.50S subunit.L10	cytosolic ribosome (sensu Eukaryota)	plastid	plastid	plastid ribosome	
AT5G13630	1040	AT5G13630.1	GUN5 (GENOMES UNCOUPLED 5)	1381	Ch/E & Ch/S	5.78999996	153.570007	metabolism vitamin and pigment & hormone	19.10 tetrapyrrole synthesis.magnesium chelatase	mitochondrion & magnesium chelatase complex	plastid	plastid	plastid	
AT5G13650	1041	AT5G13650.1	elongation factor family protein	675	Ch/S	6.8499999	74.3099976	translation stroma	29.2.4 protein.synthesis.elongation		plastid	plastid	plastid stroma	
AT5G13720	1042	AT5G13720.1	structural constituent of ribosome	262	Ch/E/IM	9.02000046	28.9099998	translation stroma ?	35.2 not assigned.unknown	chloroplast inner membrane	plastid	plastid	plastid	3.0

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AT5G14060	1043	AT5G14060.1	CARAB-AK-LYS (Lysine-sensitive aspartate kinase); amino acid binding / aspartate kinase	544	Ch/S	6.30999994	59.5999985	metabolism aa Asp	13.1.3.6.1.1 amino acid metabolism.synthesis.aspartate family.misc.homoserine.aspartate kinase		plastid	plastid	plastid	
AT5G14100	1044	AT5G14100.1	ATNAP14 (Non-intrinsic ABC protein 14)	278	Ch/E/IM	8.98999977	30.7099991	transporter ABC Co ?	34.16 transport.ABC transporters and multidrug resistance systems		plastid	plastid	plastid	
AT5G14200	1045	AT5G14200.1	3-isopropylmalate dehydrogenase, chloroplast, putative	409		5.73999977	44.1599998		13.1.4.4.3 amino acid metabolism.synthesis.branched chain group.leucine specific.3-isopropylmalate dehydrogenase	undefined			plastid stroma	
AT5G14220	1046	AT5G14220.1	HEMG2/ME E61 (maternal effect embryo arrest 61); oxidoreductase/protoporphyrinogen oxidase	508	Ch/E ??	8.35000038	55.6300011	metabolism vitamin and pigment	19.9 tetrapyrrole synthesis.protoporphyrin IX oxidase					
AT5G14260	1047	AT5G14260.1	SET domain-containing protein	514	Ch/S	6.38000011	57.5800018	unknown	27.3.69 RNA.regulation of transcription.SET-domain transcriptional regulator family			plastid	plastid	

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AT5G14320	1048	AT5G14320.1	30S ribosomal protein S13, chloroplast (CS13)	169	Ch/S & Ch/E	10.2600002	19.0900002	translation stroma	29.2.1.1.1.1.13 protein.synthesis.ribosomal.protein.prokaryotic.chloroplast.30S.subunit.S13				plastid	plastid ribosome
AT5G14590	1049	AT5G14590.1	isocitrate dehydrogenase, putative / NADP+ isocitrate dehydrogenase, putative	485		8.05000019	54.1899986		8.1.4 TCA / org.transformation.TCA.I DH	undefined	Y	C	-	
AT5G14660	1050	AT5G14660.1	PDF1B (PEPTIDE DEFORMYLASE 1B); peptide deformylase	273	Ch/S	8.92000008	30.6100006	unknown	29.4 protein.posttranslational modification				plastid	mitochondria ; plastid stroma
AT5G14740	1051	AT5G14740.2	CA2 (BETA CARBONIC ANHYDRASE 2); carbonate dehydratase/zinc ion binding	331	Ch/E & Ch/S	7.05999994	36.6100006	metabolism carbon	8.3 TCA / org.transformation.carbonic anhydrases	thylakoid membrane (sensu Viridiplantae) & cytoplasm				plastid stroma
AT5G14780	1052	AT5G14780.1	FDH (FORMATE DEHYDROGENASE); NAD binding / binding / catalytic/cofactor binding / oxidoreductase, acting on the CH-OH group of donors, NAD or NADP as acceptor	384		7.11000013	42.4099998		25.10 C1-metabolism.formate dehydrogenase	undefined	Y	M	mitochondria	
AT5G14910	1053	AT5G14910.1	heavy-metal-associated domain-containing protein	178	Ch/S & Ch/E	5.15999985	18.9500008	transporter metals ?	15.2 metal handling.binding, chelation and storage				plastid	plastid stroma

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AT5G15450	1054	AT5G15450.1	APG6/CLPB-P/CLPB3 (ALBINO AND PALE GREEN 6); ATP binding / ATPase	968	Ch/S	5.92000008	108.940002	chaperone and protease	29.6 protein.folding			plastid	plastid stroma	
AT5G15530	1055	AT5G15530.1	BCCP2 (biotin carboxyl carrier protein 2); biotin binding	255	Ch/E/IM	7.63999987	27.2800007	metabolism lipid	11.1.1 lipid metabolism. FA synthesis and FA elongation. A cetyl CoA Carboxylation	chloroplast	Y	C	envelope-inner-peripheral-stromal-side	
AT5G15880	1056	AT5G15880.1	similar to hypothetical protein [Cleome spinosa] (GB:ABD96950.1); contains InterPro domain Polyadenylate-binding protein/Hypocotyl disc protein; (InterPro:IPR002004)	348		5.32000017	39.5699997		35.2 not assigned.unknown	other (e.g. cytoplasm)			-	1.0
AT5G16010	1057	AT5G16010.1	3-oxo-5-alpha-steroid 4-dehydrogenase family protein / steroid 5-alpha-reductase family protein	268	Ch/E ??	9.36999989	30.1200008	metabolism hormone brassinosteroid	17.3.1.1.1 hormone metabolism. brassinosteroid.synthesis - degradation. BRs.DET2				envelope	6.0

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AT5G16150	1058	AT5G16150.1	GLT1/PGLCT (GLUCOSE TRANSPORTER 1); carbohydrate transmembrane transporter/sugar:hydrogen ion symporter	546	Ch/E/IM	9.06000042	56.9700012	transporter glucose ?	34.8 transport.metabolite transporters at the envelope membrane		plastid	plastid	envelope-inner-integral	12.0
AT5G16390	1059	AT5G16390.1	BCCP/BCCP1/BCCP1/CAC1-A/CAC1A (BIOTIN CARBOXYL CARRIER, BIOTIN CARBOXYL CARRIER PROTEIN 1); biotin binding	280	Ch/E/IM	9.10999966	29.6100006	metabolism lipid	11.1.1 lipid metabolism. FA synthesis and FA elongation. Acetyl CoA Carboxylation	chloroplast	Y	C	envelope-inner-peripheral-stromal-side; plastid stroma	
AT5G16440	1060	AT5G16440.1	IPP1 (ISOPENTENYL DIPHOSPHATE ISOMERASE 1); isopentenyl-diphosphate delta-isomerase	291		5.67999983	33.2099991		16.1.2.7 secondary metabolism. isoprenoids. mevalonate pathway. isopentenyl pyrophosphate:dimethylallyl pyrophosphate isomerase	chloroplast	Y	C	cytosol; plastid	
AT5G16620	1061	AT5G16620.1	PDE120 (PIGMENT DEFECTIVE EMBRYO)	447	Ch/E/IM	5.36999989	48.9000015	protein targeting Tic	29.3.3 protein targeting.chloroplast	thylakoid membrane (sensu Viridiplantae) & chloroplast	plastid	plastid	envelope-inner-integral	1.0

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AT5G16660	1062	AT5G16660.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G02900.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO62132.1)	168	Ch/E & Ch/Th	8.51000023	18.1700001	unknown	35.2 not assigned.unknown		plastid	plastid	plastid	
AT5G16710	1063	AT5G16710.1	DHAR3 (DEHYDROASCORBATE REDUCTASE 1); glutathione dehydrogenase (ascorbate)	258	Ch/S	7.59000015	28.5100002	redox	21.2.1 redox.ascorbate and glutathione.ascorbate		plastid	plastid	plastid stroma	
AT5G16715	1064	AT5G16715.1	EMB2247 (EMBRYO DEFECTIVE 2247); ATP binding / aminoacyl-tRNA ligase	970		5.94999981	110.269997		29.1.9 protein.aa activation.valine-tRNA ligase	chloroplast	Y	C	plastid stroma	
AT5G17170	1065	AT5G17170.1	ENH1 (ENHANCER OF SOS3-1); metal ion binding	271	Ch/Th	9.59000015	28.4500008	unknown	29.8 protein assembly and cofactor ligation	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	thylakoid	1.0
AT5G17520	1066	AT5G17520.1	RCP1 (ROOT CAP 1)	415	Ch/E/IM	9.36999989	45.2799988	transporter maltose	34.8 transport.metabolite transporters at the envelope membrane	chloroplast inner membrane	plastid	plastid	envelope-inner-integral	9.0
AT5G17530	1067	AT5G17530.1	phosphoglucosamine mutase family protein	581		5.86000013	62.8699989		4.2 glycolysis.PGM	undefined	Y	M	plastid stroma	
AT5G17560	1068	AT5G17560.1	BolA-like family protein	177		9.63000011	19.5300007		27.3 RNA.regulation of transcription	chloroplast	Y	C	plastid stroma	

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AT5G17630	1069	AT5G17630.1	glucose-6-phosphate/p phosphate translocator, putative	417	Ch/E/IM	9.71000004	45.7700005	transporter Pi/G6P	34.8 transport.metabolite transporters at the envelope membrane	chloroplast	Y	C	-	8.0
AT5G17670	1070	AT5G17670.1	hydrolase, acting on ester bonds	309	Ch/E & Ch/Th	5.57000017	33.4000015	metabolism lipid / vesicular trafficking?	35.2 not assigned.unknown		plastid	mitochondrion	envelope	
AT5G17710	1071	AT5G17710.1	EMB1241 (EMBRYO DEFECTIVE 1241); adenyl-nucleotide exchange factor/ chaperone binding / protein binding / protein homodimerization	324	Ch/S	4.55999994	35.4900017	chaperone and protease	29.6 protein.folding		plastid	plastid	plastid stroma	
AT5G17920	1072	AT5G17920.1	ATCIMS (COBALAMIN-INDEPENDENT METHIONINE SYNTHASE); 5-methyltetrahydropteroyltri glutamate-homocysteine S-methyltransferase/ methionine synthase	765		6.07999992	84.3499985		13.1.3.4 amino acid metabolism.synthesis.aspartate family.methionine	undefined			not plastid	

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AT5G17990	1073	AT5G17990.1	TRP1 (TRYPTOPHAN BIOSYNTHESIS 1); anthranilate phosphoribosyltransferase	444	Ch/S	6.9000001	46.5200005	metabolism amino acids Tryptophan	13.1.6.5.2 amino acid metabolism.synthesis.aromatic aa.tryptophan.anthranilate phosphoribosyltransferase			plastid	plastid stroma	
AT5G18660	1074	AT5G18660.1	DVR (PALE-GREEN AND CHLOROPHYLL B REDUCED 2); 3,8-divinyl protochlorophyllide a 8-vinyl reductase	417	Ch/E & Ch/Th	7.46999979	45.8899994	metabolism vitamin and pigment chlorophyll	19.13 tetrapyrrole synthesis.divinyl chlorophyllide-a 8-vinyl-reductase	chloroplast	plastid	plastid	plastid	
AT5G19220	1075	AT5G19220.1	ADG2 (ADPG PYROPHOSPHORYLASE 2); glucose-1-phosphate adenylyltransferase	522	Ch/S	8.02000046	57.6699982	metabolism carbon Starch biosynthesis	2.1.2.1 major CHO metabolism.synthesis.starch.AGPase		plastid	plastid	plastid stroma	
AT5G19370	1076	AT5G19370.1	rhodanese-like domain-containing protein / PPIC-type PPIASE domain-containing protein	299	Ch/S	8.61999989	32.9799995	unknown	26.23 misc.rhodanese		plastid	plastid	plastid	
AT5G19460	1077	AT5G19460.1	ATNUDT20 (Arabidopsis thaliana Nudix hydrolase homolog 20); hydrolase	374		7.55999994	41.9199982		26.13 misc.acid and other phosphatases	chloroplast	Y	C	plastid	

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AT5G19620	1078	AT5G19620.1	OEP80 (ARABIDOPSIS THALIANA OUTER ENVELOPE PROTEIN OF 80 KDA)	732	Ch/E/OM	8.40999985	79.9300003	protein targeting Toc	29.3.3 protein.targeting.chloroplast	chloroplast envelope	plastid	plastid	envelope-outer-integral	
AT5G19750	1079	AT5G19750.1	peroxisomal membrane 22 kDa family protein	288	Ch/E/IM	10.2299995	30.3600006	transporter ?	35.1 not assigned.no ontology		plastid	plastid	plastid	3.0
AT5G19850	1080	AT5G19850.1	hydrolase, alpha/beta fold family protein	359	Ch/E	6.09000015	40.0999985	hydrolase ?	35.1 not assigned.no ontology		plastid	plastid		
AT5G19855	1081	AT5G19855.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO21907.1)	203		9.67000008	23.4699993		35.2 not assigned.unknown	chloroplast	Y	C	-	
AT5G19940	1082	AT5G19940.1	plastid-lipid associated protein PAP-related / fibrillin-related	239	Ch/E & Ch/Th	9.48999977	26.4799995	PAP_fibrillin	26.31* misc.fibrillins	chloroplast envelope		plastid	thylakoid-peripheral-stromal-side	
AT5G20130	1083	AT5G20130.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO21131.1)	202	Ch/E/IM	9.57999992	21.9400005	RNA binding ?	35.2 not assigned.unknown	undefined	Y	C	-	1.0
AT5G20140	1084	AT5G20140.1	SOUL heme-binding family protein	378	Ch/E & Ch/Th	6.98000002	43.1599998	unknown	21.3 redox.heme	thylakoid membrane (sensu Viridiplantae)		plastid	thylakoid	
AT5G20250	1085	AT5G20250.1	DIN10 (DARK INDUCIBLE 10); hydrolase, hydrolyzing O-glycosyl compounds	749		6.21000004	83.1100006		3.1.2.2 minor CHO metabolism. raffinose synthases.putative	undefined			-	

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AT5G20630	1086	AT5G20630.1	GLP3 (GERMIN-LIKE PROTEIN 3); manganese ion binding / metal ion binding / nutrient reservoir	211	Ch/Th	6.25	21.8299999	unknown	20.2.99 stress.abiotic.unspecified	extracellular matrix		extracellular, endoplasmic reticulum, golgi	extracellular	2.0
AT5G20720	1087	AT5G20720.1	CPN20 (CHAPERONIN 20); calmodulin binding	253	Ch/S & Ch/E	8.85000038	26.7999992	chaperone and protease	29.6 protein.folding		plastid	plastid	plastid stroma	
AT5G21430	1088	AT5G21430.1	DNAJ heat shock N-terminal domain-containing protein	218	Ch/E & Ch/Th	5.07000017	24.4300003	NDH or chaperone and protease ?	1.1.6 PS.lightreaction.NADH DH	thylakoid membrane (sensu Viridiplantae)		plastid	thylakoid-integral	1.0
AT5G22210	1089	AT5G22210.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO48680.1)	80	CH/E ?	6.82000017	9.31000042	unknown	35.2 not assigned.unknown	undefined			-	
AT5G22510	1090	AT5G22510.1	beta-fructofuranosidase, putative / invertase, putative / saccharase, putative / beta-fructosidase, putative	617		5.8499999	69.2399979		2.2.1.3.1 major CHO metabolism.degradation.sucrose.invertases.neutral	chloroplast	Y	C	plastid stroma	
AT5G22620	1091	AT5G22620.1	phosphoglycerate/bisphosphoglycerate mutase family protein	482	Ch/S	6.63999987	53.1100006	unknown	4.11 lysis.phosphoglycerate mutase		plastid	plastid	plastid stroma	
AT5G22640	1092	AT5G22640.1	EMB1211 (EMBRYO DEFECTIVE 1211)	871	Ch/E ??	4.36000013	99.9499969	RNA binding ?	35.1 not assigned.no ontology	thylakoid membrane (sensu Viridiplantae)			plastid	
AT5G22790	1093	AT5G22790.1	RER1 (RETICULATA-RELATED 1)	433	Ch/E/IM	5.13999987	46.8300018	unknown	35.2 not assigned.unknown	chloroplast	Y	C	-	3.0

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AT5G22800	1094	AT5G22800.1	EMB1030 (EMBRYO DEFECTIVE 1030); ATP binding / alanine-tRNA ligase/ ligase, forming aminoacyl-tRNA and related compounds / nucleic acid binding	978	Ch/S	5.42000008	107.830002	translation stroma	29.1.7 protein.aa activation.alanine-tRNA ligase	mitochondrion & chloroplast	plastid	plastid	mitochondria ; plastid stroma	
AT5G22830	1095	AT5G22830.1	GMN10 (Arabidopsis thaliana Mg transporter 10)	459	Ch/E/IM	5.23000002	51.0900002	transporter Mg	34.8 transport.metabolite transporters at the envelope membrane		plastid	plastid	envelope-inner-integral	2.0
AT5G23040	1096	AT5G23040.1	CDF1 (CELL GROWTH DEFECT FACTOR 1); heat shock protein binding	258	Ch/E/IM	9.68000031	28.8099995	signalling ?	35.2 not assigned.unknown	mitochondrion	plastid	plastid	envelope	3.0
AT5G23060	1097	AT5G23060.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G59780.1); similar to extracellular Ca ²⁺ sensing receptor [Glycine max] (GB:ABY57763.1); contains InterPro domain Rhodanese-like (InterPro:IPR001763)	387	Ch/Th	9.40999985	41.2799988	PS State transition ?	1.1.30 PS.lightreaction.state transition	thylakoid membrane (sensu Viridiplantae) & mitochondrion	plastid	plastid	mitochondria ; thylakoid-integral	1.0

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AT5G23120	1098	AT5G23120.1	HCF136 (High chlorophyll fluorescence 136)	403	Ch/Th & Ch/E	6.78999996	44.0999985	chaperone and protease ?	29.8 protein assembly and cofactor ligation	thylakoid membrane (sensu Viridiplantae) & thylakoid lumen (sensu Viridiplantae) & chloroplast stromal thylakoid	plastid	plastid	thylakoid-peripheral-lumenal-side	
AT5G23890	1099	AT5G23890.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G52410.2); similar to unnamed protein product [Vitis vinifera] (GB:CAO49433.1)	946	Ch/E/IM	4.61000013	103.919998	unknown	34.8 transport.metabolite transporters at the envelope membrane	thylakoid membrane (sensu Viridiplantae) & chloroplast envelope		plastid	envelope-inner-integral	1.0
AT5G24020	1100	AT5G24020.1	MIND (ACCUMULATION AND REPLICATION OF CHLOROPLAST 11)	326	Ch/E & Ch/S	7.57999992	35.6899986	plastid division	31.2.5 cell.division.plastid	chloroplast		plastid	envelope-inner; plastid stroma	
AT5G24300	1101	AT5G24300.1	ATSS1/SSI (STARCH SYNTHASE I); transferase, transferring glycosyl groups	652	Ch/S	6.01000023	72.0899963	starch biosynthesis	2.1.2.2 major CHO metabolism.synthesis.starch.starch synthase			plastid	plastid stroma	
AT5G24400	1102	AT5G24400.1	EMB2024 (EMBRYO DEFECTIVE 2024); catalytic	325		7.63999987	35.6399994		7.1.2 OPP.oxidative PP.6-phosphogluc onolactonase	chloroplast	Y	C	plastid stroma	

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AT5G24490	1103	AT5G24490.1	30S ribosomal protein, putative	308	Ch/Th & Ch/S	6.28999996	34.8499985	translation stroma	29.2.1.1.1.1.530 protein.synthesis.ribosomal.prokaryotic.chloroplast.30S subunit.S30A		plastid	plastid	plastid ribosome	
AT5G24650	1104	AT5G24650.1	mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein	259	Ch/E/OM	9.60000038	27.7700005	protein targeting / aa channel	34.8 transport.metabolite transporters at the envelope membrane				envelope	3.0
AT5G24690	1105	AT5G24690.1	similar to RER1 (RETICULATA-RELATED 1) [Arabidopsis thaliana] (TAIR:AT5G22790.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO24736.1)	521	Ch/E/IM	9.14000034	56.8100014	unknown	35.2 not assigned.unknown	chloroplast inner membrane		plastid	plastid	3.0
AT5G24870	1106	AT5G24870.1	zinc finger (C3HC4-type RING finger) family protein	520		9.35999966	56.7900009		29.5.11.4.2 protein.degradation.ubiquitin.E3.RING	undefined			-	
AT5G25510	1107	AT5G25510.1	serine/threonine protein phosphatase 2A (PP2A) regulatory subunit B', putative	500	Ch/E ?	8.89999962	56.4199982	protein modification	29.4 protein.posttranslational modification	chloroplast	Y	C	-	
AT5G25752	1108	AT5G25752.1	rhomboid family protein	280	Ch/E/IM	9.86999989	31.5900002	chaperone and protease	29.5.5 protein.degradation.serine protease	mitochondrion	Y	M	plastid	4.0

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AT5G25940	1109	AT5G25940.1	early nodulin-related	115	Ch/E ?	10.2700005	12.2600002	unknown	33.99 development.unspecified	undefined			-	2.0
AT5G26000	1110	AT5G26000.1	TGG1 (THIOGLUCOSIDE GLUCOHYDROLASE 1); hydrolase, hydrolyzing O-glycosyl compounds	541		5.5999999	61.1300011		16.5.1 secondary metabolism.sulfur-containing.gluucosinolates	secreted		S	not plastid	
AT5G26570	1111	AT5G26570.1	PWD (PHOSPHOGLUCAN WATER DIKINASE); catalytic	1196	Ch/S	5.8499999	131.320007	metabolism starch	2.2.2.3 major CHO metabolism.degradation.starch.gluca n water dikinase	chloroplast & plastid	plastid	plastid	plastid stroma	
AT5G26742	1112	AT5G26742.1	EMB1138 (EMBRYO DEFECTIVE 1138); ATP binding / ATP-dependent helicase	747	Ch/S & Ch/E	7.23999977	81.0	RNA Binding ?	27.6* RNA.DEAD BOX helicase		plastid	plastid	plastid nucleoid	
AT5G27240	1113	AT5G27240.1	DNAJ heat shock N-terminal domain-containing protein	1104	Ch/E ?	9.02000046	124.440002	chaperone and protease ?	20.2.1 stress.abiotic .heat	other (e.g. cytoplasm)			-	
AT5G27560	1114	AT5G27560.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO17622.1)	341	Ch/S	4.73000002	38.0400009	unknown	35.2 not assigned.unkn own		plastid	plastid	plastid	
AT5G27670	1115	AT5G27670.1	HTA7; DNA binding	150	na	10.4700003	15.8999996	DNA binding	28.1.3 DNA.synthes is/chromatin structure.hist one		plastid		nucleus	

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AT5G28500	1116	AT5G28500.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G04550.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO65032.1)	434	Ch/S	4.98000002	48.2299995	unknown	35.2 not assigned.unknown				plastid	plastid stroma	
AT5G28540	1117	AT5G28540.1	BIP1; ATP binding	669	Ch/E ?	5.07999992	73.6299973	chaperone and protease	29.6 protein.foldin g	secreted		S	ER		
AT5G28750	1118	AT5G28750.1	thylakoid assembly protein, putative	147	Ch/E & Ch/Th	9.22000027	15.71	protein targeting	29.3.3 protein.target ing.chloroplast	chloroplast	Y	C	thylakoid-integral	1.0	
AT5G30510	1119	AT5G30510.1	RPS1 (ribosomal protein S1); RNA binding	416	Ch/S	5.11999989	45.1100006	translation stroma	29.2.1.1.3.1.1 protein.synthesis.ribosomal protein.prokaryotic.unknown organellar.30 S subunit.S1		plastid	plastid	plastid ribosome		
AT5G33320	1120	AT5G33320.1	CUE1 (CAB UNDEREXPRESSED 1); antiporter/triose-phosphate transmembrane transporter	408	Ch/E/IM	10.1599998	44.2200012	transporter Pi/PEP	34.8 transport.metabolite transporters at the envelope membrane	plastid inner membrane		plastid	envelope-inner-integral	6.0	
AT5G35100	1121	AT5G35100.1	peptidyl-prolyl cis-trans isomerase	281	Ch/Th	6.82000017	30.5	chaperone and protease	29.6 protein.foldin g			plastid	plastid		
AT5G35170	1122	AT5G35170.1	adenylate kinase family protein	588	Ch/Th & Ch/E & Ch/S	8.84000015	65.7300034	metabolism nucleotide	23.4.1 nucleotide metabolism.phosphotransfer and pyrophosphatases.adenylate kinase	thylakoid membrane (sensu Viridiplantae)		plastid	plastid		

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AT5G35360	1123	AT5G35360.1	CAC2 (acetyl co-enzyme A carboxylase biotin carboxylase subunit)	537	Ch/S	6.84000015	58.3800011	metabolism lipid	11.1.1 lipid metabolism. FA synthesis and FA elongation. Acetyl CoA Carboxylation			plastid	envelope-inner-peripheral-stromal-side	
AT5G35630	1124	AT5G35630.1	GS2 (GLUTAMINE SYNTHETASE 2); glutamate-ammonia ligase	430	Ch/S	6.42000008	47.4099998	metabolism carbon	12.2.2 N-metabolism. ammonia metabolism. glutamine synthase	thylakoid membrane (sensu Viridiplantae) & mitochondrion & chloroplast	plastid	plastid	plastid stroma	
AT5G35790	1125	AT5G35790.1	G6PD1 (GLUCOSE-6-PHOSPHATE DEHYDROGENASE 1); glucose-6-phosphate dehydrogenase	576	Ch/S & Ch/Th	7.61000013	65.4199982	metabolism carbon	7.1.1 OPP.oxidative PP.G6PD		plastid	plastid	plastid stroma	
AT5G35970	1126	AT5G35970.1	DNA-binding protein, putative	961	Ch/S	7.94999981	105.040001	DNA Binding ?	28.5* DNA.DEAD BOX helicase		plastid	plastid	plastid stroma	
AT5G36120	1127	AT5G36120.1	YGGT family protein	174	Ch/Th	9.89000034	18.9699993	chaperone and protease PS b6f	29.8 protein assembly and cofactor ligation		plastid	plastid	plastid	2.0
AT5G36170	1128	AT5G36170.1	HCF109 (HIGH CHLOROPHYLL FLUORESCENT 109); translation release factor	456	Ch/S	5.3499999	50.9700012	unknown	29.2.5 protein.synthesis.release	chloroplast	plastid	plastid	plastid	
AT5G36210	1129	AT5G36210.1	serine-type peptidase	730		5.11000013	75.2099991		29.5 protein.degradation	chloroplast	Y	C	-	

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AT5G36700	1130	AT5G36700.1	ATPGLP1/PGLP1 (2-PHOSPHOGLYCOLATE PHOSPHATASE 1); phosphoglycolate phosphatase	362	Ch/S	6.8899987	39.7599983	metabolism carbon	1.2.1 PS.photorepiration.phosphoglycolate phosphatase	chloroplast	Y	C	plastid stroma	
AT5G36880	1131	AT5G36880.1	acetyl-CoA synthetase, putative / acetate-CoA ligase, putative	693		5.4000001	76.7300034		11.1.8 lipid metabolism. FA synthesis and FA elongation.acyl coa ligase	chloroplast		C	plastid stroma	
AT5G36890	1132	AT5G36890.1	glycosyl hydrolase family 1 protein	490		5.3800011	56.0699997		26.3 misc.gluco-, galacto- and mannosidases	undefined		M	-	
AT5G37360	1133	AT5G37360.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO38751.1)	309	Ch/Th	7.6599985	33.4300003	unknown	35.2 not assigned.unknown	thylakoid membrane (sensu Viridiplantae)		plastid	thylakoid	2.0
AT5G38410	1134	AT5G38410.1	ribulose biphosphate carboxylase small chain 3B / RuBisCO small subunit 3B (RBCS-3B) (ATS3B)	181	Ch/S & other	8.21000004	20.2800007	metabolism carbon	1.3.2 PS.calvin cycle.rubisco small subunit	chloroplast	Y	C	plastid stroma	
AT5G38430	1135	AT5G38430.1	ribulose biphosphate carboxylase small chain 1B / RuBisCO small subunit 1B (RBCS-1B) (ATS1B)	181	Ch/S & Ch/E	7.57999992	20.2800007	metabolism carbon Calvin cycle	1.3.2 PS.calvin cycle.rubisco small subunit		plastid	plastid	plastid stroma	

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AT5G38480	1136	AT5G38480.1	GRF3 (GENERAL REGULATORY FACTOR 3); protein phosphorylated amino acid binding	255		4.73999977	28.6000004		30.7 signalling.14-3-3 proteins	other (e.g. cytoplasm)			-	
AT5G38520	1137	AT5G38520.1	hydrolase, alpha/beta fold family protein	362	Ch/E & Ch/Th	6.53999996	39.5699997	hydrolase ?	35.1 not assigned.no ontology		plastid	plastid	thylakoid	
AT5G38660	1138	AT5G38660.1	APE1 (ACCLIMATION OF PHOTOSYNTHESIS TO ENVIRONMENT)	286	Ch/Th & Ch/E	8.60000038	31.4300003	unknown	35.2 not assigned.unknown	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	thylakoid	2.0
AT5G39410	1139	AT5G39410.1	binding / catalytic	454	Ch/E/IM	8.52999973	49.6800003	metabolism aa Lys	35.2 not assigned.unknown	mitochondrion	plastid		not plastid	
AT5G39830	1140	AT5G39830.1	DEG8/DEGP8 (DEGP PROTEASE 8); peptidase/serine-type peptidase/trypsin	448	Ch/Th	8.51000023	47.4900017	chaperone and protease PS PSII	29.5.5 protein.degradation.serine protease	thylakoid lumen (sensu Viridiplantae)		plastid	thylakoid-peripheral-lumenal-side	
AT5G40370	1141	AT5G40370.1	glutaredoxin, putative	111		6.71000004	11.75		21.4 redox.glutaredoxins	undefined		S	not plastid	
AT5G40410	1142	AT5G40410.1	binding	608		8.71000004	68.6699982		35.1.5 not assigned.no ontology.pentatricopeptide (PPR) repeat-containing protein	undefined		M	-	
AT5G40950	1143	AT5G40950.1	RPL27; structural constituent of ribosome	198	Ch/E & Ch/S	9.96000004	21.7299995	translation stroma	29.2.1.1.1.2.27 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.50S subunit.L27		plastid	plastid	plastid ribosome	

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AT5G41670	1144	AT5G41670.1	6-phosphogluc onate dehydrogenase family protein	487	Ch/S	5.61999989	53.3100014	metabolism carbon	7.1.3 OPP.oxidative PP.6-phosphogluc onate dehydrogenase	mitochondrion		extracellular, endoplasmic reticulum, golgi	not plastid	
AT5G41970	1145	AT5G41970.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G49320.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO62930.1); contains InterPro domain Metal-dependent protein hydrolase (InterPro:IPR003226)	373		5.86999989	42.2999992		35.2 not assigned.unknown	undefined	Y	M	-	
AT5G42070	1146	AT5G42070.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO69519.1)	164	Ch/E & Ch/Th	8.88000011	17.6800003	unknown	35.2 not assigned.unknown	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	plastid	
AT5G42130	1147	AT5G42130.1	mitochondrial substrate carrier family protein	412	Ch/E/IM	9.36999989	44.3600006	transporter MCF Iron ?	34.8 transport.metabolite transporters at the envelope membrane		plastid		envelope-inner-integral	3.0
AT5G42270	1148	AT5G42270.1	VAR1 (VARIEGATED 1); ATP-dependent peptidase/ATPase/metallopeptidase	704	Ch/Th & Ch/E	5.36000013	75.2300034	chaperone and protease	29.5.7 protein.degradation.metall oprotease	thylakoid membrane (sensu Viridiplantae) & chloroplast	plastid	plastid	thylakoid-integral	

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AT5G42390	1149	AT5G42390.1	metalloendopeptidase	1265		6.11999989	140.600006		29.9* protein.processing	chloroplast	Y	C	plastid stroma	
AT5G42480	1150	AT5G42480.1	ARC6 (ACCUMULATION AND REPLICATION OF CHLOROPLASTS 6)	801	Ch/E/IM	4.76000023	88.2600021	plastid division	31.2.5 cell.division.plastid	chloroplast inner membrane	plastid	plastid	envelope-inner	2.0
AT5G42650	1151	AT5G42650.1	AOS (ALLENE OXIDE SYNTHASE); hydrolyase/oxygen binding	518	Ch/E & Ch/Th	8.75	58.1899986	metabolism hormone jasmonate	17.7.1.3 hormone metabolism.jasmonate.synthesis-degradation.allene oxidase synthase	thylakoid membrane (sensu Viridiplantae) & mitochondrion		plastid	thylakoid	
AT5G42765	1152	AT5G42765.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO61157.1); contains InterPro domain Twin-arginine translocation pathway signal (InterPro:IPR006311)	229	Ch/Th	5.94000006	25.0900002	unknown	35.2 not assigned.unknown			plastid	thylakoid	
AT5G42960	1153	AT5G42960.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G45170.1); similar to pore protein of 24 kD (OEP24) [Pisum sativum] (GB:CAA04468.1)	213	Ch/E/OM	9.26000023	23.4099998	transporter ion channel	34.8 transport.metabolite transporters at the envelope membrane				envelope-outer	
AT5G43745	1154	AT5G43745.1	phosphotransferase-related	817	Ch/E/IM	9.14000034	92.2099991	transporter ion channel?	35.1 not assigned.no ontology			plastid	plastid	2.0

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AT5G43780	1155	AT5G43780.1	APS4	469	Ch/S	8.8800011	52.1199989	sulfate assimilation	14.1 S-assimilation. APS	mitochondrion & chloroplast		plastid	plastid	
AT5G44316	1156	AT5G44316.1	ATP-binding-cassette transporter, putative	470		5.9299983	53.0800018		35.1 not assigned.no ontology	undefined	Y	C	-	
AT5G44340	1157	AT5G44340.1	TUB4 (tubulin beta-4 chain)	444		4.75	49.8199997		31.1 cell.organisation	undefined			-	
AT5G44520	1158	AT5G44520.1	ribose 5-phosphate isomerase-related	296		5.1300011	32.1599998		1.3.10 PS.calvin cycle.Rib5P isomerase	chloroplast	Y	C	-	
AT5G44650	1159	AT5G44650.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO44475.1)	280	Ch/Th	4.9600004	31.8099995	chaperone and protease ?	29.8 protein assembly and cofactor ligation	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	thylakoid	1.0
AT5G45170	1160	AT5G45170.1	CbbY protein-related	372	Ch/S	8.02000046	40.7400017	unknown	35.2 not assigned.unknown			plastid	plastid stroma	
AT5G45390	1161	AT5G45390.1	CLPP4 (Clp protease proteolytic subunit 4); endopeptidase Clp	292	Ch/S & Ch/E	5.3699989	31.4899998	chaperone and protease	29.5.5 protein.degradation.serine protease	thylakoid membrane (sensu Viridiplantae) & chloroplastic endopeptidase Clp complex & chloroplast stroma	plastid	plastid	plastid stroma	
AT5G45680	1162	AT5G45680.1	FK506-binding protein 1 (FKBP13)	208	Ch/Th	8.9499981	22.0400009	chaperone and protease	29.8 protein assembly and cofactor ligation	thylakoid lumen (sensu Viridiplantae)	plastid	plastid	thylakoid-peripheral-lumenal-side	
AT5G45930	1163	AT5G45930.1	CHLI2; magnesium chelatase	418	Ch/S	5.3499999	46.0900002	metabolism vitamin and pigment	19.10 tetrapyrrole synthesis.magnesium chelatase	magnesium chelatase complex & chloroplast stroma	plastid	plastid	plastid	

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AT5G46110	1164	AT5G46110.1	APE2 (ACCLIMATION OF PHOTOSYNTHESIS TO ENVIRONMENT); antiporter/triose-phosphate transmembrane transporter	410	Ch/E & Ch/Th	9.75	44.6300011	transporter Pi/TP	34.8 transport.metabolite transporters at the envelope membrane			mitochondrion	envelope-inner-integral	
AT5G46290	1165	AT5G46290.1	KAS I (3-KETOACYL-CARRIER PROTEIN SYNTHASE I); fatty-acid synthase	473	Ch/S	8.27999973	50.4099998	metabolism lipid	11.1.3 lipid metabolism. FA synthesis and FA elongation.ketoacyl ACP synthase		plastid	plastid	plastid stroma	
AT5G46420	1166	AT5G46420.1	16S rRNA processing protein RimM family	653		5.61000013	73.7799988		29.2.7* protein.synthesis.ribosome biogenesis	chloroplast	Y	C	plastid stroma	
AT5G46580	1167	AT5G46580.1	pentatricopeptide (PPR) repeat-containing protein	711	Ch/E & Ch/S	8.39999962	80.8799973	RNA Binding ?	27.7* RNA.misc.pentatricopeptide (PPR) repeat-containing protein		plastid	plastid	plastid	
AT5G47190	1168	AT5G47190.1	ribosomal protein L19 family protein	229	Ch/E & Ch/S	10.0600004	25.4599991	translation stroma	29.2.1.1.1.2.19 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.50S subunit.L19		plastid	plastid	plastid ribosome	
AT5G47840	1169	AT5G47840.1	AMK2 (ADENOSINE MONOPHOSPHATE KINASE); adenylate kinase	283	Ch/S	7.0999999	31.4500008	metabolism nucleotide	23.4.1 nucleotide metabolism.phosphotransfer and pyrophosphatases.adenylate kinase			plastid	plastid stroma	

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AT5G47860	1170	AT5G47860.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G43540.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO68746.1); contains InterPro domain Protein of unknown function DUF1350 (InterPro:IPR010765)	431		8.18999958	47.7799988		35.2 not assigned.unknown	chloroplast	Y	C	-	
AT5G48220	1171	AT5G48220.1	indole-3-glycerol phosphate synthase, putative	379	Ch/S	5.78000021	41.9599991	metabolism amino acids Tryptophan	13.1.6.5.4 amino acid metabolism.synthesis.aromatic aa.tryptophan.indole-3-glycerol phosphate synthase		plastid	plastid	plastid stroma	
AT5G48300	1172	AT5G48300.1	ADG1 (ADP GLUCOSE PYROPHOSPHORYLASE SMALL SUBUNIT 1); glucose-1-phosphate adenyltransferase	520	Ch/S	6.11999989	56.6500015	metabolism carbon	2.1.2.1 major CHO metabolism.synthesis.star ch.AGPase			plastid	plastid stroma	

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AT5G48790	1173	AT5G48790.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G73060.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO49997.1)	316	Ch/Th & Ch/E	8.11999989	35.8600006	unknown	35.2 not assigned.unknown		plastid	plastid	thylakoid	
AT5G48960	1174	AT5G48960.1	5' nucleotidase family protein	642		5.98999977	72.8899994		23.2 nucleotide metabolism.degradation	undefined	Y	C	plastid stroma	
AT5G49030	1175	AT5G49030.1	OVA2 (OVULE ABORTION 2); ATP binding / aminoacyl-tRNA ligase	1093		6.67000008	123.0		29.1.5 protein.aa activation.iso leucine-tRNA ligase	chloroplast	Y	C	plastid stroma	
AT5G49360	1176	AT5G49360.1	BXL1 (BETA-XYLOSIDASE 1); hydrolase, hydrolyzing O-glycosyl compounds	774		8.78999996	83.5199966				-	S		
AT5G49910	1177	AT5G49910.1	cpHSC70-2 (HEAT SHOCK PROTEIN 70-7); ATP binding / unfolded protein binding	718	Ch/S	5.17000008	76.9899979	chaperone and protease	29.6 protein.folding	plastid stroma	plastid	plastid	plastid stroma	
AT5G49940	1178	AT5G49940.1	NFU2 (NFU domain protein 2)	235		5.28000021	25.6200008		29.8.1* protein assembly and cofactor ligation.Fe-S assembly	chloroplast	Y	C	plastid stroma	

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AT5G50100	1179	AT5G50100.1	similar to PBng143 [Vigna radiata] (GB:BAB82450.1); contains InterPro domain Thioredoxin-like fold (InterPro:IPR012336); contains InterPro domain Putative thiol-disulphide oxidoreductase DCC (InterPro:IPR007263)	214	CH/E/IM	9.28999996	24.4300003	redox ?			Y	M		
AT5G50250	1180	AT5G50250.1	31 kDa ribonucleoprotein, chloroplast, putative / RNA-binding protein RNP-T, putative / RNA-binding protein 1/2/3, putative / RNA-binding protein cp31, putative	289		4.9000001	31.8700008		27.1.5* RNA.editing	chloroplast	Y	C	plastid stroma	
AT5G50920	1181	AT5G50920.1	CLPC (HEAT SHOCK PROTEIN 93-V); ATP binding / ATPase	929	Ch/E & Ch/S	6.36000013	103.449997	chaperone and protease	29.5.5 protein.degradation.serine protease	thylakoid membrane (sensu Viridiplantae) & mitochondrion & chloroplast stroma & chloroplast		plastid	envelope-inner-peripheral-stromal-side; plastid stroma	
AT5G51010	1182	AT5G51010.1	rubredoxin family protein	154	Ch/Th	9.89999962	17.2299995	redox	21.1 redox.thioredoxin			plastid		1.0

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AT5G51020	1183	AT5G51020.1	similar to hypothetical protein [Vitis vinifera] (GB:CAN83158.1); contains InterPro domain Protein of unknown function DUF1001 (InterPro:IPR010404)	269	Ch/E/OM	6.46000004	30.3299999	plastid division ?	31.2.5 cell.division.plastid	chloroplast		C	envelope-outer	
AT5G51070	1184	AT5G51070.1	ERD1 (EARLY RESPONSIVE TO DEHYDRATION 1); ATP binding / ATPase	945	Ch/S & Ch/E	5.88999987	103.230003	chaperone and protease	29.5.5 protein.degradation.serine protease	chloroplast & chloroplast stroma		plastid	plastid stroma	
AT5G51100	1185	AT5G51100.1	FSD2 (FE SUPEROXIDE DISMUTASE 2); iron superoxide dismutase	305	Ch/S	4.88999987	34.6599998	stress oxidative	21.6 redox.dismutases and catalases			plastid	plastid stroma	
AT5G51110	1186	AT5G51110.1	similar to dehydratase family [Arabidopsis thaliana] (TAIR:AT1G29810.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO62291.1); contains InterPro domain Transcriptional coactivator/sterin dehydratase (InterPro:IPR001533)	220		9.05000019	23.8899994		35.2 not assigned.unknown	chloroplast	Y	C	plastid stroma	

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AT5G51545	1187	AT5G51545.1	LPA2 (LOW PSII ACCUMULATION2)	185	Ch/Th	9.34000015	20.2099991	chaperone and protease	35.2 not assigned.unkn own			plastid	thylakoid-integral	
AT5G51690	1188	AT5G51690.1	ACS12 (1-Aminocyclopropane-1-carboxylate synthase 12); 1-aminocyclopropane-1-carboxylate synthase	495	Ch/E ?	7.01999998	55.2099991	metabolism hormone ethylene	17.5.1.1 hormone metabolism. ethylene.synthesis-degradation. 1-aminocyclopropane-1-carboxylate synthase	undefined		M	-	1.0
AT5G51720	1189	AT5G51720.1	similar to Os07g0467200 [Oryza sativa (japonica cultivar-group)] (GB:NP_001059590.1); similar to hypothetical protein Osl_025030 [Oryza sativa (indica cultivar-group)] (GB:EAZ03798.1); contains domain PTHR13680 (PTHR13680); contains domain PTHR13680:	108		9.32999992	11.6199999		35.2 not assigned.unkn own	undefined			plastid	
AT5G51820	1190	AT5G51820.1	PGM (PHOSPHOGLUCOMUTASE)	623	Ch/S	5.48000002	67.9800034	unknown	4.2 glycolysis.PGM	chloroplast stroma	plastid	plastid	plastid stroma	
AT5G51830	1191	AT5G51830.1	pfkB-type carbohydrate kinase family protein	343	Ch/E ?	4.98999977	37.0200005	metabolism carbon	2.2.1.1 major CHO metabolism. degradation. sucrose.fructokinase	other (e.g. cytoplasm)			-	

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AT5G52100	1192	AT5G52100.1	CRR1 (CHLOROPHYLL SYNTHESIS REDUCTASE); dihydrodipicolinate reductase	298		5.88000011	32.0299988		1.1.6.1* PS.lightreaction.NADH DH.assembly	chloroplast	Y	C	plastid stroma	
AT5G52410	1193	AT5G52410.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G23890.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO49433.1); contains InterPro domain S-layer homology region (InterPro:IPR001119)	510	Ch/E ??	5.28999996	57.7999992	unknown	35.2 not assigned.unknown				envelope	
AT5G52440	1194	AT5G52440.1	HCF106 (High chlorophyll fluorescence 106)	260	Ch/E & Ch/Th	8.92000008	28.2299995	protein targeting	29.3.3 protein.targeting.chloroplast	thylakoid & thylakoid membrane (sensu Viridiplantae)	plastid	plastid	thylakoid-integral	1.0
AT5G52520	1195	AT5G52520.1	OVA6/PRORS1 (OVULE ABORTION 6); ATP binding / aminoacyl-tRNA ligase	543	Ch/S	6.55000019	60.7400017	unknown	29.1.40 protein.aa activation.bifunctional aminoacyl-tRNA synthetase	mitochondrion & chloroplast	plastid	plastid	mitochondria; plastid stroma	

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AT5G52540	1196	AT5G52540.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G24000.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO49471.1); contains InterPro domain Protein of unknown function DUF819 (InterPro:IPR008537)	461	Ch/E/IM	9.96000004	47.6399994	transporter ?	35.2 not assigned.unkn own		plastid	plastid	envelope	9.0
AT5G52780	1197	AT5G52780.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G19100.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO49500.1)	168	Ch/Th	9.22999954	18.7399998	nd	35.2 not assigned.unkn own	thylakoid membrane (sensu Viridiplantae)	plastid	mitochondrion	thylakoid	2.0
AT5G52920	1198	AT5G52920.1	PKP-BETA1/PKP1/PKP2 (PLASTIDIC PYRUVATE KINASE 1); pyruvate kinase	579	Ch/S	6.55999994	63.5200005	nd	11.1.30 lipid metabolism. FA synthesis and FA elongation.pyruvate kinase			plastid	plastid stroma	
AT5G52960	1199	AT5G52960.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO69341.1)	170		8.26000023	19.1599998		35.2 not assigned.unkn own	chloroplast	Y	C	-	

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AT5G52970	1200	AT5G52970.1	thylakoid lumen 15.0 kDa protein	223	Ch/Th	5.65999985	24.5599995	unknown	35.1 not assigned.no ontology	thylakoid lumen (sensu Viridiplantae)		plastid	thylakoid-peripheral-lumenal-side	
AT5G53170	1201	AT5G53170.1	FTSH11 (FtsH protease 11); ATP-dependent peptidase/ATPase/metallopeptidase	806	Ch/E/IM	5.80000019	88.7099991	chaperone and protease	29.5.7 protein.degradation.metall oprotease	mitochondrion & chloroplast	plastid	plastid	mitochondria ; plastid	1.0
AT5G53460	1202	AT5G53460.1	GLT1 (NADH-dependent glutamate synthase 1 gene)	2208		5.96999979	241.899994		12.2.1.2 N-metabolism.ammonia metabolism.glutamate synthase.NADH dependent	chloroplast	Y	C	plastid	
AT5G53490	1203	AT5G53490.1	thylakoid lumenal 17.4 kDa protein, chloroplast	236	Ch/Th & Ch/E & Ch/S	5.96999979	25.6399994	RNA Binding ?	27.7* RNA.misc.pe ntatricopeptide (PPR) repeat-containing protein			plastid	thylakoid-peripheral-lumenal-side	
AT5G53580	1204	AT5G53580.1	aldo/keto reductase family protein	365	Ch/Th	9.31000042	40.5699997	metabolism vitamin and pigment vitamin b6 ?	3.5 minor CHO metabolism.others		plastid		plastid	
AT5G53850	1205	AT5G53850.1	haloacid dehalogenase-like hydrolase family protein	402		5.86999989	45.0200005		3.5 minor CHO metabolism.others	undefined			-	
AT5G53860	1206	AT5G53860.1	EMB2737 (EMBRYO DEFECTIVE 2737)	402	Ch/E ??	8.56999969	46.1500015	vesicular trafficking ?	35.2 not assigned.unknown			mitochondrion	plastid	
AT5G54190	1207	AT5G54190.1	PORA (Protochlorophyllide reductase A); oxidoreductase/protochlorophyllide reductase	405	Ch/E & Ch/Th	9.42000008	43.8600006	metabolism vitamin and pigment	19.14 tetrapyrrole synthesis.pro tochlorophyllide reductase	chloroplast	Y	C	thylakoid-peripheral-stromal-side	

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AT5G54270	1208	AT5G54270.1	LHCB3 (LIGHT-HARVESTING CHLOROPHYLL BINDING PROTEIN 3)	265	Ch/Th	4.96000004	28.7000008	PS LHCII	1.1.1.1 PS.lightreaction.photosystem II.LHC-II	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	thylakoid-integral	2.0
AT5G54600	1209	AT5G54600.1	50S ribosomal protein L24, chloroplast (CL24)	198	Ch/E & Ch/S	9.68999958	21.9699993	translation stroma	29.2.1.1.1.2.24 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.50S subunit.L24		plastid	plastid	plastid ribosome	
AT5G54770	1210	AT5G54770.1	THI1 (THIAZOLE REQUIRING)	349	Ch/S	5.80999994	36.6599998	unknown	18.2 Co-factor and vitamin metabolism.thiamine	mitochondrion & chloroplast	plastid	plastid	mitochondria ; plastid stroma	
AT5G54810	1211	AT5G54810.1	TSB1 (TRYPTOPHAN SYNTHASE BETA-SUBUNIT)	470		6.3499999	50.9199982		13.1.6.5.5 amino acid metabolism.synthesis.aromatic aa.tryptophan.tryptophan synthase	chloroplast	Y	C	plastid	
AT5G55220	1212	AT5G55220.1	trigger factor type chaperone family protein	547	Ch/S	5.25	61.7299995	chaperone and protease	29.6 protein.folding		plastid	plastid	plastid stroma	
AT5G55280	1213	AT5G55280.1	FTSZ1-1 (FtsZ1-1); structural molecule	433	Ch/S	6.92000008	45.5600014	plastid division	31.2.5 cell.division.plastid	chloroplast stroma	plastid	plastid	plastid stroma	
AT5G55510	1214	AT5G55510.1	P-P-bond-hydrolysis-driven protein transmembrane transporter	214	Ch/E/OM	9.07999992	22.5200005	protein targeting / aa channel	34.8 transport.metabolite transporters at the envelope membrane	other (e.g. cytoplasm)			envelope	
AT5G56000	1215	AT5G56000.1	heat shock protein 81-4 (HSP81-4)	699		4.96000004	80.1399994		20.2.1 stress.abiotic.heat	secreted		S	-	

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AT5G56500	1216	AT5G56500.2	ATP binding / protein binding / unfolded protein binding	597	Ch/S	5.73000002	63.3199997	chaperone and protease	29.6 protein.folding	chloroplast	Y	C	plastid stroma	
AT5G56730	1217	AT5G56730.1	peptidase M16 family protein / insulinase family protein	956	Ch/E	5.4000001	107.980003	chaperone and protease ?	29.5.7 protein.degradation.metall oprotease	undefined			-	2.0
AT5G57345	1218	AT5G57345.1	similar to unknown [Populus trichocarpa x Populus deltoides] (GB:ABK965 92.1)	188		9.18999958	20.1900005		35.2 not assigned.unknown	undefined	Y	C	-	2.0
AT5G57850	1219	AT5G57850.1	aminotransferase class IV family protein	373		8.64000034	41.0600014		26.26.1 misc.aminotransferases.aminotransferase class IV family protein	chloroplast	Y	C	plastid stroma	
AT5G57960	1220	AT5G57960.1	GTP-binding family protein	540		5.75	60.5200005		29.2.7* protein.synthesis.ribosome biogenesis	chloroplast	Y	C	plastid stroma	
AT5G58070	1221	AT5G58070.1	lipocalin, putative	186	Ch/E & other	5.96999979	21.4300003	metabolism lipid / transport ?	11 lipid metabolism	undefined			-	
AT5G58140	1222	AT5G58140.1	PHOT2 (NON PHOTOTROPIC HYPOCOTYL 1-LIKE); kinase	915	na	7.03999996	102.470001	signalling ?	29.4 protein.posttranslational modification			plastid	cytosol; golgi; plasma membrane	
AT5G58250	1223	AT5G58250.1	similar to hypothetical protein [Vitis vinifera] (GB:CAN758 40.1); contains domain PD020337 (PD020337)	211	Ch/Th	7.82000017	24.1000004	unknown	35.2 not assigned.unknown		plastid	plastid	plastid	

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AT5G58260	1224	AT5G58260.1	Encodes subunit NDH-N of NAD(P)H:plastoquinone dehydrogenase complex (Ndh complex) present in the thylakoid membrane of chloroplasts. This subunit is thought to be required for Ndh complex assembly.	209	Ch/Th	9.43000031	23.3899994	NDH	1.1.6 PS.lightreaction.NADH DH	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	thylakoid	
AT5G58270	1225	AT5G58270.1	STA1 (STAR1K 1); ATPase, coupled to transmembrane movement of substances	728	Ch/E/IM	9.27000046	80.4199982	transporter ABC	34.16 transport.ABC transporters and multidrug resistance systems	mitochondrion	plastid	mitochondrion	mitochondria	6.0
AT5G58330	1226	AT5G58330.1	malate dehydrogenase (NADP), chloroplast, putative	443	Ch/S	5.80000019	48.3100014	metabolism carbon	8.2.99 TCA / org.transformation.other organic acid transformations.misc	mitochondrion		plastid	plastid stroma	
AT5G58870	1227	AT5G58870.1	FTSH9 (FtsH protease 9); ATP-dependent peptidase/metallopeptidase	806	Ch/E	7.6500001	87.8300018	chaperone and protease	29.5.7 protein.degradation.metall oprotease	chloroplast		plastid	plastid	2.0
AT5G59250	1228	AT5G59250.1	sugar transporter family protein	558	Ch/E/IM	9.02000046	59.8300018	transporter D-xylose-H+?	34.8 transport.metabolite transporters at the envelope membrane			plastid	envelope-inner-integral	11.0

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AT5G59750	1229	AT5G59750.1	riboflavin biosynthesis protein, putative	509		5.69999981	56.1399994		18.3.1 Co-factor and vitamine metabolism.r iboflavin.GTP cyclohydrolase II	undefined	Y	M	plastid	
AT5G59870	1230	AT5G59870.1	HTA6; DNA binding	150	na	10.54	15.96	DNA binding	28.1.3 DNA.synthesis/chromatin structure.histone				nucleus	
AT5G59910	1231	AT5G59910.1	HTB4; DNA binding	150		9.98999977	16.4500008		28.1.3 DNA.synthesis/chromatin structure.histone	other (e.g. cytoplasm)			nucleus	
AT5G60600	1232	AT5G60600.1	GcpE (CHLOROPLAST BIOGENESIS 4); 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	741	Ch/S	6.01000023	82.25	metabolism isoprenoids	16.1.1.6 secondary metabolism.isoprenoids.non-mevalonate pathway.HDS	chloroplast		plastid	plastid stroma; thylakoid-peripheral-stromal-side	
AT5G60660	1233	AT5G60660.1	PIP2;4/PIP2 F (plasma membrane intrinsic protein 2;4); water channel	291	other	8.21000004	30.9500008	transporter aquaporin	34.19.1 transport.Major Intrinsic Proteins.PIP	other (e.g. cytoplasm)			-	6.0
AT5G60930	1234	AT5G60930.1	chromosome-associated kinesin, putative	1294		6.76000023	145.220001		31.1 cell.organisation	undefined			-	
AT5G61410	1235	AT5G61410.1	RPE (EMBRYO DEFECTIVE 2728); ribulose-phosphate 3-epimerase	281	Ch/S	8.23999977	30.0	metabolism carbon Calvin cycle	1.3.11 PS.calvin cycle.RPE		plastid	plastid	plastid stroma	
AT5G61790	1236	AT5G61790.1	calnexin 1 (CNX1)	530	Ch/E ?	4.80999994	60.4799995	vesicular trafficking / signalling calcium ?	30.3 signalling.calcium	secreted		S	-	1.0

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AT5G62140	1237	AT5G62140.1	similar to unknown [Populus trichocarpa] (GB:ABK94834.1)	241	Ch/E/IM	8.85000038	26.4300003	protein targeting ?	35.2 not assigned.unkn own			plastid	plastid	
AT5G62720	1238	AT5G62720.1	integral membrane HPP family protein	243	Ch/E & Ch/Th	10.1400003	25.8199997	transporter ?	35.1 not assigned.no ontology	chloroplast inner membrane		plastid	envelope-inner-integral	5.0
AT5G62790	1239	AT5G62790.1	DXR (1-DEOXY-D-XYLULOSE 5-PHOSPHATE REDUCTOISOMERASE)	477	Ch/S	6.57000017	51.9599991	metabolism isoprenoids	16.1.1.2 secondary metabolism.isoprenoids.non-mevalonate pathway.DXR		plastid	plastid	plastid stroma	
AT5G63040	1240	AT5G63040.1	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G48460.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO64290.1)	366	Ch/E/IM	9.63000011	40.6599998	unknown	35.2 not assigned.unkn own		plastid	plastid	plastid	5.0
AT5G63050	1241	AT5G63050.1	EMB2759 (EMBRYO DEFECTIVE 2759)	345	Ch/E ?	9.40999985	39.2900009	unknown	35.2 not assigned.unkn own	undefined		M	-	2.0
AT5G63310	1242	AT5G63310.1	NDPK2 (NUCLEOSIDE DIPHOSPHATE KINASE 2); ATP binding / nucleoside diphosphate kinase	231	Ch/S	9.14000034	25.5499992	metabolism nucleotide	23.4.10 nucleotide metabolism.phosphotransfer and pyrophosphatases.nucleoside diphosphate kinase	nucleus & cytoplasm	plastid	plastid	plastid stroma	
AT5G63420	1243	AT5G63420.1	EMB2746 (EMBRYO DEFECTIVE 2746); catalytic	911	Ch/S	8.42000008	100.550003	metabolism nucleotide	23.2 nucleotide metabolism.degradation		plastid	plastid	plastid stroma	

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AT5G63570	1244	AT5G63570.1	GSA1 (GLUTAMATE-1-SEMIALDEHYDE-2,1-AMINOMUTASE); glutamate-1-semialdehyde 2,1-aminomutase	474	Ch/S	6.42000008	50.3699989	metabolism vitamin and pigment	19.3 tetrapyrrole synthesis.GSA		plastid	plastid	plastid stroma	
AT5G63890	1245	AT5G63890.1	ATHDH (HISTIDINOL DEHYDROGENASE)	452	Ch/S	5.26999998	48.9500008	metabolism amino acids Histidine	13.1.7.8 amino acid metabolism.synthesis.histidine.histidinol dehydrogenase				plastid stroma	
AT5G63980	1246	AT5G63980.1	SAL1 (FIERY1); 3'(2'),5'-bisphosphate nucleotidase/inositol or phosphatidylinositol phosphatase	407		5.01999998	37.5600014		23.2 nucleotide metabolism.degradation	chloroplast	Y		plastid stroma	
AT5G64040	1247	AT5G64040.1	PSAN (photosystem I reaction center subunit PSI-N); calmodulin binding	171	Ch/Th	9.10999966	18.4200001	PS PSI	1.1.2.2 PS.lightreaction.photosystem I.PSI polypeptide subunits	thylakoid membrane (sensu Viridiplantae) & thylakoid lumen (sensu Viridiplantae) & photosystem I		plastid	thylakoid-peripheral-lumenal-side	
AT5G64050	1248	AT5G64050.1	ATERS/ERS/OVA3 (OVULE ABORTION 3); glutamate-tRNA ligase	570	Ch/S	7.61000013	63.4599991	unknown	19.1 tetrapyrrole synthesis.glu-tRNA synthetase	mitochondrion & chloroplast		mitochondrion	mitochondria ; plastid stroma	

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AT5G64280	1249	AT5G64280.1	DIT2.2 (DICARBOXYLATE TRANSPORTER 2.2); oxoglutarate: malate antiporter	549	Ch/E/IM	9.36999989	58.7400017	transporter glutamate/mal	34.8 transport.metabolite transporters at the envelope membrane			plastid	envelope	11.0
AT5G64290	1250	AT5G64290.1	DCT/DIT2.1 (DICARBOXYLATE TRANSPORT); oxoglutarate: malate antiporter	563	Ch/E & Ch/Th	9.32999992	59.9900017	transporter oxoglut/mal	34.8 transport.metabolite transporters at the envelope membrane			plastid	envelope-inner-integral	10.0
AT5G64300	1251	AT5G64300.1	ATGCH (ARABIDOPSIS THALIANA GTP CYCLOHYDROLASE II); 3,4-dihydroxy-2-butanone-4-phosphate synthase/GTP cyclohydrolase II	543		5.57999992	59.0499992		18.3.1 Co-factor and vitamine metabolism.riboflavin.GTP cyclohydrolase II	chloroplast	Y	C	plastid	
AT5G64380	1252	AT5G64380.1	fructose-1,6-bisphosphatase family protein	404		6.36999989	43.9700012		1.3.7 PS.calvin cycle.FBPase	undefined	Y	M	plastid	
AT5G64580	1253	AT5G64580.1	AAA-type ATPase family protein	855	Ch/E/IM	5.65999985	96.8499985	chaperone and protease	29.5.7 protein.degradation.metallprotease			plastid	plastid	1.0

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AT5G64816	1254	AT5G64816.1	Identical to Uncharacterized protein At5g64816 precursor [Arabidopsis Thaliana] (GB:Q8L8Q8;GB:Q9LV96); similar to unnamed protein product [Vitis vinifera] (GB:CAO22147.1)	130	Ch/E/IM	8.72999954	14.4399996	unknown	35.2 not assigned.unkn				plastid	
AT5G64860	1255	AT5G64860.1	DPE1 (DISPROPORTIONATING ENZYME); 4-alpha-glucanotransferase	576		5.44000006	64.4100037		2.2.2.4 major CHO metabolism. degradation. starch.D enzyme	undefined	Y	C	plastid	
AT5G64940	1256	AT5G64940.1	ATATH13 (ABC2 homolog 13)	761	Ch/Th	9.26000023	86.0199966	transporter ABC ?	26.56* misc.ABC1k family				plastid	envelope-inner-integral 2.0
AT5G65220	1257	AT5G65220.1	ribosomal protein L29 family protein	173	Ch/S & Ch/E & Ch/S	10.5	19.3700008	translation stroma	29.2.1.1.1.2.29 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.50S subunit.L29				plastid	plastid ribosome
AT5G65250	1258	AT5G65250.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO41077.1)	300	Ch/E/IM	9.93000031	33.2099991	unknown	35.2 not assigned.unkn				plastid	plastid 2.0
AT5G65350	1259	AT5G65350.1	histone H3	139		11.25	15.5900002		28.1.3 DNA.synthesis/chromatin structure.histone	undefined	Y	C	nucleus	

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AT5G65620	1260	AT5G65620.1	peptidase M3 family protein / thimet oligopeptidase family protein	791		5.9000001	88.75		29.5.7 protein.degradation.metall oprotease	chloroplast	Y	C	plastid stroma	
AT5G65840	1261	AT5G65840.1	similar to antioxidant/oxidoreductase [Arabidopsis thaliana] (TAIR:AT2G37240.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN81556.1); contains InterPro domain Thioredoxin-like fold (InterPro:IPR012336); contains InterPro domain Thioredo	275	Ch/S	8.57999992	29.8799992	redox	21 redox		plastid	plastid	plastid stroma	
AT5G66090	1262	AT5G66090.1	similar to unnamed protein product [Vitis vinifera] (GB:CAO23263.1); contains domain Adenine nucleotide alpha hydrolases-like (SSF52402)	210		6.21999979	22.5400009		35.2 not assigned.unknown	chloroplast	Y	C	plastid stroma	
AT5G66120	1263	AT5G66120.2	3-dehydroquinate synthase, putative	442		7.05000019	48.0600014		18.5 Co-factor and vitamin metabolism.folate & vitamin K	chloroplast	Y	C	plastid	

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AT5G66190	1264	AT5G66190.1	ATLFNR1 (LEAF FNR 1); NADPH dehydrogenase/ electron transporter, transferring electrons within the cyclic electron transport pathway of photosynthesis/ electron transporter, transferring electrons within the noncyclic electron transport pathway of ph	360	Ch/S & Ch/Th	8.31000042	40.3199997	redox	1.1.7 PS.lightreaction.ferredoxin reductase	thylakoid membrane (sensu Viridiplantae) & chloroplast stroma	plastid	plastid	thylakoid-peripheral-stromal-side	
AT5G66530	1265	AT5G66530.1	aldose 1-epimerase family protein	307	Ch/S	5.63000011	33.6899986	metabolism carbon	3.5 minor CHO metabolism. others		plastid	plastid	plastid stroma	
AT5G66550	1266	AT5G66550.1	Maf family protein	207		5.3499999	22.5599995		35.1 not assigned.no ontology	undefined		M	plastid	
AT5G66570	1267	AT5G66570.1	OE33/OEE1/OEE33/PSBO-1/PSBO1 (OXYGEN-EVOLVING ENHANCER 33); oxygen evolving/poly(U) binding	332	Ch/Th	5.53999996	35.1399994	PS PSII OEE	1.1.1.2 PS.lightreaction.photosystem II.PSII polypeptide subunits	thylakoid membrane (sensu Viridiplantae) & thylakoid lumen (sensu Viridiplantae)	plastid	plastid	thylakoid-peripheral-lumenal-side	
AT5G66720	1268	AT5G66720.1	5-azacytidine resistance protein - related	414		7.5999999	43.8699989		35.1 not assigned.no ontology	chloroplast	Y	C	not plastid	
AT5G67030	1269	AT5G67030.1	ABA1 (ABA DEFICIENT 1); zeaxanthin epoxidase	667	Ch/E & Ch/S & Ch/Th	6.5999999	73.8399963	metabolism vitamin and pigment	16.1.4 secondary metabolism.i soprenoids.c arotenoids		plastid	plastid	thylakoid	

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ATCG00020	1270	AtCg00020	Encodes chlorophyll binding protein D1, a part of the photosystem II reaction center core	353	Ch/Th	5.11999989	38.9300003	PS PSII	1.1.1.2 PS.lightreaction.photosystem II.PSII polypeptide subunits	undefined		C	thylakoid-integral	
ATCG00065	1271	AtCg00065	chloroplast gene encoding ribosomal protein s12. The gene is located in three distinct loci on the chloroplast genome and is transpliced to make one transcript.	38	Ch/S	11.5699997	13.7600002	translation stroma	29.2.1.1.1.1 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.30S subunit	undefined		C	plastid ribosome	
ATCG00120	1272	AtCg00120	Encodes the ATPase alpha subunit, which is a subunit of ATP synthase and part of the CF1 portion which catalyzes the conversion of ADP to ATP using the proton motive force. This complex is located in the thylakoid membrane of the chloroplast.	507	Ch/Th	5.17999983	55.3199997	PS ATPase	1.1.4 PS.lightreaction.ATP synthase	other (e.g. cytoplasm)		C	thylakoid-peripheral-stromal-side	
ATCG00130	1273	AtCg00130	ATPase F subunit.	184	Ch/Th	7.84000015	21.0499992	PS ATPase	1.1.4 PS.lightreaction.ATP synthase	other (e.g. cytoplasm)		C	thylakoid-integral	
ATCG00140	1274	AtCg00140	ATPase III subunit	81		4.94000006	7.96999979		1.1.4 PS.lightreaction.ATP synthase	secreted		C	thylakoid-integral	

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ATCG00150	1275	AtCg00150	Encodes a subunit of ATPase complex CF0, which is a proton channel that supplies the proton motive force to drive ATP synthesis by CF1 portion of the complex.	249		4.96000004	27.3500004		1.1.4 PS.lightreacti on.ATP synthase	undefined		C	thylakoid-integral	
ATCG00160	1276	AtCg00160	Chloroplast ribosomal protein S2	236	Ch/S	9.69999981	26.8999996	translation stroma		plastid small ribosomal subunit & chloroplast	-	C	plastid ribosome	
ATCG00170	1277	AtCg00170	RNA polymerase beta' subunit-2	1376		9.40999985	156.360001		27.2 RNA.transcri ption	undefined		C	plastid stroma	
ATCG00180	1278	AtCg00180	RNA polymerase beta' subunit-1	680		8.76000023	78.5800018		27.2 RNA.transcri ption	undefined		C	plastid stroma	
ATCG00190	1279	AtCg00190	Chloroplast DNA-dependent RNA polymerase B subunit. The transcription of this gene is regulated by a nuclear encoded RNA polymerase. This gene has been transferred to mitochondria l genome during crucifer evolution.	1072		8.68000031	121.059998		27.2 RNA.transcri ption	other (e.g. cytoplasm)		C	plastid stroma	

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ATCG00270	1280	AtCg00270	PSII D2 protein	353	Ch/Th	5.44999981	39.5400009	PS PSII	1.1.1.2 PS.lightreaction.photosystem II.PSII polypeptide subunits	other (e.g. cytoplasm)		C	thylakoid-integral	
ATCG00280	1281	AtCg00280	chloroplast gene encoding a CP43 subunit of the photosystem II reaction center. promoter contains a blue-light responsive element.	473	Ch/Th	6.69999981	51.8600006	PS PSII	1.1.1.2 PS.lightreaction.photosystem II.PSII polypeptide subunits	undefined		C	thylakoid-integral	
ATCG00330	1282	AtCg00330	30S chloroplast ribosomal protein S14	100	Ch/S	11.2299995	11.7399998	translation stroma	29.2.1.1.1.1.14 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.30S subunit.S14	undefined		C	plastid ribosome	
ATCG00340	1283	AtCg00340	Encodes the D1 subunit of photosystem I and II reaction centers.	734	Ch/Th	6.88000011	82.4700012	PS PSI	1.1.2.2 PS.lightreaction.photosystem I.PSI polypeptide subunits	mitochondrion		C	thylakoid-integral	
ATCG00350	1284	AtCg00350	Encodes psaA protein comprising the reaction center for photosystem I along with psaB protein; hydrophobic protein encoded by the chloroplast genome.	750	Ch/Th	6.5999999	83.2300034	PS PSI	1.1.2.2 PS.lightreaction.photosystem I.PSI polypeptide subunits	other (e.g. cytoplasm)		C	thylakoid-integral	

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ATCG00380	1285	AtCg00380	Chloroplast encoded ribosomal protein S4	201	Ch/S	10.3199997	23.2399998	translation stroma	29.2.1.1.1.1 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.30S subunit	undefined		C	plastid ribosome	
ATCG00420	1286	AtCg00420	Encodes NADH dehydrogenase subunit J. Its transcription is increased upon sulfur depletion.	158		6.5	18.5499992		1.1.6 PS.lightreaction.NADH DH	undefined		C	thylakoid	
ATCG00430	1287	AtCg00430	Encodes a protein which was originally thought to be part of photosystem II but its wheat homolog was later shown to encode for subunit K of NADH dehydrogenase.	225		9.17000008	25.3600006		1.1.6 PS.lightreaction.NADH DH	undefined		C	thylakoid	
ATCG00470	1288	AtCg00470	ATPase epsilon subunit	132	Ch/Th	5.82999992	14.4899998	PS ATPase	1.1.4 PS.lightreaction.ATP synthase	undefined		C	thylakoid-peripheral-stromal-side	
ATCG00480	1289	AtCg00480	chloroplast-encoded gene for beta subunit of ATP synthase	498	Ch/Th & other	5.38000011	53.9300003	PS ATPase	1.1.4 PS.lightreaction.ATP synthase	undefined		C	thylakoid-peripheral-stromal-side	
ATCG00490	1290	AtCg00490	large subunit of RUBISCO.	479	Ch	5.86999989	52.9500008	metabolism carbon	1.3.1 PS.calvin cycle.rubisco large subunit	other (e.g. cytoplasm)		C	plastid stroma	

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ATCG00500	1291	AtCg00500	Encodes the carboxytransferase beta subunit of the Acetyl-CoA carboxylase (ACCase) complex in plastids. This complex catalyzes the carboxylation of acetyl-CoA to produce malonyl-CoA, the first committed step in fatty acid synthesis.	488	Ch/E/IM	5.88999987	55.6100006	metabolism lipid	11.1.1 lipid metabolism. FA synthesis and FA elongation. Acetyl CoA Carboxylation	undefined		C	plastid stroma	
ATCG00520	1292	AtCg00520	Encodes a protein required for photosystem I assembly and stability. In cyanobacteria, loss of function mutation in this gene increases PSII/PSI ratio without any influence on photoautotrophic growth.	184		9.60999966	21.3999996		29.8 protein assembly and cofactor ligation	undefined		C	plastid stroma	

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ATCG00540	1293	AtCg00540	Encodes cytochrome f apoprotein; involved in photosynthetic electron transport chain; encoded by the chloroplast genome and is transcriptionally repressed by a nuclear gene HCF2.	320	Ch/Th	8.34000015	35.3499985	PS b6-F	1.1.3 PS.lightreaction.cytochrome b6/f	undefined		C	thylakoid-integral	
ATCG00560	1294	AtCg00560	PSII L protein	38		4.51999998	4.46999979		1.1.1.2 PS.lightreaction.photosystem II.PSII polypeptide subunits	secreted		C	thylakoid-integral	
ATCG00570	1295	AtCg00570	PSII cytochrome b559	39		10.7299995	4.42000008		1.1.1.2 PS.lightreaction.photosystem II.PSII polypeptide subunits	secreted		C	thylakoid-integral	
ATCG00580	1296	AtCg00580	PSII cytochrome b559. There have been many speculations about the function of Cyt b559, but the most favored at present is that it plays a protective role by acting as an electron acceptor or electron donor under conditions when electron flow through	83	Ch/Th	4.82999992	9.39000034	PS PSII	1.1.1.2 PS.lightreaction.photosystem II.PSII polypeptide subunits	undefined		C	thylakoid-integral	

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ATCG00630	1297	AtCg00630	Encodes subunit J of photosystem I.	44		5.86999989	5.0		1.1.2.2 PS.lightreaction.photosystem I.PSI polypeptide subunits	secreted		C	thylakoid-integral	
ATCG00640	1298	AtCg00640	encodes a chloroplast ribosomal protein L33, a constituent of the large subunit of the ribosomal complex	66		9.77999973	7.69000006		29.2.1.1.1.2 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.50S subunit	undefined		C	plastid ribosome	
ATCG00650	1299	AtCg00650	chloroplast-encoded ribosomal protein S18	101	Ch/S	12.1599998	12.0600004	translation stroma		plastid small ribosomal subunit & chloroplast	-	C	plastid ribosome	
ATCG00660	1300	AtCg00660	encodes a chloroplast ribosomal protein L20, a constituent of the large subunit of the ribosomal complex	117	Ch/S	11.8900003	14.1599998	translation stroma	29.2.1.1.1.2 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.50S subunit	undefined	Y	C	plastid ribosome	
ATCG00670	1301	AtCg00670	Encodes the only ClpP (caseinolytic protease) encoded within the plastid genome. Contains a highly conserved catalytic triad of Ser-type proteases (Ser-His-Asp). Part of the 350 kDa chloroplast Clp complex. The name reflects nomenclature described i	196	Ch/E & Ch/S	4.96999979	22.0900002	chaperone and protease	29.5.5 protein.degradation.serine protease	other (e.g. cytoplasm)		C	plastid stroma; thylakoid-inner-peripheral-stromal-side	

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ATCG00680	1302	AtCg00680	encodes for CP47, subunit of the photosystem II reaction center.	508	Ch/Th	6.3899987	56.0299988	PS PSII	1.1.1.2 PS.lightreaction.photosystem II.PSII polypeptide subunits	undefined		C	thylakoid-integral	
ATCG00710	1303	AtCg00710	Encodes a 8 kD phosphoprotein that is a component of the photosystem II oxygen evolving core. Its exact molecular function has not been determined but it may play a role in mediating electron transfer between the secondary quinone acceptors, QA and Q	73		6.0300021	7.6999981		1.1.1.2 PS.lightreaction.photosystem II.PSII polypeptide subunits	undefined		C	thylakoid-integral	
ATCG00720	1304	AtCg00720	Encodes the cytochrome b(6) subunit of the cytochrome b6f complex.	215	Ch/Th	8.8800011	24.1499996	PS b6-F	1.1.3 PS.lightreaction.cytochrome b6/f	other (e.g. cytoplasm)		C	thylakoid-integral	
ATCG00730	1305	AtCg00730	A chloroplast gene encoding subunit IV of the cytochrome b6/f complex	160	Ch/Th	6.5500019	17.4300003	PS b6-F	1.1.3 PS.lightreaction.cytochrome b6/f	other (e.g. cytoplasm)		C	thylakoid-integral	
ATCG00740	1306	AtCg00740	RNA polymerase alpha subunit	329		7.1900006	38.1300011		27.2 RNA.transcription	undefined		C	plastid stroma	
ATCG00750	1307	AtCg00750	30S chloroplast ribosomal protein S11	138	Ch/S	12.2399998	15.0200005	translation stroma		plastid small ribosomal subunit	Y	C	plastid ribosome	

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ATCG00760	1308	AtCg00760	encodes a chloroplast ribosomal protein L36, a constituent of the large subunit of the ribosomal complex	37	Ch/S	11.9099998	4.46000004	translation stroma	29.2.1.1.1.2 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.50S subunit	undefined		C	plastid ribosome	
ATCG00770	1309	AtCg00770	chloroplast 30S ribosomal protein S8	134	Ch/S	10.9300003	15.4799995	translation stroma		plastid small ribosomal subunit	-	C	plastid ribosome	
ATCG00780	1310	AtCg00780	encodes a chloroplast ribosomal protein L14, a constituent of the large subunit of the ribosomal complex	122	Ch/S	9.38000011	13.5799999	translation stroma		plastid large ribosomal subunit	-	C	plastid ribosome	
ATCG00790	1311	AtCg00790	chloroplast gene encoding a ribosomal protein L16, which is a constituent of 50S large ribosomal subunit	135	Ch/S	11.6199999	15.29	translation stroma		plastid large ribosomal subunit	-	C	plastid ribosome	
ATCG00800	1312	AtCg00800	encodes a chloroplast ribosomal protein S3, a constituent of the small subunit of the ribosomal complex	218	Ch/S	9.51000023	25.1800003	translation stroma		plastid small ribosomal subunit & chloroplast	-	C	plastid ribosome	
ATCG00810	1313	AtCg00810	encodes a chloroplast ribosomal protein L22, a constituent of the large subunit of the ribosomal complex	160	Ch/S	9.68999958	18.5799999	translation stroma	29.2.1.1.1.2 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.50S subunit	undefined		C	plastid ribosome	

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ATCG00820	1314	AtCg00820	Encodes a 6.8-kDa protein of the small ribosomal subunit.	92	Ch/S	10.7700005	10.5699997	translation stroma		plastid small ribosomal subunit & plastid ribosome	-	C	plastid ribosome	
ATCG00830	1315	AtCg00830	encodes a chloroplast ribosomal protein L2, a constituent of the large subunit of the ribosomal complex	274	Ch/S	10.8400002	29.8600006	translation stroma		plastid large ribosomal subunit	-	C	plastid ribosome	
ATCG00840	1316	AtCg00840	One of two chloroplast genes that encode chloroplast ribosomal protein L23, a constituent of the large subunit of the ribosomal complex	93	Ch/S	10.6499996	10.7799997	translation stroma	29.2.1.1.1.2 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.50S subunit	undefined		C	plastid ribosome	
ATCG00860	1317	AtCg00860	Encodes an unknown protein. This gene is regulated by AtSIG6 transcriptionally.	2294	Ch/S	8.86999989	269.559998	unknown	29.8 protein assembly and cofactor ligation	undefined		C	plastid stroma	
ATCG01060	1319	AtCg01060	Encodes the PsaC subunit of photosystem I.	81	Ch/Th	6.67000008	9.02999973	PS PSI	1.1.2.2 PS.lightreaction.photosystem I.PSI polypeptide subunits	undefined		C	thylakoid-peripheral-stromal-side	
ATCG01070	1320	AtCg01070	NADH dehydrogenase ND4L	101		8.72999954	11.2799997		1.1.6 PS.lightreaction.NADH DH	secreted		C	thylakoid-integral	
ATCG01100	1321	AtCg01100	NADH dehydrogenase ND1	360		5.55999994	40.0200005		1.1.6 PS.lightreaction.NADH DH	other (e.g. cytoplasm)		C	thylakoid-integral	

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ATCG01110	1322	AtCg01110	Encodes the 49KDa plastid NAD(P)H dehydrogenase subunit H protein. Its transcription is regulated by an ndhF-specific plastid sigma factor, SIG4.	393		5.38999987	45.5		1.1.6 PS.lightreaction.NADH DH	undefined		C	thylakoid	
ATCG01120	1323	AtCg01120	encodes a chloroplast ribosomal protein S15, a constituent of the small subunit of the ribosomal complex	88	Ch/S	10.8100004	10.71	translation stroma		plastid small ribosomal subunit	-	C	plastid ribosome	
ATCgG1130	1324	AtCg01130	hypothetical protein	1786	Ch/Th	9.73999977	213.690002	unknown	29.8 protein assembly and cofactor ligation	secreted		C	thylakoid-integral	
AT1G29920	15011	AT1G29920.1	LHCB1.1 (LHCII-1.1, CAB2) photosystem II light harvesting complex gene 1,1, CHLOROPHYLL A/B-BINDING PROTEIN 2 (CAB2), chloroplast precursor /		Ch/Th			PS LHCII	1.1.1.1 PS.lightreaction.photosystem II.LHC-II	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	thylakoid-integral	2.0
AT2G05100	15012	AT2G05100.1	LHCB2.1 (LHCII-2.1) photosystem II light harvesting complex gene 2.1, chlorophyll A-B binding protein, chloroplast precursor /		Ch/Th			PS LHCII	1.1.1.1 PS.lightreaction.photosystem II.LHC-II	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	thylakoid-integral	2.0

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AT3G27690	15013	AT3G27690.1	LHCB2.3 (LHCII-2.3) photosystem II light harvesting complex gene 2.3, chlorophyll A-B binding protein, chloroplast precursor /		Ch/Th			PS LHCII	1.1.1.1 PS.lightreaction.photosystem II.LHC-II	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	thylakoid-integral	2.0
AT1G76570	15014	AT1G76570.1	LHCB2.3-like (LHCII-2.3) photosystem II light harvesting complex gene 2.3, chlorophyll A-B binding protein, chloroplast precursor /		Ch/Th			PS LHCII	1.1.1.1 PS.lightreaction.photosystem II.LHC-II		plastid	plastid	thylakoid-integral	4.0
AT1G76450	15015	AT1G76450.1	PSBP-like 2 (OEC23-like-2) Photosystem II reaction center PsbP family protein, chloroplast precursor /		Ch/Th			PS PSII OEE ?	1.1.1.2 PS.lightreaction.photosystem II.PSII polypeptide subunits	thylakoid lumen (sensu Viridiplantae)	plastid	plastid	thylakoid-peripheral-lumenal-side	1.0
AT2G28605	15016	AT2G28605.1	PSBP-like 4-2 (OEC23-like-4) Photosystem II reaction center PsbP family protein, chloroplast precursor /		Ch/Th			PS PSII	1.1.1.2 PS.lightreaction.photosystem II.PSII polypeptide subunits		plastid	plastid	thylakoid-peripheral-lumenal-side	
AT5G11450	15017	AT5G11450.1	PSBP-like 6 (OEC23-like-6) Photosystem II reaction center PsbP family protein, chloroplast precursor /		Ch/Th			PS PSII OEE ?	1.1.1.2 PS.lightreaction.photosystem II.PSII polypeptide subunits	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	thylakoid-peripheral-lumenal-side	

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AT3G21055	15018	AT3G21055.1	PSBT (PsbTn) Photosystem II 5 kDa protein (PSII-T) (Nuclear encoded psbT) (PsbTn), chloroplast precursor /		Ch/Th			PS PSII	1.1.1.2 PS.lightreacti on.photosyst em II.PSII polypeptide subunits		plastid	plastid	thylakoid-integral	
AT1G51400	15019	AT1G51400.1	PSBT-like (PsbTn) Photosystem II 5 kDa protein (PSII-T) (Nuclear encoded psbT) (PsbTn), chloroplast precursor /		Ch/Th			PS PSII	1.1.1.2 PS.lightreacti on.photosyst em II.PSII polypeptide subunits		plastid	plastid	thylakoid-integral	
AT1G19150	15020	AT1G19150.1	LHCA6 (LHCI-6 or LHCA2.1) photosystem I light harvesting complex gene A6, chlorophyll A-B binding protein, chloroplast precursor /		Ch/Th			PS LHCI	1.1.2.1 PS.lightreacti on.photosyst em I.LHC-I		plastid	plastid	thylakoid-integral	
AT2G26500	15021	AT2G26500.3	PETM cytochrome b6/f complex subunit 7, chloroplast precursor /		Ch/Th			PS b6-f	1.1.3 PS.lightreacti on.cytochro me b6/f		plastid	plastid	thylakoid-integral	
AT1G68830	15022	AT1G68830.1	STN7 State transition 7, chloroplast precursor /		Ch/Th			PS State transition ?	1.1.30 PS.lightreacti on.state transition	chloroplast	plastid	plastid	thylakoid-integral	

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AT4G27800	15023	AT4G27800.1	TAP38 (PPH1) Thylakoid-Associated phosphatase 38 (protein phosphatase 2C, involved in LHCII dephosphorylation), chloroplast precursor /		Ch/Th			PS State transition ?	1.1.30 PS.lightreaction.state transition	nucleolus & nucleus & cytoplasm		mitochondrion	thylakoid-peripheral-stromal-side	
AT1G60950	15024	AT1G60950.1	FD2 (FER2, PETF, PETF1) Ferredoxin-2, chloroplast precursor /		Ch/Th			PS redox	1.1.5.2 PS.lightreaction.other electron carrier (ox/red).ferredoxin	chloroplast stroma	plastid	plastid	thylakoid-peripheral-stromal-side	
AT3G16250	15025	AT3G16250.1	CEF1 (PnsB3) NDH-dependent cyclic electron flow 1, NAD(P)H dehydrogenase complex subunit, involved in cyclic electron flow around photosystem I to produce ATP. Contains a 4Fe-4S cluster, chloroplast precursor /		Ch/Th			NDH or PS PSI cyclic	1.1.6 PS.lightreaction.NADH DH		plastid	plastid	thylakoid	
ATCG00440	15026	ATCG00440.1	NDHC (NDH3) NAD(P)H DEHYDROGENASE SUBUNIT C (NDHC), chloroplast encoded /		Ch/Th			NDH	1.1.6 PS.lightreaction.NADH DH	chloroplast		extracellular, endoplasmic reticulum, golgi	thylakoid-integral	

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ATCG01050	15027	ATCG01050.1	NDHD (NDH-4) NAD(P)H DEHYDROGENASE SUBUNIT D (NDHD), chloroplast encoded /		Ch/Th			NDH	1.1.6 PS.lightreaction.NADH DH			extracellular, endoplasmic reticulum, golgi	thylakoid	
ATCG01010	15028	ATCG01010.1	NDHF (NDH5) NAD(P)H DEHYDROGENASE SUBUNIT F (NDHF), chloroplast encoded /		Ch/Th			NDH	1.1.6 PS.lightreaction.NADH DH	chloroplast		extracellular, endoplasmic reticulum, golgi	thylakoid-peripheral-stromal-side	
AT1G18730	15029	AT1G18730.3	NDHF6 (PnsB4, NDF6) NDH dependent flow 6 protein, PHOTOSYNTHETIC NDH SUBCOMPLEX B 4 (PnsB4), chloroplast precursor /		Ch/Th			NDH	1.1.6 PS.lightreaction.NADH DH		plastid	plastid	thylakoid-integral	
ATCG01090	15030	ATCG01090.1	NDHI NAD(P)H DEHYDROGENASE SUBUNIT I (NDHI), chloroplast encoded /		Ch/Th			NDH	1.1.6 PS.lightreaction.NADH DH	chloroplast		mitochondrion	thylakoid-peripheral-stromal-side	
AT1G70760	15031	AT1G70760.1	NDHL NADH DEHYDROGENASE-LIKE COMPLEX L (NdhL), chloroplast precursor /		Ch/Th			NDH	1.1.6 PS.lightreaction.NADH DH		plastid	plastid	thylakoid-integral	3.0

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AT4G37925	15032	AT4G37925.1	NDHM NADH DEHYDROGENASE-LIKE COMPLEX M (NdhM), chloroplast precursor /		Ch/Th			NDH	1.1.6 PS.lightreaction.NADH DH	thylakoid membrane (sensu Viridiplantae)	plastid	mitochondrion	thylakoid	
AT4G09350	15033	AT4G09350.1	NDHT Chaperone DnaJ-domain containing NDH subunit, chloroplast precursor /		Ch/Th			NDH chaperone	1.1.6 PS.lightreaction.NADH DH				thylakoid	1.0
AT5G43750	15034	AT5G43750.1	PNSB5 (NDH18) NAD(P)H dehydrogenase 18, PHOTOSYNTHETIC NDH SUBCOMPLEX B 5 (PnsB5) /		Ch/Th			NDH	1.1.6 PS.lightreaction.NADH DH	thylakoid membrane (sensu Viridiplantae)			thylakoid-integral	2.0
AT5G47110	15035	AT5G47110.1	LIL3:1 Chlorophyll A-B binding family protein, chloroplast precursor /		Ch/Th			Stress light	1.1.8* light stress chlorophyll binding	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	thylakoid-integral	2.0
AT5G36790	15036	AT5G36790.1	PGLP1B Phosphoglycolate phosphatase 1B, chloroplastic		Ch/S			unknown	1.2.1 PS.photorespiration.phosphoglycolate phosphatase	nucleus & cytoplasm	plastid	plastid	plastid stroma	
AT5G38420	15037	AT5G38420.1	RBS2B (RBCS-2B) RuBisCO small subunit 2B, chloroplast precursor (EC 4.1.1.39) /		Ch/S ?			metabolism carbon Calvin cycle	1.3.2 PS.calvin cycle.rubisco small subunit		plastid	plastid	plastid stroma	

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AT5G18070	15038	AT5G18070.1	AGM1 (PAGM, DRT101) Phosphoacetylglucosamine mutase (PAGM) (EC 5.4.2.3) (Acetylglucosamine phosphomutase) (DNA-damage-repair/toleration protein DRT101) (N-acetylglucosamine-phosphate mutase) /		Ch/Th ??			DNA Binding	10.1 cell wall.precursor synthesis	mitochondrion				
AT4G16790	15039	AT4G16790.1	hydroxyproline-rich glycoprotein family protei		??			nd	10.5.4 cell wall.cell wall proteins.HR GP					2.0
AT4G38990	15040	AT4G38990.1	nd		??			unknown	10.6.1 cell wall.degradation.cellulases and beta -1,4-glucanases			extracellular, endoplasmic reticulum, golgi		
AT1G02640	15041	AT1G02640.1	nd		na			nd	10.6.2 cell wall.degradation.mannan-xylose-arabinose-fucose			extracellular, endoplasmic reticulum, golgi		
AT3G14310	15042	AT3G14310.1	nd		na			nd	10.8.1 cell wall.pectin*esterases.PME		plastid	extracellular, endoplasmic reticulum, golgi	not plastid	
AT3G11980	15043	AT3G11980.1	FACR2 (FAR2 MS2) Fatty acyl-CoA reductase 2, chloroplast precursor /		??			metabolism lipid ?	11.1 lipid metabolism. FA synthesis and FA elongation		plastid	plastid	plastid	

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AT5G16230	15044	AT5G16230.1	STAD3 Acyl-[acyl-carrier-protein] desaturase 3, chloroplast precursor (EC=1.14.19.2) /		??			metabolism lipid ?	11.1.15 lipid metabolism. FA synthesis and FA elongation.A CP desaturase		plastid	plastid		
AT3G02620	15045	AT3G02620.1	STAD4 (S-ACP-DES4) Acyl-[acyl-carrier-protein] desaturase 4 (Stearoyl-ACP desaturase 4), chloroplast precursor (EC 1.14.19.2) /		Ch/Th ?			metabolism lipid ?	11.1.15 lipid metabolism. FA synthesis and FA elongation.A CP desaturase		plastid	plastid		
AT3G02630	15046	AT3G02630.1	STAD5 (S-ACP-DES5) Acyl-[acyl-carrier-protein] desaturase 5, chloroplastic		Ch/Th ?			metabolism lipid	11.1.15 lipid metabolism. FA synthesis and FA elongation.A CP desaturase		plastid	plastid	plastid	
AT2G34590	15047	AT2G34590.1	PDH-E1 BETA pyruvate dehydrogenase E1 component subunit beta, transketolase activity, chloroplast precursor /		Ch/Th ?			metabolism lipid	11.1.31 lipid metabolism. FA synthesis and FA elongation.p yruvate DH		plastid	plastid	plastid	

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AT1G54570	15048	AT1G54570.1	PES1 PHYTYL ESTER SYNTHASE 1, phytyl ester synthesis and diacylglycero l acyltransfera se activities, chloroplast precursor (EC 2.3.1.-) /		Ch/Th ?			stress abiotic	11.10 lipid metabolism. glycolipid synthesis		plastid	plastid	plastoglobule s	
AT3G26840	15049	AT3G26840.1	PES2 PHYTYL ESTER SYNTHASE 2, phytyl ester synthesis and diacylglycero l acyltransfera se activities, chloroplast precursor (EC 2.3.1.-) /		Ch/Th ?			metabolism lipid ?	11.10 lipid metabolism. glycolipid synthesis		plastid	plastid	plastoglobule s	
AT2G46090	15050	AT2G46090.1	LCBK2 Long-Chain Base (LCB) Kinase 2, diacylglycero l kinase-like protein, chloroplast precursor /		Ch/Th ?			metabolism lipid	11.3 lipid metabolism. Phospholipid synthesis		plastid	plastid		
AT5G57690	15051	AT5G57690.1	DGK4 Diacylglycer ol kinase 4 (EC=2.7.1.1 07) /		??			metabolism lipid	11.3.5 lipid metabolism. Phospholipid synthesis.dia cylglycerol kinase			plastid		
AT4G15130	15052	AT4G15130.1	phosphorylc holine cytidyllyltrans ferase2		??			nd	11.3.6 lipid metabolism. Phospholipid synthesis.ch oline- phosphate cytidyllyltrans ferase					

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AT5G67050	15053	AT5G67050.1	Lipase-like alpha/beta-Hydrolases superfamily protein with Lipase class 3 domain, triglyceride lipase activity /		Ch/Th ??			metabolism lipid	11.9.2.1 lipid metabolism.lipid degradation.lipases.triacylglycerol lipase					2.0
AT4G13550	15054	AT4G13550.1	Lip-like Triacylglycerol lipase /		Ch/Th ??			metabolism lipid ?	11.9.2.1 lipid metabolism.lipid degradation.lipases.triacylglycerol lipase				plastid	
AT3G20520	15055	AT3G20520.1	SVL3 (SHV3-like 3, SEUSS-like 3) predicted glycerophosphodiester phosphodiesterase activity, chloroplast precursor /		Ch/Th ?			metabolism lipid ?	11.9.3.3 lipid metabolism.lipid degradation.lipases.glycerophosphodiester phosphodiesterase	anchored to membrane	plastid	extracellular, endoplasmic reticulum, golgi		1.0
AT3G17820	15056	AT3G17820.1	GLN13 (GS1, GLN1-3, MEB5.4) Glutamine synthetase cytosolic isozyme 1-3 (GS1) (EC 6.3.1.2) (Glutamate--ammonia ligase GLN1;3) (GLN1;3) /		na			metabolism aa glutamine	12.2.2 N-metabolism.ammonia metabolism.glutamine synthase	cytosol				
AT1G48470	15057	AT1G48470.1	GLN15 (GLN1;5) Glutamine synthetase cytosolic isozyme 1-5 (EC 6.3.1.2) (Glutamate--ammonia ligase GLN1;5) /		na			metabolism aa glutamine	12.2.2 N-metabolism.ammonia metabolism.glutamine synthase					

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AT1G74040	15058	AT1G74040.1	IPMS2 (LEU12) 2-isopropylmalate synthase 2, chloroplastic		Ch/S			metabolism amino acids branched chain	13.1.4.4.1 amino acid metabolism.synthesis.branched chain group.leucine specific.2-isopropylmalate synthase		plastid	plastid	plastid stroma	
AT3G03630	15059	AT3G03630.1	CYSK4 (OAS-TL) Probable cysteine synthase, chloroplastic (CSase) (EC 2.5.1.47) (CS26) (O-acetylserine (thiol)-lyase) (OAS-TL) (O-acetylserine sulfhydrylase), chloroplast precursor /		Ch/S ?			metabolism aa cystein	13.1.5.3.1 amino acid metabolism.synthesis.serine-glycine-cysteine group.cysteine.OASTL		plastid	plastid	plastid	2.0
AT4G39980	15060	AT4G39980.1	AROF (DAHP synthase) Phospho-2-dehydro-3-deoxyheptonate aldolase 1, chloroplast precursor (EC=2.5.1.54) /		??			metabolism aminoacids aromatic	13.1.6.1.1 amino acid metabolism.synthesis.aromatic aa.chorismate.3-deoxy-D-arabino-heptulosonate 7-phosphate synthase	chloroplast	plastid	plastid	plastid	
AT1G22410	15061	AT1G22410.1	DAHPS-like Class-II DAHP synthetase-like protein (Putative phospho-2-dehydro-3-deoxyheptonate aldolase 1), chloroplast precursor /		Ch/Th ?			metabolism aminoacids aromatic	13.1.6.1.1 amino acid metabolism.synthesis.aromatic aa.chorismate.3-deoxy-D-arabino-heptulosonate 7-phosphate synthase		plastid	plastid	plastid	

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AT4G26500	15062	AT4G26500.1	SUFE SufE-like protein		??			unknown	14 S-assimilation	mitochondrion & chloroplast stroma & chloroplast	plastid	plastid	plastid	
AT2G14750	15063	AT2G14750.1	APK1 (AKN1) Adenylyl-sulfate kinase 1, chloroplast precursor (EC=2.7.1.25) /		??			metabolism sulfur	14.15 S-assimilation. AKN	plastid	plastid	plastid	plastid	
AT3G32030	15064	AT3G32030.1	TPS30 Terpenoid synthase 30, terpenoid cyclases/Protein prenyltransferases superfamily protein /		??			metabolism isoprenoids	16.1 secondary metabolism.i soprenoids		plastid	mitochondrion		
AT2G18640	15065	AT2G18640.1	GGPP4 Geranylgeranyl pyrophosphate synthase 4 (GGPP synthase 4) (GGPS4) (EC 2.5.1.-) ((2E,6E)-farnesyl diphosphate synthase 4) (Dimethylallyltransferase 4) (EC 2.5.1.1) (Farnesyl diphosphate synthase 4) (Farnesyltransferase 4) (EC 2.5.1.29) (Ge		na			metabolism isoprenoids non-mevalonate pathway	16.1.1.10 secondary metabolism.i soprenoids.n on-mevalonate pathway.geranylgeranyl pyrophosphate synthase	endoplasmic reticulum		extracellular, endoplasmic reticulum, golgi	ER	

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AT4G19170	15066	AT4G19170.1	CCD4 (NCED4) Probable carotenoid cleavage dioxygenase 4 (AtCCD4) (EC 1.14.99.-), NINE-CIS-EPOXYCAROTENOID DIOXYGENASE 4 (NCED4), chloroplast precursor /		Ch/Th ?			metabolism vitamin and pigment	16.1.4 secondary metabolism.i soprenoids.c arotenoids		plastid	plastid	plastoglobules	
AT5G17790	15067	AT5G17790.1	VAR3 VARIEGATED 3 encodes zinc-finger protein required for chloroplast and palisade cell development , chloroplast precursor /		??			chloroplast biogenesis	16.1.4 secondary metabolism.i soprenoids.c arotenoids	chloroplast stroma & chloroplast	plastid	plastid	plastid	
AT1G10830	15068	AT1G10830.1	Z-ISO (ZCIS) 15-cis-zeta-carotene isomerase, chloroplast precursor (EC 5.2.1.12) /		Ch/Th ?			metabolism vitamin and pigment	16.1.4 secondary metabolism.i soprenoids.c arotenoids		plastid	plastid	plastid	6.0
AT5G17230	15069	AT5G17230.3	PSY1 (PSY) Phytoene synthase, chloroplast precursor (EC 2.5.1.32) /		Ch/Th ?			metabolism vitamin and pigment carotenoids	16.1.4.1 secondary metabolism.i soprenoids.c arotenoids.p hytoene synthase		plastid	plastid	plastid	

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AT2G21860	15070	AT2G21860.1	VDE-like uncharacterized plant protein with low similarity (20% identity/37% similarity) with violaxanthin de-epoxidase, chloroplast precursor /		Ch/Th ?			metabolism vitamin and pigment ?	16.1.4.21 secondary metabolism.i soprenoids.c arotenoids.vi olaxanthin de-epoxidase		plastid	plastid		
AT5G57030	15071	AT5G57030.1	LUT2 Lycopene epsilon cyclase (EC 5.5.1.18), Protein LUTEIN DEFICIENT 2 LUT2, chloroplast precursor /		Ch/Th ?			metabolism vitamin and pigment ?	16.1.4.4 secondary metabolism.i soprenoids.c arotenoids.ly copene epsilon cyclase	chloroplast	plastid	plastid	plastid	2.0
AT2G46570	15072	AT2G46570.1	Lac6 Laccase-6, Benzenediol: oxygen oxidoreductase 6, Contains 3 plastocyanin-like domains (EC=1.10.3.2) /		??			metabolism phenols ?	16.10 secondary metabolism.s imple phenols		plastid	extracellular, endoplasmic reticulum, golgi		
AT5G25980	15073	AT5G25980.2	TGG2 (BGLU37) Myrosinase 2, EC=3.2.1.147 /		na			signaling abscisic	16.5.1 secondary metabolism.s ulfur-containing.glu cosinolates			extracellular, endoplasmic reticulum, golgi	not plastid	
AT5G23010	15074	AT5G23010.1	MAM1 Methylthioalkylmalate synthase 1		??			unknown	16.5.1.1 secondary metabolism.s ulfur-containing.glu cosinolates. methylthioalkylmalate synthase		plastid	plastid	not plastid	

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AT1G64920	15075	AT1G64920.1	UDP-Glycosyltransferase superfamily protein		??			nd	16.8.1 secondary metabolism.flavonoids.antihocyanins					
AT2G42820	15076	AT2G42820.1	HVA22-like protein F/		??			metabolism hormone abscisic acid ?	17.1.1 hormone metabolism. abscisic acid.synthesis-degradation			extracellular, endoplasmic reticulum, golgi		3.0
AT5G56650	15077	AT5G56650.1	ILL1 (ILR1-like 1) IAA-amino acid hydrolase ILR1-like 1 (EC 3.5.1.-)		na			metabolism hormone auxin	17.2.1 hormone metabolism. auxin.synthesis-degradation			extracellular, endoplasmic reticulum, golgi		
AT5G35750	15078	AT5G35750.1	AHK2 Histidine kinase 2 (EC 2.7.13.3) /		na			kinase signaling	17.4.2 hormone metabolism.cytokinin.signaling transduction					4.0
AT5G25900	15079	AT5G25900.1	KO (CYP701A3, GA3, KO1) Ent-kaurene oxidase, in gibberellins (GAs) biosynthesis, GA REQUIRING 3 (GA3) (ChloroP+/TargetP Secreted), chloroplast precursor /		Ch/E/IM ? & THY ?			metabolism hormone gibberellins	17.6.1.3 hormone metabolism. gibberellin.synthesis-degradation. ent-kaurene oxidase	chloroplast outer membrane	plastid	extracellular, endoplasmic reticulum, golgi	envelope-outer	1.0
AT1G75750	15080	AT1G75750.2	GASA1 Gibberellin-regulated protein 1 (GAST1 protein homolog 1)		na			unknown	17.6.3 hormone metabolism. gibberellin.induced-regulated-responsive-activated			extracellular, endoplasmic reticulum, golgi		

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AT1G51560	15081	AT1G51560.1	PNP oxidase-like Pyridoxamine 5'-phosphate oxidase-like protein, chloroplast precursor /		Ch/S ? Or Ch/Th ?			metabolism vitamin and pigment vitamin b6 ?	18.20* Co-factor and vitamine metabolism.v itamin b6		plastid	plastid	plastid stroma	
AT3G21140	15082	AT3G21140.1	PNP oxidase-like Pyridoxamine 5'-phosphate oxidase-like protein, chloroplast precursor /		Ch/S ? Or Ch/Th ?			metabolism vitamin and pigment vitamin b6 ?	18.20* Co-factor and vitamine metabolism.v itamin b6		plastid	plastid	plastid	
AT1G21640	15083	AT1G21640.1	NADK2 NAD kinase 2, CaM binding protein, chloroplast precursor /		Ch/S ?			metabolism NAD	18.21* Co-factor and vitamine metabolism. NAD/NADP		plastid	plastid	plastid stroma	
AT4G35760	15084	AT4G35760.1	LTO1 Lumen Thiol Oxidoreductase 1 with Vitamin K epoxide reductase (VKOR) and Thioredoxin-like fold domains, chloroplast precursor /		Ch/Th ?			metabolism vitamin and pigment	18.5 Co-factor and vitamine metabolism.f olate & vitamine K		plastid	plastid	thylakoid-integral	4.0
AT1G60600	15085	AT1G60600.1	UbiA-like UbiA prenyltransferase family protein /		??			metabolism vitamin and pigment folate & vitamine K	18.5 Co-factor and vitamine metabolism.f olate & vitamine K	chloroplast		mitochondrion	plastid	7.0

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AT1G44446	15086	AT1G44446.3	CAO (CHL, CH1) Chlorophyllide a oxygenase (Chlorophyll a oxygenase) (Chlorophyll b synthase) (AtCAO), chloroplast precursor (EC 1.14.13.122) /		Ch/E ? & Ch/Th ?			metabolism vitamin and pigment chlorophyll	19.16 tetrapyrrole synthesis.chlorophyll b synthase	chloroplast & chloroplast inner membrane & thylakoid membrane	plastid	plastid	envelope-inner; thylakoid	
AT1G58290	15087	AT1G58290.1	HEMA1 (GluTR, HEMA, HEM11) Glutamyl-tRNA reductase 1 (EC 1.2.1.70), Chlorophyll and Porphyrin biosynthesis, Part of the FLU-containing chloroplast membrane complex composed of FLU, CRD1, PORB, PORC, CHLP and HEMA1, chloroplast precursor /		Ch/S ? Or Ch/Th ?			metabolism vitamin and pigment	19.2 tetrapyrrole synthesis.glu-tRNA reductase	chloroplast	plastid	plastid	plastid stroma	
AT3G59400	15088	AT3G59400.1	GUN4 Tetrapyrrole-binding protein (Genomes uncoupled 4), chloroplast precursor /		Ch/Th ?			metabolism vitamin and pigment chlorophyll and signaling plastid-to-nucleus	19.40 tetrapyrrole synthesis.regulation	chloroplast	plastid	plastid	plastid	

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AT4G18240	15089	AT4G18240.1	SS4 (SSY4) Probable starch synthase 4, chloroplast precursor /		Ch/S ?			starch biosynthesis	2.1.2.2 major CHO metabolism.synthesis.star ch.starch synthase			plastid	plastid	
AT3G01510	15090	AT3G01510.1	LSF1 Phosphoglucan phosphatase		Ch/S			metabolism starch	2.2.2.2 major CHO metabolism.degradation.starch.starch phosphorylase		plastid	plastid	plastid stroma	
AT5G47260	15091	AT5G47260.1	DRL38 Belongs to the disease resistance NB-LRR family (ChloroP-TargetPOther) /		Ch/Th ??			stress biotic	20.1 stress.biotic					
AT3G50480	15092	AT3G50480.1	HR4 homolog of RPW8 4, Powdery mildew resistance protein, RPW8 domain /		Ch/Th ??			stress biotic	20.1 stress.biotic				extracellular, endoplasmic reticulum, golgi	
AT4G16890	15093	AT4G16890.1	disease resistance protein (TIR-NBS-LRR class) /		??			nd	20.1.2 stress.biotic.receptors					
AT2G34930	15094	AT2G34930.1	LRR-like disease resistance family protein, LRR family protein /		??			stress ?	20.1.7 stress.biotic.PR-proteins				extracellular, endoplasmic reticulum, golgi	
AT1G63360	15095	AT1G63360.1	Disease resistance protein (CC-NBS-LRR class) family		??			nd	20.1.7 stress.biotic.PR-proteins					
AT1G58410	15096	AT1G58410.1	Disease resistance protein (CC-NBS-LRR class) family		??			nd	20.1.7 stress.biotic.PR-proteins					

Accession	pgID	Master Protein	Description (curated)	Length	Localization (curated)	Calculated Pi PPDB	Calculated MW PPDB	Function (putative)	MapManBin (PPDB)	Localization (TAIR)	ChloroP	TargetP	Curated localization (PPDB)	Aramemnon
AT3G25010	15097	AT3G25010.1	RLP41 Leucine-rich repeat disease resistance protein-like (Receptor like protein 41) (ChloroP-) /		Ch/Th ??			unknown	20.1.7 stress.biotic. PR-proteins			extracellular, endoplasmic reticulum, gol gi		1.0
AT2G29970	15098	AT2G29970.1	Double Clip-N motif-containing P-loop nucleoside triphosphate hydrolases superfamily protein		??			nd	20.2.1 stress.abiotic .heat					
AT1G29395	15099	AT1G29395.1	CRIM1 (COR413IM1, COR413TM1, COR414TM1) COLD REGULATED 314 INNER MEMBRANE 1, chloroplast precursor /		Ch/E/IM			stress cold	20.2.2 stress.abiotic .cold		plastid	plastid	envelope-inner-integral; envelope-inner-integral	6.0
AT4G15430	15100	AT4G15430.2	ERD (early-responsive to dehydration stress) family protein /		??			stress drought ?	20.2.3 stress.abiotic .drought/salt			extracellular, endoplasmic reticulum, gol gi		
AT3G01100	15101	AT3G01100.1	HIP1 conserved plant protein, no similarity to characterized protein, chloroplast precursor /		??			unknown	20.2.3 stress.abiotic .drought/salt		plastid	extracellular, endoplasmic reticulum, gol gi		9.0

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AT2G32920	15102	AT2G32920.1	PDIL2-3 Protein disulfide-isomerase 2-3 (AtPDIL2-3) (EC 5.3.4.1) (Protein disulfide-isomerase 5-2) (AtPDIL5-2) (Protein disulfide-isomerase 9) (PDI9)		na			redox	21.1 redox.thioredoxin		plastid	extracellular, endoplasmic reticulum, golgi		
AT1G52990	15103	AT1G52990.1	TRX-like thioredoxin family protein, Thioesterase-like protein (ChloroP-TargetPSP) /		Ch/Th ??			redox	21.1 redox.thioredoxin			extracellular, endoplasmic reticulum, golgi		
AT3G10130	15104	AT3G10130.1	Heme-binding-like protein At3g10130		Ch/S ?			unknown	21.3 redox.heme	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	plastoglobules	
AT4G28730	15105	AT4G28730.1	GRXC5 Glutaredoxin -C5		??			redox ?	21.4 redox.glutaredoxins		plastid	plastid	plastid	
AT5G23310	15106	AT5G23310.1	FSD3 Superoxide dismutase [Fe] 3, (Protein FE SUPEROXIDE DISMUTASE 3), chloroplast precursor (EC 1.15.1.1) /		Ch/S ? Or Ch/Th ?			stress oxidative	21.6 redox.dismutases and catalases	chloroplast	plastid	plastid	plastid	
AT1G32380	15107	AT1G32380.1	PRS2 (KPRS2) Ribose-phosphate pyrophosphokinase 2, chloroplast precursor (EC=2.7.6.1) /		Ch/S ? Or Ch/Th ?			metabolism nucleotide	23.1.3 nucleotide metabolism. synthesis. PR S-PP		plastid	plastid	plastid	

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AT3G46940	15108	AT3G46940.1	DUT1 Deoxyuridine 5'-triphosphate nucleotidohydrolase (dUTPase) (EC 3.6.1.23) (na			metabolism nucleotide UMP	23.5.5 nucleotide metabolism. deoxynucleotide metabolism. dUTP diphosphatase					
AT5G10610	15109	AT5G10610.1	CYP81K1 Cytochrome P450, family 81, subfamily K, polypeptide 1 /		na			redox	26.10 misc.cytochrome P450			extracellular, endoplasmic reticulum, golgi		2.0
AT3G32047	15110	AT3G32047.1	Cytochrome P450 superfamily protein;		??			nd	26.10 misc.cytochrome P450			extracellular, endoplasmic reticulum, golgi		
AT3G26300	15111	AT3G26300.1	cytochrome P450, family 71, subfamily B, polypeptide 34;putative cytochrome P450		??			nd	26.10 misc.cytochrome P450			extracellular, endoplasmic reticulum, golgi		
AT5G38450	15112	AT5G38450.1	cytochrome P450, family 735, subfamily A, polypeptide 1;member of CYP709A		??			nd	26.10 misc.cytochrome P450			extracellular, endoplasmic reticulum, golgi		
AT4G32320	15113	AT4G32320.1	APX6 Putative L-ascorbate peroxidase 6 (AtAPx08), chloroplast precursor (EC 1.11.1.11) /		Ch/Th ?			stress oxidative or redox	26.12 misc.peroxidases		plastid	plastid		

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AT5G44020	15114	AT5G44020.1	HAD-like HAD superfamily, subfamily IIIB acid phosphatase (Putative vegetative storage protein) /		Ch/Th ?			phosphatase	26.13 misc.acid and other phosphatases		plastid	extracellular, endoplasmic reticulum, golgi	not plastid	
AT3G16390	15115	AT3G16390.1	NSP3 NITRILE SPECIFIER PROTEIN 3 /		Ch/Th ??			stress biotic nitrile formation	26.16 misc.myosinases-lectin-jacalin					
AT3G61760	15116	AT3G61760.1	DRP1B (ADL1B) Dynamin-related protein 1B, GTPase activity /		Ch/Th ??			trafficking	26.17 misc.dynamin					
AT1G10290	15117	AT1G10290.1	DRP2A (ADL6) Dynamin-2A (EC 3.6.5.5) (Dynamin-like protein 6) (Dynamin-related protein 2A) /		na			trafficking	26.17 misc.dynamin	Golgi apparatus			golgi	
AT1G03160	15118	AT1G03160.1	FZL (FZO-like) determinant of thylakoid and chloroplast morphology, dynamin superfamily of membrane-remodeling GTPases, chloroplast precursor /		Ch/Th ?			unknown	26.17 misc.dynamin	chloroplast membrane	plastid	plastid	envelope-inner-integral; thylakoid-integral	
AT1G48010	15119	AT1G48010.1	Plant invertase/pectin methylesterase inhibitor superfamily protei		??			nd	26.18 misc.invertase/pectin methylesterase inhibitor family protein					

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AT4G33330	15120	AT4G33330.2	GUX2 (PGSIP3) Glycogenin-like protein 2, Plant glycogenin-like starch initiation protein 3, UDP-glucuronate: xylan alpha-glucuronosyltransferase 2 (ChloroP+) /		Ch/Th ?			cell wall biogenesis	26.2 misc.UDP glucosyl and glucoronyl transferases		plastid	extracellular, endoplasmic reticulum, golgi		
AT2G31990	15121	AT2G31990.1	HP55 Exostosin family protein with putative glycosyltransferase activity (ChloroP-/TargetPChloro) /		Ch/Th ??			unknown	26.2 misc.UDP glucosyl and glucoronyl transferases			plastid		1.0
AT3G02100	15122	AT3G02100.1	UGT83A1 (U83A1) UDP-glycosyltransferase 83A1 (ChloroP-) /		Ch/Th ??			unknown	26.2 misc.UDP glucosyl and glucoronyl transferases					
AT2G10940	15123	AT2G10940.1	LTP-like Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin-like protein, lipid transfer protein (LTP) family protein /		Ch/Th ??			unknown	26.21 misc.protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	thylakoid membrane (sensu Viridiplantae)		extracellular, endoplasmic reticulum, golgi	plastid	

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AT2G45180	15124	AT2G45180.1	Protease inhibitor/seed storage/lipid transfer protein (LTP) family protein (Putative proline-rich protein)		??			unknown	26.21 misc.protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	thylakoid membrane (sensu Viridiplantae)	plastid	extracellular, endoplasmic reticulum, golgi	not plastid	
AT4G23420	15125	AT4G23420.1	NAD(P)-binding Rossmann-fold superfamily protein /		??			nd	26.22 misc.short chain dehydrogenase/reductase (SDR)					
AT5G10050	15126	AT5G10050.1	NAD(P)-binding Rossmann-fold superfamily protein /		??			nd	26.22 misc.short chain dehydrogenase/reductase (SDR)					
AT3G25480	15127	AT3G25480.1	STR4A Rhodanese-like domain-containing protein 4A (Sulfurtransferase 4A) (AtStr4a), chloroplast precursor /		Ch/Th ?			unknown	26.23 misc.rhodanese	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	thylakoid	1.0
AT3G14210	15128	AT3G14210.1	ESM1 GDSL esterase/lipase ESM1 (EC 3.1.1.-) (Extracellular lipase ESM1) (Protein EPITHIOSPECIFIER MODIFIER 1) (AtESM1)		na			metabolism lipid	26.28 misc.GDSL-motif lipase			extracellular, endoplasmic reticulum, golgi	not plastid	
AT1G28610	15129	AT1G28610.2	GDSL-like Lipase/Acylhydrolase superfamily protein;		??			unknown	26.28 misc.GDSL-motif lipase			extracellular, endoplasmic reticulum, golgi		

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AT5G23240	15130	AT5G23240.1	DjC86 (DNAJ-like) DNAJ (type 3) heat shock family protein, chloroplast precursor /		Ch/Th ?			chaperone and protease	26.29* misc. DnaJ domain with unknown function		plastid	plastid		
AT2G42750	15131	AT2G42750.1	DNAJ-like DNAJ heat shock N-terminal domain-containing protein, chloroplast precursor /		Ch/Th ?			chaperone and protease	26.29* misc. DnaJ domain with unknown function		plastid	plastid		
AT2G26890	15132	AT2G26890.1	GRV2 (GFS2, KAM2) DnaJ homolog subfamily C GRV2 (Protein GRAVITROPISM DEFECTIVE 2) (Protein GREEN FLUORESCENT SEED 2) (Protein KATAMARI2),		na			chaperone and protease	26.29* misc. DnaJ domain with unknown function					
AT2G34860	15133	AT2G34860.1	EDA3 Embryo sac development arrest 3 protein, Heat shock protein DnaJ, chloroplast precursor /		Ch/Th ?			chaperone and protease	26.29* misc. DnaJ domain with unknown function		plastid	plastid	plastid	
AT3G45050	15134	AT3G45050.4	HP16c conserved plant protein, no similarity to characterized protein, chloroplast precursor /		Ch/Th ?			unknown	26.29* misc. DnaJ domain with unknown function		plastid	plastid		

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AT1G75690	15135	AT1G75690.1	LQY1 Protein disulfide-isomerase (EC 5.3.4.1) (Protein LOW QUANTUM YIELD OF PHOTOSYSTEM II 1), chloroplast precursor /		Ch/Th ?			PS PSII ? Or stress light	26.29* misc.DnaJ domain with unknown function	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	plastid	1.0
AT5G61670	15136	AT5G61670.1	Or-like Close homolog of Cauliflower OR (Orange) protein, induce the differentiation of noncolored plastids into chromoplasts for carotenoid accumulation, contain a Cysteine-rich zinc finger domain highly specific to DnaJ-like molecular chaperons, chlor		Ch/Th ?			chaperone and protease	26.29* misc.DnaJ domain with unknown function		plastid	plastid		2.0
AT4G00030	15137	AT4G00030.1	FIB11 (PAP11) Probable plastid-lipid-associated protein 11, chloroplastic (Fibrillin-11)		Ch/Th ?			PAP_fibrillin	26.31* misc.fibrillins		plastid	plastid	thylakoid-peripheral-stromal-side	

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AT3G26080	15138	AT3G26080.1	FIB3b (FBN3b, PAP) fibrillin 3b (FBN3b) fibrillin, plastid-lipid associated protein (PAP), chloroplast precursor /		Ch/Th ?			PAP_fibrillin	26.31* misc.fibrillins		plastid	plastid	thylakoid-peripheral-stromal-side	
AT5G48390	15139	AT5G48390.1	ZIP4-like (TPR-like) Tetratricopeptide repeat (TPR)-like superfamily protein /		Ch/Th ??			RNA Binding ?	26.33* misc.tetratricopeptide repeat (TPR) unknown function					
AT4G31390	15140	AT4G31390.1	ABC1K1 ABC1 kinase 1, Uncharacterized aarF domain-containing protein kinase, chloroplast precursor /		Ch/Th ?			kinase	26.56* misc.ABC1k family		plastid	plastid	plastoglobules	
AT1G71810	15141	AT1G71810.1	ABC1K5 ABC1 kinase 5, uncharacterized aarF domain-containing protein kinase, chloroplast precursor /		Ch/Th ?			kinase	26.56* misc.ABC1k family		plastid	plastid	plastoglobules	
AT3G24190	15142	AT3G24190.1	ABC1K6 ABC1 kinase 6, chloroplast precursor /		Ch/Th ?			kinase	26.56* misc.ABC1k family		plastid	plastid	plastoglobules	
AT5G05200	15143	AT5G05200.1	ABC1K9 ABC1 kinase 9, uncharacterized aarF domain-containing protein kinase /		Ch/Th ?			kinase	26.56* misc.ABC1k family			mitochondrion	plastoglobules	

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AT4G24810	15144	AT4G24810.3	ABC1-like Protein kinase family protein (ChloroP-TargetPOther) /		Ch/Th ??			kinase	26.56* misc.ABC1k family					
AT3G07700	15145	AT3G07700.3	MLP3.15 Protein kinase superfamily protein		Ch/Th ??			kinase	26.56* misc.ABC1k family				plastoglobules	
AT2G35660	15146	AT2G35660.1	CTF2A like oxidoreductase (Putative monooxygenase), FAD/NAD(P)-binding oxidoreductase /		Ch/Th ?			unknown	26.7 misc.oxidases - copper, flavone etc.			mitochondrion		
AT5G37980	15147	AT5G37980.1	Zinc-binding dehydrogenase family protein /		??			nd	26.7 misc.oxidases - copper, flavone etc.					
AT5G05320	15148	AT5G05320.1	FAD/NAD(P)-binding oxidoreductase family protein /		??			unknown	26.7 misc.oxidases - copper, flavone etc.					1.0
AT2G34810	15149	AT2G34810.1	BBE-like FAD-binding Berberine family protein, electron carrier activity, oxidoreductase /		Ch/Th ??			redox ?	26.8 misc.nitrilases, *nitrilases, berberine bridge enzymes, reticuline oxidases, troponine reductases				extracellular, endoplasmic reticulum, golgi	
AT5G44000	15150	AT5G44000.1	GST-like conserved protein, contains glutathione S-transferase C-terminal domain, chloroplast precursor /		Ch/E/IM ? & THY ?			stress oxidative	26.9 misc.glutathione S transferases		plastid	plastid	plastid	

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AT3G17040	15151	AT3G17040.2	HCF107 (TPR-like) Protein high chlorophyll fluorescent 107 required for normal processing of the psbB-psbT-psbH-petB-petD transcript, chloroplast precursor /		Ch/Th ?			PS PSII and b6f biogenesis RNA Binding	27.1 RNA.processing		plastid	plastid	plastid stroma	
AT2G04270	15152	AT2G04270.3	nd		Ch/S			nd	27.1 RNA.processing		plastid	plastid	plastid stroma	
AT5G53770	15153	AT5G53770.1	NTP_transf-like Nucleotidyltransferase family protein (ChloroP-/TargetP-) /		Ch/Th ??			RNA Binding ?	27.1 RNA.processing					
AT3G09650	15154	AT3G09650.1	TPR-like		??			RNA Binding ?	27.1 RNA.processing	chloroplast stroma		plastid	plastid nucleoid	
AT3G18390	15155	AT3G18390.1	CRS1/YhbY-like (EMB1865) CRM domain-containing protein, embryo defective 1865, chloroplast precursor /		Ch/Th ?			RNA Binding ?	27.1.1 RNA.processing.splicing		plastid	plastid	plastid nucleoid	
AT1G11520	15156	AT1G11520.1	HP22c conserved plant protein, low similarity to human Splicing factor 3B subunit 2, Spliceosome-associated protein-like protein (ChloroP-/TargetP-) /		Ch/Th ??			unknown	27.1.1 RNA.processing.splicing			extracellular, endoplasmic reticulum, golgi		

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AT4G37510	15157	AT4G37510.1	RNaseIII-like Ribonuclease III family protein, chloroplast precursor /		Ch/Th ?			RNA Binding	27.1.19 RNA.processing.ribonucleases		plastid	plastid	plastid	
AT3G15000	15158	AT3G15000.1	nd		??			nd	27.1.5* RNA.editing	mitochondrion	plastid	plastid	mitochondria ; plastid	
AT2G02980	15159	AT2G02980.1	PPR-like		??			nd	27.1.5* RNA.editing			plastid	plastid	
AT1G06190	15160	AT1G06190.2	RHON1 ribonucleic acid-binding protein supporting RNase E function, chloroplast precursor /		Ch/Th ?			RNA Binding	27.2 RNA.transcription		plastid	plastid	plastid nucleoid	
AT5G15700	15161	AT5G15700.1	RPOT2 DNA-directed RNA polymerase 2, chloroplastic/mitochondrial precursor (EC 2.7.7.6) /		Ch/Th ?			DNA Binding	27.2 RNA.transcription			plastid	mitochondria ; plastid	
AT5G20220	15162	AT5G20220.1	HP44 zinc knuckle (CCHC-type) family protein (chloroP+/TargetPMito) /		Ch/Th ?			transcription ?	27.3.11 RNA.regulation of transcription. C2H2 zinc finger family			mitochondrion		
AT3G46090	15163	AT3G46090.1	nd		??			nd	27.3.11 RNA.regulation of transcription. C2H2 zinc finger family					
AT1G11490	15164	AT1G11490.1	nd		??			nd	27.3.11 RNA.regulation of transcription. C2H2 zinc finger family			mitochondrion		

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AT1G10480	15165	AT1G10480.1	ZP5 (ZFP5) Zinc finger protein 5, chloroplast precursor /		Ch/Th ?			signaling gibberellic acid pathway	27.3.11 RNA.regulation of transcription. C2H2 zinc finger family		plastid	plastid		
AT5G17490	15166	AT5G17490.1	nd		na			nd	27.3.21 RNA.regulation of transcription. GRAS transcription factor family	nucleus				
AT3G13840	15167	AT3G13840.1	SCL29 Scarecrow-like protein 29 (AtSCL29) (GRAS family protein 16) (AtGRAS-16)		??			unknown	27.3.21 RNA.regulation of transcription. GRAS transcription factor family					
AT4G00730	15168	AT4G00730.1	ANL2 Homeobox-leucine zipper protein ANTHOCYANINLESS 2 (HD-ZIP protein ANL2) (Homeodomain protein AHDP) /		Ch/Th ?			transcription	27.3.22 RNA.regulation of transcription. HB,Homeobox transcription factor family		plastid			
AT1G28420	15169	AT1G28420.1	unknown		??			unknown	27.3.22 RNA.regulation of transcription. HB,Homeobox transcription factor family					
AT3G05380	15170	AT3G05380.1	nd		??			nd	27.3.25 RNA.regulation of transcription. MYB domain transcription factor family					

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AT5G10280	15171	AT5G10280.1	nd		??			nd	27.3.25 RNA.regulation of transcription. MYB domain transcription factor family					
AT4G09450	15172	AT4G09450.1	HP23c Duplicated homeodomain-like superfamily protein (ChloroP-TargetPOther) /		Ch/Th ??			DNA Binding ?	27.3.26 RNA.regulation of transcription. MYB-related transcription factor family					
AT3G11280	15173	AT3G11280.1	nd		??			nd	27.3.26 RNA.regulation of transcription. MYB-related transcription factor family					
AT3G56390	15174	AT3G56390.1	nd		??			unknown	27.3.32 RNA.regulation of transcription. WRKY domain transcription factor family					
AT1G48410	15175	AT1G48410.2	nd		??			nd	27.3.36 RNA.regulation of transcription. Argonaute	cytoplasm			cytosol	
AT1G48310	15176	AT1G48310.1	CHR18 Chromatin remodeling factor18 /		Ch/Th ??			RNA transcription ?	27.3.44 RNA.regulation of transcription. Chromatin Remodeling Factors					
AT2G40770	15177	AT2G40770.1	nd		??			nd	27.3.44 RNA.regulation of transcription. Chromatin Remodeling Factors			mitochondrion		

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AT5G09380	15178	AT5G09380.1	nd		??			nd	27.3.50 RNA.regulation of transcription. General Transcription					
AT4G38070	15179	AT4G38070.1	BH131 (bHLH131) Transcription factor bHLH131, Basic helix-loop-helix protein 131 /		Ch/Th ??			transcription	27.3.6 RNA.regulation of transcription. bHLH,Basic Helix-Loop-Helix family	mitochondrion				
AT2G14760	15180	AT2G14760.1	nd		??			nd	27.3.6 RNA.regulation of transcription. bHLH,Basic Helix-Loop-Helix family					
AT4G36540	15181	AT4G36540.1	nd		??			nd	27.3.6 RNA.regulation of transcription. bHLH,Basic Helix-Loop-Helix family					
AT5G08630	15182	AT5G08630.1	nd		??			nd	27.3.62 RNA.regulation of transcription. Nucleosome/chromatin assembly factor group					
AT4G14920	15183	AT4G14920.1	RING-like Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger protein, chloroplast precursor /		Ch/Th ?			RNA Binding ?	27.3.63 RNA.regulation of transcription. PHD finger transcription factor			plastid		2.0

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AT1G10200	15184	AT1G10200.1	Putative transcription factor (Similar to transcription factor SF3 (Pir S37656)) (Transcription factor lim1)		??			unknown	27.3.67 RNA.regulation of transcription. putative transcription regulator					
AT4G17950	15185	AT4G17950.1	nd		??			nd	27.3.67 RNA.regulation of transcription. putative transcription regulator		plastid	mitochondrion		
AT1G13790	15186	AT1G13790.1	nd		??			nd	27.3.67 RNA.regulation of transcription. putative transcription regulator					
AT1G56110	15187	AT1G56110.1	NOP56-like Homolog of nucleolar protein NOP56 (Nucleolar protein) (SAR DNA binding protein, putative) /		na			DNA Binding ?	27.3.67 RNA.regulation of transcription. putative transcription regulator	nucleolus			nucleus	
AT3G07670	15188	AT3G07670.1	MLP3.12 Putative ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit N-methyltransferase I (ChloroP+) /		Ch/Th ?			protein modification PS RBCS	27.3.69 RNA.regulation of transcription. SET-domain transcriptional regulator family		plastid	mitochondrion		

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AT2G18850	15189	AT2G18850.1	SET domain-containing protein		??			unknown	27.3.69 RNA.regulation of transcription. SET-domain transcriptional regulator family					
AT5G24330	15190	AT5G24330.1	nd		na			nd	27.3.69 RNA.regulation of transcription. SET-domain transcriptional regulator family	nucleus		mitochondrion	nucleus	
AT5G07350	15191	AT5G07350.1	nd		??			nd	27.3.73 RNA.regulation of transcription. Zn-finger(CCHC)			mitochondrion	not plastid	
AT1G64620	15192	AT1G64620.1	nd		??			nd	27.3.8 RNA.regulation of transcription. C2C2(Zn) DOF zinc finger family					
AT1G62150	15193	AT1G62150.1	HP52d Mitochondrial transcription termination factor family protein (chloroP+/TargetPMito) /		Ch/Th ??			transcription ?	27.3.99 RNA.regulation of transcription. unclassified		plastid	mitochondrion	mitochondria	
AT5G07900	15194	AT5G07900.1	nd		??			nd	27.3.99 RNA.regulation of transcription. unclassified		plastid	plastid	mitochondria	
AT2G37670	15195	AT2G37670.1	nd		??			nd	27.3.99 RNA.regulation of transcription. unclassified					

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AT5G54180	15196	AT5G54180.1	PTAC15 plastid transcriptionally active 15, mitochondria transcription termination factor (mTERF) family, chloroplast precursor /		Ch/S ?			transcription ?	27.3.99 RNA.regulation of transcription. unclassified	plastid chromosome	plastid	plastid	plastid nucleoid	
AT4G39040	15197	AT4G39040.1	CRS1/YhbY-like CRM domain-containing protein, chloroplast precursor /		Ch/Th ?			RNA Binding ?	27.4 RNA.RNA binding		plastid	plastid	plastid stroma	
AT3G10845	15198	AT3G10845.1	RNA-binding (RRM/RBD/RNP motifs) family protein		??			RNA binding ?	27.4 RNA.RNA binding					
AT4G01037	15199	AT4G01037.1	nd		Ch/S			nd	27.4 RNA.RNA binding		plastid	plastid	plastid stroma	
AT5G08610	15200	AT5G08610.1	nd		??			RNA Binding ?	27.6* RNA.DEAD BOX helicase			plastid	plastid nucleoid	
AT4G34830	15201	AT4G34830.1	MRL1 (PP349, PPR-like) conserved pentatricopeptide repeat protein, required for stabilization of rbcL mRNA, chloroplast precursor /		Ch/Th			RNA binding RBCL transcript	27.7* RNA.misc.pentatricopeptide (PPR) repeat-containing protein		plastid	plastid	plastid	1.0

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AT3G04760	15202	AT3G04760.1	PP213 (PPR-like) Pentatricopeptide repeat-containing protein, chloroplast precursor /		Ch/Th ?			RNA Binding ?	27.7* RNA.misc.pentatricopeptide (PPR) repeat-containing protein		plastid	plastid	plastid nucleoid	
AT3G29230	15203	AT3G29230.1	PP261 (PCMP-E27) Pentatricopeptide repeat-containing protein of the PCMP-E subfamily (ChloroP-TargetPMito) /		Ch/Th ??			RNA Binding ?	27.7* RNA.misc.pentatricopeptide (PPR) repeat-containing protein			mitochondrion		
AT3G53700	15204	AT3G53700.1	PP281 (MEE40, PPR-like) Pentatricopeptide repeat-containing protein (Protein MATERNAL EFFECT EMBRYO ARREST 40), chloroplast precursor /		Ch/Th ?			RNA Binding ?	27.7* RNA.misc.pentatricopeptide (PPR) repeat-containing protein		plastid	plastid	plastid	
AT5G04810	15205	AT5G04810.1	PP365 (PPR4, PPR-like) Pentatricopeptide repeat-containing protein (Maize PPR4 homolog), chloroplast precursor /		Ch/Th ?			RNA Binding ?	27.7* RNA.misc.pentatricopeptide (PPR) repeat-containing protein		plastid	plastid	plastid	
AT5G14080	15206	AT5G14080.1	PP380 (TPR-like) Tetratricopeptide repeat (TPR)-like superfamily protein /		Ch/Th ??			RNA Binding ?	27.7* RNA.misc.pentatricopeptide (PPR) repeat-containing protein			mitochondrion		

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AT5G42310	15207	AT5G42310.1	PPR-like		??			RNA Binding ?	27.7* RNA.misc.pe ntaticopeptide (PPR) repeat-containing protein		plastid	mitochondrion	plastid	
AT5G04130	15208	AT5G04130.1	GYRB2 DNA gyrase B2 (EC 5.99.1.3), chloroplast and mitochondria precursor /		Ch/Th ?			DNA Binding	28.1 DNA.synthesis/chromatin structure	mitochondrion		mitochondrion	mitochondria ; plastid nucleoid	
AT3G47490	15209	AT3G47490.1	Putative endonuclease (HNH endonuclease domain-containing protein) /		??			DNA binding ?	28.1 DNA.synthesis/chromatin structure				plastid	
AT5G67100	15210	AT5G67100.1	POLA DNA polymerase alpha catalytic subunit (EC 2.7.7.7) /		Ch/Th ??			DNA Binding	28.1 DNA.synthesis/chromatin structure					
AT1G60930	15211	AT1G60930.1	RQL4B (RECQL4B, RECQ4B) ATP-dependent DNA helicase Q-like 4B (EC 3.6.4.12) (RecQ-like protein 4B) (ChloroP-/TargetPChloro) /		Ch/Th ?			DNA Binding	28.1 DNA.synthesis/chromatin structure			plastid		2.0

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AT1G03750	15212	AT1G03750.1	SWI2 (SWITCH 2, CHR9, SNF2) DNA-binding protein with helicase activity, CHROMATIN REMODELING 9 (CHR9), SUCROSE NON-FERMENTING 2 (SNF2), SWI2, switch 2, chloroplast precursor /		Ch/Th ?			DNA Binding ?	28.1 DNA.synthesis/chromatin structure		plastid	plastid		
AT1G08880	15213	AT1G08880.1	H2AXA Probable histone H2AXa (HTA5)		na			DNA binding	28.1.3 DNA.synthesis/chromatin structure.hist one		plastid	plastid		
AT3G53650	15214	AT3G53650.1	H2B8 Histone H2B.8 (HTB6)		na			DNA binding	28.1.3 DNA.synthesis/chromatin structure.hist one					
AT1G07820	15215	AT1G07820.2	H4 Histone HA /		na			DNA synthesis/chromatin structure	28.1.3 DNA.synthesis/chromatin structure.hist one				nucleus	
AT4G31210	15216	AT4G31210.1	nd		??			nd	28.1.5* DNA.synthesis/chromatin structure.synthesis		plastid	plastid	plastid	
AT2G34640	15217	AT2G34640.1	PTAC12 Plastid transcriptionally active 12 (PTAC12)		Ch/Th ?			DNA Binding ?	28.3* DNA.plastid nucleoid interacting	plastid chromosome		plastid	nucleus; plastid nucleoid	

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AT3G09210	15218	AT3G09210.1	PTAC13 plastid transcriptionally active 13, Transcription termination factor nusG family, chloroplast precursor /		Ch/Th ?			DNA Binding ?	28.3* DNA.plastid nucleoid interacting	plastid chromosome		mitochondrion	plastid nucleoid	
AT4G20130	15219	AT4G20130.1	PTAC14 Plastid transcriptionally active 14 (PTAC14), chloroplast precursor /		Ch/Th ?			DNA Binding ?	28.3* DNA.plastid nucleoid interacting	plastid chromosome	plastid	plastid	plastid nucleoid	
AT1G21600	15220	AT1G21600.2	PTAC6 plastid transcriptionally active 6, involved in plastid gene expression, chloroplast precursor /		Ch/Th ?			DNA Binding ?	28.3* DNA.plastid nucleoid interacting	plastid chromosome	plastid	plastid	plastid nucleoid	
AT3G26580	15221	AT3G26580.1	TPR-like Tetratricopeptide repeat (TPR)-like superfamily protein, chloroplast precursor (ChloroP-/TargetPC) /		Ch/Th ?			RNA Binding ?	28.3* DNA.plastid nucleoid interacting	thylakoid membrane (sensu Viridiplantae)		plastid	plastid stroma; thylakoid	1.0
AT1G06670	15222	AT1G06670.1	NIH Nuclear DEIH-boxhelicase (ChloroP-/TargetPOther) /		na			DNA Binding ?	28.99 DNA.unspecified	nucleus				
AT5G07710	15223	AT5G07710.1	RNAse-like Polynucleotidyl transferase, ribonuclease H-like superfamily protein (ChloroP-/TargetPOther) /		Ch/Th ??			RNA Binding ?	28.99 DNA.unspecified					

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AT2G06500	15224	AT2G06500.1	transposase-like Ac-like transposase, HAT dimerisation domain-containing protein (ChloroP-/TargetPOther) /		Ch/Th ??			DNA Binding ?	28.99 DNA.unspecified					
AT5G27470	15225	AT5G27470.1	SYS (SerRS) Serine--tRNA ligase (EC 6.1.1.11) (Seryl-tRNA synthetase) (SerRS) (Seryl-tRNA(Ser/Sec) synthetase), cytosol ? /		na			protein modification	29.1.11 protein.aa activation.serine-tRNA ligase				not plastid	
ATCG01230	15226	ATCG01230.1	RPS12B 30S ribosomal protein S15, chloroplast encoded /		Ch/Th ? & Ch/S ?			translation stroma	29.2.1.1.1.1 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.30S subunit	plastid small ribosomal subunit		plastid	plastid ribosome	
ATCG01240	15227	ATCG01240.1	RPS7-2 30S ribosomal protein S7-2, chloroplast encoded /		Ch/Th ? & Ch/S ?			translation stroma	29.2.1.1.1.1 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.30S subunit	plastid small ribosomal subunit			plastid ribosome	
ATCG01020	15228	ATCG01020.1	RPL32 50S ribosomal protein L32, chloroplast encoded /		Ch/Th ? & Ch/S ?			translation stroma	29.2.1.1.1.2 protein.synthesis.ribosomal protein.prokaryotic.chloroplast.50S subunit	plastid large ribosomal subunit			plastid ribosome	

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AT3G27850	15229	AT3G27850.1	RPL12-C 50S ribosomal protein L11, chloroplast precursor /		Ch/Th ? & Ch/S ?			translation stroma	29.2.1.1.1.2.12 protein.synthesis.ribosomal.prokaryotic.chloroplast.50S subunit.L12	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	plastid ribosome	
AT1G71720	15230	AT1G71720.1	RPS1-like (PDE338) Ribosomal protein S1-like RNA-binding domain-containing protein, PIGMENT DEFECTIVE 338, chloroplast precursor /		Ch/Th ? & Ch/S ?			translation stroma ?	29.2.1.1.3.1.1 protein.synthesis.ribosomal.prokaryotic.unknown organellar.30S subunit.S1		plastid	plastid	plastid nucleoid	
AT1G72370	15231	AT1G72370.2	40S ribosomal protein Sa-1, laminin receptor homolog, cytosol /		na			translation cytosol	29.2.1.2.1.31 protein.synthesis.ribosomal.protein.eukaryotic.40S subunit.SA	small ribosomal subunit & cytosolic ribosome (sensu Eukaryota) & nucleus & cytoplasm			cytosol	
AT1G06380	15232	AT1G06380.1	RPL10a-like Weakly similar to eukaryotic 60S ribosomal subunit L1/L10e /		Ch/Th ? & Ch/S ?			translation stroma ?	29.2.1.2.2.1 protein.synthesis.ribosomal.protein.eukaryotic.60S subunit.L1			plastid	plastid stroma	
AT3G53430	15233	AT3G53430.1	RPL12B (ABIP11, RL122) 60S ribosomal protein L12-2, cytosol /		na			translation cytosol	29.2.1.2.2.12 protein.synthesis.ribosomal.protein.eukaryotic.60S subunit.L12				cytosol	
AT2G18720	15234	AT2G18720.1	nd		??			translation	29.2.3 protein.synthesis.initiation					

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AT3G13920	15235	AT3G13920.3	IF4A1 Eukaryotic initiation factor 4A-1 (eIF-4A-1) (EC 3.6.4.13) (ATP-dependent RNA helicase eIF4A-1) (DEAD-box ATP-dependent RNA helicase 4)		na			translation cytosol	29.2.3 protein.synthesis.initiation ; 27.6* RNA.DEAD BOX helicase				not plastid	
AT1G07940	15236	AT1G07940.2	eEF-1A1 (EF-1-alpha 1) Elongation factor 1-alpha 1 (EF-1-alpha 1) (eEF-1A1), Cytosol /		na			translation cytosol	29.2.4 protein.synthesis.elongation	mitochondrion				
AT5G66470	15237	AT5G66470.1	ERA-like GTP-binding protein Era, bacterial ERA was shown to specifically bind to 16S rRNA and the 30S ribosomal subunit, chloroplast precursor /		Ch/Th ? & Ch/S ?			translation stroma ?	29.2.7* protein.synthesis.ribosome biogenesis		plastid	plastid	plastid	
AT2G19870	15238	AT2G19870.1	nd		??			unknown	29.2.7* protein.synthesis.ribosome biogenesis		plastid	mitochondrion	plastid nucleoid	
AT1G71480	15239	AT1G71480.1	NTF2-like Nuclear transport factor 2 like protein, chloroplast precursor /		Ch/Th ?			transporter ?	29.3.1 protein.targeting.nucleus	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	plastid	

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AT3G16480	15240	AT3G16480.1	MPPA2 Probable mitochondrial-processing peptidase subunit alpha-2 (EC 3.4.24.64) (Alpha-MPP2) (ChloroP+) /		Ch/Th ??			chaperone and protease	29.3.2 protein.targeting.mitochondria	mitochondria l outer membrane & mitochondria n & mitochondria l inner membrane & mitochondria l matrix & mitochondria l intermembrane space	plastid	mitochondrion		
AT5G12130	15241	AT5G12130.1	PDE149 Protein pigment defective 149, Integral membrane protein TerC family, chloroplast precursor /		Ch/Th ?			unknown	29.3.3 protein.targeting.chloroplast		plastid	plastid	thylakoid-integral	8.0
AT4G14870	15242	AT4G14870.1	SECE1 Preprotein translocase subunit SECE1, interacts with SCY1 and ALB3, chloroplast precursor /		Ch/Th			protein targeting thylakoid	29.3.3 protein.targeting.chloroplast	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	thylakoid-integral	1.0
AT2G01110	15243	AT2G01110.1	TATC Chloroplast Protein Translocation (tatC), Sec-independent protein translocase, chloroplast precursor /		Ch/Th			protein targeting Tic	29.3.3 protein.targeting.chloroplast		plastid	plastid	thylakoid-integral	6.0
AT4G24840	15244	AT4G24840.1	Uncharacterized protein		na			unknown	29.3.4.2 protein.targeting.secretory.pathway.golgi		plastid			

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AT4G32640	15245	AT4G32640.2	SC24B Protein transport protein Sec24-like, chloroplast precursor /		??			protein transport ?	29.3.4.2 protein.targeting.secretory.pathway.golgi		plastid	plastid		
AT2G32850	15246	AT2G32850.2	Kinase-like Putative serine/threonine protein kinase (ChloroP-/TargetPOther) /		Ch/Th ??			kinase	29.4 protein.postranslational modification					
AT2G34290	15247	AT2G34290.1	Kinase-like Putative serine/threonine protein kinase (ChloroP-/TargetPOther) /		??			kinase	29.4 protein.postranslational modification					
AT5G46570	15248	AT5G46570.1	nd		na			nd	29.4 protein.postranslational modification					
AT3G63340	15249	AT3G63340.1	Protein phosphatase 2C family protein;		??			phosphatase	29.4 protein.postranslational modification				extracellular, endoplasmic reticulum, golgi	
AT5G20930	15250	AT5G20930.1	TOUSLED (TSL) Serine/threonine-protein kinase TOUSLED (EC 2.7.11.1), contains nuclear localization signal (NLS) but is also ChloroP+/TargetPChloro /		Ch/Th ?			kinase	29.4 protein.postranslational modification	nucleus & cytoplasm	plastid	plastid		

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AT4G11890	15251	AT4G11890.2	Kinase-like Putative serine/threonine protein kinase (ChloroP-/TargetPOther) /		??			kinase	29.4.1 protein.postranslational modification. kinase; 30.2.17 signalling.receptor kinases.DUF26					
AT3G07070	15252	AT3G07070.1	PBS1-like Serine/threonine-protein kinase (EC 2.7.11.1) /		Ch/Th ??			kinase	29.4.1.57 protein.postranslational modification. kinase.receptor like cytoplasmatic kinase VII					
AT4G33500	15253	AT4G33500.1	PP2C62 Probable protein phosphatase 2C62 (AtPP2C62) (EC 3.1.3.16)		??			phosphatase	29.4.5 protein.postranslational modification. phosphatase		plastid	plastid	plastid	
AT1G14270	15254	AT1G14270.4	CAAX-like CAAX amino terminal protease family protein, chloroplast precursor (AT1G14270.1 is ChloroP+) /		Ch/Th ?			chaperone and protease	29.5 protein.degradation					
AT3G02090	15255	AT3G02090.2	MPPB Probable mitochondrial-processing peptidase subunit beta (EC 3.4.24.64) (Beta-MPP) (ChloroP+) /		Ch/Th ??			chaperone and protease	29.5 protein.degradation	mitochondria outer membrane & mitochondrion & mitochondria inner membrane & mitochondria matrix & mitochondria intermembrane space	plastid	mitochondrion	mitochondria	

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AT1G06900	15256	AT1G06900.1	Insulinase (Peptidase family M16) family protein		??			protein degradation proteasome ?	29.5 protein.degradation					
AT2G47110	15257	AT2G47110.2	nd		na			nd	29.5.11 protein.degradation.ubiquitin					
AT5G64760	15258	AT5G64760.2	regulatory particle non-ATPase subunit 5B		??			protein degradation proteasome ?	29.5.11.20 protein.degradation.ubiquitin.proteasom	nucleus			cytosol	
AT4G31300	15259	AT4G31300.1	PSB6 (PBA1) Proteasome subunit beta type-6 (EC 3.4.25.1) (20S proteasome beta subunit A-1) (Proteasome component D) (Proteasome subunit beta type-1)		na			protein degradation proteasome ?	29.5.11.20 protein.degradation.ubiquitin.proteasom	proteasome core complex (sensu Eukaryota)			cytosol	
AT1G22500	15260	AT1G22500.1	RING/U-box superfamily protein;		??			protein degradation ubiquitin E3	29.5.11.4.2 protein.degradation.ubiquitin.E3.RING			extracellular, endoplasmic reticulum, golgi		1.0
AT5G40140	15261	AT5G40140.1	PUB40 U-box domain-containing protein 40, E3 ubiquitin ligase ?, chloroplast precursor /		??			protein degradation ubiquitin E3	29.5.11.4.2 protein.degradation.ubiquitin.E3.RING		plastid	plastid		
AT5G60250	15262	AT5G60250.1	RING-like C3H4 type zinc finger protein /		Ch/Th ??			protein degradation ubiquitin E3	29.5.11.4.2 protein.degradation.ubiquitin.E3.RING					
AT1G78100	15263	AT1G78100.1	AUF1 auxin up-regulated F-BOX protein 1 /		Ch/Th ??			protein degradation ubiquitin E3	29.5.11.4.3.2 protein.degradation.ubiquitin.E3.SCF.FBOX					

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AT4G39590	15264	AT4G39590.1	F-Box-like F-box/kelch-repeat superfamily protein /		??			protein degradation ubiquitin E3	29.5.11.4.3.2 protein.degradation.ubiquitin.E3.SCF.FBOX		plastid	plastid		
AT5G57360	15265	AT5G57360.1	nd		na			nd	29.5.11.4.3.2 protein.degradation.ubiquitin.E3.SCF.FBOX	cytosol & nucleus				
AT3G59250	15266	AT3G59250.1	F-box/RNI-like superfamily protein;		??			protein degradation ubiquitin E3	29.5.11.4.3.2 protein.degradation.ubiquitin.E3.SCF.FBOX					
AT5G03100	15267	AT5G03100.1	F-box/RNI-like superfamily protein;		??			protein degradation ubiquitin E3	29.5.11.4.3.2 protein.degradation.ubiquitin.E3.SCF.FBOX					
AT2G24540	15268	AT2G24540.1	Galactose oxidase/kelch repeat superfamily protein		??			protein degradation ubiquitin E3	29.5.11.4.3.2 protein.degradation.ubiquitin.E3.SCF.FBOX					
AT5G05560	15269	AT5G05560.1	APC1 (EMB2771) Anaphase-promoting complex subunit 1 (Cyclosome subunit 1) (Protein EMBRYO DEFECTIVE 2771) /		Ch/Th ??			protein degradation ubiquitin E3	29.5.11.4.4 protein.degradation.ubiquitin.E3.APC	ubiquitin ligase complex & cytoplasm				4.0
AT1G65630	15270	AT1G65630.1	DEGP3 Putative protease Do-like 3, mitochondria I (EC 3.4.21.-) (ChloroP+/TargetPMito) /		Ch/Th ??			chaperone and protease	29.5.5 protein.degradation.serine protease		plastid	mitochondrion		

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AT2G18080	15271	AT2G18080.1	EDA2 EMBRYO SAC DEVELOPMENT ARREST 2, Probable serine protease EDA2, chloroplast precursor (ChloroP+/TargetPS) /		Ch/Th ?			chaperone and protease	29.5.5 protein.degradation.serine protease		plastid	extracellular, endoplasmic reticulum, golgi		
AT2G32480	15272	AT2G32480.1	ARASP Arabidopsis Serin protease (ARASP), membrane zinc metalloprotease (M50), chloroplast precursor /		Ch/Th ?			chaperone and protease	29.5.7 protein.degradation.metall oprotease		plastid	plastid	envelope-inner	4.0
AT5G35220	15273	AT5G35220.1	EGY1 thylakoid ATP-independent metalloprotease required for chloroplast development , Ethylene-dependent Gravitropism -deficient and Yellow-green 1 (EGY1), chloroplast precursor /		Ch/Th			chaperone and protease	29.5.7 protein.degradation.metall oprotease	chloroplast		plastid	thylakoid-integral	8.0

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AT1G20810	15274	AT1G20810.1	FKBP18 (PP1ase, Rotamase) Peptidyl-prolyl cis-trans isomerase FKBP18 (PP1ase FKBP18) (EC 5.2.1.8) (FK506-binding protein 18) (AtFKBP18) (Immunophilin FKBP18) (Rotamase), chloroplast precursor /		Ch/Th ?			chaperone and protease	29.6 protein.foldin g	thylakoid lumen (sensu Viridiplantae)	plastid	plastid	thylakoid-peripheral-lumenal-side	1.0
AT3G60370	15275	AT3G60370.1	FKBP20-2 Peptidyl-prolyl cis-trans isomerase FKBP20-2		Ch/Th			chaperone and protease	29.6 protein.foldin g	thylakoid lumen (sensu Viridiplantae)	plastid	plastid	thylakoid-peripheral-lumenal-side	
AT1G24490	15276	AT1G24490.1	ALB4 almost identical to the Alb3/Oxa1/YidC domain of the 110 kDa inner envelope protein ARTEMIS, ALB4 is expressed as a separate 55 kDa protein and is located in the thylakoid membrane, chloroplast precursor /.		Ch/Th			chloroplast biogenesis	29.8 protein assembly and cofactor ligation	thylakoid membrane (sensu Viridiplantae) & chloroplast inner membrane	plastid	plastid	thylakoid-integral	5.0

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AT1G59840	15277	AT1G59840.2	CCB4 Cofactor assembly of complex C (CCB4), cytochrome b6 heme biogenesis, chloroplast precursor /		Ch/Th			chaperone and protease PS b6f	29.8 protein assembly and cofactor ligation			mitochondrion	plastid	
AT5G54290	15278	AT5G54290.2	CCDA Cytochrome c-type biogenesis ccda-like chloroplastic protein, Cytochrome b6f biogenesis protein CCDA, chloroplast precursor /		Ch/Th			PS b6f biogenesis	29.8 protein assembly and cofactor ligation			mitochondrion	thylakoid-integral	
AT5G52110	15279	AT5G52110.2	HCF208 HIGH CHLOROPHYLL FLUORESCENCE 208, conserved plant protein, no similarity to characterized proteins, chloroplast precursor /		Ch/Th ?			unknown	29.8 protein assembly and cofactor ligation		plastid	plastid	plastid	
ATCG01280	15280	ATCG01280.1	nd		??			nd	29.8 protein assembly and cofactor ligation	chloroplast			envelope-inner-peripheral-stromal-side	
ATCG00360	15281	ATCG00360.1	YCF3 Tetratricopeptide repeat (TPR)-like superfamily protein, PSI assembly TPR, chloroplast encoded /		Ch/Th			chaperone and protease	29.8 protein assembly and cofactor ligation	chloroplast			thylakoid-peripheral-stromal-side	

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AT5G46390	15282	AT5G46390.2	S41-like protein of the Peptidase S41 family, chloroplast precursor /		Ch/Th ?			chaperone and protease	29.9* protein.proce ssing	thylakoid lumen (sensu Viridiplantae)	plastid	plastid	thylakoid-peripheral-lumenal-side	
AT5G13000	15283	AT5G13000.1	CALS3 Callose synthase 3 (EC 2.4.1.34)		na			unknown	3.6 minor CHO metabolism.c allose			mitochondrion		10.0
AT2G13680	15284	AT2G13680.1	nd		??			nd	3.6 minor CHO metabolism.c allose			plastid		14.0
AT3G07160	15285	AT3G07160.1	nd		na			nd	3.6 minor CHO metabolism.c allose			mitochondrion	plasma membrane	16.0
AT2G13440	15286	AT2G13440.1	GIDA-like Glucose-inhibited division family A protein, similar to tRNA modification enzymes found in bacteria and mitochondria , chloroplast precursor /		Ch/Th ?			translation stroma ?	30.1.1 signalling.in sugar and nutrient physiology		plastid	plastid		
AT2G24710	15287	AT2G24710.1	GLR2.3 glutamate receptor 2.3;member of Putative ligand-gated ion channel subunit family		??			transporter ?	30.1.1 signalling.in sugar and nutrient physiology			extracellular, endoplasmic reticulum,gol gi		3.0

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AT3G26740	15288	AT3G26740.1	CCL Cytokinin-repressed protein ccr-like protein, light regulated Lir1 protein family, chloroplast precursor /		Ch/Th ?			signalling ?	30.11 signalling.lig ht		plastid	plastid	plastid	
AT2G30520	15289	AT2G30520.2	Phototropic-responsive NPH3 family protein;light inducible root phototropism 2 encoding a signal transducer of the phototropic response in Arabidopsis		??			nd	30.11 signalling.lig ht					
AT5G35840	15290	AT5G35840.1	phytochrome C, one of a family of photoreceptors that modulate plant growth and development /		??			nd	30.11 signalling.lig ht			mitochondrion		
AT1G27190	15291	AT1G27190.1	LRR-RLK Leucine-rich repeat receptor-like protein kinase (ChloroP-TargetPS) /		na			kinase	30.2.10 signalling.receptor kinases.leucine rich repeat X			extracellular, endoplasmic reticulum, golgi		1.0
AT4G28490	15292	AT4G28490.1	nd		na			nd	30.2.11 signalling.receptor kinases.leucine rich repeat XI			extracellular, endoplasmic reticulum, golgi		1.0

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AT1G08590	15293	AT1G08590.1	PXL1 Leucine-rich repeat receptor-like protein kinase PXL1 (Protein PHLOEM INTERCALATED WITH XYLEM-LIKE 1) (EC 2.7.11.1) /		Ch/Th ??			kinase	30.2.11 signalling.receptor kinases.leucine rich repeat XI			extracellular, endoplasmic reticulum, golgi		1.0
AT5G39020	15294	AT5G39020.1	nd		na			nd	30.2.16 signalling.receptor kinases.Catharanthus roseus-like RLK1			extracellular, endoplasmic reticulum, golgi		1.0
AT4G23310	15295	AT4G23310.1	CRK23 Putative cysteine-rich receptor-like protein kinase 23 (Cysteine-rich RLK23) (EC 2.7.11.-) (ChloroP+/TargetPSP) /		Ch/Th ?			kinase signaling	30.2.17 signalling.receptor kinases.DUF26		plastid	extracellular, endoplasmic reticulum, golgi		1.0
AT3G45860	15296	AT3G45860.1	CRK23 Putative cysteine-rich receptor-like protein kinase 4 (Cysteine-rich RLK4) (EC 2.7.11.-) (ChloroP+/TargetPSP) /		??			kinase signaling	30.2.17 signalling.receptor kinases.DUF26		plastid	extracellular, endoplasmic reticulum, golgi		1.0
AT5G56890	15297	AT5G56890.1	nd		na			kinase	30.2.18 signalling.receptor kinases.extensionsin		plastid	extracellular, endoplasmic reticulum, golgi		1.0
AT2G01210	15298	AT2G01210.1	nd		??			nd	30.2.3 signalling.receptor kinases.leucine rich repeat III	cell wall (sensu Magnoliophyta)		extracellular, endoplasmic reticulum, golgi	plasma membrane	1.0

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AT1G53430	15299	AT1G53430.1	LRR-RLK-like Probable LRR receptor-like serine/threonine-protein kinase EC=2.7.11.1 /		na			kinase	30.2.8.2 signalling.recptor kinases.leucine rich repeat VIII-2			extracellular, endoplasmic reticulum, golgi		1.0
AT3G05990	15300	AT3G05990.1	LRR-like Leucine-rich repeat domain-containing protein /		??			unknown	30.2.99 signalling.recptor kinases.misc		plastid	extracellular, endoplasmic reticulum, golgi		
AT3G22910	15301	AT3G22910.1	ACA13 Putative calcium-transporting ATPase 13		na			unknown	30.3 signalling.calcium					9.0
AT3G21180	15302	AT3G21180.1	ACA9 Calcium-transporting ATPase 9		na			unknown	30.3 signalling.calcium					9.0
AT4G00820	15303	AT4G00820.1	IQ-domain 17 /		??			signaling ?	30.3 signalling.calcium			mitochondrion		
AT5G53010	15304	AT5G53010.1	calcium-transporting ATPase, putative;		??			transporter ?	30.3 signalling.calcium					9.0
AT4G36080	15305	AT4G36080.1	phosphotransferases, alcohol group as acceptor;binding;inositol or phosphatidylinositol kinases;		??			nd	30.4 signalling.phosphoinositids					2.0
AT5G27540	15306	AT5G27540.1	nd		na			nd	30.5 signalling.G-proteins	mitochondrion			mitochondria	1.0
AT1G52280	15307	AT1G52280.1	nd		na			nd	30.5 signalling.G-proteins			mitochondrion		

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AT4G18430	15308	AT4G18430.1	RAA1E (RABA1e) RAB GTPase homolog A1E, Ras-related protein RABA1e /		na			signalling / SNARE effector	30.5 signalling.G-proteins					
AT5G59840	15309	AT5G59840.1	RAB-8A (ara-3) Putative GTP-binding protein ara-3 (Rab-type small GTP-binding protein-like) (Ras-related protein Rab-8A)		na			signaling	30.5 signalling.G-proteins					
AT1G06400	15310	AT1G06400.1	RABA1A (ARA-2, RAB11E) Ras-related protein RABA1a (Ras-related protein Ara-2) (Ras-related protein Rab11E) /		na			signalling / SNARE effector	30.5 signalling.G-proteins					
AT5G27510	15311	AT5G27510.1	Kinase-like Protein kinase superfamily protein, protein serine/threonine kinase activity (ChloroP-) /		Ch/Th ??			kinase	30.6 signalling.M AP kinases					
AT3G27000	15312	AT3G27000.1	ARP2 (WRM, WURM) Actin-related protein 2 /		na			cell morphogenesis cytoskeleton actin	31.1 cell.organisation	Arp2/3 protein complex				
AT1G64330	15313	AT1G64330.1	HP64c myosin heavy chain like protein /		na			cell morphogenesis cytoskeleton myosin ?	31.1 cell.organisation					

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AT4G14390	15314	AT4G14390.1	Ankyrin repeat family protein;		??			nd	31.1 cell.organisation					5.0
AT1G43700	15315	AT1G43700.1	nd		na			nd	31.1 cell.organisation	nucleus				
AT5G62700	15316	AT5G62700.1	TBB3 Tubulin beta-3 chain		na			cell morphogenesis cytoskeleton actin	31.1 cell.organisation	tubulin			not plastid	
AT5G53080	15317	AT5G53080.1	TPR-like Tetratricopeptide repeat-containing protein /		??			RNA binding ?	31.1 cell.organisation			plastid		
AT3G19720	15318	AT3G19720.3	ARC5 Dynamin-like protein ARC5 (EC=3.6.5.5) , chloroplast /		Ch/E ?			chloroplast division	31.2 cell.division				envelope-outer; peroxisome	
AT1G53720	15319	AT1G53720.1	nd		na			nd	31.3 cell.cycle	nucleus				
AT5G05010	15320	AT5G05010.2	nd		na			nd	31.4 cell.vesicle transport				plasma membrane	
AT3G50790	15321	AT3G50790.1	LEA-like esterase/lipase/thioesterase family protein, chloroplast precursor /		Ch/Th ?			unknown	33.2 development .late embryogenesis abundant		plastid	plastid		
AT2G45330	15322	AT2G45330.1	EMB1067 EMBRYO DEFECTIVE 1067, RNA 2'-phosphotransferase, Tpt1 / KptA family /		Ch/Th ?			RNA binding ?	33.99 development .unspecified		plastid	mitochondrion		

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AT5G49120	15323	AT5G49120.1	HP17z conserved plant protein, no similarity to characterized protein, chloroplast precursor /		??			unknown	33.99 development .unspecified		plastid	plastid		
AT1G45230	15324	AT1G45230.2	nd		??			nd	33.99 development .unspecified		plastid	plastid	plastid	
AT3G19490	15325	AT3G19490.1	NHD1 member of Na ⁺ /H ⁺ antiporter-Putative family with Citrate transporter-like domain, chloroplast precursor /		Ch/Th ?			transporter ?	34.12 transport.met al		plastid	plastid	not plastid	13.0
AT5G21930	15326	AT5G21930.2	PAA2 (HMA8) Copper-transporting ATPase PAA2, chloroplast precursor /		Ch/Th			transporter ATPase Cu	34.12 transport.met al	thylakoid membrane (sensu Viridiplantae)		plastid	thylakoid-integral	
AT4G04850	15327	AT4G04850.2	KEA3 K ⁺ efflux antiporter 3, putative		Ch/Th ??			transporter K ?	34.15 transport.pot assium					
AT1G51500	15328	AT1G51500.1	ABCG12 (CER5 D3 WBC12) ABC transporter G family member 12 (ABC transporter ABCG.12) (AtABCG13) (Protein ECERIFERUM 5)(White-brown complex homolog protein 12) (AtWBC12) /		na			transporter ABC	34.16 transport.ABC C transporters and multidrug resistance systems					6.0

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AT1G51460	15329	AT1G51460.1	ABCG13 (WBC13) ABC transporter G family member 13 (ABC transporter ABCG.13) (AtABCG13) (White-brown complex homolog protein 13) (AtWBC13)		na			transporter ABC	34.16 transport.ABC transporters and multidrug resistance systems					6.0
AT1G64550	15330	AT1G64550.1	general control non-repressible 3; member of GCN subfamily		??			transporter ?	34.16 transport.ABC transporters and multidrug resistance systems					
AT1G69480	15331	AT1G69480.1	PHO1A Phosphate transporter PHO1 homolog 10, plasma membrane /		na			transporter Pi	34.7 transport.phosphate					8.0
AT1G54350	15332	AT1G54350.1	ABCD2 ATP-BINDING CASSETTE D2 (ABCD2), chloroplast precursor /		Ch/Th ?			transporter ABC ?	34.8 transport.metabolite transporters at the envelope membrane		plastid	plastid	plastid	4.0
AT5G19760	15333	AT5G19760.1	nd		na			transporter MCF	34.9 transport.metabolite transporters at the mitochondria l membrane	mitochondrion			mitochondria	2.0
AT2G32040	15334	AT2G32040.1	FBT1 Folate-bioperin transporter 1, chloroplast precursor /		Ch/E/IM			transporter folate/monoglutamate	34.99 transport.misc	chloroplast envelope	plastid	plastid	envelope	11.0

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AT2G38330	15335	AT2G38330.1	MATE2 Belongs to the multi antimicrobial extrusion (MATE) (TC 2.A.66.1) family, chloroplast precursor /		??			transporter ?	34.99 transport.misc		plastid	plastid		12.0
AT2G29590	15336	AT2G29590.1	ACO-like Acyl-coenzyme A thioesterase-like protein /		na			unknown	35.1 not assigned.no ontology				peroxisome	
AT2G34680	15337	AT2G34680.1	AIR9 Outer arm dynein light chain 1 protein, AUXIN-INDUCED IN ROOT CULTURES 9 /		na			unknown	35.1 not assigned.no ontology					
AT1G29390	15338	AT1G29390.2	CRIM2 (COR413IM2, COR314TM2) cold regulated 314 thylakoid membrane 2, Integral membrane protein in the inner envelope of chloroplasts, Provide freezing tolerance, chloroplast precursor /		Ch/E/IM			stress cold	35.1 not assigned.no ontology		plastid	plastid		
AT5G58770	15339	AT5G58770.1	DDPS2 Dehydrodolic hyl diphosphate synthase 2 (Dedol-PP synthase 2) (EC 2.5.1.-) (ChloroP-/TargetPMito /		Ch/Th ??			protein modification	35.1 not assigned.no ontology			mitochondrion	plastid stroma	

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AT3G56010	15340	AT3G56010.1	HP21d conserved plant protein, no similarity to characterized protein, chloroplast precursor /		Ch/Th ?			unknown	35.1 not assigned.no ontology	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	plastid	1.0
AT2G41040	15341	AT2G41040.1	HP39 S-adenosyl-L-methionine-dependent methyltransferases superfamily protein, low similarity to Menaquinone biosynthesis methyltransferase ubiE, chloroplast precursor /		Ch/Th			unknown	35.1 not assigned.no ontology		plastid	plastid	plastoglobules	
AT2G39670	15342	AT2G39670.1	HP47b Radical SAM domain-containing protein, chloroplast precursor /		Ch/Th ?			RNA Binding ?	35.1 not assigned.no ontology		plastid	plastid	plastid	
AT4G38650	15343	AT4G38650.1	HP63 Glycosyl hydrolase family 10 protein (ChloroP-/TargetPSP) /		Ch/Th ??			unknown	35.1 not assigned.no ontology			extracellular, endoplasmic reticulum, golgi		
AT5G46190	15344	AT5G46190.1	HP69 RNA-binding KH domain-containing protein, RNA binding, nucleic acid binding /		Ch/Th ??			RNA Binding ?	35.1 not assigned.no ontology					

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AT5G50780	15345	AT5G50780.1	HP91 Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase family protein /		Ch/Th ??			unknown	35.1 not assigned.no ontology					1.0
AT1G49750	15346	AT1G49750.1	LRR-like Leucine-rich repeat domain-containing protein /		??			unknown	35.1 not assigned.no ontology			extracellular, endoplasmic reticulum, gol gi	not plastid	
AT1G53470	15347	AT1G53470.1	MSL4 Mechanosensitive ion channel protein 4 (Mechanosensitive channel of small conductance -like 4) (MscS-Like protein 4)		na			unknown	35.1 not assigned.no ontology				plasma membrane	5.0
AT1G03220	15348	AT1G03220.1	Aspartyl protease-like protein (F15K9.17 protein)		na			unknown	35.1 not assigned.no ontology		plastid	extracellular, endoplasmic reticulum, gol gi	cell wall	
AT5G06320	15349	AT5G06320.1	Harpin-induced protein-like (NDR1/HIN1-Like protein 3)		na			unknown	35.1 not assigned.no ontology	plasma membrane			plasma membrane	1.0
AT2G25830	15350	AT2G25830.1	Probable transcriptional regulatory protein		Ch/S			unknown	35.1 not assigned.no ontology			plastid	plastid stroma	
AT5G44640	15351	AT5G44640.1	beta glucosidase 13;		??			nd	35.1 not assigned.no ontology			extracellular, endoplasmic reticulum, gol gi		
AT1G47271	15352	AT1G47271.1	Cystathionine beta-synthase (CBS) family protei		??			nd	35.1 not assigned.no ontology			mitochondrion		

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AT1G79740	15353	AT1G79740.1	hAT transposon superfamily;		??			nd	35.1 not assigned.no ontology					
AT5G40290	15354	AT5G40290.1	HD domain-containing metal-dependent phosphohydrolase family protein;		??			nd	35.1 not assigned.no ontology					
AT3G08850	15355	AT3G08850.1	nd		na			nd	35.1 not assigned.no ontology					
AT5G45510	15356	AT5G45510.1	nd		na			nd	35.1 not assigned.no ontology					
AT1G32700	15357	AT1G32700.1	PLATZ transcription factor family protein;		??			nd	35.1 not assigned.no ontology					
AT1G80630	15358	AT1G80630.1	RNI-like superfamily protein;		??			nd	35.1 not assigned.no ontology					
AT3G59770	15359	AT3G59770.2	sacl homology domain-containing protein /		??			nd	35.1 not assigned.no ontology			mitochondrion		
AT3G01660	15360	AT3G01660.1	S-adenosyl-L-methionine-dependent methyltransferases superfamily protei		??			nd	35.1 not assigned.no ontology			mitochondrion		
AT4G16045	15361	AT4G16045.1	TRAF-like superfamily protein;		??			nd	35.1 not assigned.no ontology					
AT5G50970	15362	AT5G50970.1	transducin family protein / WD-40 repeat family protein;		??			nd	35.1 not assigned.no ontology					
AT1G61000	15363	AT1G61000.1	nd		na			unknown	35.1 not assigned.no ontology					5.0
AT5G22140	15364	AT5G22140.2	nd		na			unknown	35.1 not assigned.no ontology					

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AT5G43140	15365	AT5G43140.1	PMP22-like Peroxisomal membrane 22 kDa (Mpv17/PMP22) family protein		??			nd	35.1 not assigned.no ontology			mitochondrion		
AT3G63540	15366	AT3G63540.1	PsbP-like (TL19, P19) Mog1/PsbP/DUF1795-like photosystem II reaction center PsbP family protein /		Ch/Th ??			PS PSII OEE ?	35.1 not assigned.no ontology					
AT5G38510	15367	AT5G38510.2	Rhomb-like Rhomboid-related intramembrane serine protease-like protein, peptidase S54, chloroplast precursor /		Ch/Th ?			chaperone and protease ?	35.1 not assigned.no ontology			plastid		
AT1G78140	15368	AT1G78140.1	SMT-like S-adenosyl-L-methionine-dependent methyltransferases superfamily protein, chloroplast precursor /		Ch/Th ?			protein modification	35.1 not assigned.no ontology		plastid	mitochondrion	plastoglobules	
AT5G14440	15369	AT5G14440.1	SURF2 Surfeit locus protein 2		Ch/Th ??			unknown	35.1 not assigned.no ontology					
AT1G58270	15370	AT1G58270.1	TRAF-like family protein /		??			nd	35.1 not assigned.no ontology			extracellular, endoplasmic reticulum, golgi		2.0
AT1G49320	15371	AT1G49320.1	USPL1 unknown seed protein like 1 /		??			unknown	35.1 not assigned.no ontology			extracellular, endoplasmic reticulum, golgi		

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AT3G11945	15372	AT3G11945.2	VTE2-2 (HPT2, HST) Homogentisate phytyltransferase 2 (Vitamin E pathway gene 2-2 protein) (AtVTE2-2), chloroplast precursor (EC 2.5.1.n8) /		Ch/Th ?			metabolism vitamin and pigment vitamin E	35.1 not assigned.no ontology		plastid	plastid		
AT5G21920	15373	AT5G21920.1	YCF19-like YGGT family protein, chloroplast precursor /		Ch/Th ?			unknown	35.1 not assigned.no ontology		plastid	plastid		2.0
AT1G01920	15374	AT1G01920.2	SET domain-containing protein;		??			unknown	35.1.13 not assigned.no ontology.SET domain-containing protein					
AT1G53120	15375	AT1G53120.1	Putative uncharacterized protein F10L8.3 (RNA-binding S4 domain-containing protein)		??			RNA Binding ?	35.1.14 not assigned.no ontology.S RNA-binding domain-containing protein		plastid	mitochondrion	plastid	
AT3G19830	15376	AT3G19830.1	CaLB-like Calcium-dependent lipid-binding (CaLB domain) family protein, chloroplast precursor /		??			metabolism lipid ?	35.1.19 not assigned.no ontology.C2 domain-containing protein		plastid	plastid		3.0

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AT4G20080	15377	AT4G20080.1	Calcium-dependent lipid-binding (CaLB domain) plant phosphoribosyltransferase family protein;		??			nd	35.1.19 not assigned.no ontology.C2 domain-containing protein					2.0
AT3G25500	15378	AT3G25500.1	FH1 (AFH1) Formin-like protein 1 (AtFH1) (AtFORMIN-8) /		na			cell morphogenesis cytoskeleton actin	35.1.20 not assigned.no ontology.for min homology 2 domain-containing protein	membrane			plasma membrane	1.0
AT1G14710	15379	AT1G14710.2	Uncharacterized protein		na			unknown	35.1.41 not assigned.no ontology.hydroxyproline rich proteins					
AT2G18520	15380	AT2G18520.1	Pentatricopeptide repeat-containing protein		na			unknown	35.1.5 not assigned.no ontology.pentatricopeptide (PPR) repeat-containing protein			mitochondrion		
AT3G22670	15381	AT3G22670.1	PP248 Pentatricopeptide repeat-containing protein, predicted mitochondrial (TargetP) /		Ch/Th ??			RNA Binding ?	35.1.5 not assigned.no ontology.pentatricopeptide (PPR) repeat-containing protein			mitochondrion		
AT3G28660	15382	AT3G28660.1	PP260 (PCMP-E80, TPR-like) Pentatricopeptide repeat-containing protein, predicted mitochondrial (TargetP) /		Ch/Th ??			RNA Binding ?	35.1.5 not assigned.no ontology.pentatricopeptide (PPR) repeat-containing protein			mitochondrion		2.0

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AT5G24830	15383	AT5G24830.1	PP396 (TPR-like) Pentatricopeptide repeat-containing protein /		??			RNA binding ?	35.1.5 not assigned.no ontology.pentatricopeptide (PPR) repeat-containing protein			plastid		
AT5G55840	15384	AT5G55840.1	PP432 (PPR-like) Pentatricopeptide repeat-containing protein /		??			RNA Binding ?	35.1.5 not assigned.no ontology.pentatricopeptide (PPR) repeat-containing protein		plastid	mitochondrion		
AT4G13650	15385	AT4G13650.1	PPR-like		??			RNA Binding ?	35.1.5 not assigned.no ontology.pentatricopeptide (PPR) repeat-containing protein					
AT2G38420	15386	AT2G38420.1	PPR-like		??			RNA Binding ?	35.1.5 not assigned.no ontology.pentatricopeptide (PPR) repeat-containing protein			mitochondrion		
AT1G43980	15387	AT1G43980.1	PPR-like		??			RNA Binding ?	35.1.5 not assigned.no ontology.pentatricopeptide (PPR) repeat-containing protein			mitochondrion		2.0
AT5G24310	15388	AT5G24310.1	ABL interactor-like protein 3;One of four ABI-like proteins		??			nd	35.2 not assigned.unknown					

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AT3G17930	15389	AT3G17930.1	DAC protein involved in the accumulation of the cytochrome b6/f complex (DEFECTIVE ACCUMULATION OF CYTOCHROME B6/F COMPLEX), chloroplast precursor /		Ch/Th ?			PS b6-F ?	35.2 not assigned.unknown	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	plastid	2.0
AT4G31160	15390	AT4G31160.1	DCAF1 DDB1-CUL4 associated factor 1 /		??			nd	35.2 not assigned.unknown					
AT1G52590	15391	AT1G52590.1	DCC thiol-disulfide oxidoreductase family.		??			redox	35.2 not assigned.unknown		plastid	plastid		
AT5G02160	15392	AT5G02160.1	DNAJ-like conserved protein of the Heat shock protein DnaJ family, contains cysteine-rich domain, chloroplast precursor /		Ch/Th ?			chaperone and protease ?	35.2 not assigned.unknown	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	plastid	1.0
AT5G15802	15393	AT5G15802.1	HP10 conserved plant protein, no similarity to characterized protein (ChloroP-/TargetPSP) /		Ch/Th ??			unknown	35.2 not assigned.unknown			extracellular, endoplasmic reticulum, golgi		
AT5G09840	15394	AT5G09840.1	HP102 conserved plant protein, no similarity to characterized protein, Chloroplast precursor /		Ch/Th ?			RNA Binding ?	35.2 not assigned.unknown	mitochondrion	plastid	plastid		

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AT2G05310	15395	AT2G05310.1	HP13 conserved plant protein, no similarity to characterized protein, chloroplast precursor /		Ch/Th ?			unknown	35.2 not assigned.unknown		plastid	plastid	not plastid	1.0
AT4G20160	15396	AT4G20160.1	HP134z Glu-rich protein /		??			unknown	35.2 not assigned.unknown			plastid		
AT3G53470	15397	AT3G53470.2	HP15c conserved plant protein, no similarity to characterized proteins, chloroplast precursor /		Ch/Th ?			unknown	35.2 not assigned.unknown	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	thylakoid	
AT3G50685	15398	AT3G50685.1	HP16 conserved protein, weak similarity to various transporters (TatC or MFS), chloroplast precursor /		Ch/Th ?			transporter ?	35.2 not assigned.unknown		plastid	plastid		3.0
AT2G17972	15399	AT2G17972.1	HP18 conserved plant protein, no similarity to characterized proteins, chloroplast precursor /		Ch/Th ?			unknown	35.2 not assigned.unknown	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	thylakoid	1.0
AT4G13220	15400	AT4G13220.1	HP19z conserved plant protein, no similarity to characterized protein, chloroplast precursor /		??			unknown	35.2 not assigned.unknown		plastid	plastid		1.0

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AT3G12345	15401	AT3G12345.1	HP20 FKBP-type peptidyl-prolyl cis-trans isomerase, putative (Stress-enhanced protein 4), predicted mitochondria l (TargetP) /		Ch/Th ??			unknown	35.2 not assigned.unknown			mitochondrion	thylakoid	
AT2G42975	15402	AT2G42975.1	HP20b conserved protein, no similarity to characterized proteins, chloroplast precursor /		Ch/Th ?			unknown	35.2 not assigned.unknown	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	plastid	1.0
AT4G38100	15403	AT4G38100.1	HP21c conserved plant protein, no similarity to characterized protein, chloroplast precursor /		Ch/Th ?			unknown	35.2 not assigned.unknown	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	thylakoid	2.0
AT5G28885	15404	AT5G28885.1	HP21e conserved protein, no similarity to characterized protein (ChloroP-/TargetPOther) /		Ch/Th ??			unknown	35.2 not assigned.unknown					
AT1G22060	15405	AT1G22060.1	HP228 NT-C2 domain containing protein (ChloroP-/TargetPMito) /		Ch/Th ??			unknown	35.2 not assigned.unknown			mitochondrion		

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AT3G12685	15406	AT3G12685.1	HP22z Acid phosphatase /vanadium-dependent haloperoxidase-related protein, chloroplast precursor /		??			unknown	35.2 not assigned.unk nown		plastid	plastid		2.0
AT1G50020	15407	AT1G50020.1	HP23 conserved plant protein, no similarity to characterized protein, chloroplast precursor /		Ch/Th ?			unknown	35.2 not assigned.unk nown	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	plastid	1.0
AT5G41960	15408	AT5G41960.1	HP24d hypothetical protein, no similarity to characterized protein, chloroplast precursor /		Ch/Th ?			unknown	35.2 not assigned.unk nown		plastid	plastid		4.0
AT4G27390	15409	AT4G27390.1	HP25i conserved plant protein, no similarity to characterized protein, Chloroplast precursor ? (ChloroP-TargetPChloro) /		Ch/Th ?			unknown	35.2 not assigned.unk nown			plastid		2.0
AT4G01935	15410	AT4G01935.1	HP28 conserved plant protein, no similarity to characterized protein, chloroplast precursor /		Ch/Th ?			unknown	35.2 not assigned.unk nown		plastid	plastid		5.0

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AT3G09050	15411	AT3G09050.1	HP29d hypothetical protein, no similarity to characterized protein, chloroplast precursor /		Ch/Th ?			unknown	35.2 not assigned.unknown	thylakoid membrane (sensu Viridiplantae)	plastid	plastid	thylakoid	2.0
AT2G20920	15412	AT2G20920.1	HP30f conserved plant and cyanobacteria protein, similar to slr1918 protein [Synechocystis sp], no similarity to characterized protein, chloroplast precursor /		Ch/Th ?			unknown	35.2 not assigned.unknown		plastid	plastid	plastid	4.0
AT2G02730	15413	AT2G02730.1	HP30g conserved plant protein, no similarity to characterized protein (ChloroP-/TargetPSP) /		Ch/Th ??			unknown	35.2 not assigned.unknown			extracellular, endoplasmic reticulum, golgi		1.0
AT1G65230	15414	AT1G65230.1	HP32e conserved protein, no similarity to characterized proteins, chloroplast precursor /		Ch/Th ?			unknown	35.2 not assigned.unknown		plastid	plastid	thylakoid	1.0
AT4G24090	15415	AT4G24090.1	HP33b conserved protein, no similarity to characterized proteins, chloroplast precursor /		Ch/Th ?			unknown	35.2 not assigned.unknown		plastid	plastid	plastid	3.0

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AT2G34610	15416	AT2G34610.1	HP33e conserved protein, no similarity to characterized protein (ChloroP-/TargetPOther) /		Ch/Th ??			unknown	35.2 not assigned.unknown					2.0
AT4G31530	15417	AT4G31530.1	HP35f NAD(P)-binding Rossmann-fold superfamily protein, 3-beta hydroxysteroid dehydrogenase/isomerase family, chloroplast precursor /		Ch/Th ?			unknown	35.2 not assigned.unknown		plastid	plastid	plastid stroma	
AT2G04360	15418	AT2G04360.1	HP36c conserved plant protein, no similarity to characterized protein, chloroplast precursor /		Ch/Th ?			unknown	35.2 not assigned.unknown		plastid	plastid		6.0
AT5G27290	15419	AT5G27290.1	HP37 ATP-dependent Zn proteases-like protein, predicted mitochondrial (TargetP) /		Ch/Th ??			unknown	35.2 not assigned.unknown			mitochondrion		3.0
AT5G63100	15420	AT5G63100.1	HP37b S-adenosyl-L-methionine-dependent methyltransferase domain-containing protein (ChloroP-/TargetPMito) /		Ch/Th ??			protein modification ?	35.2 not assigned.unknown			mitochondrion	plastid stroma	

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AT5G22340	15421	AT5G22340.1	HP38 conserved plant protein, no similarity to characterized protein, chloroplast precursor /		Ch/Th ?			unknown	35.2 not assigned.unknown			plastid		4.0
AT3G25805	15422	AT3G25805.1	HP38 conserved plant protein, no similarity to characterized protein, chloroplast precursor /		Ch/Th ?			unknown	35.2 not assigned.unknown		plastid	mitochondrion		7.0
AT5G35066	15423	AT5G35066.1	HP4 small hypothetical protein, no similarity to characterized protein /		Ch/Th ??			unknown	35.2 not assigned.unknown					
AT3G43540	15424	AT3G43540.1	HP40d conserved plant and cyanobacteria protein, chloroplast precursor /		Ch/Th ?			unknown	35.2 not assigned.unknown		plastid	mitochondrion	plastoglobules	
AT1G52315	15425	AT1G52315.1	HP40e Regulator of Vps4 activity in the MVB (Multivesicular body) formation pathway protein (ChloroP-/TargetPMito) /		Ch/Th ??			vesicular trafficking ?	35.2 not assigned.unknown			mitochondrion		

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AT5G61200	15426	AT5G61200.3	HP45c conserved plant protein, no similarity to characterized protein, Chloroplast precursor ? (ChloroP- /TargetPChloro for AT5G61200.3) /		Ch/Th ?			unknown	35.2 not assigned.unknown					
AT3G01060	15427	AT3G01060.1	HP51 conserved protein, no similarity to characterized proteins, chloroplast precursor /		Ch/Th ?			unknown	35.2 not assigned.unknown		plastid	plastid	plastid	
AT5G19540	15428	AT5G19540.1	HP52c conserved plant protein, no similarity to characterized protein, chloroplast precursor /		Ch/Th ?			unknown	35.2 not assigned.unknown		plastid	plastid		2.0
AT3G07210	15429	AT3G07210.1	HP59z conserved protein with Trypsin-like domain /		??			chaperone and protease ?	35.2 not assigned.unknown		plastid			
AT2G45840	15430	AT2G45840.1	HP61z conserved protein with Glyco_transf_90 domain /		??			unknown	35.2 not assigned.unknown		plastid			1.0
AT3G22210	15431	AT3G22210.1	HP7 small hypothetical protein, no similarity to characterized protein /		Ch/Th ??			unknown	35.2 not assigned.unknown			extracellular, endoplasmic reticulum, golgi	not plastid	1.0

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AT5G06930	15432	AT5G06930.1	HP80z conserved plant protein, no similarity to characterized protein, chloroplast precursor /		??			unknown	35.2 not assigned.unknown		plastid	plastid		
AT3G56140	15433	AT3G56140.1	HP82 hypothetical protein, no similarity to characterized protein, chloroplast precursor /		Ch/Th ?			unknown	35.2 not assigned.unknown		plastid	plastid		2.0
AT4G08630	15434	AT4G08630.1	HP85z conserved protein, no similarity to characterized protein /		??			unknown	35.2 not assigned.unknown			plastid		
AT3G44380	15435	AT3G44380.1	LEA Late embryogenesis abundant hydroxyproline-rich glycoprotein /		Ch/Th ??			stress desiccation	35.2 not assigned.unknown					
AT1G55280	15436	AT1G55280.1	Lipase-like Lipase/lipoxygenase, PLAT/LH2 family protein, chloroplast precursor /		Ch/Th ?			metabolism lipid ?	35.2 not assigned.unknown		plastid	plastid		4.0

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AT4G28740	15437	AT4G28740.1	LPA1-like similar to Low PSII accumulation protein 1 (LPA1), integral membrane chaperone required for efficient PSII assembly, probably through direct interaction with D1 protein of PSII, (TPR)-containing protein /		Ch/Th ??			chaperone and protease ?	35.2 not assigned.unkn own				plastid	2.0
AT1G02475	15438	AT1G02475.1	LTP-like Polyketide cyclase/dehydrase and lipid transport superfamily protein, chloroplast precursor /		Ch/Th ?			transporter lipids ?	35.2 not assigned.unkn own		plastid	plastid		
AT2G32640	15439	AT2G32640.1	Lycopene_cyclase Lycopene beta/epsilon cyclase-type protein, FAD binding, chloroplast precursor /		Ch/Th ?			metabolism vitamin and pigment ?	35.2 not assigned.unkn own		plastid	plastid	thylakoid	2.0
AT5G26230	15440	AT5G26230.1	MAKR1 Probable membrane-associated kinase regulator 1, chloroplast precursor /		??			kinase regulator ?	35.2 not assigned.unkn own		plastid	plastid		
AT3G20680	15441	AT3G20680.1	Uncharacterized protein		??			unknown	35.2 not assigned.unkn own		plastid	plastid	plastid	
AT4G30720	15442	AT4G30720.1	Putative oxidoreductase/electron carrier		Ch/S			unknown	35.2 not assigned.unkn own		plastid	plastid	plastid stroma	

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AT5G04440	15443	AT5G04440.1	Uncharacterized protein		Ch/S			unknown	35.2 not assigned.unk nown		plastid	plastid	plastid stroma	
AT2G31890	15444	AT2G31890.1	Uncharacterized protein		Ch/S			unknown	35.2 not assigned.unk nown			plastid	plastid stroma	
AT5G01730	15445	AT5G01730.1	SCAR4 Protein SCAR4 (AtSCAR4) (Protein WAVE3)		??			unknown	35.2 not assigned.unk nown					
AT5G50930	15446	AT5G50930.1	Histone superfamily protein /		??			DNA binding	35.2 not assigned.unk nown			extracellular, endoplasmic reticulum,gol gi		1.0
AT5G52800	15447	AT5G52800.1	nd		??			nd	35.2 not assigned.unk nown					
AT5G04670	15448	AT5G04670.1	nd		??			nd	35.2 not assigned.unk nown			mitochondrio n		
AT1G22882	15449	AT1G22882.1	nd		??			nd	35.2 not assigned.unk nown			mitochondrio n		3.0
AT4G32900	15450	AT4G32900.2	nd		??			nd	35.2 not assigned.unk nown			mitochondrio n		
AT1G33800	15451	AT1G33800.1	nd		na			nd	35.2 not assigned.unk nown			extracellular, endoplasmic reticulum,gol gi		1.0
AT1G47470	15452	AT1G47470.1	nd		??			nd	35.2 not assigned.unk nown			extracellular, endoplasmic reticulum,gol gi		
AT5G06970	15453	AT5G06970.1	nd		na			nd	35.2 not assigned.unk nown					
AT1G17820	15454	AT1G17820.1	nd		??			nd	35.2 not assigned.unk nown			extracellular, endoplasmic reticulum,gol gi		
AT4G30200	15455	AT4G30200.3	nd		??			nd	35.2 not assigned.unk nown					

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AT4G17970	15456	AT4G17970.1	aluminum-activated, malate transporter 12;Anion transporter involved in stomatal closure. Gene has 3 splicing variants.		??			transporter ?	35.2 not assigned.unkn own					6.0
AT3G09450	15457	AT3G09450.1	nd		??			unknown	35.2 not assigned.unkn own			mitochondri on		10.0
AT3G26950	15458	AT3G26950.1	nd		??			unknown	35.2 not assigned.unkn own			mitochondri on		1.0
AT4G24030	15459	AT4G24030.1	nd		??			unknown	35.2 not assigned.unkn own			extracellular, endoplasmic reticulum, gol gi		
AT3G28430	15460	AT3G28430.1	nd		??			unknown	35.2 not assigned.unkn own			mitochondri on		
AT5G65950	15461	AT5G65950.1	nd		na			unknown	35.2 not assigned.unkn own					
AT1G67040	15462	AT1G67040.1	nd		??			unknown	35.2 not assigned.unkn own					
AT1G36745	15463	AT1G36745.1	nd		??			unknown	35.2 not assigned.unkn own					
AT3G42786	15464	AT3G42786.1	nd		??			unknown	35.2 not assigned.unkn own					
AT3G32180	15465	AT3G32180.1	nd		??			unknown	35.2 not assigned.unkn own					
AT1G27300	15466	AT1G27300.1	nd		??			unknown	35.2 not assigned.unkn own					1.0
AT5G14990	15467	AT5G14990.1	nd		??			unknown	35.2 not assigned.unkn own					
AT5G63540	15468	AT5G63540.1	nd		??			unknown	35.2 not assigned.unkn own					

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AT5G45540	15470	AT5G45540.1	nd		??			unknown	35.2 not assigned.unknown					7.0
AT5G05840	15471	AT5G05840.1	nd		??			unknown	35.2 not assigned.unknown					
AT4G20095	15472	AT4G20095.1	nd		??			unknown	35.2 not assigned.unknown					
AT3G05320	15473	AT3G05320.1	O-FucTrfase-like O-fucosyltransferase family protein /		??			protein modification ?	35.2 not assigned.unknown		plastid	mitochondrion		
AT1G64355	15474	AT1G64355.1	PLCD-like protein of unknown function with low similarity to 1-acyl-sn-glycerol-3-phosphate acyltransferase delta, chloroplast precursor /		Ch/Th ?			unknown	35.2 not assigned.unknown		plastid	plastid		3.0
AT5G05480	15475	AT5G05480.1	PNGase-like Peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase A protein /		??			unknown	35.2 not assigned.unknown			plastid		
AT1G64430	15476	AT1G64430.1	PPR-like Pentatricopeptide repeat-containing protein, chloroplast precursor /		Ch/Th ?			RNA Binding ?	35.2 not assigned.unknown		plastid	plastid		2.0
AT5G27390	15477	AT5G27390.1	PSBP-like Mog1/PsbP/DUF1795-like photosystem II reaction center PsbP family protein, chloroplast precursor /		Ch/Th ?			PS PSII ?	35.2 not assigned.unknown		plastid	plastid	plastid	

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AT1G22850	15478	AT1G22850.1	SNARE-like SNARE associated Golgi protein family, chloroplast precursor /		Ch/Th ?			unknown	35.2 not assigned.unknown		plastid	plastid	plastid	5.0
AT4G24750	15479	AT4G24750.1	Str11 Rhodanese-like domain-containing protein 11, chloroplast precursor /		Ch/Th ?			unknown	35.2 not assigned.unknown		plastid	plastid	plastid	
AT1G17850	15480	AT1G17850.1	STR8 Rhodanese-like domain-containing protein 8, chloroplast precursor /		??			unknown	35.2 not assigned.unknown		plastid	plastid		
AT2G37720	15481	AT2G37720.1	TBL15 Encodes a member of the TBL (TRICHOME BIREFRINGENCE-LIKE) gene family /		Ch/Th ??			unknown	35.2 not assigned.unknown					1.0
AT5G55710	15482	AT5G55710.1	Tic20-V (Tic20-like, IEP16-like) conserved plant and cyanobacterial protein, similar to ycf60 protein [Synechocystis sp], chloroplast encoded in red algae /		Ch/Th			protein targeting Tic ?	35.2 not assigned.unknown			plastid	envelope-inner-integral	3.0
AT2G42400	15483	AT2G42400.1	VOZ2 Transcription factor VOZ2 (Protein VASCULAR PLANT ONE-ZINC FINGER 2) (AtVOZ2) (ChloroP-) /		na			transcription nucleus ?	35.2 not assigned.unknown					

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AT5G67370	15484	AT5G67370.1	YCF36-like (CGLD27) Protein of unknown function conserved in the green lineage and diatoms (ChloroP-TargetPMito) /		Ch/Th ??			unknown	35.2 not assigned.unkn			mitochondrion		3.0
AT5G03690	15485	AT5G03690.1	Fructose-bisphosphate aldolase (EC 4.1.2.13)		??			metabolism carbon Calvin cycle	4.7 glycolysis.aldolase			mitochondrion		
AT2G27730	15486	AT2G27730.1	UMP2 conserved plant protein, low similarity to NADH-ubiquinone oxidoreductase, Mitochondria precursor /		na			resp NDH ?	9.1.1 mitochondria electron transport / ATP synthesis.NADH-DH.complex I	mitochondrion & mitochondria membrane & NADH dehydrogenase complex (ubiquinone)		mitochondrion	mitochondria	1.0
AT5G47890	15487	AT5G47890.1	NDUA2 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2, mitochondria precursor (TargetPChloro) ? /		Ch/Th ??			resp NDH ?	9.1.2 mitochondria electron transport / ATP synthesis.NADH-DH.localisation not clear			plastid	not plastid	
AT5G05370	15488	AT5G05370.1	nd		na			nd	9.5 mitochondria electron transport / ATP synthesis.cytochrome c reductase					

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AT1G49380	15489	AT1G49380.1	CCS1 Cytochrome c biogenesis protein CCS1 (C-type cytochrome synthesis protein 1), chloroplast precursor /		Ch/Th			chaperone and protease PS b6f	9.6 mitochondria I electron transport / ATP synthesis.cyt ochrome c		plastid	plastid		5.0
AT5G08690	15490	AT5G08690.1	ATPB2 ATP synthase subunit beta-2, mitochondria I precursor (EC 3.6.3.14) /		na			Mito ATPase	9.9 mitochondria I electron transport / ATP synthesis.F1-ATPase	mitochondrion		mitochondrion	mitochondria	
AT2G33040	15491	AT2G33040.1	ATPC (ATPG3) ATP synthase subunit gamma, mitochondria I (F-ATPase gamma subunit) /		na			Mito ATPase	9.9 mitochondria I electron transport / ATP synthesis.F1-ATPase	mitochondrion & nucleus & cytoplasm		mitochondrion	mitochondria	
AT2G34660	15492	AT2G34660.2	ABCC2 ABC transporter C family member 2 (ABC transporter ABCC.2) (AtABCC2) (EC 3.6.3.44) (ATP-energized glutathione S-conjugate pump 2) (Glutathione S-conjugate-transporting ATPase 2) (Multidrug resistance-associated protein 2)		na			transporter ABC						

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AT3G26085	15493	AT3G26085.3	CAAX-like CAAX amino terminal protease family protein /		Ch/Th ??			chaperone and protease						
AT3G59210	15494	AT3G59210.2	F-box/RNI-like superfamily protein;		??			nd						
AT2G07690	15495	AT2G07690.2	Minichromosome maintenance (MCM2/3/5) family protein		??			nd						
AT5G24314	15496	AT5G24314.2	PTAC7 Plastid transcriptionally active7, chloroplast precursor /		??			chloroplast transcription ?			plastid	plastid		
AT2G45280	15497	AT2G45280.2	RAD51C DNA repair protein RAD51 homolog 3 /		??			DNA binding ?				plastid		
AT1G01860	22817	At1g01860	PFC1 (PALEFACE 1); mRNA (2'-O-methyladenosine-N6-)-methyltransferase	343		8.77	38.02							
AT1G05385	22818	At1g05385	photosystem II 11 kDa protein-related	199		8.43	22.27							
AT1G06190	22819	At1g06190	ATP binding / ATPase, coupled to transmembrane movement of ions, phosphorylative mechanism	401		5.06	44.53							

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AT1G21640	22820	At1g21640	NADK2; NAD+ kinase/ calmodulin binding	999		7.5	109.19							
AT1G22410	22821	At1g22410	Amino acid biosynthesis : Phospho-2-dehydro-3-deoxyheptonate aldolase 2	507		8.93	56.15							
AT1G22530	22822	At1g22530	PATL2 (PATELLIN 2); transporter	683		4.92	76.01							
AT1G26220	22823	At1g26220	GCN5-related N-acetyltransferase (GNAT) family protein	197		9.39	21.85							
AT1G33240	22824	At1g33240	AT-GTL1 (GT2-LIKE 1); DNA binding / transcription factor	669		5.73	74.21							
AT1G42970	22825	At1g42970	GAPB (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE B SUBUNIT); glyceraldehyde-3-phosphate dehydrogenase (NADP+)/glyceraldehyde-3-phosphate dehydrogenase	447		6.33	47.66							
AT1G48350	22826	At1g48350	ribosomal protein L18 family protein	170		9.92	18.72							

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AT1G59990	22827	At1g59990	DEAD/DEAH box helicase, putative (RH22)	581		5.8	64.75							
AT1G64430	22828	At1g64430	FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; EXPRESSED IN: carpel; EXPRESSED DURING: 4 anthesis; CONTAINS InterPro DOMAIN/s: Pentatricopeptide repeat (InterPro:IPR002885); Has 22 Blast hits	559		5.73	61.62							
AT1G65960	22829	At1g65960	GAD2 (GLUTAMATE DECARBOXYLASE 2); calmodulin binding / glutamate decarboxylase	494		6.07	41.75							
AT1G72160	22830	At1g72160	SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein	490		5.21	56.11							
AT1G76890	22831	At1g76890	GT2; transcription factor	575		6.35	65.84							

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AT2G01050	22832	At2g01050	zinc ion binding;nucleic acid binding	404		8.36	56.34							
AT2G20450	22833	At2g20450	60S ribosomal protein L14 (RPL14A)	134		10.12	15.51							
AT2G21870	22834	At2g21870	unknown protein	240		6.27	27.6							
AT2G22475	22835	At2g22475	GEM (GL2-EXPRESSION MODULATOR)	299		5.27	32.22							
AT2G24395	22836	At2g24395	chaperone protein dnaJ-related	132		8.93	15.06							
AT2G27730	22837	At2g27730	unknown protein	113		9.64	11.95							
AT2G33040	22838	At2g33040	ATP synthase gamma chain, mitochondria I (ATPC)	325		9.01	35.45							
AT3G05970	22839	At3g05970	LACS6 (long-chain acyl-CoA synthetase 6); long-chain-fatty-acid-CoA ligase	701		8.11	76.6							
AT3G06980	22840	At3g06980	DEAD/DEAH box helicase, putative	781		7.56	87.43							
AT3G07070	22841	At3g07070	protein kinase family protein	414		5.35	46.07							
AT3G07670	22842	At3g07670	SET domain-containing protein	504		8.25	57.61							

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AT3G10860	22843	At3g10860	ubiquinol-cytochrome C reductase complex ubiquinone-binding protein, putative / ubiquinol-cytochrome C reductase complex 8.2 kDa protein, putative	72		9.48	8.51							
AT3G18390	22844	At3g18390	EMB1865 (embryo defective 1865); RNA binding	848		5.76	96.0							
AT3G20720	22845	At3g20720	Unknown	1199		5.19	122.85							
AT3G23070	22846	At3g23070	RNA binding	881		5.94	100.17							
AT3G52920	22847	At3g52920	unknown protein	180		6.53	20.67							
AT4G00030	22848	At4g00030	plastid-lipid associated protein PAP / fibrillin family protein	212		9.35	24.07							
AT4G12880	22849	At4g12880	plastocyanin-like domain-containing protein	141		9.25	16.13							
AT4G18740	22850	At4g18740	transcription termination factor	245		9.92	27.33							
AT4G20760	22851	At4g20760	short-chain dehydrogenase/reductase (SDR) family protein	298		9.64	32.48							
AT4G31530	22852	At4g31530	binding / catalytic	338		7.67	35.23							
AT5G01730	22853	At5g01730	AtSCAR4	1170		4.56	128.62							
AT5G10860	22854	At5g10860	CBS domain-containing protein	206		9.1	22.73							

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AT5G10910	22855	At5g10910	mraW methylase family protein	434		9.35	48.62							
AT5G16130	22856	At5g16130	40S ribosomal protein S7 (RPS7C)	190		9.75	22.06							
AT5G16840	22857	At5g16840	BPA1 (BINDINGPA RTNEROFA CD11 1); nucleic acid binding / nucleotide binding / oxidoreductase	260		5.46	27.23							
AT5G17230	22858	At5g17230	phytoene synthase (PSY) / geranylgeranyl-diphosphate geranylgeranyl transferase	437		9.22	47.49							
AT5G23760	22859	At5g23760	heavy-metal-associated domain-containing protein	103		8.61	11.57							
AT5G63060	22860	At5g63060	transporter	263		8.95	30.15							
AT5G63400	22861	At5g63400	ADK1 (ADENYLATE KINASE 1); ATP binding / adenylate kinase/ nucleobase, nucleoside, nucleotide kinase/ nucleotide kinase/ phosphotransferase, phosphate group as acceptor	246		6.91	26.93							

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ATCG00900	22862	AtCg00900	encodes a chloroplast ribosomal protein S7, a constituent of the small subunit of the ribosomal complex	155		11.28	17.36							
ATCG01020	22863	AtCg01020	encodes a chloroplast ribosomal protein L32, a constituent of the large subunit of the ribosomal complex	52		12.05	6.06							