Supplementary Table 1: Gene-ID list of rice-Arabidopsis homologous gene pairs with their corresponding functional descriptions.

Rice Gene ID	*Functional Description*	*Arabidopsis Gene ID*	*Functional Description*
10A19I.12	ADP Glucose	At1g27680	APL2 (Large Subunit Of AGP 2)
10A19I.3	Integral Membrane Protein	At1g19450	Integral Membrane Protein, Putative / Sugar Transporter Family Protein
24K23.23	Putative Amylogenin	At3g08900	RGP3 (REVERSIBLY GLYCOSYLATED POLYPEPTIDE 3); Alpha-1,4-Glucan-Protein Synthase (UDP-Forming)
49D11.23	Putative AAA-Type Atpase	At2g18330	AAA-Type Atpase Family Protein
B1011A07.10	Putative Pectinesterase	At4g02330	Pectinesterase Family Protein
B1011A07.16	Putative Pectinesterase 2.1 Precursor	At1g53830	ATPME2 (Arabidopsis Thaliana Pectin Methylesterase 2)
B1011A07.20	Putative Endo-1,3(4)-Beta-Glucanase	At4g02290	Glycosyl Hydrolase Family 9 Protein
B1011A07.31	Putative Branched Chain Alpha-Keto Acid	At3g06850	DIN3/LTA1 (DARK INDUCIBLE 3); Alpha-Ketoacid Dehydrogenase
B1012D10.16	Phospholipase-Like Protein	At2g39420	Esterase/Lipase/Thioesterase Family Protein
B1012D10.2	MCT-1 Protein-Like	At1g09150	Pseudouridine Synthase And Archaeosine Transglycosylase (PUA) Domain-Containing Protein
B1015E06.16	Putative CRK1 Protein	At1g53050	Protein Kinase Family Protein
B1015E06.2	Hypothetical Protein	At5g61500	Autophagy 3 (APG3)
B1015E06.5	Hypothetical Protein	At5g11640	Unknown Protein
B1026C12.20	Putative Speckle-Type POZ Protein	At2g39760	ATBPM3; Protein Binding
B1026C12.22	Putative Sterol 4-Alpha-Methyl-Oxidase	At2g29390	SMO2-1 (Sterol 4-Alpha-Methyl-Oxidase 1)
B1026C12.3	Putative Ethylene-Inducible Protein	At5g01410	PDX1 (PYRIDOXINE BIOSYNTHESIS 1.3); Protein Heterodimerization/ Protein Homodimerization
B1026C12.33	Unknown Protein	At1g61900	Unknown Protein
B1029H08.10	Putative Thylakoid Lumenal 21.5 Kda Protein,	At4g15510	Calcium Ion Binding
B1040D09.4	Putative RNA Helicase	At5g08610	DEAD Box RNA Helicase (RH26)
B1045D11.20	Unknown Protein	At3g53410	Zinc Finger (C3HC4-Type RING Finger) Family Protein
B1045D11.4	Putative Asparaginyl-Trna Synthetase	At1g70980	SYNC1; ATP Binding / Aminoacyl-Trna Ligase/ Asparagine-Trna Ligase/ Aspartate-Trna Ligase/ Nucleic Acid Binding
B1046G12.25	Putative Phosphoribosylaminoimidazole	At2g37690	Phosphoribosylaminoimidazole Carboxylase, Putative / AIR Carboxylase, Putative
B1047A05.37	Putative 60S Ribosomal Protein L7	At3g13580	60S Ribosomal Protein L7 (RPL7D)
B1047A05.39	Hypothetical Protein	At4g17620	Glycine-Rich Protein
B1051E10.16	Putative Serine/Threonine Protein Phosphatase	At3g05580	Serine/Threonine Protein Phosphatase, Putative
B1053A04.20-2	Sexual Differentiation Process Protein	At5g64410	ATOPT4 (Oligopeptide Transporter 4); Oligopeptide Transporter

B1056G08.109	Putative 3-Oxoacyl-[Acyl-Carrier-Protein]	At1g74960	FAB1 (FATTY ACID BIOSYNTHESIS 1); Fatty-Acid Synthase
B1056G08.112	Putative (S)-2-Hydroxy-Acid Oxidase	At3g14130	(S)-2-Hydroxy-Acid Oxidase, Peroxisomal, Putative / Glycolate Oxidase, Putative / Short Chain Alpha-Hydroxy Acid Oxidase, Putative
B1060H01.15	Putative Flavonol Glucosyltransferase	At1g01390	UDP-Glucoronosyl/UDP-Glucosyl Transferase Family Protein
B1060H01.16	Putative Flavonol Glucosyltransferase	At3g16520	UDP-Glucoronosyl/UDP-Glucosyl Transferase Family Protein
B1060H01.23	Putative Flavonol Glucosyltransferase	At5g26310	UDP-Glucoronosyl/UDP-Glucosyl Transferase Family Protein
B1060H01.29	Putative 8-Amino-7-Oxononanoate Synthase	At5g04620	ATBIOF; 8-Amino-7-Oxononanoate Synthase/ Transaminase
B1063H10.19	Putative RPR1h	At3g07040	Rpm1 (Resistance To P. Syringae Pv Maculicola 1)
B1063H10.20	Unknown Protein	At1g68220	Unknown Protein
B1063H10.8	Hypothetical Protein	At4g30410	Unknown Protein
B1064G04.16	Similar To Membrane-Associated Salt-Inducible	At1g10910	Unknown Protein
B1064G04.22	Asparaginyl Endopeptidase	At4g32940	GAMMA-VPE (Vacuolar Processing Enzyme Gamma); Cysteine-Type Endopeptidase
B1064G04.27	Putative IAA-Ala Hydrolase	At1g51760	IAR3 (IAA-ALANINE RESISTANT 3); Metallopeptidase
B1065E10.17	Putative Amino Acid Transport Protein	At5g09220	AAP2 (AMINO ACID PERMEASE 2); Amino Acid Permease
B1065E10.20	Putative Serine/Threonine Protein Kinase	At1g11050	Protein Kinase Family Protein
B1065E10.21	MADS Box Protein	At5g20240	PI (PISTILLATA); DNA Binding / Transcription Factor
B1065E10.30	Ankyrin-Like Protein	At5g64030	Dehydration-Responsive Protein-Related
B1065G12.20	Putative Peptide Transport Protein	At3g54140	Proton-Dependent Oligopeptide Transport (POT) Family Protein
B1066G12.15	Unknown Protein	At5g54860	Integral Membrane Transporter Family Protein
B1070A12.14	Putative Auxin-Responsive GH3	At5g54510	DFL1 (DWARF IN LIGHT 1); Indole-3-Acetic Acid Amido Synthetase
B1070A12.16	Hypothetical Protein	At2g16030	Unknown Protein
B1070A12.17	Hypothetical Protein	At1g55890	Pentatricopeptide (PPR) Repeat-Containing Protein
B1074C08.21	Putative RNA-Directed RNA Polymerase	At3g49500	RDR6 (RNA-DEPENDENT RNA POLYMERASE 6); Nucleic Acid Binding
B1075D06.2	Hypothetical Protein	At5g16210	HEAT Repeat-Containing Protein
B1075D06.4	Fimbrin-Like Protein (Actin Binding Motif)	At5g48460	Fimbrin-Like Protein, Putative
B1075D06.5	Putative Receptor-Like Protein Kinase	At2g01210	Leucine-Rich Repeat Transmembrane Protein Kinase, Putative
B1075D06.6	Putative Retrovirus-Related Pol Polyprotein From	At3g60170	Transposable Element Gene
B1077E10.18-1	Putative Phosphoglycolate Phosphatase Precursor	At5g47760	ATPK5 (Arabidopsis Thaliana Serine/Threonine Protein Kinase 5); Phosphoglycolate Phosphatase
B1078G07.15	Putative Pectinacetylesterase	At5g26665	Unknown Protein
B1078G07.20	Ankyrin-Kinase -Like Protein	At3g59830	Ankyrin Protein Kinase, Putative
B1078G07.4	Putative Allyl Alcohol Dehydrogenase	At1g65560	Allyl Alcohol Dehydrogenase, Putative
B1080D07.14	Ostatc	At2g01110	Apg2 (Albino And Pale Green 2)
B1080D07.15	Putative 33kda Oxygen Evolvingprotein Of	At3g50820	PSBO-2/PSBO2 (PHOTOSYSTEM II SUBUNIT O-2); Oxygen Evolving
B1088C09.1	Hypothetical Protein	At2g40400	Unknown Protein
B1088C09.4	Putative Laccase	At5g05390	LAC12 (Laccase 12); Copper Ion Binding / Oxidoreductase

B1088C09.6	Putative Leucine Zipper Protein	At1g07000	ATEXO70B2 (Exocyst Subunit EXO70 Family Protein B2); Protein Binding
B1088C09.7	Putative Leucine Zipper Protein	At2g28640	ATEXO70H5 (Exocyst Subunit EXO70 Family Protein H5); Protein Binding
B1090H08.30	Putative Cytochrome B-561	At5g38630	ACYB-1 (Arabidopsis Cytochrome B561 -1); Carbon-Monoxide Oxygenase
B1097D05.12	Putative Lycopene Epsilon-Cyclase	At5g57030	LUT2 (LUTEIN DEFICIENT 2); Lycopene Epsilon Cyclase
B1097D05.13	Putative Serine Threonine Kinase	At5g26150	Protein Kinase Family Protein
B1099D03.27	Putative S-Receptor Kinase	At2g19130	S-Locus Lectin Protein Kinase Family Protein
B1099H05.23	Putative Germin A	At5g39110	Germin-Like Protein, Putative
B1100D10.21	Putative Acyl-Coa:1-Acylglycerol-3-Phosphate	At3g18850	Lpat5
B1100D10.32	Unknown Protein	At5g54490	PBP1 (PINOID-BINDING PROTEIN 1); Calcium Ion Binding
B1100D10.34	Putative Serine/Threonine Kinase	At4g27300	S-Locus Protein Kinase, Putative
B1100H02.7	Putative ARGONAUTE9 Protein	At2g27040	Ago4 (Argonaute 4)
B1103G11.21	Putative Auxin-Independent Growth Promoter	At3g26370	Unknown Protein
B1108H10.18	Putative Exopolygalacturorase Precursor	At2g15450	Glycoside Hydrolase Family 28 Protein / Polygalacturonase (Pectinase) Family Protein
B1108H10.8	Unknown Protein	At3g17210	Stable Protein 1-Related
B1109A06.20	Unknown Protein	At2g32000	DNA Binding / DNA Topoisomerase Type I
B1111C09.4	Putative 3-Dehydroquinate Dehydratase	At3g06350	EMB3004/MEE32 (EMBRYO DEFECTIVE 3004, Maternal Effect Embryo Arrest 32); 3-Dehydroquinate Dehydratase/ NADP Binding / Shikimate 5-Dehydrogenase
B1112D09.3	Putative Root Hair Defective 3 (RHD3)	At3g13870	Rhd3 (Root Hair Defective 3)
B1114D08.16-1	Putative RNA Helicase	At1g31970	DEAD/DEAH Box Helicase, Putative
B1114D08.4	Putative Fertility Restorer Homologue	At5g61990	Pentatricopeptide (PPR) Repeat-Containing Protein
B1114E07.12	Putative Adenylate Kinase, Chloroplast	At5g35170	Nucleotide Kinase
B1116H04.25	Putative Activator Of 90 Kda Heat Shock Protein	At3g12050	Aha1 Domain-Containing Protein
B1116H04.8	Unknown Protein	At1g55230	Unknown Protein
B1120F06.103	Unknown Protein	At5g63440	Unknown Protein
B1120F06.107	Unknown Protein	At1g24310	Hypothetical Protein
B1121A12.18	Putative Auxin-Independent Growth Promoter	At5g15740	Unknown Protein
B1121A12.19	Unknown Protein	At5g55710	Unknown Protein
B1121A12.27	MAP Kinase-Like	At1g68940	Armadillo/Beta-Catenin Repeat Protein-Related / U-Box Domain-Containing Protein
B1121A12.37	Putative Protease IV	At1g73990	SPPA (Signal Peptide Peptidase); Protease IV/ Serine-Type Endopeptidase
B1130G10.10	Putative Protein Kinase	At1g52290	Protein Kinase Family Protein
B1130G10.11	Putative GTP-Binding Protein Rab7a	At3g18820	Atrabg3f/Atrab7b (Arabidopsis Rab Gtpase Homolog G3f); GTP Binding
B1130G10.13	Putative GTP-Binding Protein RIC2	At1g16920	RAB11 (ARABIDOPSIS RAB GTPASE HOMOLOG A1B); GTP Binding
B1130G10.17	Putative Gamma-Glutamyl Hydrolase	At1g78680	ATGGH2 (GAMMA-GLUTAMYL HYDROLASE 2); Gamma-Glutamyl Hydrolase
B1130G10.20	Unknown Protein	At4g18930	Cyclic Phosphodiesterase
B1130G10.22	Putative GDSL-Like Lipase/Hydrolase	At5g45670	GDSL-Motif Lipase/Hydrolase Family Protein

B1130G10.4	Hypothetical Protein	At5g46020	Unknown Protein
B1131B07.14	Putative RAB7A Protein (GTP-Binding Protein)	At4g09720	Atrabg3a; GTP Binding
B1131B07.15	Putative Zinc Finger Protein	At5g20220	Zinc Knuckle (CCHC-Type) Family Protein
B1131G07.11	Putative Elongation Factor 1-Gamma	At1g57720	Translation Elongation Factor
B1131G07.12	Elongation Factor 1-Gamma	At1g09640	Elongation Factor 1B-Gamma, Putative / Eef-1B Gamma, Putative
B1131G08.9	Hypothetical Protein	At1g29190	Pseudogene, Hypothetical Protein
B1139B11.18	Unknown Protein	At2g41640	Unknown Protein
B1139B11.7	Hypothetical Protein	At2g26870	Phosphoesterase Family Protein
B1139B11.9	Hypothetical Protein	At1g76640	Calmodulin-Related Protein, Putative
B1140D12.9	Putative Serine Carboxypeptidase II-Like	At1g73280	SCPL3 (Serine Carboxypeptidase-Like 3); Serine Carboxypeptidase
B1142B04.23	POZ Domain Protein Family-Like	At1g55760	BTB/POZ Domain-Containing Protein
B1142B04.25-1	Putative Alkaline Alpha-Galactosidase Seed	At1g55740	ATSIP1 (ARABIDOPSIS THALIANA SEED IMBIBITION 1); Hydrolase, Hydrolyzing O-Glycosyl Compounds
B1142B04.27	Putative Cytochrome C Oxidase Subunit 15(COX15)	At5g56090	Cox15 (Cytochrome C Oxidase 15)
B1142C05.18	Putative Cytidine Deaminase	At2g19570	Cda1 (Cytidine Deaminase 1)
B1142C05.30	Rev Interacting Protein-Like	At5g08420	RNA Binding
B1142C05.32	Putative Myosin Heavy Chain	At1g54560	XIE (Myosin-Like Protein XIE); Motor/ Protein Binding
B1143G03.3	Hypothetical Protein	At5g42410	Auxin-Responsive Family Protein
B1144B06.21	Unknown Protein	At1g19130	Unknown Protein
B1144D11.19	Putative Glutathione S-Transferase Osgstu4	At1g69920	ATGSTU12 (Arabidopsis Thaliana Glutathione S-Transferase (Class Tau) 12); Glutathione Transferase
B1144D11.20	Putative NADP-Specific Glutatamate	At1g51720	Glutamate Dehydrogenase, Putative
B1144D11.26	Putative Zinc Protease PQQL	At5g56730	Peptidase M16 Family Protein / Insulinase Family Protein
B1144D11.29	Putative Seryl-Trna Synthetase	At5g27470	Seryl-Trna Synthetase / Serine--Trna Ligase
B1147A04.10	Unknown Protein	At4g03290	Calcium-Binding Protein, Putative
B1147A04.12	Putative Glutathione S-Transferase GST 24	At2g29420	ATGSTU7 (GLUTATHIONE S-TRANSFERASE 25); Glutathione Transferase
B1147A04.23	Putative Zinc Finger And C2 Domain Protein	At3g07940	Zinc Finger And C2 Domain Protein, Putative
B1147B12.16	Putative Sulfate Transporter-Like	At2g25680	Sulfate Transporter
B1148D12.5	Putative Receptor Protein Kinase	At5g49760	Leucine-Rich Repeat Family Protein / Protein Kinase Family Protein
B1150F11.13	Putative Glycerol-3-Phosphate Dehydrogenase	At2g41540	GPDHC1; Glycerol-3-Phosphate Dehydrogenase (NAD+)
B1150F11.20	Putative Hexokinase	At1g50460	Hexokinase, Putative
B1151A10.15	Putative Ftsh Protease	At2g26140	FTSH4 (Ftsh Protease 4); ATP-Dependent Peptidase/ Atpase/ Metallopeptidase
B1151A10.18	Putativeethylene-Responsive Protein	At3g16050	A37 (PYRIDOXINE BIOSYNTHESIS 1.2); Protein Heterodimerization
B1155G07.14	Unknown Protein	At1g34470	Permease-Related
B1155G07.16	Putative Racc Protein	At4g28950	ARAC7/ATROP9/RAC7/ROP9 (Rho-Related Protein From Plants 9); GTP Binding

B1155G07.17	Unknown Protein	At2g14260	PIP (Proline Iminopeptidase); Prolyl Aminopeptidase
B1156H12.13	Putative DEAD BOX RNA Helicase	At5g11200	DEAD/DEAH Box Helicase, Putative
B1158C05.7	Unknown Protein	At1g06520	ATGPAT1/GPAT1 (GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE 1); 1-Acylglycerol-3-Phosphate O-Acyltransferase/ Acyltransferase
B1168F12.22	Transporter-Like Protein	At1g78130	UNE2 (Unfertilized Embryo Sac 2); Carbohydrate Transporter/ Sugar Porter
B1168F12.32	Zinc Finger (C3HC4-Type RING Finger)	At2g35330	Zinc Finger (C3HC4-Type RING Finger) Protein-Related
B1168F12.6	Putative Senc	At3g08950	Electron Transport SCO1/Senc Family Protein
B1203H11.11	Putative Fructose-Bisphosphate Aldolase	At2g36460	Fructose-Bisphosphate Aldolase, Putative
B1203H11.9	Putative MA3 Domain-Containing Protein	At4g24800	MA3 Domain-Containing Protein
B1215B07.27-2	Putative Cryptochrome 2	At1g04400	Cry2 (Cryptochrome 2)
B1215B07.31	Putative Phosphoenolpyruvate Carboxylase Kinase	At3g04530	PPCK2 (PHOSPHOENOLPYRUVATE CARBOXYLASE KINASE 2); Kinase
B1215B07.34	Putative Adenosine Kinase	At5g03300	ADK2 (ADENOSINE KINASE 2); Kinase
B1215B07.6	Putative Lysyl-Trna Synthetase	At3g13490	OVA5 (OVULE ABORTION 5); ATP Binding / Aminoacyl-Trna Ligase
B1234D02.6	Unknown Protein	At5g43410	Ethylene-Responsive Factor, Putative
B1248C03.14	Unknown Protein	At4g21630	Subtilase Family Protein
B1249D05.19	Putative Pathogenesis-Related Protein	At1g50060	Pathogenesis-Related Protein, Putative
B1249D05.22	Putative Pathogenesis-Related Protein	At5g66590	Allergen V5/Tpx-1-Related Family Protein
B1249D05.41	PR-1 Type Pathogenesis-Related Protein PR-1a	At4g25790	Allergen V5/Tpx-1-Related Family Protein
B1250G12.14	Putative Hupf2	At2g39260	RNA Binding
B1250G12.17	Putative Response Regulator	At5g24470	APRR5 (PSEUDO-RESPONSE REGULATOR 5); Transcription Regulator
B1250G12.8	Unknown Protein	At3g01440	Oxygen Evolving Enhancer 3 (Psbq) Family Protein
B1267B06.13	MYB27 Protein-Like	At2g16720	MYB7 (Myb Domain Protein 7); DNA Binding / Transcription Factor
B1267B06.22	Putative ORFX	At1g14870	Unknown Protein
B1307A11.10	Putative Protein Kinase Xa21	At3g47580	Leucine-Rich Repeat Transmembrane Protein Kinase, Putative
B1339H09.17	Putative Monoglyceride Lipase	At1g73480	Hydrolase, Alpha/Beta Fold Family Protein
B1339H09.19	Putative Annexin	At1g68090	ANNAT5 (ANN5, ANNEXIN ARABIDOPSIS 5); Calcium Ion Binding / Calcium-Dependent Phospholipid Binding
B1339H09.9	Putative Hexose Transporter	At1g05030	Hexose Transporter, Putative
B1342F01.10	Sucrose Transporter	At1g71890	ATSUC5/SUC5 (SUCROSE-PROTON SYMPORTER 5); Carbohydrate Transporter/ Sucrose:Hydrogen Symporter/ Sugar Porter
B1342F01.15	Zinc Finger (C3HC4-Type RING Finger)-Like	At5g62460	Zinc Finger (C3HC4-Type RING Finger) Family Protein
B1342F01.34	Putative UDP-Glycosyltransferase 85A8	At1g22370	UDP-Glucoronosyl/UDP-Glucosyl Transferase Family Protein
B1358B12.15	Unknown Protein	At5g40770	Atphb3 (Prohibitin 3)
B1358B12.19	Unknown Protein	At2g01770	VIT1 (VACUOLAR IRON TRANSPORTER 1); Iron Ion Transporter
B1358B12.4	Unknown Protein	At1g68610	Unknown Protein
B1364A02.11-1	Putative Glycolate Oxidase	At3g14420	(S)-2-Hydroxy-Acid Oxidase, Peroxisomal, Putative / Glycolate Oxidase, Putative / Short Chain Alpha-Hydroxy Acid Oxidase, Putative

B1364A02.2	Putative LRR Receptor-Like Kinase	At1g17230	Leucine-Rich Repeat Family Protein / Protein Kinase Family Protein
B1370C05.8	Unknown Protein	At3g51050	FG-GAP Repeat-Containing Protein
B1446H11.22	Putative Alpha-Soluble NSF Attachment Protein	At3g56190	ALPHA-SNAP2 (ALPHA-SOLUBLE NSF ATTACHMENT PROTEIN); Soluble NSF Attachment Protein
B1469H02.22-1	Putative Plasma Membrane Integral Protein	At2g37170	PIP2B (Plasma Membrane Intrinsic Protein 2;2); Water Channel
B1469H02.8	Phosphate Translocator-Like	At1g06890	Transporter-Related
C1275ERIPDM	Putative Aquaporin	At5g47450	Attip2;3 (Arabidopsis Thaliana Tonoplast Intrinsic Protein 2;3); Water Channel
H0212B02.3	Putative Peroxidase	At1g44970	Peroxidase, Putative
H0302E05.5	Putative Protein	At3g21610	Unknown Protein
H0806H05.1	Hypothetical Protein	At2g28670	Disease Resistance-Responsive Family Protein / Fibroin-Related
H0806H05.2	Cysteine Synthase	At3g61440	Atcysc1 (Beta-Substituted Ala Synthase 3;1)
H0811E11.2	Contains Similarity To F6I7.30	At4g24820	26S Proteasome Regulatory Subunit, Putative (RPN7)
I1332.2	Hypothetical Protein	At5g52060	ATBAG1 (ARABIDOPSIS THALIANA BCL-2-ASSOCIATED ATHANOGENE 1); Protein Binding
I1332.6	Unknown Protein	At3g62940	OTU-Like Cysteine Protease Family Protein
OAJNBa0031O09.09	3,4-Dihydroxy-2-Butanone Kinase	At3g17770	Dihydroxyacetone Kinase Family Protein
OAJNBa0031O09.11	Phytochrome A	At1g09570	PHYA (PHYTOCHROME A); G-Protein Coupled Photoreceptor/ Signal Transducer
OAJNBa0031O09.12	Putative Peptide Transporter Protein	At2g02040	ATPTR2-B (NITRATE TRANSPORTER 1); Transporter
OJ000126_13.4	Unknown Protein	At2g27460	Sec23/Sec24 Transport Family Protein
OJ000126_13.7	Unknown Protein	At3g52600	ATCWINV2 (ARABIDOPSIS THALIANA CELL WALL INVERTASE 2); Hydrolase, Hydrolyzing O-Glycosyl Compounds
OJ000126_13.8	Unknown Protein	At2g36190	ATCWINV4 (ARABIDOPSIS THALIANA CELL WALL INVERTASE 4); Hydrolase, Hydrolyzing O-Glycosyl Compounds
OJ000223_09.14	Unknown Protein	At3g25980	Mitotic Spindle Checkpoint Protein, Putative (MAD2)
OJ000223_09.15	Unknown Protein	At1g13440	Gapc-2
OJ000315_02.20	Unknown Protein	At5g47860	Hypothetical Protein
OJ1001_C01.113	Putative GDP Dissociation Inhibitor	At2g44100	ATGDI1 (Arabidopsis Thaliana Guanosine Diphosphate Dissociation Inhibitor 1)
OJ1001_D02.29	Putative Actin-Depolymerizing Factor	At1g01750	Actin-Depolymerizing Factor, Putative
OJ1001_D02.30	Pentatricopeptide (PPR) Repeat-Containing	At5g39350	Pentatricopeptide (PPR) Repeat-Containing Protein
OJ1001_D02.31	Putative Anthranilate Phosphoribosyltransferase	At3g57880	C2 Domain-Containing Protein
OJ1001_G01.3	Putative Transmembrane Protein	At5g12130	Pde149 (Pigment Defective 149)
OJ1001_G09.14	Cwfj / Zinc Finger(CCCH-Type)-Like Protein	At5g56900	Cwfj-Like Family Protein / Zinc Finger (CCCH-Type) Family Protein
OJ1003_A09.25	Unknown Protein	At4g31330	Unknown Protein
OJ1003_B06.7	Carboxyl-Terminal Proteinase-Like	At4g17510	Ubiquitin Carboxyl-Terminal Hydrolase, Putative / Ubiquitin Thiolesterase, Putative
OJ1003_C06.106	Putative Esterase	At5g23530	Atcxe18 (Arabidopsis Thaliana Carboxyesterase 18)
OJ1003_E05.12	Unknown Protein	At4g28430	Reticulon Family Protein
OJ1003_F04.28	Ubiquitin-Associated (UBA)/TS-N	At1g04850	Ubiquitin-Associated (UBA)/TS-N Domain-Containing Protein

OJ1003_F04.33	Kelch Repeat-Containing F-Box Protein-Like	At1g67480	Kelch Repeat-Containing F-Box Family Protein
OJ1003_F05.11	Putative Flavonoid Glucosyl-Transferase	At2g36750	UGT72C1 (UDP-Glucosyl Transferase 72C1); UDP-Glycosyltransferase/ Transferase, Transferring Glycosyl Groups
OJ1003_H02.125	Putative RSH, Disease Resistance-Related	At1g54130	RSH3 (RELA/SPOT HOMOLOG 3); Catalytic
OJ1003C07.7	Putative Myo-Inositol-1-Phosphate Synthase	At2g22240	Inositol-3-Phosphate Synthase Isozyme 2 / Myo-Inositol-1-Phosphate Synthase 2 / MI-1-P Synthase 2 / IPS 2
OJ1004_A05.11	Putative Eukaryotic Initiation Factor (Iso)4F	At5g57870	Eukaryotic Translation Initiation Factor 4F, Putative / Eif-4F, Putative
OJ1004_A05.21	Unknown Protein	At1g80860	N-Methyltransferase
OJ1004_A05.35	Putative Emperature Stress-Induced Lipocalin	At5g58070	Lipocalin, Putative
OJ1004_A05.37	Putative Calcium Binding Atopy-Related	At4g32060	Calcium-Binding EF Hand Family Protein
OJ1004_A05.39	Leucine-Rich Repeat-Like Protein	At1g15740	Leucine-Rich Repeat Family Protein
OJ1004_A05.41	Meprin And TRAF Homology Domain-Containing	At2g25320	Unknown Protein
OJ1004_A11.24	Unknown Protein	At5g42920	Hypothetical Protein
OJ1004_A11.25	Lipase Class 3-Like	At5g67050	Lipase Class 3 Family Protein
OJ1004_A11.27	Putative Flavonol Synthase	At5g08640	Fls (Flavonol Synthase)
OJ1004_E02.7	Unknown Protein	At1g77350	Unknown Protein
OJ1004_E02.9	Putative 60S Ribosomal Protein L24	At2g36620	RPL24A (RIBOSOMAL PROTEIN L24); Structural Constituent Of Ribosome
OJ1004_E04.17	Unknown Protein	At5g14390	Unknown Protein
OJ1004_E04.32	Putative Minichromosome Maintenance Deficient	At2g07690	Minichromosome Maintenance Family Protein / MCM Family Protein
OJ1004_E04.34	Putative Aspartate Transaminase	At5g19550	Asp2 (Aspartate Aminotransferase 2)
OJ1004_F02.11	Putative Membrane Protein	At1g51340	MATE Efflux Family Protein
OJ1004_H01.22	Putative Transmembrane Protein TM9SF3 (66.6 Kd)	At1g10950	Endomembrane Protein 70, Putative
OJ1004C08.10	Hypothetical Protein	At4g35760	Electron Carrier/ Protein Disulfide Oxidoreductase
OJ1004C08.14	Putative Ubiquitin Protein	At2g17190	Ubiquitin Family Protein
OJ1004C08.15	Putative Catalase	At4g35090	CAT2 (CATALASE 2); Catalase
OJ1004C08.17	Putative Protein Kinase	At2g17220	Protein Kinase, Putative
OJ1004C08.18	Putative Protein Kinase	At1g20650	Protein Kinase
OJ1004C08.6	Putative AMP-Binding Protein	At1g20510	OPCL1 (OPC-8:0 COA LIGASE1); 4-Coumarate-Coa Ligase
OJ1005_B05.29-1	Succinate Dehydrogenase Iron-Protein Subunit	At5g40650	SDH2-2 (Succinate Dehydrogenase 2-2)
OJ1005_B11.10	Putative Protein Kinase	At3g23310	Protein Kinase, Putative
OJ1005_B11.7	Putative Glucosyltransferase	At4g07960	ATCSLC12 (Cellulose Synthase-Like C12); Transferase, Transferring Glycosyl Groups
OJ1005_D12.17	Putative Glucose-6-Phosphate Isomerase	At4g24620	Pgi1 (Chloroplastic Phosphoglucose Isomerase)
OJ1005_D12.35	Unknown Protein	At4g33590	Hypothetical Protein
OJ1005_D12.36-1	Putative Calcium-Dependent Protein Kinase	At1g12680	PEPKR2 (PHOSPHOENOLPYRUVATE CARBOXYLASE-RELATED KINASE 2); Kinase
OJ1005_D12.36-2	Putative Calcium-Dependent Protein Kinase	At5g12180	CPK17 (Calcium-Dependent Protein Kinase 17); Calcium- And Calmodulin-Dependent Protein Kinase/ Kinase

OJ1005_D12.38	Putative Succinoaminoimidazolecarboximide	At3g21110	PUR7 (Purin 7); Phosphoribosylaminoimidazolesuccinocarboxamide Synthase
OJ1005_E12.1	Putative Nascent Polypeptide Associated Complex	At3g12390	Nascent Polypeptide Associated Complex Alpha Chain Protein, Putative / Alpha-NAC, Putative
OJ1005_H01.19	Putative Pectinesterase	At5g53370	Pectinesterase Family Protein
OJ1006_A02.12-1	PDR-Like ABC Transporter	At1g15520	ATPDR12/PDR12 (PLEIOTROPIC DRUG RESISTANCE 12); Atpase, Coupled To Transmembrane Movement Of Substances
OJ1006_A02.22	Putative Golgi-Associated Particle 102K Chain	At1g52360	Coatomer Protein Complex, Subunit Beta 2 (Beta Prime), Putative
OJ1006_A02.24	Putative Coatomer Protein Complex, Subunit Beta	At3g15980	Coatomer Protein Complex, Subunit Beta 2 (Beta Prime), Putative
OJ1006_A02.42	Putative Protein Kinase Xa21	At3g47090	Leucine-Rich Repeat Transmembrane Protein Kinase, Putative
OJ1006_A02.6	Putative Plastidic ATP/ADP Transporter	At1g80300	Chloroplast ADP, ATP Carrier Protein 1 / ADP, ATP Translocase 1 / Adenine Nucleotide Translocase 1 (AATP1)
OJ1006_D05.16	Putative Pectate Lyase Precursor	At1g14420	AT59 (Arabidopsis Homolog Of Tomato LAT59); Lyase/ Pectate Lyase
OJ1006_D05.27-2	Putative Histone Deacetylase HDAC3	At4g38130	Hd1 (Histone Deacetylase 19, Histone Deacetylase19)
OJ1006_D05.35	Putative Protein Kinase Xa21	At3g47580	Leucine-Rich Repeat Transmembrane Protein Kinase, Putative
OJ1006F06.12	Putative ATP Phosphoribosyl Transferase	At1g58080	Atatp-Prt1 (Atp Phosphoribosyl Transferase)
OJ1006F06.19	Unknown Protein	At1g21880	Peptidoglycan-Binding Lysm Domain-Containing Protein
OJ1006F06.4	Putative F-Box Protein	At2g17020	F-Box Family Protein (FBL10)
OJ1006F06.5	Putative Glutathione S-Transferase	At3g03190	ATGSTF11 (GLUTATHIONE S-TRANSFERASE F11); Glutathione Transferase
OJ1006F06.7	Putative Glutathione S-Transferase	At2g47730	ATGSTF8 (GLUTATHIONE S-TRANSFERASE 8); Glutathione Transferase
OJ1007_D04.17	Putative Anthranilate Phosphoribosyltransferase	At1g70570	Anthranilate Phosphoribosyltransferase, Putative
OJ1007_D04.18	Putative ATP Synthase	At2g21870	Unknown Protein
OJ1007_D04.3	Putative Polygalacturonase	At1g23460	Polygalacturonase
OJ1008_C03.10	Putative Translational Initiation Factor Eif-4A	At3g13920	EIF4A1 (Eukaryotic Translation Initiation Factor 4A-1)
OJ1008_D06.10	Putative S-Adenosyl-L-Methionine:Salicylic Acid	At5g66430	S-Adenosyl-L-Methionine:Carboxyl Methyltransferase Family Protein
OJ1008_D06.15	Putative Microtubule-Associated Protein	At5g55230	ATMAP65-1 (MICROTUBULE-ASSOCIATED PROTEINS 65-1); Microtubule Binding
OJ1008_E02.21	Putative SEC14 Cytosolic Factor	At1g19650	SEC14 Cytosolic Factor, Putative / Phosphoglyceride Transfer Protein, Putative
OJ1008_E02.6	Putative Diaminopimelate Decarboxylase	At3g14390	Diaminopimelate Decarboxylase, Putative / DAP Carboxylase, Putative
OJ1008_F08.11	Dehydrogenase-Like Protein	At5g10730	Catalytic/ Coenzyme Binding
OJ1008_F08.14	Unknown Protein	At4g21640	Subtilase Family Protein
OJ1008_F08.16	Ranbpm-Like	At1g35470	Spla/Ryanodine Receptor (SPRY) Domain-Containing Protein
OJ1012B02.1	Unknown Protein	At3g19260	Lag1 Homolog 2 (Longevity Assurance Gene1 Homolog 2)
OJ1012B02.12	Unknown Protein	At2g39970	Peroxisomal Membrane Protein (PMP36)
OJ1012B02.4	Putative Anthraniliate Synthase Alpha 2 Subunit	At2g29690	ASA2 (Anthranilate Synthase 2); Anthranilate Synthase
OJ1014_C08.12	Putative Trnahis Guanylyltransferase	At2g31580	Unknown Protein
OJ1014_E02.13	Unknown Protein	At5g49410	Unknown Protein
OJ1014_E09.29	Putative Pyruvate Kinase Isozyme A, Chloroplast	At3g22960	Pyruvate Kinase, Putative
OJ1014_E09.9	Bifunctional Phosphopantetheine Adenylyl	At2g18250	ATCOAD (4-PHOSPHOPANTETHEINE ADENYLYLTRANSFERASE); Nucleotidyltransferase/

			Pantetheine-Phosphate Adenylyltransferase
OJ1014_G12.22	Unknown Protein	At2g26690	Nitrate Transporter (NTP2)
OJ1014_G12.25	Unknown Protein	At2g23610	Esterase, Putative
OJ1014_G12.30	Putative Ca2+/H+-Exchanging Protein	At3g51860	CAX3 (Cation Exchanger 3); Cation:Cation Antiporter
OJ1014_H03.11	Putative Anther-Specific Proline-Rich Protein	At5g33370	GDSL-Motif Lipase/Hydrolase Family Protein
OJ1014_H03.14	Putative Polyribonucleotide	At5g14580	Polyribonucleotide Nucleotidyltransferase, Putative
OJ1015F07.11	Putative NAM-Like Protein	At4g36160	ANAC076/VND2 (Arabidopsis NAC Domain Containing Protein 76, VASCULAR-RELATED NAC-DOMAIN 2); Transcription Factor
OJ1015F07.14	Putative Protein Kinase	At1g12460	Leucine-Rich Repeat Transmembrane Protein Kinase, Putative
OJ1015F07.2	Putative Phosphoribosylanthranilate Transferase	At5g17990	TRP1 (TRYPTOPHAN BIOSYNTHESIS 1); Anthranilate Phosphoribosyltransferase
OJ1015F07.8	Putative Serine/Threonine Kinase	At1g01140	CIPK9 (CBL-INTERACTING PROTEIN KINASE 9); Kinase
OJ1017C11.7	Putative Squalene Monooxygenase	At1g58440	XF1; Oxidoreductase
OJ1019_E02.23	Putative Lectin-Like Protein Kinase	At5g10530	Lectin Protein Kinase, Putative
OJ1019_E02.25	Putative Insulin Degrading Enzyme	At2g41790	Peptidase M16 Family Protein / Insulinase Family Protein
OJ1019_E02.4	Floral Organ Regulator 2	At5g06870	PGIP2 (POLYGALACTURONASE INHIBITING PROTEIN 2); Protein Binding
OJ1020_C02.24	Putative Pentatricopeptide (PPR)	At1g02060	Pentatricopeptide (PPR) Repeat-Containing Protein
OJ1020_C02.26	Putative P18	At2g45640	SAP18 (SIN3 ASSOCIATED POLYPEPTIDE P18); Protein Binding / Transcription Regulator
OJ1027_G06.13	Putative ERD4 Protein	At1g30360	Erd4 (Early-Responsive To Dehydration 4)
OJ1027_G06.21	Unknown Protein	At1g17210	Zinc Ion Binding
OJ1027_G06.25	Putative CBL-Interacting Protein Kinase 23	At1g30270	CIPK23 (CBL-INTERACTING PROTEIN KINASE 23); Kinase
OJ1029_F04.24	Putative PRLI-Interacting Factor K	At4g15420	PRLI-Interacting Factor K
OJ1031_C12.26	Putative Kinetochore Protein	At1g75950	SKP1 (ARABIDOPSIS SKP1 HOMOLOGUE); Ubiquitin-Protein Ligase
OJ1041F02.16	Putative Male Fertility Protein [Zea Mays]	At3g59530	Strictosidine Synthase Family Protein
OJ1046_F07.17-1	Putative Alpha,Alpha-Trehalose-Phosphate	At2g18700	ATTPS11 (Arabidopsis Thaliana Trehalose Phosphatase/Synthase 11); Transferase, Transferring Glycosyl Groups
OJ1046_F07.26	Putative Receptor-Like Kinase Xa21-Binding	At5g07270	Ankyrin Repeat Family Protein
OJ1046_F10.128-2	Putative DNA-Dependent Protein Kinase 70 Kda	At1g16970	ATKU70/KU70 (Arabidopsis Thaliana Ku70 Homolog); Double-Stranded DNA Binding / Protein Binding
OJ1046_F10.129-1	Putative Mitogen Activated Protein Kinase	At3g04910	WNK1 (WITH NO LYSINE (K) 1); Kinase
OJ1047_A06.117	Plasma Membrane Intrinsic Protein	At3g54820	PIP2;5/PIP2D (Plasma Membrane Intrinsic Protein 2;5); Water Channel
OJ1047_A06.130	Putative 60S Ribosomal Protein L44	At4g14320	60S Ribosomal Protein L36a/L44 (RPL36aB)
OJ1047_C01.10	Arm Repeat-Containing Protein-Like Protein	At3g01400	Armadillo/Beta-Catenin Repeat Family Protein
OJ1047_C01.14	Putative Interferon-Related Protein	At1g27760	Interferon-Related Developmental Regulator Family Protein / IFRD Protein Family
OJ1047_C01.4	Hypothetical Protein	At1g75110	Rra2 (Reduced Residual Arabinose 2)
OJ1047_C01.8	Putative Eukaryotic Peptide Chain Release Factor	At3g26618	ERF1-3 (EUKARYOTIC RELEASE FACTOR 1-3); Translation Release Factor
OJ1048_C10.5	Putative Proton Myo-Inositol Transporter	At1g30220	ATINT2 (INOSITOL TRANSPORTER 2); Carbohydrate Transporter/ Sugar Porter

OJ1048_C10.6	Putative MAGE	At1g34770	MAGE-8 Antigen-Related
OJ1057_E05.110	Putative Nramp1 Protein	At1g80830	NRAMP1 (NRAMP Metal Ion Transporter 1); Manganese Ion Transporter/ Metal Ion Transporter
OJ1058_A12.123	Serine/Threonine Kinase Receptor Precursor-Like	At4g23280	Protein Kinase, Putative
OJ1058_A12.126	Serine/Threonine Kinase Receptor Precursor-Like	At4g23180	CRK10 (CYSTEINE-RICH RLK10); Kinase
OJ1058_A12.128-2	Contains EST(S): D22146(C10415)	At4g04500	Protein Kinase Family Protein
OJ1058_B11.118	Unknown Protein	At5g51150	Unknown Protein
OJ1058_C08.10	Putative Polygalacturonase	At4g23500	Glycoside Hydrolase Family 28 Protein / Polygalacturonase (Pectinase) Family Protein
OJ1058_F05.4	Unknown Protein	At1g43130	Lcv2 (Like Cov 2)
OJ1058_F05.5	Putative Polypyrimidine Track-Binding Protein	At1g43190	Polypyrimidine Tract-Binding Protein, Putative / Heterogeneous Nuclear Ribonucleoprotein, Putative
OJ1058_F07.19	Putative Class IV Chitinase (CHIV)	At3g54420	ATEP3 (Arabidopsis Thaliana Chitinase Class IV); Chitinase
OJ1058_F07.22	Putative Eukaryotic Translation Initiation	At1g73180	Eukaryotic Translation Initiation Factor-Related
OJ1060_D03.125	Amino Acid Acetyltransferase(N-Acetylglutamate	At2g22910	GCN5-Related N-Acetyltransferase (GNAT) Family Protein / Amino Acid Kinase Family Protein
OJ1063_D06.13	Putative DNA-Binding Protein	At3g61260	DNA-Binding Family Protein / Remorin Family Protein
OJ1063_D06.15	Putative Vacuolar ATP Synthase Subunit F	At4g02620	(VACUOLAR ATPASE SUBUNIT F); Hydrogen Ion Transporting ATP Synthase, Rotational Mechanism / Hydrogen Ion Transporting Atpase, Rotational Mechanism
OJ1065_B06.1	Unknown Protein	At2g44260	Unknown Protein
OJ1065_B06.19-1	Putative Photosystem I Antenna Protein	At3g61470	LHCA2 (Photosystem I Light Harvesting Complex Gene 2); Chlorophyll Binding
OJ1065_B06.2	Putative Tocopherol Polyprenyltransferase	At3g11950	ATHST; Prenyltransferase
OJ1065_B06.20	Putative Succinyl-Coa Ligase Alpha Subunit	At5g23250	Succinyl-Coa Ligase (GDP-Forming) Alpha-Chain / Succinyl-Coa Synthetase, Alpha Chain, Putative / SCS-Alpha, Putative
OJ1067_B01.11	Putative Phosphate Transporter 2-1	At5g50180	Protein Kinase, Putative
OJ1073_F05.25-1	Glycerophosphoryl Diester Phosphodiesterase 2	At5g58170	Glycerophosphoryl Diester Phosphodiesterase Family Protein
OJ1077_A12.15	Putative Aspartate Transaminase	At2g30970	Asp1 (Aspartate Aminotransferase 1)
OJ1077_A12.16	Putative SERK1 Protein	At1g60800	NIK3 (NSP-INTERACTING KINASE 3); Kinase
OJ1077_A12.17	Putative Shaggy-Related Protein Kinase Dzeta	At2g30980	Shaggy-Related Protein Kinase Delta / ASK-Delta / ASK-Dzeta (ASK4)
OJ1077_A12.6	Ribosomal Protein L11-Like	At4g18730	RPL16B (Ribosomal Protein L16B); Structural Constituent Of Ribosome
OJ1077_E05.10	Putative Vacuolar Proton-Atpase	At1g78900	VHA-A; ATP Binding / Hydrogen Ion Transporting ATP Synthase, Rotational Mechanism
OJ1079_F11.25-2	Pentatricopeptide (PPR) Repeat-Containing	At1g05750	PDE247 (PIGMENT DEFECTIVE 247); Binding
OJ1079_F11.26	Beta 1 Subunit Of 20S Proteasome	At4g31300	PBA1 (20S Proteasome Beta Subunit A 1); Peptidase
OJ1079_F11.27	Putative HYS1	At5g64930	Cpr5 (Constitutive Expression Of Pr Genes 5)
OJ1081_B12.106-3	P53 Binding Protein-Like	At1g67320	DNA Primase, Large Subunit Family
OJ1081D05.10	Unknown Protein	At2g01910	Atmap65-6
OJ1081D05.5	Putative NADPH-Dependent Oxidoreductase	At1g59950	Aldo/Keto Reductase, Putative
OJ1092_A07.116	Cytochrome C6, Chloroplast Precursor-Like	At5g45040	Cytochrome C6 (ATC6)
OJ1092_A07.123	Unknown Protein	At1g10180	Unknown Protein

OJ1092_A07.132	Putative Calcium-Dependent Protein Kinase	At5g19450	CDPK19 (CALCIUM-DEPENDENT PROTEIN KINASE 19); Calcium- And Calmodulin-Dependent Protein Kinase/ Kinase
OJ1097_A12.2	20S Proteasome Beta Subunit	At5g40580	PBB2 (20S Proteasome Beta Subunit B 2); Peptidase
OJ1111_B11.20	Putative Protein Kinase	At5g59010	ATP Binding / Binding / Protein Kinase
OJ1111_C07.25	Putative Serine Palmitoyltransferase LCB1	At4g36480	ATLCB1 (ARABIDOPSIS THALIANA SPHINGOLIPID LONGCHAIN BASE 1); Serine C-Palmitoyltransferase
OJ1111_C07.26	Putative Phosphoenolpyruvate Carboxylase Kinase	At1g08650	PPCK1 (PHOSPHOENOLPYRUVATE CARBOXYLASE KINASE); Kinase
OJ1111_E05.24	Putative Latex Protein Allergen	At2g26560	PLP2 (PHOSPHOLIPASE A 2A); Nutrient Reservoir
OJ1111_E07.25	Putative Gamma-Tocopherol Methyltransferase	At1g64970	G-Tmt (Gamma-Tocopherol Methyltransferase)
OJ1111_H02.12	Putative Blue Copper Protein Precursor	At3g60280	UCC3 (UCLACYANIN 3); Copper Ion Binding
OJ1112_E08.105	Putative Betanidin 6-O-Glucosyltransferase	At4g15280	UDP-Glucoronosyl/UDP-Glucosyl Transferase Family Protein
OJ1112_E08.119	Guanine Nucleotide-Exchange Protein-Like	At3g43300	ATMIN7 (ARABIDOPSIS THALIANA HOPM INTERACTOR 7); Guanyl-Nucleotide Exchange Factor/ Protein Binding
OJ1112_F06.15	Zinc Finger And C2 Domain Protein-Like	At1g48590	C2 Domain-Containing Protein
OJ1112_F06.16	Receptor-Like Protein Kinase-Like Protein	At1g28340	Leucine-Rich Repeat Family Protein
OJ1112_G03.18	Unknown Protein	At5g23850	Unknown Protein
OJ1112_G03.6-1	Putative RNA Helicase	At4g00660	DEAD/DEAH Box Helicase, Putative
OJ1112_G06.34	Ankyrin Repeat Protein-Like	At3g04470	Unknown Protein
OJ1112_G07.12	Putative Rar1	At5g51700	Pbs2 (Pphb Susceptible 2)
OJ1112_G07.32	Unknown Protein	At5g06270	Unknown Protein
OJ1112_G07.8	Chaperone Protein Dnaj-Related-Like	At5g61670	Encodes A Close Homolog Of The Cauliflower OR (Orange) Protein
OJ1113_E01.101	NADH-Ubiquinone Oxidoreductase 18 Kda Subunit,	At5g67590	Fro1 (Frostbite1)
OJ1113_E01.105-1	Putative Early Nodulin 8 Precursor	At3g26430	GDSL-Motif Lipase/Hydrolase Family Protein
OJ1115_A05.12-1	Putative RCH2 Protein	At3g21670	Nitrate Transporter (NTP3)
OJ1115_A05.19	Putative ASC1	At1g13580	Lag13 (Lag1 Longevity Assurance Homolog 3)
OJ1115_A07.5	Putative Sucrose-Phosphate Synthase 1	At5g20280	ATSPS1F (Sucrose Phosphate Synthase 1F); Sucrose-Phosphate Synthase/ Transferase, Transferring Glycosyl Groups
OJ1115_B01.11	Putative Cytochrome P450	At3g26300	CYP71B34 (Cytochrome P450, Family 71, Subfamily B, Polypeptide 34); Oxygen Binding
OJ1115_B01.19	Putative Cytochrome P450	At3g26210	CYP71B23 (Cytochrome P450, Family 71, Subfamily B, Polypeptide 23); Oxygen Binding
OJ1115_B01.25	Putative Zipa	At4g32190	Centromeric Protein-Related
OJ1115_B01.27	Receptor Protein Kinase PERK1-Like Protein	At3g15890	Protein Kinase Family Protein
OJ1115_B01.31	Putative Cytochrome P450	At3g26310	CYP71B35 (Cytochrome P450, Family 71, Subfamily B, Polypeptide 35); Oxygen Binding
OJ1115_D03.25	Putative GTP-Binding Protein Typa	At5g13650	Elongation Factor Family Protein
OJ1115_D03.30	Lipase Class 3-Like	At2g05260	Lipase Class 3 Family Protein
OJ1115_D04.1	Unknown Protein	At1g12790	Unknown Protein
OJ1115_D04.2	Putative Receptor Protein Kinase	At3g08680	Leucine-Rich Repeat Transmembrane Protein Kinase, Putative
OJ1115_D04.4	Putative AAA-Type Atpase	At5g17760	AAA-Type Atpase Family Protein

OJ1115_D04.5	Putative AAA-Type Atpase	At3g50930	AAA-Type Atpase Family Protein
OJ1116_A06.10	Putative Pentatricopeptide (PPR)	At2g35130	Pentatricopeptide (PPR) Repeat-Containing Protein
OJ1116_C12.15	Putative Nonspecific Lipid Transfer Protein	At5g59320	LTP3 (LIPID TRANSFER PROTEIN 3); Lipid Binding
OJ1116_E03.25-2	Putative HGA1	At1g03900	Atnap4 (Arabidopsis Thaliana Non-Intrinsic Abc Protein 4)
OJ1116_E04.6	Putative Gtpase Activating Protein	At5g54780	RAB Gtpase Activator
OJ1116_H09.4	Putative Potassium Channel	At5g46370	KCO2 (CA2+ ACTIVATED OUTWARD RECTIFYING K+ CHANNEL 2); Calcium Ion Binding / Outward Rectifier Potassium Channel
OJ1116_H09.9	Putative Multidrug Resistance Protein 1 Homolog	At1g02520	PGP11 (P-GLYCOPROTEIN 11); Atpase, Coupled To Transmembrane Movement Of Substances
OJ1117_F10.11	Putative Subtilisin-Like Proteinase	At3g14240	Subtilase Family Protein
OJ1118_A06.10	F-Box Protein Family-Like	At1g55590	F-Box Family Protein
OJ1118_A06.15	Putative Protein Phosphatase 2C	At1g16220	Protein Phosphatase 2C Family Protein / PP2C Family Protein
OJ1118_A06.9	Putative Drought-Inducible Protein 1OS	At1g80150	Pentatricopeptide (PPR) Repeat-Containing Protein
OJ1118_A10.25	Putative Trna Splicing Protein	At5g65720	Atnifs1/Nifs1 (Arabiopsis Thaliana Nitrogen Fixation S Homolog 1)
OJ1118_A10.27	Putative Delta-6-Desaturase	At2g46210	Delta-8 Sphingolipid Desaturase, Putative
OJ1118_B06.10	Putative Peroxidase	At2g22420	Peroxidase 17 (PER17) (P17)
OJ1118_C04.3	Putative Latex-Abundant Protein	At1g79330	AMC6/ATMCP2B (TYPE-II METACASPASES); Caspase/ Cysteine-Type Endopeptidase
OJ1118_C04.7	Putative SMC Protein	At5g48600	ATSMC3 (Arabidopsis Thaliana Structural Maintenance Of Chromosome 3); ATP Binding
OJ1118_D07.26-1	Putative Amino Acid Permease	At5g49630	AAP6 (AMINO ACID PERMEASE 6); Amino Acid Permease
OJ1118_D07.29	Putative Oslrk1(Receptor-Type Protein Kinase)	At5g65700	BAM1 (Big Apical Meristem 1); ATP Binding / Kinase/ Protein Serine/Threonine Kinase
OJ1118_F05.12	Unknown Protein	At1g15980	Hypothetical Protein
OJ1119_A01.20-1	Putative Phosphatidylinositol-4-Phosphate	At3g09920	PIP5K9 (PHOSPHATIDYL INOSITOL MONOPHOSPHATE 5 KINASE); 1-Phosphatidylinositol-4-Phosphate 5-Kinase
OJ1119_A01.21-1	Putative 50S Ribosomal Protein L9, Chloroplast	At3g44890	RPL9 (Ribosomal Protein L9); Structural Constituent Of Ribosome
OJ1119_B04.18	Putative Hexose Transporter	At5g26250	Sugar Transporter, Putative
OJ1119_B04.19-1	Cycloartenol-C24-Methyltransferase	At5g13710	Smt1 (Sterol Methyltransferase 1)
OJ1119_B04.25	Putative LRR Receptor-Like Kinase 2	At2g41820	Leucine-Rich Repeat Transmembrane Protein Kinase, Putative
OJ1119_B04.4	Putative DD1A Protein	At1g55360	Unknown Protein
OJ1119_B04.6	Putative X-Prolyl Aminopeptidase	At3g05350	Aminopeptidase
OJ1119_B10.28	Putative Histone Deacetylase	At5g63110	HDA6 (HISTONE DEACETYLASE 6); Histone Deacetylase
OJ1119_B10.31	Light Induced Protein Like	At4g22310	Unknown Protein
OJ1119_C05.21-2	Putative Aminoimidazolecarboximide	At2g35040	AICARFT/Impchase Bienzyme Family Protein
OJ1119_D01.17-1	Putative RNA Recognition Motif (RRM)-Containing	At5g06210	RNA-Binding Protein, Putative
OJ1119_D01.19	Putative Quinone-Oxidoreductase QR2	At5g54500	Fqr1 (Flavodoxin-Like Quinone Reductase 1)
OJ1119_D01.22	Putative Armadillo Repeat Containing Protein	At4g21350	B80; Binding / Ubiquitin-Protein Ligase
OJ1119_D01.9	Helix-Loop-Helix-Like Protein	At5g54680	ILR3 (IAA-LEUCINE RESISTANT3); DNA Binding / Transcription Factor

OJ1120_C08.21	Putative Vacuolar Protein Sorting Protein 18	At1g12470	Pep3/Vps18/Deep Orange Family Protein
OJ1121_A05.14	Putative Vacuole Membrane Protein 1	At1g05360	Unknown Protein
OJ1121_A05.15	Hypothetical Protein	At3g63170	Unknown Protein
OJ1121_A05.16	Putative Organic Cation Transporter	At3g13050	Transporter-Related
OJ1123_C12.106	Hypothetical Protein	At3g55950	Protein Kinase Family Protein
OJ1123_C12.123	Calcineurin-Like Phosphoesterase Family-Like	At1g13900	Calcineurin-Like Phosphoesterase Family Protein
OJ1123_C12.124	Putative Dimethylaniline Monooxygenase	At5g61290	Flavin-Containing Monooxygenase Family Protein / FMO Family Protein
OJ1123_E07.2	GHMP Kinase-Like Protein	At4g16130	ARA1 (ARABINOSE SENSITIVE 1); ATP Binding / Galactokinase
OJ1123_G04.15	Putative Anthocyanin Biosynthetic Gene Regulator	At5g24520	TTG1 (TRANSPARENT TESTA GLABRA 1); Nucleotide Binding
OJ1123_G04.6	MADS Box Protein	At2g45650	AGL6 (AGAMOUS LIKE-6); DNA Binding / Transcription Factor
OJ1123_G08.16	Putative Clathrin Coat Assembly Protein AP17	At2g19790	Clathrin Adaptor Complex Small Chain Family Protein
OJ1123_G09.21	Hypothetical Protein	At5g19020	Pentatricopeptide (PPR) Repeat-Containing Protein
OJ1123F12.7	Putative Sugar Kinase	At1g06730	Pfkb-Type Carbohydrate Kinase Family Protein
OJ1124_B05.20	Putative Dihydrolipoamide Acetyltransferase	At3g25860	LTA2 (PLASTID E2 SUBUNIT OF PYRUVATE DECARBOXYLASE); Dihydrolipoyllysine-Residue Acetyltransferase
OJ1124_B05.3	Myosin-Like Protein	At1g55170	Unknown Protein
OJ1124_B05.4	Putative Osrad23	At5g38470	DNA Repair Protein RAD23, Putative
OJ1124_B05.7	GF14-C Protein	At3g02520	GRF7 (General Regulatory Factor 7); Protein Phosphorylated Amino Acid Binding
OJ1124_B05.9	Putative UVB-Resistance Protein UVR8	At5g16040	Regulator Of Chromosome Condensation (RCC1) Family Protein
OJ1124_D06.10	Hypothetical Protein	At3g19870	Binding
OJ1124_D06.14	Membrane-Associated Salt-Inducible Protein-Like	At1g61870	Pentatricopeptide (PPR) Repeat-Containing Protein
OJ1124_D06.17	Pentatricopeptide Repeat-Containing	At5g48910	Pentatricopeptide (PPR) Repeat-Containing Protein
OJ1124_D06.18	Oligopeptidase A-Like	At5g65620	Peptidase M3 Family Protein / Thimet Oligopeptidase Family Protein
OJ1124_H03.12	Hypothetical Protein	At1g05440	Unknown Protein
OJ1124_H03.18	Putative WD-Repeat Protein	At5g50230	Nucleotide Binding
OJ1124_H03.2	Cysteine Synthase	At4g14880	Oasa1 (O-Acetylserine (Thiol) Lyase (Oas-Tl) Isoform A1)
OJ1124_H03.28	Putative Protein Kinase	At4g14780	Protein Kinase, Putative
OJ1124_H03.29	Putative Receptor-Associated Protein	At3g63310	Glutamate Binding
OJ1124_H03.5	Unknown Protein	At4g17420	Unknown Protein
OJ1126_B10.10	Unknown Protein	At3g27930	Unknown Protein
OJ1126_B10.14	Putative Cinnamoyl Coa Reductase	At5g14700	Cinnamoyl-Coa Reductase-Related
OJ1126_B10.4	Unknown Protein	At3g18570	Glycine-Rich Protein / Oleosin
OJ1126_B10.7	Unknown Protein	At1g26120	Esterase-Related
OJ1126_B10.8	'Unknown Protein, Contains Calcium-Binding	At1g18530	Calmodulin, Putative
OJ1126_B10.9	Putative Protein Kinase	At5g50000	Protein Kinase, Putative

OJ1126_D01.10	Putative Universal Stress Protein (USP)	At3g53990	Universal Stress Protein (USP) Family Protein
OJ1126_D09.20-1	Glycosyl Transferase-Like Protein	At5g14480	Glycosyl Transferase Family 17 Protein
OJ1126_D09.28	Putative NAD-Dependent Isocitrate Dehydrogenase	At4g35260	IDH1 (ISOCITRATE DEHYDROGENASE 1); Isocitrate Dehydrogenase (NAD+)
OJ1126B12.12	Putative Ubiquitin-Conjugating Enzyme	At3g57870	AHUS5 (EMBRYO DEFECTIVE 1637); Ubiquitin-Protein Ligase
OJ1126B12.8	Putative MADS Box-Like Protein	At4g22950	AGL19 (AGAMOUS-LIKE 19); Transcription Factor
OJ1127_B08.12	Aspartic Proteinase	At1g11910	Aspartyl Protease Family Protein
OJ1127_B08.2	Putative Protein Kinase	At2g47060	Kinase
OJ1127_B08.5	Putative Protein Kinase	At3g17510	CIPK1 (CBL-INTERACTING PROTEIN KINASE 1); Kinase
OJ1127_E01.113	Chitin-Inducible Gibberellin-Responsive Protein	At5g48150	PAT1 (PHYTOCHROME A SIGNAL TRANSDUCTION 1); Transcription Factor
OJ1127_E01.118	Yippee-Like Protein	At5g53940	Yippee Family Protein
OJ1127_E01.120	Serine/Threonine Protein Kinase PKPA-Like	At5g55560	Protein Kinase Family Protein
OJ1127_E01.125	Putative Heterogeneous Nuclear Ribonucleoprotein	At3g07810	Heterogeneous Nuclear Ribonucleoprotein, Putative / Hnrnp, Putative
OJ1131_E05.104	Putative Nucleoid DNA-Binding Protein Cnd41	At1g31450	Aspartyl Protease Family Protein
OJ1131_E09.1	Unknown Protein	At3g25040	ER Lumen Protein Retaining Receptor, Putative / HDEL Receptor, Putative
OJ1131_E09.11	Putative Protein Kinase	At3g01090	AKIN10 (Arabidopsis SNF1 Kinase Homolog 10, SNF1-RELATED PROTEIN KINASE 1.1); Protein Kinase
OJ1134_B10.8-2	Putative Poli-Like DNA Polymerase	At1g50840	POLGAMMA2 (Polymerase Gamma 2); DNA Binding / DNA-Directed DNA Polymerase
OJ1134_E08.39-1	Putative KIF4	At5g47820	FRA1 (FRAGILE FIBER 1); Microtubule Motor
OJ1134_F06.8-1	Putative Peroxisomal Targeting Signal Type 2	At1g29260	PEX7 (Peroxin 7)
OJ1134F05.13	Putatvie Subtilisin-Like Serine Protease	At4g26330	UNE17 (Unfertilized Embryo Sac 17); Subtilase
OJ1134F05.16	Putative Protein Kinase	At5g56460	Protein Kinase, Putative
OJ1134F05.19	Putative Abscisic Acid-Induced Protein	At3g22490	Late Embryogenesis Abundant Protein, Putative / LEA Protein, Putative
OJ1134F05.20	Hypothetical Protein	At2g48000	Pentatricopeptide (PPR) Repeat-Containing Protein
OJ1135_F06.11	Putative Kelch Repeat-Containing F-Box Family	At1g55270	Kelch Repeat-Containing F-Box Family Protein
OJ1135_F06.7	Unknown Protein	At2g25570	Binding
OJ1136_A05.3	Membrane Transporter PFB0275w-Like Protein	At4g36790	Transporter-Related
OJ1136_A05.4	Putative Dolichyl-Di-Phosphooligosaccharide-	At5g66680	DGL1 (Defective Glycosylation 1); Dolichyl-Diphosphooligosaccharide-Protein Glycotransferase
OJ1136_A05.5	Putative Sip1 Protein	At3g57520	ATSIP2 (ARABIDOPSIS THALIANA SEED IMBIBITION 2); Hydrolase, Hydrolyzing O-Glycosyl Compounds
OJ1136_A10.112	Putative GMP Synthetase	At1g63660	GMP Synthase (Glutamine-Hydrolyzing), Putative / Glutamine Amidotransferase, Putative
OJ1136_C04.2	Acyl-Coa Binding Protein-Like	At5g04420	Kelch Repeat-Containing Protein
OJ1136_C04.4	Putative Growth-On Protein GRO10	At1g63690	Protease-Associated (PA) Domain-Containing Protein
OJ1136_C04.9	Putative O-Diphenol-O-Methyl Transferase	At3g53140	O-Diphenol-O-Methyl Transferase, Putative
OJ1136_D12.119-1	Putative Sexual Differentiation Process Protein	At4g26590	ATOPT5 (Oligopeptide Transporter 5); Oligopeptide Transporter
OJ1136_D12.119-2	Putative Sexual Differentiation Process Protein	At5g55930	ATOPT1 (Oligopeptide Transporter 1); Oligopeptide Transporter
OJ1145_E05.10	Putative U2 Snrnp Protein A'	At1g09760	U2A' (U2 Small Nuclear Ribonucleoprotein A); Protein Binding

OJ1145_E05.12	Putative Actin Related Protein 2/3 Complex, 21	At1g60430	ARPC3 (Actin-Related Protein C3)
OJ1145_E05.4	Putative Avr9/Cf-9 Rapidly Elicited Protein	At1g29340	PUB17 (PLANT U-BOX17); Ubiquitin-Protein Ligase
OJ1145_F01.1	Unknown Protein	At1g21060	Unknown Protein
OJ1145_F01.11	Putative Limonoid UDP-Glucosyltransferase	At4g15480	UGT84A1; UDP-Glycosyltransferase/ Sinapate 1-Glucosyltransferase/ Transferase, Transferring Glycosyl Groups
OJ1145_F01.6	Putative Cinnamyl-Alcohol Dehydrogenase	At4g34230	Cad5 (Cinnamyl Alcohol Dehydrogenase 5)
OJ1149_C12.16	Putative Homoserine Kinase	At2g17265	HSK (HOMOSERINE KINASE); Homoserine Kinase
OJ1149_C12.24	Putative Callose Synthase 1 Catalytic Subunit	At5g13000	ATGSL12 (GLUCAN SYNTHASE-LIKE 12); 1,3-Beta-Glucan Synthase/ Transferase, Transferring Glycosyl Groups
OJ1149_C12.9	Unknown Protein	At3g19810	Unknown Protein
OJ1150_A11.12-1	Putative DHHC-Type Zinc Finger Domain-Containing	At3g22180	Zinc Finger (DHHC Type) Family Protein
OJ1150_A11.13	Putative Peroxisome Biogenesis Protein PEX1	At5g08470	PEX1 (PEROXISOME 1); Atpase
OJ1150_A11.17	Putative Cysteine Proteinase	At5g50260	Cysteine Proteinase, Putative
OJ1150_A11.19-1	Nucleic Acid-Binding Protein-Like	At4g24770	RBP31 (31-KDA RNA BINDING PROTEIN); RNA Binding
OJ1150_A11.24-2	Putative Cyclophilin (70.8 Kd) (Cyp-15)	At3g44600	Peptidyl-Prolyl Cis-Trans Isomerase Cyclophilin-Type Family Protein
OJ1150_A11.25	Monodehydroascorbate Reductase	At3g52880	ATMDAR1 (MONODEHYDROASCORBATE REDUCTASE 1); Monodehydroascorbate Reductase (NADH)
OJ1150_A11.26	Two-Component Phosphorelay Mediator HP2	At1g03430	AHP5 (HISTIDINE-CONTAINING PHOSPHOTRANSFER FACTOR 5); Histidine Phosphotransfer Kinase
OJ1150_A11.31	Putative 60S Ribosomal Protein L10A (RPL10aC)	At5g22440	60S Ribosomal Protein L10A (RPL10aC)
OJ1159_D09.23	Lipase-Like Protein	At4g18550	Lipase Class 3 Family Protein
OJ1159_D09.7	Lipase-Like Protein	At2g27360	Lipase, Putative
OJ1163_G04.102	Putative DEAH-Box RNA Helicase	At5g13010	EMB3011 (EMBRYO DEFECTIVE 3011); RNA Helicase
OJ1163_G08.25	Putative Histidine Amino Acid Transporter	At5g40780	LHT1 (LYSINE HISTIDINE TRANSPORTER 1); Amino Acid Transporter
OJ1163_G08.29	Putative Step II Splicing Factor SLU7	At1g65660	SMP1 (Swellmap 1); Nucleic Acid Binding
OJ1163_G08.35	Kelch Repeat-Containing Protein -Like	At1g51540	Unknown Protein
OJ1165_F02.103	WSI76 Protein Induced By Water Stress	At1g56600	ATGOLS2 (ARABIDOPSIS THALIANA GALACTINOL SYNTHASE 2); Transferase, Transferring Glycosyl Groups / Transferase, Transferring Hexosyl Groups
OJ1165_F02.106	Unknown Protein	At4g24730	Calcineurin-Like Phosphoesterase Family Protein
OJ1165_F02.107	Membrane-Associated Salt-Inducible Protein-Like	At5g65560	Pentatricopeptide (PPR) Repeat-Containing Protein
OJ1165_F02.112	Putative Importin Alpha 1	At1g09270	Protein Transporter
OJ1165_F02.119	Betaine Aldehyde Dehydrogenase-Like	At3g66658	ALDH22a1 (ALDEHYDE DEHYDROGENASE 22A1); 3-Chloroallyl Aldehyde Dehydrogenase
OJ1165_F02.125	Putative ATP-Dependent Proteinase LON2	At5g26860	LON_ARA_ARA (Lon Protease Homolog Gene); ATP Binding / ATP-Dependent Peptidase/ Serine-Type Peptidase
OJ1165_F02.126	Aminoacyl Peptidase-Like	At2g47390	Serine-Type Peptidase
OJ1165_F02.129	Nicotianamine Synthase 3	At1g09240	Nicotianamine Synthase, Putative
OJ1167_G06.104	Hypothetical Protein	At3g56220	Unknown Protein
OJ1167_G06.113	Peroxidase	At5g05340	Peroxidase, Putative

OJ1172F09.5	Unknown Protein	At2g20370	MUR3 (MURUS 3); Catalytic
OJ1175_B01.11	Putative GAMYB-Binding Protein	At1g77180	Chromatin Protein Family
OJ1175_B01.14-1	Unknown Protein	At4g24610	Unknown Protein
OJ1175_B01.14-2	Unknown Protein	At4g24610	Unknown Protein
OJ1175_B01.15	Putative Immunophilin	At5g64350	FKBP12 (FK506-Binding Protein 12 Kd); FK506 Binding / Peptidyl-Prolyl Cis-Trans Isomerase
OJ1175_B01.17	Putative Ethylene-Responsive Protein	At1g09740	Ethylene-Responsive Protein, Putative
OJ1175_B01.24	Putative MADS Box Transcription Factor	At4g24540	AGL24 (AGAMOUS-LIKE 24); Transcription Factor
OJ1175_B01.8-1	Putative F-Box Containing Protein TIR1	At4g24390	F-Box Family Protein (FBX14)
OJ1175_B01.8-2	F-Box Containing Protein TIR1-Like	At5g49980	AFB5 (AUXIN F-BOX PROTEIN 5); Ubiquitin-Protein Ligase
OJ1175C11.5	Putative Non-Symbiotic Hemoglobin 1	At2g16060	Ahb1 (Arabidopsis Hemoglobin 1)
OJ1175C11.9	Putative RING Zinc Finger Protein	At4g34370	IBR Domain-Containing Protein
OJ1177_E11.3	Putative Oxysterol Binding Protein	At4g22540	Oxysterol Binding
OJ1177_E11.4-2	Putative U3 Snornp Protein IMP4	At1g63780	Imp4
OJ1186_G01.3	Putative Chitinase Precursor	At1g05850	POM1 (POM-POM1); Chitinase
OJ1186_G01.31	Putative Signal Recognition Particle Receptor	At5g05670	Signal Recognition Particle Binding
OJ1186_G01.5	Dnaj Protein Family-Like	At1g21080	DNAJ Heat Shock N-Terminal Domain-Containing Protein
OJ1191_A10.101	Putative Auxin-Induced Protein	At3g25290	Auxin-Responsive Family Protein
OJ1191_A10.105	Putative Ribosomal Protein L32	At4g18100	60S Ribosomal Protein L32 (RPL32A)
OJ1191_A10.113	Putative GTP-Binding Protein(RAB11G)	At2g31680	Atraba5d (Arabidopsis Rab Gtpase Homolog A5d); GTP Binding
OJ1191_A10.119	Putative 70 Kda Peptidylprolyl Isomerase	At3g25230	ROF1 (ROTAMASE FKBP 1); FK506 Binding / Calmodulin Binding / Peptidyl-Prolyl Cis-Trans Isomerase
OJ1191_A10.124	Putative Type 1 Capsule Synthesis Gene(Capi)	At3g23820	GAE6 (UDP-D-GLUCURONATE 4-EPIMERASE 6); Catalytic
OJ1191_G08.12	Putative NAD(P)-Dependent Cholesterol	At2g33630	3-Beta Hydroxysteroid Dehydrogenase/Isomerase Family Protein
OJ1197_D06.101	Putative Receptor Protein Kinase	At4g20140	Leucine-Rich Repeat Transmembrane Protein Kinase, Putative
OJ1198_B10.9	Putative ABC Transporter	At3g47730	ATATH1 (ABC2 Homolog 1); Atpase, Coupled To Transmembrane Movement Of Substances
OJ1200_C08.102	Unknown Protein	At5g17780	Hydrolase, Alpha/Beta Fold Family Protein
OJ1200_C08.105	Carbonyl Reductase -Like Protein	At2g24190	Short-Chain Dehydrogenase/Reductase (SDR) Family Protein
OJ1200_C08.118	Unknown Protein	At1g08400	Chromosome Structural Maintenance Protein-Related
OJ1200_C08.121	Putative Arabinoxylan Narabinofuranohydrolase	At3g10740	ASD1 (ALPHA-L-ARABINOFURANOSIDASE); Hydrolase, Acting On Glycosyl Bonds
OJ1200_C08.122	Putative Serine/Threonine Kinase	At2g26980	CIPK3 (CBL-INTERACTING PROTEIN KINASE 3); Kinase
OJ1200_C08.124-1	Calmodulin	At3g43810	CAM7 (CALMODULIN 7); Calcium Ion Binding
OJ1202_E07.17	Zinc Finger-Like	At3g09320	Zinc Finger (DHHC Type) Family Protein
OJ1208D02.10	Putative Proton-Dependent Oligopeptide	At1g62200	Proton-Dependent Oligopeptide Transport (POT) Family Protein
OJ1211_G06.4	Putative Calcium-Dependent Protein Kinase	At1g18890	ATCDPK1; Calcium- And Calmodulin-Dependent Protein Kinase/ Kinase/ Protein Kinase
OJ1212_A08.12	Unknown Protein	At1g73240	Unknown Protein

OJ1212_C01.15	Putative Lung Seven Transmembrane Receptor 1	At3g09570	Unknown Protein
OJ1212_C05.11	Putative Zinc Transporter	At5g59520	ZIP2 (ZINC TRANSPORTER 2 PRECURSOR); Transferase, Transferring Glycosyl Groups / Zinc Ion Transporter
OJ1212_C05.3	Unknown Protein	At2g44310	Calcium-Binding EF Hand Family Protein
OJ1212_D02.6	Unknown Protein	At5g40640	Unknown Protein
OJ1212_D02.8	Putative B-Keto Acyl Reductase	At1g67730	B-Keto Acyl Reductase, Putative (GLOSSY8)
OJ1214_E03.13	Putative 60S Ribosomal Protein L37a	At3g60240	Eif4g (Eukaryotic Translation Initiation Factor 4g)
OJ1214_E03.14	Unknown Protein	At3g15180	Proteasome-Related
OJ1214_E03.15	Unknown Protein	At1g28380	Nsl1 (Necrotic Spotted Lesions 1)
OJ1214_E03.16	Unknown Protein	At4g21700	Unknown Protein
OJ1214_E03.3	Putative Ribosomal Protein L35A	At1g41880	60S Ribosomal Protein L35a (RPL35aB)
OJ1214_E03.5	Putative Dynamin	At5g42080	ADL1 (ARABIDOPSIS DYNAMIN-LIKE PROTEIN); GTP Binding
OJ1214_E03.9	Putative T-Complex Protein 1 Beta Subunit	At5g20890	Chaperonin, Putative
OJ1217_D10.10	Endo-1,3	At3g23570	Dienelactone Hydrolase Family Protein
OJ1217_D10.25	Putative Flavonol 3-Sulfotransferase	At1g28170	Sulfotransferase Family Protein
OJ1217_D10.27	Putative Flavonol 3-Sulfotransferase	At5g43690	Sulfotransferase Family Protein
OJ1217B09.14	Putative Alcohol Dehydrogenase	At1g22430	Oxidoreductase/ Zinc Ion Binding
OJ1217B09.18	Hypothetical Protein	At1g60600	ABC4 (ABERRANT CHLOROPLAST DEVELOPMENT 4); 1,4-Dihydroxy-2-Naphthoate Octaprenyltransferase/ Prenyltransferase
OJ1217B09.20	Putative Ubiquitin-Specific Protease 3	At4g39910	ATUBP3 (UBIQUITIN-SPECIFIC PROTEASE 3); Ubiquitin-Specific Protease
OJ1218_D07.5	Putative Short-Chain Dehydrogenase/Reductase	At5g19200	Short-Chain Dehydrogenase/Reductase (SDR) Family Protein
OJ1224_G08.21	SWP1 Protein-Like	At3g04740	Swp (Struwwelpeter)
OJ1225_F07.14	Unknown Protein	At5g12960	Catalytic
OJ1225_F07.15	Putative Zinc-Finger Protein	At1g51200	DNA Binding / Zinc Ion Binding
OJ1234_B11.20	Putative Alcohol Oxidase	At4g28570	Alcohol Oxidase-Related
OJ1234_B11.27	Putative Protein Kinase (ADK1)	At1g03930	ADK1 (DUAL SPECIFICITY KINASE 1); Kinase
OJ1249_F12.2	Putative Nucleotide Sugar Epimerase	At4g30440	GAE1 (UDP-D-GLUCURONATE 4-EPIMERASE 1); UDP-Glucuronate 4-Epimerase/ Catalytic
OJ1249_F12.29	Unknown Protein	At3g01780	Encodes TPLATE, A Cytokinesis Protein Targeted To The Cell Plate
OJ1261C08.11	Hypothetical Protein	At2g39710	Aspartyl Protease Family Protein
OJ1263_E10.15	Protein Phosphatase 2A B'kappa Subunit	At5g25510	Serine/Threonine Protein Phosphatase 2A (PP2A) Regulatory Subunit B', Putative
OJ1263_E10.4	Putative Syntaxin 71 (SYP71)	At3g09740	Syp71 (Syntaxin Of Plants 71)
OJ1263_E10.5	Putative Anti-Silencing Protein	At5g38110	ASF1B/SGA01/SGA1 (Anti- Silencing Function 1b)
OJ1263_E10.7	Putative MATE Efflux Protein	At1g71140	MATE Efflux Family Protein
OJ1263_E10.8	Putative 50S Ribosomal Protein L12	At1g70190	Ribosomal Protein L12 Family Protein
OJ1263_E10.9	Putative Phosphatidylserine Synthase	At1g15110	Phosphatidyl Serine Synthase Family Protein
OJ1263H11.6	Unknown Protein	At5g51880	Oxidoreductase, Acting On Paired Donors, With Incorporation Or Reduction Of Molecular

			Oxygen, 2-Oxoglutarate As One Donor, And Incorporation Of One Atom Each Of Oxygen Into Both Donors
OJ1263H11.7	Putative Phospholipase D Beta 2	At2g42010	PLDBETA1 (PHOSPHOLIPASE D BETA 1); Phospholipase D
OJ1264_A04.18	Unknown Protein	At5g27400	Unknown Protein
OJ1264_A04.20	Putative Mitogen-Activated Protein Kinase	At5g19010	MPK16 (Mitogen-Activated Protein Kinase 16); MAP Kinase
OJ1268_B08.20	Hypothetical Protein	At2g12210	Transposable Element Gene
OJ1268_B08.7	Putative Malate Dehydrogenase	At3g15020	Malate Dehydrogenase (NAD)
OJ1268_B08.8	GTP-Binding Nuclear Protein RAN-B1	At5g55190	RAN3; GTP Binding
OJ1276_B06.27	Unknown Protein	At3g27670	RST1 (RESURRECTION1); Binding
OJ1276_B06.28	Putative Alliinase	At4g24670	Alliinase Family Protein
OJ1281_H05.4	Putative 60S Ribosomal Protein L36	At3g53740	60S Ribosomal Protein L36 (RPL36B)
OJ1281_H05.5	Putative Hsp70	At3g12580	HSP70 (Heat Shock Protein 70); ATP Binding
OJ1281_H05.8	'GTP Cyclohydrolase	At5g59750	Riboflavin Biosynthesis Protein, Putative
OJ1282_E10.12-2	Putative Na+/H+ Antiporter	At2g31910	Atchx21 (Cation/H+ Exchanger 21)
OJ1282_E10.22-2	Putative Peroxidase	At5g42180	Peroxidase 64 (PER64) (P64) (PRXR4)
OJ1282_E10.7	Pentatricopeptide (PPR) Repeat-Containing	At2g27610	Pentatricopeptide (PPR) Repeat-Containing Protein
OJ1282_H11.16-2	Asparaginyl Endopeptidase REP-2	At1g62710	BETA-VPE (Vacuolar Processing Enzyme Beta); Cysteine-Type Endopeptidase
OJ1287_H05.17-1	Putative Vacuolar Protein Sorting Homolog	At1g77140	VPS45 (VACUOLAR PROTEIN SORTING 45); Protein Transporter
OJ1288_G09.15	Putative Trehalose-6-Phosphate Phosphatase	At4g12430	Trehalose-6-Phosphate Phosphatase, Putative
OJ1288_G09.19	Putative Elicitor-Inducible Protein EIG-J7	At2g22170	Lipid-Associated Family Protein
OJ1293_A01.6	Putative Cellulase	At3g43860	Glycosyl Hydrolase Family 9 Protein
OJ1293_E04.24	Glutathione S-Transferase C-Terminal	At5g44000	Glutathione S-Transferase C-Terminal Domain-Containing Protein
OJ1293_E04.26	Putative Ribosomal Protein L37	At3g16080	60S Ribosomal Protein L37 (RPL37C)
OJ1294_F06.14	Putative Cytochrome P450	At5g25120	CYP71B11 (Cytochrome P450, Family 71, Subfamily B, Polypeptide 11); Oxygen Binding
OJ1294_F06.17	Putative Signal Recognition Particle Receptor	At2g45770	CPFTSY (Ferric Reductase Deficient 4); GTP Binding
OJ1294_F06.9	Putative Receptor Protein Kinase	At3g28040	Leucine-Rich Repeat Transmembrane Protein Kinase, Putative
OJ1294_G06.18	Putative Ribulose-1,5 Bisphosphate	At1g14030	Ribulose-1,5 Bisphosphate Carboxylase Oxygenase Large Subunit N-Methyltransferase, Putative
OJ1294_G06.25	Putative Auxin-Independent Growth Promoter	At5g65470	Unknown Protein
OJ1297_C09.31	Proteasome Subunit Beta Type 3	At1g21720	PBC1 (20S Proteasome Beta Subunit C1); Peptidase
OJ1301_C12.3	Putative Sorbitol Transporter	At3g18830	ATPLT5 (POLYOL TRANSPORTER 5); D-Ribose Transporter/ D-Xylose Transporter/ Carbohydrate Transporter/ Galactose Transporter/ Glucose Transporter/ Glycerol Transporter/ Hydrogen:Sugar Symporter/ Mannitol Transporter/ Monosaccharide Transporter/ Myo-Inositol
OJ1310_F05.15	Putative Poly(A)-Binding Protein	At4g34110	PAB2 (POLY(A)-BINDING PROTEIN 2); RNA Binding
OJ1311_D08.27	Putative Lysine-Ketoglutarate	At4g33150	Lkr (Saccharopine Dehydrogenase)
OJ1311_H06.22	Receptor Protein Kinase-Like	At1g11330	S-Locus Lectin Protein Kinase Family Protein
OJ1311_H06.4	Dek1-Calpain-Like Protein	At1g55350	DEK1 (DEFECTIVE KERNEL 1); Calpain/ Cysteine-Type Endopeptidase

OJ1316_A04.104	Putative Glycosyltransferase	At3g06260	GATL4 (Galacturonosyltransferase-Like 4); Polygalacturonate 4-Alpha-Galacturonosyltransferase/ Transferase, Transferring Glycosyl Groups / Transferase, Transferring Hexosyl Groups
OJ1316_A04.107	Unknown Protein	At4g17270	Mo25 Family Protein
OJ1316_E06.11-2	Protein Kinase-Like	At5g57610	Protein Kinase Family Protein
OJ1323_A06.27	Putative Membrane Protein	At5g07250	Rhomboid Family Protein
OJ1339_B08.1-1	Putative Membrane Related Protein CP5	At5g54170	Unknown Protein
OJ1339_F05.120-2	Unknown Protein	At1g56660	Unknown Protein
OJ1339_F05.125	Putative Receptor-Like Protein Kinase	At5g10020	Leucine-Rich Repeat Transmembrane Protein Kinase, Putative
OJ1340_C08.105	Unknown Protein	At4g01870	Tolb Protein-Related
OJ1340_C08.107	Putative RAB24 Protein	At1g48130	ATPER1 (Arabidopsis Thaliana 1-Cysteine Peroxiredoxin 1); Antioxidant
OJ1340_C08.130	Pyrrolidone Carboxyl Peptidase-Like Protein	At1g56700	Pyrrolidone-Carboxylate Peptidase Family Protein
OJ1340_C08.131	Putative Eukaryotic Translation Initiation	At3g55620	EMB1624 (EMBRYO DEFECTIVE 1624); Translation Initiation Factor
OJ1340_C08.132	Putative Thymidylate Kinase	At5g59440	Thymidylate Kinase Family Protein
OJ1342_D02.28	Putative Cinnamate 4-Hydroxylase	At2g30490	Atc4h (Cinnamate-4-Hydroxylase)
OJ1342_D02.35	Unknown Protein	At2g34570	MEE21 (Maternal Effect Embryo Arrest 21)
OJ1342_D02.8	Putative Oscttp	At5g26220	Chac-Like Family Protein
OJ1343_B12.129	Putative Kinetochore Protein	At1g20140	ASK4 (ARABIDOPSIS SKP1-LIKE 4); Ubiquitin-Protein Ligase
OJ1343_D04.112	Putative Sex Determination Protein Tasselseed 2	At3g26770	Short-Chain Dehydrogenase/Reductase (SDR) Family Protein
OJ1343_D04.115	Putative Sex Determination Protein Tasselseed 2	At4g03140	Oxidoreductase
OJ1343_D04.123	Putative Sex Determination Protein Tasselseed 2	At3g51680	Short-Chain Dehydrogenase/Reductase (SDR) Family Protein
OJ1343_D04.124	Putative Sex Determination Protein Tasselseed 2	At3g26760	Short-Chain Dehydrogenase/Reductase (SDR) Family Protein
OJ1345_B12.1	Putative Regulator Of Chromosome Condensation	At5g42140	Zinc Finger Protein, Putative / Regulator Of Chromosome Condensation (RCC1) Family Protein
OJ1345_B12.10	Putative Apoptosis-Related Protein	At1g29850	Double-Stranded DNA-Binding Family Protein
OJ1345_B12.11	Unknown Protein	At3g20550	Ddl (Dawdle)
OJ1345_D02.3	Pentatricopeptide (PPR) Repeat-Containing	At2g44880	Pentatricopeptide (PPR) Repeat-Containing Protein
OJ1345_D02.4	Heat Shock Protein 82	At5g56030	HSP81-2 (EARLY-RESPONSIVE TO DEHYDRATION 8); ATP Binding
OJ1349_D05.117	Unknown Protein	At1g06050	Unknown Protein
OJ1349_D05.131	Putative Pentatricopeptide (PPR)	At4g02750	Pentatricopeptide (PPR) Repeat-Containing Protein
OJ1349_D05.133	Hypothetical Protein	At5g24600	Unknown Protein
OJ1349_D05.141	Putative Pectinesterase	At4g12420	SKU5 (Skewed 5); Copper Ion Binding
OJ1351_C05.110	S-Receptor Kinase PK3 Precursor-Like Protein	At1g67000	Kinase
OJ1351_C05.112	Probable Photosystem II Oxygen-Evolving Complex	At1g06680	PSBP-1 (OXYGEN-EVOLVING ENHANCER PROTEIN 2); Calcium Ion Binding
OJ1359_D06.12	Putative Ribosomal Protein S4	At5g58420	40S Ribosomal Protein S4 (RPS4D)
OJ1359_D06.20	Vacuolar Acid Invertase	At1g62660	Beta-Fructosidase (BFRUCT3) / Beta-Fructofuranosidase / Invertase, Vacuolar
OJ1359_D06.29	Unknown Protein	At1g33230	Unknown Protein

OJ1361_E02.101	Tetratricopeptide Repeat (TPR)-Containing	At4g02680	EOL1 (ETO1-LIKE 1); Binding
OJ1362_G11.1	Putative Exostosin-2	At5g04500	Glycosyltransferase Family Protein 47
OJ1362_G11.18	Putative 60S Ribosomal L28 Protein	At2g19730	60S Ribosomal Protein L28 (RPL28A)
OJ1362_G11.23	Putative LEA Protein	At5g44310	Late Embryogenesis Abundant Domain-Containing Protein / LEA Domain-Containing Protein
OJ1364E02.4	Putative LIM-Domain Protein	At2g39900	LIM Domain-Containing Protein
OJ1364E02.5	Unknown Protein	At2g29560	Enolase, Putative
OJ1364E02.6	Putative Class I Low-Molecular-Weight Heat Shock	At5g59720	Hsp18.2 (Heat Shock Protein 18.2)
OJ1365_D05.10	Putative Response Regulator Protein(Receiver	At3g04280	Arr22 (Arabidopsis Response Regulator 22)
OJ1365_D05.6	Putative Protein Transport SEC23-Related	At5g43670	Transport Protein, Putative
OJ1369_G08.17	Putative CCR4-NOT Transcription Complex, Subunit	At5g59710	VIP2 (VIRE2 INTERACTING PROTEIN2); Transcription Regulator
OJ1369_G08.3	Lipase Class 3 Protein-Like	At3g14070	CAX9 (CATION EXCHANGER 9); Cation:Cation Antiporter
OJ1369_G08.6	Putative Polygalacturonase	At1g19170	Glycoside Hydrolase Family 28 Protein / Polygalacturonase (Pectinase) Family Protein
OJ1371_D04.6	Putative Cysteine Proteinase 1 Precursor	At4g39090	RD19 (RESPONSIVE TO DEHYDRATION 19); Cysteine-Type Peptidase
OJ1372_D06.21	Kinetochore Protein-Like	At5g35520	Kinetochore Protein-Related
OJ1372_D06.24	Unknown Protein	At4g10300	Unknown Protein
OJ1372_D06.35	Putative CER1 Protein	At1g02190	CER1 Protein, Putative
OJ1372_D12.114	Putative PDR-Like ABC Transporter	At2g36380	ATPDR6/PDR6 (PLEIOTROPIC DRUG RESISTANCE 6); Atpase, Coupled To Transmembrane Movement Of Substances
OJ1372_D12.115	Putative Ionotropic Glutamate Receptor Homolog	At1g05200	ATGLR3.4 (Arabidopsis Thaliana Glutamate Receptor 3.4)
OJ1378_A04.7	Hypothetical Protein	At1g22540	Proton-Dependent Oligopeptide Transport (POT) Family Protein
OJ1384D03.15	Putative CELL DIVISION CONTROL PROTEIN 2 HOMOLOG	At3g48750	CDC2/CDC2A/CDC2AAT/CDK2/CDKA;1 (CELL DIVISION CONTROL 2); Cyclin-Dependent Protein Kinase/ Kinase/ Protein Binding
OJ1402_H07.4	Putative CDC6	At4g14700	ATORC1A/ORC1A (ORIGIN OF REPLICATION COMPLEX 1A); DNA Binding
OJ1402_H07.8	Putative AUX1-Like Permease	At2g38120	AUX1 (AUXIN RESISTANT 1); Amino Acid Permease/ Transporter
OJ1409_C08.14-1	Putative Serine/Threonine Kinase	At5g58380	CIPK10 (CBL-INTERACTING PROTEIN KINASE 10); Kinase
OJ1409_C08.19	Putative Potassium Transporter	At2g40540	Kt2 (Potassium Transporter 2)
OJ1409_C08.26	Putative Alpha-Galactosidase	At3g56310	Alpha-Galactosidase, Putative / Melibiase, Putative / Alpha-D-Galactoside Galactohydrolase, Putative
OJ1414_E05.15	Putative GA 2-Oxidase	At1g30040	ATGA2OX2; Gibberellin 2-Beta-Dioxygenase
OJ1414_E05.17	Calcyclin Binding Protein-Like	At1g30070	SGS Domain-Containing Protein
OJ1414_E05.5	Unknown Protein	At1g29980	Unknown Protein
OJ1414_E05.8	Putative Potassium Channel	At5g46240	KAT1 (K+ Atpase 1); Cyclic Nucleotide Binding / Inward Rectifier Potassium Channel
OJ1435_F07.15	Putative Amino Acid Transporter	At1g77380	AAP3 (Amino Acid Permease 3); Amino Acid Permease
OJ1435_F07.21	Unknown Protein	At5g61230	Ankyrin Repeat Family Protein
OJ1435_F07.24-2	Unknown Protein	At5g45560	Pleckstrin Homology (PH) Domain-Containing Protein / Lipid-Binding START Domain-Containing Protein

OJ1435_F07.26	Putative Rubisco Subunit Binding-Protein Beta	At1g55490	CPN60B (CHAPERONIN 60 BETA); ATP Binding / Protein Binding / Unfolded Protein Binding
OJ1435_F07.30	Putative Nodulin Mtn21	At4g01440	Nodulin Mtn21 Family Protein
OJ1435_F07.31	Putative 60S Ribosomal Protein L9	At1g33140	60S Ribosomal Protein L9 (RPL90A/C)
OJ1435_F07.7	Putative Family II Extracellular Lipase 3	At1g75900	Family II Extracellular Lipase 3 (EXL3)
OJ1435_F07.8-1	Putative Hydroxypyruvate Reductase	At1g68010	HPR (Hydroxypyruvate Reductase); NAD Binding / Cofactor Binding / Oxidoreductase, Acting On The CH-OH Group Of Donors, NAD Or NADP As Acceptor
OJ1442_E05.17	Putative Iron-Phytosiderophore Transporter	At3g17650	YSL5 (YELLOW STRIPE LIKE 5); Oligopeptide Transporter
OJ1442_E05.18	Putative Forever Young Oxidoreductase	At4g27760	FEY (FOREVER YOUNG); Oxidoreductase
OJ1442_E05.22	Putative 15.9 Kda Subunit Of RNA Polymerase II	At5g09920	RPB15.9 (RNA Polymerase II 15.9)
OJ1442_E05.24	Unknown Protein	At1g73060	Unknown Protein
OJ1442_E05.26	Putative Minor Histocompatibility Antigen H13	At2g03120	Signal Peptide Peptidase Family Protein
OJ1442_E05.31	UDP-Glucose Pyrophosphorylase	At5g17310	UTP--Glucose-1-Phosphate Uridylyltransferase, Putative / UDP-Glucose Pyrophosphorylase, Putative / Ugpase, Putative
OJ1448_G06.10	Putative Dnak-Type Molecular Chaperone	At5g09590	Mthsc70-2 (HEAT SHOCK PROTEIN 70); ATP Binding / Unfolded Protein Binding
OJ1448_G06.11	Putative DNA-3-Methyladenine Glycosylase	At3g12040	DNA-3-Methyladenine Glycosylase (MAG)
OJ1448_G06.19	Putative Cation Diffusion Facilitator 8	At3g58060	Cation Efflux Family Protein / Metal Tolerance Protein, Putative (Mtpc3)
OJ1457_D07.109-1	Putative Regulator Of Nonsense Transcripts 1	At5g47010	LBA1/UPF1 (LOW-LEVEL BETA-AMYLASE 1); RNA Helicase
OJ1457_D07.114	GTP-Binding Protein Rab6	At2g44610	RAB6; GTP Binding
OJ1457_D07.117	Putative Malate Dehydrogenase	At2g13560	Malate Oxidoreductase, Putative
OJ1458_B07.103	Putative Adapter Protein ATH-55	At5g28740	Transcription-Coupled DNA Repair Protein-Related
OJ1458_B07.124	Unknown Protein	At5g19250	Hypothetical Protein
OJ1460_H08.3	Hypothetical Protein	At3g23610	Dual Specificity Protein Phosphatase (Dsptp1)
OJ1470_H06.117	Putative Photosystem II 10 Kd Polypeptide	At1g79040	PSBR (Photosystem II Subunit R)
OJ1476_F05.35	Putative Pentatricopeptide (PPR)	At1g19520	NFD5 (NUCLEAR FUSION DEFECTIVE 5); Transcription Factor
OJ1477_F01.104-1	XIAP Associated Factor-1-Like Protein	At1g09920	TRAF-Type Zinc Finger-Related
OJ1477_F01.111	Unknown Protein	At5g12150	Pleckstrin Homology (PH) Domain-Containing Protein / Rhogap Domain-Containing Protein
OJ1477_F01.112	Putative Ferredoxin-Dependent Glutamate	At5g04140	Glu1 (Ferredoxin-Dependent Glutamate Synthase 1)
OJ1477_F01.114	Nucleoid DNA-Binding-Like Protein	At3g54400	Aspartyl Protease Family Protein
OJ1477_F01.115	Phosphatidylinositol-4-Phosphate 5-Kinase-Like	At3g56960	Phosphatidylinositol-4-Phosphate 5-Kinase Family Protein
OJ1477_F01.124	Putative Condensin Subunit 1	At3g57060	Binding
OJ1477_F01.127	Putative Developmental Protein Sina	At3g61790	Seven In Absentia (SINA) Family Protein
OJ1479_B11.10	Putative Glycosyl Hydrolase Family 35	At2g16730	BGAL13 (Beta-Galactosidase 13); Beta-Galactosidase
OJ1479_B11.11	Putative Acyl Carrier Protein III, Chloroplast	At4g25050	Acp4 (Acyl Carrier Protein 4)
OJ1479_B11.20	Putative 21D7	At1g20200	EMB2719 (EMBRYO DEFECTIVE 2719); Binding
OJ1479_B11.21	Putative Ripening Regulated Protein DDTFR18	At1g47530	Ripening-Responsive Protein, Putative
OJ1479_B11.3	Proteasome Alpha Subunit	At5g66140	PAD2 (20S Proteasome Alpha Subunit D2); Peptidase

OJ1479_B11.7	Typical P-Type R2R3 Myb Protein	At5g14340	Atmyb40 (Myb Domain Protein 40); DNA Binding / Transcription Factor
OJ1479_B11.9	Putative Peroxisome Type Ascorbate Peroxidase	At4g35000	APX3 (ASCORBATE PEROXIDASE 3); L-Ascorbate Peroxidase
OJ1479_B12.21	Putative Mono- Or Diacylglycerol	At3g51520	Diacylglycerol Acyltransferase Family
OJ1479_B12.23	Putative Diphosphate-Fructose-6-Phosphate	At1g76550	Pyrophosphate--Fructose-6-Phosphate 1-Phosphotransferase Alpha Subunit, Putative / Pyrophosphate-Dependent 6-Phosphofructose-1-Kinase, Putative
OJ1479_B12.26	Putative Phosphoribosyl Pyrophosphate	At2g42910	Ribose-Phosphate Pyrophosphokinase 4 / Phosphoribosyl Diphosphate Synthetase 4 (PRS4)
OJ1479_B12.9	Putative NADPH-Thioredoxin Reductase	At4g35460	NTR1 (NADPH-Dependent Thioredoxin Reductase 1)
OJ1484_G09.129-1	Phosphoenolpyruvate Carboxylase	At1g53310	ATPPC1 (PHOSPHOENOLPYRUVATE CARBOXYLASE 1); Phosphoenolpyruvate Carboxylase
OJ1485_B09.5	Hypothetical Protein	At1g74680	Exostosin Family Protein
OJ1485_B09.6	Putative Leucine Zipper Protein	At5g50380	ATEXO70F1 (Exocyst Subunit EXO70 Family Protein F1); Protein Binding
OJ1486_E07.21	Unknown Protein	At2g23940	Unknown Protein
OJ1489_G03.3	Putative NAD-/NADP-Dependent Oxidoreductase	At1g54870	Oxidoreductase
OJ1489_G03.7	Unknown Protein	At4g15520	Trna/Rrna Methyltransferase (Spou) Family Protein
OJ1489_G03.9	Unknown Protein	At3g05170	Phosphoglycerate/Bisphosphoglycerate Mutase Family Protein
OJ1499_D04.6	Expressed Protein	At2g21640	Unknown Protein
OJ1499_D04.8	Putative Leucine-Rich Repeat Receptor Kinase	At4g39270	Leucine-Rich Repeat Transmembrane Protein Kinase, Putative
OJ1499_D04.9	Putative Cellular Retinaldehyde-Binding Protein	At1g75170	Transporter
OJ1506_A04.23	WD-40 Repeat Protein-Like	At2g19430	Transducin Family Protein / WD-40 Repeat Family Protein
OJ1506_A04.26	Putative Adhesion Of Calyx Edges Protein ACE	At1g72970	HTH (HOTHEAD); Aldehyde-Lyase
OJ1506_F01.10	Putative Aminotransferase	At2g13360	Agt (Alanine:Glyoxylate Aminotransferase)
OJ1506_F01.29	Putative Sodium-Dicarboxylate Cotransporter	At5g47560	ATSDAT/ATTDT (TONOPLAST DICARBOXYLATE TRANSPORTER); Malate Transporter/ Sodium:Dicarboxylate Symporter
OJ1513_F02.123	Pentatricopeptide (PPR) Repeat-Containing	At4g37380	Pentatricopeptide (PPR) Repeat-Containing Protein
OJ1513_F02.135	Casein Kinase II Alpha Subunit	At3g50000	CKA2 (Casein Kinase II Alpha Chain 2); Kinase
OJ1521_G02.18	Ankyrin-Like Protein	At2g31820	Ankyrin Repeat Family Protein
OJ1521_G02.8	Putative 60S Ribosomal Protein L7 (RPL7A)	At1g80750	60S Ribosomal Protein L7 (RPL7A)
OJ1521_G02.9	Putative Resistance Gene Analog PIC27	At3g50950	Disease Resistance Protein (CC-NBS-LRR Class), Putative
OJ1523_A02.1	Reversibly Glycosylated Polypeptide	At5g15650	RGP2 (Reversibly Glycosylated Polypeptide-3); DNA Binding / Alpha-1,4-Glucan-Protein Synthase (UDP-Forming)
OJ1523_A02.10	Putative Chromosome Condensation Regulator	At3g02300	Regulator Of Chromosome Condensation (RCC1) Family Protein
OJ1523_A02.3	Unknown Protein, 5'-Partial	At2g03730	Acr5 (Act Domain Repeat 5)
OJ1524_D08.15	Putative Copper-Transporting P-Type Atpase	At1g63440	HMA5 (HEAVY METAL ATPASE 5); Atpase, Coupled To Transmembrane Movement Of Ions, Phosphorylative Mechanism
OJ1524_D08.16	Putative Exopolygalacturonase Precursor	At3g14040	Exopolygalacturonase / Galacturan 1,4-Alpha-Galacturonidase / Pectinase
OJ1524_D08.17	Putative Fumarylacetoacetate Hydrolase	At1g12050	Fumarylacetoacetase, Putative
OJ1524_D08.18	Putative 3-Oxoacyl Carrier Protein Synthase	At2g04540	3-Oxoacyl-(Acyl-Carrier-Protein) Synthase II, Putative
OJ1524_D08.2	Putative Dnaj Homolog, Subfamily C, Member 9	At3g12170	DNAJ Heat Shock N-Terminal Domain-Containing Protein

OJ1524_D08.8	Putative Outer Envelope Membrane Protein OEP75	At5g19620	Oep80 (Arabidopsis Thaliana Outer Envelope Protein Of 80 Kda)
OJ1528D07.7	Putative Glyceraldehyde-3-Phosphate	At1g42970	GAPB (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE B SUBUNIT); Glyceraldehyde-3-Phosphate Dehydrogenase
OJ1529_G03.13	Hypothetical Protein	At3g11460	Pentatricopeptide (PPR) Repeat-Containing Protein
OJ1529_G03.7	Ubiquitin Conjugating Enzyme	At3g08690	UBC11 (Ubiquitin-Conjugating Enzyme 11); Ubiquitin-Protein Ligase
OJ1532_D06.3	Unknown Protein	At1g32250	Calmodulin, Putative
OJ1532_D06.5	Unknown Protein	At3g26420	ATRZ-1A; RNA Binding / Nucleotide Binding
OJ1532_D06.6	Unknown Protein	At2g21660	ATGRP7 (COLD, CIRCADIAN RHYTHM, AND RNA BINDING 2); RNA Binding
OJ1534_E09.14	Receptor Protein Kinase PERK1-Like	At2g26330	Er (Erecta, Quantitative Resistance To Plectosphaerella 1)
OJ1534_E09.18	Putative Myosin Heavy Chain	At1g54560	Member Of Myosin-Like Proteins
OJ1534_E09.23	Putative Isoleucyl-Trna Synthetase	At5g49030	OVA2 (OVULE ABORTION 2); ATP Binding / Aminoacyl-Trna Ligase
OJ1534_E09.9-2	Unknown Protein	At5g35560	DENN (AEX-3) Domain-Containing Protein
OJ1538_H05.7	Putative CLB1 Protein	At1g20080	C2 Domain-Containing Protein
OJ1540_G08.30	Putative SKP1 Interacting Partner 1	At5g57900	Skip1 (Skp1 Interacting Partner 1)
OJ1540_H01.1	Heat Shock Protein 90	At4g24190	SHD (SHEPHERD); ATP Binding
OJ1540_H01.10	Putative Receptor Protein Kinase	At1g75820	CLV1 (CLAVATA 1); ATP Binding / Kinase/ Protein Serine/Threonine Kinase
OJ1540_H01.2	Putative Senescence-Associated Protein	At3g21600	Senescence/Dehydration-Associated Protein-Related
OJ1540_H01.3	Putative Zinc Finger Protein	At5g66070	Protein Binding / Zinc Ion Binding
OJ1540_H01.4	Putative Protein Phosphatase	At3g51370	Protein Phosphatase 2C, Putative / PP2C, Putative
OJ1548_F12.19	Hypothetical Protein	At5g46760	Basic Helix-Loop-Helix (Bhlh) Family Protein
OJ1548_F12.23	Putative Quinone Oxidoreductase	At4g21580	Oxidoreductase, Zinc-Binding Dehydrogenase Family Protein
OJ1548_F12.27-1	GCN5-Related N-Acetyltransferase (GNAT) Family	At2g39000	GCN5-Related N-Acetyltransferase (GNAT) Family Protein
OJ1548_F12.6	Putative Methyltransferase	At5g57280	Unknown Protein
OJ1559_F09.109	Ribosomal Protein S15	At5g59850	40S Ribosomal Protein S15A (RPS15aF)
OJ1559_F09.120	Cellulose Synthase-4	At5g05170	CESA3 (CELLULASE SYNTHASE 3); Cellulose Synthase/ Transferase, Transferring Glycosyl Groups
OJ1562_B11.104	Unknown Protein	At5g19850	Hydrolase, Alpha/Beta Fold Family Protein
OJ1562_H01.1	Unknown Protein	At1g64890	Integral Membrane Transporter Family Protein
OJ1562_H01.2	'Unknown Protein, Contains	At1g31500	Endonuclease/Exonuclease/Phosphatase Family Protein
OJ1562_H01.5	Putative Cdc2 Protein Kinase	At5g10270	CDKC;1 (CYCLIN-DEPENDENT KINASE C;1); Kinase
OJ1567_G09.101	Zinc Finger And C2 Domain Protein-Like	At1g73580	C2 Domain-Containing Protein
OJ1567_G09.119	Putative 60S Ribosomal Protein	At3g24830	60S Ribosomal Protein L13A (RPL13aB)
OJ1567_G09.130	Putative GTP Binding Protein	At1g50920	GTP-Binding Protein-Related
OJ1567_G09.131-2	Putative Ferredoxin	At4g21090	Electron Carrier
OJ1568_B05.11	SNF7-Like Protein	At2g19830	SNF7 Family Protein
OJ1568_B05.15	Putative Arp3	At1g13180	DIS1 (DISTORTED TRICHOMES 1); Structural Constituent Of Cytoskeleton

OJ1568_B05.16	Rjs-Like Protein	At3g26100	Regulator Of Chromosome Condensation (RCC1) Family Protein
OJ1568_B05.21	NBS-LRR Disease Resistance Protein-Like	At1g58400	Disease Resistance Protein (CC-NBS-LRR Class), Putative
OJ1568_B05.26	Ubiquitin-Like Protein	At5g40630	Ubiquitin Family Protein
OJ1568_B05.3	Putative Cellulase	At5g16700	Glycosyl Hydrolase Family 5 Protein / Cellulase Family Protein
OJ1568_B05.8	Putative Cytochrome P450	At5g63450	CYP94B1 (Cytochrome P450, Family 94, Subfamily B, Polypeptide 1); Oxygen Binding
OJ1572_F02.14	Unknown Protein	At5g32440	Unknown Protein
OJ1572_F02.2	BRAP2-Like Protein	At2g26000	Catalytic
OJ1572_F02.9	Putative Ankyrin Repeat-Containing Protein	At5g20350	Tip1 (Tip Growth Defective 1)
OJ1575_B01.20	Putative Preprotein Translocase Secy Subunit,	At2g18710	SCY1 (SECY HOMOLOG 1); Protein Translocase
OJ1575_B01.21	Putative Cyclic Nucleotide-Gated	At3g48010	ATCNGC16 (Cyclic Nucleotide Gated Channel 16); Calmodulin Binding / Cyclic Nucleotide Binding / Ion Channel
OJ1579_C03.5	Unknown Protein	At5g39360	Circadian Clock Coupling Factor-Related
OJ1581_H09.6	DEAD/DEAH Box Helicase-Like	At1g12770	Emb1586 (Embryo Defective 1586)
OJ1582_D10.10	Unknown Protein	At2g32280	Unknown Protein
OJ1582_D10.12	Histone H2A	At4g27230	Histone H2A, Putative
OJ1582_D10.6	Putative Oxygen-Evolving Enhancer Protein 3-1,	At4g21280	PSBQ/PSBQ-1/PSBQA; Calcium Ion Binding
OJ1595_D08.27-1	Unknown Protein	At3g03570	Unknown Protein
OJ1606_D04.114	Putative Protein Kinase Xa21, Receptor Type	At1g35710	Leucine-Rich Repeat Transmembrane Protein Kinase, Putative
OJ1607A12.21	Putative Sulfate Transporter ATST1	At3g51895	SULTR3;1 (SULFATE TRANSPORTER 1); Sulfate Transporter
OJ1607A12.3	Hypothetical Protein	At3g56640	Exocyst Complex Subunit Sec15-Like Family Protein
OJ1607A12.5	Putative Glutathione Reductase	At3g54660	GR (GLUTATHIONE REDUCTASE); Glutathione-Disulfide Reductase
OJ1607A12.7	Hypothetical Protein	At3g23020	Pentatricopeptide (PPR) Repeat-Containing Protein
OJ1611_C08.15	Unknown Protein	At3g17740	Hypothetical Protein
OJ1611_C08.2-1	1-Aminocyclopropane-1-Carboxylate Oxidase	At1g05010	EFE (Ethylene Forming Enzyme)
OJ1611_C08.25	Universal Stress Protein / Early Nodulin	At3g03270	Universal Stress Protein (USP) Family Protein / Early Nodulin ENOD18 Family Protein
OJ1611_C08.26	Putative 1-Aminocyclopropane-1-Carboxylate	At1g48420	D-CDES (D-CYSTEINE DESULFHYDRASE); 1-Aminocyclopropane-1-Carboxylate Deaminase/ D-Cysteine Desulfhydrase/ Catalytic
OJ1611_C08.28	Putative Cyclic Nucleotide-Binding Transporter	At3g17700	CNBT1 (CYCLIC NUCLEOTIDE-BINDING TRANSPORTER 1); Calmodulin Binding / Cyclic Nucleotide Binding / Ion Channel
OJ1611_C08.4	Putative Beta-1,3-Glucanase Precursor	At5g55180	Glycosyl Hydrolase Family 17 Protein
OJ1611_C08.7	Unknown Protein	At2g32970	Unknown Protein
OJ1612_A04.101	Putative Isopentenyl	At3g02780	IPP2 (ISOPENTENYL PYROPHOSPHATE:DIMETHYLLALLYL PYROPHOSPHATE ISOMERASE 2); Isopentenyl-Diphosphate Delta-Isomerase
OJ1612_A04.108	Putative Phototropic Response Protein Family	At5g48800	Phototropic-Responsive NPH3 Family Protein
OJ1612_A04.112	Putative Translation Releasing Factor2	At5g36170	HCF109 (HIGH CHLOROPHYLL FLUORESCENT 109); Translation Release Factor
OJ1613_G04.16	Putative 33 Kda Secretory Protein	At4g20670	Lipase
OJ1613_G04.20	Putative Polycomb Group Protein FIE2	At3g20740	FIE (FERTILIZATION-INDEPENDENT ENDOSPERM 1); Nucleotide Binding / Transcription

			Factor
OJ1613_G04.21	Putative Actin-Related Protein 4 (ARP4)	At1g18450	ATARP4 (ACTIN-RELATED PROTEIN 4); Structural Constituent Of Cytoskeleton
OJ1626_B09.15	Unknown Protein	At5g08320	Unknown Protein
OJ1626_B09.4	Alpha 2 Subunit Of 20S Proteasome	At1g16470	PAB1 (20S Proteasome Alpha Subunit B1); Peptidase
OJ1626_B09.8	Putative Nitrilase 2	At5g22300	Nit4 (Nitrilase 4)
OJ1626B05.9	Putative Steroid 22-Alpha-Hydroxylase	At3g50660	Dwf4 (Dwarf 4)
OJ1634_B10.107	Pentatricopeptide (PPR) Repeat-Containing	At1g26460	Pentatricopeptide (PPR) Repeat-Containing Protein
OJ1634_B10.122	Putative WD-Repeat Protein 12	At5g15550	Transducin Family Protein / WD-40 Repeat Family Protein
OJ1634_H04.114	Putative DNA-Directed RNA Polymerase Iia	At5g51940	DNA-Directed RNA Polymerase II, Putative
OJ1634_H04.119	Putative RES Protein	At3g61180	Zinc Finger (C3HC4-Type RING Finger) Family Protein
OJ1641_C04.101	Putative NAD Synthetase	At1g55090	Carbon-Nitrogen Hydrolase Family Protein
OJ1643_A10.16	Membrane-Associated Salt-Inducible Protein Like	At4g36680	Pentatricopeptide (PPR) Repeat-Containing Protein
OJ1643_A10.19	Putative Replication Protein A2	At3g02920	Replication Protein-Related
OJ1643_A10.2	Putative ADP-Ribosylation Factor-Directed Gtpase	At1g60860	ARF Gtpase-Activating Domain-Containing Protein
OJ1643_A10.31	Unknown Protein	At5g23200	Unknown Protein
OJ1643_A10.33-1	Putative Carboxypeptidase D	At5g23210	Scpl34
OJ1643_A10.34	Putative Ubiquitin-Conjugating Enzyme E2	At5g25760	PEX4 (PEROXIN4); Ubiquitin-Protein Ligase
OJ1651_G11.6	Unknown Protein	At1g05130	Unknown Protein
OJ1653_D06.5	Putative Phosphoribosylglycinamide	At1g31220	Phosphoribosylglycinamide Formyltransferase
OJ1654_A02.17	Unknown Protein	At3g27470	Unknown Protein
OJ1655_B12.15	Putative Trehalose-6-Phosphate	At1g68020	ATTPS6 (Arabidopsis Thaliana Trehalose Phosphatase/Synthase 6); Trehalose-Phosphatase
OJ1655_B12.16	Leaf Senescence Protein-Like	At5g64020	Hypothetical Protein
OJ1655_B12.20	Putative Nuclear Protein P30	At5g16940	Carbon-Sulfur Lyase
OJ1655_B12.22	Putative FEG Protein	At2g01730	ATCPSF73-II (CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR 73 KDA SUBUNIT-II); Catalytic
OJ1656_A11.18	Unknown Protein	At1g08200	Axs2 (Udp-D-Apiose/Udp-D-Xylose Synthase 2)
OJ1656_A11.4	Aspartyl Aminopeptidase-Like Protein	At5g04710	Aspartyl Aminopeptidase, Putative
OJ1656_A11.6	Similar To Root Cap Protein	At5g54370	Late Embryogenesis Abundant Protein-Related / LEA Protein-Related
OJ1656_A11.8	Similar To Root Cap Protein	At3g19430	Late Embryogenesis Abundant Protein-Related / LEA Protein-Related
OJ1656_E11.135	Putative AKT1-Like Potassium Channel	At2g26650	AKT1 (ARABIDOPSIS K TRANSPORTER 1); Cyclic Nucleotide Binding / Inward Rectifier Potassium Channel
OJ1657_H11.2	Putative Inosine-Uridine Preferring Nucleoside	At5g18860	Inosine-Uridine Preferring Nucleoside Hydrolase Family Protein
OJ1661_C12.17-1	Putative Avr9 Elicitor Response Protein	At1g05170	Galactosyltransferase Family Protein
OJ1661_C12.7	Unknown Protein	At3g01670	Unknown Protein
OJ1664_D08.101-1	Unknown Protein	At5g19050	Unknown Protein
OJ1664_D08.105	Putative Mrna Binding Protein Precursor	At3g63140	Mrna-Binding Protein, Putative

OJ1664_D08.106	Mutt-Like Protein	At3g12600	ATNUDT16 (Arabidopsis Thaliana Nudix Hydrolase Homolog 16)
OJ1669_F01.30	Putative GCPE Protein	At5g60600	Gcpe (CHLOROPLAST BIOGENESIS 4); 4-Hydroxy-3-Methylbut-2-En-1-Yl Diphosphate Synthase
OJ1679_B08.15	Putative Molybdopterin Synthase Large Subunit	At2g43760	Molybdopterin Biosynthesis Moae Family Protein
OJ1679_B08.28	Avrrpt2-Induced Protein 2-Like	At2g24390	Unknown Protein
OJ1679_B08.9	Putative Cycloartenol Synthase	At2g07050	Cas1 (Cycloartenol Synthase 1)
OJ1695_A02.17	Putative D-Protein	At3g07720	Kelch Repeat-Containing Protein
OJ1695_A02.21	Integral Membrane Protein-Like	At5g02060	Integral Membrane Protein, Putative
OJ1695_A02.23	Putative U4/U6-Associated RNA Splicing Factor	At1g28060	Small Nuclear Ribonucleoprotein Family Protein / Snrnp Family Protein
OJ1695_A02.24	Phosphatase 2A Regulatory A Subunit	At3g25800	PDF1 (65 KDA REGULATORY SUBUNIT OF PROTEIN PHOSPHATASE 2A); Protein Phosphatase Type 2A Regulator
OJ1695_A02.34	Putative Ferredoxin-Thioredoxin Reductase	At2g04700	Ferredoxin Thioredoxin Reductase Catalytic Beta Chain Family Protein
OJ1695_H09.11	Unknown Protein	At3g54360	Binding / Protein Binding / Zinc Ion Binding
OJ1695_H09.19	Putative DEAD Box-Like RNA Helicase	At4g15850	ATRH1 (Arabidopsis Thaliana RNA Helicase 1); ATP-Dependent Helicase
OJ1695_H09.27-1	Putative CCR4-NOT Transcription Complex Subunit	At1g80780	CCR4-NOT Transcription Complex Protein, Putative
OJ1699_E05.18	Putative Carboxyl-Terminal Proteinase	At3g13510	Unknown Protein
OJ1699_E05.21	Putative CMP-Sialic Acid Transporter	At5g41760	Nucleotide-Sugar Transporter
OJ1699_E05.34	Unknown Protein	At5g55170	Sum3 (Small Ubiquitin-Like Modifier 3)
OJ1699_E05.4	Putative GDP-Fucose Protein-O-Fucosyltransferase	At5g50420	Unknown Protein
OJ1699_E05.40	Tubulin Alpha-1 Chain	At5g19780	TUA5 (Tubulin Alpha-5)
OJ1705_A03.38	Putative Threonyl-Trna Synthetase	At5g26830	Threonyl-Trna Synthetase / Threonine--Trna Ligase (THRRS)
OJ1705_C03.129	Unknown Protein	At5g46060	Unknown Protein
OJ1705_E12.26	Putative Citrate Synthase, Glyoxysomal Precursor	At2g42790	CSY3 (CITRATE SYNTHASE 3); Citrate (SI)-Synthase
OJ1705_E12.28	Disease Resistance Protein Cf-2.1-Like	At1g53440	Leucine-Rich Repeat Family Protein / Protein Kinase Family Protein
OJ1705_E12.35	Las17 Binding Protein	At1g29800	Zinc Ion Binding
OJ1705B08.11	Putative CAF Protein	At1g01040	DCL1 (DICER-LIKE1); ATP-Dependent Helicase/ Ribonuclease III
OJ1705B08.7	Putative Peroxidase	At1g05260	RCI3 (RARE COLD INDUCIBLE GENE 3); Peroxidase
OJ1710_H11.105-1	Putative CND41, Chloroplast Nucleoid DNA Binding	At3g50050	Aspartyl Protease Family Protein
OJ1710_H11.110	Putative Nt-Gh3 Deduced Protein	At4g37390	YDK1 (AUXIN UPREGULATED1, YADOKARI 1); Indole-3-Acetic Acid Amido Synthetase
OJ1712_E04.5	Putative Gamma Hydroxybutyrate Dehydrogenase	At3g25530	ATGHBDH/GHBDH; Phosphogluconate Dehydrogenase (Decarboxylating)
OJ1714_H10.115	Unknown Protein	At3g11780	MD-2-Related Lipid Recognition Domain-Containing Protein / ML Domain-Containing Protein
OJ1714_H10.119-1	Putative MADS-Box Transcription Factor CDM51	At1g69180	CRC (CRABS CLAW); Transcription Factor
OJ1714_H10.124	Unknown Protein	At5g57040	Lactoylglutathione Lyase Family Protein / Glyoxalase I Family Protein
OJ1714_H10.127	GPI-Anchored Protein -Like	At3g52370	Beta-Ig-H3 Domain-Containing Protein / Fasciclin Domain-Containing Protein
OJ1714_H10.135	Putative Calcium-Dependent Protein Kinase 2	At3g10660	CPK2 (CALMODULIN-DOMAIN PROTEIN KINASE CDPK ISOFORM 2); Calcium- And Calmodulin-Dependent Protein Kinase/ Kinase

OJ1714_H10.149	Putative Cell Death Associated Protein	At5g06570	Hydrolase
OJ1715_A07.16	Putative Beta-1,3-Galactosyltransferase 5	At5g62620	Galactosyltransferase Family Protein
OJ1715_H01.26	26S Proteasome Regulatory Particle Triple-A	At1g53750	RPT1A (Regulatory Particle Triple-A 1A); Atpase
OJ1715_H01.42	Putative Ribosomal Protein L35A	At1g74270	60S Ribosomal Protein L35a (RPL35aC)
OJ1715_H01.9	Lysine-Ketoglutarate Reductase/Saccharopine	At4g33150	Lkr (Saccharopine Dehydrogenase)
OJ1717_A09.24	Putative Protein Phosphatase 2C	At5g06750	Protein Phosphatase 2C Family Protein / PP2C Family Protein
OJ1717_A09.30	Putative Ring Finger Protein	At1g20823	Zinc Finger (C3HC4-Type RING Finger) Family Protein
OJ1717_A09.34	Putative Aspartate-Trna Ligase	At4g31180	Aspartyl-Trna Synthetase, Putative / Aspartate--Trna Ligase, Putative
OJ1717_A09.37	Putative GAMM1 Protein	At5g41970	Unknown Protein
OJ1717_A09.39	Unknown Protein	At4g17670	Senescence-Associated Protein-Related
OJ1720_F04.113	Putative Ikappab Kinase Complex-Associated	At5g13680	ABO1/ELO2 (ABA-OVERLY SENSITIVE 1); Transcriptional Elongation Regulator
OJ1723_B06.130	Unknown Protein	At5g39650	Unknown Protein
OJ1725_H08.12-2	Mechanosensitive Ion Channel Domain-Containing	At1g53470	Mechanosensitive Ion Channel Domain-Containing Protein / MS Ion Channel Domain-Containing Protein
OJ1729_E01.2	Putative Serine/Threonine Kinase -Related	At4g05200	Protein Kinase Family Protein
OJ1729_E01.7	Putative Serine/Threonine Kinase -Related	At4g11530	Protein Kinase Family Protein
OJ1734_E02.30	Alpha-Expansin Osexp5	At1g62980	Atexpa18 (Arabidopsis Thaliana Expansin A18)
OJ1734_E02.35	Putative Soluble Starch Synthase 2	At3g01180	Glycogen Synthase, Putative
OJ1734_E02.38	Putative Geranylgeranyl Reductase	At1g74470	Geranylgeranyl Reductase
OJ1734_E02.41	Putative Atpase	At5g60730	Anion-Transporting Atpase Family Protein
OJ1734_E02.43	Putative Major Intrinsic Protein	At2g34390	NIP2;1/NLM4 (NOD26-LIKE INTRINSIC PROTEIN 2;1); Water Channel
OJ1734_E04.11	Putative Iron Transporter Fe2	At1g10970	ZIP4 (ZINC TRANSPORTER 4 PRECURSOR); Cation Transporter
OJ1734_E04.23	Unknown Protein	At1g25510	Aspartyl Protease Family Protein
OJ1734_E04.4	Putative UDP-N-Acetylglucosamine	At1g31070	UDP-N-Acetylglucosamine Pyrophosphorylase-Related
OJ1741_B01.9	Voltage-Dependent Anion-Selective Channel (VDAC)	At5g15090	Porin, Putative / Voltage-Dependent Anion-Selective Channel Protein, Putative
OJ1743_B12.18	Putative Cell Division Control Protein CDC91	At1g12730	Cell Division Cycle Protein-Related
OJ1743_B12.21-2	Putative Purine Permease	At1g44750	ATPUP11 (Arabidopsis Thaliana Purine Permease 11)
OJ1743_B12.30	Putative Peptide Transporter	At1g32450	Proton-Dependent Oligopeptide Transport (POT) Family Protein
OJ1743_B12.36	Unknown Protein	At2g30530	Unknown Protein
OJ1743_B12.39	Putative Immediate-Early Fungal Elicitor Protein	At1g49780	U-Box Domain-Containing Protein
OJ1743_B12.40	Putative Clathrin Coat Assembly Protein AP50	At5g46630	Clathrin Adaptor Complexes Medium Subunit Family Protein
OJ1743_B12.5	Putative Serine Carboxypeptidase	At1g33540	SCPL18 (Serine Carboxypeptidase-Like 18); Serine Carboxypeptidase
OJ1743A09.16	Putative Leucine-Rich Repeat Transmembrane	At1g48480	RKL1 (Receptor-Like Kinase 1); ATP Binding / Kinase/ Protein Serine/Threonine Kinase
OJ1743A09.2	Putative Homocysteine S-Methyltransferase-1	At3g25900	ATHMT-1/HMT-1; Homocysteine S-Methyltransferase
OJ1743A09.5	Putative Beta-1,3-Glucanase	At2g01630	Glycosyl Hydrolase Family 17 Protein / Beta-1,3-Glucanase, Putative

OJ1743A09.9	Putative Topoisomerase	At1g22730	MA3 Domain-Containing Protein
OJ1753_E03.106	Putative Adenine Phosphoribosyl Transferase	At4g22570	APT3 (ADENINE PHOSPHORIBOSYL TRANSFERASE 3); Adenine Phosphoribosyltransferase
OJ1753_E03.112	Putative Beta-Alanine Synthases	At5g64370	BETA-UP (BETA-UREIDOPROPIONASE); Beta-Ureidopropionase
OJ1754_E06.14	Chalcone Isomerase	At3g55120	TT5 (TRANSPARENT TESTA 5); Chalcone Isomerase
OJ1754_E06.16	Ethylene-Responsive Small GTP-Binding Protein	At3g46060	Ara3
OJ1754_E06.24	Unknown Protein	At3g46450	SEC14 Cytosolic Factor Family Protein / Phosphoglyceride Transfer Family Protein
OJ1754_E06.24	Unknown Protein	At5g02500	HSC70-1 (Heat Shock Cognate 70 Kda Protein 1); ATP Binding
OJ1754_E06.32	Hypothetical Protein	At1g08070	Pentatricopeptide (PPR) Repeat-Containing Protein
OJ1754_E06.9	Putative Leukotriene A-4 Hydrolase	At5g13520	Peptidase M1 Family Protein
OJ1756_H07.11	Putative Ribosomal Protein S3a, Cytosolic	At4g34670	40S Ribosomal Protein S3A (RPS3aB)
OJ1756_H07.55	Putative Pentatricopeptide (PPR)	At5g08490	Pentatricopeptide (PPR) Repeat-Containing Protein
OJ1756_H07.62	Putative Dipeptidyl Peptidase IV	At5g24260	Prolyl Oligopeptidase Family Protein
OJ1767_D02.15-1	Putative Inorganic Pyrophosphatase	At5g09650	Inorganic Pyrophosphatase Family Protein
OJ1767_D02.9-1	Emp24/Gp25l/P24-Like	At1g09580	Emp24/Gp25l/P24 Family Protein
OJ1770_H02.15	PIN1-Like Auxin Transport Protein-Like	At5g15100	PIN8 (PIN-FORMED 8); Auxin:Hydrogen Symporter/ Transporter
OJ1770_H02.17	Putative Proteasome Subunit Beta Type 1	At3g60820	PBF1 (20S Proteasome Beta Subunit F1); Peptidase
OJ1773_H01.102	Putative Lysine Ketoglutarate Reductase	At1g61240	Unknown Protein
OJ1773_H01.103	Putative 40S Ribosomal Protein S11	At5g23740	RPS11-BETA (RIBOSOMAL PROTEIN S11-BETA); Structural Constituent Of Ribosome
OJ1773_H01.109	Unknown Protein	At2g13330	Transposable Element Gene; Gypsy-Like Retrotransposon Family,
OJ1773_H01.113	Putative Lysophospholipase Homolog	At1g11090	Hydrolase, Alpha/Beta Fold Family Protein
OJ1785_A05.14	Putative Pentatricopeptide Repeat Containing	At3g24000	Pentatricopeptide (PPR) Repeat-Containing Protein
OJ1789_C07.10	Putative Ribosomal Protein L17	At1g67430	60S Ribosomal Protein L17 (RPL17B)
OJ1789_C07.13	Moco Containing Protein(Osmcp)	At3g01910	Sox (Sulfite Oxidase)
OJ1789_C07.19	Putative Diphosphonucleotide Phosphatase	At1g13750	Calcineurin-Like Phosphoesterase Family Protein
OJ1789_C07.21	Putative Microtubule-Associated Protein	At1g27920	Microtubule Associated Protein (MAP65/ASE1) Family Protein
OJ1789_C07.8	Putative Uridine Kinase/Uracil	At5g40870	ATUK/UPRT1; ATP Binding / Kinase/ Uracil Phosphoribosyltransferase/ Uridine Kinase
OJ1789_D08.10	Glutaredoxin-Like	At5g14070	Glutaredoxin Family Protein
OJ1790_D02.27	Putative Brassinosteroid Receptor	At1g55610	BRL1 (BRI 1 LIKE); Kinase
OJ1790_D02.29-1	Putative Aspartate Kinase, Homoserine	At4g19710	Ak-Hsdh/Ak-Hsdh Ii
OJ1791_B03.16	Putative 26S Proteasome Non-Atpase Regulatory	At4g24820	26S Proteasome Regulatory Subunit, Putative (RPN7)
OJ1791_B03.34	Putative Glyceraldehyde-3-Phosphate	At3g04120	GAPC (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE C SUBUNIT); Glyceraldehyde-3-Phosphate Dehydrogenase
OJ1791_B03.38	Putative Pentatricopeptide (PPR)	At3g04130	Binding
OJ1791_B03.41	Ankyrin Repeat-Like Protein	At3g01750	Ankyrin Repeat Family Protein
OJ1791_B03.50-2	2 Coiled Coil Domains Of Eukaryotic Origin (31.3	At3g18790	Unknown Protein

OJ1793_E11.105	Putative 5-Alpha-Taxadienol-10-Beta-Hydroxylase	At5g36110	CYP716A1 (Cytochrome P450, Family 716, Subfamily A, Polypeptide 1); Oxygen Binding
OJ1793_E11.124	Unknown Protein	At1g50900	Unknown Protein
OJ2056_H01.1	Putative Delta-12 Oleate Desaturase	At3g12120	Fad2 (Fatty Acid Desaturase 2)
OJ2056_H01.13	Unknown Protein	At2g42210	ATOEP16-3; Protein Translocase
OJ2056_H01.18	Unknown Protein	At5g48020	Hypothetical Protein
OJ2056_H01.22-1	Putative 60S Ribosomal Protein L31	At2g19740	60S Ribosomal Protein L31 (RPL31A)
OJ2056_H01.23	Unknown Protein	At5g13070	MSF1-Like Family Protein
OJ2056_H01.33	ATP/ADP Translocator	At3g08580	AAC1 (ADP/ATP CARRIER 1); Binding
OJ2056_H01.36	Putative Fimbrin	At5g35700	Fimbrin-Like Protein, Putative
OJ2056_H01.9	Unknown Protein	At5g19630	Hypothetical Protein
OJ9003_G05.12	Putative Serine/Threonine Kinase	At5g07070	CIPK2 (CBL-INTERACTING PROTEIN KINASE 2); Kinase
OJ9003_G05.21	Putative SNF2 Domain-Containing Protein	At3g54280	ATP Binding / DNA Binding / Helicase
OJ9003_G05.28	Polyubiquitin 6	At4g05320	Ubq10 (Polyubiquitin 10)
OJ9003_G05.34	Putative Ribosomal Protein S14	At3g52580	40S Ribosomal Protein S14 (RPS14C)
OJ991113_30.18	Unknown Protein	At1g06710	Pentatricopeptide (PPR) Repeat-Containing Protein
OJ991113_30.3	Unknown Protein	At1g67600	Unknown Protein
OJ991113_30.4	Unknown Protein	At5g03860	Malate Synthase, Putative
OJ991113_30.7	Unknown Protein	At1g27190	Leucine-Rich Repeat Transmembrane Protein Kinase, Putative
OJ991113_30.8	Unknown Protein	At3g22320	ATRPABC24.3 ("Arabidopsis Thaliana RNA Polymerase I, II And III 24.3 Kda Subunit"); DNA Binding / DNA-Directed RNA Polymerase
OJ991214_12.1	Unknown Protein	At5g50250	31 Kda Ribonucleoprotein, Chloroplast, Putative / RNA-Binding Protein RNP-T, Putative / RNA-Binding Protein 1/2/3, Putative / RNA-Binding Protein Cp31, Putative
OJ991214_12.11	Unknown Protein	At3g53980	Protease Inhibitor/Seed Storage/Lipid Transfer Protein (LTP) Family Protein
OJ991214_12.3	Unknown Protein	At1g08380	PSAO (Photosystem I Subunit O)
OJA1212_C06.18	Putative Gtpase	At3g47450	Atnos1/Nos1
OJA1212_C06.25	Lactate Dehydrogenase	At4g17260	L-Lactate Dehydrogenase, Putative
OJA1325D05.4	Putative HNH Endonuclease	At1g18680	HNH Endonuclease Domain-Containing Protein
OJA1364E02.1	Putative Heat Shock Protein	At3g46230	ATHSP17.4 (Arabidopsis Thaliana Heat Shock Protein 17.4)
OJA1364E02.2	Putative Fructose-1,6-Biphosphotase, Chloroplast	At3g54050	Fructose-1,6-Bisphosphatase, Putative / D-Fructose-1,6-Bisphosphate 1-Phosphohydrolase, Putative / Fbpase, Putative
OSJNAa0087H07.7	Putative Aldehyde Oxidase	At3g43600	Aao2 (Aldehyde Oxidase 2)
OSJNAb0015J03.9	Putative Enolase (2-Phospho-D-Glycerate)	At2g36530	LOS2 (Low Expression Of Osmotically Responsive Genes 1); Phosphopyruvate Hydratase
OSJNBa0001K12.13	Putative Alcohol Oxidase	At4g19380	Alcohol Oxidase-Related
OSJNBa0001K12.5	Putative Alcohol Oxidase	At3g23410	Alcohol Oxidase-Related
OSJNBa0001O14.1	Putative Protein Phosphatase 2C	At4g38520	Protein Phosphatase 2C Family Protein / PP2C Family Protein
OSJNBa0001O14.11	Putative Cora-Like Mg2+ Transporter Protein	At3g58970	Magnesium Transporter Cora-Like Family Protein

OSJNBa0001O14.15	Hypothetical Protein	At5g04480	Unknown Protein
OSJNBa0001O14.3	Putative C-4 Sterol Methyl Oxidase	At4g12110	SMO1-1 (STEROL-4ALPHA-METHYL OXIDASE 1-1); Catalytic
OSJNBa0001O14.6	Unknown Protein	At5g03460	Unknown Protein
OSJNBa0002I03.12	Unknown Protein (C-Terminus Truncated)	At1g47550	Unknown Protein
OSJNBa0002I03.14	Putative U3 Small Nucleolar Ribonucleoprotein	At4g05410	Transducin Family Protein / WD-40 Repeat Family Protein
OSJNBa0002I03.18	Putative Inositol Polyphosphate 5-Phosphatase	At1g47510	Endonuclease/Exonuclease/Phosphatase Family Protein
OSJNBa0002I03.19	Putative LIM Domain Containing Protein	At5g17890	LIM Domain-Containing Protein / Disease Resistance Protein-Related
OSJNBa0002J24.3	Putative Peroxidase	At4g37530	Peroxidase, Putative
OSJNBa0002J24.4	Putative Peroxidase	At3g49960	Peroxidase, Putative
OSJNBa0002J24.6	Putative Casein Kinase Alpha Subunit	At2g23070	Casein Kinase II Alpha Chain, Putative
OSJNBa0003G23.3	Putative Ubiquitin-Conjugating Enzyme E2	At5g42990	UBC18 (Ubiquitin-Conjugating Enzyme 16); Ubiquitin-Protein Ligase
OSJNBa0003O19.10	Putative Enoyl-Coa-Hydratase	At5g65940	Chy1 (Beta-Hydroxyisobutyryl-Coa Hydrolase 1)
OSJNBa0003O19.2	Unknown Protein	At4g17870	Unknown Protein
OSJNBa0003O19.22	Putative Adenosine Kinase	At4g27600	Pfkb-Type Carbohydrate Kinase Family Protein
OSJNBa0003O19.4	Unknown Protein	At4g17890	UBP20 (UBIQUITIN-SPECIFIC PROTEASE 20); DNA Binding
OSJNBa0003O19.5	Unknown Protein	At2g26890	GRV2 (KATAMARI2); Binding / Heat Shock Protein Binding
OSJNBa0003O19.6	Unknown Protein	At2g38710	AMMECR1 Family
OSJNBa0003O19.7	Putative Carnitine/Acylcarnitine Translocase	At5g46800	BOU (A BOUT DE SOUFFLE); Binding
OSJNBa0004A10.16	Putative RNA-Binding Protein	At1g74230	GR-RBP5 (Glycine-Rich RNA-Binding Protein 5); RNA Binding
OSJNBa0004B24.15	Putative Cytochrome P450tyr	At2g22330	CYP79B3 (Cytochrome P450, Family 79, Subfamily B, Polypeptide 3); Oxygen Binding
OSJNBa0004B24.2	Putative Purple Acid Phosphatase	At3g20500	ATPAP18/PAP18 (Purple Acid Phosphatase 18); Acid Phosphatase/ Protein Serine/Threonine Phosphatase
OSJNBa0004B24.22	Putative Membrane-Associated Salt-Inducible	At5g08310	Pentatricopeptide (PPR) Repeat-Containing Protein
OSJNBa0004B24.3	Hypothetical Protein	At1g50740	Unknown Protein
OSJNBa0004E08.1	Putative Cyclophilin	At2g16600	ROC3 (Rotamase Cyp 3)
OSJNBa0004E08.10	Putative Aldose 1-Epimerase - Like Protein	At3g17940	Aldose 1-Epimerase Family Protein
OSJNBa0004E08.12	Putative Receptor-Like Protein Kinase	At1g17750	Leucine-Rich Repeat Transmembrane Protein Kinase, Putative
OSJNBa0004G17.1	Putative Phosphatidylinositol 4-Phosphate	At1g21980	ATPIP5K1 (Arabidopsis Thaliana 1-Phosphatidylinositol-4-Phosphate 5-Kinase 1); 1-Phosphatidylinositol-4-Phosphate 5-Kinase
OSJNBa0004L11.15	Putative Beta-Glucosidase	At3g18080	Glycosyl Hydrolase Family 1 Protein
OSJNBa0004L11.21	Putative UDP-Glucoronosyl And UDP-Glucosyl	At2g22590	Glycosyltransferase Family Protein
OSJNBa0004L11.6	Expressed Protein	At1g71940	Unknown Protein
OSJNBa0004N05.4	Unknown Protein	At4g26740	ATS1 (ARABIDOPSIS THALIANA SEED GENE 1); Calcium Ion Binding
OSJNBa0004N05.7	Unknown Protein	At2g33380	RD20 (RESPONSIVE TO DESSICATION 20); Calcium Ion Binding
OSJNBa0004N05.8	Unknown Protein	At4g16480	ATINT4 (INOSITOL TRANSPORTER 4); Carbohydrate Transporter/ Myo-Inositol:Hydrogen Symporter/ Sugar Porter

OSJNBa0004P12.3	Putative Endonuclease	At1g02270	Endonuclease/Exonuclease/Phosphatase Family Protein / Calcium-Binding EF Hand Family Protein
OSJNBa0005K07.1	Actin	At5g09810	ACT7 (Actin 7)
OSJNBa0005K07.2	Unknown Protein	At4g10440	Dehydration-Responsive Family Protein
OSJNBa0005K07.3	Putative Kinase	At2g46700	Calcium-Dependent Protein Kinase, Putative / CDPK, Putative
OSJNBa0005K07.4	Putative Serine Peptidase	At4g36190	Serine Carboxypeptidase S28 Family Protein
OSJNBa0005N02.3	Unknown Protein	At1g48410	Ago1 (Argonaute 1)
OSJNBa0005N02.7	Unknown Protein	At1g08430	ALMT1/ATALMT1 (AL-ACTIVATED MALATE TRANSPORTER 1); Malate Transporter
OSJNBa0006A01.11	Unknown Protein	At5g01120	Unknown Protein
OSJNBa0006A01.17	Unknown Protein	At1g32160	Unknown Protein
OSJNBa0006A01.18	Unknown Protein	At1g68310	Unknown Protein
OSJNBa0006A01.21	Unknown Protein	At1g32050	Secretory Carrier Membrane Protein (SCAMP) Family Protein
OSJNBa0006A01.5	Unknown Protein	At1g32340	NHL8 (NDR1/HIN1-Like 8); Protein Binding / Zinc Ion Binding
OSJNBa0006B20.20	Unknown Protein	At1g21370	Unknown Protein
OSJNBa0006B20.3	Unknown Protein	At1g04290	Thioesterase Family Protein
OSJNBa0006B20.4	Unknown Protein	At1g21750	ATPDIL1-1 (PDI-LIKE 1-1); Protein Disulfide Isomerase
OSJNBa0006B20.8	Unknown Protein	At3g26540	Pentatricopeptide (PPR) Repeat-Containing Protein
OSJNBa0006L06.1	Putative Amylase	At3g23920	BMY7/TR-BAMY (Beta-Amylase 7); Beta-Amylase
OSJNBa0006L06.21	Putative Protein Kinase	At5g44700	EDA23 (Embryo Sac Development Arrest 23); ATP Binding / Protein Serine/Threonine Kinase
OSJNBa0006L06.28	Putative Ribosomal Protein L11	At4g35490	Ribosomal Protein L11 Family Protein
OSJNBa0006L06.3	60S Ribosomal Protein L21	At1g57860	60S Ribosomal Protein L21
OSJNBa0006L06.5	Putative WD-Repeat Containing Protein	At1g04510	Nucleotide Binding
OSJNBa0006L06.7	60S Ribosomal Protein L17	At3g04400	EMB2171 (EMBRYO DEFECTIVE 2171); Structural Constituent Of Ribosome
OSJNBa0006L06.8	Putative Peroxin	At3g04460	Apm4/Atpex12/Pex12 (Peroxin-12)
OSJNBa0006L06.9	Cap-Binding Protein P28	At5g35620	LSP1 (LOSS OF SUSCEPTIBILITY TO POTYVIRUSES); RNA Binding / Translation Initiation Factor
OSJNBa0006M15.16	Unknown Protein	At2g20860	LIP1 (Lipoic Acid Synthase 1); Lipoic Acid Synthase
OSJNBa0006M15.17	Unknown Protein	At1g22200	Unknown Protein
OSJNBa0006O14.4	Unknown Protein	At3g18350	Unknown Protein
OSJNBa0006O15.16	Putative Lecithin-Cholesterol Acyl Transferase	At1g27480	Lecithin:Cholesterol Acyltransferase Family Protein / LACT Family Protein
OSJNBa0006O15.28	Serine/Threonine-Protein Kinase Nek4-Like	At3g20860	Protein Kinase Family Protein
OSJNBa0007H12.40	Putative Isocitrate Lyase	At3g21720	Isocitrate Lyase, Putative
OSJNBa0007M04.13	Putative RNA Binding Protein	At5g04600	RNA Recognition Motif (RRM)-Containing Protein
OSJNBa0007M04.24	Putative Cell Division Cycle Protein	At3g53230	Cell Division Cycle Protein 48, Putative / CDC48, Putative
OSJNBa0007M04.45	Putative Trehalose-6-Phosphate Synthase	At1g60140	ATTPS10 (Arabidopsis Thaliana Trehalose Phosphatase/Synthase 10); Transferase, Transferring Glycosyl Groups / Trehalose-Phosphatase

OSJNBa0008C07.10	Putative Wax Synthase	At5g55380	Membrane Bound O-Acyl Transferase (MBOAT) Family Protein / Wax Synthase-Related
OSJNBa0008C11.15	Leucine Zipper Protein-Like Protein	At2g28650	ATEXO70H8 (Exocyst Subunit EXO70 Family Protein H8); Protein Binding
OSJNBa0008C11.35	Unknown Protein	At3g23590	Unknown Protein
OSJNBa0008C11.37	Kinase Associated Protein Phosphatase	At5g19280	KAPP (Kinase-Associated Protein Phosphatase); Protein Phosphatase Type 2C
OSJNBa0008J01.16	Putative S6 Ribosomal Protein Kinase	At3g08720	ATPK19/ATPK2 (ARABIDOPSIS THALIANA SERINE/THREONINE PROTEIN KINASE 19, ARABIDOPSIS THALIANA SERINE/THREONINE PROTEIN KINASE 2); Kinase
OSJNBa0008J01.17	Putative Translation Initiation Factor Eif-2	At5g20920	Eif2 Beta (Embryo Defective 1401)
OSJNBa0008J01.18	Putative Receptor-Like Protein Kinase	At5g58300	Leucine-Rich Repeat Transmembrane Protein Kinase, Putative
OSJNBa0008J01.21	Putative Syringolide-Induced Protein	At2g38600	Acid Phosphatase Class B Family Protein
OSJNBa0008J01.23	Putative Cytochrome P450	At5g24900	CYP714A2 (Cytochrome P450, Family 714, Subfamily A, Polypeptide 2); Oxygen Binding
OSJNBa0008J01.24	Putative Avr9/Cf-9 Rapidly Elicited Protein 31	At4g20780	Calcium-Binding Protein, Putative
OSJNBa0008J01.6	Putative Vacuolar Targeting Receptor	At3g52850	Atelp1 (Vacuolar Sorting Receptor Homolog)
OSJNBa0008M17.11	Unknown Protein	At1g31280	Ago2 (Argonaute 2)
OSJNBa0008M17.4	Unknown Protein	At3g22200	POP2 (POLLEN-PISTIL INCOMPATIBILITY 2); 4-Aminobutyrate Transaminase
OSJNBa0009C07.16	Putative Auxin-Regulated Protein	At2g46370	Jar1 (Jasmonate Resistant 1)
OSJNBa0009C07.5	Unknown Protein	At1g64110	AAA-Type Atpase Family Protein
OSJNBa0009C07.9	Putative Calcium-Dependent Protein Kinase	At4g23650	CDPK6 (CALCIUM-DEPENDENT PROTEIN KINASE 6); Anion Channel/ Calcium- And Calmodulin-Dependent Protein Kinase/ Kinase
OSJNBa0009C08.12	Unknown Protein	At3g61320	Unknown Protein
OSJNBa0009C08.14	Putative Aminotransferase	At5g65780	ATBCAT-5; Branched-Chain-Amino-Acid Transaminase/ Catalytic
OSJNBa0009E21.4	Unknown Protein	At4g31130	Unknown Protein
OSJNBa0009H03.25	Putative Phosphoprotein Phosphatase	At5g55260	PPX2 (Protein Phosphatase X-2); Protein Serine/Threonine Phosphatase
OSJNBa0009K15.12	Unknown Protein	At3g51970	Long-Chain-Alcohol O-Fatty-Acyltransferase Family Protein / Wax Synthase Family Protein
OSJNBa0009L15.1	Unknown Protein	At5g41880	DNA Primase Small Subunit Family
OSJNBa0009L15.3	Putative Protein Phosphatase 2C	At3g05640	Protein Phosphatase 2C, Putative / PP2C, Putative
OSJNBa0010D21.3	Unknown Protein	At1g74180	Leucine-Rich Repeat Family Protein
OSJNBa0010E04.10	Putative Phospholipase	At1g07230	Phosphoesterase Family Protein
OSJNBa0010E04.11	Anthranilate Synthase Alpha 1 Subunit	At5g05730	ASA1 (ANTHRANILATE SYNTHASE ALPHA SUBUNIT 1); Anthranilate Synthase
OSJNBa0010E04.12	Putative Small Nuclear Ribonucleoprotein	At3g47120	RNA Recognition Motif (RRM)-Containing Protein
OSJNBa0010E04.19	Putative Ion Antiporter	At3g17630	ATCHX19 (CATION/H+ EXCHANGER 19); Monovalent Cation:Proton Antiporter
OSJNBa0010E04.5	Putative Organic Solute Transporter	At5g26734	Unknown Protein
OSJNBa0010H02.13	Unknown Protein	At1g19800	Tgd1 (Trigalactosyldiacylglycerol 1)
OSJNBa0010H02.16	Unknown Protein	At5g47500	Pectinesterase Family Protein
OSJNBa0010H02.2	Unknown Protein	At4g38390	Unknown Protein
OSJNBa0010H02.23	Unknown Protein	At1g12090	ELP (EXTENSIN-LIKE PROTEIN); Lipid Binding
OSJNBa0010H02.6	Unknown Protein	At3g20050	ATTCP-1 (Arabidopsis Thaliana T-Complex Protein 1 Alpha Subunit); ATP Binding / Protein

			Binding / Unfolded Protein Binding
OSJNBa0010H02.9	Unknown Protein	At2g45080	CYCP3;1 (Cyclin P3;1); Cyclin-Dependent Protein Kinase
OSJNBa0010K01.7	Putative Receptor Protein Kinase	At1g28440	HSL1 (HAESA-LIKE 1); ATP Binding / Kinase/ Protein Serine/Threonine Kinase
OSJNBa0010K08.8-1	Putative Zinc Finger Protein	At1g01350	Zinc Finger (CCCH-Type/C3HC4-Type RING Finger) Family Protein
OSJNBa0010N03.13	Putative Serine/Threonine Protein Kinase	At4g14580	CIPK4 (CBL-INTERACTING PROTEIN KINASE 4); Kinase
OSJNBa0011F23.4	Unknown Protein	At5g57330	Aldose 1-Epimerase Family Protein
OSJNBa0011F23.7	Unknown Protein	At1g73110	Ribulose Bisphosphate Carboxylase/Oxygenase Activase, Putative / Rubisco Activase, Putative
OSJNBa0011H24.1	Putative Fatty Acid Elongase	At5g04530	Beta-Ketoacyl-Coa Synthase Family Protein
OSJNBa0011H24.11	Putative Fatty Acid Elongase	At2g28630	Beta-Ketoacyl-Coa Synthase Family Protein
OSJNBa0011H24.19	Putative Capping Protein Beta Subunit	At1g71790	F-Actin Capping Protein Beta Subunit Family Protein
OSJNBa0011H24.21	Putative Aldose 1-Epimerase	At3g47800	Aldose 1-Epimerase Family Protein
OSJNBa0011J03.9	Hypothetical Protein	At4g38680	GRP2 (COLD SHOCK DOMAIN PROTEIN 2); Nucleic Acid Binding
OSJNBa0011J08.12	Unknown Protein	At1g01590	FRO1 (FERRIC REDUCTION OXIDASE 1); Ferric-Chelate Reductase
OSJNBa0011K22.4	Unknown Protein	At3g02740	Aspartyl Protease Family Protein
OSJNBa0011L07.13	Unknown Protein	At3g58690	Protein Kinase Family Protein
OSJNBa0011L07.8	Unknown Protein	At4g34660	SH3 Domain-Containing Protein 2 (SH3P2)
OSJNBa0011L09.11	Putative Serine/Threonine Protein Kinase	At2g05940	Protein Kinase, Putative
OSJNBa0011L09.20	Putative Cucumisin-Like Serine Protease	At2g05920	Subtilase Family Protein
OSJNBa0011L09.6	Hypothetical Protein	At5g14710	Unknown Protein
OSJNBa0011L14.1	Putative Phosphoserine Aminotransferase	At4g35630	PSAT (Phosphoserine Aminotransferase); Phosphoserine Transaminase
OSJNBa0011L14.11	Putative Atfp6-Like Protein	At5g17450	Heavy-Metal-Associated Domain-Containing Protein / Copper Chaperone (CCH)-Related
OSJNBa0011L14.5	Putative FH Protein Interacting Protein FIP2	At5g55000	FIP2 (FH Protein Interacting Protein 2); Voltage-Gated Potassium Channel
OSJNBa0011N12.22	Glutelin C Precursor	At5g44120	CRA1 (CRUCIFERINA); Nutrient Reservoir
OSJNBa0012K14.33	Putative ATP Binding Protein Associated With	At2g18990	Txnd9 (Thioredoxin Domain-Containing Protein 9 Homolog)
OSJNBa0012L23.32	Putative Transcription Factor	At1g73230	Nascent Polypeptide-Associated Complex (NAC) Domain-Containing Protein
OSJNBa0013A09.12	Expressed Protein	At1g69450	Unknown Protein
OSJNBa0013A09.13	Putative Inositol 1,3,4-Trisphosphate	At4g08170	Inositol 1,3,4-Trisphosphate 5/6-Kinase Family Protein
OSJNBa0013A09.14	Alpha Tubulin	At1g50010	TUA2 (Tubulin Alpha-2 Chain)
OSJNBa0013D02.10	Putative Ascorbate Peroxidase	At1g07890	Apx1 (Ascorbate Peroxidase 1, Maternal Effect Embryo Arrest 6)
OSJNBa0013D02.14	Hypothetical Protein	At5g02830	Pentatricopeptide (PPR) Repeat-Containing Protein
OSJNBa0013D02.19	Hypothetical Protein	At3g45740	Hydrolase Family Protein / HAD-Superfamily Protein
OSJNBa0013D02.6	Putative Phosphate/Phosphoenolpyruvate	At5g05820	Phosphate Translocator-Related
OSJNBa0013D02.9	Putative MAP Kinase 1	At3g45640	ATMPK3 (MITOGEN-ACTIVATED PROTEIN KINASE 3); MAP Kinase/ Kinase/ Protein Kinase
OSJNBa0013H03.27	Putative Peptidyl-Prolyl Cis-Trans Isomerase,	At3g01480	Peptidyl-Prolyl Cis-Trans Isomerase, Putative / Cyclophilin, Putative / Rotamase, Putative
OSJNBa0013K16.2	Unknown Protein	At4g35310	CPK5 (CALMODULIN-DOMAIN PROTEIN KINASE 5); Calcium- And Calmodulin-Dependent

			Protein Kinase/ Kinase
OSJNBa0013K16.8	Unknown Protein	At1g42540	ATGLR3.3 (Arabidopsis Thaliana Glutamate Receptor 3.3)
OSJNBa0013M12.16	Hypothetical Protein	At4g30880	Protease Inhibitor/Seed Storage/Lipid Transfer Protein (LTP) Family Protein
OSJNBa0013M12.21	Hypothetical Protein	At5g61190	Zinc Finger Protein-Related
OSJNBa0013M12.4	Putative Vesicle Soluble NSF Attachment Protein	At3g17440	NPSN13 (Novel Plant SNARE 13)
OSJNBa0013M12.6	Unknown Protein	At3g21550	Unknown Protein
OSJNBa0013M12.7	Putative Cytochrome P450-Related Protein	At2g46950	CYP709B2 (Cytochrome P450, Family 709, Subfamily B, Polypeptide 2); Oxygen Binding
OSJNBa0013M12.9	Putative Peroxidase	At5g58390	Peroxidase, Putative
OSJNBa0013O08.2	Putative Mucin	At2g02880	Mucin-Related
OSJNBa0014E22.2	Putative F-Box Protein FBL2	At5g23340	Protein Binding
OSJNBa0014E22.23-1	Unknown Protein	At5g23390	Unknown Protein
OSJNBa0014E22.8	ABA-Responsive Protein-Like	At5g13200	GRAM Domain-Containing Protein / ABA-Responsive Protein-Related
OSJNBa0014G15.2	Putative Splicing Regulatory Protein	At5g46870	RNA Recognition Motif (RRM)-Containing Protein
OSJNBa0014G15.3	Putative Reductase	At5g37510	EMB1467 (EMBRYO DEFECTIVE 1467); NADH Dehydrogenase
OSJNBa0014G15.4	Putative GTP-Binding Protein	At1g14830	ADL1C (DYNAMIN-LIKE PROTEIN 5); GTP Binding / Gtpase
OSJNBa0014K14.4	Unknown Protein	At1g80530	Nodulin Family Protein
OSJNBa0014M17.24	Putative Immediate-Early Fungal Elicitor	At3g52450	U-Box Domain-Containing Protein
OSJNBa0014O06.13	Putative Integral Membrane Protein	At2g23150	NRAMP3 (NRAMP Metal Ion Transporter 3); Manganese Ion Transporter/ Metal Ion Transporter
OSJNBa0014O06.18	Putative Methionyl-Trna Synthetase	At3g55400	Ova1 (Ovule Abortion 1)
OSJNBa0014O06.3	Hypothetical Protein	At1g03010	Phototropic-Responsive NPH3 Family Protein
OSJNBa0015G17.1	Putative Cytochrome P450 Protein, 3'-Partial	At5g38970	BR6OX1 (BRASSINOSTEROID-6-OXIDASE); Oxygen Binding
OSJNBa0015G17.23	Putative Peptidyl-Prolyl Cis-Trans Isomerase	At1g13690	ATE1 (Atpase E1); Nucleic Acid Binding
OSJNBa0015J15.10	Hypothetical Protein	At3g61410	Unknown Protein
OSJNBa0015J15.13	Putative Lipid Transfer Protein	At4g12490	Protease Inhibitor/Seed Storage/Lipid Transfer Protein (LTP) Family Protein
OSJNBa0015J15.3	Putative Trehalose-6-Phosphate Phosphatase	At4g22590	Trehalose-6-Phosphate Phosphatase, Putative
OSJNBa0015J15.31	Putative Proline Oxidase	At5g38710	Proline Oxidase, Putative / Osmotic Stress-Responsive Proline Dehydrogenase, Putative
OSJNBa0015J15.32	Unknown Protein	At5g47570	Unknown Protein
OSJNBa0015J15.7	Putative Lipid Transfer Protein	At4g12520	Protease Inhibitor/Seed Storage/Lipid Transfer Protein (LTP) Family Protein
OSJNBa0015K02.10	Unknown Protein	At4g27650	PEL1 (PELOTA); Translation Release Factor
OSJNBa0015K02.13	Unknown Protein	At5g16510	Reversibly Glycosylated Polypeptide, Putative
OSJNBa0015K02.14	Unknown Protein	At3g13530	MAPKKK7 (MAP3K EPSILON PROTEIN KINASE); Kinase
OSJNBa0015K02.18	Unknown Protein	At1g59312	Unknown Protein
OSJNBa0015K02.19	Unknown Protein	At5g64910	Unknown Protein
OSJNBa0015K02.2	Unknown Protein	At5g35630	Gs2 (Glutamine Synthetase 2)
OSJNBa0015K02.7	Unknown Protein	At5g24940	Protein Phosphatase 2C, Putative / PP2C, Putative

OSJNBa0015N08.11	Putative Basic Blue Copper Protein	At2g02850	ARPN (PLANTACYANIN); Copper Ion Binding
OSJNBa0015N08.12	Putative Transcription Factor	At1g17880	Nascent Polypeptide-Associated Complex (NAC) Domain-Containing Protein / BTF3b-Like Transcription Factor, Putative
OSJNBa0015N08.13	Translational Elongation Factor Tu	At4g02930	Elongation Factor Tu, Putative / EF-Tu, Putative
OSJNBa0015N08.15	Putative Proteasome Regulatory Non-Atpase	At5g09900	Emb2107 (Embryo Defective 2107)
OSJNBa0015N08.20	Unknown Protein	At4g35450	AKR2 (ANKYRIN REPEAT-CONTAINING PROTEIN 2); Protein Binding
OSJNBa0015N08.21	Pantoate--Beta-Alanine Ligase	At5g48840	PANC (Arabidopsis Homolog Of Bacterial Panc); Pantoate-Beta-Alanine Ligase
OSJNBa0015N08.24	Putative Der1-Like Protein	At4g04860	Der1-Like Family Protein / Degradation In The ER-Like Family Protein
OSJNBa0015N08.28	Hypothetical Protein	At1g12700	Helicase Domain-Containing Protein / Pentatricopeptide (PPR) Repeat-Containing Protein
OSJNBa0015N08.5	Putative Aspartate Kinase	At5g13280	Ak-Lys1 (Aspartate Kinase 1)
OSJNBa0015N08.9	Putative	At1g01630	SEC14 Cytosolic Factor, Putative / Phosphoglyceride Transfer Protein, Putative
OSJNBa0015O22.19	Putative Peroxidase	At5g06720	Peroxidase, Putative
OSJNBa0015O22.21	Putative Peroxidase	At5g19890	Peroxidase, Putative
OSJNBa0016A21.104	ABC1 Family Protein Kinase-Like Protein	At5g05200	ABC1 Family Protein
OSJNBa0016A21.128-2	Putative 40S Ribosomal Protein S12	At2g32060	40S Ribosomal Protein S12 (RPS12C)
OSJNBa0016C11.4	Zinc Finger Protein-Like	At3g47550	Zinc Finger (C3HC4-Type RING Finger) Family Protein
OSJNBa0016G10.11	Phosphodiesterase/Alkaline Phosphatase D-Like	At5g42370	Unknown Protein
OSJNBa0016G10.14	Unknown Protein	At5g27830	Hypothetical Protein
OSJNBa0016G10.4	Putative 60S Ribosomal Protein L6 (RPL6C)	At1g74050	60S Ribosomal Protein L6 (RPL6C)
OSJNBa0016G10.5	Putative Brix Domain-Containing Protein	At1g52930	Brix Domain-Containing Protein
OSJNBa0016G10.6-2	Putative AAK1 Protein	At2g32850	Protein Kinase Family Protein
OSJNBa0016I09.14	Hypothetical Protein	At5g64700	Nodulin Mtn21 Family Protein
OSJNBa0016I09.24	Putative Phosphoenolpyruvate Carboxylase	At3g14940	ATPPC3 (PHOSPHOENOLPYRUVATE CARBOXYLASE 3); Phosphoenolpyruvate Carboxylase
OSJNBa0016I09.29	Putative 14-3-3-Like Protein	At1g26480	GRF12 (GENERAL REGULATORY FACTOR 12); Protein Phosphorylated Amino Acid Binding
OSJNBa0016I09.3	ATF6I18_13(AL022198|Pid:G2980770) Arabidopsis	At5g45820	CIPK20 (CBL-INTERACTING PROTEIN KINASE 20); Kinase
OSJNBa0016I09.7	Hypothetical Protein	At3g14920	Unknown Protein
OSJNBa0016I09.8	Putative S-Adenosyl-L-Methionine Synthetase	At1g02500	SAM1 (S-Adenosylmethionine Synthetase 1); Methionine Adenosyltransferase
OSJNBa0016N23.106	Putative Beta-Glucosidase Isozyme 2 Precursor	At2g44480	Glycosyl Hydrolase Family 1 Protein
OSJNBa0016N23.121	Putative High-Affinity Potassium Transporter	At1g31120	KUP10 (K+ Transporter 10); Potassium Ion Transporter
OSJNBa0016N23.122	Putative Alcohol Dehydrogenase Homolog	At1g62610	Oxidoreductase
OSJNBa0016O02.24	Unknown Protein	At5g47810	Phosphofructokinase Family Protein
OSJNBa0016O02.3	Unknown Protein	At5g08170	EMB1873 (EMBRYO DEFECTIVE 1873); Agmatine Deiminase
OSJNBa0016O02.9	Unknown Protein	At5g48220	Indole-3-Glycerol-Phosphate Synthase
OSJNBa0017B10.17	Unknown Protein	At2g25720	Unknown Protein
OSJNBa0017E08.10	Putative Pre-Mrna Splicing Factor	At4g03430	STA1 (STABILIZED1); RNA Splicing Factor, Transesterification Mechanism

OSJNBa0017E08.12	Putative Epoxide Hydrolase	At3g51000	Epoxide Hydrolase, Putative
OSJNBa0017E08.18	Putative Membrane-Associated Protein	At1g12700	Helicase Domain-Containing Protein / Pentatricopeptide (PPR) Repeat-Containing Protein
OSJNBa0017E08.4	Putative Lanthionine Synthetase	At1g52920	Catalytic
OSJNBa0017E08.8	Putative Dehydrogenase	At4g27440	PORB (PROTOCHLOROPHYLLIDE OXIDOREDUCTASE B); Oxidoreductase/ Protochlorophyllide Reductase
OSJNBa0017J22.12	Unknown Protein	At3g55070	Unknown Protein
OSJNBa0017J22.13	Putative Ubiquitin / Ribosomal Protein S27a	At2g47110	UBQ6 (Ubiquitin 6); Protein Binding
OSJNBa0017J22.5	Unknown Protein	At3g17205	UPL6 (UBIQUITIN PROTEIN LIGASE 6); Ubiquitin-Protein Ligase
OSJNBa0017J22.6	Unknown Protein	At1g09330	Hypothetical Protein
OSJNBa0017N12.13	Putative Phosphate Synthase	At1g22410	2-Dehydro-3-Deoxyphosphoheptonate Aldolase, Putative / 3-Deoxy-D-Arabino-Heptulosonate 7-Phosphate Synthase, Putative / DAHP Synthetase, Putative
OSJNBa0017N12.5	Histone H3.2 Protein	At5g10980	Histone H3
OSJNBa0017N12.8	Abscisic Acid-Inducible Protein Kinase	At1g78290	Serine/Threonine Protein Kinase, Putative
OSJNBa0018H01.3	Unknown Protein	At2g34690	Acd11 (Accelerated Cell Death 11)
OSJNBa0018H01.6	Putative Basic Protein	At2g26720	Plastocyanin-Like Domain-Containing Protein / Mavicyanin, Putative
OSJNBa0018H01.7	Putative Glutathione S-Transferase	At1g65820	Microsomal Glutathione S-Transferase, Putative
OSJNBa0018H01.9	Putative Snrnp Protein	At2g33730	DEAD Box RNA Helicase, Putative
OSJNBa0018I03.26	Atpase-Like Protein	At5g44240	Haloacid Dehalogenase-Like Hydrolase Family Protein
OSJNBa0018K15.1	Putative Arm Repeat Protein	At5g01830	Armadillo/Beta-Catenin Repeat Family Protein / U-Box Domain-Containing Protein
OSJNBa0018M05.1	Unknown Protein	At1g47875	Pseudogene, Hypothetical Protein
OSJNBa0018M05.13	Unknown Protein	At3g18620	Zinc Finger (DHHC Type) Family Protein
OSJNBa0018M05.14	Unknown Protein	At1g65730	YSL7 (YELLOW STRIPE LIKE 7); Oligopeptide Transporter
OSJNBa0018M05.15	Unknown Protein	At5g16370	AMP-Binding Protein, Putative
OSJNBa0018M05.16	Unknown Protein	At1g48930	Endo-1,4-Beta-Glucanase, Putative / Cellulase, Putative
OSJNBa0018M05.18	Unknown Protein	At5g23110	Zinc Finger (C3HC4-Type RING Finger) Family Protein
OSJNBa0018M05.19	Unknown Protein	At5g23240	DNAJ Heat Shock N-Terminal Domain-Containing Protein
OSJNBa0018M05.20	Unknown Protein	At1g34130	STT3B (STAUROSPORIN AND TEMPERATURE SENSITIVE 3-LIKE B); Oligosaccharyl Transferase
OSJNBa0018M05.21	Unknown Protein	At1g63070	Pentatricopeptide (PPR) Repeat-Containing Protein
OSJNBa0018M05.8	Unknown Protein	At3g17670	Binding
OSJNBa0018M05.9	Unknown Protein	At2g03690	Coenzyme Q Biosynthesis Coq4 Family Protein / Ubiquinone Biosynthesis Coq4 Family Protein
OSJNBa0018M09.11	Putative SERK2 Protein	At5g10290	Leucine-Rich Repeat Family Protein / Protein Kinase Family Protein
OSJNBa0019D11.15	Unknown Protein	At3g62470	Pentatricopeptide (PPR) Repeat-Containing Protein
OSJNBa0019D11.19	Unknown Protein	At5g54140	ILL3 (IAA-Amino Acid Hydrolase ILR1-Like 3); Metallopeptidase
OSJNBa0019D11.5	Unknown Protein	At1g03360	ATRRP4; Exonuclease
OSJNBa0019F11.10	Hypothetical Protein	At1g19370	Unknown Protein

OSJNBa0019F11.13	Putative 60S Ribosomal Protein	At3g49010	ATBBC1 (Breast Basic Conserved 1)
OSJNBa0019F11.19	Putative Syntaxin Protein	At3g05710	SYP43 (Syntaxin 43); T-SNARE
OSJNBa0019F11.23	Putative Plastid Protein	At1g32580	Plastid Developmental Protein DAG, Putative
OSJNBa0019F11.5	Unknown Protein	At5g17210	Unknown Protein
OSJNBa0019G23.2	Unknown Protein	At5g04360	ATPU1 (PULLULANASE 1); Alpha-Amylase/ Limit Dextrinase
OSJNBa0019G23.3	Unknown Protein	At1g20030	Pathogenesis-Related Thaumatin Family Protein
OSJNBa0019G23.6	Unknown Protein	At1g30890	Integral Membrane HRF1 Family Protein
OSJNBa0019G23.8	Unknown Protein	At3g08980	Signal Peptidase I Family Protein
OSJNBa0019K04.15	Unknown Protein	At5g62220	Exostosin Family Protein
OSJNBa0019K04.19	Unknown Protein	At1g01930	Zinc Finger Protein-Related
OSJNBa0019K04.2	Unknown Protein	At4g25480	DREB1A (DEHYDRATION RESPONSE ELEMENT B1A); DNA Binding / Transcription Factor/ Transcriptional Activator
OSJNBa0019K04.6	Unknown Protein	At4g11810	SPX (SYG1/Pho81/XPR1) Domain-Containing Protein
OSJNBa0019K04.7	Unknown Protein	At1g12570	Glucose-Methanol-Choline (GMC) Oxidoreductase Family Protein
OSJNBa0019K04.9	Unknown Protein	At5g51750	Subtilase Family Protein
OSJNBa0020E23.9	Unknown Protein	At5g02910	F-Box Family Protein
OSJNBa0020H02.1	Putative Heat Shock Protein	At5g15450	APG6/CLPB-P/CLPB3 (ALBINO AND PALE GREEN 6); ATP Binding / Atpase
OSJNBa0020H14.13	Putative Plastid Division Protein Ftsz	At3g52750	FTSZ2-2 (Ftsz2-2); Structural Molecule
OSJNBa0020H14.6	Putative Myb-Like Transcription Factor	At4g09450	Myb Family Transcription Factor
OSJNBa0020I02.14	Unknown Protein	At1g09770	ATCDC5 (Arabidopsis Thaliana Homolog Of Cdc5); DNA Binding / Transcription Factor
OSJNBa0020I02.8	Unknown Protein	At5g51340	Binding
OSJNBa0020J04.12	Unknown Protein	At5g41890	GDSL-Motif Lipase/Hydrolase Family Protein
OSJNBa0020J04.13	Unknown Protein	At5g17570	Tatd-Related Deoxyribonuclease Family Protein
OSJNBa0020J04.7	Unknown Protein	At2g16530	3-Oxo-5-Alpha-Steroid 4-Dehydrogenase Family Protein / Steroid 5-Alpha-Reductase Family Protein
OSJNBa0020J04.9	Unknown Protein	At2g21270	Ubiquitin Fusion Degradation UFD1 Family Protein
OSJNBa0020P07.11	Unknown Protein	At1g01090	PDH-E1 ALPHA (PYRUVATE DEHYDROGENASE E1 ALPHA); Pyruvate Dehydrogenase (Acetyl-Transferring)
OSJNBa0020P07.12	Unknown Protein	At1g64720	Cp5
OSJNBa0020P07.16	Unknown Protein	At3g29775	Transposable Element Gene
OSJNBa0020P07.4	Unknown Protein	At2g18040	PIN1AT (Parvulin 1At)
OSJNBa0020P07.6	Unknown Protein	At3g57430	Pentatricopeptide (PPR) Repeat-Containing Protein
OSJNBa0022D10.11	Unknown Protein	At2g42490	Copper Amine Oxidase, Putative
OSJNBa0022H21.12	Unknown Protein	At1g14130	2-Oxoglutarate-Dependent Dioxygenase, Putative
OSJNBa0022H21.21	Unknown Protein	At5g50170	C2 Domain-Containing Protein / GRAM Domain-Containing Protein
OSJNBa0022H21.3	Unknown Protein	At5g42260	Glycosyl Hydrolase Family 1 Protein

OSJNBa0022J22.7	Putative Nucleoid DNA-Binding Protein	At3g59080	DNA Binding
OSJNBa0022J22.8	Putative Ubiquitin	At2g46500	Phosphatidylinositol 3- And 4-Kinase Family Protein / Ubiquitin Family Protein
OSJNBa0023I13.30	Unknown Protein	At1g16080	Unknown Protein
OSJNBa0023I17.12	Putative Receptor Protein Kinase PERK	At3g14840	Leucine-Rich Repeat Family Protein / Protein Kinase Family Protein
OSJNBa0023I17.4	Putative Pentatricopeptide (PPR)	At2g36730	Pentatricopeptide (PPR) Repeat-Containing Protein
OSJNBa0023I17.7	Unknown Protein	At1g50670	OTU-Like Cysteine Protease Family Protein
OSJNBa0023I19.10	Putative Purple Acid Phosphatase	At1g14700	ATPAP3/PAP3 (Purple Acid Phosphatase 3)
OSJNBa0023J03.8	Unknown Protein	At1g71100	RSW10 (RADIAL SWELLING 10); Ribose-5-Phosphate Isomerase
OSJNBa0024F18.3	Putative NAC-Domain Protein	At4g35580	No Apical Meristem (NAM) Family Protein
OSJNBa0024J22.1	Unknown Protein	At1g79940	Heat Shock Protein Binding / Unfolded Protein Binding
OSJNBa0024K17.10	Putative Translation Elongation Factor	At3g22980	Elongation Factor Tu Family Protein
OSJNBa0024K17.17	Expressed Protein	At5g17830	Unknown Protein
OSJNBa0025J22.1	Putative Multiple Stress-Responsive Zinc-Finger	At4g22820	Zinc Finger (AN1-Like) Family Protein
OSJNBa0025J22.10	Putative 60S Ribosomal Protein L31	At5g56710	60S Ribosomal Protein L31 (RPL31C)
OSJNBa0025J22.21	Putative DNA-Damage-Repair/Toleration Protein	At3g12610	DRT100 (DNA-DAMAGE REPAIR/TOLERATION 100); Protein Binding
OSJNBa0025J22.3	Putative Protein Kinase (KIPK)	At4g26610	Protein Kinase, Putative
OSJNBa0025J22.9	Unknown Protein	At3g57780	Unknown Protein
OSJNBa0025P09.18	Putative Cytokinin Dehydrogenase	At2g41510	ATCKX1/CKX1 (CYTOKININ OXIDASE/DEHYDROGENASE 1); Cytokinin Dehydrogenase
OSJNBa0025P13.1	Putative Protein Kinase	At4g08850	Leucine-Rich Repeat Family Protein / Protein Kinase Family Protein
OSJNBa0026A15.13	Hypothetical Protein	At2g26680	Unknown Protein
OSJNBa0026A15.3	Putative Translation Initiation Factor	At3g19760	Eukaryotic Translation Initiation Factor 4A, Putative / Eif-4A, Putative / DEAD Box RNA Helicase, Putative
OSJNBa0026E05.10	Putative UOS1	At1g16720	Oxidoreductase/ Transcriptional Repressor
OSJNBa0026E05.30	Putative Calcium Exchanger (CAX2)	At1g55730	ATCAX5 (Calcium Exchanger 5); Cation:Cation Antiporter
OSJNBa0026E05.33	Unknown Protein	At5g58110	Unknown Protein
OSJNBa0026E05.37	Putative Beta-1,3-Glucanase	At5g58090	Glycosyl Hydrolase Family 17 Protein
OSJNBa0026J14.20	Pectate Lyase-Like Protein	At3g55140	Pectate Lyase Family Protein
OSJNBa0026L12.2	Putative Cytochrome P450	At1g64950	CYP89A5 (Cytochrome P450, Family 87, Subfamily A, Polypeptide 5); Oxygen Binding
OSJNBa0026L12.23	Putative Nodulin-26	At4g10380	NIP5;1/NLM6/NLM8 (NOD26-Like Intrinsic Protein 5;1); Boron Transporter/ Water Channel
OSJNBa0026L12.31	Putative Non-LTR Retroelement Reverse	At2g45230	Transposable Element Gene
OSJNBa0026L12.5	Putative Cytochrome P450	At1g64900	CYP89A2 (CYTOCHROME P450 89A2); Oxygen Binding
OSJNBa0026O12.11	Putative Esterase	At5g62930	GDSL-Motif Lipase/Hydrolase Family Protein
OSJNBa0026O12.9	Hypothetical Protein	At3g23300	Dehydration-Responsive Protein-Related
OSJNBa0027G07.7	Unknown Protein	At1g34580	Monosaccharide Transporter, Putative
OSJNBa0027H06.5	Unknown Protein	At3g14540	Terpene Synthase/Cyclase Family Protein

OSJNBa0027H09.13	Unknown Protein	At1g04610	Flavin-Containing Monooxygenase / FMO (YUCCA3)
OSJNBa0027H16.15	Hypothetical Protein	At3g60150	Unknown Protein
OSJNBa0027L23.3	Putative Plastid-Lipid Associated Protein	At2g35490	Plastid-Lipid Associated Protein PAP, Putative
OSJNBa0027L23.4	Unknown Protein	At3g18410	NADH-Ubiquinone Oxidoreductase-Related
OSJNBa0027L23.5	Putative Inositol 1,3,4-Trisphosphate	At5g16760	Inositol 1,3,4-Trisphosphate 5/6-Kinase
OSJNBa0027L23.9	Unknown Protein	At1g65020	Unknown Protein
OSJNBa0027N13.142	Unknown Protein	At2g32380	Unknown Protein
OSJNBa0027O01.6	Unknown Protein	At4g14420	Lesion Inducing Protein-Related
OSJNBa0027P08.12	Unknown Protein	At1g65010	Unknown Protein
OSJNBa0027P08.14	Unknown Protein	At5g46290	KAS I (3-KETOACYL-ACYL CARRIER PROTEIN SYNTHASE I); Fatty-Acid Synthase
OSJNBa0027P08.15	Unknown Protein	At1g19120	Small Nuclear Ribonucleoprotein, Putative / Snrnp, Putative / Sm Protein, Putative
OSJNBa0027P08.6	Unknown Protein	At5g49740	ATFRO7/FRO7 (FERRIC REDUCTION OXIDASE 7); Ferric-Chelate Reductase/ Oxidoreductase
OSJNBa0027P08.7	Unknown Protein	At2g02470	PHD Finger Family Protein
OSJNBa0027P08.8	Unknown Protein	At3g02850	SKOR (Stelar K+ Outward Rectifier); Cyclic Nucleotide Binding / Outward Rectifier Potassium Channel
OSJNBa0027P10.1	Putative Palmitoyl-Protein Thioesterase	At3g60340	Palmitoyl Protein Thioesterase Family Protein
OSJNBa0027P10.10	Putative Ribosomal Protein L27	At4g15000	60S Ribosomal Protein L27 (RPL27C)
OSJNBa0027P10.11	Putative Arm Repeat Protein	At2g44900	Armadillo/Beta-Catenin Repeat Family Protein / F-Box Family Protein
OSJNBa0027P10.14	Putative WD-40 Protein	At5g07590	WD-40 Repeat Protein Family
OSJNBa0027P10.16	Hypothetical Protein	At2g44740	CYCP4;1 (Cyclin P4;1); Cyclin-Dependent Protein Kinase
OSJNBa0027P10.3	Putative Peptide Methionine Sulfoxide Reductase	At4g25130	Peptide Methionine Sulfoxide Reductase, Putative
OSJNBa0027P10.4	Putative Nucleoside Diphosphate Kinase	At4g09320	NDPK1 (Nucleoside Diphosphate Kinase 1); ATP Binding / Nucleoside Diphosphate Kinase
OSJNBa0027P10.5	Putative Nucleic Acid Binding Protein	At4g26000	PEP (PEPPER); Nucleic Acid Binding
OSJNBa0027P10.8	Putative Casein Kinase II Beta Subunit	At2g44680	CKB4 (CASEIN KINASE II BETA SUBUNIT 4); Protein Kinase CK2 Regulator
OSJNBa0028I23.19	Unknown Protein	At1g43690	Ubiquitin Interaction Motif-Containing Protein
OSJNBa0028I23.24	Unknown Protein	At5g45370	Nodulin-Related / Integral Membrane Family Protein
OSJNBa0029C04.10	Unknown Protein	At2g13000	Transposable Element Gene
OSJNBa0029C15.2	Putative Thioredoxin-Like U5 Small	At5g08290	YLS8 (Yellow-Leaf-Specific Gene 8); Catalytic
OSJNBa0029C15.3	Putative Cytochrome P450 Protein	At5g23190	CYP86B1 (Cytochrome P450, Family 86, Subfamily B, Polypeptide 1); Oxygen Binding
OSJNBa0029C15.7	Anther-Specific Protein YY2	At1g02050	Chalcone And Stilbene Synthase Family Protein
OSJNBa0029H02.14	Unknown Protein	At5g48930	Transferase Family Protein
OSJNBa0029H02.16	Unknown Protein	At3g55280	60S Ribosomal Protein L23A (RPL23aB)
OSJNBa0029H02.19	Unknown Protein	At2g24240	Potassium Channel Tetramerisation Domain-Containing Protein
OSJNBa0029H02.21	Unknown Protein	At5g17410	Tubulin Family Protein
OSJNBa0029H02.22	Unknown Protein	At2g24290	Unknown Protein

OSJNBa0029H02.25	Unknown Protein	At5g11040	Unknown Protein
OSJNBa0029H02.4	Unknown Protein	At2g03670	CDC48B; Atpase
OSJNBa0029H02.6	Unknown Protein	At5g25050	Integral Membrane Transporter Family Protein
OSJNBa0029P06.15	Putative Alpha-Mannosidase	At5g66150	Glycosyl Hydrolase Family 38 Protein
OSJNBa0029P16.14	Putative Proton Pump	At2g21410	(VACUOLAR PROTON ATPASE A2); Atpase
OSJNBa0030G18.4	SWP1 Protein-Like	At3g04740	Swp (Struwwelpeter)
OSJNBa0030I14.5	Putative Early-Responsive To Dehydration Stress	At3g21620	Early-Responsive To Dehydration Protein-Related / ERD Protein-Related
OSJNBa0030I14.9	UDP-Glucose 4-Epimerase	At4g23920	UGE2 (UDP-D-Glucose/UDP-D-Galactose 4-Epimerase 2); UDP-Glucose 4-Epimerase/ Protein Dimerization
OSJNBa0030J19.9	Putative Ribosomal Protein L27a	At1g70600	60S Ribosomal Protein L27A (RPL27aC)
OSJNBa0030M21.36	Eukaryotic Translation Initiation Factor 1A	At2g04520	Eukaryotic Translation Initiation Factor 1A, Putative / Eif-1A, Putative / Eif-4C, Putative
OSJNBa0030M21.4	Putative Lectin-Like Receptor Kinase 7	At5g01550	Lectin Protein Kinase, Putative
OSJNBa0031C24.124	Putative Cytochrome P450	At3g53280	CYP71B5 (CYTOCHROME P450 71B5); Oxygen Binding
OSJNBa0031C24.143	Putative Cytochrome P450	At5g25140	CYP71B13 (Cytochrome P450, Family 71, Subfamily B, Polypeptide 13); Oxygen Binding
OSJNBa0031I04.2	Putative Calcineurin	At1g64480	Cbl8 (Calcineurin B-Like Protein 5)
OSJNBa0031O09.02	Predicted Protein	At5g43950	Unknown Protein
OSJNBa0031O09.03	Similar To Histone 2A Domain	At1g54690	Histone H2A, Putative
OSJNBa0031O09.05	Putative Myb/Myb-Related Protein	At4g33450	Atmyb69 (Myb Domain Protein 69); DNA Binding / Transcription Factor
OSJNBa0032B23.5	Unknown Protein	At5g51660	Cleavage And Polyadenylation Specificity Factor (CPSF) A Subunit C-Terminal Domain-Containing Protein
OSJNBa0032F06.12	Unknown Protein	At5g53470	Acbp1 (Acyl-Coa Binding Protein)
OSJNBa0032F06.13	Unknown Protein	At3g59950	Autophagy 4b (APG4b)
OSJNBa0032F06.14	Unknown Protein	At5g18400	Unknown Protein
OSJNBa0032F06.15	Unknown Protein	At1g63220	C2 Domain-Containing Protein
OSJNBa0032F06.16	Unknown Protein	At2g45790	Eukaryotic Phosphomannomutase Family Protein
OSJNBa0032F06.7	Unknown Protein	At4g27780	Acbp2 (Acyl-Coa Binding Protein Acbp 2)
OSJNBa0032G08.1	Putative Dihydroflavonal-4-Reductase	At4g33360	Terpene Cyclase/Mutase-Related
OSJNBa0032G08.17	Unknown Protein	At4g33250	EIF3K (Eukaryotic Translation Initiation Factor 3K)
OSJNBa0032G08.18	Putative 40S Ribosomal Protein	At3g04770	RPSAB (40S Ribosomal Protein SA B); Structural Constituent Of Ribosome
OSJNBa0032G08.3	Putative Protein With Similarity To Putative	At3g19230	Leucine-Rich Repeat Family Protein
OSJNBa0032G08.4	Putative Glycogenin	At1g54940	Glycogenin Glucosyltransferase (Glycogenin)-Related
OSJNBa0032G08.6	Putative Plasma Membrane Proton Atpase	At1g17260	AHA10 (AUTOINHIBITED H(+)-ATPASE ISOFORM 10); Atpase
OSJNBa0032G08.7	Putative Leucine-Rich Repeat Transmembrane	At1g53730	Leucine-Rich Repeat Transmembrane Protein Kinase, Putative
OSJNBa0032G11.10	Putative Methyl Chloride Transferase	At2g43910	Thiol Methyltransferase, Putative
OSJNBa0032G11.11	Putative Poly(ADP-Ribose) Glycohydrolase	At2g31870	Tej (Sanskrit For 'Bright')
OSJNBa0032G11.13	Putative Protein Kinase	At3g59350	Kinase

OSJNBa0032G11.16	Putative B' Regulatory Subunit Of Protein	At3g26020	Protein Phosphatase Type 2A Regulator
OSJNBa0032G11.17	Putative GDSL-Like Lipase/Acylhydrolase	At3g48460	GDSL-Motif Lipase/Hydrolase Family Protein
OSJNBa0032G11.2	Putative Oxidoreductase	At4g10020	Short-Chain Dehydrogenase/Reductase (SDR) Family Protein
OSJNBa0032G11.22	Putative Pirin-Like Protein	At1g50590	Pirin, Putative
OSJNBa0032G11.28	Putative AMP-Binding Protein	At4g14070	AAE15 (ACYL-ACTIVATING ENZYME 15); Acyl-ACP Synthetase
OSJNBa0032G11.5	Putative Late Embryogenesis Abundant Protein	At2g44060	Late Embryogenesis Abundant Family Protein / LEA Family Protein
OSJNBa0032H19.14	Unknown Protein	At2g05640	Transposable Element Gene
OSJNBa0032H19.2	Unknown Protein	At2g31890	Protein Contains Putative RNA Binding Domain.
OSJNBa0032H19.22	Putative Stearoyl-Acyl-Carrier Protein	At5g16230	Acyl-(Acyl-Carrier-Protein) Desaturase, Putative / Stearoyl-ACP Desaturase, Putative
OSJNBa0032H19.25	Hypothetical Protein	At5g39250	F-Box Family Protein
OSJNBa0032H19.8	Putative Ribosomal Protein S19	At5g61170	40S Ribosomal Protein S19 (RPS19C)
OSJNBa0032I19.1	Unknown Protein	At1g10810	Aldo/Keto Reductase Family Protein
OSJNBa0032I19.2	Unknown Protein	At1g60690	Aldo/Keto Reductase Family Protein
OSJNBa0032N04.1	Hypothetical Protein	At5g63560	Transferase Family Protein
OSJNBa0033G05.14	Unknown Protein	At2g12550	Ubiquitin-Associated (UBA)/TS-N Domain-Containing Protein
OSJNBa0033G05.20	Unknown Protein	At5g33280	Chloride Channel-Like (CLC) Protein, Putative
OSJNBa0033G05.7	Unknown Protein	At4g30560	ATCNGC9 (CYCLIC NUCLEOTIDE GATED CHANNEL 9); Calmodulin Binding / Cyclic Nucleotide Binding / Ion Channel
OSJNBa0033G05.8	Unknown Protein	At1g80550	Pentatricopeptide (PPR) Repeat-Containing Protein
OSJNBa0033G16.4	Unknown Protein	At3g44220	Harpin-Induced Family Protein / HIN1 Family Protein / Harpin-Responsive Family Protein
OSJNBa0033G16.6	Unknown Protein	At3g11680	Unknown Protein
OSJNBa0033H08.6	Unknown Protein	At1g62940	4-Coumarate--Coa Ligase Family Protein / 4-Coumaroyl-Coa Synthase Family Protein
OSJNBa0033P04.2	Putative Rubisco Subunit Binding-Protein Alpha	At2g28000	CPN60A (Chloroplast / 60 Kda Chaperonin Alpha Subunit); ATP Binding / Protein Binding / Unfolded Protein Binding
OSJNBa0033P04.20	Putative DNA Binding Protein	At3g23240	ATERF1/ERF1 (ETHYLENE RESPONSE FACTOR 1); DNA Binding / Transcription Factor/ Transcriptional Activator
OSJNBa0033P04.26	Putative Pentatricopeptide Repeat Containing	At5g52850	Pentatricopeptide (PPR) Repeat-Containing Protein
OSJNBa0034B05.21	Putative Protein Kinase	At1g50700	CPK33 (Calcium-Dependent Protein Kinase 33); Calcium- And Calmodulin-Dependent Protein Kinase/ Kinase
OSJNBa0034B05.23	Putative Synaptobrevin-Like Protein	At5g22360	ATVAMP714 (Vesicle-Associated Membrane Protein 714)
OSJNBa0034B05.25	Putative Protein Kinase	At3g06030	ANP3 (Arabidopsis NPK1-Related Protein Kinase 3); Kinase
OSJNBa0034D21.15	Putative Antifungal Zeamatin-Like Protein	At4g11650	Atosm34 (Osmotin 34)
OSJNBa0034E08.23	Putative Piwi Domain Containing Protein	At1g69440	Ago7 (Argonaute7)
OSJNBa0034E08.30	Putative Mitotic Checkpoint Protein	At1g49910	WD-40 Repeat Family Protein / Mitotic Checkpoint Protein, Putative
OSJNBa0035A24.10	Prefoldin-Related KE2-Like	At3g52400	SYP122 (Syntaxin 122); T-SNARE
OSJNBa0035A24.17	Hypothetical Protein	At3g18440	Unknown Protein
OSJNBa0035A24.45	RAD23 Protein-Like	At1g79650	RAD23; Damaged DNA Binding

OSJNBa0035A24.50	Putative Sterol Delta-7 Reductase	At1g50430	Dwf5 (Dwarf 5)
OSJNBa0035H01.10	Putative Cellulose Synthase	At3g03050	CSLD3 (CELLULOSE SYNTHASE-LIKE 3); Cellulose Synthase/ Transferase, Transferring Glycosyl Groups
OSJNBa0035H01.8	Putative Acyltransferase	At1g32200	Ats1 (Acyltransferase 1)
OSJNBa0035I03.10	Putative Inorganic Pyrophosphatase	At1g15690	AVP1 (Vacuolar-Type H+-Pumping Pyrophosphatase 1)
OSJNBa0035I03.11	Unknown Protein	At5g34940	Glycosyl Hydrolase Family 79 N-Terminal Domain-Containing Protein
OSJNBa0035I03.17	Putative DNA-Binding Protein Phosphatase 2C	At2g25620	Protein Phosphatase 2C, Putative / PP2C, Putative
OSJNBa0035I03.35	Putative Plasma Membrane H+-Atpase	At3g42640	AHA8 (ARABIDOPSIS H(+)-ATPASE 8); Atpase
OSJNBa0035I24.3	Expressed Protein	At4g33700	CBS Domain-Containing Protein
OSJNBa0035M09.11	Unknown Protein	At2g15410	Transposable Element Gene
OSJNBa0035M09.16	Unknown Protein	At5g10620	Unknown Protein
OSJNBa0035M09.17	Unknown Protein	At5g19940	Plastid-Lipid Associated Protein PAP-Related / Fibrillin-Related
OSJNBa0035M09.18	Unknown Protein	At4g25870	Unknown Protein
OSJNBa0035M09.2	Unknown Protein	At5g57110	ACA8 (AUTOINHIBITED CA2+ -ATPASE, ISOFORM 8); Calmodulin Binding
OSJNBa0035M09.7	Unknown Protein	At1g51590	Calcium Ion Binding / Mannosyl-Oligosaccharide 1,2-Alpha-Mannosidase
OSJNBa0035O13.14	Unknown Protein	At3g62700	ATMRP10 (Arabidopsis Thaliana Multidrug Resistance-Associated Protein 10)
OSJNBa0035O13.9	Unknown Protein	At5g45890	SAG12 (SENESCENCE-ASSOCIATED GENE 12); Cysteine-Type Peptidase
OSJNBa0036B21.10	Unknown Protein	At4g39640	GGT1; Gamma-Glutamyltransferase
OSJNBa0036B21.13	Unknown Protein	At1g34210	SERK2 (SOMATIC EMBRYOGENESIS RECEPTOR-LIKE KINASE 2); Kinase
OSJNBa0036B21.20	Unknown Protein	At5g27870	Pectinesterase Family Protein
OSJNBa0036B21.21	Unknown Protein	At3g28860	ATMDR11/ATPGP19/MDR1/MDR11/PGP19 (P-GLYCOPROTEIN 19); Atpase, Coupled To Transmembrane Movement Of Substances / Auxin Efflux Transporter
OSJNBa0036B21.6	Unknown Protein	At1g15820	LHCB6 (LIGHT HARVESTING COMPLEX PSII); Chlorophyll Binding
OSJNBa0036D19.6	Putative Senescence-Associated Protein 15	At1g01120	KCS1 (3-KETOACYL-COA SYNTHASE 1); Acyltransferase
OSJNBa0036E02.13	Putative DNA-Binding Protein	At1g80270	DNA-Binding Protein, Putative
OSJNBa0036E02.23	Putative Coatmer Beta Subunit (Beta-Coat	At4g31480	Coatomer Beta Subunit, Putative / Beta-Coat Protein, Putative / Beta-COP, Putative
OSJNBa0036E02.3	Putative Na+-Dependen Inorganic Phosphate	At5g44370	Transporter-Related
OSJNBa0036E02.4	Putative Leucine-Rich Repeat Protein LRP	At5g21090	Leucine-Rich Repeat Protein, Putative
OSJNBa0036E02.7	Putative Transcription Factor HBP-1b - Wheat	At5g06950	AHBP-1B (Bzip Transcription Factor HBP-1b Homolog)
OSJNBa0036E17.10	Cytosolic Pyruvate Orthophosphate Dikinase	At4g15530	Ppdk (Pyruvate Orthophosphate Dikinase)
OSJNBa0036E17.12	Expressed Protein	At2g14680	MEE13 (Maternal Effect Embryo Arrest 13)
OSJNBa0038E22.11	Putative Polyprotein	At2g15100	Transposable Element Gene
OSJNBa0038F22.1	Receptor Protein Kinase-Like	At2g21480	Protein Kinase Family Protein
OSJNBa0038F22.14	Putative Isp4 Protein	At4g10770	ATOPT7 (Oligopeptide Transporter 7); Oligopeptide Transporter
OSJNBa0038F22.17	Putative Ribonucleoside-Diphosphate Reductase	At3g27060	TSO2 (TSO2); Ribonucleoside-Diphosphate Reductase
OSJNBa0038F22.20	Unknown Protein	At5g01460	LMBR1 Integral Membrane Family Protein

OSJNBa0038J17.19	Unknown Protein	At5g45920	Carboxylic Ester Hydrolase
OSJNBa0038J17.26	Unknown Protein	At1g28590	Lipase, Putative
OSJNBa0038J17.27	Hypothetical Protein	At1g15000	SCPL50 (Serine Carboxypeptidase-Like 50); Serine Carboxypeptidase
OSJNBa0038O10.10	Unknown Protein	At5g64500	Membrane Protein-Related
OSJNBa0038O10.17	Unknown Protein	At5g08350	GRAM Domain-Containing Protein / ABA-Responsive Protein-Related
OSJNBa0038O10.7	Unknown Protein	At5g23140	CLPP2 (Clp Protease Proteolytic Subunit 2); Endopeptidase Clp
OSJNBa0038P21.6	Unknown Protein	At1g62670	Pentatricopeptide (PPR) Repeat-Containing Protein
OSJNBa0038P21.9	Unknown Protein	At5g14770	Pentatricopeptide (PPR) Repeat-Containing Protein
OSJNBa0039C07.14	Unknown Protein	At5g45880	Pollen Ole E 1 Allergen And Extensin Family Protein
OSJNBa0039C07.2	Unknown Protein	At1g28110	SCPL45; Serine Carboxypeptidase
OSJNBa0039C07.3	Unknown Protein	At1g32210	Atdad1 (Defender Against Apoptotic Death 1)
OSJNBa0039C07.4	Unknown Protein	At5g50920	CLPC (HEAT SHOCK PROTEIN 93-V); ATP Binding / Atpase
OSJNBa0039G19.10	Unknown Protein	At1g21100	O-Methyltransferase, Putative
OSJNBa0039K24.10	Unknown Protein	At5g14130	Peroxidase, Putative
OSJNBa0039K24.19	Unknown Protein	At1g49730	Protein Kinase Family Protein
OSJNBa0039K24.21	Unknown Protein	At1g05970	Nucleotide Binding
OSJNBa0039K24.22	Unknown Protein	At1g75030	ATLP-3 (Arabidopsis Thaumatin-Like Protein 3)
OSJNBa0039K24.28	Unknown Protein	At1g44575	Npq4 (Nonphotochemical Quenching)
OSJNBa0039K24.3	Unknown Protein	At1g18740	Unknown Protein
OSJNBa0039N21.16	Putative Transposon Protein	At1g34660	Transposable Element Gene
OSJNBa0039N21.4	Putative Glucose-6-Phosphate Dehydrogenase	At5g35790	G6PD1 (GLUCOSE-6-PHOSPHATE DEHYDROGENASE 1); Glucose-6-Phosphate 1-Dehydrogenase
OSJNBa0039N21.9	Putative Glycosyltransferase Protein	At1g18580	GAUT11 (Galacturonosyltransferase 11); Polygalacturonate 4-Alpha-Galacturonosyltransferase
OSJNBa0039O18.13	Putative RNA Helicase	At5g60990	DEAD/DEAH Box Helicase, Putative (RH10)
OSJNBa0039O18.8	Putative Beta 1,3-Glucanase	At2g16230	Glycosyl Hydrolase Family 17 Protein
OSJNBa0039O18.9	Guanine Nucleotide-Binding Protein Beta Subunit	At4g34460	Agb1 (Gtp Binding Protein Beta 1)
OSJNBa0040D17.13	Unknown Protein	At1g53390	Atpase, Coupled To Transmembrane Movement Of Substances
OSJNBa0040D23.4	Putative Transmembrane Protein	At1g14530	(TOM THREE HOMOLOG); Virion Binding
OSJNBa0040E01.14	Putative Glucosyltransferase	At5g59590	UDP-Glucoronosyl/UDP-Glucosyl Transferase Family Protein
OSJNBa0040E01.26	Putative Ankyrin	At2g03430	Ankyrin Repeat Family Protein
OSJNBa0040E01.5	Putative Glucosyltransferase	At3g02100	UDP-Glucoronosyl/UDP-Glucosyl Transferase Family Protein
OSJNBa0040E01.6	Unknown Protein	At5g07960	Unknown Protein
OSJNBa0040E01.8	Putative UDP-Glucose Dehydrogenase	At5g15490	UDP-Glucose 6-Dehydrogenase, Putative
OSJNBa0040E17.10	Hypothetical Protein	At2g14610	Pr1 (Pathogenesis-Related Gene 1)
OSJNBa0040K22.111	Putative UVB-Resistance Protein UVR8	At3g15430	Regulator Of Chromosome Condensation (RCC1) Family Protein

OSJNBa0041A02.10	Unknown Protein	At4g09010	APX4 (ASCORBATE PEROXIDASE 4); Peroxidase
OSJNBa0041A02.11	Unknown Protein	At1g31410	Putrescine-Binding Periplasmic Protein-Related
OSJNBa0041A02.14	Unknown Protein	At5g45280	Pectinacetylesterase, Putative
OSJNBa0041A02.18	Unknown Protein	At5g23320	ATSTE14 (PRENYLCYSTEINE ALPHA-CARBOXYL METHYLTRANSFERASE 14A); Protein-S-Isoprenylcysteine O-Methyltransferase
OSJNBa0041A02.24	Unknown Protein	At4g30160	VLN4 (ARABIDOPSIS THALIANA VILLIN 4); Actin Binding
OSJNBa0041A02.25	Unknown Protein	At5g57550	XTR3 (XYLOGLUCAN ENDOTRANSGLYCOSYLASE 3); Hydrolase, Acting On Glycosyl Bonds
OSJNBa0041A02.26	Unknown Protein	At4g30270	MERI5B (MERISTEM-5); Hydrolase, Acting On Glycosyl Bonds
OSJNBa0041C07.40	Putative Leucyl-Trna Synthetase	At1g09620	ATP Binding / Aminoacyl-Trna Ligase
OSJNBa0041M21.2	Unknown Protein	At1g73040	Jacalin Lectin Family Protein
OSJNBa0041P03.12	Putative Chloroplast RNA Processing Protein	At1g64580	Pentatricopeptide (PPR) Repeat-Containing Protein
OSJNBa0041P03.13	Putative Chloroplast RNA Processing Protein	At1g12300	Pentatricopeptide (PPR) Repeat-Containing Protein
OSJNBa0041P03.2	Putative Signal Tranduction Protein	At1g15130	Hydroxyproline-Rich Glycoprotein Family Protein
OSJNBa0041P03.4	Putative ABC Transporter	At1g17840	ABC Transporter Family Protein
OSJNBa0041P03.5	Unknown Protein	At4g03420	Unknown Protein
OSJNBa0042E19.39	Putative Chloroplast RNA Processing Protein	At3g04260	PTAC3 (PLASTID TRANSCRIPTIONALLY ACTIVE3); DNA Binding
OSJNBa0042E19.4	Putative Oxygen Evolving Complex Protein	At3g55330	Photosystem II Reaction Center Psbp Family Protein
OSJNBa0042F15.2	Unknown Protein	At5g11560	Catalytic
OSJNBa0042F21.13	Unknown Protein	At3g55800	SBPASE (Sedoheptulose-Bisphosphatase); Phosphoric Ester Hydrolase
OSJNBa0042H09.16	Hypothetical Protein	At2g45010	Unknown Protein
OSJNBa0042H24.55-1	Serine/Threonine-Specific Receptor Protein	At4g29990	Light Repressible Receptor Protein Kinase
OSJNBa0042H24.55-2	Leucine-Rich Repeat Protein Kinase-Like	At1g51860	Leucine-Rich Repeat Protein Kinase, Putative
OSJNBa0042H24.8-2	Bystin (51.6 Kd)-Like	At1g31660	Unknown Protein
OSJNBa0042I09.17	Putative Receptor-Like Protein Kinase	At1g34300	Lectin Protein Kinase Family Protein
OSJNBa0042I09.24	Putative Nicotinate Phosphoribosyltransferase	At2g23420	Nicotinate Phosphoribosyltransferase Family Protein / Naprtase Family Protein
OSJNBa0042I09.26	Cellulose Synthase	At4g39350	CESA2 (CELLULASE SYNTHASE 2); Cellulose Synthase/ Transferase, Transferring Glycosyl Groups
OSJNBa0042I09.9	Putative Oxygenase	At3g24200	Monooxygenase
OSJNBa0042I15.10	Unknown Protein	At1g08250	Prephenate Dehydratase Family Protein
OSJNBa0042I15.17	Unknown Protein	At3g09970	Calcineurin-Like Phosphoesterase Family Protein
OSJNBa0042I15.19	Unknown Protein	At5g22510	Beta-Fructofuranosidase, Putative / Invertase, Putative / Saccharase, Putative / Beta-Fructosidase, Putative
OSJNBa0042I15.9	Unknown Protein	At5g04660	CYP77A4 (Cytochrome P450, Family 77, Subfamily A, Polypeptide 4); Oxygen Binding
OSJNBa0042L16.13	Unknown Protein	At4g36940	Nicotinate Phosphoribosyltransferase
OSJNBa0042L16.16	Unknown Protein	At1g49740	Phospholipase C
OSJNBa0042L16.3	Unknown Protein	At4g14110	Cop9 (Constitutive Photomorphogenic 9)

OSJNBa0042P21.23	Putative Protein Kinase	At1g70520	Protein Kinase Family Protein
OSJNBa0042P21.27	Putative Polygalacturonase	At3g26610	Polygalacturonase, Putative / Pectinase, Putative
OSJNBa0043A12.13	Unknown Protein	At5g15710	F-Box Family Protein
OSJNBa0043A12.14	Unknown Protein	At1g13640	Phosphatidylinositol 3- And 4-Kinase Family Protein
OSJNBa0043A12.21	Unknown Protein	At4g22300	Carboxylic Ester Hydrolase
OSJNBa0043A12.24	Unknown Protein	At1g49820	ATMTK; S-Methyl-5-Thioribose Kinase
OSJNBa0043A12.26	Unknown Protein	At3g19460	Reticulon Family Protein (RTNLB11)
OSJNBa0043A12.28	Unknown Protein	At5g43060	Cysteine Proteinase, Putative / Thiol Protease, Putative
OSJNBa0043A12.35	Unknown Protein	At1g34270	Exostosin Family Protein
OSJNBa0043A12.38	Unknown Protein	At2g37250	ADK/ATPADK1 (ADENOSINE KINASE); Nucleotide Kinase
OSJNBa0043A12.5	Unknown Protein	At5g56180	ATARP8 (ACTIN-RELATED PROTEIN 8); Structural Constituent Of Cytoskeleton
OSJNBa0043A12.6	Unknown Protein	At5g53300	UBC10 (Ubiquitin-Conjugating Enzyme 10); Ubiquitin-Protein Ligase
OSJNBa0043L09.15	Unknown Protein	At2g20900	Diacylglycerol Kinase
OSJNBa0043L09.27	Unknown Protein	At5g13780	GCN5-Related N-Acetyltransferase, Putative
OSJNBa0043L09.28	Unknown Protein	At5g54260	MRE11 (MEIOTIC RECOMBINATION 11); Protein Serine/Threonine Phosphatase
OSJNBa0043L24.12	Unknown Protein	At1g23360	Ubie/COQ5 Methyltransferase Family Protein
OSJNBa0043L24.16	Unknown Protein	At5g14590	Isocitrate Dehydrogenase, Putative / NADP+ Isocitrate Dehydrogenase, Putative
OSJNBa0043L24.17	Unknown Protein	At5g40370	Glutaredoxin, Putative
OSJNBa0043L24.22	Unknown Protein	At2g38970	Zinc Finger (C3HC4-Type RING Finger) Family Protein
OSJNBa0043L24.23	Unknown Protein	At1g05055	Member Of Transcription Factor TFIIH Complex
OSJNBa0043L24.4	Unknown Protein	At3g24320	CHM (CHLOROPLAST MUTATOR); ATP Binding / Damaged DNA Binding
OSJNBa0044A10.21	Putative Oxidoreductase	At4g09670	Oxidoreductase Family Protein
OSJNBa0044E16.22	Carboxyl-Terminal Peptidase-Like	At5g18460	Hypothetical Protein
OSJNBa0044E16.26	Pfkb Type Carbohydrate Kinase Protein	At5g43910	Pfkb-Type Carbohydrate Kinase Family Protein
OSJNBa0044E16.36	Type 1 Membrane Protein -Like	At3g24160	Pmp (Putative Type 1 Membrane Protein)
OSJNBa0044K18.7	Unknown Protein	At3g27540	Glycosyl Transferase Family 17 Protein
OSJNBa0044M19.10	Unknown Protein	At1g27990	Unknown Protein
OSJNBa0045C13.16	Putative Vacuolar Sorting Receptor Protein	At2g14740	Vacuolar Sorting Receptor, Putative
OSJNBa0045O17.6	Unknown Protein	At3g29732	Transposable Element Gene
OSJNBa0047A17.12-1	Unknown Protein	At2g29590	Thioesterase Family Protein
OSJNBa0047A17.6	Putative Copine III	At5g07300	Bon2 (Bonzai 2)
OSJNBa0047E24.13	Putative Ribosomal Protein L6	At1g05190	EMB2394 (EMBRYO DEFECTIVE 2394); Structural Constituent Of Ribosome
OSJNBa0047E24.17	Putative Oligopeptide Transporter Protein	At4g16370	ATOPT3 (OLIGOPEPTIDE TRANSPORTER); Oligopeptide Transporter
OSJNBa0047E24.19	Expressed Protein	At2g04900	Unknown Protein
OSJNBa0047E24.21	Putative Transcriptional Adaptor	At3g07740	ADA2A (Arabidopsis Adaptor 2A Homolog)

OSJNBa0047E24.27	Putative Stress-Related Protein	At3g11930	Universal Stress Protein (USP) Family Protein
OSJNBa0047E24.7	Putative Potassium Channel Protein	At5g55630	KCO1 (CA2+ ACTIVATED OUTWARD RECTIFYING K+ CHANNEL 1); Calcium-Activated Potassium Channel/ Outward Rectifier Potassium Channel
OSJNBa0047E24.9	Phytochrome C	At5g35840	Phyc (Phytochrome Defective C)
OSJNBa0047G15.10	Hypothetical Protein	At3g07510	Unknown Protein
OSJNBa0048A13.16	Putative Zinc-Finger Motif	At4g39100	Shl1 (Short Life)
OSJNBa0048A13.17	Unknown Protein	At5g38880	Unknown Protein
OSJNBa0048K16.23	Putative UDP-Glycosyltransferase	At1g22400	UGT85A1 (UDP-Glucosyl Transferase 85A1); UDP-Glycosyltransferase/ Transferase, Transferring Glycosyl Groups / Transferase, Transferring Hexosyl Groups
OSJNBa0049O12.19	Proliferating Cell Nuclear Antigen (PCNA)	At2g29570	PCNA2 (PROLIFERATING CELL NUCLEAR 2); DNA Binding / DNA Polymerase Processivity Factor
OSJNBa0049O12.2	Putative Starch Synthase	At4g18240	Starch Synthase-Related Protein
OSJNBa0049O12.9	Hypothetical Protein	At5g60700	Glycosyltransferase Family Protein 2
OSJNBa0050E08.8	Putative Alcohol Dehydrogenase	At1g64710	Oxidoreductase/ Zinc Ion Binding
OSJNBa0050F10.19	Putative Gibberellin 20-Dioxygenase	At5g51810	ATGA20OX2/GA20OX2 (Gibberellin 20 Oxidase 2); Gibberellin 20-Oxidase
OSJNBa0050F10.25	Putative Branched-Chain Alpha-Keto Acid	At1g55510	BCDH BETA1 (BRANCHED-CHAIN ALPHA-KETO ACID DECARBOXYLASE E1 BETA SUBUNIT); 3-Methyl-2-Oxobutanoate Dehydrogenase (2-Methylpropanoyl-Transferring)
OSJNBa0050F10.39-1	Putative SHOOT1 Protein	At1g55480	Binding / Protein Binding
OSJNBa0050F10.4	Putative Polynucleotide Phosphorylase	At3g03710	RIF10 (RESISTANT TO INHIBITION WITH FSM 10); 3'-5'-Exoribonuclease/ RNA Binding / Nucleic Acid Binding
OSJNBa0050F10.40	Galactose-1-Phosphate Uridylyltransferase-Like	At5g18200	UDP-Glucose:Hexose-1-Phosphate Uridylyltransferase
OSJNBa0050H14.4	Hypothetical Protein	At1g72620	Hydrolase, Alpha/Beta Fold Family Protein
OSJNBa0050H14.9	Hypothetical Protein	At1g10460	GLP7 (GERMIN-LIKE PROTEIN 7); Manganese Ion Binding / Metal Ion Binding / Nutrient Reservoir
OSJNBa0050N08.15	Putative Methionyl-Trna Synthetase	At4g13780	Methionine--Trna Ligase, Putative / Methionyl-Trna Synthetase, Putative / Metrs, Putative
OSJNBa0050N08.17	Putative Selenium-Binding Protein-Like	At2g22410	Pentatricopeptide (PPR) Repeat-Containing Protein
OSJNBa0051D19.17	Putative Tam3-Transposase	At1g42110	Transposable Element Gene; Hat-Like Transposase Family (Hobo/Ac/Tam3),
OSJNBa0051D19.18	Putative Alpha-Galactosidase	At5g08380	ATAGAL1 (ARABIDOPSIS THALIANA ALPHA-GALACTOSIDASE 1); Alpha-Galactosidase
OSJNBa0051D19.19	Putative Beta-Tonoplast Intrinsic Protein	At1g17810	BETA-TIP (BETA-TONOPLAST INTRINSIC PROTEIN); Water Channel
OSJNBa0051D19.25	Putative Basic Secretory Protein	At2g15220	Secretory Protein, Putative
OSJNBa0051D19.7	Putative Chloroplast Inner Envelope Protein	At1g06950	Attic110/Tic110 (Translocon At The Inner Envelope Membrane Of Chloroplasts 110)
OSJNBa0051H17.18	Putative Cdc21 Protein	At2g16440	DNA Replication Licensing Factor, Putative
OSJNBa0051J07.8	Putative Nodulin Protein	At1g21890	Nodulin Mtn21 Family Protein
OSJNBa0052F07.1	Putative Vacuolar Sorting-Associated Protein,	At2g17790	Hypothetical Protein
OSJNBa0052F07.11	Putative Argonaute Protein	At2g27880	Argonaute Protein, Putative / AGO, Putative
OSJNBa0052F07.12	Unknown Protein	At1g03910	Hypothetical Protein
OSJNBa0052F07.14	Putative Membrane Protein	At3g52190	PHF1 (PHOSPHATE TRANSPORTER TRAFFIC FACILITATOR1); Nucleotide Binding
OSJNBa0052F07.23	Unknown Protein	At3g23090	Unknown Protein

OSJNBa0052K01.16	Unknown Protein	At3g47560	Esterase/Lipase/Thioesterase Family Protein
OSJNBa0052K01.18	Putative Nucleosome Assembly Protein	At5g56950	NAP1;3 (NUCLEOSOME ASSEMBLY PROTEIN1;3); DNA Binding
OSJNBa0052K01.19	Unknown Protein	At2g26070	Rte1 (Reversion-To-Ethylene Sensitivity1)
OSJNBa0052K01.2	Putative Protein Phosphatase 2C	At1g72770	Hab1 (Homology To Abi1)
OSJNBa0052K01.23	Putative Flap Endonuclease 1	At5g26675	Unknown Protein
OSJNBa0052K15.13-1	Putative Cyclic Nucleotide-Gated	At5g53130	CNGC1 (CYCLIC NUCLEOTIDE GATED CHANNEL 1); Calmodulin Binding / Cation Channel/ Cyclic Nucleotide Binding / Inward Rectifier Potassium Channel
OSJNBa0052K15.15	Putative 40S Ribosomal Protein S15A	At4g29430	RPS15AE (Ribosomal Protein S15A E); Structural Constituent Of Ribosome
OSJNBa0052M16.38	Acetolactate Synthase	At3g48560	Csr1 (Chlorsulfuron/Imidazolinone Resistant 1)
OSJNBa0052O12.10	Putative Serine Palmitoyltransferase	At5g23670	LCB2 (Serine Palmitoyltransferase LCB2 (Long Chain Base) Subunit Gene); Serine C-Palmitoyltransferase
OSJNBa0052O12.15	Putative Carbonyl Reductase-Like Protein	At5g61830	Short-Chain Dehydrogenase/Reductase (SDR) Family Protein
OSJNBa0052O21.10	Unknown Protein	At2g43820	GT/UGT74F2 (UDP-GLUCOSYLTRANSFERASE 74F2); UDP-Glucosyltransferase/ UDP-Glycosyltransferase/ Transferase, Transferring Glycosyl Groups / Transferase, Transferring Hexosyl Groups
OSJNBa0052O21.15	Unknown Protein	At1g05680	UDP-Glucoronosyl/UDP-Glucosyl Transferase Family Protein
OSJNBa0053B21.10	Unknown Protein	At1g36590	Transposable Element Gene
OSJNBa0053C23.17	Hypothetical Protein	At5g41900	Hydrolase, Alpha/Beta Fold Family Protein
OSJNBa0053C23.2	Putative Glyoxylate Reductase	At1g01510	An (Angustifolia)
OSJNBa0053C23.23	Hypothetical Protein	At5g52810	Ornithine Cyclodeaminase/Mu-Crystallin Family Protein
OSJNBa0053C23.4	Putative Serine/Threonine Protein Kinase	At4g01370	ATMPK4 (MAP KINASE 4); MAP Kinase/ Kinase
OSJNBa0053C23.5	Unknown Protein	At4g25660	Unknown Protein
OSJNBa0053C23.6	Putative Receptor-Like Protein Kinase	At2g39360	Protein Kinase Family Protein
OSJNBa0053D03.12	Putative Flavonoid 3'-Hydroxylase	At5g07990	TT7 (TRANSPARENT TESTA 7); Flavonoid 3'-Monooxygenase/ Oxygen Binding
OSJNBa0053E05.18	Putative ATP-Dependent Clp Protease Subunit	At1g33360	ATP-Dependent Clp Protease ATP-Binding Subunit Clpx, Putative
OSJNBa0053K19.11	Unknown Protein	At1g11860	Aminomethyltransferase, Putative
OSJNBa0053K19.19	Unknown Protein	At1g11720	ATSS3 (STARCH SYNTHASE 3); Starch Synthase/ Transferase, Transferring Glycosyl Groups
OSJNBa0053K19.7	Unknown Protein	At5g26940	Exonuclease Family Protein
OSJNBa0053K19.9	Unknown Protein	At4g18360	(S)-2-Hydroxy-Acid Oxidase, Peroxisomal, Putative / Glycolate Oxidase, Putative / Short Chain Alpha-Hydroxy Acid Oxidase, Putative
OSJNBa0053L11.25	F-Box Family Protein-Like	At1g56240	ATPP2-B13 (Phloem Protein 2-B13)
OSJNBa0053L11.26-1	Glutathione Reductase	At3g24170	ATGR1; Glutathione-Disulfide Reductase
OSJNBa0053L11.32	Putative LEUNIG	At2g32700	WD-40 Repeat Family Protein
OSJNBa0053L11.37	Unknown Protein	At3g07090	Unknown Protein
OSJNBa0054H04.30	Expressed Protein	At5g67370	Unknown Protein
OSJNBa0054K20.1	Putative Pathogenesis-Related Protein PR-1	At4g30320	Allergen V5/Tpx-1-Related Family Protein
OSJNBa0054K20.10	Putative MAP Kinase Kinase	At3g21220	ATMKK5 (MITOGEN-ACTIVATED PROTEIN KINASE KINASE 5); Kinase

OSJNBa0054K20.13	RING Zinc Finger Protein-Like	At4g32600	Zinc Finger (C3HC4-Type RING Finger) Family Protein
OSJNBa0054K20.15-1	Putative Glutamate Receptor Subunit Kainate	At2g29100	ATGLR2.9 (Arabidopsis Thaliana Glutamate Receptor 2.9)
OSJNBa0054K20.17	Diacylglycerol Kinase-Like	At4g30340	ATDGK7 (DIACYLGLYCEROL KINASE 7); Diacylglycerol Kinase
OSJNBa0054K20.22	Putative Initiation Factor 3g	At3g11400	EIF3G1 (Eukaryotic Translation Initiation Factor 3G1); RNA Binding / Translation Initiation Factor
OSJNBa0054K20.23	Unknown Protein	At3g09250	DNA Binding / Nuclease
OSJNBa0054K20.28-2	Amino Acid Transporter-Like	At5g02180	Amino Acid Transporter Family Protein
OSJNBa0054K20.32	Cyclic Nucleotide-Gated Calmodulin-Binding Ion	At4g30360	ATCNGC17 (Cyclic Nucleotide Gated Channel 17); Calmodulin Binding / Cyclic Nucleotide Binding / Ion Channel
OSJNBa0054K20.36	Putative Dem Protein	At3g19240	Unknown Protein
OSJNBa0054K20.8	Putative Serine Threonine Kinase	At1g16760	Protein Kinase Family Protein
OSJNBa0054L03.39-2	Putative Poli-Like DNA Polymerase	At1g50840	POLGAMMA2 (Polymerase Gamma 2); DNA Binding / DNA-Directed DNA Polymerase
OSJNBa0055C08.1	Unknown Protein	At3g27020	YSL6 (YELLOW STRIPE LIKE 6); Oligopeptide Transporter
OSJNBa0055C08.14	Unknown Protein	At4g24990	ATGP4 (Arabidopsis Thaliana Geranylgeranylated Protein)
OSJNBa0055C08.3	Unknown Protein	At5g50700	Short-Chain Dehydrogenase/Reductase (SDR) Family Protein
OSJNBa0055E23.6	Putative Peptide Chain Release Factor	At3g62910	APG3 (ALBINO AND PALE GREEN); Translation Release Factor
OSJNBa0055E23.9	Putative Cupin	At3g62020	GLP10 (GERMIN-LIKE PROTEIN 10); Manganese Ion Binding / Metal Ion Binding / Nutrient Reservoir
OSJNBa0055O03.14	Putative Ferulate-5-Hydroxylase	At4g36220	FAH1 (FERULATE-5-HYDROXYLASE 1); Ferulate 5-Hydroxylase
OSJNBa0055P24.13	Putative Pol Polyprotein	At3g59280	Txr1 (Thaxtomin A Resistant 1)
OSJNBa0055P24.3	Cytoplasmic Malate Dehydrogenase	At5g43330	Malate Dehydrogenase, Cytosolic, Putative
OSJNBa0056A15.4	Putative Receptor-Like Protein Kinase	At4g00960	Protein Kinase Family Protein
OSJNBa0056A20.5	Putative Ribosomal Protein L7Ae-Like	At4g22380	Ribosomal Protein L7Ae/L30e/S12e/Gadd45 Family Protein
OSJNBa0056E06.11	Putative Small GTP-Binding Protein	At5g45130	Rha1
OSJNBa0056E06.17	Putative Apical-Basal Pattern Formation Protein	At5g39500	Pattern Formation Protein, Putative
OSJNBa0056E06.2	Putative Metal Transporter (With Alternative	At1g31260	ZIP10 (ZINC TRANSPORTER 10 PRECURSOR); Cation Transporter
OSJNBa0056E06.20	Hypothetical Protein	At3g22540	Unknown Protein
OSJNBa0056E06.3	Putative Metal Transporter (With Alternative	At2g04032	ZIP7 (ZINC TRANSPORTER 7 PRECURSOR); Cation Transporter
OSJNBa0056E06.4	Expressed Protein	At1g79120	Unknown Protein
OSJNBa0056E06.9	Expressed Protein	At1g31300	Unknown Protein
OSJNBa0056G17.11	Putative Serine/Threonine Kinase	At5g63610	HEN3 (HUA ENHANCER 3); Kinase
OSJNBa0056G17.13	Putative Ubiquinone Oxidoreductase Subunit	At3g03100	Oxidoreductase
OSJNBa0056G17.14	Unknown Protein	At1g32090	Early-Responsive To Dehydration Protein-Related / ERD Protein-Related
OSJNBa0056G17.15	Putative Cholinephosphate Cytidylyltransferase	At4g15130	Cholinephosphate Cytidylyltransferase, Putative / Phosphorylcholine Transferase, Putative / CTP:Phosphocholine Cytidylyltransferase, Putative
OSJNBa0056G17.16	Putative Cellulose Synthase 5-Partial	At5g16910	ATCSLD2 (Cellulose Synthase-Like D2); Cellulose Synthase/ Transferase, Transferring Glycosyl Groups

OSJNBa0056G17.2	Unknown Protein	At1g32080	Membrane Protein, Putative
OSJNBa0056G17.32	Putative Gypsy-Type Retrotransposon Protein	At5g59210	Myosin Heavy Chain-Related
OSJNBa0056G17.4	Putative Urea Active Transport Protein	At5g45380	Sodium:Solute Symporter Family Protein
OSJNBa0056G17.5	Putative Ankyrin Protein	At2g01680	Ankyrin Repeat Family Protein
OSJNBa0056G17.6	Putative Clp Protease	At5g45390	CLPP4 (Clp Protease Proteolytic Subunit 4); Endopeptidase Clp
OSJNBa0056G17.7	Unknown Protein	At5g45410	Unknown Protein
OSJNBa0056G17.9	Putative ADP-Ribosylation Factor	At5g17060	ADP-Ribosylation Factor, Putative
OSJNBa0056O06.5	Putative Microtubial Binding Protein	At1g62040	ATG8C (AUTOPHAGY 8C); Microtubule Binding
OSJNBa0056O06.9-1	Glyoxalase I	At1g11840	ATGLX1 (GLYOXALASE I HOMOLOG); Lactoylglutathione Lyase
OSJNBa0057E11.25	Putative Receptor-Like Kinase, 5'-Partial	At4g21380	ARK3 (Arabidopsis Receptor Kinase 3); Kinase
OSJNBa0057G07.14	Putative WD Repeat-Protein	At2g26490	Transducin Family Protein / WD-40 Repeat Family Protein
OSJNBa0057G07.15	Lipoxygenase L-2	At1g55020	LOX1 (Lipoxygenase 1); Lipoxygenase
OSJNBa0057G07.17	Putative Glycine Hydroxymethyltransferase	At4g37930	SHM1 (SERINE HYDROXYMETHYLTRANSFERASE 1); Glycine Hydroxymethyltransferase
OSJNBa0057G07.3	Unknown Protein	At1g56290	Cwfj-Like Family Protein
OSJNBa0057G07.4	Putative Deoxyhypusine Synthase	At5g05920	Dhs (Dhs)
OSJNBa0057L21.1	Putative Phragmoplastin	At3g60190	ADL4/ADLP2/DRP1E/EDR3 (DYNAMIN-LIKE PROTEIN 4); GTP Binding / Gtpase
OSJNBa0057L21.15	Hypothetical Protein	At5g46920	Intron Maturase, Type II Family Protein
OSJNBa0057L21.19	Putative Peroxidase	At5g17820	Peroxidase 57 (PER57) (P57) (PRXR10)
OSJNBa0057L21.9	Putative Chlorophyll Synthase	At1g44446	CH1 (CHLORINA 1); Chlorophyll A Oxygenase
OSJNBa0057M23.115	Unknown Protein	At2g16070	Pdv2 (Plastid Division2)
OSJNBa0057M23.117	PRLI-Interacting Factor G-Like Protein	At3g50780	Unknown Protein
OSJNBa0058D03.10	Formamidopyrimidine-DNA Glycosylase-Like	At1g52500	ATFPG-1/ATFPG-2/ATMMH-1/ATMMH-2/FPG-1/FPG-2 (FORMAMIDOPYRIMIDINE-DNA GLYCOSYLASE 1, FORMAMIDOPYRIMIDINE-DNA GLYCOSYLASE 2); DNA N-Glycosylase
OSJNBa0058E19.16	Putative Disease Resistance Protein	At2g25790	Leucine-Rich Repeat Transmembrane Protein Kinase, Putative
OSJNBa0058G03.1	Unknown Protein	At1g57680	Unknown Protein
OSJNBa0058G03.4	Unknown Protein	At5g57580	Calmodulin-Binding Protein
OSJNBa0058G03.7	Unknown Protein	At1g29150	ATS9 (19S PROTEOSOME SUBUNIT 9); Binding
OSJNBa0058K23.10	Unknown Protein	At2g02870	Kelch Repeat-Containing F-Box Family Protein
OSJNBa0058K23.13	Unknown Protein	At1g30570	Protein Kinase Family Protein
OSJNBa0058K23.14	Unknown Protein	At5g21040	F-Box Family Protein / WD-40 Repeat Family Protein
OSJNBa0058K23.17	Unknown Protein	At2g34660	ATMRP2 (MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN 2); Atpase, Coupled To Transmembrane Movement Of Substances
OSJNBa0058K23.7	Unknown Protein	At5g46330	FLS2 (FLAGELLIN-SENSITIVE 2); ATP Binding / Kinase/ Protein Binding / Protein Serine/Threonine Kinase/ Transmembrane Receptor Protein Serine/Threonine Kinase
OSJNBa0059E14.14	Unknown Protein	At1g55340	Unknown Protein
OSJNBa0059E14.17	Putative Ubiquinol-Cytochrome C Reductase	At5g25450	Ubiquinol-Cytochrome C Reductase Complex 14 Kda Protein, Putative

OSJNBa0059E14.19	Hypothetical Protein	At5g28150	Unknown Protein
OSJNBa0059E14.8	Putative 40S Ribosomal Protein S2	At3g57490	40S Ribosomal Protein S2 (RPS2D)
OSJNBa0059E14.9	Unknown Protein	At3g08030	Unknown Protein
OSJNBa0059G06.10	Putative Chromosome Region Maintenance Protein	At5g17020	XPO1A (Exportin 1A); Protein Transporter
OSJNBa0059G06.13	Unknown Protein	At5g38060	Unknown Protein
OSJNBa0059G06.2	Putative Lipase/Acylhydrolase	At1g20120	Family II Extracellular Lipase, Putative
OSJNBa0059G06.22	Putative Gibberelin 20-Oxidase	At4g25420	GA5 (GA REQUIRING 5); Gibberellin 20-Oxidase/ Gibberellin 3-Beta-Dioxygenase
OSJNBa0059G06.4	Putative Mate Efflux Family Protein	At4g22790	MATE Efflux Family Protein
OSJNBa0059G06.5	Unknown Protein	At3g60810	Unknown Protein
OSJNBa0060A14.12	Putative Glucosyltransferase	At5g03760	ATCSLA09 (RESISTANT TO AGROBACTERIUM TRANSFORMATION 4); Transferase, Transferring Glycosyl Groups
OSJNBa0060A14.17	Putative Pectin Methylesterase	At3g29090	Pectinesterase Family Protein
OSJNBa0060B20.12	Unknown Protein	At1g31850	Dehydration-Responsive Protein, Putative
OSJNBa0060B20.9	Unknown Protein	At5g16860	Pentatricopeptide (PPR) Repeat-Containing Protein
OSJNBa0060D06.18	Unknown Protein	At3g13320	CAX2 (CATION EXCHANGER 2); Calcium:Hydrogen Antiporter
OSJNBa0060G17.3	Hypothetical Protein	At5g07790	Unknown Protein
OSJNBa0060K08.15	Putative Molybdenum Cofactor Biosynthesis	At2g31950	Molybdopterin Synthase (CNX2)
OSJNBa0060K08.30	Unknown Protein	At5g16730	Unknown Protein
OSJNBa0060K08.35	F-Box-Like Protein	At3g61590	F-Box Family Protein
OSJNBa0060K08.43	Putative BTB/POZ Domain-Containing Protein	At3g61600	ATPOB1 (Arabidopsis Thaliana POZ/BTB Containing-Protein 1); Protein Binding
OSJNBa0060M17.1	Putative Polygalacturonase	At3g57510	ADPG1 (Endo-Polygalacturonase 1); Polygalacturonase
OSJNBa0060M17.7	Putative Calmodulin-Domain Protein Kinase	At3g57530	CPK32 (CALCIUM-DEPENDENT PROTEIN KINASE 32); Calcium- And Calmodulin-Dependent Protein Kinase/ Kinase
OSJNBa0060N03.10	Unknown Protein	At5g20810	Calmodulin Binding
OSJNBa0060N03.11	Unknown Protein	At5g05680	Nuclear Pore Complex Protein-Related
OSJNBa0060N03.23	Unknown Protein	At1g22280	Protein Phosphatase 2C, Putative / PP2C, Putative
OSJNBa0061E21.10	Chloroplast RNA Processing Protein-Like Protein	At5g55840	Pentatricopeptide (PPR) Repeat-Containing Protein
OSJNBa0061E21.13	Putative Phosphatidylinositol 3-Kinase	At1g60490	ATVPS34 (Arabidopsis Thaliana Vacuolar Protein Sorting 34); Phosphatidylinositol 3-Kinase
OSJNBa0061E21.29	Putative TGF-Beta Receptor-Interacting Protein	At2g46280	TRIP-1 (TGF-BETA RECEPTOR INTERACTING PROTEIN 1); Nucleotide Binding
OSJNBa0061G20.2	Unknown Protein	At4g27210	Transposable Element Gene
OSJNBa0061H20.1	Putative Cytochrome P450	At2g45580	CYP76C3 (Cytochrome P450, Family 76, Subfamily C, Polypeptide 3); Oxygen Binding
OSJNBa0061K21.15	Putative Epimerase/Dehydratase	At5g28840	GME (GDP-D-MANNOSE 3',5'-EPIMERASE); GDP-Mannose 3,5-Epimerase/ NAD Binding / Catalytic
OSJNBa0061K21.20	Putative Histone H2A	At5g02560	Histone H2A, Putative
OSJNBa0061K21.21	Putative Calcium-Transporting Atpase	At3g22910	Calcium-Transporting Atpase, Plasma Membrane-Type, Putative / Ca(2+)-Atpase, Putative (ACA13)
OSJNBa0061L20.103	Putative Zinc Transporter Protein ZIP1	At1g05300	ZIP5 (ZINC TRANSPORTER 5 PRECURSOR); Cation Transporter

OSJNBa0061L20.107-1	Putative Nucleic Acid Binding Protein	At3g11200	PHD Finger Family Protein
OSJNBa0061L20.107-2	Nucleic Acid Binding Protein-Like	At1g14510	PHD Finger Family Protein
OSJNBa0062C05.1	Putative Malate Oxidoreductase, 5'-Partial	At4g00570	Malate Oxidoreductase, Putative
OSJNBa0062C05.25	Putative PPR Repeat Containing Protein	At3g60050	Pentatricopeptide (PPR) Repeat-Containing Protein
OSJNBa0062C05.29	Putative TPR (Tetratricopeptide Repeat) Domain	At1g33400	Tetratricopeptide Repeat (TPR)-Containing Protein
OSJNBa0062G05.28	PPR-Repeat Protein-Like	At4g39530	Pentatricopeptide (PPR) Repeat-Containing Protein
OSJNBa0063C18.16	Unknown Protein	At1g69670	ATCUL3B/CUL3B (Cullin 3B); Protein Binding / Ubiquitin-Protein Ligase
OSJNBa0063C18.17	Unknown Protein	At3g58730	(VACUOLAR ATP SYNTHASE SUBUNIT D); Hydrogen Ion Transporting ATP Synthase, Rotational Mechanism / Hydrogen Ion Transporting Atpase, Rotational Mechanism
OSJNBa0063C18.18	Unknown Protein	At3g25660	Glutamyl-Trna(Gln) Amidotransferase, Putative
OSJNBa0063C18.19	Unknown Protein	At1g62640	KAS III (3-KETOACYL-ACYL CARRIER PROTEIN SYNTHASE III); 3-Oxoacyl-[Acyl-Carrier-Protein] Synthase
OSJNBa0063E14.35	Putative 68 Kda Protein HP68	At4g19210	ATRLI2 (Arabidopsis Thaliana Rnase L Inhibitor Protein 2)
OSJNBa0063H21.19	Unknown Protein	At2g11890	Adenylate Cyclase
OSJNBa0063K04.14	Pentatricopeptide (PPR) Repeat-Containing	At4g01400	Pentatricopeptide (PPR) Repeat-Containing Protein
OSJNBa0064D20.11	Unknown Protein	At1g59750	ARF1 (AUXIN RESPONSE FACTOR 1); Transcription Factor
OSJNBa0064D20.8	Unknown Protein	At1g59740	Proton-Dependent Oligopeptide Transport (POT) Family Protein
OSJNBa0064D20.9	Unknown Protein	At5g08500	Transmembrane CLPTM1 Family Protein
OSJNBa0064E16.10	Putative Membrane Protein	At4g12980	Auxin-Responsive Protein, Putative
OSJNBa0064E16.11	Unknown Protein	At5g48750	Auxin-Responsive Protein, Putative
OSJNBa0064E16.15	Unknown Protein	At5g55530	C2 Domain-Containing Protein
OSJNBa0064E16.4	Putative Sulfate Transporter	At1g22150	SULTR1;3 (Sulfate Transporter); Sulfate Transporter
OSJNBa0064E16.6	Putative Sulfate Transporter	At5g10180	AST68 (Sulfate Transporter 2.1)
OSJNBa0064E16.9	Putative Transaminase	At4g33680	AGD2 (ABERRANT GROWTH AND DEATH 2); Transaminase
OSJNBa0064G10.13	Unknown Protein	At1g08590	CLAVATA1 Receptor Kinase (CLV1)
OSJNBa0064G10.14	Unknown Protein	At5g36970	Nhl25 (Ndr1/Hin1-Like 25)
OSJNBa0064G10.16	Unknown Protein	At5g08570	Pyruvate Kinase, Putative
OSJNBa0064G16.2	Putative Sucrose-Phosphatase	At1g51420	Sucrose-Phosphatase, Putative
OSJNBa0064H22.10	Unknown Protein	At2g03200	Aspartyl Protease Family Protein
OSJNBa0064H22.16	Unknown Protein	At5g67030	ABA1 (ABA DEFICIENT 1); Zeaxanthin Epoxidase
OSJNBa0064H22.19	Unknown Protein	At1g14070	FUT7 (Fucosyltransferase 7); Fucosyltransferase/ Transferase, Transferring Glycosyl Groups
OSJNBa0064H22.2	Unknown Protein	At5g17330	GAD (Glutamate Decarboxylase 1); Calmodulin Binding
OSJNBa0064H22.21	Unknown Protein	At4g37030	Unknown Protein
OSJNBa0064H22.6	Unknown Protein	At2g02010	Glutamate Decarboxylase, Putative
OSJNBa0064H22.7	Unknown Protein	At3g20300	Extracellular Ligand-Gated Ion Channel

OSJNBa0064M23.11	Unknown Protein	At3g02310	SEP2 (SEPALLATA2); DNA Binding / Transcription Factor
OSJNBa0064M23.12	Unknown Protein	At3g61460	BRH1 (BRASSINOSTEROID-RESPONSIVE RING-H2); Protein Binding / Zinc Ion Binding
OSJNBa0064M23.14	Unknown Protein	At5g24530	Oxidoreductase, 2OG-Fe(II) Oxygenase Family Protein
OSJNBa0064M23.15	Unknown Protein	At4g10500	Oxidoreductase, 2OG-Fe(II) Oxygenase Family Protein
OSJNBa0065B15.8	Unknown Protein	At4g39330	Oxidoreductase/ Zinc Ion Binding
OSJNBa0065C16.14	Profilin A	At2g19770	PRF5 (PROFILIN5); Actin Binding / Actin Monomer Binding
OSJNBa0065C16.15	Putative Beta-Glucosidase	At1g26560	Glycosyl Hydrolase Family 1 Protein
OSJNBa0065F09.11	Putative GTP-Binding Protein	At5g52210	ATGB1 (Arabidopsis Thaliana GTP-Binding Protein 1)
OSJNBa0065J17.11	Putative Peroxidase	At5g66390	Peroxidase 72 (PER72) (P72) (PRXR8)
OSJNBa0065O17.14	Unknown Protein	At4g00460	ATROPGEF3/ROPGEF3 (KINASE PARTNER PROTEIN-LIKE); Rho Guanyl-Nucleotide Exchange Factor
OSJNBa0066H10.123	KH Domain-Like Protein	At3g08620	KH Domain-Containing Protein
OSJNBa0066H15.11	Putative TNFR-Like Receptor Kinase	At3g59420	ACR4 (ARABIDOPSIS CRINKLY4); Kinase
OSJNBa0066H15.13	Putative Leucine-Rich Receptor-Like Protein	At4g18670	Leucine-Rich Repeat Family Protein / Extensin Family Protein
OSJNBa0066H15.17	Putative Gag And Pol Polyprotein	At1g11265	Transposable Element Gene; Copia-Like Retrotransposon Family,
OSJNBa0066H15.19	Putative LSTK-1-Like Kinase	At1g54510	Protein Kinase Family Protein
OSJNBa0066H15.2	Putative Protein Kinase	At3g22750	Protein Kinase, Putative
OSJNBa0066I08.2	Hypothetical Protein	At3g15480	Unknown Protein
OSJNBa0067E01.3	Putative Thiamin Biosynthesis Protein	At2g29630	Thiamine Biosynthesis Family Protein / Thic Family Protein
OSJNBa0067G20.8	Unknown Protein	At1g70080	Terpene Synthase/Cyclase Family Protein
OSJNBa0067K08.12	Unknown Protein	At3g59820	Calcium Ion Binding
OSJNBa0067K08.13	Unknown Protein	At5g16970	AT-AER (ALKENAL REDUCTASE); 2-Alkenal Reductase
OSJNBa0067K08.22	Unknown Protein	At1g22450	COX6B (CYTOCHROME C OXIDASE 6B); Cytochrome-C Oxidase
OSJNBa0067K08.23	Unknown Protein	At3g02470	Samdc (S-Adenosylmethionine Decarboxylase)
OSJNBa0067K08.3	Unknown Protein	At3g07565	Unknown Protein
OSJNBa0067K08.7	Unknown Protein	At3g59710	Short-Chain Dehydrogenase/Reductase (SDR) Family Protein
OSJNBa0067K08.8	Unknown Protein	At5g16250	Unknown Protein
OSJNBa0067N01.14	Putative Cell Death Suppressor Protein	At3g44880	Acd1 (Accelerated Cell Death 1, Pheophorbide A Oxygenase)
OSJNBa0067N01.16	Tonoplast Intrinsic Protein	At2g36830	GAMMA-TIP (Tonoplast Intrinsic Protein (TIP) Gamma); Water Channel
OSJNBa0067N01.17	Putative GTP-Binding Protein	At5g03530	ATRAB ALPHA (Arabidopsis Rab Gtpase Homolog C2a); GTP Binding
OSJNBa0067N01.22	Putative Zfwd1 Protein With Similarity To Myosin	At4g25440	ZFWD1 (Zinc Finger WD40 Repeat Protein 1); Nucleic Acid Binding / Zinc Ion Binding
OSJNBa0068A07.14	Putative Translation Initiation Factor 2B Beta	At3g07300	GTP Binding / Translation Initiation Factor
OSJNBa0068A07.23	Putative Lipase	At1g28570	GDSL-Motif Lipase, Putative
OSJNBa0068L06.10	Unknown Protein	At5g64440	Amidase Family Protein
OSJNBa0068L06.2	Unknown Protein	At5g06900	CYP93D1 (Cytochrome P450, Family 93, Subfamily D, Polypeptide 1); Oxygen Binding

OSJNBa0068L06.3	Unknown Protein	At1g03620	Phagocytosis And Cell Motility Protein ELMO1-Related
OSJNBa0068L06.7	Unknown Protein	At1g58140	Transposable Element Gene; Copia-Like Retrotransposon Family,
OSJNBa0068L06.8	Unknown Protein	At5g64460	Unknown Protein
OSJNBa0068L06.9	Unknown Protein	At1g06200	Serine-Type Peptidase
OSJNBa0069D17.1	Unknown Protein	At4g13010	Oxidoreductase, Zinc-Binding Dehydrogenase Family Protein
OSJNBa0069E14.13	Putative Dehydrogenase	At3g03980	Short-Chain Dehydrogenase/Reductase (SDR) Family Protein
OSJNBa0069E14.2	Putative RNA-Binding Protein	At3g13460	Ect2
OSJNBa0069E14.3	Putative Growth Inhibitory Protein	At1g54390	PHD Finger Protein-Related
OSJNBa0069E14.8	Putative Exohydrolase	At5g20950	Glycosyl Hydrolase Family 3 Protein
OSJNBa0069P02.20	Putative 2-Oxoacid-Dependent Oxidase	At3g49620	DIN11 (DARK INDUCIBLE 11); Oxidoreductase
OSJNBa0070C17.12	Unknown Protein	At1g30630	Coatomer Protein Epsilon Subunit Family Protein / COPE Family Protein
OSJNBa0070C17.14	Unknown Protein	At1g79490	EMB2217 (EMBRYO DEFECTIVE 2217); Binding
OSJNBa0070C17.16	Unknown Protein	At4g20050	Qrt3 (Quartet 3)
OSJNBa0070C17.2	Unknown Protein	At4g13840	Transferase Family Protein
OSJNBa0070C17.23	Unknown Protein	At2g35060	KUP11 (K+ Uptake Permease 11); Potassium Ion Transporter
OSJNBa0070C17.24	Unknown Protein	At2g29260	Tropinone Reductase, Putative / Tropine Dehydrogenase, Putative
OSJNBa0070M12.12	Unknown Protein	At2g46860	Inorganic Pyrophosphatase, Putative (Soluble) / Pyrophosphate Phospho-Hydrolase, Putative / Ppase, Putative
OSJNBa0070M12.4	Unknown Protein	At2g35930	U-Box Domain-Containing Protein
OSJNBa0070M12.7	Unknown Protein	At3g15130	Pentatricopeptide (PPR) Repeat-Containing Protein
OSJNBa0070M12.8	Unknown Protein	At1g49180	Protein Kinase Family Protein
OSJNBa0070N04.14	Putative Oxidoreductase	At1g75200	Flavodoxin Family Protein / Radical SAM Domain-Containing Protein
OSJNBa0070N04.15	Hypothetical Protein	At2g22070	Pentatricopeptide (PPR) Repeat-Containing Protein
OSJNBa0070N04.26	Hypothetical Protein	At5g03030	DNAJ Heat Shock N-Terminal Domain-Containing Protein
OSJNBa0070N04.5	Phosphoglucose Isomerase (Pgi-A)	At5g42740	Glucose-6-Phosphate Isomerase, Cytosolic (PGIC)
OSJNBa0070N04.6	Putative Kinase	At1g49270	Protein Kinase Family Protein
OSJNBa0070N04.9	Unknown Protein	At1g05070	Unknown Protein
OSJNBa0070O11.10	Unknown Protein	At5g10790	UBP22 (UBIQUITIN-SPECIFIC PROTEASE 22); Ubiquitin-Specific Protease
OSJNBa0070O11.5	Unknown Protein	At4g32140	Unknown Protein
OSJNBa0071I13.11	Unknown Protein	At4g30190	AHA2 (Arabidopsis H(+)-Atpase 2); Atpase
OSJNBa0071I13.13	Unknown Protein	At2g18980	Peroxidase, Putative
OSJNBa0071I20.6	Putative Ribosomal Protein S10p/S20e	At3g47370	Structural Constituent Of Ribosome
OSJNBa0071K18.5	Putative WD Domain Containing Protein	At2g20330	Transducin Family Protein / WD-40 Repeat Family Protein
OSJNBa0071K18.7	Unknown Protein	At1g07040	Unknown Protein
OSJNBa0071K19.11	Putative Notchless Protein Homolog	At5g52820	WD-40 Repeat Family Protein / Notchless Protein, Putative

OSJNBa0071K19.14	Putative Chromomethylase	At1g69770	Cmt3 (Chromomethylase 3)
OSJNBa0071M09.1	Hypothetical Protein	At3g11670	DGD1 (DIGALACTOSYL DIACYLGLYCEROL DEFICIENT 1); Galactolipid Galactosyltransferase
OSJNBa0071M09.22	SR-Rich Pre-Mrna Splicing Activator	At2g29210	Splicing Factor PWI Domain-Containing Protein
OSJNBa0071M09.8	Hypothetical Protein	At5g06060	Tropinone Reductase, Putative / Tropine Dehydrogenase, Putative
OSJNBa0072D21.10	Unknown Protein	At3g48530	CBS Domain-Containing Protein
OSJNBa0072D21.14	Unknown Protein	At2g05170	ATVPS11 (Arabidopsis Thaliana Vacuolar Protein Sorting 11); Transporter
OSJNBa0072D21.2	Unknown Protein	At4g33650	ADL2 (ARABIDOPSIS DYNAMIN-LIKE 2); GTP Binding / Gtpase
OSJNBa0072D21.3	Unknown Protein	At1g78560	Bile Acid:Sodium Symporter Family Protein
OSJNBa0072F16.1	Unknown Protein	At1g12900	Gapa-2
OSJNBa0072F16.19	Unknown Protein	At1g25530	Lysine And Histidine Specific Transporter, Putative
OSJNBa0072F16.3	Unknown Protein	At1g18800	NRP2 (NAP1-RELATED PROTEIN 2); DNA Binding / Chromatin Binding / Histone Binding
OSJNBa0072F16.4	Unknown Protein	At5g39840	ATP-Dependent RNA Helicase
OSJNBa0072F16.5	Unknown Protein	At5g39830	DEGP8 (DEGP PROTEASE 8); Serine-Type Peptidase/ Trypsin
OSJNBa0072H09.17	Extracellular Calcium Sensing Receptor	At5g23060	Unknown Protein
OSJNBa0072I06.4	Unknown Protein	At2g04039	Unknown Protein
OSJNBa0072K14.12	Unknown Protein	At4g23160	Protein Kinase Family Protein
OSJNBa0072K14.18	Unknown Protein	At3g26810	AFB2 (AUXIN SIGNALING F-BOX 2); Auxin Binding / Ubiquitin-Protein Ligase
OSJNBa0072K14.5	Unknown Protein	At5g55070	2-Oxoacid Dehydrogenase Family Protein
OSJNBa0073A18.26-1	Unknown Protein	At5g42570	Unknown Protein
OSJNBa0073A18.28	Putative Ribosomal Protein L10a	At2g27530	60S Ribosomal Protein L10A (RPL10aB)
OSJNBa0073A21.16	SAM-Dependent Methyltransferase-Like	At1g54310	RNA Binding
OSJNBa0073A21.17	LEM3 (Ligand-Effect Modulator 3)-Like	At3g12740	LEM3 (Ligand-Effect Modulator 3) Family Protein / CDC50 Family Protein
OSJNBa0073A21.22	Serine/Threonine Protein Kinase	At2g24360	Serine/Threonine/Tyrosine Kinase, Putative
OSJNBa0073A21.31	Putative High Affinity Potassium Transporter	At4g10310	HKT1 (HIGH-AFFINITY K+ TRANSPORTER 1); Sodium Ion Transporter
OSJNBa0073A21.8-1	Putative Cytochrome P450	At4g15110	CYP97B3 (Cytochrome P450, Family 97, Subfamily B, Polypeptide 3); Oxygen Binding
OSJNBa0073E02.3	Unknown Protein	At1g08630	Tha1 (Threonine Aldolase 1)
OSJNBa0073E02.7	Unknown Protein	At2g31190	Hypothetical Protein
OSJNBa0073G17.1	Putative WD Repeat Protein	At5g08560	Transducin Family Protein / WD-40 Repeat Family Protein
OSJNBa0073L01.1	Putative Histidine Kinase	At5g35750	Ahk2 (Arabidopsis Histidine Kinase 2)
OSJNBa0073L01.13	Hypothetical Protein	At4g38270	GAUT3 (Galacturonosyltransferase 3); Polygalacturonate 4-Alpha-Galacturonosyltransferase/ Transferase, Transferring Glycosyl Groups
OSJNBa0073L01.2	Putative Acetyl-Coa Carboxylase	At1g36160	ACC1 (ACETYL-COENZYME A CARBOXYLASE 1); Acetyl-Coa Carboxylase
OSJNBa0073L01.3	Putative Kelch-Containing Protein	At1g22040	Kelch Repeat-Containing F-Box Family Protein
OSJNBa0073L04.3	Unknown Protein	At3g52820	ATPAP22/PAP22 (Purple Acid Phosphatase 22); Acid Phosphatase/ Protein Serine/Threonine Phosphatase

OSJNBa0073L04.5	Unknown Protein	At2g36290	Hydrolase, Alpha/Beta Fold Family Protein
OSJNBa0073L04.7	Unknown Protein	At2g27510	ATFD3 (FERREDOXIN 3); Electron Carrier
OSJNBa0073L04.8	Unknown Protein	At2g27500	Hydrolase, Hydrolyzing O-Glycosyl Compounds
OSJNBa0073L04.9	Unknown Protein	At3g52720	Carbonic Anhydrase Family Protein
OSJNBa0073L20.20	Putative Crooked Neck Protein	At3g13210	Crooked Neck Protein, Putative / Cell Cycle Protein, Putative
OSJNBa0073L20.5	Putative CDP-Diacylglycerol Synthetase	At4g26770	Phosphatidate Cytidylyltransferase, Putative / CDP-Diglyceride Synthetase, Putative
OSJNBa0074P11.1	'Unknown Protein, Contains TPR Domain'	At1g53300	TTL1 (TETRATRICOPETIDE-REPEAT THIOREDOXIN-LIKE 1); Binding
OSJNBa0074P11.10	'Unknown Protein, Contains PPR Repeat'	At3g49170	EMB2261 (EMBRYO DEFECTIVE 2261); Binding
OSJNBa0074P11.13	Unknown Protein	At2g46420	Unknown Protein
OSJNBa0075A22.20	TATA-Binding Protein TBP2	At1g55520	TBP2 (TATA Binding Protein 2); DNA Binding / RNA Polymerase II Transcription Factor
OSJNBa0075A22.22	Putative Beta-1,3-Glucanase	At1g64760	Hydrolase, Hydrolyzing O-Glycosyl Compounds
OSJNBa0075A22.24	Putative Sodium/Calcium Exchanger Protein	At5g17860	Cation Exchanger, Putative (CAX7)
OSJNBa0075A22.29	Putative 3-Isopropylmalate Dehydrogenase	At1g80560	3-Isopropylmalate Dehydrogenase, Chloroplast, Putative
OSJNBa0075G19.1	N-Hydroxycinnamoyl/Benzoyltransferase-Like Protein	At5g07850	Transferase Family Protein
OSJNBa0075G19.13	Hypothetical Protein	At1g62730	Unknown Protein
OSJNBa0075G19.5	Putative Acyl-Coa Oxidase	At4g16760	Acx1 (Acyl-Coa Oxidase 1)
OSJNBa0075N02.110	Tubulin-Related Protein-Like Peotein	At4g37190	Unknown Protein
OSJNBa0075N02.115	Synbindin-Like Protein	At5g02280	Synbindin, Putative
OSJNBa0075N02.118	Tetratricopeptide Repeat (TPR)-Containing	At5g17270	Tetratricopeptide Repeat (TPR)-Containing Protein
OSJNBa0076F20.10	Putative Cytochrome	At5g53560	ATB5-A (Cytochrome B5 A)
OSJNBa0076F20.16	Putative Aldo/Keto Reductase	At5g53580	Aldo/Keto Reductase Family Protein
OSJNBa0076F20.2	Putative Receptor Protein Kinase	At4g10390	Protein Kinase Family Protein
OSJNBa0076F20.3	Putative Electron Transfer Oxidoreductase	At2g43400	ETFQO (ELECTRON-TRANSFER FLAVOPROTEIN:UBIQUINONE OXIDOREDUCTASE); Catalytic/ Electron Acceptor
OSJNBa0076F20.4	Unknown Protein	At1g64980	Unknown Protein
OSJNBa0076F20.6	Putative Gamma-Lyase	At1g64660	ATMGL; Catalytic/ Methionine Gamma-Lyase
OSJNBa0076F20.9	Putative Retrotransposon Polyprotein	At4g21360	Transposable Element Gene
OSJNBa0076N16.21	Unknown Protein	At2g43330	ATINT1 (INOSITOL TRANSPORTER 1); Carbohydrate Transporter/ Sugar Porter
OSJNBa0076N16.22	Unknown Protein	At1g65430	Zinc Finger Protein-Related
OSJNBa0077F02.122	Putative Alpha Subunit Of F-Actin Capping	At3g05520	F-Actin Capping Protein Alpha Subunit Family Protein
OSJNBa0077J18.6	Putative Chalcone Synthase 1	At5g13930	CHS (CHALCONE SYNTHASE); Naringenin-Chalcone Synthase
OSJNBa0077M12.117	Receptor Like Protein	At4g22140	DNA Binding
OSJNBa0078A17.10	Unknown Protein	At3g17800	Unknown Protein
OSJNBa0078A17.11	Putative Anthranilate Synthase Beta Subunit	At5g57890	Anthranilate Synthase Beta Subunit, Putative
OSJNBa0078A17.12	Actin	At3g12110	ACT11 (ACTIN-11); Structural Constituent Of Cytoskeleton

OSJNBa0078A17.13	Putative Transposase	At4g38180	FRS5 (FAR1-RELATED SEQUENCE 5); Zinc Ion Binding
OSJNBa0078A17.19	Putative Root-Specific Protein	At4g12470	Protease Inhibitor/Seed Storage/Lipid Transfer Protein (LTP) Family Protein
OSJNBa0078A17.4	Gibberellin-Induced Receptor-Like Kinase TMK	At1g66150	Tmk1 (Transmembrane Kinase 1)
OSJNBa0078A17.8	Putative Splicing Factor	At5g06160	Splicing Factor-Related
OSJNBa0078D03.20	Putative Na+/K+/Cl-Cotransport Protein	At1g30450	CCC1; Cation:Chloride Symporter
OSJNBa0078D06.30	Putative Protein Phosphatase 2C	At3g17090	Protein Phosphatase Type 2C
OSJNBa0078D06.32	Putative Galactose Kinase	At3g06580	GAL1 (GALACTOSE KINASE 1); ATP Binding / Galactokinase
OSJNBa0078D06.36	Unknown Protein	At4g01880	Unknown Protein
OSJNBa0078D06.37	Unknown Protein, 5'-Partial	At1g20980	SPL14 (SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 14); DNA Binding / Transcription Factor
OSJNBa0078K05.12	Putative Sesquiterpene Cyclase	At3g14520	Terpene Synthase/Cyclase Family Protein
OSJNBa0078N11.28-1	Chromosome Structural Maintenance Protein-Like	At3g47700	Mag2
OSJNBa0078N11.31	Kelch Repeat-Containing F-Box-Like	At1g74510	Kelch Repeat-Containing F-Box Family Protein
OSJNBa0078N11.41	Transitional Endoplasmic Reticulum Atpase-Like	At1g50140	AAA-Type Atpase Family Protein
OSJNBa0078O01.10	Putative Leaf Protein	At3g18110	EMB1270 (EMBRYO DEFECTIVE 1270); Binding
OSJNBa0078O01.25	Putative Leaf Protein	At1g60770	Pentatricopeptide (PPR) Repeat-Containing Protein
OSJNBa0078O01.26	Putative Leaf Protein	At2g20710	Pentatricopeptide (PPR) Repeat-Containing Protein
OSJNBa0078O01.6	Unknown Protein	At3g47160	Protein Binding / Zinc Ion Binding
OSJNBa0078O01.9	Putative Pkcq-Interacting Protein	At4g04950	Thioredoxin Family Protein
OSJNBa0079A21.10	Unknown Protein	At2g44830	Protein Kinase, Putative
OSJNBa0079A21.12	Unknown Protein	At3g27660	Oleo4 (Oleosin4)
OSJNBa0079A21.20	Unknown Protein	At5g47310	Unknown Protein
OSJNBa0079B05.15	Unknown Protein	At2g26500	Cytochrome B6f Complex Subunit (Petm), Putative
OSJNBa0079B15.25	Putative Aurora-Related Kinase	At2g45490	ATAUR3 (ATAURORA3); ATP Binding / Histone Serine Kinase(H3-S10 Specific) / Protein Kinase
OSJNBa0079B15.8	Unknown Protein	At3g18940	Clast3-Related
OSJNBa0079L16.13	Putative Peptide Transport Protein	At5g46050	ATPTR3/PTR3 (PEPTIDE TRANSPORTER PROTEIN 3); Transporter
OSJNBa0079L16.17	Putative CER1	At2g37700	CER1 Protein, Putative
OSJNBa0079M09.13	Unknown Protein	At3g45780	PHOT1 (Phototropin 1); Kinase
OSJNBa0079M09.14	Unknown Protein	At4g37940	AGL21 (AGAMOUS-LIKE 21); Transcription Factor
OSJNBa0081C01.1	Unknown Protein	At2g20770	Lanthionine Synthetase C-Like Family Protein
OSJNBa0081C01.11	Unknown Protein	At5g10560	Glycosyl Hydrolase Family 3 Protein
OSJNBa0081C01.12	Unknown Protein	At1g13250	GATL3 (Galacturonosyltransferase-Like 3); Polygalacturonate 4-Alpha-Galacturonosyltransferase/ Transferase, Transferring Glycosyl Groups / Transferase, Transferring Hexosyl Groups
OSJNBa0081C01.15	Unknown Protein	At3g49640	FAD Binding / Oxidoreductase
OSJNBa0081C01.16	Unknown Protein	At2g37710	RLK (RECEPTOR LECTIN KINASE); Kinase

OSJNBa0081C01.3	Unknown Protein	At2g20780	Mannitol Transporter, Putative
OSJNBa0081C01.5	Unknown Protein	At2g20750	Atexpb1 (Arabidopsis Thaliana Expansin B1)
OSJNBa0081C01.8	Unknown Protein	At1g51740	SYP81 (Syntaxin 81)
OSJNBa0081C13.10	Sec13p	At2g30050	Transducin Family Protein / WD-40 Repeat Family Protein
OSJNBa0081C13.26	Putative WD Repeat Domain 11	At3g33530	Transducin Family Protein / WD-40 Repeat Family Protein
OSJNBa0081C13.27	Unknown Protein	At3g10250	Unknown Protein
OSJNBa0081C13.28	Putative 50S Ribosomal Protein L3	At2g43030	Ribosomal Protein L3 Family Protein
OSJNBa0081C13.30	Putative Splicing Factor 3b, Subunit 3, 130kda	At3g55220	Splicing Factor, Putative
OSJNBa0081L15.13	Unknown Protein	At2g04660	APC2 (Anaphase-Promoting Complex/Cyclosome 2); Ubiquitin-Protein Ligase
OSJNBa0081L15.14	Unknown Protein	At5g50320	ELO3 (ELONGATA 3); N-Acetyltransferase/ Catalytic/ Hydrogen Ion Transporting ATP Synthase, Rotational Mechanism / Hydrogen Ion Transporting Atpase, Rotational Mechanism / Iron Ion Binding
OSJNBa0081L15.18	Unknown Protein	At5g40760	G6PD6 (GLUCOSE-6-PHOSPHATE DEHYDROGENASE 6); Glucose-6-Phosphate 1-Dehydrogenase
OSJNBa0081L15.3	Unknown Protein	At3g27390	Unknown Protein
OSJNBa0081P02.1	Hypothetical Protein	At1g25190	Unknown Protein
OSJNBa0081P02.15	Putative Protein Kinase	At5g66790	Protein Kinase Family Protein
OSJNBa0081P02.7	Unknown Protein	At1g73500	ATMKK9 (Arabidopsis Thaliana MAP Kinase Kinase 9); Kinase
OSJNBa0082M15.18	Putative	At1g63680	PDE316 (PIGMENT DEFECTIVE EMBRYO); ATP Binding / Ligase
OSJNBa0082M15.3	Putative Outer Envelope Protein	At2g16640	ATTOC132/TOC132 (MULTIMERIC TRANSLOCON COMPLEX IN THE OUTER ENVELOPE MEMBRANE 132); Transmembrane Receptor
OSJNBa0082M15.4	Beta-Expansin	At1g65680	Atexpb2 (Arabidopsis Thaliana Expansin B2)
OSJNBa0082M15.7	Putative WW-Domain Oxidoreductase	At4g11410	Short-Chain Dehydrogenase/Reductase (SDR) Family Protein
OSJNBa0083F15.12	Putative Sesquiterpene Synthase	At5g23960	Terpene Synthase/Cyclase Family Protein
OSJNBa0083F15.15	Putative Ubiquitin Conjugation Factor	At5g15400	U-Box Domain-Containing Protein
OSJNBa0083M08.1	Putative Trna Synthetase	At5g26707	Unknown Protein
OSJNBa0083M16.19	Putative Receptor Kinase	At1g68400	Leucine-Rich Repeat Transmembrane Protein Kinase, Putative
OSJNBa0083M16.25	Putative Endo-1,4-Beta-Xylanase X-1	At1g10050	Glycosyl Hydrolase Family 10 Protein / Carbohydrate-Binding Domain-Containing Protein
OSJNBa0083M16.34	Putative 16.9 Kda Heat Shock Protein	At1g53540	17.6 Kda Class I Small Heat Shock Protein (HSP17.6C-CI) (AA 1-156)
OSJNBa0083N12.1	Unknown Protein	At1g21230	WAK5 (WALL ASSOCIATED KINASE 5); Kinase/ Protein Serine/Threonine Kinase
OSJNBa0083N12.12	Unknown Protein	At3g22370	AOX1A (Alternative Oxidase 1A); Alternative Oxidase
OSJNBa0083N12.15	Unknown Protein	At1g64990	Unknown Protein
OSJNBa0083N12.20	Unknown Protein	At1g64850	Calcium-Binding EF Hand Family Protein
OSJNBa0083N12.23	Unknown Protein	At3g01390	Vma10 (Vacuolar Membrane Atpase 10)
OSJNBa0083N12.6	Unknown Protein	At1g80480	Ptac17 (Plastid Transcriptionally Active17)
OSJNBa0083N12.7	Unknown Protein	At4g33270	CDC20.1; Signal Transducer
OSJNBa0084A10.10	Unknown Protein	At2g18540	Cupin Family Protein

OSJNBa0084A10.7	Unknown Protein	At1g21760	F-Box Family Protein
OSJNBa0084K01.10	Unknown Protein	At3g51240	F3H (TRANSPARENT TESTA 6); Naringenin 3-Dioxygenase
OSJNBa0084K01.13	Unknown Protein	At5g13240	Unknown Protein
OSJNBa0084K01.16	Unknown Protein	At2g30000	Unknown Protein
OSJNBa0084K01.19	Unknown Protein	At5g39590	Unknown Protein
OSJNBa0084K01.2	Unknown Protein	At5g20990	B73 (CHLORATE RESISTANT 6); Molybdenum Ion Binding
OSJNBa0084K01.4	Unknown Protein	At5g03220	Transcriptional Co-Activator-Related
OSJNBa0084K01.5	Unknown Protein	At5g05780	Athmov34 (Asymmetric Leaves Enhancer3)
OSJNBa0084K01.7	Unknown Protein	At3g45380	Unknown Protein
OSJNBa0084K11.12	Unknown Protein	At4g35750	Rho-Gtpase-Activating Protein-Related
OSJNBa0084K11.14	Unknown Protein	At1g20380	Prolyl Oligopeptidase, Putative / Prolyl Endopeptidase, Putative / Post-Proline Cleaving Enzyme, Putative
OSJNBa0084K11.15	Unknown Protein	At1g16210	Unknown Protein
OSJNBa0084K11.2	Unknown Protein	At4g00430	TMP-C (Plasma Membrane Intrinsic Protein 1;4)
OSJNBa0084K11.20	Unknown Protein	At1g47670	Amino Acid Transporter Family Protein
OSJNBa0084K11.4	Unknown Protein	At1g01600	CYP86A4 (Cytochrome P450, Family 86, Subfamily A, Polypeptide 4); Oxygen Binding
OSJNBa0084K11.6	Unknown Protein	At3g10390	FLD (FLOWERING LOCUS D); Amine Oxidase
OSJNBa0084K11.9	Unknown Protein	At1g76040	CPK29 (Calcium-Dependent Protein Kinase 29); Calcium- And Calmodulin-Dependent Protein Kinase/ Kinase
OSJNBa0084K20.14	Unknown Protein	At5g36790	Phosphoglycolate Phosphatase, Putative
OSJNBa0084K20.3	Unknown Protein	At1g35460	Basic Helix-Loop-Helix (Bhlh) Family Protein
OSJNBa0084K20.5	Unknown Protein	At1g67530	Armadillo/Beta-Catenin Repeat Family Protein / U-Box Domain-Containing Family Protein
OSJNBa0084K20.6	Unknown Protein	At5g14220	HEMG2/MEE61 (Maternal Effect Embryo Arrest 61); Oxidoreductase/ Protoporphyrinogen Oxidase
OSJNBa0084K20.9	Unknown Protein	At5g14230	Ankyrin Repeat Family Protein
OSJNBa0084P08.2	Putative Plasma Membrane Associated Protein	At1g04560	AWPM-19-Like Membrane Family Protein
OSJNBa0085I10.11	Unknown Protein	At1g13270	MAP1C (METHIONINE AMINOPEPTIDASE 1B); Metalloexopeptidase
OSJNBa0085I10.13	Unknown Protein	At5g09400	KUP7 (K+ Uptake Permease 7); Potassium Ion Transporter
OSJNBa0085I10.14	Unknown Protein	At1g03475	LIN2 (LESION INITIATION 2); Coproporphyrinogen Oxidase
OSJNBa0085I10.18	Unknown Protein	At1g30900	Vacuolar Sorting Receptor, Putative
OSJNBa0085I10.3	Unknown Protein	At1g79350	EMB1135 (EMBRYO DEFECTIVE 1135); DNA Binding
OSJNBa0085K21.31	Putative Thiosulfate Transferase	At1g79230	St1 (Mercaptopyruvate Sulfurtransferase 1)
OSJNBa0085K21.33	Tubulin Beta Chain	At5g62700	TUB3 (Tubulin Beta-3); Structural Molecule
OSJNBa0085K21.46	Putative TIP120 Protein	At2g02560	CAND1 (CULLIN-ASSOCIATED AND NEDDYLATION DISSOCIATED, HEMIVENATA); Binding
OSJNBa0086A10.12	Putative Serine/Threonine-Specific Protein	At4g24400	Cipk8 (Cbl-Interacting Protein Kinase 8)
OSJNBa0086B14.2	Unknown Protein	At5g65400	Unknown Protein

OSJNBa0086B14.22	Unknown Protein	At1g34750	Protein Phosphatase 2C, Putative / PP2C, Putative
OSJNBa0086B14.23	Unknown Protein	At4g08920	Cry1 (Cryptochrome 1, Out Of Phase 2)
OSJNBa0086B14.3	Unknown Protein	At5g09450	Pentatricopeptide (PPR) Repeat-Containing Protein
OSJNBa0086F04.36	Putative Fertility Restorer Homologue	At5g01110	Pentatricopeptide (PPR) Repeat-Containing Protein
OSJNBa0086F04.42	Putative Farnesylated Protein	At1g22990	Heavy-Metal-Associated Domain-Containing Protein / Copper Chaperone (CCH)-Related
OSJNBa0086N05.101	Unknown Protein	At5g01750	Unknown Protein
OSJNBa0086N05.115	Putative Amino Acid Transport Protein	At3g11900	ANT1 (AROMATIC AND NEUTRAL TRANSPORTER 1); Amino Acid Permease/ Amino Acid Transporter
OSJNBa0086N11.18	Putative Glutathione Transferase	At5g45020	Unknown Protein
OSJNBa0086N11.31	Putative Iron/Ascorbate-Dependent	At5g54000	Oxidoreductase, 2OG-Fe(II) Oxygenase Family Protein
OSJNBa0086O06.1	Unknown Protein	At3g60160	ATMRP9 (Arabidopsis Thaliana Multidrug Resistance-Associated Protein 9)
OSJNBa0086O06.10	Unknown Protein	At1g78800	Glycosyl Transferase Family 1 Protein
OSJNBa0086O06.11	Unknown Protein	At3g19380	U-Box Domain-Containing Protein
OSJNBa0086O06.12	Unknown Protein	At1g32560	Late Embryogenesis Abundant Group 1 Domain-Containing Protein / LEA Group 1 Domain-Containing Protein
OSJNBa0086O06.18	Unknown Protein	At5g59450	Scarecrow-Like Transcription Factor 11 (SCL11)
OSJNBa0086O06.23	Unknown Protein	At1g43000	Zinc-Binding Family Protein
OSJNBa0086P08.13	Putative Branched-Chain Amino Acid	At5g57850	Aminotransferase Class IV Family Protein
OSJNBa0086P08.14	Hypothetical Protein	At4g28440	DNA-Binding Protein-Related
OSJNBa0086P08.22	Putative Heat Shock Protein 40	At4g28480	Heat Shock Protein Binding / Unfolded Protein Binding
OSJNBa0087C10.12	Putative RNA Helicase	At3g18600	DEAD/DEAH Box Helicase, Putative
OSJNBa0087C10.14	Putative AAA-Type Atpase	At3g28580	AAA-Type Atpase Family Protein
OSJNBa0087C10.22	Unknow Protein	At5g23330	Riboflavin Biosynthesis Protein-Related
OSJNBa0087C10.23	Putative Vacuolar Protein Sorting-Associated	At1g75850	Unknown Protein
OSJNBa0087C10.4	Putative Oxidoreductase	At3g28480	Oxidoreductase, 2OG-Fe(II) Oxygenase Family Protein
OSJNBa0087C10.9	Synaptobrevin-Like Protein	At1g04750	Vamp7b (Vesicle-Associated Membrane Protein 7b)
OSJNBa0087F21.31	Putative Plasma Membrane H+-Atpase	At2g18960	AHA1 (PLASMA MEMBRANE PROTON ATPASE); Atpase
OSJNBa0087G11.19	Putative 1,3-Beta-Glucanase	At5g20870	Glycosyl Hydrolase Family 17 Protein
OSJNBa0087G11.20	Putative Pre-Mrna Splicing Factor	At1g10580	Transducin Family Protein / WD-40 Repeat Family Protein
OSJNBa0087G11.4	Unknown Protein	At4g33160	F-Box Family Protein (FBX13)
OSJNBa0087M10.1	Ribosomal Protein L15	At4g17390	60S Ribosomal Protein L15 (RPL15B)
OSJNBa0087M10.16	Putative Pentatricopeptide Repeat Protein	At3g53700	MEE40 (Maternal Effect Embryo Arrest 40); Binding
OSJNBa0087M10.8	Putative ACT Domain Repeat Protein	At1g69040	ACR4 (ACT REPEAT 4); Amino Acid Binding
OSJNBa0087O09.19	Putative Aldehyde Oxidase	At5g20960	Aao1 (Aldehyde Oxidase 1)
OSJNBa0087O24.20	Unknown Protein	At5g65930	ZWI (ZWICHEL); Calmodulin Binding / Microtubule Motor
OSJNBa0087O24.21	Unknown Protein	At1g78690	Phospholipid/Glycerol Acyltransferase Family Protein

OSJNBa0087O24.6	Unknown Protein	At5g55280	FTSZ1-1 (Ftsz1-1); Structural Molecule
OSJNBa0088A01.11	Unknown Protein	At5g13770	Pentatricopeptide (PPR) Repeat-Containing Protein
OSJNBa0088A01.16	Unknown Protein	At5g56320	Atexpa14 (Arabidopsis Thaliana Expansin A14)
OSJNBa0088H09.1	Unknown Protein	At5g41180	Leucine-Rich Repeat Protein Kinase, Putative
OSJNBa0088H09.10	Unknown Protein	At2g36060	Mmz3 (Mms Zwei Homologe 3)
OSJNBa0088H09.11	Unknown Protein	At5g22250	CCR4-NOT Transcription Complex Protein, Putative
OSJNBa0088H09.15	Unknown Protein	At3g11650	NHL2 (NDR1/HIN1-Like 2)
OSJNBa0088H09.16	Unknown Protein	At3g11660	NHL1 (NDR1/HIN1-Like 1)
OSJNBa0088H09.18	Unknown Protein	At5g03540	(EXOCYST SUBUNIT EXO70 FAMILY PROTEIN A1); Protein Binding
OSJNBa0088H09.2	Unknown Protein	At3g48990	AMP-Dependent Synthetase And Ligase Family Protein
OSJNBa0088H09.3	Unknown Protein	At4g11610	NTRB (NADPH-Dependent Thioredoxin Reductase B)
OSJNBa0088H09.6	Unknown Protein	At5g41260	Protein Kinase Family Protein
OSJNBa0088I06.1	Putative 60S Ribosomal Protein L30	At3g18740	60S Ribosomal Protein L30 (RPL30C)
OSJNBa0088I06.10	Unknown Protein	At5g21170	AMP-Activated Protein Kinase
OSJNBa0088I06.13	Hypothetical Protein	At5g19360	CPK34 (Calcium-Dependent Protein Kinase 34); Calcium- And Calmodulin-Dependent Protein Kinase/ Kinase
OSJNBa0088I06.19	Hypothetical Protein	At5g06150	CYC1BAT (CYCLIN B 1;2); Cyclin-Dependent Protein Kinase Regulator
OSJNBa0088I06.20	Putative Nodulin Mtn21 Protein	At5g07050	Nodulin Mtn21 Family Protein
OSJNBa0088I06.5	'Unknown Protein, Conatins SET Domain'	At5g04940	Suvh1 (Su(Var)3-9 Homolog 1)
OSJNBa0088I06.9	Putative Calmodulin	At5g37780	CAM1 (CALMODULIN 1); Calcium Ion Binding
OSJNBa0088I22.12	Unknown Protein	At1g12740	CYP87A2 (Cytochrome P450, Family 87, Subfamily A, Polypeptide 2); Oxygen Binding
OSJNBa0088I22.7	Unknown Protein	At5g52120	ATPP2-A14 (Phloem Protein 2-A14)
OSJNBa0088K19.13	Unknown Protein	At1g72090	Radical SAM Domain-Containing Protein / TRAM Domain-Containing Protein
OSJNBa0088M05.16	Putative Annexin	At2g38760	ANNAT3 (ANNEXIN 3, ANNEXIN ARABIDOPSIS 3); Calcium Ion Binding / Calcium-Dependent Phospholipid Binding
OSJNBa0088M06.1	Unknown Protein	At1g56130	Leucine-Rich Repeat Family Protein / Protein Kinase Family Protein;
OSJNBa0088O14.4	Pathogenesis-Related Protein 1	At3g19690	Pathogenesis-Related Protein, Putative
OSJNBa0089K21.2	Unknown Protein	At4g02840	Small Nuclear Ribonucleoprotein D1, Putative / Snrnp Core Protein D1, Putative / Sm Protein D1, Putative
OSJNBa0089K21.6	Unknown Protein	At5g23810	AAP7 (Amino Acid Permease 7)
OSJNBa0089K24.1	Putative Peroxidase	At2g41480	Peroxidase
OSJNBa0089K24.15	Putative MRP-Like ABC Transporter	At3g13080	ATMRP3 (Arabidopsis Thaliana Multidrug Resistance-Associated Protein 3)
OSJNBa0089K24.24	Unknown Protein	At5g20060	Carboxylic Ester Hydrolase
OSJNBa0089K24.3	Hypothetical Protein	At1g24090	Rnase H Domain-Containing Protein
OSJNBa0089N06.12	Unknown Protein	At3g21820	SET Domain-Containing Protein
OSJNBa0089N06.26	Unknown Protein	At1g61720	Ban (Banyuls)

OSJNBa0089N06.6	Unknown Protein	At3g01190	Peroxidase 27 (PER27) (P27) (PRXR7)
OSJNBa0090H18.25	Putative Chaperonin Containing TCP1, Subunit 3	At5g26360	Chaperonin, Putative
OSJNBa0090H18.33	Putative Drought-Induced Protein RDI	At1g53210	Sodium/Calcium Exchanger Family Protein / Calcium-Binding EF Hand Family Protein
OSJNBa0090L05.7	Hypothetical Protein	At1g64140	Unknown Protein
OSJNBa0090O10.11	Hypothetical Protein	At2g40780	RNA Binding / Translation Initiation Factor
OSJNBa0090O10.18	Putative Transporter	At1g64650	Unknown Protein
OSJNBa0090O10.21	Hypothetical Protein	At1g01220	GHMP Kinase-Related
OSJNBa0090O10.22	Hypothetical Protein	At3g13230	Nucleic Acid Binding
OSJNBa0090O10.25	Hypothetical Protein	At4g24050	Short-Chain Dehydrogenase/Reductase (SDR) Family Protein
OSJNBa0091C07.1	Unknown Protein	At1g74580	Pentatricopeptide (PPR) Repeat-Containing Protein
OSJNBa0091C12.3	Unknown Protein	At4g38580	ATFP6 (FARNESYLATED PROTEIN 6); Metal Ion Binding
OSJNBa0091C16.21	Lipase Class 3-Like	At3g07400	Lipase Class 3 Family Protein
OSJNBa0091C18.37	Putative Actin Related Protein 2	At3g27000	ARP2 (WURM); Structural Constituent Of Cytoskeleton
OSJNBa0091C18.39	Hypothetical Protein	At5g25790	Transcription Factor
OSJNBa0091D06.12	Unknown Protein	At2g01660	33 Kda Secretory Protein-Related
OSJNBa0091D06.17	Unknown Protein	At3g43630	Nodulin, Putative
OSJNBa0091E13.20	Hypothetical Protein	At3g19540	Unknown Protein
OSJNBa0091E23.2	Rice Pathogenesis-Related Protein Class 1	At4g33720	Pathogenesis-Related Protein, Putative
OSJNBa0091E23.5	Putative Benzoyltransferase	At1g27620	Transferase Family Protein
OSJNBa0091J19.1	Putative Inosine Monophosphate Dehydrogenase	At1g16350	Inosine-5'-Monophosphate Dehydrogenase, Putative
OSJNBa0091J19.10	Unknown Protein	At5g44450	Unknown Protein
OSJNBa0091J19.11	Putative Actin-Depolymerizing Factor	At2g31200	ADF6 (ACTIN DEPOLYMERIZING FACTOR 6); Actin Binding
OSJNBa0091J19.14	Hypothetical Protein	At3g12870	Unknown Protein
OSJNBa0091J19.15	Putative Fatty Acid Hydroxylase	At4g20870	Fatty Acid Hydroxylase, Putative
OSJNBa0091J19.7	Unknown Protein	At3g10260	Reticulon Family Protein
OSJNBa0091J19.9	Putative GTP-Binding Protein	At1g56050	GTP-Binding Protein-Related
OSJNBa0091P11.1	Sucrose Transporter, 5'-Partial	At1g09960	SUT4 (SUCROSE TRANSPORTER 4); Carbohydrate Transporter/ Sucrose:Hydrogen Symporter/ Sugar Porter
OSJNBa0091P11.10	Ribulose-5-Phosphate-3-Epimerase	At5g61410	RPE (EMBRYO DEFECTIVE 2728); Ribulose-Phosphate 3-Epimerase
OSJNBa0091P11.12	Putative Plant Cytochrome P-450 Protein	At1g69500	Oxygen Binding
OSJNBa0091P11.14	Putative Male Sterility Protein	At3g11980	Ms2 (Male Sterility 2)
OSJNBa0091P11.22	Putative Pentatricopeptide Repeat Containing	At5g56310	Pentatricopeptide (PPR) Repeat-Containing Protein
OSJNBa0091P11.24	Putative Auxin Independent Growth-Related	At2g03280	Unknown Protein
OSJNBa0091P11.6	Unknown Protein	At3g28760	Unknown Protein
OSJNBa0092M19.24	Putative Glycosyl Transferase	At1g19300	GATL1/GLZ1/PARVUS (Galacturonosyltransferase-Like 1); Polygalacturonate 4-Alpha-Galacturonosyltransferase/ Transferase, Transferring Glycosyl Groups / Transferase,

			Transferring Hexosyl Groups
OSJNBa0092M19.27	Putative Vacuolar Protein Sorting-Associated	At5g53530	Vacuolar Protein Sorting-Associated Protein 26, Putative / VPS26, Putative
OSJNBa0092M19.3	Hypothetical Protein	At4g16010	Transposable Element Gene
OSJNBa0092N12.12	Putative Receptor-Like Protein Kinase	At2g01950	BRL2 (BRI1-LIKE 2); ATP Binding / Protein Serine/Threonine Kinase
OSJNBa0093F16.23	Auxin Response Factor 2	At5g20730	NPH4 (NON-PHOTOTROPHIC HYPOCOTYL); Transcription Factor
OSJNBa0093M23.10	Germin-Like Protein	At1g09560	GLP5 (GERMIN-LIKE PROTEIN 5); Manganese Ion Binding / Metal Ion Binding / Nutrient Reservoir
OSJNBa0093O08.1	Unknown Protein	At1g56130	Leucine-Rich Repeat Family Protein / Protein Kinase Family Protein;
OSJNBa0093O08.12	Unknown Protein	At4g14630	GLP9 (GERMIN-LIKE PROTEIN 9); Manganese Ion Binding / Metal Ion Binding / Nutrient Reservoir
OSJNBa0093O08.13	Unknown Protein	At3g14580	Pentatricopeptide (PPR) Repeat-Containing Protein
OSJNBa0093P23.1	Unknown Protein	At2g13610	ABC Transporter Family Protein
OSJNBa0094F01.1	Putative 40S Ribosomal Protein S15	At5g09510	40S Ribosomal Protein S15 (RPS15D)
OSJNBa0094F01.10	Unknown Protein	At1g04230	Unknown Protein
OSJNBa0094F01.18	Putative Indole-3-Glycerol Phosphate Lyase	At4g02610	Tryptophan Synthase, Alpha Subunit, Putative
OSJNBa0094F01.24	Putative 60S Ribosomal Protein L1	At3g09630	Structural Constituent Of Ribosome
OSJNBa0094H06.16	Unknown Protein	At1g71050	Heavy-Metal-Associated Domain-Containing Protein / Copper Chaperone (CCH)-Related
OSJNBa0094J08.10	Unknown Protein	At3g11030	Steroid Hormone Receptor/ Transcription Factor
OSJNBa0094J08.18	Putative Amino Acid Transporter	At5g16740	Amino Acid Transporter Family Protein
OSJNBa0094J08.21	Putative Polyprotein	At4g03810	Retrotransposon Protein
OSJNBa0094J08.24	Hypothetical Protein	At1g68930	Pentatricopeptide (PPR) Repeat-Containing Protein
OSJNBa0094J08.29	Putative Protein Kinase	At3g27560	ATN1; Kinase/ Protein Threonine/Tyrosine Kinase
OSJNBa0094J08.6	Putative Cinnamoyl-Coa Reductase	At5g58490	Cinnamoyl-Coa Reductase Family
OSJNBa0094J08.7	Putative Multiple Inositol Polyphosphate	At1g09870	Histidine Acid Phosphatase Family Protein
OSJNBa0094J09.17	Putative Protein	At3g63220	Kelch Repeat-Containing F-Box Family Protein
OSJNBa0094P09.18	Unknown Protein	At1g17200	Integral Membrane Family Protein
OSJNBa0095C06.17	Putative Pyridoxamine 5-Phosphate Oxidase	At5g49970	Pyridoxamine 5'-Phosphate Oxidase-Related
OSJNBa0095C07.1	Putative Beta-Phosphoglucomutase	At2g38740	Haloacid Dehalogenase-Like Hydrolase Family Protein
OSJNBa0095C07.3	Putative Eukaryotic Initiation Factor Subunit	At5g27640	TIF3B1 (EUKARYOTIC TRANSLATION INITIATION FACTOR 3B); Nucleic Acid Binding / Translation Initiation Factor
OSJNBa0095C07.4	Putative Nuclear Protein	At2g44525	Unknown Protein
OSJNBa0095C07.5	Putative Pyruvate Kinase	At1g32440	Pyruvate Kinase, Putative
OSJNBa0095C07.6	Putative Protein Kinase	At4g35470	Leucine-Rich Repeat Family Protein
OSJNBa0095C07.6	Putative Protein Kinase	At5g46570	Protein Kinase Family Protein
OSJNBa0095C07.8	Putative Leucine-Rich Repeat Protein	At3g07010	Pectate Lyase Family Protein
OSJNBa0095H06.5	Unknown Protein	At1g66510	AAR2 Protein Family

OSJNBa0095H06.6	Unknown Protein	At3g24240	Leucine-Rich Repeat Transmembrane Protein Kinase, Putative
OSJNBa0095N06.18	Putative MATE Efflux Family Protein	At3g21690	MATE Efflux Family Protein
OSJNBa0096E22.2	Hypothetical Protein	At3g49790	ATP Binding
OSJNBa0096F01.13	Unknown Protein	At2g47140	Short-Chain Dehydrogenase/Reductase (SDR) Family Protein
OSJNBa0096F01.2	Unknown Protein	At5g43530	SNF2 Domain-Containing Protein / Helicase Domain-Containing Protein / RING Finger Domain-Containing Protein
OSJNBa0096F01.6	Unknown Protein	At5g43500	ATARP9 (ACTIN-RELATED PROTEIN 9); Protein Binding
OSJNBa0096F01.8	Unknown Protein	At3g26290	CYP71B26 (Cytochrome P450, Family 71, Subfamily B, Polypeptide 26); Oxygen Binding
OSJNBa0096I06.11	Putative Ferredoxin	At1g10960	ATFD1 (FERREDOXIN 1); Electron Carrier/ Iron Ion Binding
OSJNBa0096I06.14	Putative Transcription Factor	At3g05420	ACBP4 (ACYL-COA BINDING PROTEIN 4, ACYL-COA-BINDING DOMAIN 4); Acyl-Coa Binding
OSJNBa0096I06.26	Putative Deoxycytidine Deaminase	At5g28050	Hydrolase/ Zinc Ion Binding
OSJNBa0096I06.27	Putative Polygalacturonase	At3g62110	Glycoside Hydrolase Family 28 Protein / Polygalacturonase (Pectinase) Family Protein
OSJNBa0096I06.33	Putative Hydroxysteroiddehydrogenase	At3g29260	Short-Chain Dehydrogenase/Reductase (SDR) Family Protein
OSJNBb0002J01.12	Las17 Binding Protein-Like	At3g43230	Zinc Finger (FYVE Type) Family Protein
OSJNBb0002J11.14	Unknown Protein	At4g28740	Unknown Protein
OSJNBb0002J11.20	Unknown Protein	At3g04290	ATLTL1/LTL1 (LI-TOLERANT LIPASE 1); Carboxylic Ester Hydrolase
OSJNBb0002J11.22	Unknown Protein	At5g63010	WD-40 Repeat Family Protein
OSJNBb0002N06.2	Unknown Protein	At3g42100	AT Hook Motif-Containing Protein-Related
OSJNBb0003A12.10	Unknown Protein	At2g38940	ATPT2 (PHOSPHATE TRANSPORTER 2); Carbohydrate Transporter/ Phosphate Transporter/ Sugar Porter
OSJNBb0003A12.6	Unknown Protein	At2g32830	PHT5 (Phosphate Transporter 5); Inorganic Phosphate Transporter/ Phosphate Transporter
OSJNBb0003E08.13	Putative Nitrate Transporter NRT1-5	At5g62680	Proton-Dependent Oligopeptide Transport (POT) Family Protein
OSJNBb0003E08.15	Putative Thioredoxin	At5g39950	ATTRX2 (Arabidopsis Thioredoxin H2, Thioredoxin H-Type 1); Thiol-Disulfide Exchange Intermediate
OSJNBb0003E08.20	Plasma Membrane H+ Atpase	At5g62670	AHA11 (ARABIDOPSIS H(+)-ATPASE 11); Atpase
OSJNBb0003E08.26	Putative Pentatricopeptide (PPR)	At1g59720	Pentatricopeptide (PPR) Repeat-Containing Protein
OSJNBb0003H03.24	Aspartate Carbamoyltransferase	At3g20330	Aspartate Carabmoyltransferase, Chloroplast / Aspartate Transcarbamylase / Atcase (PYRB)
OSJNBb0003H03.27	Putative ADP-Ribosylation Factor 3	At5g14670	ATARFA1B (ADP-Ribosylation Factor A1B); GTP Binding / Phospholipase Activator/ Protein Binding
OSJNBb0003H22.12	Putative Pectin-Glucuronyltransferase	At5g61840	GUT1; Catalytic
OSJNBb0003H22.2	Mutt-Like Protein	At3g26690	ATNUDT13 (ARABIDOPSIS THALIANA NUDIX HYDROLASE HOMOLOG 13); Hydrolase
OSJNBb0004A06.10	Unknown Protein	At3g21380	Unknown Protein
OSJNBb0004A17.1	Unknown Protein	At1g65840	ATPAO4 (POLYAMINE OXIDASE 4); Amine Oxidase
OSJNBb0004A17.12	Unknown Protein	At1g10820	Unknown Protein
OSJNBb0004A17.3	Unknown Protein	At3g02720	DJ-1 Family Protein / Protease-Related
OSJNBb0004A17.6	Unknown Protein	At2g02220	ATPSKR1 (PHYTOSULFOKIN RECEPTOR 1); ATP Binding / Peptide Receptor/ Protein Serine/Threonine Kinase

OSJNBb0004A17.9	Unknown Protein	At3g50420	Pentatricopeptide (PPR) Repeat-Containing Protein
OSJNBb0004G23.3	Unknown Protein	At2g46890	Oxidoreductase
OSJNBb0004G23.4	Unknown Protein	At1g18010	Unknown Protein
OSJNBb0004M10.7	Putative Myosin Heavy Chain-Like	At2g26570	Unknown Protein
OSJNBb0005B05.10	Unknown Protein	At2g44210	Unknown Protein
OSJNBb0005F01.1	Putative Helicase	At1g72680	Cinnamyl-Alcohol Dehydrogenase, Putative
OSJNBb0005G07.107	Putative Lateral Organ Boundaries (LOB) Domain	At2g30340	LOB Domain Protein 13 / Lateral Organ Boundaries Domain Protein 13 (LBD13)
OSJNBb0005G07.112	Putative Short-Root Transcription Factor	At3g49950	Scarecrow Transcription Factor Family Protein
OSJNBb0005G07.114	Putative WD Repeat Protein	At5g66240	Transducin Family Protein / WD-40 Repeat Family Protein
OSJNBb0005J14.19	Putative Glutathione S-Transferase	At1g10360	ATGSTU18 (GLUTATHIONE S-TRANSFERASE 29); Glutathione Transferase
OSJNBb0005J14.27	Cytochrome P450-Like Protein	At2g45510	CYP704A2 (Cytochrome P450, Family 704, Subfamily A, Polypeptide 2); Oxygen Binding
OSJNBb0005J14.3	Putative Serine Protease	At1g04110	SDD1 (STOMATAL DENSITY AND DISTRIBUTION); Subtilase
OSJNBb0006H05.17	Hypothetical Protein	At5g24710	Unknown Protein
OSJNBb0006H05.29	NADP-Specific Isocitrate Dehydrogenase	At1g65930	Isocitrate Dehydrogenase, Putative / NADP+ Isocitrate Dehydrogenase, Putative
OSJNBb0006L01.1	Unknown Protein	At1g06650	2-Oxoglutarate-Dependent Dioxygenase, Putative
OSJNBb0006L01.3	Unknown Protein	At5g47020	Glycine-Rich Protein
OSJNBb0006L01.7	Unknown Protein	At1g59520	Cw7
OSJNBb0006L10.23	Scramblase-Like	At2g04940	Scramblase-Related
OSJNBb0006L10.5	Putative Spermine Synthase	At5g19530	Acl5 (Acaulis 5)
OSJNBb0006N15.11	Unknown Protein	At1g24360	3-Oxoacyl-(Acyl-Carrier Protein) Reductase, Chloroplast / 3-Ketoacyl-Acyl Carrier Protein Reductase
OSJNBb0006N15.13	Unknown Protein	At1g10840	TIF3H1 (Eukaryotic Translation Initiation Factor 3 Subunit H1); Translation Initiation Factor
OSJNBb0006N15.8	Unknown Protein	At5g02610	60S Ribosomal Protein L35 (RPL35D)
OSJNBb0006O08.13	Unknown Protein	At5g46720	Unknown Protein
OSJNBb0006O08.14	Putative Zinc Finger Protein	At5g46750	AGD8 (ARF-GAP DOMAIN 8); DNA Binding
OSJNBb0006O08.2	Putative Cleavage And Polyadenylation Specifity	At1g61010	Hydrolase
OSJNBb0007E22.1	Putative NPH3 Family Protein	At2g14820	Phototropic-Responsive NPH3 Family Protein
OSJNBb0007E22.16	Putative Aldo/Keto Reductase Family Protein	At1g04420	Aldo/Keto Reductase Family Protein
OSJNBb0007E22.7	Putative Serpin	At1g47710	Serpin, Putative / Serine Protease Inhibitor, Putative
OSJNBb0008A05.2	Unknown Protein	At3g29240	Unknown Protein
OSJNBb0008A05.25	Putative Beta-Galactosidase	At5g20710	BGAL7 (Beta-Galactosidase 7); Beta-Galactosidase
OSJNBb0008A05.9	Putative Mevalonate Kinase	At5g27450	MK/MVK; Mevalonate Kinase
OSJNBb0008D07.22	Hypothetical Protein, Similar To Oryza	At5g27370	Unknown Protein
OSJNBb0009C07.1	Unknown Protein	At2g45620	Nucleotidyltransferase Family Protein
OSJNBb0009C07.2	Putative Transcription Initiation Factor	At4g12610	ATRAP74/RAP74; Transcription Initiation Factor

OSJNBb0011A08.1	Putative Rnase	At3g01410	Rnase H Domain-Containing Protein
OSJNBb0011A08.13	Putative Helicase	At3g30560	Transposable Element Gene
OSJNBb0011A08.2	Putative Thiolase	At2g33150	PED1 (PEROXISOME DEFECTIVE 1); Acetyl-Coa C-Acyltransferase
OSJNBb0011H13.18	Putative P-Type Atpase	At1g10130	ECA3 (ENDOPLASMIC RETICULUM-TYPE CALCIUM-TRANSPORTING ATPASE 3); Calcium-Transporting Atpase/ Calmodulin Binding
OSJNBb0011H13.3	Unknown Protein	At1g17870	Unknown Protein
OSJNBb0011H15.39-1	Putative NADPH-Dependent Reductase	At4g35250	Vestitone Reductase-Related
OSJNBb0011H15.4	Putative Auxin Induced Protein	At1g29430	Auxin-Responsive Family Protein
OSJNBb0011H15.42	Putative MYST1	At4g24430	Lyase
OSJNBb0011J16.13	Expressed Protein	At4g21170	Pentatricopeptide (PPR) Repeat-Containing Protein
OSJNBb0011N17.14	Unknown Protein	At5g55370	Long-Chain-Alcohol O-Fatty-Acyltransferase Family Protein / Wax Synthase Family Protein
OSJNBb0011N17.16	Unknown Protein	At5g61640	PMSR1 (PEPTIDEMETHIONINE SULFOXIDE REDUCTASE 1); Protein-Methionine-S-Oxide Reductase
OSJNBb0011N17.19	Unknown Protein	At3g03420	Ku70-Binding Family Protein
OSJNBb0011N17.9	Unknown Protein	At3g01660	Methyltransferase
OSJNBb0012A20.13	Unknown Protein	At1g52200	Unknown Protein
OSJNBb0012A20.16	Putative Endosomal Protein	At1g14670	Endomembrane Protein 70, Putative
OSJNBb0012A20.18	Putative NADPH-Dependent Oxidoreductase	At1g59960	Aldo/Keto Reductase, Putative
OSJNBb0012E08.10	Unknown Protein	At5g61790	Calnexin 1 (CNX1)
OSJNBb0012E08.6	Unknown Protein	At1g37110	Transposable Element Gene; Copia-Like Retrotransposon Family,
OSJNBb0012E08.8	Unknown Protein	At3g26680	Snm1 (Sensitive To Nitrogen Mustard 1)
OSJNBb0012E24.2	Unknown Protein	At3g47420	Glycerol-3-Phosphate Transporter, Putative / Glycerol 3-Phosphate Permease, Putative
OSJNBb0012E24.3	Unknown Protein	At1g60170	Emb1220 (Embryo Defective 1220)
OSJNBb0012E24.4	Unknown Protein	At2g45540	WD-40 Repeat Family Protein / Beige-Related
OSJNBb0012E24.7	Unknown Protein	At4g11640	ATSR (ARABIDOPSIS THALIANA SIGNAL-RESPONSIVE); Serine Racemase
OSJNBb0012E24.9	Unknown Protein	At4g11600	ATGPX6 (GLUTATHIONE PEROXIDASE 6); Glutathione Peroxidase
OSJNBb0012I09.11	Putative SKP1	At4g34210	ASK11 (ARABIDOPSIS SKP1-LIKE 11); Ubiquitin-Protein Ligase
OSJNBb0012J10.18	Putative ADH Glutamate Dehydrogenase	At5g07440	GDH2 (GLUTAMATE DEHYDROGENASE 2); Oxidoreductase
OSJNBb0012J10.19	Unknown Protein	At5g51170	Unknown Protein
OSJNBb0013J13.11	Unknown Protein	At5g35820	Transposable Element Gene
OSJNBb0013K01.1	Putative Replication Factor C 36kda Subunit	At1g77470	Replication Factor C 36 Kda, Putative
OSJNBb0013K01.36	Replication Protein A 70kda	At2g06510	Replication Protein, Putative
OSJNBb0013K01.4	Kinesin Motor Protein 1-Like	At5g06670	Kinesin Motor Protein-Related
OSJNBb0013K08.1	Unknown Protein, 5' Partial	At4g36860	LIM Domain-Containing Protein
OSJNBb0013K08.2	Putative Multidrug Efflux Protein	At3g26590	MATE Efflux Family Protein
OSJNBb0013K08.3	Putative Calcineurin B-Like Protein	At4g26570	Atcbl3 (Calcineurin B-Like 3)

OSJNBb0013K08.9	Putative Nucleotide-Binding Protein	At4g19540	Unknown Protein
OSJNBb0014I10.10	Putative Apyrase	At5g18280	Atapy2 (Apyrase 2)
OSJNBb0014I11.10	Putative Oxysterol-Binding Protein	At4g08180	Oxysterol-Binding Family Protein
OSJNBb0014I11.12	Putative Flavin-Containing Monooxygenase	At1g12140	Flavin-Containing Monooxygenase Family Protein / FMO Family Protein
OSJNBb0014I11.9	Putative Nitrate Transporter	At1g12110	NRT1.1 (Nitrate Transporter 1.1); Transporter
OSJNBb0014K18.13	Unknown Protein	At2g40900	Nodulin Mtn21 Family Protein
OSJNBb0014K18.8	Putative 1-Deoxy-D-Xylulose-5-Phosphate	At4g15560	Cla1 (Cloroplastos Alterados 1)
OSJNBb0015G09.5	Unknown Protein	At1g11410	S-Locus Protein Kinase, Putative
OSJNBb0015I02.11	Putative TCP-1/Cpn60 Chaperonin Family Protein	At3g03960	Chaperonin, Putative
OSJNBb0015I02.14	Putative Helicase	At2g42520	DEAD Box RNA Helicase, Putative
OSJNBb0015I02.15	Serine/Threonine Protein Phosphatase PP2A-2	At2g42500	PP2A-4 (Protein Phosphatase 2A-4); Protein Phosphatase Type 2A/ Protein Serine/Threonine Phosphatase
OSJNBb0015I02.16	Putative Phosphatase	At3g58490	Phosphatidic Acid Phosphatase Family Protein / PAP2 Family Protein
OSJNBb0015I02.17	Putative Acyl-Activating Enzyme	At1g55320	Unknown Protein
OSJNBb0015I11.10	Putative Pollen Allergen	At3g45970	Atexla1 (Arabidopsis Thaliana Expansin-Like A1)
OSJNBb0015I11.13	Protein Kinase-Like Protein	At4g35230	Protein Kinase Family Protein
OSJNBb0015I11.17	Mucin-Like Protein	At3g51420	Strictosidine Synthase Family Protein
OSJNBb0015I11.26	Putative Protein Phosphatase-2C	At2g33700	Protein Phosphatase 2C, Putative / PP2C, Putative
OSJNBb0015K05.11	Putative Dnaj Domain Containing Protein	At2g35720	DNAJ Heat Shock N-Terminal Domain-Containing Protein
OSJNBb0015N08.10	Unknown Protein	At2g19330	Leucine-Rich Repeat Family Protein
OSJNBb0015N08.12	Unknown Protein	At5g57110	ACA8 (AUTOINHIBITED CA2+ -ATPASE, ISOFORM 8); Calmodulin Binding
OSJNBb0016D16.5	Unknown Protein	At4g18200	Unknown Protein
OSJNBb0016D16.6	Unknown Protein	At1g19260	Hat Dimerisation Domain-Containing Protein
OSJNBb0016G07.10	Unknown Protein	At1g28580	GDSL-Motif Lipase, Putative
OSJNBb0016G07.8	'Unknown Protein, Contains GDSL-Like	At5g45910	GDSL-Motif Lipase/Hydrolase Family Protein
OSJNBb0016H12.13	Putative Endo-1,4-Beta-Glucanase	At5g49720	KOR1 (KORRIGAN); Hydrolase, Hydrolyzing O-Glycosyl Compounds
OSJNBb0016H12.15	Putative Cytokinesis-Specific Syntaxin-Related	At1g08560	SYP111 (Syntaxin 111); T-SNARE
OSJNBb0016H12.19	Unknown Protein	At5g10860	CBS Domain-Containing Protein
OSJNBb0016H12.23	Unknown Protein	At1g28010	PGP14 (P-GLYCOPROTEIN 14); Atpase, Coupled To Transmembrane Movement Of Substances
OSJNBb0016H12.26	Unknown Protein	At5g58730	Pfkb-Type Carbohydrate Kinase Family Protein
OSJNBb0016M10.2	Putative AUX1-Like Permease	At2g21050	Amino Acid Permease, Putative
OSJNBb0016P23.14	Putative GDSL-Like Lipase/Acylhydrolase	At5g55050	GDSL-Motif Lipase/Hydrolase Family Protein
OSJNBb0016P23.2	Unknown Protein	At2g32480	Membrane-Associated Zinc Metalloprotease, Putative
OSJNBb0016P23.5	Putative Ribosomal Protein L19	At3g16780	60S Ribosomal Protein L19 (RPL19B)
OSJNBb0017F17.11	Hypothetical Protein	At1g55000	Peptidoglycan-Binding Lysm Domain-Containing Protein

OSJNBb0017F17.13	Silencing Group B Protein	At1g03150	GCN5-Related N-Acetyltransferase (GNAT) Family Protein
OSJNBb0017F17.15	Pescadillo-Like Protein	At5g14520	Pescadillo-Related
OSJNBb0017F17.16	Lethal(2)Denticleless-Like Protein	At3g27640	Transducin Family Protein / WD-40 Repeat Family Protein
OSJNBb0017F17.18	Putative Acyl-Coa Independent Ceramide Synthase	At4g22330	ATCES1 (ATCES1); Catalytic
OSJNBb0017F17.21	Putative Zinc Binding Protein	At2g40110	Yippee Family Protein
OSJNBb0017F17.22	Putative ABC Transporter	At2g40090	ATATH9 (ABC2 Homolog 9)
OSJNBb0017F17.24	Hypothetical Protein, 5'-Partial	At5g14940	Proton-Dependent Oligopeptide Transport (POT) Family Protein
OSJNBb0017I01.22	Unknown Protein	At1g26700	MLO14 (MILDEW RESISTANCE LOCUS O 14); Calmodulin Binding
OSJNBb0017I01.27	Unknown Protein	At3g15380	Choline Transporter-Related
OSJNBb0017I01.6	Unknown Protein	At3g09010	Protein Kinase Family Protein
OSJNBb0017I01.8	Unknown Protein	At3g15450	Unknown Protein
OSJNBb0018A10.13	Unknown Protein	At1g44070	Transposable Element Gene; CACTA-Like Transposase Family (Tnp2/En/Spm),
OSJNBb0018B10.16	Unknown Protein	At4g10790	UBX Domain-Containing Protein
OSJNBb0018B10.19	Putative Trehalase	At4g24040	ATTRE1 (TREHALASE 1); Trehalase
OSJNBb0018B10.27	Putative Shaggy Protein Kinase (5' Partial)	At3g05840	ATSK12 (Arabidopsis Thaliana SHAGGY-Like Kinase 12); Protein Kinase
OSJNBb0018G11.20	Nucleoporin-Like Protein	At1g33410	Unknown Protein
OSJNBb0018H10.28	Putative WD Repeat Protein	At5g14050	Transducin Family Protein / WD-40 Repeat Family Protein
OSJNBb0018J12.16	Unknown Protein	At2g45440	DHDPS2 (DIHYDRODIPICOLINATE SYNTHASE); Dihydrodipicolinate Synthase
OSJNBb0018L13.8	Putative Peroxisome Assembly Protein 10	At2g26350	PEX10 (Peroxin 10); Protein Binding / Zinc Ion Binding
OSJNBb0020J19.1	Unknown Protein	At1g10940	ASK1 (ARABIDOPSIS SERINE/THREONINE KINASE 1); Kinase
OSJNBb0020J19.10	Unknown Protein	At1g77610	Glucose-6-Phosphate/Phosphate Translocator-Related
OSJNBb0020J19.11	Unknown Protein	At3g10220	Tubulin Folding Cofactor B
OSJNBb0020J19.4	Unknown Protein	At5g11570	Proton-Dependent Oligopeptide Transport (POT) Family Protein
OSJNBb0020O11.14	Unknown Protein	At3g47430	Peroxisomal Biogenesis Factor 11 Family Protein / PEX11 Family Protein
OSJNBb0020O11.6	Unknown Protein	At1g12240	ATBETAFRUCT4/VAC-INV (VACUOLAR INVERTASE); Beta-Fructofuranosidase/ Hydrolase, Hydrolyzing O-Glycosyl Compounds
OSJNBb0021A09.5	Unknown Protein	At4g23630	Bti1 (Virb2-Interacting Protein 1)
OSJNBb0021C10.25	Hypothetical Protein	At1g51130	Unknown Protein
OSJNBb0021O11.12	Putative Oxalate Oxidase	At1g18970	GLP4 (GERMIN-LIKE PROTEIN 4); Manganese Ion Binding / Metal Ion Binding / Nutrient Reservoir
OSJNBb0021O11.14	Putative Oxalate Oxidase	At1g18980	Germin-Like Protein, Putative
OSJNBb0021O11.23	Unknown Protein	At1g59650	Cw14
OSJNBb0021O11.3	Putative Valyl Trna Synthetase	At1g14610	TWN2 (TWIN 2); ATP Binding / Aminoacyl-Trna Ligase
OSJNBb0021O11.5	Putative Ribosomal Protein L18	At5g27820	Ribosomal Protein L18 Family Protein
OSJNBb0021O11.8	Putative Permease	At1g49960	Xanthine/Uracil Permease Family Protein
OSJNBb0021P10.3	20S Proteasome Beta 4 Subunit	At4g14800	PBD2 (20S PROTEASOME BETA SUBUNIT 2); Peptidase

OSJNBb0021P10.4	Putative CLC-D Chloride Channel Protein	At5g26240	CLC-D (Chloride Channel D); Anion Channel/ Voltage-Gated Chloride Channel
OSJNBb0022E02.1	Putative FK506-Binding Protein, 5'-Partial	At1g18170	Immunophilin / FKBP-Type Peptidyl-Prolyl Cis-Trans Isomerase Family Protein
OSJNBb0022E02.10	Unknown Protein	At1g18180	Unknown Protein
OSJNBb0022E02.2	Unknown Protein	At1g18470	Zinc Finger (C3HC4-Type RING Finger) Family Protein
OSJNBb0022F16.7	Unknown Protein	At1g22920	AJH1 (COP9-Signalosome 5A)
OSJNBb0022F23.3	Unknown Protein	At2g04780	Fla7 (Fla7)
OSJNBb0022F23.4	Unknown Protein	At4g26690	MRH5/SHV3 (Morphogenesis Of Root Hair 5); Glycerophosphodiester Phosphodiesterase/ Kinase
OSJNBb0022F23.9	Unknown Protein	At5g06850	C2 Domain-Containing Protein
OSJNBb0022I16.5	Putative Cytosolic Trna-Ala Synthetase	At1g50200	ALATS (ALANYL-TRNA SYNTHETASE); ATP Binding / Alanine-Trna Ligase/ Nucleic Acid Binding
OSJNBb0022P19.1	Unknown Protein	At2g47800	ATMRP4 (Arabidopsis Thaliana Multidrug Resistance-Associated Protein 4)
OSJNBb0023M11.20	Putative 1,4-Beta-Xylanase	At4g33830	Glycosyl Hydrolase Family 10 Protein
OSJNBb0024A20.12	Hypothetical Protein	At2g31670	Unknown Protein
OSJNBb0024A20.19	Putative 40S Ribosomal Protein	At2g31610	40S Ribosomal Protein S3 (RPS3A)
OSJNBb0024A20.6	Unknown Protein	At3g22990	Binding
OSJNBb0024B16.2	Putative Ran Binding Protein	At5g19820	EMB2734 (EMBRYO DEFECTIVE 2734); Lyase
OSJNBb0024B16.3	Putative Sugar-Starvation Induced Protein	At2g32150	Haloacid Dehalogenase-Like Hydrolase Family Protein
OSJNBb0024B16.4	Putative Long Chain Fatty Acid Elongation	At3g06470	GNS1/SUR4 Membrane Family Protein
OSJNBb0024B16.5	Ethylene Responsive Factor, 5'-Partial	At1g66340	ETR1 (ETHYLENE RESPONSE 1); Two-Component Response Regulator
OSJNBb0024B16.7	Putative Lipoxygenase	At3g22400	Lipoxygenase, Putative
OSJNBb0024J04.2	Expressed Protein	At3g58520	Unknown Protein
OSJNBb0024J04.20	Putative Calcium-Dependent Protein Kinase	At5g04870	CPK1 (Calcium-Dependent Protein Kinase Isoform AK1); Calcium- And Calmodulin-Dependent Protein Kinase/ Kinase
OSJNBb0024J04.21	Expressed Protein	At2g35860	Beta-Ig-H3 Domain-Containing Protein / Fasciclin Domain-Containing Protein
OSJNBb0024J04.3	Putative N2,N2-Dimethylguanosine Trna	At5g15810	N2,N2-Dimethylguanosine Trna Methyltransferase Family Protein
OSJNBb0024J04.5	Expressed Protein	At5g16280	Binding
OSJNBb0024J04.6	Putative Syntaxin	At3g11820	SYP121 (Syntaxin 121); T-SNARE
OSJNBb0024J04.8	Putative Calmodulin-Binding Protein	At3g22190	IQD5 (IQ-Domain 5); Calmodulin Binding
OSJNBb0024J04.9	Putative Dnaj Like Protein	At3g44110	ATJ3 (Arabidopsis Thaliana Dnaj Homologue 3)
OSJNBb0024J13.13-2	Unknown Protein	At1g80540	Unknown Protein
OSJNBb0024K03.1	Sterol Desaturase-Like	At1g69640	Acid Phosphatase, Putative
OSJNBb0024K03.30	Putative ABA-Responsive Protein	At1g74520	ATHVA22A (Arabidopsis Thaliana HVA22 Homologue A)
OSJNBb0024K03.4	Putative Cullin 3	At1g26830	ATCUL3/ATCUL3A/CUL3/CUL3A (Cullin 3A); Protein Binding / Ubiquitin-Protein Ligase
OSJNBb0026I12.4	Unknown Protein	At1g73370	SUS6; UDP-Glycosyltransferase/ Sucrose Synthase
OSJNBb0026L04.10	Unknown Protein	At1g62860	Hypothetical Protein

OSJNBb0027B08.33	Putative Hydrolase	At4g02340	Epoxide Hydrolase, Putative
OSJNBb0027B08.34	Putative Isomerase	At4g15940	Fumarylacetoacetate Hydrolase Family Protein
OSJNBb0027B08.7	Putative 5'-Phosphoribosyl-5-Aminoimidazole	At3g55010	Phosphoribosylformylglycinamidine Cyclo-Ligase, Chloroplast / Phosphoribosyl-Aminoimidazole Synthetase / AIR Synthase (PUR5)
OSJNBb0027B08.8	Hypothetical Protein	At3g62640	Unknown Protein
OSJNBb0028C01.25	Putative Anthocyanidin Hydroxylase	At1g35190	Oxidoreductase, 2OG-Fe(II) Oxygenase Family Protein
OSJNBb0028C01.26	Unknown Protein	At3g61060	Atpp2-A13
OSJNBb0028C01.28	Putative Shaggy-Like Kinase	At4g00720	Shaggy-Related Protein Kinase Theta / ASK-Theta (ASK8)
OSJNBb0028C01.32	Putative Arm Repeat Containing Protein	At2g45720	Binding
OSJNBb0028C01.45	Hypothetical Protein	At1g74300	Esterase/Lipase/Thioesterase Family Protein
OSJNBb0031B09.19	Putative Multidrug Resistance P-Glycoprotein	At3g28345	ABC Transporter Family Protein
OSJNBb0031B09.22	Putative Lycopene Beta-Cyclase	At3g10230	Lyc (Lycopene Cyclase)
OSJNBb0031B09.25	Putative Cgi67 Serine Protease	At3g01690	Unknown Protein
OSJNBb0031F05.13	Putative Transposase	At1g35590	Transposable Element Gene
OSJNBb0031F05.17	Putative Mechanosensitive Ion Channel Protein	At1g58200	Msl3 (Mscs-Like 3)
OSJNBb0032D24.14	Unknown Protein	At3g15310	Transposable Element Gene
OSJNBb0032E06.11	Unknown Protein	At1g63120	ATRBL2 (ARABIDOPSIS THALIANA RHOMBOID-LIKE 2); Serine-Type Endopeptidase
OSJNBb0032E06.5	Unknown Protein	At1g63170	Zinc Finger (C3HC4-Type RING Finger) Family Protein
OSJNBb0032E06.6	Unknown Protein	At1g63160	Replication Factor C 40 Kda, Putative
OSJNBb0032E06.7	Unknown Protein	At5g17320	Homeobox-Leucine Zipper Family Protein / Lipid-Binding START Domain-Containing Protein
OSJNBb0032E15.114	Putative Myrosinase Precursor	At1g80910	Unknown Protein
OSJNBb0032K15.14	Putative Ketol-Acid Reductoisomerase	At3g58610	Ketol-Acid Reductoisomerase
OSJNBb0032K15.17	Hypothetical Protein	At5g15900	Unknown Protein
OSJNBb0032K15.9	Unknown Protein	At1g29050	Unknown Protein
OSJNBb0033J23.1	Unknown Protein,3'-Partial	At5g27540	EMB2473 (EMBRYO DEFECTIVE 2473); GTP Binding / Calcium Ion Binding
OSJNBb0033J23.12	Putative Cyclophilin	At2g38730	Peptidyl-Prolyl Cis-Trans Isomerase, Putative / Cyclophilin, Putative / Rotamase, Putative
OSJNBb0033J23.13	Putative RNA Binding Protein	At5g12190	RNA Recognition Motif (RRM)-Containing Protein
OSJNBb0033J23.17	Putative DNA Gyrase Subunit	At3g10690	DNA Gyrase Subunit A Family Protein
OSJNBb0033J23.3	Putative Short Chain Alcohol Dehydrogenase	At1g52340	ABA2 (ABA DEFICIENT 2); Oxidoreductase
OSJNBb0033J23.4	Putative Phospholipase	At5g04040	SDP1 (SUGAR-DEPENDENT1); Triacylglycerol Lipase
OSJNBb0033N16.11	Putative Alpha-Coat Protein	At2g21390	Coatomer Protein Complex, Subunit Alpha, Putative
OSJNBb0033N16.16	Putative DNA-Binding Protein	At1g70660	MMZ2 (MMS ZWEI HOMOLOGE 2); Ubiquitin-Protein Ligase
OSJNBb0033N16.3	Putative Protein Kinase	At3g17850	Protein Kinase, Putative
OSJNBb0033N16.4	Putative Receptor Kinase	At3g17840	RLK902 (Receptor-Like Kinase 902); ATP Binding / Kinase/ Protein Serine/Threonine Kinase
OSJNBb0033N16.5	Phosphoglucomutase	At1g70730	Phosphoglucomutase, Cytoplasmic, Putative / Glucose Phosphomutase, Putative

OSJNBb0034G17.19	Unknown Protein	At2g01480	Unknown Protein
OSJNBb0034G17.8	Unknown Protein	At3g57560	Aspartate/Glutamate/Uridylate Kinase Family Protein
OSJNBb0034G17.9	Unknown Protein	At2g44990	CCD7 (More Axillary Growth 3)
OSJNBb0034I13.1	Unknown Protein	At2g20810	GAUT10/LGT4 (Galacturonosyltransferase 10); Polygalacturonate 4-Alpha-Galacturonosyltransferase/ Transferase, Transferring Glycosyl Groups / Transferase, Transferring Hexosyl Groups
OSJNBb0034I13.12	Unknown Protein	At1g01320	Tetratricopeptide Repeat (TPR)-Containing Protein
OSJNBb0034I13.13	Unknown Protein	At5g10030	TGA4 (TGACG MOTIF-BINDING FACTOR 4); DNA Binding / Calmodulin Binding / Transcription Factor
OSJNBb0034I13.21	Unknown Protein	At5g39090	Transferase Family Protein
OSJNBb0034I13.5	Unknown Protein	At5g03250	Phototropic-Responsive NPH3 Family Protein
OSJNBb0035I14.16	Uroporphyrin-III C-Methyltransferase-Like	At5g40850	UPM1 (UROPHORPHYRIN METHYLASE 1); Uroporphyrin-III C-Methyltransferase
OSJNBb0035N08.27	Putative Sds22+	At5g19680	Leucine-Rich Repeat Family Protein
OSJNBb0035N08.29	Unknown Protein	At3g58800	Unknown Protein
OSJNBb0035N08.30	Putative Protodermal Factor	At2g42840	Pdf1 (Protodermal Factor 1)
OSJNBb0035N21.11	Unknown Protein, Contains Hat Family	At3g42170	Transposase
OSJNBb0035N21.12	Unknown Protein, Contains Hat Family	At3g14800	Unknown Protein
OSJNBb0035N21.18	Putative Polyprenyl Diphosphate Synthase,	At1g78510	Solanesyl Diphosphate Synthase (SPS)
OSJNBb0035N21.6	Putative Late Embryogenesis Abundant Protein	At2g46140	Late Embryogenesis Abundant Protein, Putative / LEA Protein, Putative
OSJNBb0036F07.1	Hypothetical Protein	At3g04750	Pentatricopeptide (PPR) Repeat-Containing Protein
OSJNBb0036F07.12	Putative Beige Protein	At1g03060	WD-40 Repeat Family Protein / Beige-Related
OSJNBb0036F07.14	Unknown Protein	At1g62250	Unknown Protein
OSJNBb0036F07.15	Putative Cop-Coated Vesicle Membrane Protein	At3g22845	Emp24/Gp25l/P24 Protein-Related
OSJNBb0036F07.3	Putative Histone H2 Protein	At3g54560	Histone H2A.F/Z
OSJNBb0036F07.7	Putative ATP Sulfurylase	At3g22890	APS1 (ATP Sulfurylase 3)
OSJNBb0036G09.12	Putative NADPH-Dependent FMN And FAD Containing	At3g02280	Flavodoxin Family Protein
OSJNBb0036G09.15	Hypothetical Protein	At1g16740	Ribosomal Protein L20 Family Protein
OSJNBb0036G09.18	Cytochrome B245 Beta Chain Homolog Rboha	At1g64060	ATRBOH F (RESPIRATORY BURST OXIDASE PROTEIN F); NAD(P)H Oxidase
OSJNBb0036G09.3	Putative GTP-Binding Protein	At5g11480	GTP Binding
OSJNBb0036G09.6	Putative Dimethylaniline Monooxygenase	At4g13260	YUC2 (YUCCA2); Monooxygenase/ Oxidoreductase
OSJNBb0037J12.26	Putative Cytosolic Chaperonin Delta-Subunit	At3g18190	Chaperonin, Putative
OSJNBb0038A07.4	Putative Glutathione S-Transferase	At1g59700	ATGSTU16 (Arabidopsis Thaliana Glutathione S-Transferase (Class Tau) 16); Glutathione Transferase
OSJNBb0038A07.5	Putative Glutathione S-Transferase	At1g59670	ATGSTU15 (Arabidopsis Thaliana Glutathione S-Transferase (Class Tau) 15); Glutathione Transferase
OSJNBb0038F03.4	Unknown Protein	At2g19170	SLP3 (Subtilisin-Like Serine Protease 3); Subtilase
OSJNBb0038F20.15-1	Chloride Channel	At5g49890	CLC-C (Chloride Channel C); Anion Channel/ Voltage-Gated Chloride Channel

OSJNBb0038F20.4	Putative NTGP4	At1g33970	GTP Binding
OSJNBb0038H12.1	Putative Ubiquitin-Conjugating Enzyme	At2g18600	RUB1-Conjugating Enzyme, Putative
OSJNBb0038H12.19	Putative Plastidic Phosphoglucomutase	At5g51820	Pgm (Phosphoglucomutase)
OSJNBb0039L24.1	Unknown Protein	At3g61220	Short-Chain Dehydrogenase/Reductase (SDR) Family Protein
OSJNBb0039L24.15	Unknown Protein	At4g25570	ACYB-2 (Arabidopsis Cytochrome B561 -2); Carbon-Monoxide Oxygenase
OSJNBb0039L24.21	Unknown Protein	At1g63420	Unknown Protein
OSJNBb0039L24.7	Unknown Protein	At3g61230	LIM Domain-Containing Protein
OSJNBb0040D15.1	Unknown Protein	At3g58670	Unknown Protein
OSJNBb0040H10.1	Alpha/Beta Hydrolase-Like Protein	At3g29770	Hydrolase, Alpha/Beta Fold Family Protein
OSJNBb0040H10.15	Translocase Inner Membrane-Like Protein	At1g20350	ATTIM17-1 (Arabidopsis Thaliana Translocase Inner Membrane Subunit 17-1); Protein Translocase
OSJNBb0040H10.21	Putative Reversibly Glycosylated Polypeptide	At3g02230	Rgp1 (Reversibly Glycosylated Polypeptide 1)
OSJNBb0040H10.26	MADS Box Protein, MADS2	At1g69120	AP1 (APETALA1); DNA Binding / Transcription Factor
OSJNBb0040H10.5	Putative Cytochrome P-450	At1g74110	CYP78A10 (Cytochrome P450, Family 78, Subfamily A, Polypeptide 10); Oxygen Binding
OSJNBb0040H10.7	Unknown Protein	At5g61370	Pentatricopeptide (PPR) Repeat-Containing Protein
OSJNBb0040H10.9	Putative 6-Phosphogluconolactonase	At1g13700	Glucosamine/Galactosamine-6-Phosphate Isomerase Family Protein
OSJNBb0041A22.12	Putative Inorganic Pyrophosphatase	At3g53620	Inorganic Pyrophosphatase, Putative (Soluble) / Pyrophosphate Phospho-Hydrolase, Putative / Ppase, Putative
OSJNBb0041A22.22	Unknown Protein	At4g22000	Unknown Protein
OSJNBb0041A22.4	Unknown Protein	At2g35030	Pentatricopeptide (PPR) Repeat-Containing Protein
OSJNBb0041A22.5	'Unknown Protein, Contains ACT Domain, PF01842'	At2g39570	ACT Domain-Containing Protein
OSJNBb0041A22.7	Putative Na+/H+ Antiporter	At3g53720	ATCHX20 (CATION/H+ EXCHANGER 20); Monovalent Cation:Proton Antiporter
OSJNBb0041A22.8	Putative Actin-Depolymerizing Factor 1 (Adf 1)	At5g59890	ADF4 (ACTIN DEPOLYMERIZING FACTOR 4); Actin Binding
OSJNBb0041B22.109	Putative S-Receptor Kinase KIK1 Precursor	At4g21390	B120; Protein Kinase/ Sugar Binding
OSJNBb0041J06.115	Putative ATP Synthase Gamma Chain 1, Chloroplast	At4g04640	ATPC1 (ATP Synthase Gamma Chain 1)
OSJNBb0041J20.7	Putative RNA Polymerase III	At5g45140	NRPC2 (Nuclear RNA Polymerase C 2); DNA Binding / DNA-Directed RNA Polymerase
OSJNBb0042J17.1	Unknown Protein	At2g18840	Integral Membrane Yip1 Family Protein
OSJNBb0042J17.15	Putative Pentatricopeptide Repeat-Containing	At2g20540	Pentatricopeptide (PPR) Repeat-Containing Protein
OSJNBb0042J17.6	Putative Tubby Protein	At1g76900	Attlp1 (TUBBY LIKE PROTEIN 1); Phosphoric Diester Hydrolase/ Transcription Factor
OSJNBb0042K11.1	Methylenetetrahydrofolate Reductase, 3-Partial	At3g59970	MTHFR1 (METHYLENETETRAHYDROFOLATE REDUCTASE 1); Methylenetetrahydrofolate Reductase (NADPH)
OSJNBb0042K11.2	Ribosomal Protein L17-Like Protein	At3g54210	Ribosomal Protein L17 Family Protein
OSJNBb0042N11.19	Putative Cytochrome P450	At3g26320	CYP71B36 (Cytochrome P450, Family 71, Subfamily B, Polypeptide 36); Oxygen Binding
OSJNBb0043C10.11	Putative 40S Ribosomal Protein S17	At3g10610	40S Ribosomal Protein S17 (RPS17C)
OSJNBb0043C10.12	Putative Homeodomain-Leucine Zipper Protein	At5g60690	REV (REVOLUTA); DNA Binding / Lipid Binding / Transcription Factor
OSJNBb0043C10.13	Putative Lysine Decarboxylase-Like Protein	At3g53450	Unknown Protein

OSJNBb0043H09.9	Unknown Protein	At5g42150	Electron Carrier/ Protein Disulfide Oxidoreductase
OSJNBb0043H23.1	Unknown Protein	At1g16560	Per1-Like Family Protein
OSJNBb0043H23.11	Putative ATP-Dependent Transmembrane	At1g51500	CER5 (ECERIFERUM 5); Atpase, Coupled To Transmembrane Movement Of Substances
OSJNBb0043H23.7	Unknown Protein	At5g11500	Unknown Protein
OSJNBb0043P23.23	Putative RNA Polymerase	At3g59600	DNA-Directed RNA Polymerase I, II, And III, Putative
OSJNBb0043P23.8	Putative Protein Kinase	At4g13020	MHK; Kinase
OSJNBb0044B19.2	Putative Casein Kinase	At3g23340	CKL10 (Casein Kinase I-Like 10); Casein Kinase I/ Kinase
OSJNBb0044B19.4	Putative Polyubiquitin	At5g20620	UBQ4 (Ubiquitin 4); Protein Binding
OSJNBb0044B19.7	Hypothetical Protein	At1g03950	SNF7 Family Protein
OSJNBb0044I14.4	Putative Serine /Threonine Kinase Similar To	At2g02800	APK2B (PROTEIN KINASE 2B); Kinase
OSJNBb0044I14.9	Putative Sucrose Transporter	At1g22710	SUC2 (SUCROSE-PROTON SYMPORTER 2); Carbohydrate Transporter/ Sucrose:Hydrogen Symporter/ Sugar Porter
OSJNBb0046O12.20	Glycerophosphoryl Diester Phosphodiesterase 2	At1g66980	Protein Kinase Family Protein / Glycerophosphoryl Diester Phosphodiesterase Family Protein
OSJNBb0048A17.1	Casein Kinase II Alpha Subunit, 5'-Partial	At5g67380	CKA1 (CASEIN KINASE ALPHA 1); Kinase
OSJNBb0048A17.10	Unknown Protein	At1g77360	Pentatricopeptide (PPR) Repeat-Containing Protein
OSJNBb0048A17.11	Putative Serine Protease	At5g67360	ARA12; Subtilase
OSJNBb0048A17.17	Putative Cytochrome P450	At4g37360	CYP81D2 (Cytochrome P450, Family 81, Subfamily D, Polypeptide 2); Oxygen Binding
OSJNBb0048A17.2	Translation Initiation Factor 5A	At1g69410	Eukaryotic Translation Initiation Factor 5A, Putative / Eif-5A, Putative
OSJNBb0048A17.4	Putative Cytochrome P450	At4g37320	CYP81D5 (Cytochrome P450, Family 81, Subfamily D, Polypeptide 5); Oxygen Binding
OSJNBb0048A17.5	Unknown Protein	At4g34270	TIP41-Like Family Protein
OSJNBb0048A17.6	Putative Dehydrogenase Precursor	At1g14810	Semialdehyde Dehydrogenase Family Protein
OSJNBb0048A17.8	Putative Protein Phosphatase	At4g33920	Protein Phosphatase 2C Family Protein / PP2C Family Protein
OSJNBb0048A17.9	Putative Methyltransferase	At5g65860	Protein Binding
OSJNBb0048D20.14	Alpha-Expansin	At2g03090	Atexpa15 (Arabidopsis Thaliana Expansin A15)
OSJNBb0048D20.7	Putative Amino Acid Transporter	At3g13620	Amino Acid Permease Family Protein
OSJNBb0048D20.9	Putative Cystathionine Gamma Synthase	At3g01120	Mto1 (Methionine Overaccumulation 1)
OSJNBb0048E02.1	Unknown Protein	At4g22150	Pux3 (Lant Ubx Domain-Containing Protein 3)
OSJNBb0048E02.12	Unknown Protein	At1g24020	Bet V I Allergen Family Protein
OSJNBb0048E02.13	Unknown Protein	At4g11130	RDR2 (RNA-DEPENDENT RNA POLYMERASE 2); RNA-Directed RNA Polymerase
OSJNBb0048E02.7	Unknown Protein	At5g47000	Peroxidase, Putative
OSJNBb0048I21.10	Putative Deoxyribonucleoside Kinase	At1g72040	Deoxynucleoside Kinase Family
OSJNBb0048I21.11	Unknown Protein	At1g34320	Hypothetical Protein
OSJNBb0048I21.12	Putative GTP-Binding Protein	At4g02790	GTP-Binding Family Protein
OSJNBb0048I21.13	Unknown Protein	At2g21120	Unknown Protein
OSJNBb0048I21.14	Putative Amidophosphoribosyltransferase	At2g16570	ATASE (GLN PHOSPHORIBOSYL PYROPHOSPHATE AMIDOTRANSFERASE 1); Amidophosphoribosyltransferase

OSJNBb0048I21.15	Putative Oligopeptide Transporter	At2g02020	Proton-Dependent Oligopeptide Transport (POT) Family Protein
OSJNBb0048I21.6	Putative Dienelactone Hydrolase	At1g35420	Dienelactone Hydrolase Family Protein
OSJNBb0048I21.7	Putative Anthranilate Phosphoribosyltransferase	At1g22610	C2 Domain-Containing Protein
OSJNBb0048O22.2	Unknown Protein	At1g27530	Unknown Protein
OSJNBb0048O22.3	Putative Phosphoenolpyruvate Carboxykinase	At4g37870	ATP Binding / Phosphoenolpyruvate Carboxykinase (ATP)
OSJNBb0048O22.8	Putatputative ABC Transporter	At2g29940	ATPDR3/PDR3 (PLEIOTROPIC DRUG RESISTANCE 3); Atpase, Coupled To Transmembrane Movement Of Substances
OSJNBb0049A16.3	Putative Myosin	At3g19960	ATATM (Myosin 1); Motor
OSJNBb0049A16.4	Putative C-Myc Binding Protein	At5g23290	C-Myc Binding Protein, Putative / Prefoldin, Putative
OSJNBb0050N02.3	Unknown Protein	At3g49070	Unknown Protein
OSJNBb0050O03.10	Unknown Protein	At3g17360	POK1 (PHRAGMOPLAST ORIENTING KINESIN 1); Microtubule Motor
OSJNBb0050O03.11	Unknown Protein	At5g19610	Sec7 Domain-Containing Protein
OSJNBb0050O03.15	Unknown Protein	At4g38890	Dihydrouridine Synthase Family Protein
OSJNBb0050O03.5	Unknown Protein	At1g24470	Short-Chain Dehydrogenase/Reductase (SDR) Family Protein
OSJNBb0051N19.2	Unknown Protein	At2g23000	SCPL10 (Serine Carboxypeptidase-Like 10); Serine Carboxypeptidase
OSJNBb0052C09.16	Putative Integral Membrane Protein	At5g52450	MATE Efflux Protein-Related
OSJNBb0053G03.10	Putative Nuclear Matrix Constituent Protein 1	At1g13220	Nuclear Matrix Constituent Protein-Related
OSJNBb0053G03.17	Putative Regulatory Protein NPR1 (Nonexpresser	At5g45110	NPR3 (NPR1-LIKE PROTEIN 3); Protein Binding
OSJNBb0053G03.3	Hypothetical Protein	At2g24970	Unknown Protein
OSJNBb0054B09.7	Unknown Protein	At1g20390	Hypothetical Protein
OSJNBb0055I24.101	Leaf Senescence Related Protein-Like	At2g14530	Unknown Protein
OSJNBb0055I24.109	Putative Peroxidase Prx15 Precursor	At1g30870	Cationic Peroxidase, Putative
OSJNBb0055I24.131	Chitinase III-Like Protein	At1g70800	C2 Domain-Containing Protein
OSJNBb0056B16.16	Putative Vps52 / Sac2 Family Protein	At1g71270	Pok (Poky Pollen Tube)
OSJNBb0056F09.6	Unknown Protein	At5g12890	UDP-Glucoronosyl/UDP-Glucosyl Transferase Family Protein
OSJNBb0056I22.32	Putative GTP-Binding Protein Yptm3	At4g17170	AT-RAB2 (Arabidopsis Rab Gtpase Homolog B1c); GTP Binding
OSJNBb0057P11.2	Putative Chelatase Subunit	At5g45930	CHLI2; Magnesium Chelatase
OSJNBb0058B20.18	Putative Cell Elongation Protein DIMINUTO (Cell	At3g19820	DWF1 (DIMINUTO 1); Catalytic
OSJNBb0058B20.19	Putative Transcription Initiation Factor IIE,	At4g20330	Transcription Initiation Factor-Related
OSJNBb0058B20.9	Putative Disease Resistance Response Protein	At1g65870	Disease Resistance-Responsive Family Protein
OSJNBb0059K02.12	Unknown Protein	At1g59840	Unknown Protein
OSJNBb0059K02.13	Unknown Protein	At3g50100	Exonuclease Family Protein
OSJNBb0059K02.15	Unknown Protein	At4g34200	EDA9 (Embryo Sac Development Arrest 9); NAD Binding / Amino Acid Binding / Cofactor Binding / Oxidoreductase, Acting On The CH-OH Group Of Donors, NAD Or NADP As Acceptor / Phosphoglycerate Dehydrogenase
OSJNBb0059K02.16	Unknown Protein	At5g13690	Alpha-N-Acetylglucosaminidase Family / NAGLU Family

OSJNBb0059K02.23	Unknown Protein	At1g23090	AST91 (SULFATE TRANSPORTER 91); Sulfate Transporter
OSJNBb0059K02.8	Unknown Protein	At1g47128	Cysteine Proteinase (RD21A) / Thiol Protease
OSJNBb0059K02.9	Unknown Protein	At1g53920	GLIP5 (GDSL-Motif Lipase 5); Carboxylic Ester Hydrolase
OSJNBb0060E08.16	Unknown Protein	At1g05230	Homeobox-Leucine Zipper Family Protein / Lipid-Binding START Domain-Containing Protein
OSJNBb0060I05.12	Hypothetical Protein	At1g63830	Proline-Rich Family Protein
OSJNBb0060I05.3	Putative Transcription Factor	At4g11880	AGL14 (AGAMOUS-LIKE 14); DNA Binding / Transcription Factor
OSJNBb0060J21.1	Putative Ribosomal Protein S18A	At4g09800	RPS18C (S18 RIBOSOMAL PROTEIN); Structural Constituent Of Ribosome
OSJNBb0060J21.12	Putative Serine/Threonine Protein Kinase	At5g18190	Protein Kinase Family Protein
OSJNBb0060J21.16	Putative Zinc Finger Protein	At2g36320	Zinc Finger (AN1-Like) Family Protein
OSJNBb0060J21.19	Putative Beta-1,3 Glucanase	At2g19440	Glycosyl Hydrolase Family 17 Protein
OSJNBb0060J21.2	Glutamate Dehydrogenase	At5g18170	GDH1 (GLUTAMATE DEHYDROGENASE 1); Oxidoreductase
OSJNBb0060J21.20	Putative Replication Factor	At5g27740	Nucleoside-Triphosphatase/ Nucleotide Binding
OSJNBb0060J21.21	Expressed Protein	At3g03740	ATBPM4 (BTB-POZ AND MATH DOMAIN 4); Protein Binding
OSJNBb0060J21.23	Expressed Protein	At5g35220	EGY1 (ETHYLENE-DEPENDENT GRAVITROPISM-DEFICIENT AND YELLOW-GREEN 1); Sterol Regulatory Element-Binding Protein Site 2 Protease
OSJNBb0060J21.31	Putative Vesicle Trafficking Protein	At1g11890	SEC22 (Secretion 22); Transporter
OSJNBb0060J21.5	Putative Acetyltransferase	At2g32030	GCN5-Related N-Acetyltransferase (GNAT) Family Protein
OSJNBb0060M15.2	Unknown Protein	At1g19920	Aps2 (Atp Sulfurylase Precursor)
OSJNBb0060O16.24	Ethylene-Responsive Protein-Like	At5g14680	Universal Stress Protein (USP) Family Protein
OSJNBb0060O16.25-3	Carbamoyl-Phosphate Synthetase Small	At3g27740	Cara (Carbamoyl Phosphate Synthetase A)
OSJNBb0060O16.26	Uridine Kinase-Like Protein	At1g26190	Phosphoribulokinase/Uridine Kinase Family Protein
OSJNBb0060O16.28	Putative Kinesin Light Chain	At1g27500	Kinesin Light Chain-Related
OSJNBb0060O16.41	Putative Histidinol-Phosphate Transaminase	At5g10330	Emb2196 (Embryo Defective 2196)
OSJNBb0061C13.16	Unknown Protein	At5g20660	24 Kda Vacuolar Protein, Putative
OSJNBb0061C13.5	Unknown Protein	At3g53260	PAL2 (Phenylalanine Ammonia-Lyase 2); Phenylalanine Ammonia-Lyase
OSJNBb0061I18.14	Conserved Unknown Protein With Similarity To	At1g72320	APUM23 (ARABIDOPSIS PUMILIO 23); RNA Binding
OSJNBb0061I18.20	Putative Red Chlorophyll Catabolite Reductase	At4g37000	Acd2 (Accelerated Cell Death 2)
OSJNBb0062D12.107	Unknown Protein	At4g21570	Unknown Protein
OSJNBb0062D12.120	Hypothetical Protein	At5g58040	ATFIP1[V] (ARABIDOPSIS HOMOLOG OF YEAST FIP1 [V]); RNA Binding
OSJNBb0062D12.125	Putative Protein Phosphatase Type 2C	At3g15260	Protein Phosphatase 2C, Putative / PP2C, Putative
OSJNBb0062D12.129-2	Putative MAP4 Kinase	At3g15220	Protein Kinase, Putative
OSJNBb0062G19.12	Putative Acyl Carrier Protein	At1g54630	Acp3 (Acyl Carrier Protein 3)
OSJNBb0062G19.5	Expressed Protein	At5g42960	Unknown Protein
OSJNBb0062G19.9	Putative Carboxylate Oxidase	At1g17020	SRG1 (SENESCENCE-RELATED GENE 1); Oxidoreductase, Acting On Paired Donors, With Incorporation Or Reduction Of Molecular Oxygen, 2-Oxoglutarate As One Donor, And

			Incorporation Of One Atom Each Of Oxygen Into Both Donors
OSJNBb0062H02.1	Unknown Protein	At5g15220	Ribosomal Protein L27 Family Protein
OSJNBb0062H02.10	Unknown Protein	At4g04510	Protein Kinase Family Protein
OSJNBb0062H02.2	Unknown Protein	At4g10710	SPT16 (GLOBAL TRANSCRIPTION FACTOR C); Metalloexopeptidase
OSJNBb0062H02.3	Unknown Protein	At3g25420	SCPL21 (Serine Carboxypeptidase-Like 21); Serine Carboxypeptidase
OSJNBb0062P14.106	Putative Cytochrome P450 77A3	At2g42250	CYP712A1 (Cytochrome P450, Family 712, Subfamily A, Polypeptide 1); Oxygen Binding
OSJNBb0062P14.116-1	Putative ORMDL2	At1g01230	ORMDL Family Protein
OSJNBb0064I19.17	Cyt-P450 Monooxygenase	At2g45570	CYP76C2 (Cytochrome P450, Family 76, Subfamily C, Polypeptide 2); Oxygen Binding
OSJNBb0064I19.32	Unknown Protein	At5g27990	Unknown Protein
OSJNBb0064P21.2	Calcium-Dependent Protein Kinase	At2g17290	CPK6 (CALCIUM-DEPENDENT PROTEIN KINASE 6); Anion Channel/ Calcium- And Calmodulin-Dependent Protein Kinase/ Kinase
OSJNBb0064P21.3	Putative Sugar Transporter	At4g35300	TMT2 (TONOPLAST MONOSACCHARIDE TRANSPORTER2); Carbohydrate Transporter/ Sugar Porter
OSJNBb0065J09.13	Unknown Protein	At5g22790	Rer1 (Reticulata-Related 1)
OSJNBb0065J09.8	Unknown Protein	At3g53150	UGT73D1 (UDP-Glucosyl Transferase 73D1); UDP-Glycosyltransferase
OSJNBb0065L13.7	Unknown Protein	At4g13510	AMT1;1 (AMMONIUM TRANSPORT 1); Ammonium Transporter
OSJNBb0066C12.30	Putative Apoplastic Invertase	At1g55120	ATFRUCT5 (BETA-FRUCTOFURANOSIDASE 5); Hydrolase, Hydrolyzing O-Glycosyl Compounds / Levanase
OSJNBb0067G11.10	Unknown Protein	At1g18070	Translation Factor, Nucleic Acid Binding
OSJNBb0067G11.11	Unknown Protein	At5g55940	Emb2731 (Embryo Defective 2731)
OSJNBb0067G11.13	Unknown Protein	At5g55760	SRT1 (SIRTUIN 1); DNA Binding
OSJNBb0067G11.14	Unknown Protein	At5g10480	Pas2 (Pasticcino 2)
OSJNBb0067H15.19	'Unknown Protein, Contains BURP Domain,	At5g25610	Rd22 (Responsive To Dessication 22)
OSJNBb0070J16.2	Unknown Protein	At4g21760	BGLU47 (Beta-Glucosidase 47); Hydrolase, Hydrolyzing O-Glycosyl Compounds
OSJNBb0070J16.3	Unknown Protein	At1g61820	BGLU46; Hydrolase, Hydrolyzing O-Glycosyl Compounds
OSJNBb0070O09.2	Unknown Protein	At3g18140	Nucleotide Binding
OSJNBb0070O09.3	Putative Protein Phosphatase 2A Regulatory	At3g09880	ATB' BETA (Arabidopsis Thaliana Serine/Threonine Protein Phosphatase 2A 55 Kda Regulatory Subunit B Prime Beta); Protein Phosphatase Type 2A Regulator
OSJNBb0070O09.5	Hypothetical Protein	At2g28120	Nodulin Family Protein
OSJNBb0071D01.2	Unknown Protein	At1g76020	Unknown Protein
OSJNBb0072E24.1	Putative Angio-Associated Migratory Cell	At4g02730	Transducin Family Protein / WD-40 Repeat Family Protein
OSJNBb0072E24.15	Putative Ubiquitin Protein Ligase	At3g53090	UPL7 (Ubiquitin-Protein Ligase 7); Ubiquitin-Protein Ligase
OSJNBb0072E24.2	Putative Glutamine Synthetase	At4g30550	Glutamine Amidotransferase Class-I Domain-Containing Protein
OSJNBb0072E24.7	Putative Proline-Rich Protein	At5g03820	GDSL-Motif Lipase/Hydrolase Family Protein
OSJNBb0072M01.1	Unknown Protein	At3g09040	Pentatricopeptide (PPR) Repeat-Containing Protein
OSJNBb0072M01.6	Unknown Protein	At5g44100	CKL7 (Casein Kinase I-Like 7); Casein Kinase I/ Kinase

OSJNBb0072M01.9	Unknown Protein	At2g20450	60S Ribosomal Protein L14 (RPL14A)
OSJNBb0073N24.1	Putative Glutamyl-Trna Reductase	At1g58290	HEMA1; Glutamyl-Trna Reductase
OSJNBb0073N24.11	Putative Hypersensitivity-Related (Hsr)Protein	At5g17540	Transferase Family Protein
OSJNBb0073N24.22	Putative Rhizobium-Induced Nodule Development	At3g48880	F-Box Family Protein
OSJNBb0073N24.9	Putative LIM Domain Protein	At1g01780	LIM Domain-Containing Protein
OSJNBb0074M06.14	Putative Polyprotein	At3g61330	Transposable Element Gene
OSJNBb0074M06.8	Putative Trypanothione-Dependent Peroxidase	At1g60420	DC1 Domain-Containing Protein
OSJNBb0075E08.37	Putative DNA-Binding Protein AT-Hook 2	At4g22810	DNA-Binding Protein-Related
OSJNBb0075O18.121	Osh45	At5g25220	Knat3 (Knotted1-Like Homeobox Gene 3)
OSJNBb0076A22.1	Unknown Protein	At1g80570	F-Box Family Protein (FBL14)
OSJNBb0076H04.26	Putative Trna (Guanine-N2-)-Methyltransferase,	At3g02320	RNA Binding / Trna (Guanine-N2-)-Methyltransferase
OSJNBb0076H04.3	Putative Mannitol Transporter Protein	At2g18480	Mannitol Transporter, Putative
OSJNBb0076N15.1	Putative Lipoxygenase	At1g72520	Lipoxygenase, Putative
OSJNBb0076N15.12	Putative Fiddlehead-Like Protein	At2g26250	FDH (FIDDLEHEAD); Acyltransferase
OSJNBb0076N15.5	Putative Alpha 1 Subunit Of 20S Proteasome	At2g05840	PAA2 (20S Proteasome Alpha Subunit A2); Peptidase
OSJNBb0076O03.29	RNA Helicase-Like	At1g32490	EMB2733/ESP3 (EMBRYO DEFECTIVE 2733); ATP-Dependent RNA Helicase
OSJNBb0078D11.10	Unknown Protein	At4g35620	CYCB2;2 (CYCLIN B2;2); Cyclin-Dependent Protein Kinase Regulator
OSJNBb0078D11.5	Unknown Protein	At1g76270	Unknown Protein
OSJNBb0079B02.14	Unknown Protein	At5g62500	ATEB1B (Arabidopsis Thaliana Microtubule End Binding Protein EB1A); Microtubule Binding
OSJNBb0079B02.2	Unknown Protein	At2g21940	ATP Binding / Shikimate Kinase
OSJNBb0079B02.3	Unknown Protein	At5g64570	XYL4 (Beta-Xylosidase 4); Hydrolase, Hydrolyzing O-Glycosyl Compounds
OSJNBb0079B02.9	Unknown Protein	At1g14340	RNA Recognition Motif (RRM)-Containing Protein
OSJNBb0079B16.5	Putative Pentatricopeptide Repeat Protein	At5g66500	Pentatricopeptide (PPR) Repeat-Containing Protein
OSJNBb0079L11.8	Putative Isovaleryl-Coa Dehydrogenase	At3g45300	Ivd (Isovaleryl-Coa-Dehydrogenase)
OSJNBb0080H08.21	Unknown Protein	At3g07020	UDP-Glucose:Sterol Glucosyltransferase (UGT80A2)
OSJNBb0080H08.3	Unknown Protein	At1g60500	Dynamin Family Protein
OSJNBb0081B07.10	Ras-Related GTP-Binding Protein	At1g07410	Atraba2b (Arabidopsis Rab Gtpase Homolog A2b); GTP Binding
OSJNBb0081B07.12	Putative Peptide Transport Protein	At3g53960	Proton-Dependent Oligopeptide Transport (POT) Family Protein
OSJNBb0081B07.15	Putative Sugar Transporter Protein	At5g59250	Sugar Transporter Family Protein
OSJNBb0081B07.16	Putative Receptor-Like Protein Kinase	At3g53810	Lectin Protein Kinase, Putative
OSJNBb0081B07.19	Putative Hsp70 Binding Protein	At3g53800	Armadillo/Beta-Catenin Repeat Family Protein
OSJNBb0081B07.22	Unknown Protein	At2g37660	Catalytic/ Coenzyme Binding
OSJNBb0081B07.24	Alpha-Expansin	At2g39700	Atexpa4 (Arabidopsis Thaliana Expansin A4)
OSJNBb0081B07.25	Putative Protein Kinase	At2g28930	APK1B (Arabidopsis Protein Kinase 1B); Kinase
OSJNBb0081B07.5	Unknown Protein	At3g13440	Hypothetical Protein

OSJNBb0081B07.6	Putative Chloroplast RNA Processing Protein	At1g74850	PTAC2 (PLASTID TRANSCRIPTIONALLY ACTIVE2); Binding
OSJNBb0081F12.23	Unknown Protein	At5g62290	Nucleotide-Sensitive Chloride Conductance Regulator (Icln) Family Protein
OSJNBb0081K01.19	Putative ABC (ATP-Binding Cassette) Transporter	At5g39040	ATTAP2 (Arabidopsis Thaliana Transporter Associated With Antigen Processing Protein 2); Atpase, Coupled To Transmembrane Movement Of Substances
OSJNBb0081K01.23	Putative Phytochelatin Synthetase, 3'-Partial	At3g02210	Phytochelatin Synthetase Family Protein / COBRA Cell Expansion Protein COBL3
OSJNBb0081K01.9	Putative Ribosomal Protein L13a	At5g48760	60S Ribosomal Protein L13A (RPL13aD)
OSJNBb0084L07.12	Methylmalonate Semi-Aldehyde Dehydrogenase	At2g14170	ALDH6B2 (Aldehyde Dehydrogenase 6B2)
OSJNBb0084L07.3	Putative Nodule-Specific Protein	At2g39210	Nodulin Family Protein
OSJNBb0085C12.13	Unknown Protein	At3g27260	GTE8 (GLOBAL TRANSCRIPTION FACTOR GROUP E8); DNA Binding
OSJNBb0085C12.17	Unknown Protein	At2g43020	ATPAO2 (POLYAMINE OXIDASE 2); Amine Oxidase
OSJNBb0085F13.1	Unknown Protein	At1g62780	Unknown Protein
OSJNBb0085F13.13	Unknown Protein	At1g12550	Oxidoreductase Family Protein
OSJNBb0085F13.14	Unknown Protein	At2g16500	Adc1 (Arginine Decarboxylase 1)
OSJNBb0085F13.17	Unknown Protein	At5g52640	HSP81-1 (HEAT SHOCK PROTEIN 81-1); ATP Binding / Unfolded Protein Binding
OSJNBb0085F13.5	Unknown Protein	At4g08900	Arginase
OSJNBb0085I16.13	Unknown Protein	At1g53400	Unknown Protein
OSJNBb0085I16.26	ATP-NAD Kinase Protein-Like	At1g78590	ATNADK-3/NADK3 (NAD(H) Kinase 3); NAD+ Kinase/ NADH Kinase
OSJNBb0085I16.5	Flavonoid 7-O-Methyltransferase-Like	At1g33030	O-Methyltransferase Family 2 Protein
OSJNBb0086G13.14	Unknown Protein	At1g77290	Tetrachloro-P-Hydroquinone Reductive Dehalogenase-Related
OSJNBb0086G13.15	Unknown Protein	At5g63860	Uvr8 (Uvb-Resistance 8)
OSJNBb0086G17.10	Putative SMC5 Protein	At5g15920	Structural Maintenance Of Chromosomes (SMC) Family Protein (MSS2)
OSJNBb0088C09.12	Unknown Protein	At1g43580	Unknown Protein
OSJNBb0088N06.1	Putative Adenosine Monophosphate Binding	At1g20560	AMP-Dependent Synthetase And Ligase Family Protein
OSJNBb0088N06.11	Putative Serine/Threonine Protein Kinase	At2g17700	Protein Kinase Family Protein
OSJNBb0088N06.16	Ubiquitin-Conjugating Enzyme	At4g27960	UBC9 (UBIQUITIN CONJUGATING ENZYME 9); Ubiquitin-Protein Ligase
OSJNBb0088N06.17	Small GTP-Binding Protein RACBP	At3g51300	ARAC11/Atrop1/ROP1/ROP1AT (Rho-Related Protein From Plants 1); GTP Binding / Gtpase/ Protein Binding
OSJNBb0088N06.19	Putative Glutamate-Trna Ligase	At5g64050	ATERS/ERS/OVA3 (OVULE ABORTION 3); Glutamate-Trna Ligase
OSJNBb0088N06.2	Unknown Protein	At5g42320	Zinc Carboxypeptidase Family Protein
OSJNBb0088N06.23	Peptidylprolyl Isomerase Cyp2	At2g21130	Peptidyl-Prolyl Cis-Trans Isomerase / Cyclophilin (CYP2) / Rotamase
OSJNBb0088N06.3	Putative Syntaxin Of Plants 52	At1g16240	Syp51 (Syntaxin Of Plants 51)
OSJNBb0088N06.8	Putative Aminoalcoholphosphotransferase	At1g13560	AAPT1 (AMINOALCOHOLPHOSPHOTRANSFERASE 1); Phosphatidyltransferase
OSJNBb0089A17.11	Putative Hexose Carrier Protein	At5g61520	Hexose Transporter, Putative
OSJNBb0089A17.2	Putative Protein Kinase	At5g61550	Protein Kinase Family Protein
OSJNBb0089A17.8	Putative Myb-Related Protein	At5g61620	Myb Family Transcription Factor
OSJNBb0089A17.9	Unknown Protein	At4g17430	Unknown Protein

OSJNBb0089B03.4	Unknown Protein	At1g08550	Npq1 (Non-Photochemical Quenching 1)
OSJNBb0089B03.6	Unknown Protein	At2g43710	SSI2 (Fatty Acid Biosynthesis 2); Acyl-[Acyl-Carrier-Protein] Desaturase
OSJNBb0089F16.6	Unknown Protein	At5g55510	Protein Translocase
OSJNBb0089K06.20	Unknown Protein	At3g04580	Ein4 (Ethylene Insensitive 4)
OSJNBb0089K24.8	Unknown Protein	At1g58190	Leucine-Rich Repeat Family Protein
OSJNBb0091E11.23	Unknown Protein	At3g07570	Membrane Protein, Putative
OSJNBb0091E11.4	Unknown Protein	At4g34530	Basic Helix-Loop-Helix (Bhlh) Family Protein
OSJNBb0091N21.27	Putative Stress-Responsive Protein	At5g62350	Invertase/Pectin Methylesterase Inhibitor Family Protein / DC 1.2 Homolog (FL5-2I22)
OSJNBb0091N21.29	Putative Methionine Aminopeptidase	At2g45240	MAP1A (METHIONINE AMINOPEPTIDASE 1A); Methionyl Aminopeptidase
OSJNBb0091N21.33	Unknown Protein	At3g49550	Unknown Protein
OSJNBb0092C08.10	Putative Tawin2	At1g78300	GRF2 (GENERAL REGULATORY FACTOR 2); Protein Phosphorylated Amino Acid Binding
OSJNBb0092C08.2	Putative Flavonol Synthase	At4g10490	Oxidoreductase, 2OG-Fe(II) Oxygenase Family Protein
OSJNBb0092C08.24	Putative Avr9/Cf-9 Rapidly Elicited Protein	At5g42340	Binding / Ubiquitin-Protein Ligase
OSJNBb0092C08.31	Putative Glutamate/Malate Translocator	At5g64290	DCT/DIT2.1 (DICARBOXYLATE TRANSPORT); Oxoglutarate:Malate Antiporter
OSJNBb0092C08.34	Putative Riboflavin Biosynthesis Protein Riba	At5g64300	ATGCH (Arabidopsis Thaliana GTP Cyclohydrolase II); 3,4-Dihydroxy-2-Butanone-4-Phosphate Synthase/ GTP Cyclohydrolase II
OSJNBb0092C08.9	Unknown Protein	At1g16430	Surfeit Locus Protein 5 Family Protein / SURF5 Family Protein
OSJNBb0092E21.11	Putative Gibberellin 20-Oxidase	At5g07200	YAP169 (Gibberellin 20 Oxidase 3); Gibberellin 20-Oxidase
OSJNBb0092E21.3	Cytochrome C	At4g10040	CYTC-2 (CYTOCHROME C-2); Electron Carrier
OSJNBb0092E21.8	Putative Tetratricopeptide Repeat	At5g10200	Binding
OSJNBb0092G21.1	Unknown Protein	At5g05480	Unknown Protein
OSJNBb0092G21.11	Unknown Protein	At5g19080	Zinc Finger (C3HC4-Type RING Finger) Family Protein
OSJNBb0092G21.15	Unknown Protein	At3g63120	CYCP1;1 (Cyclin P1;1); Cyclin-Dependent Protein Kinase
OSJNBb0092G21.7	Unknown Protein	At3g06150	Unknown Protein
OSJNBb0093E13.1	Unknown Protein	At3g22290	Unknown Protein
OSJNBb0093E13.11	Putative Clathrin Assembly Protein	At4g35410	Clathrin Adaptor Complex Small Chain Family Protein
OSJNBb0093E13.2	Ferredoxin-NADP+ Reductase	At1g30510	ATRFNR2 (ROOT FNR 2); Oxidoreductase
OSJNBb0093E13.3	Putative Cell Differentiation Protein	At3g20800	Rcd1-Like Cell Differentiation Protein, Putative
OSJNBb0093G06.10	Unknown Protein	At2g16850	PIP2;8/PIP3B (Plasma Membrane Intrinsic Protein 2;8); Water Channel
OSJNBb0094K03.15	Unknown Protein	At3g24180	Catalytic
OSJNBb0094K03.17	Putative ATP-Dependent RNA Helicase	At2g35920	Helicase Domain-Containing Protein
OSJNBb0094O03.14	Putative Kinesin-Like Protein	At3g49650	Kinesin Motor Protein-Related
OSJNBb0094O03.16	Putative Glyoxysomal Malate Dehydrogenase	At5g09660	Pmdh2 (Peroxisomal Nad-Malate Dehydrogenase 2)
OSJNBb0094P23.28	Putative GTP-Binding Protein	At1g30580	GTP Binding
OSJNBb0094P23.29	Putative Acyl-[Acyl-Carrier Protein] Desaturase,	At3g02610	Acyl-[Acyl-Carrier-Protein] Desaturase

OSJNBb0095H08.30	Putative Tyrosine Decarboxylase	At2g20340	Tyrosine Decarboxylase, Putative
OSJNBb0095H08.9	Hypothetical Protein	At1g04780	Ankyrin Repeat Family Protein
OSJNBb0096M04.115	Unknown Protein	At5g48660	Unknown Protein
OSJNBb0096M04.130	Putative Phytase	At3g07130	ATPAP15/PAP15 (Purple Acid Phosphatase 15); Acid Phosphatase/ Protein Serine/Threonine Phosphatase
OSJNBb0096M04.15	Putative Cytochrome P450	At3g26330	CYP71B37 (Cytochrome P450, Family 71, Subfamily B, Polypeptide 37); Oxygen Binding
OSJNBb0096M04.25	Putative Reductase	At3g01980	Short-Chain Dehydrogenase/Reductase (SDR) Family Protein
OSJNBb0096M04.40	Hypothetical Protein	At3g18840	Binding
OSJNBb0096M04.45	Putative Conserved Oligomeric Golgi Complex	At4g24840	Unknown Protein
OSJNBb0099O15.10	Putative Cation/Hydrogen Exchanger (CHX6a)	At2g13620	ATCHX15 (Cation/Hydrogen Exchanger 15); Monovalent Cation:Proton Antiporter
OSJNBb0099O15.15	Putative L-Ascorbate Oxidase	At3g13390	SKS11 (SKU5 Similar 11); Copper Ion Binding / Oxidoreductase
OSJNBb0099O15.8	Unknown Protein	At5g20640	Unknown Protein
OSJNBb0099P06.1	Unknown Protein	At3g17470	Rela/Spot Domain-Containing Protein / Calcium-Binding EF-Hand Family Protein
OSJNBb0099P06.11	Putative Glutaryl-Coa Dehydrogenase	At3g51840	ACX4 (ACYL-COA OXIDASE 4); Oxidoreductase
OSJNBb0099P06.14	'Putative 6-Phosphofructo-2-Kinase (EC	At1g07110	F2KP (FRUCTOSE-2,6-BISPHOSPHATASE); Fructose-2,6-Bisphosphate 2-Phosphatase
OSJNBb0099P06.4	Putative Receptor-Like Protein Kinase	At3g46290	Protein Kinase, Putative
OSJNBb0099P06.6	Putative Arginyl-Trna Synthetase	At4g26300	EMB1027 (EMBRYO DEFECTIVE 1027); ATP Binding / Arginine-Trna Ligase
OSJNBb0099P06.8	Putative PRP8 Protein	At1g80070	Sus2 (Abnormal Suspensor 2)
OSJNBb0103I08.15	Unknown Protein	At5g24380	YSL2 (YELLOW STRIPE LIKE 2); Oligopeptide Transporter
OSJNBb0103I08.5	Unknown Protein	At5g23450	Atlcbk1 (A. Thaliana Long-Chain Base (Lcb) Kinase 1); Diacylglycerol Kinase
OSJNBb0103I08.9	Unknown Protein	At3g45270	Transposable Element Gene
OSJNBb0106M04.19	Cold Acclimation Protein WCOR413-Like Protein	At3g50830	COR413-PM2 (Cold Regulated 413 Plasma Membrane 2)
OSJNBb0106M04.22	Putative Thioredoxin-Like Protein	At4g37200	HCF164 (High Chlorophyll Fluorescence 164); Thiol-Disulfide Exchange Intermediate
OSJNBb0106M04.24	Putative Allene Oxide Synthase	At5g42650	AOS (ALLENE OXIDE SYNTHASE); Hydro-Lyase/ Oxygen Binding
OSJNBb0108E08.15	Expressed Protein	At1g17460	TRFL3 (TRF-LIKE 3); DNA Binding / Transcription Factor
OSJNBb0108E17.13	Putative NADH-Ubiquinone Oxidoreductase	At4g02580	NADH-Ubiquinone Oxidoreductase 24 Kda Subunit, Putative
OSJNBb0108E17.14	Unknown Protein	At3g04820	Pseudouridylate Synthase
OSJNBb0108E17.2	Hypothetical Protein	At1g09850	XBCP3 (XYLEM BARK CYSTEINE PEPTIDASE 3); Cysteine-Type Peptidase
OSJNBb0108E17.4	Putative Thioredoxin H-Type (TRX-H) (Trxta)	At5g42980	ATTRX3 (Thioredoxin H-Type 3); Thiol-Disulfide Exchange Intermediate
OSJNBb0111B07.11	Putative Vesicle Transport-Related Protein	At2g17980	ATSLY1; Protein Transporter
OSJNBb0111K12.10	Putative Beta-Glucosidase	At4g27820	Glycosyl Hydrolase Family 1 Protein
OSJNBb0113I20.23	Putative Xylan Xylanohydrolase Isoenzyme	At1g58370	RXF12; Hydrolase, Hydrolyzing O-Glycosyl Compounds
OSJNBb0116K07.13	Unknown Protein	At3g19320	Leucine-Rich Repeat Family Protein
OSJNBb0116K07.15	Unknown Protein	At3g50120	Unknown Protein
OSJNBb0116K07.19	Unknown Protein	At5g63930	Leucine-Rich Repeat Transmembrane Protein Kinase, Putative

OSJNBb0116K07.3	Unknown Protein	At1g80050	APT2 (ADENINE PHOSPHORIBOSYL TRANSFERASE 2); Adenine Phosphoribosyltransferase
OSJNBb0118P14.11	Unknown Protein	At1g47980	Unknown Protein
OSJNBb0118P14.12	Unknown Protein	At5g36880	AMP Binding / Acetate-Coa Ligase/ Catalytic
OSJNBb0118P14.5	Unknown Protein	At1g76130	AMY2/ATAMY2 (ALPHA-AMYLASE-LIKE 2); Alpha-Amylase
OSJNOa018M17.6	Putative Endo-Beta-1,4-Glucanase Precursor	At2g32990	Glycosyl Hydrolase Family 9 Protein
OSJNOa283G08.2	Glycolipid Transfer Protein-Like	At2g33470	Gltp1 (Glycolipid Transfer Protein 1)
P0003D09.18	Unknown Protein	At5g62270	Unknown Protein
P0003D09.22	Putative 4-Diphosphocytidyl-2-C-Methyl-D-	At2g26930	ATCDPMEK (PIGMENT DEFECTIVE 277); 4-(Cytidine 5'-Diphospho)-2-C-Methyl-D-Erythritol Kinase
P0003E08.13	Putative Mitogen-Activated Protein Kinase	At2g42880	ATMPK20 (Arabidopsis Thaliana MAP Kinase 20); MAP Kinase
P0003E08.5	Hypothetical Protein	At1g29820	Unknown Protein
P0003E08.6	Hypothetical Protein	At2g42960	Protein Kinase Family Protein
P0004D12.18	Rapamycin-Binding Protein-Like	At3g25220	FKBP15-1 (FK506-Binding Protein 15 Kd-1); FK506 Binding / Peptidyl-Prolyl Cis-Trans Isomerase
P0004D12.9	Leaf Senescence Related Protein-Like	At4g25360	Unknown Protein
P0005A05.10	Unknown Protein	At1g19600	Pfkb-Type Carbohydrate Kinase Family Protein
P0005A05.13	Putative Isoflavone Reductase Homolog IRL	At4g39230	Isoflavone Reductase, Putative
P0005A05.14	Putative Isoflavone Reductase Homolog IRL	At1g75280	Isoflavone Reductase, Putative
P0005A05.15	Hypothetical Protein	At5g60030	Unknown Protein
P0005E02.105	Putative Phi-1(Phosphate-Induced Protein 1)	At2g17230	Phosphate-Responsive 1 Family Protein
P0005E02.109	Putative Pngase (Peptide N-Glycanase)	At5g49570	Transglutaminase-Like Family Protein
P0005E02.119	Unknown Protein	At4g20150	Unknown Protein
P0005H10.12	Putative Aldose Reductase	At3g53880	Aldo/Keto Reductase Family Protein
P0005H10.17	Putative Delta L Pyrroline-5-Carboxylate	At2g39800	P5cs1 (Delta1-Pyrroline-5-Carboxylate Synthase 1)
P0005H10.21	Ras-Related GTP-Binding Protein	At3g46830	Atraba2c/Atrab11a (Arabidopsis Rab Gtpase Homolog A2c); GTP Binding
P0006C01.14	Beta-Adaptin-Like Protein A	At5g11490	Adaptin Family Protein
P0006C01.2	Sgt1	At4g11260	SGT1B (Enhanced Downy Mildew 1b); Binding
P0006C08.21	Putative Vacuolar Protein Sorting	At3g47810	MAG1 (MAIGO 1); Protein Serine/Threonine Phosphatase
P0006C08.29-1	Putative 24 Kda Seed Maturation Protein	At4g11220	Bti2 (Virb2-Interacting Protein 2)
P0006C08.30	Putative Phosphoribosylanthranilate Isomerase 1	At1g07780	PAI1 (PHOSPHORIBOSYLANTHRANILATE ISOMERASE 1); Phosphoribosylanthranilate Isomerase
P0006E02.16	Putative Octicosapeptide/Phox/Bem1p (PB1)	At1g62390	Octicosapeptide/Phox/Bem1p (PB1) Domain-Containing Protein / Tetratricopeptide Repeat (TPR)-Containing Protein
P0007D08.10-1	Putative Sac Domain-Containing Inositol	At1g22620	ATSAC1 (SUPPRESSOR OF ACTIN 1); Phosphoinositide 5-Phosphatase
P0007D08.11	Putative Alcohol Dehydrogenase (Zn	At5g63620	Oxidoreductase, Zinc-Binding Dehydrogenase Family Protein
P0007D08.12	Putative Adenylate Kinase, Chloroplast (ATP-AMP	At5g47840	Adenylate Kinase, Chloroplast, Putative / ATP-AMP Transphosphorylase, Putative
P0007D08.23	Putative PIR7A Protein	At1g33990	Hydrolase, Alpha/Beta Fold Family Protein

P0007D08.28	Putative PPR Protein	At3g07290	Pentatricopeptide (PPR) Repeat-Containing Protein
P0007D08.32	Unknown Protein	At5g11730	Unknown Protein
P0007D08.34	Putative Arm Repeat-Containing Protein	At2g23140	Armadillo/Beta-Catenin Repeat Family Protein / U-Box Domain-Containing Protein
P0009G03.13	Hypothetical Protein	At3g12570	Fyd
P0010B10.22	Secretory Carrier Membrane Protein	At1g61250	SC3 (SECRETORY CARRIER 3); Carrier
P0010B10.27	Putative Vacuolar Protein Sorting-Associated	At4g21560	Vacuolar Protein Sorting-Associated Protein 28 Family Protein / VPS28 Family Protein
P0010C01.12-1	WD-40 Repeat Protein-Like	At3g15470	WD-40 Repeat Family Protein
P0010C01.12-2	WD-40 Repeat Protein-Like	At5g54200	WD-40 Repeat Family Protein
P0010C01.19	Putative Beta-Expansin	At4g28250	Atexpb3 (Arabidopsis Thaliana Expansin B3)
P0010C01.20	Putative Sphingolipid Delta 4 Desaturase	At4g04930	DES-1-LIKE (Fatty Acid Desaturase 1-Like); Oxidoreductase
P0010C01.26	Putative Thioredoxin M-Type, Chloroplast	At1g76760	ATY1 (Arabidopsis Thioredoxin Y1); Thiol-Disulfide Exchange Intermediate
P0010D04.10	Putative Protein Translation Factor Sui1	At1g54290	Eukaryotic Translation Initiation Factor SUI1, Putative
P0011G08.16	Putative Receptor-Like Protein Kinase	At5g61350	Protein Kinase Family Protein
P0012A04.17	Bola-Like Family Protein / Fe-S Metabolism	At4g26500	ATSUFE/CPSUFE/EMB1374 (EMBRYO DEFECTIVE 1374); Enzyme Activator/ Transcription Regulator
P0012A04.3	Unknown Protein	At3g57620	Glyoxal Oxidase-Related
P0013B04.13	Unknown Protein	At3g50340	Unknown Protein
P0013B04.16	Putative Glycoprotein	At1g49710	FUT12 (Fucosyltransferase 12); Fucosyltransferase/ Transferase, Transferring Glycosyl Groups
P0013B04.19	Putative Cytochrome P450	At3g19270	CYP707A4 (Cytochrome P450, Family 707, Subfamily A, Polypeptide 4); Oxygen Binding
P0013F10.1	Hypothetical Protein	At2g47160	Bor1 (Requires High Boron 1)
P0013F10.14	Hypothetical Protein	At1g52780	Unknown Protein
P0013F10.7	Putative Glucosyl Transferase	At2g36790	UGT73C6 (UDP-Glucosyl Transferase 73C6); UDP-Glucosyltransferase/ UDP-Glycosyltransferase/ Transferase, Transferring Glycosyl Groups
P0013G02.12	Putative Ribosomal RNA Apurinic Site Specific	At1g55030	F-Box Family Protein
P0014E08.3	Unknown Protein	At5g58740	Nuclear Movement Family Protein
P0015C07.26-2	Serine/Threonine Protein Kinase-Like	At4g35780	Protein Kinase Family Protein
P0015C07.29	Putative Chain A, C-Terminal Domain Of Mouse	At1g25280	Attlp10 (TUBBY LIKE PROTEIN 10); Phosphoric Diester Hydrolase/ Transcription Factor
P0015C07.31	MAP3K-Like Protein Kinase	At3g19310	Phospholipase C
P0015C07.39-1	Putative Remembr-H2 Protein	At1g71980	Protease-Associated Zinc Finger (C3HC4-Type RING Finger) Family Protein
P0016F11.27	Putative Cinnamoyl Coa Reductase	At1g80820	Ccr2 (Cinnamoyl Coa Reductase)
P0016F11.32	Putative Translation Initiation Factor Eif-2B	At2g34970	Eif4-Gamma/Eif5/Eif2-Epsilon Domain-Containing Protein
P0017C12.1	Serine/Threonine-Specific Receptor Protein	At4g32710	Kinase
P0017C12.24	U5 Snrnp-Specific Protein-Like	At5g04990	Sad1/Unc-84 Protein-Related
P0017C12.29	Putative Mevalonate Disphosphate Decarboxylase	At2g38700	MVD1 (Mevalonate Diphosphate Decarboxylase 1)
P0017H11.13	Dnaj Protein-Like	At5g16650	DNAJ Heat Shock N-Terminal Domain-Containing Protein
P0017H11.16	Unknown Protein	At4g17790	Unknown Protein

P0017H11.19-1	MDR-Like ABC Transporter	At4g25960	PGP2 (P-GLYCOPROTEIN 2); Atpase, Coupled To Transmembrane Movement Of Substances
P0017H11.19-2	Putative MDR-Like ABC Transporter	At1g10680	PGP10 (P-GLYCOPROTEIN 10); Atpase, Coupled To Transmembrane Movement Of Substances
P0017H11.7	Putative Zinc-Binding Protein	At4g17900	Zinc-Binding Family Protein
P0018C07.101	BLE2 Protein-Like	At3g06210	Binding
P0018C07.116	Putative Zinc Finger POZ Domain Protein	At3g06190	ATBPM2; Protein Binding
P0018C07.117	Putative Placental Protein 6	At3g07950	Rhomboid Protein-Related
P0018C07.120	Pectin Methylesterase-Like Protein	At5g55590	QRT1 (QUARTET 1); Pectinesterase
P0018C07.124	Integral Membrane Protein-Like	At1g03260	Hypothetical Protein
P0018C10.26	Unknown Protein	At1g77130	Glycogenin Glucosyltransferase (Glycogenin)-Related
P0018C10.28	Putative Pectin Methylesterase	At5g09760	Pectinesterase Family Protein
P0018C10.29	Hypothetical Protein	At1g48880	Unknown Protein
P0018C10.31	Putative Stearoyl-Acyl Carrier Protein	At1g43800	Acyl-(Acyl-Carrier-Protein) Desaturase, Putative / Stearoyl-ACP Desaturase, Putative
P0018C10.32	Hypothetical Protein	At3g21470	Pentatricopeptide (PPR) Repeat-Containing Protein
P0018C10.38	Scarecrow-Like Protein	At1g21450	SCL1 (SCARECROW-LIKE 1); Transcription Factor
P0018C10.44	Unknown Protein	At1g21410	F-Box Family Protein
P0019D06.2	Putative AAA-Type Atpase	At2g27600	AAA-Type Atpase Family Protein / Vacuolar Sorting Protein-Related
P0019E03.1	Putative Purine Permease	At1g30840	ATPUP4 (Arabidopsis Thaliana Purine Permease 4); Purine Transporter
P0019E03.16	NADH-Dependent Glutamate Synthase	At5g53460	GLT1 (NADH-Dependent Glutamate Synthase 1 Gene)
P0019E03.18	Putative GPAA1 - Like Protein	At5g19130	GPI Transamidase Component Family Protein / Gaa1-Like Family Protein
P0019E03.5	Hypothetical Protein	At3g61750	Auxin-Responsive Protein -Related
P0020B10.26	Glucose-6-Phosphate/Phosphate Translocator	At5g54800	GPT1 (Glucose-6-Phosphate Transporter 1); Antiporter/ Glucose-6-Phosphate Transporter
P0020C11.10	Putative Glutathione S-Transferase	At2g02390	ATGSTZ1 (GLUTATHIONE S-TRANSFERASE 18); Glutathione Transferase
P0020C11.11	Putative Nucleic Acid Binding Protein	At5g26210	PHD Finger Family Protein
P0020C11.16	Putative Prgr1	At5g23550	Unknown Protein
P0020C11.29-1	Putative Pentatricopeptide (PPR)	At1g09900	Pentatricopeptide (PPR) Repeat-Containing Protein
P0020C11.30	Putative Protein Kinase 1	At2g41970	Protein Kinase, Putative
P0020D05.17	Unknown Protein	At4g08240	Unknown Protein
P0020D05.19	Putative Calmodulin-Binding Protein Phosphatase	At1g47380	Protein Phosphatase 2C-Related / PP2C-Related
P0020D05.7	Unknown Protein	At4g16830	Nuclear RNA-Binding Protein (RGGA)
P0020D05.9	Unknown Protein	At1g50630	Extracellular Ligand-Gated Ion Channel
P0020E09.15	Hypothetical Protein	At1g11290	Pentatricopeptide (PPR) Repeat-Containing Protein
P0020E09.19	Putative Uncoupling Protein	At3g54110	ATPUMP1/UCP1 (UNCOUPLING PROTEIN 1); Binding / Oxidative Phosphorylation Uncoupler
P0020E09.22	Putative Cinnamoyl-Coa Reductase	At2g02400	Cinnamoyl-Coa Reductase Family
P0021G06.107	Putative Vesicle-Associated Membrane Protein	At2g32670	ATVAMP725 (Arabidopsis Thaliana Vesicle-Associated Membrane Protein 725)

P0021G06.114	Putative IAA Amidohydrolase	At3g02875	ILR1 (IAA-LEUCINE RESISTANT 1); Metallopeptidase
P0022B05.111	Putative Pollen-Specific Protein NTP303	At5g66920	SKS17 (SKU5 Similar 17); Copper Ion Binding / Oxidoreductase
P0022B05.116	Hypothetical Protein	At1g09310	Unknown Protein
P0022E03.24	Photosystem I Protein-Like Protein	At1g30380	Psak (Photosystem I Subunit K)
P0022E03.6-1	Ferredoxin--NADP Reductase, Embryo Isozyme,	At4g05390	ATRFNR1 (ROOT FNR 1); Oxidoreductase
P0022E03.9	Putative Flavonol 3-O-Glucosyltransferase	At5g17050	UDP-Glucoronosyl/UDP-Glucosyl Transferase Family Protein
P0022F10.12	Unknown Protein	At1g79750	ATNADP-ME4 (NADP-MALIC ENZYME 4); Malate Dehydrogenase (Oxaloacetate-Decarboxylating) (NADP+)/ Malic Enzyme/ Oxidoreductase, Acting On NADH Or NADPH, NAD Or NADP As Acceptor
P0022F10.18	Putative ABC Transporter	At1g59870	PDR8/PEN3 (PLEIOTROPIC DRUG RESISTANCE8); Atpase, Coupled To Transmembrane Movement Of Substances
P0022F10.23	Hypothetical Protein	At5g11580	UVB-Resistance Protein-Related / Regulator Of Chromosome Condensation (RCC1) Family Protein
P0022F12.20	Putative Receptor-Like Protein	At2g45340	Leucine-Rich Repeat Transmembrane Protein Kinase, Putative
P0022F12.21	Putative Rad51C Protein	At2g45280	ATRAD51C (Arabidopsis Thaliana Ras Associated With Diabetes Protein 51C); ATP Binding / Damaged DNA Binding
P0024C06.22	Putative Flavonol 3'-Sulfotransferase	At3g45070	Sulfotransferase Family Protein
P0024C06.31	Putative Fatty Acyl Coa Reductase	At5g22500	Acyl Coa Reductase, Putative / Male-Sterility Protein, Putative
P0024G09.11	Unknown Protein	At3g55600	Unknown Protein
P0024G09.18	Unknown Protein	At3g49720	Unknown Protein
P0024G09.4	Putative Peptide Transport Protein	At5g01180	Proton-Dependent Oligopeptide Transport (POT) Family Protein
P0025A05.3	Unknown Protein	At5g15240	Amino Acid Transporter Family Protein
P0025A05.6	Putative Glucosyltransferase IS5a,	At2g15480	UGT73B5 (UDP-Glucosyl Transferase 73B5); UDP-Glycosyltransferase/ Transferase, Transferring Glycosyl Groups
P0025D09.105-1	Unknown Protein	At2g45990	Unknown Protein
P0025H06.10	Ferredoxin-Nitrite Reductase	At2g15620	NIR1 (NITRITE REDUCTASE); Ferredoxin-Nitrate Reductase
P0026F07.24	Putative Caffeoyl-Coa O-Methyltransferase 1	At4g34050	Caffeoyl-Coa 3-O-Methyltransferase, Putative
P0026F07.9	Putative Transmembrane 9 Superfamily Protein	At4g12650	Endomembrane Protein 70, Putative
P0026H03.15	Calcium-Binding EF Hand-Like Protein	At3g24110	Calcium-Binding EF Hand Family Protein
P0026H03.20-2	Subtilisin-Like Serine Protease AIR3-Like	At5g59810	Subtilase Family Protein
P0026H03.22	Unknown Protein	At4g12690	Unknown Protein
P0026H03.23	Ribosomal Protein L12-Like Protein	At3g06040	Ribosomal Protein L12 Family Protein
P0026H03.8	Unknown Protein	At3g27340	Unknown Protein
P0027A02.29	Putative Senescence-Associated Protein	At2g19580	Tet2 (Tetraspanin2)
P0027A02.9	Putative Serine Threonine Kinase	At5g12000	Kinase
P0027G10.1	Putative Avr9/Cf-9 Rapidly Elicited Protein 276	At1g60190	Armadillo/Beta-Catenin Repeat Family Protein / U-Box Domain-Containing Protein
P0027G10.24	Putative Beta-Glucan Binding Protein	At5g15870	Glycosyl Hydrolase Family 81 Protein
P0027G10.30-1	Acyl-Activating Enzyme 17-Like Protein	At5g23050	Acyl-Activating Enzyme 17 (AAE17)

P0028A08.21	Putative Heat-Shock Protein	At2g04030	CR88 (EMBRYO DEFECTIVE 1956); ATP Binding
P0028G04.28	Hypothetical Protein	At2g46930	Pectinacetylesterase, Putative
P0028G04.9	Hypothetical Protein	At5g19290	Esterase/Lipase/Thioesterase Family Protein
P0030D07.10	Hypothetical Protein	At3g44530	HIRA (ARABIDOPSIS HOMOLOG OF HISTONE CHAPERONE HIRA); Nucleotide Binding / Protein Binding
P0030D07.11	Putative Magnesium/Proton Exchanger	At2g47600	ATMHX (MAGNESIUM/PROTON EXCHANGER); Cation:Cation Antiporter
P0030D07.8	Pentatricopeptide (PPR) Repeat-Containing	At2g26790	Pentatricopeptide (PPR) Repeat-Containing Protein
P0030D07.9-1	Putative Acyl-ACP Thioesterase	At1g08510	FATB (FATTY ACYL-ACP THIOESTERASES B); Acyl Carrier/ Acyl-ACP Thioesterase
P0030G02.24-1	Unknown Protein	At1g16290	Unknown Protein
P0030G02.26	Putative Glyceraldehyde-3-Phosphate	At1g79530	GAPCP-1; Glyceraldehyde-3-Phosphate Dehydrogenase
P0030G02.51	Putative Copper-Exporting Atpase	At5g44790	RAN1 (RESPONSIVE-TO-ANTAGONIST1); Atpase, Coupled To Transmembrane Movement Of Ions, Phosphorylative Mechanism
P0030G11.13	Putative Hosphatidylinositol/Phophatidylcholine	At4g39170	SEC14 Cytosolic Factor, Putative / Phosphoglyceride Transfer Protein, Putative
P0030G11.15	Putative SMC3 Protein	At2g27170	Ttn7 (Titan7)
P0030H07.1	Unknown Protein	At2g37540	Short-Chain Dehydrogenase/Reductase (SDR) Family Protein
P0030H07.13	Putative Protein Kinase Xa21	At3g47110	Leucine-Rich Repeat Transmembrane Protein Kinase, Putative
P0030H07.20	Putative Aspartate--Trna Ligase	At4g33760	Trna Synthetase Class II (D, K And N) Family Protein
P0031D02.12	Unknown Protein	At3g56290	Unknown Protein
P0031D11.14	Hypothetical Protein	At3g55350	Unknown Protein
P0031D11.4	Unknown Protein	At2g39450	Cation Efflux Family Protein
P0031D11.6	Putative Protein Kinase AFC1	At3g53570	AFC1 (ARABIDOPSIS FUS3-COMPLEMENTING GENE 1); Kinase
P0034A04.112	26S Proteasome Regulatory Subunit 4 Homolog	At4g29040	RPT2A (Regulatory Particle Triple-A 2A); Atpase
P0034A04.121	Putative DNA Repair Protein Rhp54	At3g42670	CHR38 (Chromatin Remodeling 38); ATP Binding / DNA Binding / Helicase
P0034A04.123	Putative Ubiquitin-Activating Enzyme	At5g06460	ATUBA2 (Arabidopsis Thaliana Ubiquitin Activating Enzyme 2); Ubiquitin Activating Enzyme
P0034A04.127-2	Pyruvate Decarboxylase Isozyme 3	At4g33070	Pyruvate Decarboxylase, Putative
P0034A04.134-1	Putative Omega-3 Fatty Acid Desaturase	At5g05580	FAD8 (FATTY ACID DESATURASE 8); Omega-3 Fatty Acid Desaturase
P0034C09.19	Putative Ser/Thr Protein Phosphatase	At1g50370	Serine/Threonine Protein Phosphatase, Putative
P0034C11.11	Putative Receptor Protein Kinase	At1g78530	Protein Kinase Family Protein
P0034C11.24	Unknown Protein	At3g12530	Psf2
P0034E02.1	Similar To Phosphate/Phosphoenolpyruvate	At2g25520	Phosphate Translocator-Related
P0034E02.27	Cytochrome P450-Like Protein	At3g56630	CYP94D2 (Cytochrome P450, Family 94, Subfamily D, Polypeptide 2); Oxygen Binding
P0034E02.36	Putative Glucosyltransferase	At2g30140	UDP-Glucoronosyl/UDP-Glucosyl Transferase Family Protein
P0034E02.39	Hypothetical Protein	At2g26770	Plectin-Related
P0034E02.40	Tubulin Beta Chain	At5g12250	Tub6 (Beta-6 Tubulin)
P0035F12.15	Putative Reca Protein	At2g19490	Reca Family Protein
P0035F12.16	Unknown Protein	At5g55120	VTC5; Galactose-1-Phosphate Guanylyltransferase (GDP)

P0035H10.13	Putative Knotted1-Type Homeobox Protein	At4g08150	KNAT1 (BREVIPEDICELLUS 1); Transcription Factor
P0036E06.15	Phospholipid/Glycerol Acyltransferase-Like	At2g38110	ATGPAT6/GPAT6 (GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE 6); 1-Acylglycerol-3-Phosphate O-Acyltransferase/ Acyltransferase
P0036E06.16	Putative SKP1 Interacting Partner	At3g61350	Skip4 (Skp1 Interacting Partner 4)
P0036E06.27-2	Catalase (EC 1.11.1.6) Cata-Like Protein	At1g20630	CAT1 (CATALASE 1); Catalase
P0036E06.29	Putative Dnak-Type Molecular Chaperone Bip	At5g42020	BIP (LUMINAL BINDING PROTEIN); ATP Binding
P0038C05.1	Hypothetical Protein	At3g15600	Unknown Protein
P0038C05.12	Putative Peroxidase	At4g36430	Peroxidase, Putative
P0038C05.26	Hypothetical Protein	At3g30390	Amino Acid Transporter Family Protein
P0038D11.18	Unknown Protein	At1g15490	Hydrolase, Alpha/Beta Fold Family Protein
P0038D11.19	Hypothetical Protein	At1g35110	Ulp1 Protease Family Protein
P0038F09.39	Gamma-Glutamylcysteine Synthetase	At4g23100	Rml1 (Phytoalexin Deficient 2, Root Meristemless 1)
P0039A07.11	Putative Ammonium Transporter	At2g38290	Atamt2 (Ammonium Transporter 2)
P0039G05.11	Florfenicol Resistance Protein-Like	At1g60230	Radical SAM Domain-Containing Protein
P0039H02.103	Putative Syntaxin-Related Protein	At5g08080	SYP132 (Syntaxin 132); T-SNARE
P0039H02.105	Putative Alpha 3 Glucosyltransferase	At5g38460	ALG6, ALG8 Glycosyltransferase Family Protein
P0039H02.111	Putative Prolyl-Trna Synthetase	At5g52520	OVA6 (OVULE ABORTION 6); ATP Binding / Aminoacyl-Trna Ligase
P0039H02.112	Putative Anthranilate Phosphoribosyltransferase	At5g17980	C2 Domain-Containing Protein
P0039H02.131	Unknown Protein	At4g24290	Unknown Protein
P0039H02.137	Putative Brassinosteroid LRR Receptor Kinase	At3g03770	Leucine-Rich Repeat Transmembrane Protein Kinase, Putative
P0039H02.138-1	Osrad6	At2g02760	ATUBC2 (UBIQUITING-CONJUGATING ENZYME 2); Ubiquitin-Protein Ligase
P0040B10.15	Putative Esterase	At1g10740	Hypothetical Protein
P0040B10.2	Putative Leucine-Rich Repeat Family Protein	At1g03440	Leucine-Rich Repeat Family Protein
P0040B10.4	Putative WD-40 Repeat Protein	At4g03020	Transducin Family Protein / WD-40 Repeat Family Protein
P0040B10.6	Unknown Protein	At5g27320	Atgid1c/Gid1c (Ga Insensitive Dwarf1c)
P0040H05.31	Unknown Protein	At1g79390	Unknown Protein
P0041A24.3	Unknown Protein	At1g10240	FRS11 (FAR1-RELATED SEQUENCE 11); Zinc Ion Binding
P0042A10.14	Hypothetical Protein	At1g26310	CAL (CAULIFLOWER); DNA Binding / Transcription Factor
P0042A10.6	Similar To Phytochrome A Supressor	At1g53090	SPA4 (SPA1-RELATED 4); Signal Transducer
P0042A10.7	Hypothetical Protein	At1g28290	Pollen Ole E 1 Allergen And Extensin Family Protein
P0042B03.17	Putative Trehalose-Phosphatase	At1g35910	Trehalose-6-Phosphate Phosphatase, Putative
P0042B03.35	Transporter-Like Protein	At5g10190	Transporter-Related
P0042D01.4	Putative Phenylalanine Ammonia-Lyase	At2g37040	PAL1 (PHE AMMONIA LYASE 1); Phenylalanine Ammonia-Lyase
P0043B10.5	Putative DNA-Dependent Atpase	At3g06400	CHR11 (CHROMATIN-REMODELING PROTEIN 11); DNA-Dependent Atpase
P0044F08.16	Putative WD40-Repeat Protein	At3g18060	Transducin Family Protein / WD-40 Repeat Family Protein

P0044F08.18	Putative Spore Coat Protein	At1g23010	Multi-Copper Oxidase Type I Family Protein
P0045D08.22	Putative Ca2+-Dependent Lipid-Binding Protein	At5g11100	C2 Domain-Containing Protein
P0046D03.133	Putative Prohibitin	At4g28510	Atphb1 (Prohibitin 1)
P0047B07.110-1	Protoporphyrin IX Magnesium Chelatase (EC	At5g13630	Gun5 (Genomes Uncoupled 5)
P0047B07.111	Hypothetical Protein	At2g41770	Unknown Protein
P0047B07.116	Putative Serine Carboxypeptidase II-3 Precursor	At3g63470	SCPL40 (Serine Carboxypeptidase-Like 40); Serine Carboxypeptidase
P0047E05.15-1	Putative Ubiquitin Activating Enzyme	At1g05350	Thif Family Protein
P0048B08.24-1	Putative Cell Division Protein Ftsh3	At3g47060	FTSH7 (Ftsh Protease 7); ATP-Dependent Peptidase/ Atpase/ Metallopeptidase
P0048B08.24-2	Cell Division Protein Ftsh3-Like	At5g58870	FTSH9 (Ftsh Protease 9); ATP-Dependent Peptidase/ Atpase/ Metallopeptidase
P0048D08.104	MET-10+Related Protein-Like	At4g04670	Met-10+ Like Family Protein / Kelch Repeat-Containing Protein
P0048D08.105	CDP2_ORYSA Calcium-Dependent Protein Kinase	At4g04720	CPK21 (Calcium-Dependent Protein Kinase 21); Calcium- And Calmodulin-Dependent Protein Kinase/ Kinase
P0048F12.1	Unknown Protein	At5g15930	PAM1 (PLANT ADHESION MOLECULE 1); RAB Gtpase Activator
P0048F12.11	Putative Phospholipid/Glycerol Acyltransferase	At1g02390	ATGPAT2/GPAT2 (GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE 2); Acyltransferase
P0135D07.12	Dehydration-Responsive Family Protein-Like	At4g00750	Dehydration-Responsive Family Protein
P0135D07.18	Membrane Bound O-Acyl Transferase-Like	At1g63050	Membrane Bound O-Acyl Transferase (MBOAT) Family Protein
P0135D07.26	Membrane Protein-Like	At4g23030	MATE Efflux Protein-Related
P0135D07.43	Putative CRT/DRE Binding Factor 1	At4g25470	CBF2 (FREEZING TOLERANCE QTL 4); DNA Binding / Transcription Factor/ Transcriptional Activator
P0264G11.2-2	Putative Racd Protein	At4g35020	ARAC3/ATROP6/RHO1PS/ROP6 (Rho-Related Protein From Plants 6); GTP Binding / Gtpase
P0401G10.21	Putative Glucose Inhibited Division Protein A	At2g13440	Glucose-Inhibited Division Family A Protein
P0401G10.8	Putative MLH1	At4g09140	ATMLH1 (Arabidopsis Thaliana Mutl-Homologue 1)
P0403C05.17	Putative Formamidase	At4g37550	Formamidase
P0403C05.18	Hypothetical Protein	At2g33760	Pentatricopeptide (PPR) Repeat-Containing Protein
P0403C05.2	Hypothetical Protein	At5g61010	ATEXO70E2 (EXOCYST SUBUNIT EXO70 FAMILY PROTEIN E2); Protein Binding
P0403C05.9	Putative Chorismate Mutase Precursor	At1g69370	CM3 (CHORISMATE MUTASE 3); Chorismate Mutase
P0404D10.16	Stress Inducible Protein-Like	At1g22700	Binding
P0404G11.106-1	Putative ATP/GTP Nucleotide-Binding Protein	At5g61450	2-Phosphoglycerate Kinase-Related
P0406E03.14-2	GDSL-Motif Lipase/Hydrolase-Like	At2g04570	GDSL-Motif Lipase/Hydrolase Family Protein
P0406E03.15	SWIB Complex BAF60b Domain-Containing	At4g26810	SWIB Complex BAF60b Domain-Containing Protein
P0406E03.18	Putative NADPH-Dependent Retinol	At4g05530	Short-Chain Dehydrogenase/Reductase (SDR) Family Protein
P0406E03.32-1	Putative Chloroplast Drought-Induced Stress	At4g04020	FIB (FIBRILLIN); Structural Molecule
P0406E03.33	Transcriptional Regulators Of Nagc/Xylr	At1g30540	Atpase, Badf/Badg/Bcra/Bcrd-Type Family
P0406F06.16	Putative Organic Cation Transporter	At1g79360	Transporter-Related
P0406F06.33	Putative Chlorophyll A-B Binding Protein Of	At5g54270	Lhcb3 (Light-Harvesting Chlorophyll Binding Protein 3)
P0406G08.10	Laccase	At5g60020	LAC17 (Laccase 17); Copper Ion Binding / Oxidoreductase

P0406G08.13	Putative AAA-Metalloprotease	At2g29080	FTSH3 (Ftsh Protease 3); ATP-Dependent Peptidase/ Atpase
P0407A09.6-1	Transmembrane Protein-Like	At4g09810	Transporter-Related
P0407B12.19	Putative UTP-Glucose Glucosyltransferase	At1g01420	UDP-Glucoronosyl/UDP-Glucosyl Transferase Family Protein
P0407H12.144	Breast Adenocarcinoma Marker-Like	At2g06530	SNF7 Family Protein
P0408C03.13	Putative SLT1 Protein (Ion Homeostasis Related	At2g37570	Slt1 (Sodium- And Lithium-Tolerant 1)
P0408C03.24	Hypothetical Protein	At3g46550	Sos5 (Salt Overly Sensitive 5)
P0408C03.8	Putative Ubiquitin Carrier Protein UBC7	At3g46460	UBC13 (Ubiquitin-Conjugating Enzyme 13); Ubiquitin-Protein Ligase
P0408C03.9	Osmotin-Like Protein	At2g28790	Osmotin-Like Protein, Putative
P0408G07.2	Hypothetical Protein	At2g03880	Pentatricopeptide (PPR) Repeat-Containing Protein
P0409B08.17	Putative Reductase	At1g68540	Oxidoreductase Family Protein
P0409B08.21	Putative Mannose-6-Phosphate Isomerase	At3g02570	MEE31 (Maternal Effect Embryo Arrest 31); Mannose-6-Phosphate Isomerase
P0409B08.27	Putative Bifunctional Nuclease	At1g68290	Bifunctional Nuclease, Putative
P0409B08.4	Putative Transcription Factor	At3g48670	XH/XS Domain-Containing Protein / XS Zinc Finger Domain-Containing Protein
P0409B11.10	Putative Phosphoadenylyl-Sulfate Reductase	At1g62180	Apr2 (5'adenylylphosphosulfate Reductase 2)
P0409B11.17-2	Putative Beta-1,3-Glucanase	At1g11820	Hydrolase, Hydrolyzing O-Glycosyl Compounds
P0409B11.19	Putative Glucosyltransferase	At5g66690	UDP-Glucoronosyl/UDP-Glucosyl Transferase Family Protein
P0409B11.32	Putative PS60	At1g76160	SKS5 (SKU5 Similar 5); Copper Ion Binding / Oxidoreductase
P0410E01.3	Hypothetical Protein	At3g15650	Phospholipase/Carboxylesterase Family Protein
P0410E01.31	Putative Acetyl Transferase	At3g62160	Transferase Family Protein
P0410E02.2	Putative Ethylene-Responsive Transcriptional	At2g42680	ATMBF1A/MBF1A (MULTIPROTEIN BRIDGING FACTOR 1A); DNA Binding / Transcription Coactivator
P0410E02.38	Hypothetical Protein	At5g05010	Clathrin Adaptor Complexes Medium Subunit-Related
P0410E03.13	Putative H+-Transporting Atpase	At4g32530	Vacuolar ATP Synthase, Putative / V-Atpase, Putative
P0410E03.18	Unknown Protein	At5g27490	Integral Membrane Yip1 Family Protein
P0410E03.20	Hypothetical Protein	At1g11020	Zinc Finger (C3HC4-Type RING Finger) Family Protein
P0410E03.24	Unknown Protein	At5g11420	Unknown Protein
P0410E03.26	Putative GTP-Binding Protein	At5g20010	RAN-1 (Ras-Related GTP-Binding Nuclear Protein 1); GTP Binding
P0410E11.123-2	Putative Glucose-1-Phosphate	At5g48300	ADG1 (ADP GLUCOSE PYROPHOSPHORYLASE SMALL SUBUNIT 1); Glucose-1-Phosphate Adenylyltransferase
P0413A11.18	Peroxisomal Fatty Acid Beta-Oxidation	At4g29010	AIM1 (ABNORMAL INFLORESCENCE MERISTEM); Enoyl-Coa Hydratase
P0413A11.38-1	Putative Sugar Transporter	At1g79820	SGB1; Carbohydrate Transporter/ Sugar Porter
P0413A11.38-2	Putative Sugar Transporter	At1g67300	Hexose Transporter, Putative
P0413C03.28	Putative Ubiquitin-Like Protein	At5g48710	Ubiquitin-Related
P0413C03.5	Putative Gamma-Adaptin 1	At1g31730	Epsilon-Adaptin, Putative
P0413C03.8	Putative Selenium Binding Protein	At4g14030	Selenium-Binding Protein, Putative
P0413C03.9	Putative Glycine-Rich RNA-Binding Protein 2	At5g61030	GR-RBP3 (Glycine-Rich RNA-Binding Protein 3); RNA Binding

P0413G02.1	Putative Cytokinin Oxidase	At1g75450	CKX5 (CYTOKININ OXIDASE 5); Cytokinin Dehydrogenase
P0413G02.11	Putative Purple Acid Phosphatase	At2g16430	PAP10; Acid Phosphatase/ Protein Serine/Threonine Phosphatase
P0413G02.15	Putative Low Density Lipoprotein	At5g16300	Hypothetical Protein
P0413H11.35	Putative Chlorophyll A/B-Binding Protein	At3g47470	LHCA4 (Photosystem I Light Harvesting Complex Gene 4); Chlorophyll Binding
P0413H11.37	Putative Polypyrimidine Tract-Binding Protein	At3g01150	PTB (POLYPYRIMIDINE TRACT-BINDING); RNA Binding
P0415A04.13	Peroxidase-Like Protein	At5g15180	Peroxidase, Putative
P0415A04.19	Unknown Protein	At5g10300	Hydrolase, Alpha/Beta Fold Family Protein
P0415A04.24	Putative Nuclear Transport Factor 2	At1g27970	Ntf2b (Nuclear Transport Factor 2b)
P0415A04.26	Putative Pectin Esterase	At1g11580	Pectin Methylesterase, Putative
P0415A04.27	Disease Resistance Protein-Like	At5g43740	Disease Resistance Protein (CC-NBS-LRR Class), Putative
P0415B12.4	RNA Binding Protein Rp120	At5g07350	Tudor Domain-Containing Protein / Nuclease Family Protein
P0415C01.11	Unknown Protein	At5g64780	Unknown Protein
P0416G11.10	Unknown Protein	At2g47970	NPL4 Family Protein
P0416G11.15	Putative Peroxidase Isozyme 38K Precursor	At2g39040	Peroxidase, Putative
P0417F02.7	Hexokinase II	At1g47840	Hexokinase, Putative
P0417G05.10	Putative Receptor Kinase	At4g23740	Leucine-Rich Repeat Transmembrane Protein Kinase, Putative
P0418E08.114	Putative UDP-Glucosyltransferase	At3g11340	UDP-Glucoronosyl/UDP-Glucosyl Transferase Family Protein
P0418E08.117	Putative UDP-Glucosyltransferase	At3g55710	UDP-Glucoronosyl/UDP-Glucosyl Transferase Family Protein
P0419A09.30	Putative Ethylene Response Factor	At5g25390	SHN2 (SHINE2); DNA Binding / Transcription Factor
P0419A09.31	Putative DEAD Box	At3g01540	DRH1 (DEAD Box RNA Helicase 1)
P0419A09.34	Putative SPX (SYG1/Pho81/XPR1) Domain-Containing	At2g26660	SPX (SYG1/Pho81/XPR1) Domain-Containing Protein
P0419A09.6-1	26S Proteasome Regulatory Particle Triple-A	At1g45000	26S Proteasome Regulatory Complex Subunit P42d, Putative
P0419A09.7	Putative SEC14 Cytosolic Factor (SEC14)	At1g55840	SEC14 Cytosolic Factor (SEC14) / Phosphoglyceride Transfer Protein
P0419B01.17	Hypothetical Protein	At4g36690	ATU2AF65A; RNA Binding
P0419B01.2	Nucleotide Pyrophosphatase Homolog	At4g29680	Type I Phosphodiesterase/Nucleotide Pyrophosphatase Family Protein
P0419B01.5	Cytochrome P450-Like Protein	At3g13730	CYP90D1 (CYTOCHROME P450, FAMILY 90, SUBFAMILY D, POLYPEPTIDE 1); Oxidoreductase, Acting On Paired Donors, With Incorporation Or Reduction Of Molecular Oxygen, NADH Or NADPH As One Donor, And Incorporation Of One Atom Of Oxygen / Oxygen Binding
P0419B01.6	Putative Ethylene-Responsive RNA Helicase	At1g55150	DEAD Box RNA Helicase, Putative (RH20)
P0419C03.10-1	Unknown Protein	At1g14780	Unknown Protein
P0419C04.13	Hypothetical Protein	At5g56530	Hypothetical Protein
P0419C04.2	Unknow Protein	At3g51610	Unknown Protein
P0419C04.8	'Putative 60S Ribosomal Protein, L10'	At1g26910	60S Ribosomal Protein L10 (RPL10B)
P0419H03.23	Phytosulfokine Receptor Precursor-Like	At1g17240	Leucine-Rich Repeat Family Protein

P0419H03.34	Putative Receptor Mediated Endocytosis RME-1	At4g05520	Calcium-Binding EF Hand Family Protein
P0419H03.37	Putative Chain C, Structure Of The Plant	At1g71260	Atwhy2 (A. Thaliana Whirly 2); Dna Binding
P0421H07.18	RING Zinc Finger Protein	At4g26580	Protein Binding / Zinc Ion Binding
P0421H07.20	Putative Farnesyl-Pyrophosphate Synthetase	At5g47770	FPS1 (FARNESYL DIPHOSPHATE SYNTHASE 1); Dimethylallyltranstransferase/ Geranyltranstransferase
P0423A12.15	Hypothetical Protein	At4g31380	Flp1 (Fpf1-Like Protein 1)
P0423A12.18	Putative Glutathione S-Transferase	At3g62760	ATGSTF13 (Arabidopsis Thaliana Glutathione S-Transferase (Class Phi) 13); Glutathione Transferase
P0423A12.19	Hypothetical Protein	At3g62770	Atatg18a (Arabidopsis Thaliana Homolog Of Yeast Autophagy 18 (ATG18) A)
P0423B08.13	Putative I-Box Binding Factor	At5g04760	Myb Family Transcription Factor
P0423B08.7	Unknown Protein	At5g06140	Phox (PX) Domain-Containing Protein
P0426D06.10	Unknown Protein	At4g01810	Protein Transport Protein-Related
P0426D06.17	Unknown Protein	At1g73720	Transducin Family Protein / WD-40 Repeat Family Protein
P0426D06.20	Putative Protein Kinase	At1g56720	Protein Kinase Family Protein
P0426D06.21	Putative Pto Kinase Interactor 1	At3g17410	Serine/Threonine Protein Kinase, Putative
P0426D06.8	Putative Seca-Type Chloroplast Protein Transport	At4g01800	Preprotein Translocase Seca Subunit, Putative
P0427D10.102	Putative ATP-Dependent RNA Helicase	At3g09720	DEAD/DEAH Box Helicase, Putative
P0427G12.14	Putative Endoglucanase 1 Precursor	At1g02800	ATCEL2 (Arabidopsis Thaliana Cellulase 2); Hydrolase, Hydrolyzing O-Glycosyl Compounds
P0427G12.16	Putative Oxidase-Like	At2g46760	FAD-Binding Domain-Containing Protein
P0428D12.112	Putative Ubiquitin-Specific Protease	At5g06600	UBP12 (UBIQUITIN-SPECIFIC PROTEASE 12); Ubiquitin-Specific Protease
P0429B05.10	Putative Receptor-Like Protein Kinase	At1g73080	PEPR1 (PEP1 RECEPTOR 1); ATP Binding / Kinase/ Protein Binding / Protein Serine/Threonine Kinase
P0429B05.26	Putative Phosphoglycerate Dehydrogenase	At1g17740	Unknown Protein
P0429B05.28	Suppressor-Like Protein	At5g65490	Unknown Protein
P0429B05.37	Putative Adenylyl Cyclase Associated Protein	At4g34490	Atcap1 (Cyclase Associated Protein 1)
P0429B05.38	Putative 4-Coumarate-Coa Ligase	At3g21240	4CL2 (4-Coumarate:Coa Ligase 2); 4-Coumarate-Coa Ligase
P0430F03.1	Putative MATE Efflux Protein Family Protein	At3g23560	ALF5 (ABERRANT LATERAL ROOT FORMATION 5); Antiporter/ Transporter
P0430F03.13	Putative Glucosyltransferase	At2g18570	UDP-Glucoronosyl/UDP-Glucosyl Transferase Family Protein
P0431A02.33	Putative Zeta-Carotene Desaturase Precursor	At3g04870	ZDS (ZETA-CAROTENE DESATURASE); Carotene 7,8-Desaturase
P0431A03.1	Unknown Protein	At1g68660	Unknown Protein
P0431A03.16	Putative Transmembrane Protein	At1g25520	Unknown Protein
P0431A03.17	Unknown Protein	At1g70900	Unknown Protein
P0431A03.26	Ribonuclease	At1g26820	RNS3 (RIBONUCLEASE 3); Endoribonuclease
P0431B06.14	Pentatricopeptide (PPR) Repeat-Containing	At4g39620	EMB2453 (EMBRYO DEFECTIVE 2453); Binding
P0431B06.16	Putative NTGP5	At1g22050	Ubiquitin Family Protein
P0431B06.25	Aspartyl Protease-Like	At5g10080	Aspartyl Protease Family Protein

P0431B06.40	Putative Phosphoglycerate Mutase	At1g22170	Phosphoglycerate/Bisphosphoglycerate Mutase Family Protein
P0431B06.41	Putative Inositol Polyphosphate 5-Phosphatase I	At5g65090	BST1 (BRISTLED1); Hydrolase
P0431B06.43	Putative Beta-D-Xylosidase	At1g78060	Glycosyl Hydrolase Family 3 Protein
P0431B06.5	Putative SEC6	At1g71820	Unknown Protein
P0431G06.20	Putative NADPH:Quinone Oxidoreductase	At3g27890	NQR (NADPH:QUINONE OXIDOREDUCTASE); FMN Reductase
P0431G06.4	Hypothetical Protein	At5g19420	Zinc Finger Protein, Putative / Regulator Of Chromosome Condensation (RCC1) Family Protein
P0431H09.18	Unknown Protein	At4g25940	Epsin N-Terminal Homology (ENTH) Domain-Containing Protein
P0432B10.6	Putative 60S Ribosomal Protein L30	At1g36240	60S Ribosomal Protein L30 (RPL30A)
P0432C03.20	Hypothetical Protein	At3g10150	ATPAP16/PAP16 (Purple Acid Phosphatase 16); Acid Phosphatase/ Protein Serine/Threonine Phosphatase
P0432C03.7	Beta 1,3-Glucanase	At3g57270	BG1 (BETA-1,3-GLUCANASE 1); Hydrolase, Hydrolyzing O-Glycosyl Compounds
P0434A03.105-2	Putative NEP1-Interacting Protein 2	At2g17730	Zinc Finger (C3HC4-Type RING Finger) Family Protein
P0434A03.107	Putative Mannose-P-Dolichol Utilization Defect 1	At5g59470	PQ-Loop Repeat Family Protein / Transmembrane Family Protein
P0434A03.108	Carboxypeptidase C Cbp31	At3g10410	SCPL49 (Serine Carboxypeptidase-Like 49); Serine Carboxypeptidase
P0434A03.111-2	Unknown Protein	At5g22950	SNF7 Family Protein
P0434A03.134	Putative Xyloglucan Endo-Transglycosylase	At2g36870	Xyloglucan:Xyloglucosyl Transferase, Putative / Xyloglucan Endotransglycosylase, Putative / Endo-Xyloglucan Transferase, Putative
P0434A03.135	Putative Cysteine Proteinase	At3g54940	Cysteine Proteinase, Putative
P0434A03.138	Unknown Protein	At4g38430	ATROPGEF1/ROPGEF1 (KINASE PARTNER PROTEIN-LIKE); Rho Guanyl-Nucleotide Exchange Factor/ Protein Binding
P0434B04.10	Putative Triose-Phosphate Isomerase	At3g55440	ATCTIMC (CYTOSOLIC TRIOSE PHOSPHATE ISOMERASE); Triose-Phosphate Isomerase
P0434B04.12	Putative CER3	At5g02310	CER3 (ECERIFERUM 3); Protein Binding / Ubiquitin-Protein Ligase/ Zinc Ion Binding
P0434B04.3	Unknown Protein	At1g32130	Unknown Protein
P0434B04.34	Putative Glycoprotein	At3g55360	ATTSC13/CER10/ECR/TSC13 (ENOYL-COA REDUCTASE); 3-Oxo-5-Alpha-Steroid 4-Dehydrogenase/ Fatty Acid Elongase/ Trans-2-Enoyl-Coa Reductase (NADPH)
P0434C04.32	Putative Seven Transmembrane Protein	At4g02600	ATMLO1/MLO1 (MILDEW RESISTANCE LOCUS O 1); Calmodulin Binding
P0434E03.15	Putative Avr9 Elicitor Response Protein	At5g53340	Transferase, Transferring Hexosyl Groups
P0434E03.23	Unknown Protein	At1g11540	Unknown Protein
P0434E03.25	Putative Cellulase	At4g23560	Glycosyl Hydrolase Family 9 Protein
P0435B05.15	Putative Ribosomal Protein L18a, Cytosolic	At2g34480	60S Ribosomal Protein L18A (RPL18aB)
P0435B05.19	Putative GTP-Binding Protein	At2g31060	GTP Binding / Translation Elongation Factor
P0435B05.32	Putative Glucan Synthase	At4g03550	ATGSL05 (GLUCAN SYNTHASE-LIKE 5); 1,3-Beta-Glucan Synthase/ Transferase, Transferring Glycosyl Groups
P0435E12.12	Putative 12-Oxophytodienoic Acid Reductase	At1g76680	OPR1 (12-Oxophytodienoate Reductase 1); 12-Oxophytodienoate Reductase
P0435E12.43	Unknown Protein	At2g44090	Unknown Protein
P0436B05.15	Hypothetical Protein	At5g24630	Bin4 (Brassinosteroid-Insensitive4)
P0436B06.11	Putative UDP-Glucose 4-Epimerase	At4g10960	UGE5 (UDP-D-Glucose/UDP-D-Galactose 4-Epimerase 5); UDP-Glucose 4-Epimerase/ Protein Dimerization

P0436B06.29	Selenium-Binding Protein-Like	At3g25970	Pentatricopeptide (PPR) Repeat-Containing Protein
P0436D06.12	Putative Oxalyl-Coa Decarboxylase	At5g17380	Pyruvate Decarboxylase Family Protein
P0436D06.2	Hypothetical Protein	At1g15170	MATE Efflux Family Protein
P0436E04.21	Putative Benzoyltransferase	At2g40230	Transferase Family Protein
P0436E04.9	Putative Receptor Ser/Thr Protein Kinase	At1g52310	Protein Kinase Family Protein / C-Type Lectin Domain-Containing Protein
P0437G01.10	Putative Cytochrome P450 Reductase	At4g30210	Atr2 (Arabidopsis P450 Reductase 2)
P0437G01.11	Putative HAD-Superfamily Hydrolase	At4g25840	GPP1 (GLYCEROL-3-PHOSPHATASE 1); Hydrolase
P0437G01.17	Unknown Protein	At5g57460	Protein Binding / Protein Transporter
P0437H03.127	Unknown Protein	At2g22370	Unknown Protein
P0437H03.131	Putative SWIRM Domain-Containing Protein	At2g33610	ATSWI3B (Arabidopsis Thaliana Switching Protein 3B); DNA Binding
P0437H03.132	Citrate Synthase	At2g44350	ATCS (CITRATE SYNTHASE 4); Citrate (SI)-Synthase
P0437H03.136	Putative Extra Sporogenous Cells	At5g07280	EMS1 (EXCESS MICROSPOROCYTES1); Kinase
P0438H08.18	Putative Vesicle-Associated Membrane	At2g45140	Vesicle-Associated Membrane Protein, Putative / VAMP, Putative
P0438H08.20	Putative Ribosomal Protein L34	At1g26880	60S Ribosomal Protein L34 (RPL34A)
P0438H08.29	Putative Caffeic Acid 3-O-Methyltransferase	At5g54160	Atomt1 (O-Methyltransferase 1)
P0439B06.12	Unknown Protein	At1g68780	Leucine-Rich Repeat Family Protein
P0439B06.21	Putative E12A11 Protein	At1g18100	E12A11; Phosphatidylethanolamine Binding
P0439B06.32	Unknown Protein	At3g03440	Armadillo/Beta-Catenin Repeat Family Protein
P0439B06.7	Putative Acetoacyl-Coa-Thiolase	At5g47720	Acetyl-Coa C-Acetyltransferase
P0439B07.24	Putative Dihydroneopterin Aldolase	At5g62980	Dihydroneopterin Aldolase, Putative
P0439B07.4	Putative PHG1A Protein	At2g24170	Endomembrane Protein 70, Putative
P0439E07.11	Putative Hexokinase I	At4g29130	ATHXK1 (GLUCOSE INSENSITIVE 2); ATP Binding / Hexokinase
P0439E07.15	Putative Pectin Methylesterase	At5g19730	Pectinesterase Family Protein
P0439E07.9	Putative Dehydrogenase	At4g29120	6-Phosphogluconate Dehydrogenase NAD-Binding Domain-Containing Protein
P0439E11.14	Unknown Protein	At5g19090	Heavy-Metal-Associated Domain-Containing Protein
P0439E11.8	Unknown Protein	At1g31470	Nfd4 (Nuclear Fusion Defective 4)
P0440D10.18	Putative Tetrafunctional Protein Of Glyoxysomal	At3g06860	MFP2 (MULTIFUNCTIONAL PROTEIN); Enoyl-Coa Hydratase
P0440D10.23	Mannose-Binding Rice Lectin	At1g19720	Pentatricopeptide (PPR) Repeat-Containing Protein
P0441A12.12-1	Putative AKIN Beta3	At2g28060	Protein Kinase-Related
P0441A12.23	Putative Syringolide-Induced Protein B13-1-1	At4g39830	L-Ascorbate Oxidase, Putative
P0443G08.126	Putative Tyrosyl-Trna Synthetase	At2g33840	Trna Synthetase Class I (W And Y) Family Protein
P0443G08.138	Putative Monodehydroascorbate Reductase	At1g63940	Monodehydroascorbate Reductase, Putative
P0443H10.10	Unknown Protein	At1g51580	KH Domain-Containing Protein
P0444A09.11	Putative Kaurene Synthase A	At4g02780	GA1 (GA REQUIRING 1); Ent-Copalyl Diphosphate Synthase
P0445D12.3	Putative ABC Transporter	At2g01320	ABC Transporter Family Protein

P0445D12.4	Unknown Protein	At1g71070	Glycosyltransferase Family 14 Protein / Core-2/I-Branching Enzyme Family Protein
P0445E10.3	Putative CAD Atpase	At1g80350	ERH3 (ECTOPIC ROOT HAIR 3); ATP Binding / Nucleoside-Triphosphatase/ Nucleotide Binding
P0446B05.17	Putative Protein Phosphatase 2C	At1g07430	Protein Phosphatase 2C, Putative / PP2C, Putative
P0446B05.2	Unknown Protein	At5g02190	PCS1 (PROMOTION OF CELL SURVIVAL1); Aspartic-Type Endopeptidase/ Peptidase
P0446B05.20	Ankyrin-Like Protein	At2g39750	Dehydration-Responsive Family Protein
P0446B05.22	Unknown Protein	At3g55580	Regulator Of Chromosome Condensation (RCC1) Family Protein
P0446F04.116	Putative 1-Aminocyclopropane-1-Carboxylate	At1g50960	ATGA2OX7 (GIBBERELLIN 2-OXIDASE 7); Gibberellin 2-Beta-Dioxygenase/ Gibberellin 20-Oxidase
P0446G04.10	Putative NADH Dehydrogenase	At1g07180	NDA1 (ALTERNATIVE NAD(P)H DEHYDROGENASE 1); NADH Dehydrogenase
P0446G04.23	Unknown Protein	At5g58560	Phosphatidate Cytidylyltransferase Family Protein
P0446G04.4	Hypothetical Protein	At3g57070	Glutaredoxin Family Protein
P0446G04.7	Putative NAD-Malate Dehydrogenase	At3g47520	MDH (Malate Dehydrogenase); Malate Dehydrogenase
P0446G04.9	Putative ABC Transporter	At4g04770	Atabc1 (Arabidopsis Thaliana Nucleosome Assembly Protein 1)
P0446G09.124	Putative Pentatricopeptide (PPR)	At1g71490	Pentatricopeptide (PPR) Repeat-Containing Protein
P0448B11.50-1	DNA Helicase-Like	At5g35970	DNA-Binding Protein, Putative
P0450A04.116	Putative Sodium/Proton Antiporter	At3g05030	NHX2 (Sodium Proton Exchanger 2)
P0450A04.117	Putative Tubby Related Protein	At2g47900	Attlp3 (TUBBY LIKE PROTEIN 3); Phosphoric Diester Hydrolase/ Transcription Factor
P0450A04.119	Putative Beta-Amylase	At5g18670	BMY3 (Beta-Amylase 3); Beta-Amylase
P0450A04.129	Putative CRK1 Protein(Cdc2-Related Kinase 1)	At1g54610	Protein Kinase Family Protein
P0450B04.1	Putative P450	At2g30770	CYP71A13 (Cytochrome P450, Family 71, Subfamily A, Polypeptide 13); Oxygen Binding
P0450B04.20-1	Putative GDP-Mannose Transporter	At2g13650	Gonst1 (Golgi Nucleotide Sugar Transporter 1)
P0450B04.21	Putative Shwachman-Bodian-Diamond Syndrome	At1g43860	Transcription Factor
P0450B04.29	Putative Mago Nashi	At1g02140	MEE63 (Maternal Effect Embryo Arrest 63)
P0450B04.3-1	Putative Cytochrome P450 71C4	At4g13310	CYP71A20 (Cytochrome P450, Family 71, Subfamily A, Polypeptide 20); Oxygen Binding
P0451A10.15	Putative Vacuolar ATP Synthase 16 Kda	At1g19910	AVA-P2 (Vacuolar-H+-Pumping Atpase 16 Kda Proteolipid Subunit 2); Atpase
P0451A10.27	Putative Alkaline/Neutral Invertase	At4g09510	Beta-Fructofuranosidase, Putative / Invertase, Putative / Saccharase, Putative / Beta-Fructosidase, Putative
P0451A10.31	Putative Polymyositis/Scleroderma Autoantigen 1	At3g60500	3' Exoribonuclease Family Protein
P0451A10.34-2	Putative Far-Red Impaired Response Protein	At5g18960	FRS12 (FAR1-RELATED SEQUENCE 12); Zinc Ion Binding
P0451A10.9-1	Unknown Protein	At2g17050	Disease Resistance Protein (TIR-NBS-LRR Class), Putative
P0451D05.22	Putative Mutator-Like Transposase	At3g04605	Transposable Element Gene
P0451D05.26	Hypothetical Protein	At3g24420	Hydrolase, Alpha/Beta Fold Family Protein
P0451G12.16	Putative SEC23	At2g21630	Transport Protein, Putative
P0451G12.21	Putative Prmc3	At1g47480	Unknown Protein
P0451G12.24	Putative Prmc3	At3g48690	Unknown Protein

P0451G12.3	Alpha-Amylase Isozyme 3E Precursor	At4g25000	AMY1 (ALPHA-AMYLASE-LIKE); Alpha-Amylase
P0451H06.1	Putative Poly(A)-Binding Protein	At1g49760	PAB8 (POLY(A) BINDING PROTEIN 8); RNA Binding / Translation Initiation Factor
P0452F04.18-2	Putative Non-Transporter ABC Protein Abcf1	At1g64550	ATGCN3 (Arabidopsis Thaliana General Control Non-Repressible 3)
P0452F04.20	Putative Disease Resistance Protein Hcr2-5D	At3g15410	Leucine-Rich Repeat Family Protein
P0452F04.25	Putative Prolyl 4-Hydroxylase	At1g20270	Oxidoreductase, 2OG-Fe(II) Oxygenase Family Protein
P0452F04.30	Unknown Protein	At5g08400	Unknown Protein
P0452F04.33-1	UDP-Glucoronosyl/UDP-Glucosyl Transferase Family	At1g64100	DNA Binding / Binding
P0452F04.34	Unknown Protein	At1g73390	Unknown Protein
P0452F04.36	Unknown Protein	At3g19990	Binding
P0452F10.16	Hypothetical Protein	At3g24570	Peroxisomal Membrane 22 Kda Family Protein
P0452F10.19	Putative Caulobacter Crescentus D-Isomer	At1g79870	Oxidoreductase Family Protein
P0452F10.6	RAS-Related GTP-Binding Protein Rab7 Family	At1g52280	Atrabg3d (Arabidopsis Rab Gtpase Homolog G3d); GTP Binding
P0453D01.16-1	Unknown Protein	At2g35150	Phosphate-Responsive 1 Family Protein
P0453D01.4	Putative High Affinity Sulfate Transporter	At4g08620	SULTR1;1 (Sulfate Transporter 1;1); Sulfate Transporter
P0453E03.104	Unknown Protein	At3g57320	Unknown Protein
P0453E03.107	Pentatricopeptide (PPR)Repeat-Containing	At1g01970	Pentatricopeptide (PPR) Repeat-Containing Protein
P0453E03.111	Putative Translation Elongation Factor Eef-1	At5g19510	Elongation Factor 1B Alpha-Subunit 2 (Eef1balpha2)
P0453E03.113	Selenium-Binding Protein-Like	At2g29760	Pentatricopeptide (PPR) Repeat-Containing Protein
P0453E05.113	Putative Cyclin-Dependent Kinase CDC2C	At1g18670	IBS1 (IMPAIRED IN BABA-INDUCED STERILITY 1); Kinase
P0453E05.118	Translation Initiation Factor 5A	At1g13950	EIF-5A (Eukaryotic Translation Initiation Factor 5A-1); Translation Initiation Factor
P0453E05.123	Unknown Protein	At5g39410	Unknown Protein
P0453E05.124	Putative Brassinosteroid Insensitive 1	At1g74360	Leucine-Rich Repeat Transmembrane Protein Kinase, Putative
P0453G03.27	Putative Geranylgeranyl Diphosphate Synthase	At4g36810	GGPS1 (GERANYLGERANYL PYROPHOSPHATE SYNTHASE 1); Farnesyltranstransferase
P0453G03.28	Transporter-Related-Like	At5g57100	Transporter-Related
P0453H10.11	Putative Protein Phosphatase 2A 48 Kda	At5g28900	Calcium-Binding EF Hand Family Protein
P0453H10.23	Unknown Protein	At1g52000	Jacalin Lectin Family Protein
P0453H10.31	Putative Cellulose Synthase-Like Protein	At5g22740	ATCSLA02 (Cellulose Synthase-Like A2); Transferase, Transferring Glycosyl Groups
P0454A11.10	NPK1-Related Protein Kinase-Like Protein	At3g07980	MAPKKK6 (MAP3K EPSILON PROTEIN KINASE 2); Kinase
P0454A11.12	NPK1-Related Protein Kinase-Like Protein	At5g08590	ASK2 (ARABIDOPSIS SERINE/THREONINE KINASE 2); Kinase
P0454A11.14	Putative Plasma Membrane Associated Protein	At1g29520	AWPM-19-Like Membrane Family Protein
P0454A11.19	Putative Flavonoid 3',5'-Hydroxylase	At5g44620	CYP706A3 (Cytochrome P450, Family 706, Subfamily A, Polypeptide 3); Oxygen Binding
P0454H12.12	Putative 2,3-Bisphosphoglycerate-Independent	At3g08590	2,3-Biphosphoglycerate-Independent Phosphoglycerate Mutase, Putative / Phosphoglyceromutase, Putative
P0454H12.13	Unknown Protein	At2g38630	Unknown Protein
P0454H12.17	Hypothetical Protein	At5g09950	Pentatricopeptide (PPR) Repeat-Containing Protein

P0454H12.21	Hypothetical Protein	At1g06840	Leucine-Rich Repeat Transmembrane Protein Kinase, Putative
P0454H12.5	Unknown Protein	At4g10360	Unknown Protein
P0455A11.11	Putative Mrna Cap Methyltransferase	At3g20650	Mrna Capping Enzyme Family Protein
P0455A11.13	SET Domain-Containing Protein-Like	At4g15180	SET Domain-Containing Protein
P0455C04.24	Hypothetical Protein	At5g04850	SNF7 Family Protein
P0455C04.25	Putative Peptide Transporter-Like Protein	At5g13400	Proton-Dependent Oligopeptide Transport (POT) Family Protein
P0455C04.26	Putative C-8,7 Sterol Isomerase	At1g20050	Hyd1 (Hydra 1)
P0455H11.113	Putative Rab GTP-Binding Protein Rab11a	At5g47520	Atraba5a (Arabidopsis Rab Gtpase Homolog A5a); GTP Binding
P0455H11.115	Ripening-Related Protein-Like	At5g59480	Haloacid Dehalogenase-Like Hydrolase Family Protein
P0455H11.118-1	Putative Pectinacetylesterase Precursor	At1g57590	Carboxylic Ester Hydrolase
P0455H11.122	Myb-Like DNA-Binding Protein-Like	At5g56110	Atmyb103/Atmyb80 (Myb Domain Protein 103, Myb Domain Protein 80); DNA Binding / Transcription Factor
P0456A01.12	Putative Cytochrome P450	At3g14680	CYP72A14 (Cytochrome P450, Family 72, Subfamily A, Polypeptide 14); Oxygen Binding
P0456A01.31	Putative Trehalose-6-Phosphate Synthase	At1g06410	ATTPS7 (Arabidopsis Thaliana Trehalose-Phosphatase/Synthase 7); Transferase, Transferring Glycosyl Groups / Trehalose-Phosphatase
P0456A01.5	Subtilisin-Like Protease	At5g45650	Subtilase Family Protein
P0456B03.101	Putative Betaine-Aldehyde Dehydrogenase	At3g48170	ALDH10A9 (Aldehyde Dehydrogenase 10A9); 3-Chloroallyl Aldehyde Dehydrogenase
P0456B03.116	Inositol Polyphosphate-5-Phosphatase-Like	At2g01900	Endonuclease/Exonuclease/Phosphatase Family Protein
P0456F08.13	Putative WD-Repeat Protein RBAP1	At2g19520	Fve (Fve)
P0456F08.17	Putative Lipase	At2g42690	Lipase, Putative
P0456F08.19	Putative H+-Transporting ATP Synthase	At4g38510	(VACUOLAR ATP SYNTHASE SUBUNIT B2); Hydrogen Ion Transporting ATP Synthase, Rotational Mechanism
P0456F08.2	Unknown Protein	At2g26180	IQD6 (IQ-Domain 6); Calmodulin Binding
P0456F08.24	Putative Glycine Dehydrogenase	At2g26080	Glycine Dehydrogenase (Decarboxylating), Putative / Glycine Decarboxylase, Putative / Glycine Cleavage System P-Protein, Putative
P0458A05.17	Hypothetical Protein	At1g74160	Unknown Protein
P0458A05.20	Unknown Protein	At3g59770	SAC9 (Suppressor Of Actin 9)
P0458B05.10	ATP-Dependent Clp Protease ATP-Binding Subunit	At5g51070	ERD1 (EARLY RESPONSIVE TO DEHYDRATION 1); ATP Binding / Atpase
P0458B05.20	Putative DNA Repair Protein Rad8	At5g22750	RAD5; ATP Binding / DNA Binding / Helicase/ Protein Binding / Zinc Ion Binding
P0458B05.4	Unknown Protein	At5g27730	Hypothetical Protein
P0458D06.46	Unknown Protein	At1g74530	Unknown Protein
P0458E05.19	Similar To 5-Oxoprolinase	At5g37830	Hydantoinase/Oxoprolinase Family Protein
P0458E05.25	Unknown Protein	At3g11530	Vacuolar Protein Sorting 55 Family Protein / VPS55 Family Protein
P0458E05.28	Unknown Protein	At3g62840	Unknown Protein
P0458E05.31	Putative Rac Gtpase Activating Protein	At5g22400	Rac Gtpase Activating Protein, Putative
P0458E05.6	Putative Chromosome Condensation Factor	At1g76950	Zinc Finger Protein (PRAF1) / Regulator Of Chromosome Condensation (RCC1) Family Protein
P0458G06.122	Leaf Senescence Related Protein-Like Protein	At4g01080	Unknown Protein

P0458H05.109	Putative Serine/Threonine Kinase Protein	At3g45860	Receptor-Like Protein Kinase, Putative
P0458H05.127	Putative Serine/Threonine Kinase Protein	At4g23140	Crk6 (Cysteine-Rich Rlk 6)
P0459B01.11	Phosphoribulokinase Precursor	At1g32060	PRK (PHOSPHORIBULOKINASE); ATP Binding / Phosphoribulokinase/ Protein Binding
P0459B01.28	Putative 60S Ribosomal Protein L12	At2g37190	60S Ribosomal Protein L12 (RPL12A)
P0459B01.29	Putative DNA Topoisomerase II	At3g23890	TOPII (TOPOISOMERASE II); ATP Binding / DNA Binding / DNA Topoisomerase (ATP-Hydrolyzing)
P0459B01.30-2	Unknown Protein	At1g47250	PAF2 (20S Proteasome Alpha Subunit F2); Peptidase
P0459B01.40	Putative Amino Acid Transporter	At1g31830	Amino Acid Permease Family Protein
P0459B01.42-1	Putative Serine/Threonine-Protein Kinase Mak	At4g10010	Protein Kinase Family Protein
P0459B01.7	26S Proteosome Regulatory Subunit-Like	At3g03060	Atpase
P0459B01.8	Unknown Protein	At1g31940	Unknown Protein
P0459B04.13	Putative Myb Factor Protein	At3g46130	MYB111 (Myb Domain Protein 111)
P0459B04.17	Putative Tonoplast Membrane Integral Protein	At4g01470	GAMMA-TIP3/TIP1;3 (Tonoplast Intrinsic Protein 1;3); Water Channel
P0459B04.20	Putative Legumin-Like Protein	At2g28680	Cupin Family Protein
P0460C04.10	Hypothetical Protein	At5g39980	Pentatricopeptide (PPR) Repeat-Containing Protein
P0460C04.11	Hypothetical Protein	At3g55960	NLI Interacting Factor (NIF) Family Protein
P0460C04.21	Putative Vacuolar Proton-Atpase Subunit 1	At2g28520	VHA-A1 (VACUOLAR PROTON ATPASE A 1); Atpase
P0460C04.4	Putative Calcium-Dependent Protein Kinase	At1g74740	CPK30 (Calcium-Dependent Protein Kinase 30); Calcium- And Calmodulin-Dependent Protein Kinase/ Kinase/ Protein Kinase
P0460E08.9	Ospk7	At4g18700	CIPK12 (CIPK12); Kinase
P0460H02.14	Hypothetical Protein	At3g26840	Esterase/Lipase/Thioesterase Family Protein
P0460H02.16	Unknown Protein	At5g58920	Unknown Protein
P0460H02.3	Hypothetical Protein	At2g27490	ATCOAE; ATP Binding / Dephospho-Coa Kinase
P0461A06.1	Unknown Protein	At1g16860	Merozoite Surface Protein-Related
P0461A06.15	Putative Germin Protein Type 1	At3g05950	Germin-Like Protein, Putative
P0461A06.7	Unknown Protein	At5g45100	Protein Binding / Zinc Ion Binding
P0461B08.19	Protein Kinase-Like	At2g45910	Protein Kinase Family Protein / U-Box Domain-Containing Protein
P0461B08.25	Aquaporin	At4g23400	PIP1;5/PIP1D (Plasma Membrane Intrinsic Protein 1;5); Water Channel
P0461B08.26	Putative MAP3K Alpha 1 Protein Kinase	At1g63700	YDA (YODA); Kinase
P0461B08.29	Putative Cytochrome P450	At4g00360	CYP86A2 (ABERRANT INDUCTION OF TYPE THREE GENES 1); Oxygen Binding
P0461B08.35	Putative Uracil Transport Protein	At5g03560	Nucleobase:Cation Symporter
P0461B08.4-2	Putative Tripeptidyl Peptidase II	At4g20850	TPP2 (TRIPEPTIDYL PEPTIDASE II); Subtilase
P0461D06.12	Putative High-Affinity Potassium Transporter	At2g30070	ATKT1 (Arabidopsis Thaliana K+ Uptake 1); Potassium Ion Transporter
P0461D06.24-1	ATP/GTP Binding Protein-Like	At5g10010	Unknown Protein
P0461D06.32	Putative Elongation Factor 2	At1g56075	Putative Elongation Factor
P0461D06.6	Unknown Protein	At3g26670	Unknown Protein

P0461F06.19	Putative Dioscorin Class A Precursor	At1g08065	Carbonate Dehydratase/ Zinc Ion Binding
P0461F06.39	Putative Zinc-Finger Protein	At5g22480	Zinc Finger (ZPR1-Type) Family Protein
P0462E11.12	Putative (+)-Delta-Cadinene Sythase	At3g14490	Terpene Synthase/Cyclase Family Protein
P0462E11.7	Putative Ubiquinone Oxidoreductase Subunit 1	At2g47910	Crr6 (Chlororespiratory Reduction 6)
P0462H08.25	Unknown Protein	At5g03430	Phosphoadenosine Phosphosulfate (PAPS) Reductase Family Protein
P0462H08.5	Unknown Protein	At5g24860	Fpf1 (Flowering Promoting Factor 1)
P0463A02.18	Putative NAD+ ADP-Ribosyltransferase	At4g02390	APP (ARABIDOPSIS POLY(ADP-RIBOSE) POLYMERASE); NAD+ ADP-Ribosyltransferase
P0463A02.24	Hypothetical Protein	At1g17010	Oxidoreductase, 2OG-Fe(II) Oxygenase Family Protein
P0463G12.43-1	Putative Aminopropyl Transferase	At5g53120	Spds3 (Spermidine Synthase 3)
P0466H10.25	Putative Pyrroline-5-Carboxylate Reductas	At5g14800	P5cr (Pyrroline-5- Carboxylate (P5c) Reductase)
P0466H10.27	Hypothetical Protein	At1g20780	Armadillo/Beta-Catenin Repeat Protein-Related / U-Box Domain-Containing Protein
P0466H10.3	Putative Glucan Endo-1,3-Beta-D-Glucosidase	At3g57260	BGL2 (PATHOGENESIS-RELATED PROTEIN 2); Glucan 1,3-Beta-Glucosidase/ Hydrolase, Hydrolyzing O-Glycosyl Compounds
P0467G09.22	Putative Catechol O-Methyltransferase	At4g35160	O-Methyltransferase Family 2 Protein
P0468B07.16	Hypothetical Protein	At3g56840	FAD-Dependent Oxidoreductase Family Protein
P0468B07.17	Hypothetical Protein	At3g60360	EDA14/UTP11 (U3 SMALL NUCLEOLAR RNA-ASSOCIATED PROTEIN 11, Embryo Sac Development Arrest 14)
P0468B07.18	Hypothetical Protein	At4g37510	Ribonuclease III Family Protein
P0468B07.19	Putative Calmodulin	At3g56800	CAM3 (CALMODULIN 3); Calcium Ion Binding
P0468B07.27	Proteasome Subunit Alpha Type 3	At2g27020	PAG1 (20S Proteasome Alpha Subunit G1); Peptidase
P0470A03.13-1	Putative Protein Phosphatase-2C	At5g36250	Protein Phosphatase 2C, Putative / PP2C, Putative
P0470A03.14	Putative Ser/Thr Specific Protein Phosphatase 2A	At1g17720	ATB BETA (Arabidopsis Thaliana Serine/Threonine Protein Phosphatase 2A 55 Kda Regulatory Subunit B Beta Isofor); Nucleotide Binding
P0470A12.34	Putative Peptide Transporter	At1g69870	Proton-Dependent Oligopeptide Transport (POT) Family Protein
P0470A12.38	Putative Rho GDP-Dissociation Inhibitor	At3g07880	Rho GDP-Dissociation Inhibitor Family Protein
P0470A12.8	Putative ABC Transporter	At1g70610	ATTAP1 (Arabidopsis Thaliana Transporter Associated With Antigen Processing Protein 1); Atpase, Coupled To Transmembrane Movement Of Substances
P0470B03.25	Nitrate Reductase Apoenzyme	At1g77760	Nia1 (Nitrate Reductase 1)
P0470D12.102	Selenium-Binding Protein-Like Protein	At4g32430	Pentatricopeptide (PPR) Repeat-Containing Protein
P0470D12.125	Putative Stress-Related Protein	At3g05500	Rubber Elongation Factor (REF) Family Protein
P0470D12.138	Putative TGF(Transfoming Growth Factor) Beta	At5g06360	Ribosomal Protein S8e Family Protein
P0470D12.142-1	Universal Stress Protein USP1-Like Protein	At2g47710	Universal Stress Protein (USP) Family Protein
P0470D12.145	SKP1(S-Phase Kinase Associated Protein)	At4g29370	Kelch Repeat-Containing F-Box Family Protein
P0470F10.1	Putative Osnac7 Protein	At2g46770	NST1 (NAC SECONDARY WALL THICKENING PROMOTING FACTOR1); Transcription Factor
P0470F10.11	Putative Acidic Ribosomal Protein P1a	At1g01100	60S Acidic Ribosomal Protein P1 (RPP1A)
P0470F10.14	Putative Avr9 Elicitor Response Protein	At1g32930	Galactosyltransferase Family Protein
P0470F10.18	Putative 40S RIBOSOMAL PROTEIN S13	At4g00100	ATRPS13A (RIBOSOMAL PROTEIN S13A); Structural Constituent Of Ribosome

P0470F10.20	Putative Calmodulin	At1g12310	Calmodulin, Putative
P0470G10.10	Transcriptional Coactivator P15 (PC4) Family	At5g09250	KIWI; DNA Binding / Transcription Coactivator
P0470G10.17	Putative Suppressor Of Actin 1	At5g66020	ATSAC1B/IBS2 (IMPAIRED IN BABA-INDUCED STERILITY 2); Phosphoinositide 5-Phosphatase
P0470G10.26	Putative Purine Nucleotide Binding Protein	At5g22370	EMB1705 (EMBRYO DEFECTIVE 1705); ATP Binding
P0470G10.35	Putative DNA J Domain Protein	At1g76700	DNAJ Heat Shock N-Terminal Domain-Containing Protein
P0471A11.10	Putative Phi-1	At1g35140	Phi-1 (Phosphate-Induced 1)
P0471A11.31-1	Putative Poly(A) Binding Protein	At5g10350	Polyadenylate-Binding Protein Family Protein / PABP Family Protein
P0471A11.34	LMBR1 Integral Membrane Protein-Like	At5g65290	LMBR1 Integral Membrane Family Protein
P0471A11.43	Unknown Protein	At1g72210	Basic Helix-Loop-Helix (Bhlh) Family Protein (Bhlh096)
P0471A11.50	Pentatricopeptide (PPR) Repeat-Containing	At1g73400	Pentatricopeptide (PPR) Repeat-Containing Protein
P0471B04.12	Putative Receptor Protein Kinase	At1g72180	Leucine-Rich Repeat Transmembrane Protein Kinase, Putative
P0471B04.13	Putative Amino Acid Permease 6	At1g10010	AAP8 (Amino Acid Permease 8); Amino Acid Permease
P0471B04.18	Hypothetical Protein	At4g15090	FAR1 (FAR-RED IMPAIRED RESPONSE 1); Zinc Ion Binding
P0471B04.23	Hypothetical Protein	At5g67540	Glycosyl Hydrolase Family Protein 43
P0471B04.4	Hypothetical Protein	At5g49880	Mitotic Checkpoint Family Protein
P0471B04.5	Putative Elicitor Response Protein	At1g33430	Galactosyltransferase Family Protein
P0472F10.2	Putative Serine Decarboxylase	At1g43710	EMB1075 (EMBRYO DEFECTIVE 1075); Carboxy-Lyase
P0472F10.24	Putative WD Repeat Domain 5B	At5g64730	Transducin Family Protein / WD-40 Repeat Family Protein
P0473D02.16	Putative NADH Dehydrogenase	At4g05020	NDB2 (NAD(P)H DEHYDROGENASE B2); Disulfide Oxidoreductase
P0473D02.40-1	N-Acetylglucosaminyltransferase-Like Protein	At1g03520	Glycosyltransferase Family 14 Protein / Core-2/I-Branching Enzyme Family Protein
P0473F05.0-3	Disease Resistance Protein RPM1-Like	At3g46710	Disease Resistance Protein (CC-NBS-LRR Class), Putative
P0473H02.4	Putative Glycoprotease	At4g22720	Glycoprotease M22 Family Protein
P0473H02.6	Putative	At4g32840	Phosphofructokinase Family Protein
P0474F07.6	Ripening-Related Protein-Like	At4g12390	Invertase/Pectin Methylesterase Inhibitor Family Protein
P0474F11.12	Kinesin Light Chain-Like	At2g31240	Tetratricopeptide Repeat (TPR)-Containing Protein
P0474F11.13	Putative Anthocyanin Acyltransferase	At3g29635	Transferase Family Protein
P0474F11.25-1	Putative Fibrillarin	At4g25630	Fib2 (Fibrillarin 2)
P0474F11.3	Putative Protein Serine/Threonine Kinase	At3g09830	Protein Kinase, Putative
P0474F11.34-1	Putative Ubiquitin C-Terminal Hydrolase	At1g65650	Ubiquitin Carboxyl-Terminal Hydrolase Family 1 Protein
P0474F11.8	Protein Phosphatase	At2g39840	TOPP4 (Type One Serine/Threonine Protein Phosphatase 4); Protein Phosphatase Type 1
P0475C12.28	Unknown Protein	At3g44830	Lecithin:Cholesterol Acyltransferase Family Protein / LACT Family Protein
P0475E07.126	Putative Phosphoglucomutase Precursor,	At5g17530	Phosphoglucosamine Mutase Family Protein
P0475F05.14-1	Unknown Protein	At3g52920	Unknown Protein
P0475F05.16	Branching Enzyme-3 Precursor	At5g03650	Sbe2.2 (Starch Branching Enzyme 2.2)

P0475F05.7	Putative CTR1-Like Protein Kinase	At5g03730	CTR1 (CONSTITUTIVE TRIPLE RESPONSE 1); Kinase
P0475H04.11	Unknown Protein	At1g10320	U2 Snrnp Auxiliary Factor-Related
P0476C12.12	Putative 26S Proteasome Regulatory Particle	At5g58290	RPT3 (Root Phototropism 3); Atpase
P0476C12.36	C2 Domain-Containing Protein-Like	At3g17980	C2 Domain-Containing Protein
P0476H10.11	PDR-Like ABC Transporter	At3g53480	ATPDR9/PDR9 (PLEIOTROPIC DRUG RESISTANCE 9); Atpase, Coupled To Transmembrane Movement Of Substances
P0476H10.22	Putative SNAP25	At1g13890	SNAP30 (Synaptosomal-Associated Protein 30)
P0476H10.24	Putative Galactomannan Galactosyltransferase	At5g07720	Galactosyl Transferase GMA12/MNN10 Family Protein
P0476H10.25	Putative 60S Acidic Ribosomal Protein P2A	At3g44590	60S Acidic Ribosomal Protein P2 (RPP2D)
P0476H10.42	Putative Seed Maturation Protein	At5g22470	NAD+ ADP-Ribosyltransferase
P0477A12.39	Unknown Protein	At5g60930	Chromosome-Associated Kinesin, Putative
P0477A12.6	Putative Ubiquitin / Ribosomal Protein CEP52	At3g52590	UBQ1 (EARLY-RESPONSIVE TO DEHYDRATION 16, UBIQUITIN EXTENSION PROTEIN 1); Protein Binding
P0477B05.11	Putative Nicotianamine Aminotransferase A	At5g36160	Aminotransferase-Related
P0477F03.101	Unknown Protein	At5g23040	CDF1 (CELL GROWTH DEFECT FACTOR 1); Heat Shock Protein Binding
P0477F03.105	Putative 2-Oxoglutarate-Dependent Dioxygenase	At1g52820	2-Oxoglutarate-Dependent Dioxygenase, Putative
P0478E02.11	Unknown Protein	At5g66090	Unknown Protein
P0478F09.14	Putative Extensin	At3g24480	Leucine-Rich Repeat Family Protein / Extensin Family Protein
P0478H03.1	Unknown Protein	At5g49540	Unknown Protein
P0478H03.16	Unknown Protein	At1g15160	MATE Efflux Family Protein
P0479C12.25-1	Putative Trehalose-6-Phosphate Synthase	At1g23870	ATTPS9 (Arabidopsis Thaliana Trehalose-Phosphatase/Synthase 9); Transferase, Transferring Glycosyl Groups / Trehalose-Phosphatase
P0479C12.38	Putative Receptor-Like Protein Kinase	At1g73080	PEPR1 (PEP1 RECEPTOR 1); ATP Binding / Kinase/ Protein Binding / Protein Serine/Threonine Kinase
P0479D12.11	MAP Kinase MAPK2	At1g10210	ATMPK1 (MITOGEN-ACTIVATED PROTEIN KINASE 1); MAP Kinase/ Kinase
P0479D12.34	Exocyst Subunit EXO70-Like Protein	At4g31540	ATEXO70G1 (Exocyst Subunit EXO70 Family Protein G1); Protein Binding
P0480C01.20	Putative PGPD14 Protein (Pollen Germination	At5g22920	Zinc Finger (C3HC4-Type RING Finger) Family Protein
P0480C01.27	Putative MRP Protein (ATP/GTP-Binding Protein)	At3g24430	HCF101 (HIGH-CHLOROPHYLL-FLUORESCENCE 101); ATP Binding
P0480E02.11	Nucleoid DNA-Binding Protein Cnd41-Like Protein	At3g18490	Aspartyl Protease Family Protein
P0481E12.1	Putative (1-4)-Beta-Mannan Endohydrolase	At4g28320	Glycosyl Hydrolase Family 5 Protein / Cellulase Family Protein
P0481E12.10	Putative Dihydroorotase	At4g22930	PYR4 (DIHYDROOROTASE, PYRIMIDIN 4, Dihydroorotase); Dihydroorotase
P0481E12.26	Unknown Protein	At1g29690	CAD1 (CONSTITUTIVELY ACTIVATED CELL DEATH 1); Oxidoreductase
P0481E12.28	Hypothetical Protein	At5g45690	Unknown Protein
P0481E12.30	Hypothetical Protein	At5g42660	Hypothetical Protein
P0481E12.31	Putative Ribosomal Protein L13	At1g78630	EMB1473 (EMBRYO DEFECTIVE 1473); Structural Constituent Of Ribosome
P0481F05.16	Putative Potential Copper-Transporting Atpase	At4g33520	PAA1 (Metal-Transporting P-Type Atpase 1)
P0482C06.15	Putative Prolyl Endopeptidase	At1g76140	Prolyl Oligopeptidase

P0482C06.2	1-Deoxy-D-Xylulose-5-Phosphate Reductoisomerase	At5g62790	Dxr (1-Deoxy-D-Xylulose 5-Phosphate Reductoisomerase)
P0482C06.5	Putative Protein Kinase	At1g62400	HT1 (HIGH LEAF TEMPERATURE 1); Kinase/ Protein Threonine/Tyrosine Kinase
P0482D04.13	Unknown Protein	At5g15790	Zinc Finger (C3HC4-Type RING Finger) Family Protein
P0482D04.17	Unknown Protein	At1g27440	GUT2; Catalytic
P0482D04.4	Enoyl Coa Hydratase-Like Protein	At5g43280	Atdci1 (Delta(3,5),Delta(2,4)-Dienoyl-Coa Isomerase 1)
P0482D04.5	Hypothetical Protein	At5g41060	Zinc Ion Binding
P0482D04.9	Putative Ubiquitin Conjugating Enzyme	At5g50870	UBC27 (Ubiquitin-Conjugating Enzyme 26); Ubiquitin-Protein Ligase
P0482F12.1-1	Bax Inhibitor-1 (BI-1) (Osbi-1)	At5g47120	Atbi-1 (Arabidopsis Bax Inhibitor 1)
P0482F12.19	Putative 28 Kda Golgi SNARE Protein	At2g45200	GOS12 (GOLGI SNARE 12); SNARE Binding
P0482F12.21-1	Putative TPR Repeat Containing Protein	At3g04830	Binding
P0482F12.5	Putative Alkaline/Neutral Invertase	At4g34860	Beta-Fructofuranosidase
P0483C08.42	Putative 40S Ribosomal Protein S8	At5g20290	40S Ribosomal Protein S8 (RPS8A)
P0483C08.45	Putative O-Linked N-Acetyl Glucosamine	At3g04240	SEC (SECRET AGENT); Transferase, Transferring Glycosyl Groups
P0483D07.1	'Unknown Protein, WD Domain, G-Beta Repeat,	At1g15440	Transducin Family Protein / WD-40 Repeat Family Protein
P0483D07.18	'Unknown Protein, Contains Histidine-Containing	At3g16360	AHP4 (HPT PHOSPHOTRANSMITTER 4); Histidine Phosphotransfer Kinase/ Transferase, Transferring Phosphorus-Containing Groups
P0483D07.2	'Unknown Protein, Similar To DJ-1/Pfpi Family,	At1g53280	DJ-1 Family Protein
P0483D07.3	Putative Heat Shock Protein HSP101	At1g74310	ATHSP101 (HEAT SHOCK PROTEIN 101); ATP Binding / Atpase
P0483D07.5	Putative Oligosaccharyl Transferase STT3	At5g19690	STT3A (STAUROSPORIN AND TEMPERATURE SENSITIVE 3-LIKE A); Oligosaccharyl Transferase
P0483D07.6	Unknown Protein	At3g03010	Unknown Protein
P0483E06.129	Putative Phosphoglycerate Dehydrogenase	At1g72190	Oxidoreductase Family Protein
P0483G10.1	Unknown Protein	At3g01650	Copine-Related
P0483G10.13	Unknown Protein	At5g11870	Unknown Protein
P0483G10.17	Putative Peroxidase	At1g71695	Peroxidase 12 (PER12) (P12) (PRXR6)
P0483G10.3	Putative Nitrate Transporter	At3g45680	Proton-Dependent Oligopeptide Transport (POT) Family Protein
P0485B12.35	Alpha-Expansin	At1g69530	Atexpa1 (Arabidopsis Thaliana Expansin A1)
P0485G01.13	Ubiquitin-Conjugating Enzyme E2	At1g16890	UBC36; Ubiquitin-Protein Ligase
P0485G01.25	Unknown Protein	At4g13240	ATROPGEF9/ROPGEF9 (KINASE PARTNER PROTEIN-LIKE); Rho Guanyl-Nucleotide Exchange Factor
P0485G01.26	Peroxiredoxin	At1g65970	TPX2 (THIOREDOXIN-DEPENDENT PEROXIDASE 2); Antioxidant
P0486F07.29	Putative Equilibrative Nucleoside Transporter	At1g70330	ENT1,AT (EQUILIBRATIVE NUCLEOTIDE TRANSPORTER 1); Nucleoside Transporter
P0486F07.35	Putative Copper Chaperone	At5g02600	Heavy-Metal-Associated Domain-Containing Protein
P0486F07.4	Putative Integral Membrane Protein	At5g19980	Integral Membrane Family Protein
P0486G03.16	N-Type ATP Pyrophosphatase-Like	At2g44270	Unknown Protein
P0486G03.2	Putative Peptidylprolyl Isomerase D	At2g15790	Sqn (Squint)

P0486G03.3	Armadillo/Beta-Catenin Repeat Protein-Like	At4g33940	Zinc Finger (C3HC4-Type RING Finger) Family Protein
P0486G03.5	Zinc Metalloproteinase-Like	At1g49630	ATPREP2; Metalloendopeptidase
P0486G03.7	Unknown Protein	At4g33380	Unknown Protein
P0487D09.13	Ankyrin-Like Protein	At2g01680	Ankyrin Repeat Family Protein
P0487D09.19	Putative Myosin II Heavy Chain	At1g68060	ATMAP70-1 (MICROTUBULE-ASSOCIATED PROTEINS 70-1); Microtubule Binding
P0487D09.22	Putative Dihydropyrimidine Dehydrogenase	At3g17810	Dihydroorotate Dehydrogenase Family Protein / Dihydroorotate Oxidase Family Protein
P0487D09.5	Erwinia Induced Protein 2	At5g17190	Unknown Protein
P0487D09.7	Putative Zn-Dependent Protease With Chaperone	At5g51740	Peptidase M48 Family Protein
P0487D09.8	Glutamine Synthetase Shoot Isozyme	At5g37600	ATGSR1 (Arabidopsis Thaliana Glutamine Synthase Clone R1); Glutamate-Ammonia Ligase
P0487E11.17	Putative GTP-Binding Protein	At4g02080	ASAR1 (Arabidopsis Thaliana Secretion-Associated RAS Super Family 2); GTP Binding
P0487H02.5	Putative Mtn21	At1g09380	Integral Membrane Family Protein / Nodulin Mtn21-Related
P0487H05.14	Putative Riboflavin Biosynthesis Protein Ribd	At3g47390	Cytidine/Deoxycytidylate Deaminase Family Protein
P0487H05.16-2	Nucellin-Like Aspartic Protease-Like	At1g05840	Aspartyl Protease Family Protein
P0487H05.39	Putative Importin 7<Ran-Binding Protein 7	At2g31660	SAD2 (SUPER SENSITIVE TO ABA AND DROUGHT2); Protein Transporter
P0488B06.38-1	Unknown Protein	At1g15080	ATPAP2 (PHOSPHATIDIC ACID PHOSPHATASE 2); Phosphatidate Phosphatase
P0489A01.10	Hypothetical Protein	At4g18010	IP5PII (INOSITOL POLYPHOSPHATE 5-PHOSPHATASE II); Inositol-Polyphosphate 5-Phosphatase
P0489A01.13	Putative Cytochrome P450	At2g21910	CYP96A5 (Cytochrome P450, Family 96, Subfamily A, Polypeptide 5); Oxygen Binding
P0489A01.17	Hypothetical Protein	At1g65710	Unknown Protein
P0489A01.9	Hypothetical Protein	At3g10530	Transducin Family Protein / WD-40 Repeat Family Protein
P0489A05.24	Putative Major Intrinsic Protein	At4g18910	NIP1;2/NLM2 (NOD26-Like Intrinsic Protein 1;2); Water Channel
P0489A05.5	Putative MADS-Box Protein	At2g42830	SHP2 (SHATTERPROOF 2); Transcription Factor
P0489B03.15	Putative 60S Ribosomal Protein	At1g08360	60S Ribosomal Protein L10A (RPL10aA)
P0489G09.22	Putative Endo-Beta-1,4-Glucanase	At1g64390	Endo-1,4-Beta-Glucanase, Putative / Cellulase, Putative
P0491E01.9	Cyclin-Like	At3g21870	CYCP2;1 (Cyclin P2;1); Cyclin-Dependent Protein Kinase
P0491F11.12	Putative 5-3 Exoribonuclease	At5g42540	XRN2 (EXORIBONUCLEASE 2); 5'-3' Exonuclease/ Nucleic Acid Binding
P0491F11.13	Putative 3-Phosphoinositide-Dependent Protein	At3g10540	3-Phosphoinositide-Dependent Protein Kinase, Putative
P0491F11.16	Putative Amidophosphoribosyltransferase	At4g34740	ATASE2/ATD2 (GLN PHOSPHORIBOSYL PYROPHOSPHATE AMIDOTRANSFERASE 2); Amidophosphoribosyltransferase
P0491F11.2	Hypothetical Protein	At1g72140	Proton-Dependent Oligopeptide Transport (POT) Family Protein
P0492E07.108	Spermidine Synthase 1	At1g23820	Spds1 (Spermidine Synthase 1)
P0492E07.115	Putative CLB1 Protein (Calcium-Dependent Lipid	At3g61050	Lipid Binding
P0492E07.120	UIP2-Like Protein	At5g42190	ASK2 (ARABIDOPSIS SKP1-LIKE 2); Ubiquitin-Protein Ligase
P0492E07.128	Unknown Protein	At3g13930	Dihydrolipoamide S-Acetyltransferase, Putative
P0492F05.14	3-Methyl-2-Oxobutanoate	At2g46110	KPHMT1/PANB1 (KETOPANTOATE HYDROXYMETHYLTRANSFERASE 1); 3-Methyl-2-Oxobutanoate Hydroxymethyltransferase

P0492F05.17	Putative Late Embryogenesis Abundant Protein	At1g01470	Lea14 (Late Embryogenesis Abundant 14)
P0492F05.28	Hypothetical Protein	At4g12550	AIR1 (Auxin-Induced In Root Cultures 1); Lipid Binding
P0492F05.5	Dimethylaniline Monooxygenase-Like Protein	At5g25620	YUC6 (YUCCA6); Monooxygenase
P0492G09.17	Putative Ethylene-Forming Enzyme	At3g21420	Oxidoreductase, 2OG-Fe(II) Oxygenase Family Protein
P0492G09.19	Putative HAK2 (K+ Transporter)	At3g02050	KUP3 (K+ Uptake Permease 3); Potassium Ion Transporter
P0492G09.21	Putative Cytochrome C1 Precursor	At5g40810	Cytochrome C1, Putative
P0492G09.25	Putative Serine/Threonine Kinase PBS1 Protein	At5g18610	Protein Kinase Family Protein
P0492G09.26	Unknown Protein	At5g18630	Lipase Class 3 Family Protein
P0492G09.7	Pir7b Protein (Pseudomonas Inducible Protein)	At2g23600	ACL (ACETONE-CYANOHYDRIN LYASE); Hydrolase
P0493A04.32	Unknown Protein	At1g02180	Ferredoxin-Related
P0493A04.9	Plastid (P)Ppgpp Synthase	At3g14050	RSH2 (RELA-SPOT HOMOLOG); Catalytic
P0494A10.15	Putative Fructose-Bisphosphate Aldolase	At2g01140	Fructose-Bisphosphate Aldolase, Putative
P0494A10.16	Putative ATP-Dependent RNA Helicase A	At1g48650	Helicase Domain-Containing Protein
P0494D11.1	Putative 3-Glucanase	At4g31140	Glycosyl Hydrolase Family 17 Protein
P0494D11.3	Putative Proteasome 26S Non-Atpase Subunit 1	At2g32730	26S Proteasome Regulatory Subunit, Putative
P0494D11.7	Putative Phosphoethanolamine	At2g38670	PECT1 (PHOSPHORYLETHANOLAMINE CYTIDYLYLTRANSFERASE 1); Ethanolamine-Phosphate Cytidylyltransferase
P0495C02.18	Putative Peroxisomal Membrane Protein 22 Kda	At4g04470	PMP22 (Peroxisomal Membrane Protein 22)
P0495H05.17	Hypothetical Protein	At1g58060	Helicase Domain-Containing Protein
P0495H05.31	Hypothetical Protein	At1g12720	Mutator-Like Transposase Family
P0495H05.61	Putative UDP-Glucose 4-Epimerase	At1g30620	Mur4 (Murus 4)
P0496C02.103	Unknown Protein	At4g21770	Pseudouridine Synthase Family Protein
P0496D04.15	Putative DNA-Directed RNA Polymerase II 13.6K	At3g52090	ATRPB13.6 (Arabidopsis Thaliana RNA Polymerase II 13.6 Kda Subunit); DNA Binding / DNA-Directed RNA Polymerase
P0496D04.20-1	Putative Integral Membrane Protein	At2g32040	Integral Membrane Transporter Family Protein
P0496D04.21	Hypothetical Protein	At4g14830	Unknown Protein
P0496E03.28	Putative Protein Kinase Xa21 D, Receptor Type	At3g47570	Leucine-Rich Repeat Transmembrane Protein Kinase, Putative
P0496E03.6	Putative Ankyrin-Kinase	At1g14000	Protein Kinase Family Protein / Ankyrin Repeat Family Protein
P0496E03.9	Putative Acetolactate Synthase Small Subunit	At2g31810	Acetolactate Synthase Small Subunit, Putative
P0496H05.17	Putative Cyt-P450 Monooxygenase	At2g45550	CYP76C4 (Cytochrome P450, Family 76, Subfamily C, Polypeptide 4); Oxygen Binding
P0496H05.25	Putative Peptidylprolyl Isomerase	At5g48570	Peptidyl-Prolyl Cis-Trans Isomerase, Putative / FK506-Binding Protein, Putative
P0497A05.15	Unknown Protein	At1g05690	BT3 (BTB And TAZ Domain Protein 3); Protein Binding / Transcription Regulator
P0497A05.18	Proline Transport Protein-Like	At2g39890	Prot1 (PROLINE TRANSPORTER 1)
P0498E12.107	Putative Reticuline Oxidase Precursor	At5g44400	FAD-Binding Domain-Containing Protein
P0498H04.1	Putative Bile Acid Beta-Glucosidase	At1g33700	Unknown Protein
P0498H04.19	Putative AER	At5g67150	Transferase Family Protein

P0498H04.25	Unknown Protein	At1g08480	Unknown Protein
P0498H04.26	Putative GDSL-Motif Lipase/Hydrolase Protein	At1g29670	GDSL-Motif Lipase/Hydrolase Family Protein
P0498H04.27	Putative Peroxidase 47 Precursor	At4g33420	Peroxidase, Putative
P0498H04.29	Putative Fructokinase	At4g10260	Pfkb-Type Carbohydrate Kinase Family Protein
P0499G10.13-2	GEKO1-Like Protein	At2g03800	Gek1 (Geko1)
P0499G10.22	Putative ABI3-Interacting Protein 2	At3g22440	Hydroxyproline-Rich Glycoprotein Family Protein
P0501E09.27	Putative UNC50	At2g15240	UNC-50 Family Protein
P0501E09.36-2	Putative Na+/H+ Antiporter Precursor	At3g19490	ATNHD1 (Arabidopsis Thaliana Na/H Antiporter 1); Sodium:Hydrogen Antiporter
P0501G01.15	Hypothetical Protein	At5g24030	C4-Dicarboxylate Transporter/Malic Acid Transport Family Protein
P0501G01.21	Putative Endopolygalacturonase	At3g59850	Polygalacturonase, Putative / Pectinase, Putative
P0501G01.24	Hypothetical Protein	At1g07380	Ceramidase Family Protein
P0501G01.6	Hypothetical Protein	At4g01210	Glycosyltransferase Family Protein 1
P0501G01.7	Putative Uroporphyrinogen Decarboxylase	At3g14930	HEME1; Uroporphyrinogen Decarboxylase
P0501G04.11	Putative Pentatricopeptide (PPR)	At2g37230	Pentatricopeptide (PPR) Repeat-Containing Protein
P0501G04.26	Putative Wall-Associated Kinase	At1g21270	WAK2 (Wall-Associated Kinase 2); Protein Serine/Threonine Kinase
P0501G04.29	Putative CLAVATA1 Receptor Kinase	At4g28650	Leucine-Rich Repeat Transmembrane Protein Kinase, Putative
P0501G04.4	Kinesin Light Chain-Like Protein	At4g10840	Kinesin Light Chain-Related
P0501G04.9	Hydroperoxide Lyase	At4g15440	HPL1 (HYDROPEROXIDE LYASE 1); Heme Binding / Iron Ion Binding / Monooxygenase
P0503B05.26	Putative Hydroquinone Glucosyltransferase	At4g01070	UDP-Glucoronosyl/UDP-Glucosyl Transferase Family Protein
P0503C12.1	Putative Oxidoreductase-Like Protein	At3g15090	Oxidoreductase, Zinc-Binding Dehydrogenase Family Protein
P0503D09.101	Unknown Protein	At5g46090	Unknown Protein
P0503E05.6	Putative Hydoxyethylthiazole Kinase	At3g24030	Hydroxyethylthiazole Kinase Family Protein
P0504A05.1	Unknown Protein	At4g29850	Unknown Protein
P0504A05.24	Putative 4-Coumarate Coenzyme A Ligase	At1g51680	4cl1 (4-Coumarate:Coa Ligase 1)
P0504A05.25	Integral Membrane Protein-Like	At2g35760	Integral Membrane Family Protein
P0504A05.26	Putative Calmodulin-Binding Protein	At4g25800	Calmodulin-Binding Protein
P0504D03.19	Unknown Protein	At1g51160	Synbindin, Putative
P0504D03.20	Unknown Protein	At3g23620	Brix Domain-Containing Protein
P0504D03.3	Putative ARG1 Protein (Altered Response To	At1g68370	Arg1 (Altered Response To Gravity 1)
P0504E02.19	Photosystem II Protein W-Like Protein	At4g28660	Photosystem II Reaction Centre W (Psbw) Family Protein
P0504E02.20	Putative Ribonucleoprotein	At4g03110	RNA-Binding Protein, Putative
P0504E02.27	Putative Type IIB Calcium Atpase	At3g57330	Calcium-Transporting Atpase, Plasma Membrane-Type, Putative / Ca2+-Atpase, Putative (ACA11)
P0504E02.3	Putative Dermal Glycoprotein Precursor	At1g03230	Extracellular Dermal Glycoprotein, Putative / EDGP, Putative
P0505D12.20	Putative Histone H3	At5g65360	Histone H3

P0505D12.22	Fructose-1,6-Bisphosphatase	At1g43670	Fructose-1,6-Bisphosphatase, Putative / D-Fructose-1,6-Bisphosphate 1-Phosphohydrolase, Putative / Fbpase, Putative
P0505D12.23	Hypothetical Protein	At1g01050	Inorganic Pyrophosphatase, Putative (Soluble) / Pyrophosphate Phospho-Hydrolase, Putative / Ppase, Putative
P0505D12.6	Putative Uricase	At2g26230	Uricase / Urate Oxidase / Nodulin 35, Putative
P0505H05.2	Putative Cysteine Proteinase	At2g27420	Cysteine Proteinase, Putative
P0506A10.22	Hypothetical Protein	At2g45750	Dehydration-Responsive Family Protein
P0506B12.12	Putative Respiratory Burst Oxidase Protein	At5g60010	Ferric Reductase-Like Transmembrane Component Family Protein
P0506B12.16	Putative Histone H4	At5g59970	Histone H4
P0506B12.20	Putative ABC Transporter-Like Protein	At3g55090	ABC Transporter Family Protein
P0506B12.23	Unknown Protein	At5g18520	Unknown Protein
P0506B12.26	Unknown Protein	At3g12360	Ankyrin Repeat Family Protein
P0506B12.36	40S Ribosomal Protein	At5g02960	40S Ribosomal Protein S23 (RPS23B)
P0506B12.4	Putative CAAT-Box DNA Binding Protein	At4g14540	CCAAT-Box Binding Transcription Factor Subunit B (NF-YB) (HAP3) (AHAP3) Family
P0506C07.14	Putative Disease Resistance Protein RPR1	At1g58410	Disease Resistance Protein (CC-NBS-LRR Class), Putative
P0506C07.2	Thioredoxin H-Type (TRX-H)	At1g19730	ATTRX4 (Thioredoxin H-Type 4); Thiol-Disulfide Exchange Intermediate
P0506C07.26	Putative Actin Interacting Protein	At4g36400	FAD Linked Oxidase Family Protein
P0506E04.16	Putative Thiamine Pyrophosphokinase	At2g44750	Thiamin Pyrophosphokinase, Putative
P0506E04.5	Hypothetical Protein	At3g25270	Unknown Protein
P0506F02.101	Unknown Protein	At2g22010	Zinc Finger (C3HC4-Type RING Finger) Family Protein
P0506F02.102	Putative 4-Alpha-Glucanotransferase	At5g64860	DPE1 (DISPROPORTIONATING ENZYME); 4-Alpha-Glucanotransferase
P0506F02.114	Putative GTP-Binding Protein DRG	At4g39520	GTP-Binding Protein, Putative
P0506F02.124	Putative Receptor-Like Protein Kinase 4	At4g23160	Protein Kinase Family Protein
P0506F02.128	Putative Myb Protein	At3g47600	MYB94 (Myb Domain Protein 94); DNA Binding / Transcription Factor
P0507H06.12	Unknown Protein	At5g43660	Oxidoreductase, Acting On Paired Donors, With Incorporation Or Reduction Of Molecular Oxygen, 2-Oxoglutarate As One Donor, And Incorporation Of One Atom Each Of Oxygen Into Both Donors
P0507H12.6	Putative Succinate Dehydrogenase Flavoprotein	At5g66760	SDH1-1 (Succinate Dehydrogenase 1-1)
P0508B05.10	Unknown Protein	At5g46960	Invertase/Pectin Methylesterase Inhibitor Family Protein
P0508B05.30	Putative Vacuolar-Type H+-Translocating	At1g16780	Vacuolar-Type H+-Translocating Inorganic Pyrophosphatase, Putative
P0509B06.12	Putative 0-Deacetylbaccatin III-10-O-Acetyl	At3g03480	CHAT (ACETYL COA:(Z)-3-HEXEN-1-OL ACETYLTRANSFERASE); Acetyl Coa:(Z)-3-Hexen-1-Ol Acetyltransferase
P0509B06.2	Putative Aspartate Transaminase	At1g80360	Aminotransferase Class I And II Family Protein
P0510C12.1	Putative Polyubiquitin	At1g65350	UBQ13 (Ubiquitin 13)
P0510F09.19	Hypothetical Protein	At5g11960	Hypothetical Protein
P0510F09.21	Lysine Decarboxylase-Like Protein	At5g11950	Hypothetical Protein
P0510F09.22	SPP30 Homolog	At5g58030	Transport Protein Particle (TRAPP) Component Bet3 Family Protein

P0512C01.16	Putative Peptide Transporter	At1g52190	Proton-Dependent Oligopeptide Transport (POT) Family Protein
P0512C01.2	Putative Permease 1	At2g34190	Xanthine/Uracil Permease Family Protein
P0512C01.25	Glutelin Type I Precursor	At1g03890	Cupin Family Protein
P0512C01.3	Putative Dynein Light Chain	At5g20110	Dynein Light Chain, Putative
P0512C01.36	Putative Glycerophosphoryl Diester	At5g08030	Glycerophosphoryl Diester Phosphodiesterase Family Protein
P0512C01.5	Unknown Protein	At1g52240	ATROPGEF11/ROPGEF11 (KINASE PARTNER PROTEIN-LIKE); Rho Guanyl-Nucleotide Exchange Factor
P0512C01.6	Hypothetical Protein	At4g23440	Transmembrane Receptor
P0512C01.8	Aspartate Aminotransferase	At5g11520	Asp3 (Aspartate Aminotransferase 3)
P0512G09.14	Unknown Protein	At3g46480	Oxidoreductase, 2OG-Fe(II) Oxygenase Family Protein
P0512G09.7	Unknown Protein	At5g11700	Glycine-Rich Protein
P0512H04.9-2	Unknown Protein	At2g25800	Unknown Protein
P0514G12.27	Unknown Protein	At3g53210	Nodulin Mtn21 Family Protein
P0514G12.39	Oseya1	At2g35320	ATEYA (ARABIDOPSIS THALIANA EYES ABSENT HOMOLOG); Protein Tyrosine Phosphatase, Metal-Dependent
P0514G12.8	Ferredoxin-NADP+ Reductase	At1g20020	Atlfnr2 (Leaf Fnr 2)
P0514H03.3	Hypothetical Protein	At4g21300	Pentatricopeptide (PPR) Repeat-Containing Protein
P0515A04.20	Putative Elicitor Inducible Beta-1,3-Glucanase	At4g17180	Glycosyl Hydrolase Family 17 Protein
P0515A04.25	Cation Exchanger-Like Protein	At1g54110	Cation Exchanger, Putative (CAX10)
P0515A04.36	Putative NBS-LRR Type Disease Resistance	At4g26090	Rps2 (Resistant To P. Syringae 2)
P0516G10.12-1	Putative Proline-Rich Protein APG	At1g33810	Unknown Protein
P0516G10.12-2	Unknown Protein	At2g23540	GDSL-Motif Lipase/Hydrolase Family Protein
P0518C01.10	Putative Cytochrome B5	At2g32720	B5 #4 (Cytochrome B5 Family Protein #4); Heme Binding / Transition Metal Ion Binding
P0518C01.3	Unknown Protein	At3g27110	Peptidase M48 Family Protein
P0518C01.6	Unknown Protein	At3g48250	Pentatricopeptide (PPR) Repeat-Containing Protein
P0518C01.9	Putative Cysteine Proteinase	At1g20850	XCP2 (XYLEM CYSTEINE PEPTIDASE 2); Cysteine-Type Peptidase/ Peptidase
P0518F01.10	Hypothetical Protein	At4g29530	2,3-Diketo-5-Methylthio-1-Phosphopentane Phosphatase Family
P0518F01.14	Putative Chlorophyll A/B-Binding Protein 2	At2g34430	LHB1B1 (Photosystem II Light Harvesting Complex Gene 1.4); Chlorophyll Binding
P0518F01.24	Putative Cytochrome P450	At3g14630	CYP72A9 (Cytochrome P450, Family 72, Subfamily A, Polypeptide 9); Oxygen Binding
P0518F01.9	Hypothetical Protein	At4g13650	Pentatricopeptide (PPR) Repeat-Containing Protein
P0519A12.14	Putative Glutaredoxin I	At1g77370	Glutaredoxin, Putative
P0519A12.15	Putative Aldehyde Dehydrogenase	At1g44170	Aldh3h1 (Aldehyde Dehydrogenase 4)
P0519D04.19	Hypothetical Protein	At5g11540	FAD-Binding Domain-Containing Protein
P0519E02.19	Unknown Protein	At5g49830	Hypothetical Protein
P0519E02.23	Putative Squalene Synthase	At4g34640	SQS1 (SQUALENE SYNTHASE 1); Farnesyl-Diphosphate Farnesyltransferase
P0519E06.15	Amino Acid Permease-Like	At1g05940	CAT9 (CATIONIC AMINO ACID TRANSPORTER 9); Cationic Amino Acid Transporter

P0519E06.2	Unknown Protein	At2g44850	Unknown Protein
P0519E06.25	Putative Cell Division Cycle Protein 23	At3g48150	APC8 (Anaphase-Promoting Complex/Cyclosome 8); Binding
P0519E12.121	Putative Transmembrane Protein	At1g14010	Emp24/Gp25l/P24 Family Protein
P0519E12.133	DEAD Box Protein-Like	At1g16280	DEAD/DEAH Box Helicase, Putative
P0519E12.134	Unknown Protein	At4g08810	SUB1 (Short Under Blue Light 1)
P0520B06.15	Putative TATA Binding Protein-Associated Factor	At1g04950	TAFII59 (TATA Box Associated Factor II 59); Transcription Initiation Factor
P0520B06.18	Unknown Protein	At1g68300	Universal Stress Protein (USP) Family Protein
P0520B06.19	Unknown Protein	At4g05400	Unknown Protein
P0520B06.20	Putative 26S Proteasome Subunit	At5g45620	26S Proteasome Regulatory Subunit, Putative (RPN9)
P0520B06.4	Oryza Sativa MAP Kinase Kinase 1	At5g56580	ATMKK6 (ARABIDOPSIS NQK1); Kinase
P0521F09.28	Putative Uracil Phosphoribosyltransferase	At1g55810	Uracil Phosphoribosyltransferase, Putative / UMP Pyrophosphorylase, Putative / Uprtase, Putative
P0523A04.108	Unknown Protein	At5g05950	MEE60 (Maternal Effect Embryo Arrest 60)
P0523B07.38-1	Putative Polyphosphoinositide Binding Protein	At5g47730	SEC14 Cytosolic Factor, Putative / Polyphosphoinositide-Binding Protein, Putative
P0523B07.45	Putative Protein Kinase G11A	At5g47750	Protein Kinase, Putative
P0523B07.46	Putative Ribosomal Protein L17	At1g27400	60S Ribosomal Protein L17 (RPL17A)
P0523B07.7	Putative Flavonol 4'-Sulfotransferase	At5g07010	Sulfotransferase Family Protein
P0524E08.104	Hydrolase-Like Protein	At5g09430	Hydrolase
P0524E08.106	Unknown Protein	At1g34640	Unknown Protein
P0524E08.108	Unknown Protein	At1g78190	TRM112-Like Protein
P0524E08.116	Unknown Protein	At1g35780	Unknown Protein
P0524E08.130	Putative Trehalose-6-Phosphate Phosphatase	At5g65140	Trehalose-6-Phosphate Phosphatase, Putative
P0524E08.133	UMP/CMP Kinase A	At3g60180	Uridylate Kinase, Putative / Uridine Monophosphate Kinase, Putative / UMP Kinase, Putative
P0524F03.27	Putative Golgi SNARE Protein	At1g15880	GOS11 (GOLGI SNARE 11); SNARE Binding
P0524F03.3	Exostosin Family-Like Protein	At3g03650	EDA5 (Embryo Sac Development Arrest 5); Catalytic
P0524G08.101	Unknown Protein	At3g12260	Complex 1 Family Protein / LVR Family Protein
P0524G08.102	Putative Xylulose Kinase	At5g49650	Xylulose Kinase, Putative
P0524G08.110	Putative Calcium/Calmodulin-Dependent Protein	At2g41140	CRK1 (CDPK-RELATED KINASE 1); Calcium Ion Binding / Calcium-Dependent Protein Serine/Threonine Phosphatase/ Kinase
P0524G08.116	10 Kda Chaperonin	At5g20720	CPN20 (CHAPERONIN 20); Calmodulin Binding
P0524G08.122	Lipase-Like Protein	At1g28600	Carboxylic Ester Hydrolase
P0524G08.123	Transport Protein Particle Component Bet3-Like	At5g54750	Transport Protein Particle (TRAPP) Component Bet3, Putative
P0524G08.134	Putative Transcription Factor APFI	At1g47260	APFI; Carbonate Dehydratase
P0528B09.18	Glyceraldehyde-3-Phosphate Dehydrogenase	At2g24270	ALDH11A3 (Aldehyde Dehydrogenase 11A3); 3-Chloroallyl Aldehyde Dehydrogenase
P0528B09.19	Putative Omega-6 Fatty Acid Desaturase,	At4g30950	FAD6 (FATTY ACID DESATURASE 6); Omega-6 Fatty Acid Desaturase
P0528B09.25	Putative CBL-Interacting Protein Kinase	At4g30960	CIPK6 (CBL-INTERACTING PROTEIN KINASE 6); Kinase

P0528B09.35-1	Putative Cinnamoyl-Coa Reductase	At1g15950	Ccr1 (Cinnamoyl Coa Reductase 1)
P0528B09.37	Putative Chorimate Mutase	At5g10870	ATCM2 (CHORISMATE MUTASE 2); Chorismate Mutase
P0529E05.10	Hypothetical Protein	At3g09060	Pentatricopeptide (PPR) Repeat-Containing Protein
P0529E05.11	Hypothetical Protein	At3g09050	Unknown Protein
P0529E05.15	Unknown Protein	At2g39940	COI1 (CORONATINE INSENSITIVE 1); Ubiquitin-Protein Ligase
P0529H11.17	Putative Laccase	At3g09220	LAC7 (Laccase 7); Copper Ion Binding / Oxidoreductase
P0529H11.19	Unknown Protein	At2g37970	SOUL Heme-Binding Family Protein
P0529H11.24	Ataxin 3-Like Protein	At3g54130	Josephin Family Protein
P0529H11.26	Putative Steroid Reductase DET2	At2g38050	Det2 (De-Etiolated 2)
P0529H11.27	Alpha 1,4-Glucan Phosphorylase H Isozyme	At3g46970	ATPHS2/PHS2 (ALPHA-GLUCAN PHOSPHORYLASE 2); Phosphorylase/ Transferase, Transferring Glycosyl Groups
P0529H11.3	Unknown Protein	At3g54020	Phosphatidic Acid Phosphatase-Related / PAP2-Related
P0529H11.31	Hypothetical Protein	At3g46980	Carbohydrate Transporter/ Sugar Porter
P0530H10.9	Putative Ferrochelatase II	At2g30390	Ferrochelatase II
P0533E11.20	Cytokinesis-Related Sec1 Protein-Like	At1g12360	KEU (KEULE); Protein Transporter
P0534A03.127	Putative Vacuolar ATP Synthase Subunit H	At3g42050	Vacuolar ATP Synthase Subunit H Family Protein
P0534H07.20	Extensin-Like Protein	At3g22800	Leucine-Rich Repeat Family Protein / Extensin Family Protein
P0534H07.34	Putative Z-Protein	At1g03070	Glutamate Binding
P0534H07.8	Putative Inositol-1,4,5-Trisphosphate	At3g63240	Endonuclease/Exonuclease/Phosphatase Family Protein
P0537A05.2	Putative Peroxidase	At5g64120	Peroxidase, Putative
P0537A05.24	Hypothetical Protein	At5g30145	Unknown Protein
P0539D10.15	Putative Xyloglucan Fucosyltransferase	At2g03220	FT1 (FUCOSYLTRANSFERASE 1); Fucosyltransferase/ Transferase, Transferring Glycosyl Groups
P0539D10.17	Putative Light-Harvesting Chlorophyll-A/B	At1g45474	LHCA5 (Photosystem I Light Harvesting Complex Gene 5)
P0539D10.4	Hypothetical Protein	At5g37770	TCH2 (TOUCH 2); Calcium Ion Binding
P0543C11.29	Putative Nicotianamine Aminotransferase A	At5g53970	Aminotransferase, Putative
P0543C11.34	Putative Dnaj-Like Protein	At2g20560	DNAJ Heat Shock Family Protein
P0543C11.35	Putative Guanylate Binding Protein	At5g46070	GTP Binding / Gtpase
P0543C11.42	Hypothetical Protein	At1g19480	Hhh-GPD Base Excision DNA Repair Family Protein
P0543D10.15	Putative Aminopeptidase N	At1g63770	Peptidase M1 Family Protein
P0543D10.17-1	Putative Ripening Regulated Protein DDTFR18	At4g25640	MATE Efflux Family Protein
P0543D10.26	Putative SAP1 Protein	At3g04570	DNA-Binding Protein-Related
P0543D10.30	Putative Bet1/Sft1-Related SNARE (Atbs14a)	At3g58170	ATBS14A; Protein Transporter
P0544B02.10	Putative Glossy1 Protein	At5g57800	WAX2; Catalytic
P0544B02.16	Putative Glutamine Amidotransferase Class-I	At2g23970	Defense-Related Protein, Putative
P0544B02.21	Putative RAD23 Protein	At1g16190	DNA Repair Protein RAD23, Putative

P0544B02.25	Putative Adiponectin Receptor 1	At4g30850	Hhp2 (Heptahelical Transmembrane Protein2)
P0544B02.28	Unknown Protein	At4g30790	Unknown Protein
P0544B02.31	Putative Protein Phosphatase Type-2C	At4g31860	Protein Phosphatase 2C, Putative / PP2C, Putative
P0544B02.33	Unknown Protein	At2g24020	Unknown Protein
P0544B02.5	Putative Dem Protein	At4g33400	Dem Protein-Related / Defective Embryo And Meristems Protein-Related
P0544G09.12	Putative Cytochrome P450 (CYP78A9)	At3g61880	CYP78A9 (CYTOCHROME P450 78A9); Oxygen Binding
P0544G09.23	Putative Pepper Esterase	At5g62180	ATCXE20 (ARABIDOPSIS THALIANA CARBOXYESTERASE 20); Carboxylesterase
P0544G09.25	Putative P450 Monooxygenase	At4g12310	CYP706A5 (Cytochrome P450, Family 706, Subfamily A, Polypeptide 5); Oxygen Binding
P0544G09.31	Putative ER Lumen Protein-Retaining Receptor	At1g75760	ER Lumen Protein Retaining Receptor Family Protein
P0544G09.37	Putative Armadillo Repeat Containing Protein	At5g66200	Armadillo/Beta-Catenin Repeat Family Protein
P0544G09.9	Putative Gtpase-Activating Protein GYP7 (GAP For	At5g53570	Rabgap/TBC Domain-Containing Protein
P0544H11.26	Putative Cytochrome P450 Monooxygenase	At2g26710	BAS1 (PHYB ACTIVATION TAGGED SUPPRESSOR 1); Oxygen Binding
P0544H11.36	Unknown Protein	At4g32460	Unknown Protein
P0544H11.38	26S Proteasome Regulatory Particle Triple-A	At5g19990	ATSUG1; Atpase
P0544H11.39	Putative Serine-Threonine Kinase	At3g15610	Transducin Family Protein / WD-40 Repeat Family Protein
P0544H11.40	Putative Beta-Ketoacyl-Coa-Synthase	At2g26640	Beta-Ketoacyl-Coa Synthase, Putative
P0547A06.49	Roc1(Homeobox Protein)	At4g04890	PDF2 (PROTODERMAL FACTOR2); DNA Binding / Transcription Factor
P0552F09.101	Sucrose Synthase 3 (Sucrose-UDP	At3g43190	SUS4; UDP-Glycosyltransferase/ Sucrose Synthase/ Transferase, Transferring Glycosyl Groups
P0552F09.104	Disease Resistance Response Protein-Like	At5g42500	Disease Resistance-Responsive Family Protein
P0552F09.120	Putative Alanine Aminotransferase	At1g72330	Alaat2 (Alanine Aminotransferase 2)
P0554D10.14	Putative Polygalacturonase PG2	At1g48100	Glycoside Hydrolase Family 28 Protein / Polygalacturonase (Pectinase) Family Protein
P0554D10.25	Putative Lipase Homolog	At1g09390	GDSL-Motif Lipase/Hydrolase Family Protein
P0554D10.26	Bromelain-Like Thiol Protaease	At2g34080	Cysteine Proteinase, Putative
P0554F08.13	Putative Peptidyl-Trna Hydrolase (PTH)	At1g18440	Peptidyl-Trna Hydrolase Family Protein
P0554F08.4	Putative P-Glycoprotein	At2g47000	PGP4 (P-GLYCOPROTEIN 4, P-GLYCOPROTEIN4); Atpase, Coupled To Transmembrane Movement Of Substances / Xenobiotic-Transporting Atpase
P0554F08.6	Putative Phosphoethanolamine	At1g48600	Phosphoethanolamine N-Methyltransferase 2, Putative (NMT2)
P0554F08.7	Unknown Protein	At1g14910	Epsin N-Terminal Homology (ENTH) Domain-Containing Protein
P0556A11.20	Putative KH Domain Protein	At5g46190	KH Domain-Containing Protein
P0557A01.5	Hypothetical Protein	At1g68980	Pentatricopeptide (PPR) Repeat-Containing Protein
P0557D09.17	RRM-Containing RNA-Binding Protein-Like	At1g07360	Zinc Finger (CCCH-Type) Family Protein / RNA Recognition Motif (RRM)-Containing Protein
P0557D09.31	Putative Aldehyde Oxidase	At2g27150	Aao3 (Abscisic Aldehyde Oxidase 3)
P0560B06.13	Putative DNA-Dependent Atpase	At3g06400	CHR11 (CHROMATIN-REMODELING PROTEIN 11); DNA-Dependent Atpase
P0560B06.28	Hypothetical Protein	At5g18600	Glutaredoxin Family Protein
P0560B06.30	Cullin-Like Protein	At1g43140	Hypothetical Protein

P0560B06.33	Putative Potassium Transporter	At4g33530	KUP5 (K+ Uptake Permease 5); Potassium Ion Transporter
P0560B08.103	Putative Dihydropterin Pyrophosphokinase	At4g30000	Dihydropterin Pyrophosphokinase, Putative / Dihydropteroate Synthase, Putative / DHPS, Putative
P0560B08.106	Putative Caltractin	At3g50360	ATCEN2 (CENTRIN2); Calcium Ion Binding
P0560B08.109	Myosin Heavy Chain-Like	At4g33390	Unknown Protein
P0560C03.1	Putative Threonine Synthase	At4g29840	MTO2 (METHIONINE OVER-ACCUMULATOR); Threonine Synthase
P0560C03.15	Unknown Protein	At3g18390	Emb1865 (Embryo Defective 1865)
P0562A06.20	Putative Gibberellin Action Negative Regulator	At3g11540	Spy (Spindly)
P0562A06.21	Cyclophilin	At2g36130	Peptidyl-Prolyl Cis-Trans Isomerase, Putative / Cyclophilin, Putative / Rotamase, Putative
P0562A06.23	Putative Dihydroxy-Acid Dehydratase	At3g23940	Dehydratase Family
P0562A06.4	Putative Auxin-Regulated Protein	At5g03880	Unknown Protein
P0562A06.8	Putative Vesicle-Associated Membrane Protein 725	At3g54300	ATVAMP727 (Arabidopsis Thaliana Vesicle-Associated Membrane Protein 727)
P0564H06.1	Putative GST6 Protein	At1g17180	ATGSTU25 (Arabidopsis Thaliana Glutathione S-Transferase (Class Tau) 25); Glutathione Transferase
P0564H06.14	Putative Polyamine Oxidase Precursor	At5g13700	APAO/ATPAO1 (POLYAMINE OXIDASE 1); FAD Binding / Polyamine Oxidase
P0564H06.24	Hypothetical Protein	At1g11660	ATP Binding
P0565A07.136	Putative Ethylene-Responsive Small GTP-Binding	At5g59840	Ras-Related GTP-Binding Family Protein
P0565A07.137	Unknown Protein	At2g35730	Heavy-Metal-Associated Domain-Containing Protein
P0567H04.15	Chlorophyll A/B-Binding Protein	At5g01530	Chlorophyll A-B Binding Protein CP29 (LHCB4)
P0567H04.16-1	Inositol Phosphatase-Like Protein	At2g20890	Psb29 (Thylakoid Formation1)
P0567H04.24	Membrane Lipoprotein Lipid Attachment	At5g54240	Unknown Protein
P0567H04.30	Arm Repeat Containing Protein-Like	At1g61350	Armadillo/Beta-Catenin Repeat Family Protein
P0571D04.111	Putative Expansin Protein Family (EXPL2)	At4g38400	Atexla2 (Arabidopsis Thaliana Expansin-Like A2)
P0571D04.117	Putative EBNA1-Binding Protein Homolog	At3g22660	Rrna Processing Protein-Related
P0572D06.34	Putative N7 Protein	At4g05490	F-Box Family Protein (FBL22)
P0572D06.37-1	Putative Nonclathrin Coat Protein Zeta2-COP	At1g60970	Clathrin Adaptor Complex Small Chain Family Protein
P0574F11.14	Putative Acetyl-Coa C-Acyltransferase	At5g48230	ACAT2/EMB1276 (ACETOACETYL-COA THIOLASE 2, EMBRYO DEFECTIVE 1276); Acetyl-Coa C-Acetyltransferase
P0574F11.31	Putative Ubiquitin-Protein Ligase 1	At1g70320	UPL2 (UBIQUITIN-PROTEIN LIGASE 2); Ubiquitin-Protein Ligase
P0574F11.34	NOI Protein	At1g35940	AT Hook Motif-Containing Protein-Related
P0574F11.8	C2 Domain-Containing Protein-Like	At5g47710	C2 Domain-Containing Protein
P0575F10.12	Putative Eukaryotic Translation Initiation	At3g56150	Eif3c (Eukaryotic Translation Initiation Factor 3)
P0575F10.14	Putative NADPH-Dependent Mannose 6-Phosphate	At2g21250	Mannose 6-Phosphate Reductase (NADPH-Dependent), Putative
P0575F10.15	Phosphatidylinositol Synthase	At4g38570	CDP-Diacylglycerol--Inositol 3-Phosphatidyltransferase, Putative / Phosphatidylinositol Synthase, Putative
P0575F10.36	Putative 3-Isopropylmalate Dehydratase Large	At4g13430	Aconitase Family Protein / Aconitate Hydratase Family Protein
P0575F10.6-1	Putative Arginine/Serine-Rich Splicing Factor	At4g25500	ATRSP35 (Arabidopsis Thaliana Arginine/Serine-Rich Splicing Factor 35)

P0576F08.10	Putative SINA2 Protein,Seven In Absentia	At3g58040	Seven In Absentia (SINA) Family Protein
P0576F08.1-1	Putative Phosphoribosyl Pyrophosphate Synthase	At2g44530	Ribose-Phosphate Pyrophosphokinase, Putative / Phosphoribosyl Diphosphate Synthetase, Putative
P0576F08.2	Putative Xyloglucan Endo-1,4-Beta-D-Glucanase	At1g32170	XTR4 (XYLOGLUCAN ENDOTRANSGLYCOSYLASE 4); Hydrolase, Acting On Glycosyl Bonds
P0576F08.31	Hypothetical Protein	At5g17670	Hydrolase
P0576F08.33	Putative Amidotransferase	At5g60540	ATPDX2/EMB2407/PDX2 (PYRIDOXINE BIOSYNTHESIS 2); Glutaminase/ Glutamyl-Trna(Gln) Amidotransferase/ Protein Heterodimerization
P0577B11.124	Putative CTP:Phosphorylcholine	At2g32260	Cholinephosphate Cytidylyltransferase, Putative / Phosphorylcholine Transferase, Putative / CTP:Phosphocholine Cytidylyltransferase, Putative
P0577B11.125	Putative Heat Shock Protein 40	At1g10350	DNAJ Heat Shock Protein, Putative
P0577B11.132	WD-40 Repeat Protein-Like	At1g15750	Tpl/Wsip1 (Wus-Interacting Protein 1)
P0580A11.104	Putative DNA Repair Protein	At1g05120	SNF2 Domain-Containing Protein / Helicase Domain-Containing Protein / RING Finger Domain-Containing Protein
P0581F09.10	Hypothetical Protein	At5g12260	Hypothetical Protein
P0581F09.16	Hypothetical Protein	At3g17610	Unknown Protein
P0582D05.112	Putative Cold Shock Protein-1	At2g21060	ATGRP2B (GLYCINE-RICH PROTEIN 2B); Nucleic Acid Binding
P0582D05.130-1	60S Acidic Ribosomal Protein P0	At2g40010	60S Acidic Ribosomal Protein P0 (RPP0A)
P0582D05.131	Putative Non-Phototropic Hypocotyl 3	At1g30440	Phototropic-Responsive NPH3 Family Protein
P0582D05.138	Putative Pentatricopeptide (PPR)	At1g53600	Pentatricopeptide (PPR) Repeat-Containing Protein
P0582D05.139	Putative Cytochrome P450 Protein	At1g01280	CYP703A2 (Cytochrome P450, Family 703, Subfamily A, Polypeptide 2); Oxygen Binding
P0583B06.11	Putative RAE1 (RNA Export 1, S.Pombe) Homolog	At1g80670	Transducin Family Protein / WD-40 Repeat Family Protein
P0583G08.11	Putative Receptor-Like Kinase	At4g33430	BAK1 (BRI1-ASSOCIATED RECEPTOR KINASE); Kinase
P0584E12.40-1	Unknown Protein	At5g15880	Unknown Protein
P0585B01.16	Putative L-Aspartate Oxidase	At5g14760	AO (L-ASPARTATE OXIDASE); L-Aspartate Oxidase
P0585B01.25	Putative Blast And Wounding Induced	At3g18040	MPK9 (MAP KINASE 9); MAP Kinase
P0585B01.27	Putative Tyrosine Kinase Wee1	At1g02970	WEE1 (Arabidopsis Wee1 Kinase Homolog); Kinase/ Protein Kinase
P0585B01.29-1	Putative HGA1	At3g57380	Unknown Protein
P0585B01.29-2	Putative HGA1	At3g18170	Unknown Protein
P0585B01.3	Putative Proteasome Subunit Alpha Type 1	At5g42790	PAF1 (Proteasome Alpha Subunit F1); Peptidase
P0585G03.10	Putative Permease 1	At5g62890	Permease, Putative
P0585G03.19	Small GTP-Binding Protein Osrac3	At5g62880	ARAC10/ATRAC10/Atrop11 (Rho-Related Protein From Plants 11); GTP Binding
P0585G03.2	Putative Altered Response To Gravity	At1g24120	ARL1 (ARG1-LIKE1); Heat Shock Protein Binding / Unfolded Protein Binding
P0585G03.23	Putative Degp2 Protease	At5g40200	DEGP9 (DEGP PROTEASE 9); Serine-Type Peptidase/ Trypsin
P0585G03.4	Putative Mannosyl-Oligosaccharide	At1g27520	Glycoside Hydrolase Family 47 Protein
P0585H11.109	Putative Phytosulfokine Receptor	At5g53890	Leucine-Rich Repeat Transmembrane Protein Kinase, Putative
P0589E08.4	Putative N-Acetylglucosamine-Phosphate Mutase	At5g18070	DRT101 (DNA-DAMAGE-REPAIR/TOLERATION 101); Intramolecular Transferase, Phosphotransferases

P0592C06.112	Putative Eif3e (Subunits Of Eukaryotic	At3g57290	EIF3E (Eukaryotic Translation Initiation Factor 3E)
P0592G05.19	Unknown Protein	At1g27340	F-Box Family Protein
P0594D10.112	Putative Clathrin-Adaptor Medium Chain Apm 4	At4g24550	Clathrin Adaptor Complexes Medium Subunit Family Protein
P0594D10.119	Putative D-Type Cyclin	At2g22490	CYCD2;1 (CYCLIN D2;1); Cyclin-Dependent Protein Kinase Regulator/ Protein Binding
P0594D10.123	Putative FH Protein Interacting Protein FIP1	At1g28200	Fip1 (Fh Interacting Protein 1)
P0594D10.125	Putative DEAD/H (Asp-Glu-Ala-Asp/His) Box	At4g01020	Helicase Domain-Containing Protein / IBR Domain-Containing Protein / Zinc Finger Protein-Related
P0594D10.128	Putative Alcohol Dehydrogenase	At1g22440	Alcohol Dehydrogenase, Putative
P0594D10.134	Putative Protein Kinase Hvpkaba1(Abcisic	At4g33950	OST1 (OPEN STOMATA 1); Kinase/ Protein Kinase
P0594D10.135	Putative 40S Ribosomal Protein S6	At5g10360	EMB3010 (EMBRYO DEFECTIVE 3010); Structural Constituent Of Ribosome
P0597G07.107	Protein Phosphatase 2C-Like	At1g09160	Protein Phosphatase 2C-Related / PP2C-Related
P0597G07.115	Putative Pectin Methylesterase	At3g05610	Pectinesterase Family Protein
P0599F09.13	Putative Serine/Threonine-Protein Kinase 16	At5g08160	ATPK3 (Arabidopsis Thaliana Serine/Threonine Protein Kinase 3); Kinase
P0599F09.17	Brain Protein 44-Like	At5g20090	Unknown Protein
P0599F09.21	Putative Strictosidine Synthase	At1g74000	Ss3 (Strictosidine Synthase 3)
P0604E01.20	Putative Polcalcin Phl P 7 (Calcium-Binding	At1g73630	Calcium-Binding Protein, Putative
P0604E01.39	Putative Mtn21	At3g18200	Nodulin Mtn21 Family Protein
P0604E01.45	Putative Expansin 11 Precursor	At2g37640	Atexpa3 (Arabidopsis Thaliana Expansin A3)
P0604E01.47	Putative Malate Dehydrogenase [NADP],	At5g58330	Malate Dehydrogenase (NADP), Chloroplast, Putative
P0604E01.52	Putative AER	At5g23940	EMB3009 (EMBRYO DEFECTIVE 3009); Transferase
P0604E01.8	Putative Iron Deficiency Protein Ids3	At2g44800	Oxidoreductase, 2OG-Fe(II) Oxygenase Family Protein
P0605D08.24	Putative Germin-Like Protein	At3g10080	Germin-Like Protein, Putative
P0610E02.28	Hypothetical Protein	At1g50660	Unknown Protein
P0610E02.30	Auxin Efflux Carrier Protein-Like	At1g71090	Auxin Efflux Carrier Family Protein
P0610E02.32	Putative Aconitate Hydratase	At2g05710	Aconitate Hydratase, Cytoplasmic, Putative / Citrate Hydro-Lyase/Aconitase, Putative
P0610E02.33	Putative Glycinamide Ribonucleotide Synthetase	At1g09830	Phosphoribosylamine--Glycine Ligase (PUR2)
P0613B07.138	Putative Plastidic Glucose 6-Phosphate	At5g13110	G6PD2 (GLUCOSE-6-PHOSPHATE DEHYDROGENASE 2); Glucose-6-Phosphate 1-Dehydrogenase
P0613F08.1	Bet V I Allergen-Like	At5g53160	Unknown Protein
P0613F08.20	Unknown Protein	At5g24130	Unknown Protein
P0613F08.9	Putative Polygalacturonase	At4g23820	Glycoside Hydrolase Family 28 Protein / Polygalacturonase (Pectinase) Family Protein
P0614D08.19	Hypothetical Protein	At3g10140	Reca Family Protein
P0614D08.31	Putative Glucan Endo-1,3-Beta-D-Glucosidase	At3g23770	Glycosyl Hydrolase Family 17 Protein
P0616D06.101	Putative 60S Ribosomal Protein L27a	At1g23290	RPL27A (RIBOSOMAL PROTEIN L27A); Structural Constituent Of Ribosome
P0616D06.103	Putative Exportin, Trna	At1g72560	Psd (Paused)
P0616D06.115	Unknown Protein	At1g19110	Inter-Alpha-Trypsin Inhibitor Heavy Chain-Related

P0616D06.117	Elongation Factor 1 Beta	At1g30230	Elongation Factor 1-Beta / EF-1-Beta
P0616D06.120	Putative Ids-4 Protein	At2g45130	SPX (SYG1/Pho81/XPR1) Domain-Containing Protein
P0616D06.127-1	Putative Oligouridylate Binding Protein	At3g14100	Oligouridylate-Binding Protein, Putative
P0616D06.132	Putative RNA Polymerase II Subunit 14.5 Kd	At3g16980	DNA-Directed RNA Polymerase II, Putative
P0617A09.16	Putative Potassium Transporter HAK2p	At5g14880	Potassium Transporter, Putative
P0617A09.20	Putative Nucellin-Like Aspartic Protease	At1g49050	Aspartyl Protease Family Protein
P0617C02.115	Kinesin-Related Protein KLPA-Like Protein	At4g05190	ATK5 (Arabidopsis Thaliana Kinesin 5); Microtubule Motor
P0617C02.122-1	Unknown Protein	At4g11800	Calcineurin-Like Phosphoesterase Family Protein
P0617C02.124-2	Putative Glucose Transport Protein STP1	At1g11260	STP1 (SUGAR TRANSPORTER 1); Carbohydrate Transporter/ Sugar Porter
P0617H07.4	Putative MRP-Like ABC Transporter	At3g21250	ATMRP6 (Arabidopsis Thaliana Multidrug Resistance-Associated Protein 6)
P0617H07.5	Putative Pollen Specific Protein SF21	At5g56750	Ndr Family Protein
P0618H09.1	Putative 60S Ribosomal Protein L22	At3g05560	Structural Constituent Of Ribosome
P0618H09.12	Hypothetical Protein	At3g16670	Unknown Protein
P0618H09.15	Putative Cytoplasmic Ribosomal Protein L18	At5g27850	60S Ribosomal Protein L18 (RPL18C)
P0618H09.21	Putative Pectinesterase	At3g14310	ATPME3 (Arabidopsis Thaliana Pectin Methylesterase 3)
P0618H09.27	Putative Tyrosyl-Trna Synthetase	At1g28350	ATP Binding / Aminoacyl-Trna Ligase
P0620H05.25	Putative CLAVATA1 Receptor Kinase	At5g25930	Leucine-Rich Repeat Family Protein / Protein Kinase Family Protein
P0620H05.3	Putative Pentatricopeptide (PPR)	At4g31850	PGR3 (PROTON GRADIENT REGULATION 3); Binding
P0620H05.37	Putative 40S Ribosomal Protein S24	At3g04920	40S Ribosomal Protein S24 (RPS24A)
P0620H05.9	Putative Poly(A) Polymerase	At4g32850	Npap (NUCLEAR POLY(A) POLYMERASE); Nucleotidyltransferase
P0622F08.20	Putative Fruit Protein	At1g15140	Oxidoreductase NAD-Binding Domain-Containing Protein
P0623F08.33	Putative Hydroxymethylglutaryl Coenzyme A	At4g11820	BAP1 (Hydroxymethylglutaryl-Coa Synthase)
P0623F08.37	Putative Sorbitol Dehydrogenase	At5g51970	Sorbitol Dehydrogenase, Putative / L-Iditol 2-Dehydrogenase, Putative
P0623F08.6	Putative Hydroxyanthranilate	At1g31490	Transferase Family Protein
P0625E02.103	Putative Triacylglycerol Lipase	At5g18640	Lipase Class 3 Family Protein
P0625E02.108-2	DNA Polymerase Zeta Catalytic Subunit-Like	At1g67500	ATREV3 (Arabidopsis Thaliana Recovery Protein 3); DNA Binding
P0627E03.1	Tetratricopeptide Repeat(TPR)-Containing	At5g65160	Tetratricopeptide Repeat (TPR)-Containing Protein
P0627E03.16	Putative Toc64	At5g09420	Chloroplast Outer Membrane Translocon Subunit, Putative
P0627E03.18	Putative Histidine-Trna Ligase	At3g46100	ATHRS1 (HISTIDYL-TRNA SYNTHETASE 1); Histidine-Trna Ligase
P0627E03.20	Disulfide Isomerase	At1g34780	ATAPRL4 (APR-LIKE 4); Electron Carrier/ Protein Disulfide Oxidoreductase
P0627E03.21	Putative Early-Responsive To Dehydration Stress	At1g13860	Dehydration-Responsive Protein-Related
P0627E03.33	Putative UDP-Glucose Glucosyltransferase1	At1g22360	UDP-Glycosyltransferase
P0627E03.4	Putative Annexin P35	At5g10230	ANN7 (ANN7, ANNEXIN ARABIDOPSIS 7); Calcium Ion Binding / Calcium-Dependent Phospholipid Binding
P0627E03.41	Putative Phi-1	At4g08950	Phosphate-Responsive Protein, Putative (EXO)

P0627E10.1	Putative Phosphoinositide-Specific Phospholipase	At3g08510	ATPLC2 (PHOSPHOLIPASE C 2); Phospholipase C
P0627E10.11	Putative Prephenate Dehydratase	At3g07630	Prephenate Dehydratase Family Protein
P0627E10.20	Putative Protein Serine/Threonine Kinase BNK1	At5g02800	Protein Kinase Family Protein
P0627E10.26	Putative 2-Oxoglutarate Dehydrogenase, E1	At5g65750	2-Oxoglutarate Dehydrogenase E1 Component, Putative / Oxoglutarate Decarboxylase, Putative / Alpha-Ketoglutaric Dehydrogenase, Putative
P0627E10.6	Putative Peroxidase	At2g37130	Peroxidase 21 (PER21) (P21) (PRXR5)
P0628H02.1	Putative Crooked Neck Protein	At5g45990	Crooked Neck Protein, Putative / Cell Cycle Protein, Putative
P0636F09.3	Putative Glycogenin	At3g18660	PGSIP1 (PLANT GLYCOGENIN-LIKE STARCH INITIATION PROTEIN 1); Transferase, Transferring Glycosyl Groups
P0640E12.105	Peptidyl-Prolyl Cis-Trans Isomerase	At3g66654	Peptidyl-Prolyl Cis-Trans Isomerase Cyclophilin-Type Family Protein
P0643A10.18	Putative Avr9/Cf-9 Rapidly Elicited Protein 276	At3g46510	Armadillo/Beta-Catenin Repeat Family Protein / U-Box Domain-Containing Family Protein
P0643A10.20	Unknown Protein	At3g60000	Unknown Protein
P0643A10.22	Putative ADP-Ribosylation Factor	At5g37680	ATARLA1A (ADP-Ribosylation Factor-Like A1A); GTP Binding
P0643A10.26	Unknown Protein	At1g23230	Unknown Protein
P0643A10.27	GDSL-Motif Lipase/Hydrolase-Like	At1g74460	GDSL-Motif Lipase/Hydrolase Family Protein
P0643A10.28	Unknown Protein	At5g57930	Apo2 (Accumulation Of Photosystem One 2)
P0643A10.32	Putative Endo-1,4-Beta-Glucanase	At1g70710	CEL1 (Cellulase 1); Hydrolase, Hydrolyzing O-Glycosyl Compounds
P0643A10.40	SET Domain-Containing Protein-Like	At1g24610	SET Domain-Containing Protein
P0643A10.49	Mutt/Nudix-Like	At1g73540	ATNUDT21 (Arabidopsis Thaliana Nudix Hydrolase Homolog 21); Hydrolase
P0643A10.51	Putative Caleosin	At1g70670	Caleosin-Related Family Protein
P0643A10.55	33 Kda Secretory Protein-Like	At5g41280	Unknown Protein
P0643D11.18	Unknown Protein	At3g47610	Transcription Regulator/ Zinc Ion Binding
P0643F09.13	Haloacid Dehalogenase-Like Hydrolase-Like	At2g33250	Unknown Protein
P0643F09.20	ABC1-Like	At3g24190	ABC1 Family Protein
P0643F09.23	Putative NADH Dehydrogenase	At2g20360	Catalytic/ Coenzyme Binding
P0643F09.26	Putative Myosin Subfamily XI Heavy Chain	At5g43900	Mya2 (Arabidopsis Myosin)
P0643F09.32	Putative Arp2/3 Complex 41kd Subunit	At2g31300	ARPC1b (Actin-Related Protein C1b); Nucleotide Binding
P0643F09.35	Putative Potassium Channel Beta Subunit	At1g04690	KAB1 (POTASSIUM CHANNEL BETA SUBUNIT); Potassium Channel
P0643F09.4	Alcohol Dehydrogenase Class III	At5g43940	ADH2 (ALCOHOL DEHYDROGENASE 2); Formaldehyde Dehydrogenase (Glutathione)
P0643F09.5	Diphthamide Synthesis DPH2-Like	At5g62030	Diphthamide Synthesis DPH2 Family Protein
P0643F09.7	Exoribonuclease-Like	At5g38890	Exoribonuclease-Related
P0644G05.16	Unknown Protein	At3g60900	FLA10 (Fasciclin-Like Arabinogalactan-Protein 10)
P0644G05.33	Hypothetical Protein	At3g16720	ATL2 (Arabidopsis T?Xicos En Levadura 2); Protein Binding / Zinc Ion Binding
P0645D04.22-1	Putative Ras-Related Protein RGP1	At5g47960	SMG1 (SMALL MOLECULAR WEIGHT G-PROTEIN 1); GTP Binding
P0646B04.11	Cyclase-Like Protein	At1g44542	Cyclase Family Protein
P0646B04.12	Putative DNA-Directed RNA Polymerase II	At2g15430	RBP36A (RNA Polymerase II 36 Kda Polypeptide A); DNA Binding / DNA-Directed RNA

			Polymerase
P0646B04.51	Putative Avr9/Cf-9 Rapidly Elicited Protein	At1g47056	VFB1 (VIER F-BOX PROTEINE 1); Ubiquitin-Protein Ligase
P0646B04.7	Putative Receptor-Like Kinase RHG1	At2g23300	Leucine-Rich Repeat Transmembrane Protein Kinase, Putative
P0646B04.9	PPR Protein-Like Protein	At1g79540	Pentatricopeptide (PPR) Repeat-Containing Protein
P0650H04.11	Putative Cinnamyl Alcohol Dehydrogenase	At4g37980	ELI3-1 (ELICITOR-ACTIVATED GENE 3); Oxidoreductase/ Zinc Ion Binding
P0650H04.32	Putative White Pigment Protein	At2g39350	ABC Transporter Family Protein
P0651G05.38	Putative Fiber Protein Fb34	At1g13380	Unknown Protein
P0654A08.41	Putative Cytochrome P450 Monooxygenase	At2g30750	CYP71A12 (Cytochrome P450, Family 71, Subfamily A, Polypeptide 12); Oxygen Binding
P0654B04.16-2	WD-40 Repeat Protein-Like	At3g13340	WD-40 Repeat Family Protein
P0654B04.19	Putative Phosphatidylinositol Transfer	At1g55690	SEC14 Cytosolic Factor Family Protein / Phosphoglyceride Transfer Family Protein
P0654B04.3	Putative Chloroplast Nucleoid DNA-Binding	At5g10770	Chloroplast Nucleoid DNA-Binding Protein, Putative
P0654B04.31	Putative Zinc Finger And C2 Domain Protein	At4g05330	Agd13 (Arf-Gap Domain 13)
P0654B04.5	Putative Chloride Channel Protein	At1g55620	CLC-F (CHLORIDE CHANNEL F); Voltage-Gated Chloride Channel
P0656C04.104-1	Unknown Protein	At3g05000	Transport Protein Particle (TRAPP) Component Bet3 Family Protein
P0656C04.124	Putative 60S Ribosomal Protein L30	At2g44860	60S Ribosomal Protein L24, Putative
P0657H12.1	Aluminum-Activated Malate Transporter-Like	At1g08440	Unknown Protein
P0657H12.28	GL2-Type Homeobox Genes	At3g61150	HDG1 (HOMEODOMAIN GLABROUS1); DNA Binding / Transcription Factor
P0660F12.13	Hypothetical Protein	At1g07130	OB-Fold Nucleic Acid Binding Domain-Containing Protein
P0660F12.17	Putative Beta 1,3-Glucanase	At5g42720	Glycosyl Hydrolase Family 17 Protein
P0660F12.24	Unknown Protein	At2g01170	Amino Acid Permease Family Protein
P0663C08.12	Unknown Protein	At5g12010	Unknown Protein
P0663C08.13	Putative Vacuolar ATP Synthase Subunit C	At1g12840	Det3 (De-Etiolated 3)
P0663C08.15	Putative Protein Kinase ADK1	At1g72710	Casein Kinase, Putative
P0663C08.2	Unknown Protein	At5g28540	Luminal Binding Protein 1 (Bip-1) (BP1)
P0663C08.5	Putative Hypersensitive-Induced Response	At5g62740	Band 7 Family Protein
P0663C08.7	Unknown Protein	At1g49970	CLPR1 (Clp Protease Proteolytic Subunit 5); Endopeptidase Clp
P0663C08.8	Putative DNA Damage Binding Protein 1	At4g05420	DDB1A (UV-Damaged DNA-Binding Protein 1A); DNA Binding
P0663C08.9	Unknown Protein	At2g28360	SIT4 Phosphatase-Associated Family Protein
P0663E10.7	Putative Transcription Factor X1	At1g15910	XH/XS Domain-Containing Protein / XS Zinc Finger Domain-Containing Protein
P0663F07.1	SPX (SYG1/Pho81/XPR1) Domain-Containing	At1g63010	SPX (SYG1/Pho81/XPR1) Domain-Containing Protein
P0663F07.14	Pentatricopeptide (PPR) Repeat-Containing	At1g74900	Pentatricopeptide (PPR) Repeat-Containing Protein
P0663F07.33	Fringe-Related Protein-Like	At5g41460	Fringe-Related Protein
P0663F07.43	Putative Serine/Threonine-Specific Protein	At2g33580	Protein Kinase Family Protein / Peptidoglycan-Binding Lysm Domain-Containing Protein
P0663F07.5	Dtdp-D-Glucose 4,6-Dehydratase-Like	At1g63000	Nrs/Er (Nucleotide-Rhamnose Synthase/Epimerase-Reductase)
P0665A11.10	Hypothetical Protein	At3g49200	Unknown Protein

P0665A11.26	Putative Ubiquitin Carboxyl-Terminal Hydrolase	At3g11910	Ubiquitin-Specific Protease, Putative
P0665A11.3	Hypothetical Protein	At3g22270	Unknown Protein
P0665A11.6	Putative Serine Proteinase	At4g20430	Subtilase Family Protein
P0665A11.7	Putative Receptor-Protein Kinase	At3g51550	Protein Kinase Family Protein
P0665C04.29	Putative Ubiquitin-Specific Protease Otubain 1	At1g28120	Unknown Protein
P0665C04.3	PHO85-Like Protein	At3g02040	SRG3 (SENESCENCE-RELATED GENE 3); Glycerophosphodiester Phosphodiesterase
P0665C04.30	AP2 Domain-Containing Protein AP29-Like	At1g52630	Unknown Protein
P0665C04.32	Putative Glycyl-Trna Synthetase	At1g29880	Glycyl-Trna Synthetase / Glycine--Trna Ligase
P0665D10.14	Unknown Protein	At5g04560	Encodes A DNA Glycosylase DEMETER (DME)
P0665D10.18	Unknown Protein	At1g65480	Ft (Flowering Locus T)
P0665D10.20	Putative Phophatidylethanolamine Binding	At5g16880	VHS Domain-Containing Protein / GAT Domain-Containing Protein
P0666E12.11	Putative Target Of Myb1	At3g04090	Sip1;1 (Small And Basic Intrinsic Protein 1a)
P0666G04.16	Unknown Protein	At1g79930	HSP91 (Heat Shock Protein 91)
P0666G10.104	Putative Retinoblastoma Protein	At3g12280	Rbr1 (Retinoblastoma-Related 1)
P0666G10.106	Putative Pentatricopeptide (PPR)	At3g12770	Pentatricopeptide (PPR) Repeat-Containing Protein
P0666G10.108	Putative DHHC-Type Zinc Finger Domain-Containing	At3g48760	Zinc Finger (DHHC Type) Family Protein
P0666G10.131	Putative Anthocyanin-Related Membrane Protein 1	At3g59310	Unknown Protein
P0666G10.132	Putative Biotin Synthase	At2g43360	BIO2 (BIOTIN AUXOTROPH 2); Biotin Synthase
P0668C05.107	Transducin /WD-40 Repeat Protein Family-Like	At2g47990	SWA1 (SLOW WALKER1); Nucleotide Binding
P0668C05.111	Osnac3 Protein	At5g63790	ANAC102 (Arabidopsis NAC Domain Containing Protein 102); Transcription Factor
P0668H12.10	Putative Ankyrin Protein	At3g04710	Binding
P0668H12.19	Putative 26S Proteasome Regulatory Subunit	At2g39990	EIF2 (Eukaryotic Translation Initiation Factor 2); Translation Initiation Factor
P0668H12.20	Putative Methionine S-Methyltransferase (EC	At5g49810	MMT (Methionine S-Methyltransferase); S-Adenosylmethionine-Dependent Methyltransferase
P0668H12.21	Putative GTP-Binding Protein	At1g09630	ATRAB11C (ARABIDOPSIS RAB GTPASE HOMOLOG A2A); GTP Binding
P0668H12.7	Unknown Protein	At3g27030	Unknown Protein
P0669G09.11	Putative GDP-Fucose	At3g05320	Unknown Protein
P0669G09.12	Unknown Protein	At3g02070	OTU-Like Cysteine Protease Family Protein
P0669G09.15-2	Putative Porphobilinogen Deaminase	At5g08280	HEMC (HYDROXYMETHYLBILANE SYNTHASE); Hydroxymethylbilane Synthase
P0669G09.17	Unknown Protein	At1g56180	Unknown Protein
P0669G09.19	Putative Phosphoglycerate Kinase, Cytosolic	At1g79550	Pgk (Phosphoglycerate Kinase)
P0669G09.32	Putative Inositol-1-Monophosphatase	At1g31190	Inositol Monophosphatase Family Protein
P0669G09.6	Putative 4-Hydroxyphenylpyruvate Dioxygenase	At1g06570	Pds1 (Phytoene Desaturation 1)
P0669G10.5-1	Putative Protein Kinase ADK1	At5g43320	CKL8 (Casein Kinase I-Like 8); Casein Kinase I/ Kinase
P0669G10.7	Putative Glyoxalase I	At1g67280	Lactoylglutathione Lyase, Putative / Glyoxalase I, Putative

P0669G10.9	Putative Iron/Ascorbate-Dependent	At5g20400	Oxidoreductase, 2OG-Fe(II) Oxygenase Family Protein
P0669H03.9	Putative Cellulose Synthase-8	At4g39350	CESA2 (CELLULASE SYNTHASE 2); Cellulose Synthase/ Transferase, Transferring Glycosyl Groups
P0670E08.10	Putative Polygalacturonase	At4g18180	Glycoside Hydrolase Family 28 Protein / Polygalacturonase (Pectinase) Family Protein
P0670E08.9	Putative Glycosyltransferase	At5g47780	GAUT4 (Galacturonosyltransferase 4); Polygalacturonate 4-Alpha-Galacturonosyltransferase/ Transferase, Transferring Glycosyl Groups
P0671B11.20	Putative 1-Aminocyclopropane-1-Carboxylic Acid	At4g26200	ACS7 (1-Amino-Cyclopropane-1-Carboxylate Synthase 7); 1-Aminocyclopropane-1-Carboxylate Synthase
P0671B11.35	Putative Regulatory Protein NPR1	At1g64280	NPR1 (NONEXPRESSER OF PR GENES 1); Protein Binding
P0671D01.17	Putative Nifu-Like Protein	At3g01020	ATISU2/ISU2 (Iscu-Like 2); Structural Molecule
P0671D01.24	Putative Mannan Endo-1,4-Beta-Mannosidase	At5g66460	(1-4)-Beta-Mannan Endohydrolase, Putative
P0671D01.25	Putative Aspartic Protease	At4g04460	Aspartyl Protease Family Protein
P0671D01.4	Hypothetical Protein	At3g12470	Nucleic Acid Binding
P0671F11.27	Putative 2-Oxoglutarate-Dependent Oxygenase	At2g30830	2-Oxoglutarate-Dependent Dioxygenase, Putative
P0672C09.17	Putative Beta-Galactosidase	At3g13750	BGAL1 (BETA GALACTOSIDASE 1); Beta-Galactosidase
P0672C09.22	Putative 1-Aminocyclopropane-1-Carboxylate	At2g19590	ACO1 (ACC OXIDASE 1); 1-Aminocyclopropane-1-Carboxylate Oxidase
P0672D01.114	Putative RNA Helicase	At1g20920	DEAD Box RNA Helicase, Putative
P0672D01.115	Unknown Protein	At3g02950	Unknown Protein
P0672D08.18	Hypothetical Protein	At3g48610	Phosphoesterase Family Protein
P0672D08.27	Hypothetical Protein	At5g13100	Oxidoreductase
P0672D08.30	Putative DNA Repair And Recombination Protein	At2g18760	CHR8 (Chromatin Remodeling 8); ATP Binding / DNA Binding / Helicase
P0672D08.33	Hypothetical Protein	At3g10640	SNF7 Family Protein
P0672D08.4	Hypothetical Protein	At5g16520	Unknown Protein
P0672D08.5	Putative 40S Ribosomal Protein S5	At2g37270	ATRPS5B (RIBOSOMAL PROTEIN 5B); Structural Constituent Of Ribosome
P0672D08.7	Putative Sphingosine-1-Phosphate Lyase	At1g27980	Pyridoxal-Dependent Decarboxylase Family Protein
P0673E01.19	Putative SNF2 Domain/Helicase Domain-Containing	At2g16390	DRD1 (DEFECTIVE IN RNA-DIRECTED DNA METHYLATION 1); ATP Binding / DNA Binding / Helicase/ Nucleic Acid Binding
P0673E01.23	26S Proteasome Regulatory Particle Non-Atpase	At1g64520	26S Proteasome Regulatory Subunit, Putative (RPN12)
P0674H09.13	Hypothetical Protein	At5g48340	Unknown Protein
P0674H09.17	Putative Beta-Glucosidase	At5g36890	Hydrolase, Hydrolyzing O-Glycosyl Compounds
P0674H09.28	Patatin-Like Protein	At4g37050	PLA V/PLP4 (Patatin-Like Protein 4); Nutrient Reservoir
P0676F10.11	Unknown Protein	At5g03740	HD2C (HISTONE DEACETYLASE 2C); Nucleic Acid Binding / Zinc Ion Binding
P0676F10.14	Unknown Protein	At5g08180	Ribosomal Protein L7Ae/L30e/S12e/Gadd45 Family Protein
P0676F10.33	Putative Curly Leaf Protein	At2g23380	CLF (CURLY LEAF); Transcription Factor
P0676F10.7	Unknown Protein	At5g15890	Unknown Protein
P0676G05.12	Putative RNA Polymerase II Fifth Largest	At4g14660	RNA Polymerase Rpb7 N-Terminal Domain-Containing Protein
P0676G05.13	Unknown Protein	At3g17020	Universal Stress Protein (USP) Family Protein

P0676G05.6	Putative Disulfide Isomerase	At2g47470	ATPDIL2-1/MEE30/UNE5 (PDI-LIKE 2-1, Maternal Effect Embryo Arrest 30, Unfertilized Embryo Sac 5)
P0676G05.7	Unknown Protein	At3g62600	DNAJ Heat Shock Family Protein
P0676G05.8	Putative Tubulin Gamma-2 Chain (Gamma-2	At3g61650	TUBG1 (GAMMA-TUBULIN); Structural Molecule
P0676G05.9	Putative Dihydrolipoamide Dehydrogenase	At3g16950	Lpd1 (Lipoamide Dehydrogenase 1)
P0676H02.1	Putative Glutathione S-Transferase	At3g09270	ATGSTU8 (Arabidopsis Thaliana Glutathione S-Transferase (Class Tau) 8); Glutathione Transferase
P0676H02.3	Putative Purine Permease	At1g28220	ATPUP3 (Arabidopsis Thaliana Purine Permease 3); Purine Transporter
P0676H02.31-1	Putative Isoamylase-Type Starch Debranching	At4g09020	ATISA3/ISA3 (ISOAMYLASE 3); Alpha-Amylase
P0676H02.7	Putative Ripening Regulated Protein DDTFR18	At5g65380	Ripening-Responsive Protein, Putative
P0676H03.17	Putative Cytochrome B5 Reductase	At5g17770	Atcbr (Nadh:Cytochrome B5 Reductase 1)
P0676H03.26	Unknown Protein	At1g52890	ANAC019 (Arabidopsis NAC Domain Containing Protein 19); Transcription Factor
P0676H03.28	Putative Microtubule Associated Protein	At2g35630	Mor1 (Microtubule Organization 1)
P0676H03_3	ADP-Ribosylation Factor	At2g47170	ARF1A1c (ADP-RIBOSYLATION FACTOR 1); GTP Binding / Phospholipase Activator/ Protein Binding
P0677G01.47	Avr9/Cf-9 Rapidly Elicited Protein-Like	At3g07360	Armadillo/Beta-Catenin Repeat Family Protein / U-Box Domain-Containing Protein
P0677H08.18	Putative Subtilisin-Like Protease	At1g01900	Subtilase Family Protein
P0677H08.24	Unknown Protein	At1g21790	Unknown Protein
P0678F11.2	Ubiquitin-Like Protein	At5g55160	Sum2 (Small Ubiquitin-Like Modifier 2)
P0678F11.21	Hypothetical Protein	At1g65320	CBS Domain-Containing Protein
P0679C08.10	Unknown Protein	At5g42090	Unknown Protein
P0679C08.19	Rice Waxy Protein	At1g32900	Starch Synthase, Putative
P0679C08.26	Unknown Protein	At5g51550	Phosphate-Responsive 1 Family Protein
P0679C08.28	Putative Transketolase	At2g45290	Transketolase, Putative
P0679C08.29	3-Phosphoshikimate 1-Carboxyvinyltransferase	At2g45300	3-Phosphoshikimate 1-Carboxyvinyltransferase / 5-Enolpyruvylshikimate-3-Phosphate / EPSP Synthase
P0679C08.30	40S Ribosomal Protein S20	At5g62300	40S Ribosomal Protein S20 (RPS20C)
P0679C08.31	Unknown Protein	At2g45330	EMB1067 (EMBRYO DEFECTIVE 1067); Trna 2'-Phosphotransferase
P0679C12.16	Putative Beta-1,3-Glucanase	At1g32860	Glycosyl Hydrolase Family 17 Protein
P0679C12.26	Hypothetical Protein	At3g52570	Unknown Protein
P0679C12.4	Hypothetical Protein	At1g67190	F-Box Family Protein
P0680A05.37	Putative Hydrolase	At4g36610	Hydrolase, Alpha/Beta Fold Family Protein
P0680A05.39	Putative Cytosolic Monodehydroascorbate	At3g27820	ATMDAR4 (MONODEHYDROASCORBATE REDUCTASE 4); Monodehydroascorbate Reductase (NADH)
P0680F05.36	Phosphate/Phosphoenolpyruvate Translocator	At3g14410	Transporter-Related
P0680F05.38	Copine I-Like Protein	At1g79380	Copine-Related
P0680F05.45	Putative Tryptophan Synthase Beta-Subunit	At4g27070	TSB2 (TRYPTOPHAN SYNTHASE BETA-SUBUNIT); Tryptophan Synthase

P0680F05.51	Putative 33-Kda Secretory Protein	At1g63600	Protein Kinase-Related
P0681B11.1	Putative Protein Kinase APK1B	At3g13690	Protein Kinase Family Protein
P0681B11.19	Unknown Protein	At3g02420	Unknown Protein
P0681F05.106-2	Putative Thiamine Biosynthesis Protein	At5g54770	Thi1 (Thiazole Requiring)
P0681F05.108-1	Putative Endoxyloglucan Transferase	At5g13870	EXGT-A4 (ENDOXYLOGLUCAN TRANSFERASE A4); Hydrolase, Acting On Glycosyl Bonds
P0681F05.108-2	Xyloglucan Endotransglycosylase-Like Protein	At3g44990	XTR8 (Xyloglucan:Xyloglucosyl Transferase 8); Hydrolase, Acting On Glycosyl Bonds
P0681F05.120	Putative ATP/GTP-Binding Protein	At4g21210	Encodes A PPDK Regulatory Protein That Has Both Protein Kinase And Protein Phosphatase Activities Towards PPDK (Pyruvate Orthophosphate Dikinase).
P0681F05.131-1	Putative Peroxidase	At4g11290	Peroxidase, Putative
P0681F05.132	Hypothetical Protein	At4g05220	Harpin-Induced Protein-Related / HIN1-Related / Harpin-Responsive Protein-Related
P0681F05.133	Putative 1-Acyl-Sn-Glycerol-3-Phosphate	At5g60620	Phospholipid/Glycerol Acyltransferase Family Protein
P0682A06.20	Putative GDP-Mannose Pyrophosphorylase	At2g39770	CYT1 (CYTOKINESIS DEFECTIVE 1); Nucleotidyltransferase
P0682A06.39	Putative Endo-1,3	At3g23600	Hydrolase
P0682B08.20	Hypothetical Protein	At1g02370	Pentatricopeptide (PPR) Repeat-Containing Protein
P0682B08.6	Putative ATP Citrate Lyase	At5g49460	ACLB-2 (ATP-Citrate Lyase B-2)
P0682B08.8	Putative Pm5 Collagenase	At3g62360	Unknown Protein
P0683B11.11	Putative Embryonic Abundant Protein-Like	At5g10830	Embryo-Abundant Protein-Related
P0683B11.24	Putative Alliinase	At1g34060	Alliinase Family Protein
P0683B11.27	Hypothetical Protein	At3g12630	Zinc Finger (AN1-Like) Family Protein
P0683F02.10	Putative G10 Protein	At4g21110	G10 Family Protein
P0683F02.14	Putative Cytochrome P450	At2g27690	CYP94C1 (Cytochrome P450, Family 94, Subfamily C, Polypeptide 1); Oxygen Binding
P0683F02.2	Hypothetical Protein	At5g05710	Pleckstrin Homology (PH) Domain-Containing Protein
P0683F02.22	Unknown Protein	At3g48410	Hydrolase, Alpha/Beta Fold Family Protein
P0683F02.6	Putative 3-Deoxy-D-Manno-Octulosonic-Acid	At5g03770	3-Deoxy-D-Manno-Octulosonic Acid Transferase-Related
P0683F02.7	Unknown Protein	At1g48640	Lysine And Histidine Specific Transporter, Putative
P0683F02.8	Putative Permease 1	At4g38050	Permease
P0683F12.13	Putative Phosphatidylinositol-Specific	At3g55940	Phosphoinositide-Specific Phospholipase C, Putative
P0683F12.15	Putative Dnaj	At3g08910	DNAJ Heat Shock Protein, Putative
P0683F12.16	Putative Leucoanthocyanidin Dioxygenase (EC	At3g11180	Oxidoreductase, 2OG-Fe(II) Oxygenase Family Protein
P0683F12.6	Putative Senescence-Associated Protein	At3g12090	Tet6 (Tetraspanin6)
P0684A08.22	Putative Bzip Protein	At4g35240	Unknown Protein
P0684A08.25	Unknown Protein	At5g43800	Transposable Element Gene
P0684A08.36	Putative Amino Acid Transport Protein	At4g38250	Amino Acid Transporter Family Protein
P0684B02.1	Putative Clathrin-Associated Protein	At1g60780	Clathrin Adaptor Complexes Medium Subunit Family Protein
P0684B02.7	Putative High Affinity Nitrate Transporter	At1g12940	ATNRT2.5 (NITRATE TRANSPORTER2.5); Nitrate Transporter

P0684C01.11	Unknown Protein	At1g15010	Unknown Protein
P0684C01.4	Putative Eukaryotic Translation Initiation	At4g11420	EIF3A (Eukaryotic Translation Initiation Factor 3A)
P0684C02.14	Putative Retrotransposon Polyprotein	At1g21945	Transposable Element Gene; Copia-Like Retrotransposon Family,
P0684C02.5	Unknown Protein	At4g27020	Unknown Protein
P0684E06.22	Acidic Class III Chitinase Oschib3a	At5g24090	Acidic Endochitinase (CHIB1)
P0684E06.23	Putative Pyruvate Kinase	At5g52920	Pyruvate Kinase, Putative
P0684E06.8	Putative YLP	At1g64200	VHA-E3 (VACUOLAR H+-ATPASE SUBUNIT E ISOFORM 3); Hydrogen Ion Transporting ATP Synthase, Rotational Mechanism / Hydrogen Ion Transporting Atpase, Rotational Mechanism
P0684F11.15	Putative Dynamin Homolog	At1g59610	Adl3 (Arabidopsis Dynamin-Like 3)
P0684F11.16	Putative Helicase	At1g70070	PDE317 (PIGMENT DEFECTIVE 317); ATP-Dependent Helicase
P0684F11.2	Putative Immediate-Early Fungal Elicitor Protein	At5g37490	U-Box Domain-Containing Protein
P0684F11.21	Putative Avr9/Cf-9 Rapidly Elicited Protein 231	At1g70090	GATL9/LGT8 (Galacturonosyltransferase-Like 9); Polygalacturonate 4-Alpha-Galacturonosyltransferase/ Transferase, Transferring Glycosyl Groups / Transferase, Transferring Hexosyl Groups
P0684F11.25	Putative Pyruvate Dehydrogenase E1 Alpha	At1g59900	AT-E1 ALPHA (Pyruvate Dehydrogenase Complex E1 Alpha Subunit); Pyruvate Dehydrogenase (Acetyl-Transferring)
P0685G12.19	Putative SNF5 Homolog BSH (Bsh)	At3g17590	BSH (Bushy Growth)
P0685G12.41	Sucrase-Like Protein	At5g55900	Sucrase-Related
P0685G12.43	Putative Ribulose-1,5-Bisphosphate	At3g07670	SET Domain-Containing Protein
P0685G12.44-1	Cellulose Synthase-Like Protein Oscsle2	At1g55850	ATCSLE1 (Cellulose Synthase-Like E1); Cellulose Synthase/ Transferase, Transferring Glycosyl Groups
P0686C03.126	Unknown Protein	At4g38160	Pde191 (Pigment Defective 191)
P0686E09.12	Putative CTP Synthase	At3g12670	EMB2742 (EMBRYO DEFECTIVE 2742); CTP Synthase
P0686E09.16	Unknown Protein	At1g80410	EMB2753 (EMBRYO DEFECTIVE 2753); Binding
P0686H11.17	Zinc Finger Protein Family-Like	At2g04240	XERICO; Protein Binding / Zinc Ion Binding
P0686H11.30	Putative Receptor Protein Kinase	At5g56040	ATP Binding / Protein Serine/Threonine Kinase
P0686H11.31	Putative Signal Transducer And Activator Of	At1g49540	Nucleotide Binding
P0686H11.32	Unknown Protein	At5g56050	Unknown Protein
P0686H11.35	Copine I-Like	At5g14420	Copine-Related
P0688A04.10	Putative Cytochrome P450	At3g14690	CYP72A15 (Cytochrome P450, Family 72, Subfamily A, Polypeptide 15); Oxygen Binding
P0688A04.27	Putative Cytochrome P450	At3g14650	CYP72A11 (Cytochrome P450, Family 72, Subfamily A, Polypeptide 11); Oxygen Binding
P0688A04.29	Hypothetical Protein	At5g10060	Unknown Protein
P0688A04.9	Putative Cytochrome P450	At3g14660	CYP72A13 (Cytochrome P450, Family 72, Subfamily A, Polypeptide 13); Oxygen Binding
P0688H12.36	Nuclear Protein-Like	At1g25682	Cell Cycle Control Protein-Related
P0689E12.19	Putative Stress Related-Like Protein Interactor	At2g24420	DNA Repair Atpase-Related
P0689E12.34	Putative Ribosomal Large Subunit Pseudouridine	At1g78910	Pseudouridine Synthase Family Protein
P0689H05.20	Putative Ent-Kaurene Synthase B	At1g79460	GA2 (GA REQUIRING 2); Ent-Kaurene Synthase

P0690B02.26	S-Adenosylmethionine:2-Demethylmenaquinone	At5g16450	Dimethylmenaquinone Methyltransferase Family Protein
P0690B02.4	Unknown Protein	At1g73010	Phosphoric Monoester Hydrolase
P0690B02.7	Putative Serine Acetyltransferase	At5g56760	Atserat1;1 (SERINE ACETYLTRANSFERASE 52); Serine O-Acetyltransferase
P0690E03.3	Putative 12-Oxophytodienoate Reductase	At2g06050	Opr3 (Opda-Reductase 3)
P0690E03.8	Germin-Like Protein	At1g72610	GLP1 (GERMIN-LIKE PROTEIN 1); Manganese Ion Binding / Metal Ion Binding / Nutrient Reservoir
P0691E06.15	Putative Latex-Abundant Protein	At1g79340	Latex-Abundant Protein, Putative (AMC7) / Caspase Family Protein
P0691E06.20	Unknown Protein	At5g44860	Unknown Protein
P0691E06.21	PPR-Repeat Protein -Like	At5g15300	Pentatricopeptide (PPR) Repeat-Containing Protein
P0691E06.27	Putative Exodeoxyribonuclease	At2g41460	ARP (Apurinic Endonuclease-Redox Protein)
P0691F12.18	Putative Pectinesterase 2.1 Precursor	At4g33220	Pectinesterase Family Protein
P0692C11.26	Putative Vesicle Transport V-SNARE Protein	At3g29100	VTI13 (Vesicle Transport V-SNARE 13); SNARE Binding / Receptor
P0692C11.3	WSI18 Protein	At3g15670	Late Embryogenesis Abundant Protein, Putative / LEA Protein, Putative
P0693E08.4	Alpha-Expansin Osexpa13	At1g20190	Atexpa11 (Arabidopsis Thaliana Expansin A11)
P0695H10.11	Hypothetical Protein	At5g39990	Glycosyltransferase Family 14 Protein / Core-2/I-Branching Enzyme Family Protein
P0695H10.12	Putative Casein Kinase	At3g03940	Protein Kinase Family Protein
P0695H10.14	Putative Signal Recognition Particle 54K	At1g48900	Signal Recognition Particle 54 Kda Protein 3 / SRP54 (SRP-54C)
P0695H10.9	Putative Transcription Initiation Factor	At1g75510	Transcription Initiation Factor IIF Beta Subunit (TFIIF-Beta) Family Protein
P0696F12.7	Putative Serine/Threonine-Specific Protein	At4g23200	Protein Kinase Family Protein
P0696F12.9	Putative Serine/Threonine-Specific Protein	At4g38830	Protein Kinase Family Protein
P0696G06.11	Unknown Protein	At1g05720	Selenoprotein Family Protein
P0696G06.15	Putative Chloroplast Membrane-Associated 30 Kd	At1g65260	Ptac4 (Plastid Transcriptionally Active4)
P0696G06.20	Putative Calreticulin	At1g09210	Calreticulin 2 (CRT2)
P0696G06.26	Unknown Protein	At5g36800	Unknown Protein
P0696G06.30	Putative 60S Ribosomal Protein L5	At5g39740	60S Ribosomal Protein L5 (RPL5B)
P0696G06.32	Putative Cyclin-Dependent Kinase B1-1	At2g38620	CDKB1;2 (Cyclin-Dependent Kinase B1;2); Kinase
P0696G06.7	Hypothetical Protein	At3g03300	Dcl2 (Dicer-Like 2)
P0696G06.9	Putative Fructokinase I	At2g31390	Pfkb-Type Carbohydrate Kinase Family Protein
P0698A04.23	Putative Leucyl-Trna Synthetase	At4g04350	EMB2369 (EMBRYO DEFECTIVE 2369); ATP Binding / Aminoacyl-Trna Ligase
P0698A10.11	Putative Hydroxymethyltransferase	At1g36370	SHM7 (Serine Hydroxymethyltransferase 7); Glycine Hydroxymethyltransferase
P0698A10.13	Hypothetical Protein	At1g22030	Unknown Protein
P0698G06.1	Putative Sec61 Alpha Form 2	At2g34250	Protein Translocase
P0698G06.3	Putative Histone Acetyltransferase HAT B	At5g56740	Histone Acetyltransferase Family Protein
P0698H10.12	Unknown Protein	At2g39670	Radical SAM Domain-Containing Protein
P0698H10.9	Hypothetical Protein	At1g10750	Unknown Protein

P0699H05.16	Putative 3-Hydroxybutyryl-Coa Dehydrogenase	At3g15290	3-Hydroxybutyryl-Coa Dehydrogenase, Putative
P0700A11.12	Putative Vacuolar ATP Synthase Subunit D	At3g28715	H+-Transporting Two-Sector Atpase, Putative
P0700D12.114-2	Oxysterol-Binding Protein-Like	At4g25850	Oxysterol-Binding Family Protein
P0700D12.116	30S Ribosomal Protein S16-Like	At5g56940	Ribosomal Protein S16 Family Protein
P0700F06.13	Putative Rieske Iron-Sulfur Protein Tic55	At2g24820	TIC55 (TRANSLOCON AT THE INNER ENVELOPE MEMBRANE OF CHLOROPLASTS 55); Oxidoreductase
P0700F06.14	Putative Tumor Differentially Expressed Protein	At1g16180	TMS Membrane Family Protein / Tumour Differentially Expressed (TDE) Family Protein
P0700F06.15-1	Zinc Finger (CCCH-Type) Protein-Like	At2g24830	Zinc Finger (CCCH-Type) Family Protein / D111/G-Patch Domain-Containing Protein
P0700F06.17	Unknown Protein	At3g01780	Encodes TPLATE, A Cytokinesis Protein Targeted To The Cell Plate
P0700F06.22	Cytochrome B5 Domain-Containing Protein-Like	At3g48890	ATMP2 (ARABIDOPSIS THALIANA MEMBRANE-ASSOCIATED PROGESTERONE BINDING PROTEIN 3); Heme Binding / Transition Metal Ion Binding
P0700F06.24	Unknown Protein	At1g76820	Putative Translation Initiation Factor IF-2.
P0700F06.32	Translation Initiation Factor IF-3-Like	At2g24060	Translation Initiation Factor 3 (IF-3) Family Protein
P0700F06.34-3	Putative Carboxypeptidase D	At4g30610	Brs1 (Bri1 Suppressor 1)
P0700F06.36	Putative Leucine Aminopeptidase	At2g24200	Cytosol Aminopeptidase
P0701D05.3	Putative RNA Helicase	At5g05450	DEAD/DEAH Box Helicase, Putative (RH18)
P0701D05.34	Thioredoxin-Like Protein	At3g08710	ATH9 (Thioredoxin H-Type 9)
P0701D05.8	Hypothetical Protein	At5g64190	Unknown Protein
P0701E06.10	Putative Enoyl-ACP Reductase	At2g05990	MOD1 (MOSAIC DEATH 1); Enoyl-[Acyl-Carrier-Protein] Reductase (NADH)/ Oxidoreductase
P0701F11.30	Zinc Finger (C3HC4-Type RING Finger)-Like	At3g53690	Zinc Finger (C3HC4-Type RING Finger) Family Protein
P0701F11.5-1	Putative CBL-Interacting Protein Kinase	At5g10930	CIPK5 (CBL-INTERACTING PROTEIN KINASE 5); Kinase
P0701F11.5-2	Putative CBL-Interacting Protein Kinase	At5g25110	CIPK25 (CBL-INTERACTING PROTEIN KINASE 25); Kinase
P0702B09.7	Putative Dihydropyrimidinase	At5g12200	Dihydropyrimidinase / Dhpase / Dihydropyrimidine Amidohydrolase / Hydantoinase (PYD2)
P0702C09.13-1	Unknown Protein	At5g14790	Binding
P0702C09.33	Putative Mtn3	At5g50790	Nodulin Mtn3 Family Protein
P0702E04.10	MADS Box Protein	At1g24260	SEP3 (SEPALLATA3); Transcription Factor
P0702E04.15	Ftsj Cell Division Protein-Like	At5g09530	Hydroxyproline-Rich Glycoprotein Family Protein
P0702E04.16	Putative Glutamate-1-Semialdehyde	At3g48730	GSA2 (GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOMUTASE 2); Glutamate-1-Semialdehyde 2,1-Aminomutase
P0702E04.18	Nuclear Transport Factor 2 (NTF-2)	At1g27310	NTF2A (NUCLEAR TRANSPORT FACTOR 2A); Ran Gtpase Binding / Protein Transporter
P0702E04.19	Nodulin-Related Protein-Like	At5g14120	Nodulin Family Protein
P0702E04.22	Putative Peroxidase	At4g37520	Peroxidase 50 (PER50) (P50) (PRXR2)
P0702E04.27	Coated Vesicle Membrane Protein-Like	At3g07680	Emp24/Gp25l/P24 Family Protein
P0702F05.10	Unknown Protein	At4g23850	Long-Chain-Fatty-Acid--Coa Ligase / Long-Chain Acyl-Coa Synthetase
P0702F05.23	Unknown Protein	At3g59140	ATMRP14 (Arabidopsis Thaliana Multidrug Resistance-Associated Protein 14)
P0702G08.13	Unknown Protein	At5g46950	Invertase/Pectin Methylesterase Inhibitor Family Protein

P0702G08.2	Gtpase Activator Protein-Like	At3g07890	RAB Gtpase Activator
P0702G08.21	Enhancer Of Polycomb-Like Protein	At1g79020	Transcription Factor-Related
P0702H08.19	Putative Carboxymethylenebutenolidase	At2g32520	Dienelactone Hydrolase Family Protein
P0703B01.25	Putative Non-Cell-Autonomous Protein Pathway2	At5g15140	Aldose 1-Epimerase Family Protein
P0703B01.8	Unknown Protein	At4g39860	Unknown Protein
P0703B11.26	Hypothetical Protein	At3g56370	Leucine-Rich Repeat Transmembrane Protein Kinase, Putative
P0703B11.29	Similar To Protein Kinase Atsik	At3g08760	ATSIK; Kinase
P0703C03.43	60S Ribosomal Protein L7A	At3g62870	60S Ribosomal Protein L7A (RPL7aB)
P0704D04.1	Hypothetical Protein	At1g66770	Nodulin Mtn3 Family Protein
P0704D04.27	Receptor-Like Protein Kinase-Like	At2g26730	Leucine-Rich Repeat Transmembrane Protein Kinase, Putative
P0705A04.46	Putative Dentritic Cell 2 Protein<DC2 Protein	At4g29870	Unknown Protein
P0705A05.111	Putative Iron Inhibited ABC Transporter 2	At5g60790	ATGCN1 (Arabidopsis Thaliana General Control Non-Repressible 1)
P0705A05.112-3	Putative P-Glycoprotein 1	At2g36910	ATPGP1 (ARABIDOPSIS THALIANA P GLYCOPROTEIN1); Calmodulin Binding
P0705A05.133	Putative SET1	At4g13460	SUVH9 (SU(VAR)3-9 HOMOLOG 9); Histone-Lysine N-Methyltransferase/ Zinc Ion Binding
P0706E03.1	Putative Proteasome 26S Non-Atpase Subunit 2	At2g20580	Atrpn1a/RPN1A (26S Proteasome Regulatory Subunit S2 1A); Binding
P0706E03.4-1	Putative Eukaryotic Translation Initiation	At1g36730	Eukaryotic Translation Initiation Factor 5, Putative / Eif-5, Putative
P0706E03.6	Putative GTP-Binding Protein	At5g60860	Atraba1f (Arabidopsis Rab Gtpase Homolog A1f); GTP Binding
P0706E03.9	Apospory-Associated Protein C-Like	At5g66530	Aldose 1-Epimerase Family Protein
P0707C02.27	Dehydration-Responsive Protein-Like	At1g26850	Dehydration-Responsive Family Protein
P0707C02.28	Putative Phosphofructokinase	At2g22480	Phosphofructokinase Family Protein
P0707C02.31	Putative Glucose Transporter	At4g02050	Sugar Transporter, Putative
P0707D10.20	Unknown Protein	At5g11320	YUC4 (YUCCA4); Monooxygenase
P0707D10.27	Hypothetical Protein	At1g80310	Sulfate Transporter
P0707D10.28	Hypothetical Protein	At3g22690	Pentatricopeptide (PPR) Repeat-Containing Protein
P0707D10.7	Hypothetical Protein	At5g17460	Unknown Protein
P0708B04.1	Putative Male Fertility Protein	At1g74020	SS2 (STRICTOSIDINE SYNTHASE 2); Strictosidine Synthase
P0708B04.21	Putative Senescence-Associated Protein	At2g23810	Tet8 (Tetraspanin8)
P0708B04.23	Splicing Factor 3B Subunit 5-Like Protein	At3g23320	Unknown Protein
P0708B04.3-1	Putative Calcineurin B Subunit	At3g18430	Calcium-Binding EF Hand Family Protein
P0708D12.3	Putative Casein Kinase	At3g13670	Protein Kinase Family Protein
P0708H12.35	Trehalose-6-Phosphate Phosphatase	At5g51460	ATTPPA (Arabidopsis Thaliana Trehalose-6-Phosphate Phosphatase); Trehalose-Phosphatase
P0708H12.4-1	F-Box Protein-Like	At5g51380	F-Box Family Protein
P0709D11.15	Putative Oxidoreductase, Zinc-Binding	At1g23740	Oxidoreductase, Zinc-Binding Dehydrogenase Family Protein
P0709D11.28	Putative Polygalacturonase Isoenzyme 1 Beta	At1g70370	BURP Domain-Containing Protein / Polygalacturonase, Putative
P0710A02.3	Putative Protein Kinase AFC3	At4g32660	AME3; Kinase

P0710A02.4	Cytosolic Aldehyde Dehydrogenase	At3g48000	ALDH2B4 (ALDEHYDE DEHYDROGENASE 2); 3-Chloroallyl Aldehyde Dehydrogenase/ Aldehyde Dehydrogenase (NAD)
P0710F09.119	Putative Chalcone Synthase	At4g34850	Chalcone And Stilbene Synthase Family Protein
P0711A01.29-1	Putative HAK2	At1g60160	Potassium Transporter Family Protein
P0711F01.27	Putative Protein-Arginine N-Methyltransferase	At4g29510	Protein Arginine N-Methyltransferase, Putative
P0711F01.41	Putative FAE1	At4g34510	KCS2 (3-Ketoacyl-Coa Synthase 2); Acyltransferase
P0711F01.51	ATP-Binding Cassette Transporter Atabca1-Like	At3g47780	ATATH6 (ABC2 Homolog 6); Atpase, Coupled To Transmembrane Movement Of Substances
P0711F01.53	Putative Serine/Threonine Protein Kinase	At5g15080	Protein Kinase, Putative
P0711F01.56-1	Voltage-Dependent Anion Channel	At3g01280	Porin, Putative
P0711H09.10-1	Putative AT-Hook DNA-Binding Protein	At2g33620	DNA-Binding Family Protein / AT-Hook Protein 1 (AHP1)
P0711H09.13	Protein Cdc2 Kinase	At1g20930	CDKB2;2 (CYCLIN-DEPENDENT KINASE B2;2); Kinase
P0711H09.15	3-Hydroxy-3-Methylglutaryl-Coenzyme A Reductase	At1g76490	Hmg1 (3-Hydroxy-3-Methylglutaryl Coa Reductase)
P0711H09.20	Unknown Protein	At3g18240	Unknown Protein
P0711H09.4	Unknown Protein	At2g17350	Unknown Protein
P0711H09.5	Putative Aminoacylase	At4g38220	Aminoacylase, Putative / N-Acyl-L-Amino-Acid Amidohydrolase, Putative
P0711H09.9	Putative Rab Geranylgeranyltransferase, Beta	At5g12210	Geranylgeranyl Transferase Type II Beta Subunit, Putative / RAB Geranylgeranyltransferase Beta Subunit, Putative
P0712E02.24	Unknown Protein	At1g69800	CBS Domain-Containing Protein
P0712E02.8	Unknown Protein	At5g35460	Unknown Protein
P0724B10.10	Putative Syntaxin	At5g16830	SYP21 (Syntaxin 21); T-SNARE
P0724B10.17	Putative Cytochrome P450	At4g19230	CYP707A1 (Cytochrome P450, Family 707, Subfamily A, Polypeptide 1); Oxygen Binding
P0724B10.23	Nodulin-Like Protein	At4g30420	Nodulin Mtn21 Family Protein
P0724B10.24	Putative 9-Cis-Epoxycarotenoid Dioxygenase	At4g19170	Nced4 (Nine-Cis-Epoxycarotenoid Dioxygenase 4)
P0724B10.3-1	Putative Protein Kinase Yaka	At5g35980	Kinase
P0724B10.35	Phosphatidic Acid Phosphatase-Like	At5g66450	Phosphatidic Acid Phosphatase-Related / PAP2-Related
P0724B10.38	Putative Ornithine Carbamoyltransferase	At1g75330	OTC (ORNITHINE CARBAMOYLTRANSFERASE); Amino Acid Binding / Carboxyl- And Carbamoyltransferase
P0724B10.42	Putative Phenylcoumaran Benzylic Ether Reductase	At4g34540	Isoflavone Reductase Family Protein
P0724B10.43	Hydrolase, Alpha/Beta Fold Family-Like	At4g36530	Hydrolase, Alpha/Beta Fold Family Protein
P0724B10.5	Unknown Protein	At1g31650	ATROPGEF14/ROPGEF14 (KINASE PARTNER PROTEIN-LIKE); Rho Guanyl-Nucleotide Exchange Factor
P0758B01.6-1	Putative Thromboxane-A Synthase	At2g26170	CYP711A1 (MORE AXILLARY BRANCHES 1); Oxygen Binding
PPR683	Hypothetical Protein	At1g63130	Pentatricopeptide (PPR) Repeat-Containing Protein
PPR762	Hypothetical Protein	At1g62910	Pentatricopeptide (PPR) Repeat-Containing Protein
q3037.18	Hypothetical Protein	At1g63930	Unknown Protein
q3037.20	Similar To Medicago Nodulin N21 (Mtn21)	At1g68170	Nodulin Mtn21 Family Protein
W455ERIPDK	Putative GTP-Binding Protein	At1g02130	ATRAB1B (Arabidopsis Thaliana Responsive To Abscisic Acid 1B); GTP Binding

Supplementary Table 2: Libraries and signature counts in Rice

Code	Title	No. of Signatures
9LA	Leaves	1,606,175
9LB	Leaves - Replicate	1,005,937
9LC	Leaves	1,144,192
9LD	Leaves - Replicate	1,146,212
9ME	Merismatic Tissue	2,112,790
9RO	Roots	2,162,940
9RR	Roots - Replicate	2,156,164
FLA	F1 Hybrid 60days Mature Leaf Replicate A	1,171,478
FLB	F1 Hybrid 60days Mature Leaf Replicate B	1,040,468
FLC	F1 Hybrid 60days Mature Leaf Replicate C	1,056,621
FLD	F1 Hybrid 60days Mature Leaf Replicate D	1,419,115
FME	F1 Hybrid 60days Meristematic tissue	3,045,290
FRO	F1 Hybrid 60days Mature Root	2,436,387
FRR	F1 Hybrid 60days Mature Root-Repl	2,205,884
MC00	Mock treatment-0hr	1,372,860
MC24	Mock treatment-24hr	1,402,116
MR03	M. grisea-R-3hr	1,422,272
MR06	M. grisea-R-6hr	1,054,700
MR12	M. grisea-R-12hr	1,331,343
MR24	M. grisea-R-24hr	1,435,098
MR48	M. grisea-R-48hr	1,367,250
MS03	M. grisea-S-3hr	1,584,229
MS06	M. grisea-S-6hr	1,354,948
MS12	M. grisea-S-12hr	1,086,361
MS24	M. grisea-S-24hr	1,022,535
MS48	M. grisea-S-48hr	1,518,407
MS96	M. grisea-S-96hr	1,061,873
NCA	35 days - Callus	2,131,255
NCL	14 days - Young leaves stressed in 4C cold for 24h	2,322,924

NCR	14 days - Young roots stressed in 4C cold for 24h	2,401,553
NDL	14 days - Young leaves stressed in drought for 5 days	2,613,140
NDR	14 days - Young roots stressed in drought for 5 days	2,190,870
NGD	10 days - Germinating seedlings grown in dark	2,512,579
NGS	3 days - Germinating seed	1,861,571
NIP	90 days - Immature panicle	2,661,421
NL4	Leaf - Combination of Replicates	4,940,921
NLA	60 days - Mature Leaves - Replicate A	1,073,991
NLB	60 days - Mature Leaves - Replicate B	1,348,557
NLC	60 days - Mature Leaves - Replicate C	1,263,549
NLD	60 days - Mature Leaves - Replicate D	1,254,824
NME	60 days - Crown vegetative meristematic tissue	2,568,641
NOS	Ovary and mature stigma	2,499,264
NPO	Mature Pollen	2,310,574
NR2	Root - Combination of Replicates	5,293,337
NRA	60 days - Mature Roots - Replicate A	2,675,567
NRB	60 days - Mature Roots - Replicate B	2,617,770
NSL	14 days - Young leaves stressed in 250 mM NaCl for 24h	2,531,362
NSR	14 days - Young roots stressed in 250 mM NaCl for 24h	1,842,226
NST	60 days - Stem	2,095,983
NYL	14 days - Young leaves	2,249,147
NYR	14 days - Young Roots	1,944,785
PLA	rice leaf, beet armyworm damaged, 24 hr(99-1726)	1,150,869
PLC	rice leaf, mechanical damaged, 24 hr	1,213,577
PLW	rice leaf, water weevil damaged, 24 hr	1,012,170
PSC	rice developing seeds, 6 days old cypress high milling(99-1710)	1,266,713
PSI	rice developing seeds,6 days old, Ilpumbyeo - High Taste	1,201,584

PSL	rice developing seeds, 6 days old, LaGrue-Low Milling	1,082,099
PSN	rice developing seed, 6 days old, Nipponbare-Grain quality control	1,207,914
PSY	rice developing seeds,6 days old, YR15965Acp33 - Low Taste	1,190,250
XC00	Unwounded Control-Nipponbare Xa21-0hr	1,190,318
XC06	Mock treatment-6hr	1,367,076
XC24	Mock treatment-24hr	1,165,716
XR03	X.oryzae-R-3hr	1,134,269
XR06	X.oryzae-R-6hr	1,269,616
XR12	X.oryzae-R-12hr	1,542,183
XR24	X.oryzae-R-24hr	1,055,586
XR48	X.oryzae- R-48hr	1,248,814
XS03	X.oryzae-S-3hr	1,466,965
XS06	X.oryzae-S-6hr	1,419,178
XS12	X.oryzae- S-12hr	1,444,840
XS24	X.oryzae- S-24hr	1,264,383
XS48	X.oryzae-S-48hr	1,175,368

Supplementary Table 3: Libraries and signature counts in Arabidopsis

Library	Code	Description	Total Signatures
Callus	CAF	actively growing, classic MPSS	1,959,539
Infloresence	INF	mixed stage, immature buds, classic MPSS	1,774,306
Leaves	LEF	21 day, untreated, classic MPSS	2,884,598
Root	ROF	21 day, untreated, classic MPSS	3,642,632
Silique	SIF	24 to 48 hr post-fertilization, classic MPSS	2,012,859
apl-10 inflorsenece	AP1	mixed stage, immature buds	2,964,724
ap3-6 infloresence	AP3	mixed stage, immature buds	2,435,965
Agamous infloresence	AGM	mixed stage, immature buds	2,575,670
Infloresence	INS	mixed stage, immature buds	2,890,894
Root	ROS	21 day, untreated	2,458,436
sup/ap1 infloresence	SAP	mixed stage, immature buds	2,310,350
Leaves,	S04	4 hr after salicylic acid treatment	3,006,975
Leaves,	S52	52 hr after salicylic acid treatment	2,964,840
Leaves	LES	21 day, untreated	3,109,385
Germinating seedlings	GSE	Germinating seedlings	2,550,655
Callus	CAS	actively growing, signature MPSS	1,919,458
Silique	SIS	24 to 48 hr post-fertilization, signature MPSS	2,349,283

Supplementary Table 4: Details of rice-Arabidopsis housekeeping homologous gene-pairs with their corresponding short functional description. Dn represents non-synonymous substitution rates, Ds represents synonymous substitution rates, Exp_rank corresponds to expression rank for individual rice genes, GC_3 represents GC content at synonymous third codon position. wRn stands for error minimization values and FFE represents free folding energy of rice genes.

Rice Housekeeping Gene ID	***Functional Description***	***Arabidopsis Gene ID***	***Functional description***	***Dn***	***Ds***	***Exp_rank***	***GC_3***	***wRn***	***FFE***
B1011A07.31	Putative Branched Chain Alpha-Keto Acid	At3g06850	DIN3/LTA1 (DARK INDUCIBLE 3); Alpha-Ketoacid Dehydrogenase	0.3377	2.3877	1	47.4470	-0.1220	-0.0249
B1116H04.25	Putative Activator Of 90 Kda Heat Shock Protein	At3g12050	Aha1 Domain-Containing Protein	0.2758	4.0649	1	83.6990	-0.4609	-0.0430
B1120F06.103	Unknown Protein	At5g63440	Unknown Protein	0.1327	3.7843	1	48.8260	0.0135	-0.0810
B1131G08.9	Hypothetical Protein	At1g29190	Hypothetical Protein	0.4423	3.5749	1	91.0110	-0.4516	-0.1236
OJ1003_E05.12	Unknown Protein	At4g28430	Reticulon Family Protein	0.7466	3.5888	1	73.8370	-0.2062	-0.0830
OJ1004C08.18	Putative Protein Kinase	At1g20650	Protein Kinase	0.3943	4.2327	1	61.9570	-0.1400	-0.0504
OJ1008_D06.10	Putative S-Adenosyl-L-Methionine:Salicylic Acid	At5g66430	S-Adenosyl-L-Methionine:Carboxyl Methyltransferase Family Protein	0.6264	4.1153	1	86.9080	-0.4801	-0.0408
OJ1014_H03.11	Putative Anther-Specific Proline-Rich Protein	At5g33370	GDSL-Motif Lipase/Hydrolase Family Protein	0.2670	4.1522	1	90.8570	-0.4465	-0.0354
OJ1047_C01.14	Putative Interferon-Related Protein	At1g27760	Interferon-Related Developmental Regulator Family Protein / IFRD Protein Family	0.5031	2.9312	1	43.6590	-0.1589	-0.0260
OJ1057_E05.110	Putative Nramp1 Protein	At1g80830	NRAMP1 (NRAMP Metal Ion Transporter 1); Manganese Ion Transporter/ Metal Ion Transporter	0.3917	4.5023	1	77.5000	-0.4968	-0.0217
OJ1081_B12.106-3	P53 Binding Protein-Like	At1g67320	DNA Primase, Large Subunit Family	0.3462	3.2364	1	51.9570	-0.1473	-0.0505
OJ1111_C07.25	Putative Serine Palmitoyltransferase LCB1	At4g36480	ATLCB1 (ARABIDOPSIS THALIANA SPHINGOLIPID LONGCHAIN BASE 1); Serine C-Palmitoyltransferase	0.2450	2.3034	1	37.7230	-0.0794	-0.0547
OJ1111_C07.26	Putative Phosphoenolpyruvate Carboxylase Kinase	At1g08650	PPCK1 (PHOSPHOENOLPYRUVATE CARBOXYLASE KINASE); Kinase	0.4265	3.8441	1	96.7150	-0.3681	-0.0761
OJ1112_G07.12	Putative Rar1	At5g51700	Pbs2 (Pphb Susceptible 2)	0.2779	3.5972	1	35.6320	-0.0390	-0.1028
OJ1119_A01.21-1	Putative 50S Ribosomal Protein L9, Chloroplast	At3g44890	RPL9 (Ribosomal Protein L9); Structural Constituent Of Ribosome	0.2662	3.6649	1	59.1950	-0.1830	-0.0471
OJ1119_B10.31	Light Induced Protein Like	At4g22310	Unknown Protein	0.1204	3.1667	1	37.0370	0.0837	-0.1128
OJ1126B12.12	Putative Ubiquitin-Conjugating Enzyme	At3g57870	AHUS5 (EMBRYO DEFECTIVE 1637); Ubiquitin-Protein Ligase	0.0852	3.3972	1	58.4420	-0.5007	-0.1119
OJ1126B12.8	Putative MADS Box-Like Protein	At4g22950	AGL19 (AGAMOUS-LIKE 19); Transcription Factor	0.5405	3.4458	1	55.7250	-0.4748	-0.1086
OJ1134_F06.8-1	Putative Peroxisomal Targeting	At1g29260	PEX7 (Peroxin 7)	0.304	4.0848	1	94.8550	-0.3608	-0.0795

	Signal Type 2			8						
OJ1150_A11.12-1	Putative DHHC-Type Zinc Finger Domain-Containing	At3g22180	Zinc Finger (DHHC Type) Family Protein	0.4643	4.7025	1	59.0980	-0.2672	-0.0175
OJ1175_B01.14-2	Unknown Protein	At4g24610	Unknown Protein	0.3058	4.9323	1	44.9700	-0.1046	-0.0244
OJ1175C11.9	Putative RING Zinc Finger Protein	At4g34370	IBR Domain-Containing Protein	0.3217	4.4045	1	51.3940	-0.2428	-0.0293
OJ1191_A10.101	Putative Auxin-Induced Protein	At3g25290	Auxin-Responsive Family Protein	0.4616	4.2146	1	80.6280	-0.5002	-0.0679
OJ1214_E03.9	Putative T-Complex Protein 1 Beta Subunit	At5g20890	Chaperonin, Putative	0.0736	3.9506	1	46.5650	-0.3498	-0.0273
OJ1263_E10.15	Protein Phosphatase 2A B'kappa Subunit	At5g25510	Serine/Threonine Protein Phosphatase 2A (PP2A) Regulatory Subunit B', Putative	0.2441	4.6214	1	57.0230	-0.3946	-0.0359
OJ1263H11.6	Unknown Protein	At5g51880	Oxidoreductase, Acting On Paired Donors, With Incorporation Or Reduction Of Molecular Oxygen, 2-Oxoglutarate As One Donor, And Incorporation Of One Atom Each Of Oxygen Into Both Donors	0.3713	3.8191	1	54.5850	-0.4277	-0.0763
OJ1276_B06.27	Unknown Protein	At3g27670	RST1 (RESURRECTION1); Binding	0.6371	1.6701	1	42.5140	-0.0162	-0.0211
OJ1311_D08.27	Putative Lysine-Ketoglutarate	At4g33150	Lkr (Saccharopine Dehydrogenase)	0.3367	1.7409	1	38.4150	-0.0135	-0.0126
OJ1365_D05.6	Putative Protein Transport SEC23-Related	At5g43670	Transport Protein, Putative	0.3253	3.6904	1	55.6800	-0.3236	-0.0350
OJ1372_D06.24	Unknown Protein	At4g10300	Unknown Protein	0.3674	3.2763	1	91.7430	-0.4120	-0.1018
OJ1378_A04.7	Hypothetical Protein	At1g22540	Proton-Dependent Oligopeptide Transport (POT) Family Protein	0.4631	4.3594	1	92.7950	-0.3550	-0.0301
OJ1442_E05.22	Putative 15.9 Kda Subunit Of RNA Polymerase II	At5g09920	RPB15.9 (RNA Polymerase II 15.9)	0.1592	3.3908	1	96.8250	-0.4680	-0.0951
OJ1442_E05.24	Unknown Protein	At1g73060	Unknown Protein	0.2615	2.3707	1	55.3670	-0.3962	-0.0416
OJ1457_D07.109-1	Putative Regulator Of Nonsense Transcripts 1	At5g47010	LBA1/UPF1 (LOW-LEVEL BETA-AMYLASE 1); RNA Helicase	0.1631	5.0465	1	44.9850	0.0583	-0.0102
OJ1524_D08.2	Putative Dnaj Homolog, Subfamily C, Member 9	At3g12170	DNAJ Heat Shock N-Terminal Domain-Containing Protein	0.2548	2.8260	1	51.4170	-0.2883	-0.0550
OJ1534_E09.9-2	Unknown Protein	At5g35560	DENN (AEX-3) Domain-Containing Protein	0.5141	4.7785	1	43.1510	0.3659	-0.0686
OJ1548_F12.23	Putative Quinone Oxidoreductase	At4g21580	Oxidoreductase, Zinc-Binding Dehydrogenase Family Protein	0.2647	1.7860	1	63.3990	-0.5881	-0.0576
OJ1579_C03.5	Unknown Protein	At5g39360	Circadian Clock Coupling Factor-Related	0.2125	3.8690	1	67.6600	-0.3931	-0.0915
OJ1643_A10.16	Membrane-Associated Salt-Inducible Protein Like	At4g36680	Pentatricopeptide (PPR) Repeat-Containing Protein	0.6373	2.1844	1	71.7700	-0.3287	-0.0402
OJ1695_A02.23	Putative U4/U6-Associated RNA Splicing Factor	At1g28060	Small Nuclear Ribonucleoprotein Family Protein / Snrnp Family Protein	0.2440	4.2665	1	40.5150	-0.0816	-0.0246
OJ1695_A02.34	Putative Ferredoxin-Thioredoxin Reductase	At2g04700	Ferredoxin Thioredoxin Reductase Catalytic Beta Chain Family Protein	0.2790	3.4271	1	49.6400	-0.2345	-0.0582
OJ1705_A03.38	Putative Threonyl-Trna Synthetase	At5g26830	Threonyl-Trna Synthetase / Threonine--Trna Ligase (THRRS)	0.2207	4.5367	1	47.8770	-0.2876	-0.0239
OJ1710_H11.105-1	Putative CND41, Chloroplast	At3g50050	Aspartyl Protease Family Protein	0.370	2.0856	1	46.5120	-0.2476	-0.0409

	Nucleoid DNA Binding			8						
OJ1717_A09.37	Putative GAMM1 Protein	At5g41970	Unknown Protein	0.1909	4.1041	1	54.2680	-0.3442	-0.0693	
OJ1743_B12.40	Putative Clathrin Coat Assembly Protein AP50	At5g46630	Clathrin Adaptor Complexes Medium Subunit Family Protein	0.0422	3.5074	1	44.4170	-0.2375	-0.0372	
OJ1789_D08.10	Glutaredoxin-Like	At5g14070	Glutaredoxin Family Protein	0.3382	3.3431	1	97.6560	-0.2983	-0.2044	
OJ1791_B03.50-2	2 Coiled Coil Domains Of Eukaryotic Origin (31.3	At3g18790	Unknown Protein	0.2277	3.8953	1	87.5490	-0.6059	-0.0505	
OSJNBa0003O19.5	Unknown Protein	At2g26890	GRV2 (KATAMARI2); Binding / Heat Shock Protein Binding	0.1999	5.0206	1	37.0370	-0.0182	-0.0110	
OSJNBa0004B24.2	Putative Purple Acid Phosphatase	At3g20500	ATPAP18/PAP18 (Purple Acid Phosphatase 18); Acid Phosphatase/ Protein Serine/Threonine Phosphatase	0.1965	2.2081	1	50.0000	-0.1335	-0.0081	
OSJNBa0004E08.1	Putative Cyclophilin	At2g16600	ROC3 (Rotamase Cyp 3)	0.3264	3.6366	1	97.1590	-0.4355	-0.1011	
OSJNBa0006B20.3	Unknown Protein	At1g04290	Thioesterase Family Protein	0.4990	2.2975	1	83.4480	-0.4955	-0.1261	
OSJNBa0009C08.12	Unknown Protein	At3g61320	Unknown Protein	0.3682	2.2535	1	70.2920	-0.5081	-0.0326	
OSJNBa0010E04.12	Putative Small Nuclear Ribonucleoprotein	At3g47120	RNA Recognition Motif (RRM)-Containing Protein	0.4499	3.8781	1	56.0280	-0.1794	-0.0462	
OSJNBa0010H02.13	Unknown Protein	At1g19800	Tgd1 (Trigalactosyldiacylglycerol 1)	0.4284	4.2276	1	75.5160	-0.5293	-0.0247	
OSJNBa0010H02.2	Unknown Protein	At4g38390	Unknown Protein	0.4124	4.4123	1	47.8990	0.1563	-0.0439	
OSJNBa0010K01.7	Putative Receptor Protein Kinase	At1g28440	HSL1 (HAESA-LIKE 1); ATP Binding / Kinase/ Protein Serine/Threonine Kinase	0.3438	4.9159	1	79.1400	-0.4180	-0.0091	
OSJNBa0013D02.9	Putative MAP Kinase 1	At3g45640	ATMPK3 (MITOGEN-ACTIVATED PROTEIN KINASE 3); MAP Kinase/ Kinase/ Protein Kinase	0.1833	4.0862	1	92.4700	-0.4447	-0.0333	
OSJNBa0014O06.3	Hypothetical Protein	At1g03010	Phototropic-Responsive NPH3 Family Protein	0.6305	4.5377	1	91.6810	-0.3821	-0.0342	
OSJNBa0015K02.7	Unknown Protein	At5g24940	Protein Phosphatase 2C, Putative / PP2C, Putative	0.1902	3.9330	1	40.9770	-0.2716	-0.0762	
OSJNBa0016N23.122	Putative Alcohol Dehydrogenase Homolog	At1g62610	Oxidoreductase	0.3792	4.1158	1	61.3970	-0.2628	-0.1004	
OSJNBa0016O02.3	Unknown Protein	At5g08170	EMB1873 (EMBRYO DEFECTIVE 1873); Agmatine Deiminase	0.3471	2.8158	1	46.0320	-0.0659	-0.0385	
OSJNBa0019D11.19	Unknown Protein	At5g54140	ILL3 (IAA-Amino Acid Hydrolase ILR1-Like 3); Metallopeptidase	0.3504	1.9783	1	53.9640	-0.5149	-0.0162	
OSJNBa0019F11.23	Putative Plastid Protein	At1g32580	Plastid Developmental Protein DAG, Putative	0.2813	3.8312	1	78.0950	-0.4428	-0.0907	
OSJNBa0019F11.5	Unknown Protein	At5g17210	Unknown Protein	0.6164	3.6961	1	62.4200	-0.0849	-0.1037	
OSJNBa0022H21.12	Unknown Protein	At5g50170	C2 Domain-Containing Protein / GRAM Domain-Containing Protein	0.4648	3.9862	1	98.5960	-0.4272	-0.0623	
OSJNBa0023I17.12	Putative Receptor Protein Kinase PERK	At3g14840	Leucine-Rich Repeat Family Protein / Protein Kinase Family Protein	0.5562	4.1754	1	39.0710	0.1442	-0.0384	
OSJNBa0024J22.1	Unknown Protein	At1g79940	Heat Shock Protein Binding / Unfolded Protein Binding	0.2118	1.7743	1	50.7250	-0.2040	-0.0225	

OSJNBa0026E05.33	Unknown Protein	At5g58110	Unknown Protein	0.3110	2.4383	1	65.9340	-0.4600	-0.1020
OSJNBa0027P08.15	Unknown Protein	At1g19120	Small Nuclear Ribonucleoprotein, Putative / Snrnp, Putative / Sm Protein, Putative	0.1622	1.8355	1	45.5280	-0.3557	-0.1368
OSJNBa0031O09.03	Similar To Histone 2A Domain	At1g54690	Histone H2A, Putative	0.0974	3.4848	1	95.4200	-0.5160	-0.1277
OSJNBa0032G08.4	Putative Glycogenin	At1g54940	Glycogenin Glucosyltransferase (Glycogenin)-Related	0.5336	4.3813	1	96.8970	-0.3674	-0.0322
OSJNBa0032G11.13	Putative Protein Kinase	At3g59350	Kinase	0.1716	4.1600	1	37.4270	0.3225	-0.0293
OSJNBa0034B05.23	Putative Synaptobrevin-Like Protein	At5g22360	ATVAMP714 (Vesicle-Associated Membrane Protein 714)	0.1403	3.7908	1	69.3020	-0.4133	-0.0776
OSJNBa0035A24.10	Prefoldin-Related KE2-Like	At3g52400	SYP122 (Syntaxin 122); T-SNARE	1.4085	2.2482	1	51.2990	-0.2903	-0.1285
OSJNBa0035I03.17	Putative DNA-Binding Protein Phosphatase 2C	At2g25620	Protein Phosphatase 2C, Putative / PP2C, Putative	0.5238	2.4156	1	49.4440	-0.2149	-0.0412
OSJNBa0036B21.10	Unknown Protein	At4g39640	GGT1; Gamma-Glutamyltransferase	0.3112	2.2018	1	65.7660	-0.4467	-0.0368
OSJNBa0038J17.19	Unknown Protein	At5g45920	Carboxylic Ester Hydrolase	0.3577	1.5981	1	69.4690	-0.1762	-0.0920
OSJNBa0039C07.3	Unknown Protein	At1g32210	Atdad1 (Defender Against Apoptotic Death 1)	0.0969	2.9715	1	52.2120	-0.4317	-0.1377
OSJNBa0039N21.9	Putative Glycosyltransferase Protein	At1g18580	GAUT11 (Galacturonosyltransferase 11); Polygalacturonate 4-Alpha-Galacturonosyltransferase	0.2764	4.4416	1	45.9410	-0.1687	-0.0571
OSJNBa0041C07.40	Putative Leucyl-Trna Synthetase	At1g09620	ATP Binding / Aminoacyl-Trna Ligase	0.2296	3.9567	1	43.3070	-0.3159	-0.0119
OSJNBa0042H24.8-2	Bystin (51.6 Kd)-Like	At1g31660	Unknown Protein	0.2760	3.8511	1	46.7580	-0.2134	-0.0316
OSJNBa0050E08.8	Putative Alcohol Dehydrogenase	At1g64710	Oxidoreductase/ Zinc Ion Binding	0.2951	3.3563	1	65.1520	-0.4795	-0.0711
OSJNBa0052K01.17	Putative ADP/ATP Translocase	At5g56450	Substrate Carrier Family Protein	0.2664	3.6006	1	64.4260	-0.4141	-0.0380
OSJNBa0053C23.5	Unknown Protein	At4g25660	Unknown Protein	0.2896	3.7633	1	70.3060	-0.3237	-0.0455
OSJNBa0054K20.17	Diacylglycerol Kinase-Like	At4g30340	ATDGK7 (DIACYLGLYCEROL KINASE 7); Diacylglycerol Kinase	0.3701	4.0242	1	51.2300	-0.1564	-0.0531
OSJNBa0054K20.36	Putative Dem Protein	At3g19240	Unknown Protein	0.3197	4.5357	1	68.6110	-0.5069	-0.0314
OSJNBa0055C08.14	Unknown Protein	At4g24990	ATGP4 (Arabidopsis Thaliana Geranylgeranylated Protein)	0.2933	1.6259	1	64.2860	-0.5326	-0.0622
OSJNBa0056G17.7	Unknown Protein	At5g45410	Unknown Protein	0.4379	1.7909	1	46.9030	-0.0019	-0.0295
OSJNBa0060D06.18	Unknown Protein	At3g13320	CAX2 (CATION EXCHANGER 2); Calcium:Hydrogen Antiporter	0.2519	1.8479	1	43.5770	0.1216	-0.0333
OSJNBa0061L20.103	Putative Zinc Transporter Protein ZIP1	At1g05300	ZIP5 (ZINC TRANSPORTER 5 PRECURSOR); Cation Transporter	0.4482	4.1577	1	93.9480	-0.4258	-0.0546
OSJNBa0063K04.14	Pentatricopeptide (PPR) Repeat-Containing	At4g01400	Pentatricopeptide (PPR) Repeat-Containing Protein	0.1453	3.0704	1	58.4070	-0.0546	-0.0555
OSJNBa0064D20.9	Unknown Protein	At5g08500	Transmembrane CLPTM1 Family Protein	0.153	4.4529	1	52.0210	-0.0692	-0.0516

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OSJNBa0064E16.11	Unknown Protein	At5g48750	Auxin-Responsive Protein, Putative	0.7521	3.6443	1	95.8330	-0.2934	-0.1181
OSJNBa0064E16.15	Unknown Protein	At5g55530	C2 Domain-Containing Protein	0.4792	4.1649	1	49.4680	-0.3545	-0.0221
OSJNBa0068A07.14	Putative Translation Initiation Factor 2B Beta	At3g07300	GTP Binding / Translation Initiation Factor	0.2225	1.6346	1	43.9900	-0.3566	-0.0435
OSJNBa0068L06.9	Unknown Protein	At1g06200	Serine-Type Peptidase	0.3355	1.7749	1	54.6390	-0.1668	-0.0524
OSJNBa0070C17.23	Unknown Protein	At2g35060	KUP11 (K+ Uptake Permease 11); Potassium Ion Transporter	0.1998	1.5766	1	53.2300	-0.3677	-0.0126
OSJNBa0073A18.26-1	Unknown Protein	At5g42570	Unknown Protein	0.4234	1.8549	1	70.8740	-0.6031	-0.0761
OSJNBa0073A21.8-1	Putative Cytochrome P450	At4g15110	CYP97B3 (Cytochrome P450, Family 97, Subfamily B, Polypeptide 3); Oxygen Binding	0.2139	1.8190	1	50.4660	-0.1566	-0.0424
OSJNBa0073L01.13	Hypothetical Protein	At4g38270	GAUT3 (Galacturonosyltransferase 3); Polygalacturonate 4-Alpha-Galacturonosyltransferase/ Transferase, Transferring Glycosyl Groups	0.3124	2.7820	1	51.2910	-0.0738	-0.0187
OSJNBa0075A22.20	TATA-Binding Protein TBP2	At1g55520	TBP2 (TATA Binding Protein 2); DNA Binding / RNA Polymerase II Transcription Factor	0.0453	3.7557	1	46.3540	-0.1984	-0.0837
OSJNBa0081P02.7	Unknown Protein	At1g73500	ATMKK9 (Arabidopsis Thaliana MAP Kinase Kinase 9); Kinase	0.5081	4.0719	1	92.4530	-0.4380	-0.0292
OSJNBa0083N12.20	Unknown Protein	At1g64850	Calcium-Binding EF Hand Family Protein	0.3586	3.5304	1	91.7720	-0.4888	-0.0913
OSJNBa0088H09.6	Unknown Protein	At5g41260	Protein Kinase Family Protein	0.2275	4.4032	1	47.4730	-0.2472	-0.0486
OSJNBa0089K24.15	Putative MRP-Like ABC Transporter	At3g13080	ATMRP3 (Arabidopsis Thaliana Multidrug Resistance-Associated Protein 3)	0.3188	2.6248	1	63.2100	-0.3346	-0.0137
OSJNBa0090O10.19	Putative Inner Membrane Protein	At1g72750	ATTIM23-2 (Arabidopsis Thaliana Translocase Inner Membrane Subunit 23-2); Protein Translocase	0.3435	3.6816	1	94.1800	-0.4742	-0.0990
OSJNBa0090O10.21	Hypothetical Protein	At1g01220	GHMP Kinase-Related	0.2955	1.8900	1	47.3430	-0.3511	-0.0197
OSJNBa0093O08.1	Unknown Protein	At1g56130	Leucine-Rich Repeat Family Protein / Protein Kinase Family Protein;	0.5410	3.5231	1	62.4060	-0.2482	-0.0878
OSJNBa0094J08.29	Putative Protein Kinase	At3g27560	ATN1; Kinase/ Protein Threonine/Tyrosine Kinase	0.3825	2.3417	1	52.3940	-0.3380	-0.0287
OSJNBb0004A17.3	Unknown Protein	At3g02720	DJ-1 Family Protein / Protease-Related	0.1697	1.6746	1	48.9190	-0.2271	-0.0367
OSJNBb0006L10.5	Putative Spermine Synthase	At5g19530	Acl5 (Acaulis 5)	0.2583	4.1250	1	74.8430	-0.3296	-0.0238
OSJNBb0015I02.16	Putative Phosphatase	At3g58490	Phosphatidic Acid Phosphatase Family Protein / PAP2 Family Protein	0.3519	1.9494	1	61.4250	-0.3425	-0.0318
OSJNBb0017F17.18	Putative Acyl-Coa Independent Ceramide Synthase	At4g22330	ATCES1 (ATCES1); Catalytic	0.2032	2.3443	1	47.3900	-0.1454	-0.0405
OSJNBb0021O11.8	Putative Permease	At1g49960	Xanthine/Uracil Permease Family Protein	0.3201	4.5193	1	81.9390	-0.3387	-0.0250
OSJNBb0034G17.19	Unknown Protein	At2g01480	Unknown Protein	0.6163	4.2363	1	48.4260	0.0816	-0.0507

OSJNBb0035I14.16	Uroporphyrin-III C-Methyltransferase-Like	At5g40850	UPM1 (UROPHORPHYRIN METHYLASE 1); Uroporphyrin-III C-Methyltransferase	0.2736	2.2590	1	60.4970	-0.4790	-0.0245
OSJNBb0036F07.7	Putative ATP Sulfurylase	At3g22890	APS1 (ATP Sulfurylase 3)	0.2212	2.1076	1	62.9460	-0.2669	-0.0486
OSJNBb0039L24.21	Unknown Protein	At1g63420	Unknown Protein	0.5293	4.4424	1	82.9520	-0.3380	-0.0441
OSJNBb0041A22.5	'Unknown Protein, Contains ACT Domain, PF01842'	At2g39570	ACT Domain-Containing Protein	0.4396	2.9725	1	59.1220	-0.0735	-0.0452
OSJNBb0044I14.4	Putative Serine /Threonine Kinase Similar To	At2g02800	APK2B (PROTEIN KINASE 2B); Kinase	0.2934	4.2864	1	49.5120	-0.1040	-0.0376
OSJNBb0053G03.17	Putative Regulatory Protein NPR1 (Nonexpresser	At5g45110	NPR3 (NPR1-LIKE PROTEIN 3); Protein Binding	0.3948	4.5346	1	56.3330	0.1638	-0.0268
OSJNBb0059K02.15	Unknown Protein	At4g34200	EDA9 (Embryo Sac Development Arrest 9); NAD Binding / Amino Acid Binding / Cofactor Binding / Oxidoreductase, Acting On The CH-OH Group Of Donors, NAD Or NADP As Acceptor / Phosphoglycerate Dehydrogenase	0.2019	1.3993	1	58.0870	-0.6057	-0.0183
OSJNBb0060J21.23	Expressed Protein	At5g35220	EGY1 (ETHYLENE-DEPENDENT GRAVITROPISM-DEFICIENT AND YELLOW-GREEN 1); Sterol Regulatory Element-Binding Protein Site 2 Protease	0.1945	2.2249	1	37.9000	0.1489	-0.0303
OSJNBb0062H02.2	Unknown Protein	At4g10710	SPT16 (GLOBAL TRANSCRIPTION FACTOR C); Metalloexopeptidase	0.2139	3.1605	1	41.7270	-0.1957	-0.0096
OSJNBb0064I19.32	Unknown Protein	At5g27990	Unknown Protein	0.6580	1.8255	1	61.7490	-0.5119	-0.1192
OSJNBb0072E24.1	Putative Angio-Associated Migratory Cell	At4g02730	Transducin Family Protein / WD-40 Repeat Family Protein	1.0649	2.6386	1	47.1430	0.0034	-0.0258
OSJNBb0073N24.1	Putative Glutamyl-Trna Reductase	At1g58290	HEMA1; Glutamyl-Trna Reductase	0.2625	4.4780	1	64.0820	-0.5049	-0.0468
OSJNBb0076O03.29	RNA Helicase-Like	At1g32490	EMB2733/ESP3 (EMBRYO DEFECTIVE 2733); ATP-Dependent RNA Helicase	0.2021	4.8634	1	39.9790	-0.0398	-0.0174
OSJNBb0085F13.13	Unknown Protein	At1g12550	Oxidoreductase Family Protein	0.3917	4.1173	1	91.9190	-0.3667	-0.0630
OSJNBb0086G17.10	Putative SMC5 Protein	At5g15920	Structural Maintenance Of Chromosomes (SMC) Family Protein (MSS2)	0.3324	4.9149	1	47.9340	-0.2483	-0.0173
OSJNBb0091N21.29	Putative Methionine Aminopeptidase	At2g45240	MAP1A (METHIONINE AMINOPEPTIDASE 1A); Methionyl Aminopeptidase	0.1811	4.1877	1	38.6170	0.2498	-0.0527
OSJNBb0092C08.9	Unknown Protein	At1g16430	Surfeit Locus Protein 5 Family Protein / SURF5 Family Protein	0.2854	2.0547	1	63.7680	-0.2262	-0.2061
OSJNBb0093E13.11	Putative Clathrin Assembly Protein	At4g35410	Clathrin Adaptor Complex Small Chain Family Protein	0.0733	3.4787	1	52.9760	-0.5010	-0.0577
OSJNBb0096M04.115	Unknown Protein	At5g48660	Unknown Protein	0.3122	3.8335	1	76.9230	-0.5396	-0.1000
OSJNBb0116K07.3	Unknown Protein	At1g80050	APT2 (ADENINE PHOSPHORIBOSYL TRANSFERASE 2); Adenine Phosphoribosyltransferase	0.2620	2.0646	1	57.8680	-0.1287	-0.0542
P0007D08.23	Putative PIR7A Protein	At1g33990	Hydrolase, Alpha/Beta Fold Family Protein	0.2479	4.1441	1	64.2470	-0.5081	-0.0565
P0009G03.13	Hypothetical Protein	At3g12570	Fyd	0.3216	4.4156	1	51.0980	-0.0343	-0.0242

P0010C01.26	Putative Thioredoxin M-Type, Chloroplast	At1g76760	ATY1 (Arabidopsis Thioredoxin Y1); Thiol-Disulfide Exchange Intermediate	0.8795	2.4702	1	70.3030	-0.4297	-0.0457
P0019D06.2	Putative AAA-Type Atpase	At2g27600	AAA-Type Atpase Family Protein / Vacuolar Sorting Protein-Related	0.1625	1.5607	1	58.4860	-0.3710	-0.0287
P0019E03.5	Hypothetical Protein	At3g61750	Auxin-Responsive Protein -Related	0.4956	4.1990	1	81.8920	-0.4547	-0.0704
P0020D05.9	Unknown Protein	At1g50630	Extracellular Ligand-Gated Ion Channel	0.5286	4.2318	1	97.9310	-0.4586	-0.0563
P0024G09.11	Unknown Protein	At3g55600	Unknown Protein	0.4913	3.9146	1	66.9490	-0.6185	-0.0356
P0035F12.15	Putative Reca Protein	At2g19490	Reca Family Protein	0.2369	2.1083	1	36.5380	-0.1881	-0.0366
P0035F12.16	Unknown Protein	At5g55120	VTC5; Galactose-1-Phosphate Guanylyltransferase (GDP)	0.4078	1.5518	1	48.4570	-0.3143	-0.0247
P0041A24.3	Unknown Protein	At1g10240	FRS11 (FAR1-RELATED SEQUENCE 11); Zinc Ion Binding	0.2916	2.4241	1	65.7560	-0.4183	-0.0293
P0401G10.21	Putative Glucose Inhibited Division Protein A	At2g13440	Glucose-Inhibited Division Family A Protein	0.1904	4.6648	1	40.5710	0.1032	-0.0156
P0407H12.144	Breast Adenocarcinoma Marker-Like	At2g06530	SNF7 Family Protein	0.1159	3.7349	1	43.3500	-0.2517	-0.0729
P0409B08.21	Putative Mannose-6-Phosphate Isomerase	At3g02570	MEE31 (Maternal Effect Embryo Arrest 31); Mannose-6-Phosphate Isomerase	0.3966	2.3912	1	61.1680	-0.5694	-0.0449
P0410E03.18	Unknown Protein	At5g27490	Integral Membrane Yip1 Family Protein	0.2337	4.1021	1	69.1230	-0.5216	-0.0551
P0410E03.26	Putative GTP-Binding Protein	At5g20010	RAN-1 (Ras-Related GTP-Binding Nuclear Protein 1); GTP Binding	0.0399	3.6042	1	59.5240	-0.4990	-0.0661
P0419A09.6-1	26S Proteasome Regulatory Particle Triple-A	At1g45000	26S Proteasome Regulatory Complex Subunit P42d, Putative	0.0628	3.0483	1	50.5430	-0.5646	-0.0560
P0419H03.37	Putative Chain C, Structure Of The Plant	At1g71260	Atwhy2 (A. Thaliana Whirly 2); Dna Binding	0.4873	2.1788	1	46.7890	0.2341	-0.0504
P0423B08.13	Putative I-Box Binding Factor	At5g04760	Myb Family Transcription Factor	0.3980	3.4084	1	92.6830	-0.3660	-0.0913
P0431B06.16	Putative NTGP5	At1g22050	Ubiquitin Family Protein	0.2236	3.3497	1	57.1430	-0.0593	-0.1336
P0435B05.19	Putative GTP-Binding Protein	At2g31060	GTP Binding / Translation Elongation Factor	0.1737	1.7564	1	46.0420	-0.1263	-0.0312
P0437G01.17	Unknown Protein	At5g57460	Protein Binding / Protein Transporter	0.3530	4.6558	1	66.6110	-0.4279	-0.0212
P0437H03.127	Unknown Protein	At2g22370	Unknown Protein	0.1767	1.9829	1	43.0620	-0.1732	-0.0750
P0438H08.18	Putative Vesicle-Associated Membrane	At2g45140	Vesicle-Associated Membrane Protein, Putative / VAMP, Putative	0.2561	2.0448	1	56.7570	-0.2456	-0.0720
P0441A12.23	Putative Syringolide-Induced Protein B13-1-1	At4g39830	L-Ascorbate Oxidase, Putative	0.3070	4.3852	1	98.7410	-0.4129	-0.0292
P0445D12.4	Unknown Protein	At1g71070	Glycosyltransferase Family 14 Protein / Core-2/I-Branching Enzyme Family Protein	0.3644	3.1227	1	65.0130	-0.2079	-0.0527
P0451D05.26	Hypothetical Protein	At3g24420	Hydrolase, Alpha/Beta Fold Family Protein	0.5314	3.8372	1	93.1410	-0.3860	-0.1007
P0453D01.4	Putative High Affinity Sulfate Transporter	At4g08620	SULTR1;1 (Sulfate Transporter 1;1); Sulfate Transporter	0.2570	1.5917	1	45.7140	-0.0913	-0.0171

P0453G03.28	Transporter-Related-Like	At5g57100	Transporter-Related	1.1110	4.1900	1	80.1100	-0.5575	-0.0552
P0454A11.12	NPK1-Related Protein Kinase-Like Protein	At5g08590	ASK2 (ARABIDOPSIS SERINE/THREONINE KINASE 2); Kinase	1.1265	4.1394	1	83.7540	-0.3409	-0.0758
P0459B01.40	Putative Amino Acid Transporter	At1g31830	Amino Acid Permease Family Protein	0.2743	4.4651	1	92.7880	-0.2976	-0.0565
P0461A06.1	Unknown Protein	At1g16860	Merozoite Surface Protein-Related	0.1905	2.3908	1	37.9020	-0.0485	-0.0282
P0461B08.29	Putative Cytochrome P450	At4g00360	CYP86A2 (ABERRANT INDUCTION OF TYPE THREE GENES 1); Oxygen Binding	0.2485	4.2856	1	95.8580	-0.3864	-0.0147
P0471A11.34	LMBR1 Integral Membrane Protein-Like	At5g65290	LMBR1 Integral Membrane Family Protein	0.2532	2.0741	1	41.7740	-0.0430	-0.0184
P0473H02.4	Putative Glycoprotease	At4g22720	Glycoprotease M22 Family Protein	0.1645	4.1875	1	68.7320	-0.4278	-0.0713
P0476H10.42	Putative Seed Maturation Protein	At5g22470	NAD+ ADP-Ribosyltransferase	0.3359	4.6458	1	50.2960	-0.3457	-0.0185
P0482D04.9	Putative Ubiquitin Conjugating Enzyme	At5g50870	UBC27 (Ubiquitin-Conjugating Enzyme 26); Ubiquitin-Protein Ligase	0.2420	3.6675	1	67.9350	-0.4845	-0.0554
P0482F12.19	Putative 28 Kda Golgi SNARE Protein	At2g45200	GOS12 (GOLGI SNARE 12); SNARE Binding	0.1949	3.8668	1	78.0170	-0.5693	-0.1206
P0485B12.35	Alpha-Expansin	At1g69530	Atexpa1 (Arabidopsis Thaliana Expansin A1)	0.2325	3.8187	1	94.7790	-0.4658	-0.0466
P0486F07.29	Putative Equilibrative Nucleoside Transporter	At1g70330	ENT1,AT (EQUILIBRATIVE NUCLEOTIDE TRANSPORTER 1); Nucleoside Transporter	0.2684	1.7503	1	66.6670	-0.3971	-0.0176
P0492G09.21	Putative Cytochrome C1 Precursor	At5g40810	Cytochrome C1, Putative	0.1208	4.0842	1	41.9010	-0.0885	-0.0507
P0493A04.32	Unknown Protein	At1g02180	Ferredoxin-Related	0.6463	3.3731	1	63.5140	-0.5617	-0.1314
P0494D11.7	Putative Phosphoethanolamine	At2g38670	PECT1 (PHOSPHORYLETHANOLAMINE CYTIDYLYLTRANSFERASE 1); Ethanolamine-Phosphate Cytidylyltransferase	0.3279	4.2269	1	39.1200	-0.0886	-0.0336
P0504D03.19	Unknown Protein	At1g51160	Synbindin, Putative	0.2306	3.6105	1	70.2860	-0.3664	-0.1346
P0504E02.3	Putative Dermal Glycoprotein Precursor	At1g03230	Extracellular Dermal Glycoprotein, Putative / EDGP, Putative	0.7315	4.1978	1	94.1180	-0.3208	-0.0249
P0512C01.6	Hypothetical Protein	At4g23440	Transmembrane Receptor	0.3575	3.4267	1	42.8270	-0.0801	-0.0163
P0528B09.25	Putative CBL-Interacting Protein Kinase	At4g30960	CIPK6 (CBL-INTERACTING PROTEIN KINASE 6); Kinase	0.3011	4.2575	1	96.2000	-0.4571	-0.0251
P0529H11.24	Ataxin 3-Like Protein	At3g54130	Josephin Family Protein	0.2707	3.9131	1	58.8820	-0.6036	-0.0452
P0560B08.106	Putative Caltractin	At3g50360	ATCEN2 (CENTRIN2); Calcium Ion Binding	0.1338	3.2715	1	40.0000	-0.1383	-0.1355
P0562A06.20	Putative Gibberellin Action Negative Regulator	At3g11540	Spy (Spindly)	0.1719	4.8396	1	41.8100	-0.1133	-0.0174
P0572D06.34	Putative N7 Protein	At4g05490	F-Box Family Protein (FBL22)	0.6863	2.0516	1	61.8120	-0.4523	-0.0759
P0575F10.36	Putative 3-Isopropylmalate Dehydratase Large	At4g13430	Aconitase Family Protein / Aconitate Hydratase Family Protein	0.1717	2.5431	1	56.5840	-0.5567	-0.0304
P0576F08.1-1	Putative Phosphoribosyl	At2g44530	Ribose-Phosphate Pyrophosphokinase, Putative /	0.190	2.8029	1	41.5790	-0.1319	-0.0359

	Pyrophosphate Synthase		Phosphoribosyl Diphosphate Synthetase, Putative	5					
P0640E12.105	Peptidyl-Prolyl Cis-Trans Isomerase	At3g66654	Peptidyl-Prolyl Cis-Trans Isomerase Cyclophilin-Type Family Protein	0.3736	3.8356	1	41.5180	-0.3059	-0.0438
P0643A10.22	Putative ADP-Ribosylation Factor	At5g37680	ATARLA1A (ADP-Ribosylation Factor-Like A1A); GTP Binding	0.0593	1.4481	1	48.5880	-0.3194	-0.1005
P0663F07.1	SPX (SYG1/Pho81/XPR1) Domain-Containing	At1g63010	SPX (SYG1/Pho81/XPR1) Domain-Containing Protein	0.2531	1.6175	1	52.7030	0.0074	-0.0161
P0666G04.16	Unknown Protein	At3g04090	Sip1;1 (Small And Basic Intrinsic Protein 1a)	0.3962	1.5755	1	85.1240	-0.4389	-0.0638
P0669G09.11	Putative GDP-Fucose	At3g05320	Unknown Protein	0.3819	4.3184	1	49.4000	-0.1574	-0.0277
P0669G09.15-2	Putative Porphobilinogen Deaminase	At5g08280	HEMC (HYDROXYMETHYLBILANE SYNTHASE); Hydroxymethylbilane Synthase	0.1850	3.9306	1	35.7140	0.4281	-0.0534
P0671B11.35	Putative Regulatory Protein NPR1	At1g64280	NPR1 (NONEXPRESSER OF PR GENES 1); Protein Binding	0.4441	1.6640	1	60.1110	-0.1373	-0.0321
P0676G05.8	Putative Tubulin Gamma-2 Chain (Gamma-2	At3g61650	TUBG1 (GAMMA-TUBULIN); Structural Molecule	0.0467	1.8143	1	45.6470	-0.0800	-0.0324
P0680F05.45	Putative Tryptophan Synthase Beta-Subunit	At4g27070	TSB2 (TRYPTOPHAN SYNTHASE BETA-SUBUNIT); Tryptophan Synthase	0.1851	3.3379	1	65.1580	-0.4847	-0.0550
P0681B11.1	Putative Protein Kinase APK1B	At3g13690	Protein Kinase Family Protein	0.2771	4.7184	1	41.3010	-0.0629	-0.0273
P0683B11.11	Putative Embryonic Abundant Protein-Like	At5g10830	Embryo-Abundant Protein-Related	0.4532	3.8516	1	94.3550	-0.4047	-0.0555
P0683F02.2	Hypothetical Protein	At5g05710	Pleckstrin Homology (PH) Domain-Containing Protein	0.1685	3.2828	1	95.2700	-0.5021	-0.1525
P0683F12.13	Putative Phosphatidylinositol-Specific	At3g55940	Phosphoinositide-Specific Phospholipase C, Putative	0.4149	4.5339	1	80.6160	-0.4177	-0.0318
P0686C03.126	Unknown Protein	At4g38160	Pde191 (Pigment Defective 191)	0.3605	4.0803	1	76.4330	-0.6886	-0.0387
P0710A02.4	Cytosolic Aldehyde Dehydrogenase	At3g48000	ALDH2B4 (ALDEHYDE DEHYDROGENASE 2); 3-Chloroallyl Aldehyde Dehydrogenase/ Aldehyde Dehydrogenase (NAD)	0.3561	4.3912	1	90.4860	-0.5239	-0.0317
P0724B10.42	Putative Phenylcoumaran Benzylic Ether Reductase	At4g34540	Isoflavone Reductase Family Protein	0.3545	1.6140	1	55.5560	-0.0414	-0.0722
10A19I.3	Similar To Gb|U43629 Integral Membrane Protein From	At1g19450	Integral Membrane Protein, Putative / Sugar Transporter Family Protein	0.2055	3.2132	2	54.6390	-0.2572	-0.0351
B1026C12.33	Unknown Protein	At1g61900	Unknown Protein	0.4298	2.4504	2	54.8240	-0.5420	-0.0286
B1046G12.25	Putative Phosphoribosylaminoimidazole	At2g37690	Phosphoribosylaminoimidazole Carboxylase, Putative / AIR Carboxylase, Putative	0.3112	1.6345	2	46.4880	-0.1763	-0.0091
B1088C09.1	Hypothetical Protein	At2g40400	Unknown Protein	0.3151	1.6165	2	47.2140	-0.1093	-0.0151
B1144B06.21	Unknown Protein	At1g19130	Unknown Protein	0.3240	3.6476	2	61.5380	-0.5951	-0.0923
H0811E11.2	Contains Similarity To F6I7.30	At4g24820	26S Proteasome Regulatory Subunit, Putative (RPN7)	0.1697	3.6433	2	70.9840	-0.5248	-0.0938
I1332.6	Unknown Protein	At3g62940	OTU-Like Cysteine Protease Family Protein	0.2816	2.1755	2	54.0350	-0.4220	-0.0679
OJ1005_D12.36-1	Putative Calcium-Dependent Protein Kinase	At1g12680	PEPKR2 (PHOSPHOENOLPYRUVATE CARBOXYLASE-RELATED KINASE 2); Kinase	0.3736	4.3703	2	63.8100	-0.3505	-0.0499

OJ1005_D12.38	Putative Succinoaminoimidazolecarboximide	At3g21110	PUR7 (Purin 7); Phosphoribosylaminoimidazolesuccinocarboxamide Synthase	0.3320	1.7523	2	54.3770	-0.4539	-0.0422
OJ1008_E02.6	Putative Diaminopimelate Decarboxylase	At3g14390	Diaminopimelate Decarboxylase, Putative / DAP Carboxylase, Putative	0.2362	2.0064	2	53.9610	-0.2206	-0.0182
OJ1079_F11.25-2	Pentatricopeptide (PPR) Repeat-Containing	At1g05750	PDE247 (PIGMENT DEFECTIVE 247); Binding	0.4315	4.2910	2	92.8060	-0.4542	-0.0144
OJ1111_E07.25	Putative Gamma-Tocopherol Methyltransferase	At1g64970	G-Tmt (Gamma-Tocopherol Methyltransferase)	0.3107	4.1547	2	64.7060	-0.2329	-0.0541
OJ1118_A10.27	Putative Delta-6-Desaturase	At2g46210	Delta-8 Sphingolipid Desaturase, Putative	0.3271	4.2172	2	87.7190	-0.4072	-0.0481
OJ1119_A01.20-1	Putative Phosphatidylinositol-4-Phosphate	At3g09920	PIP5K9 (PHOSPHATIDYL INOSITOL MONOPHOSPHATE 5 KINASE); 1-Phosphatidylinositol-4-Phosphate 5-Kinase	0.2470	4.7647	2	44.7920	-0.1263	-0.0133
OJ1124_H03.5	Unknown Protein	At4g17420	Unknown Protein	0.2640	3.9453	2	50.9090	-0.1252	-0.0369
OJ1145_E05.10	Putative U2 Snrnp Protein A'	At1g09760	U2A' (U2 Small Nuclear Ribonucleoprotein A); Protein Binding	0.2131	1.8471	2	48.4380	-0.1853	-0.0482
OJ1186_G01.3	Putative Chitinase Precursor	At1g05850	POM1 (POM-POM1); Chitinase	0.3171	2.6258	2	68.1060	-0.4963	-0.1228
OJ1263_E10.9	Putative Phosphatidylserine Synthase	At1g15110	Phosphatidyl Serine Synthase Family Protein	0.2401	2.5516	2	52.7090	-0.3099	-0.0284
OJ1340_C08.131	Putative Eukaryotic Translation Initiation	At3g55620	EMB1624 (EMBRYO DEFECTIVE 1624); Translation Initiation Factor	0.0621	1.7990	2	46.5220	-0.3746	-0.0412
OJ1567_G09.119	Putative 60S Ribosomal Protein	At3g24830	60S Ribosomal Protein L13A (RPL13aB)	0.1586	3.7248	2	86.0820	-0.6284	-0.0932
OJ1607A12.21	Putative Sulfate Transporter ATST1	At3g51895	SULTR3;1 (SULFATE TRANSPORTER 1); Sulfate Transporter	0.2118	4.5663	2	90.8790	-0.3821	-0.0279
OJ1611_C08.28	Putative Cyclic Nucleotide-Binding Transporter	At3g17700	CNBT1 (CYCLIC NUCLEOTIDE-BINDING TRANSPORTER 1); Calmodulin Binding / Cyclic Nucleotide Binding / Ion Channel	0.3495	4.6637	2	35.3260	0.2680	-0.0091
OJ1643_A10.2	Putative ADP-Ribosylation Factor-Directed Gtpase	At1g60860	ARF Gtpase-Activating Domain-Containing Protein	0.3519	4.6554	2	34.0400	0.1855	-0.0113
OJ1767_D02.9-1	Emp24/Gp25l/P24-Like	At1g09580	Emp24/Gp25l/P24 Family Protein	0.3203	2.9847	2	58.8240	-0.0294	-0.0972
OJ2056_H01.13	Unknown Protein	At2g42210	ATOEP16-3; Protein Translocase	0.2935	3.3589	2	82.0690	-0.4811	-0.1180
OSJNBa0006L06.3	60S Ribosomal Protein L21	At1g57860	60S Ribosomal Protein L21	0.0863	1.7057	2	83.4390	-0.6023	-0.1579
OSJNBa0008J01.16	Putative S6 Ribosomal Protein Kinase	At3g08720	ATPK19/ATPK2 (ARABIDOPSIS THALIANA SERINE/THREONINE PROTEIN KINASE 19, ARABIDOPSIS THALIANA SERINE/THREONINE PROTEIN KINASE 2); Kinase	0.1770	1.8795	2	60.4100	-0.4348	-0.0232
OSJNBa0008M17.11	Unknown Protein	At1g31280	Ago2 (Argonaute 2)	0.5762	4.9119	2	64.3790	-0.5929	-0.0230
OSJNBa0013M12.6	Unknown Protein	At3g21550	Unknown Protein	0.4393	3.5662	2	97.8950	-0.4105	-0.1306
OSJNBa0027P10.1	Putative Palmitoyl-Protein Thioesterase	At3g60340	Palmitoyl Protein Thioesterase Family Protein	0.2735	2.4602	2	54.3170	-0.1283	-0.0556
OSJNBa0027P10.8	Putative Casein Kinase II Beta	At2g44680	CKB4 (CASEIN KINASE II BETA SUBUNIT 4);	0.192	3.8947	2	53.0530	-0.1105	-0.0511

	Subunit		Protein Kinase CK2 Regulator	4					
OSJNBa0032G11.17	Putative GDSL-Like Lipase/Acylhydrolase	At3g48460	GDSL-Motif Lipase/Hydrolase Family Protein	0.3759	4.0633	2	95.7870	-0.4575	-0.0305
OSJNBa0032G11.2	Putative Oxidoreductase	At4g10020	Short-Chain Dehydrogenase/Reductase (SDR) Family Protein	0.2907	4.1849	2	93.3730	-0.4184	-0.0507
OSJNBa0040E01.26	Putative Ankyrin	At2g03430	Ankyrin Repeat Family Protein	0.3195	1.5540	2	54.4300	-0.5513	-0.0976
OSJNBa0047G15.10	Hypothetical Protein	At3g07510	Unknown Protein	0.3501	3.5781	2	97.9490	-0.4158	-0.0764
OSJNBa0053L11.25	F-Box Family Protein-Like	At1g56240	ATPP2-B13 (Phloem Protein 2-B13)	0.7745	2.2719	2	66.4180	-0.3862	-0.0717
OSJNBa0058K23.10	Unknown Protein	At2g02870	Kelch Repeat-Containing F-Box Family Protein	0.5277	4.1933	2	45.2870	-0.1315	-0.0220
OSJNBa0059G06.22	Putative Gibberelin 20-Oxidase	At4g25420	GA5 (GA REQUIRING 5); Gibberellin 20-Oxidase/ Gibberellin 3-Beta-Dioxygenase	0.3408	4.0519	2	92.8990	-0.3360	-0.0365
OSJNBa0061L20.107-1	Putative Nucleic Acid Binding Protein	At3g11200	PHD Finger Family Protein	0.2025	3.7908	2	75.6640	-0.3577	-0.0738
OSJNBa0073E02.3	Unknown Protein	At1g08630	Tha1 (Threonine Aldolase 1)	0.2949	1.9190	2	55.0900	-0.4439	-0.0676
OSJNBa0076F20.1	Putative Glycine Decarboxylase Subunit	At1g32470	Glycine Cleavage System H Protein	0.2141	1.6304	2	71.7110	-0.3531	-0.0988
OSJNBa0081C01.8	Unknown Protein	At1g51740	SYP81 (Syntaxin 81)	0.3599	3.6258	2	48.0970	-0.3697	-0.0671
OSJNBa0085K21.46	Putative TIP120 Protein	At2g02560	CAND1 (CULLIN-ASSOCIATED AND NEDDYLATION DISSOCIATED, HEMIVENATA); Binding	0.1616	5.0723	2	38.8060	-0.1199	-0.0062
OSJNBa0090O10.25	Hypothetical Protein	At4g24050	Short-Chain Dehydrogenase/Reductase (SDR) Family Protein	0.2642	4.1384	2	91.5360	-0.4263	-0.0554
OSJNBa0094F01.10	Unknown Protein	At1g04230	Unknown Protein	0.3411	2.2512	2	46.4650	-0.1937	-0.0686
OSJNBb0012A20.16	Putative Endosomal Protein	At1g14670	Endomembrane Protein 70, Putative	0.1443	1.7746	2	55.4620	-0.4046	-0.0332
OSJNBb0013K08.3	Putative Calcineurin B-Like Protein	At4g26570	Atcbl3 (Calcineurin B-Like 3)	0.0700	3.8235	2	52.9410	-0.2507	-0.0991
OSJNBb0017F17.13	Silencing Group B Protein	At1g03150	GCN5-Related N-Acetyltransferase (GNAT) Family Protein	0.0746	2.1488	2	62.5770	-0.1369	-0.0431
OSJNBb0028C01.26	Unknown Protein	At3g61060	Atpp2-A13	0.3480	3.9905	2	69.7280	-0.4521	-0.0465
OSJNBb0035N21.18	Putative Polyprenyl Diphosphate Synthase,	At1g78510	Solanesyl Diphosphate Synthase (SPS)	0.2475	4.1600	2	46.2910	0.1438	-0.0300
OSJNBb0036F07.15	Putative Cop-Coated Vesicle Membrane Protein	At3g22845	Emp24/Gp25l/P24 Protein-Related	0.2086	1.6077	2	63.7760	0.0880	-0.0719
OSJNBb0040H10.26	MADS Box Protein, MADS2	At1g69120	AP1 (APETALA1); DNA Binding / Transcription Factor	0.4236	3.7494	2	55.3100	0.1418	-0.0394
OSJNBb0048O22.8	Putatputative ABC Transporter	At2g29940	ATPDR3/PDR3 (PLEIOTROPIC DRUG RESISTANCE 3); Atpase, Coupled To Transmembrane Movement Of Substances	0.2668	2.8067	2	42.2710	0.2624	-0.0116
OSJNBb0062H02.3	Unknown Protein	At3g25420	SCPL21 (Serine Carboxypeptidase-Like 21); Serine Carboxypeptidase	0.3632	2.5963	2	59.0340	-0.1242	-0.0337
OSJNBb0080H08.3	Unknown Protein	At1g60500	Dynamin Family Protein	0.443	4.5786	2	93.1360	-0.4674	-0.0163

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OSJNBb0091E11.4	Unknown Protein	At4g34530	Basic Helix-Loop-Helix (Bhlh) Family Protein	1.1848	3.0786	2	70.9460	-0.4670	-0.0494
OSJNBb0094K03.15	Unknown Protein	At3g24180	Catalytic	0.1837	2.7019	2	41.0380	0.1915	-0.0365
OSJNBb0108E17.13	Putative NADH-Ubiquinone Oxidoreductase	At4g02580	NADH-Ubiquinone Oxidoreductase 24 Kda Subunit, Putative	0.1511	4.7965	2	53.5430	-0.2483	-0.0781
P0006C08.21	Putative Vacuolar Protein Sorting	At3g47810	MAG1 (MAIGO 1); Protein Serine/Threonine Phosphatase	0.0665	3.6604	2	80.2200	-0.5230	-0.1207
P0408C03.8	Putative Ubiquitin Carrier Protein UBC7	At3g46460	UBC13 (Ubiquitin-Conjugating Enzyme 13); Ubiquitin-Protein Ligase	0.0817	3.4838	2	48.1250	-0.2196	-0.0964
P0423A12.19	Hypothetical Protein	At3g62770	Atatg18a (Arabidopsis Thaliana Homolog Of Yeast Autophagy 18 (ATG18) A)	0.3082	4.3293	2	63.1580	-0.2805	-0.0256
P0438H08.20	Putative Ribosomal Protein L34	At1g26880	60S Ribosomal Protein L34 (RPL34A)	0.1005	3.2594	2	73.0430	-0.4597	-0.1500
P0450B04.21	Putative Shwachman-Bodian-Diamond Syndrome	At1g43860	Transcription Factor	0.3045	4.1017	2	70.1860	-0.4196	-0.0482
P0452F10.19	Putative Caulobacter Crescentus D-Isomer	At1g79870	Oxidoreductase Family Protein	0.2708	3.9430	2	96.6890	-0.4589	-0.0573
P0472F10.2	Putative Serine Decarboxylase	At1g43710	EMB1075 (EMBRYO DEFECTIVE 1075); Carboxy-Lyase	0.1808	4.3969	2	66.6670	-0.4721	-0.0373
P0473D02.40-1	N-Acetylglucosaminyltransferase-Like Protein	At1g03520	Glycosyltransferase Family 14 Protein / Core-2/I-Branching Enzyme Family Protein	0.2923	4.3299	2	72.7070	-0.4594	-0.0624
P0474F11.25-1	Putative Fibrillarin	At4g25630	Fib2 (Fibrillarin 2)	0.1452	1.5434	2	64.2860	-0.4915	-0.0477
P0474F11.8	Protein Phosphatase	At2g39840	TOPP4 (Type One Serine/Threonine Protein Phosphatase 4); Protein Phosphatase Type 1	0.1611	4.0539	2	52.6670	-0.2045	-0.0472
P0487E11.17	Putative GTP-Binding Protein	At4g02080	ASAR1 (Arabidopsis Thaliana Secretion-Associated RAS Super Family 2); GTP Binding	0.0532	3.6367	2	72.5270	-0.6617	-0.0964
P0491F11.2	Hypothetical Protein	At1g72140	Proton-Dependent Oligopeptide Transport (POT) Family Protein	0.4655	4.4213	2	94.2490	-0.4191	-0.0370
P0504A05.26	Putative Calmodulin-Binding Protein	At4g25800	Calmodulin-Binding Protein	0.3779	4.3994	2	41.6960	0.0118	-0.0381
P0504D03.20	Unknown Protein	At3g23620	Brix Domain-Containing Protein	0.2816	2.0108	2	57.4390	-0.5795	-0.0655
P0518F01.5	Unknown Protein	At4g29480	ATP Synthase G Subunit Family Protein	0.2492	1.9271	2	71.4290	-0.1689	-0.1959
P0519A12.14	Putative Glutaredoxin I	At1g77370	Glutaredoxin, Putative	0.3455	2.8738	2	51.1810	-0.3637	-0.1168
P0524F03.27	Putative Golgi SNARE Protein	At1g15880	GOS11 (GOLGI SNARE 11); SNARE Binding	0.1838	3.7467	2	39.1300	0.0930	-0.0945
P0534H07.34	Putative Z-Protein	At1g03070	Glutamate Binding	0.2333	3.7918	2	87.8660	-0.5117	-0.0631
P0552F09.120	Putative Alanine Aminotransferase	At1g72330	Alaat2 (Alanine Aminotransferase 2)	0.1463	1.7416	2	40.0000	0.1774	-0.0455
P0560C03.1	Putative Threonine Synthase	At4g29840	MTO2 (METHIONINE OVER-ACCUMULATOR); Threonine Synthase	0.2320	4.3971	2	83.3330	-0.5531	-0.0223
P0562A06.21	Cyclophilin	At2g36130	Peptidyl-Prolyl Cis-Trans Isomerase, Putative / Cyclophilin, Putative / Rotamase, Putative	0.1081	3.5650	2	62.5810	-0.3100	-0.1317
P0562A06.8	Putative Vesicle-Associated	At3g54300	ATVAMP727 (Arabidopsis Thaliana Vesicle-	0.148	3.7780	2	70.7960	-0.5034	-0.0589

	Membrane Protein 725		Associated Membrane Protein 727)	5						
P0585B01.29-2	Putative HGA1	At3g18170	Unknown Protein	0.4869	4.0080	2		89.6070	-0.4860	-0.0299
P0618H09.21	Putative Pectinesterase	At3g14310	ATPME3 (Arabidopsis Thaliana Pectin Methylesterase 3)	0.4894	4.4153	2		95.3490	-0.3948	-0.0090
P0627E10.6	Putative Peroxidase	At2g37130	Peroxidase 21 (PER21) (P21) (PRXR5)	0.3622	3.9251	2		91.9610	-0.3381	-0.0706
P0671D01.17	Putative Nifu-Like Protein	At3g01020	ATISU2/ISU2 (Iscu-Like 2); Structural Molecule	0.2890	3.6120	2		75.4720	-0.3968	-0.1357
P0671D01.25	Putative Aspartic Protease	At4g04460	Aspartyl Protease Family Protein	0.4202	1.9774	2		55.6660	-0.5991	-0.0264
P0692C11.26	Putative Vesicle Transport V-SNARE Protein	At3g29100	VTI13 (Vesicle Transport V-SNARE 13); SNARE Binding / Receptor	0.2031	3.8492	2		60.8910	-0.5306	-0.0824
P0700A11.12	Putative Vacuolar ATP Synthase Subunit D	At3g28715	H+-Transporting Two-Sector Atpase, Putative	0.0633	4.0187	2		55.0000	-0.1083	-0.0607
P0700F06.36	Putative Leucine Aminopeptidase	At2g24200	Cytosol Aminopeptidase	0.1571	1.7937	2		55.9080	-0.4867	-0.0221
P0707C02.28	Putative Phosphofructokinase	At2g22480	Phosphofructokinase Family Protein	0.1721	4.2802	2		35.1530	0.0612	-0.0254
P0711F01.56-1	Voltage-Dependent Anion Channel	At3g01280	Porin, Putative	0.2475	2.5263	2		56.9290	-0.4019	-0.0799
P0711H09.10-1	Putative AT-Hook DNA-Binding Protein	At2g33620	DNA-Binding Family Protein / AT-Hook Protein 1 (AHP1)	0.3565	1.8935	2		51.1900	0.1403	-0.1062
P0712E02.24	Unknown Protein	At1g69800	CBS Domain-Containing Protein	0.2888	2.1143	2		41.6670	-0.2021	-0.0098
OJ1115_A05.19	Putative ASC1	At1g13580	Lag13 (Lag1 Longevity Assurance Homolog 3)	0.2152	2.5283	3		45.0510	-0.0233	-0.0790
OJ1124_B05.9	Putative UVB-Resistance Protein UVR8	At5g16040	Regulator Of Chromosome Condensation (RCC1) Family Protein	0.1653	2.9537	3		60.5900	-0.1520	-0.0585
OJ1127_E01.118	Yippee-Like Protein	At5g53940	Yippee Family Protein	0.4506	3.2793	3		70.8740	-0.3686	-0.1045
OJ1150_A11.17	Putative Cysteine Proteinase	At5g50260	Cysteine Proteinase, Putative	0.3225	4.0908	3		96.1220	-0.3759	-0.0608
OJ1163_G08.29	Putative Step II Splicing Factor SLU7	At1g65660	SMP1 (Swellmap 1); Nucleic Acid Binding	0.1385	4.3941	3		45.7020	-0.2115	-0.0284
OJ1186_G01.31	Putative Signal Recognition Particle Receptor	At5g05670	Signal Recognition Particle Binding	0.3177	2.0494	3		47.8990	-0.0646	-0.0684
OJ1540_H01.2	Putative Senescence-Associated Protein	At3g21600	Senescence/Dehydration-Associated Protein-Related	0.7858	2.0761	3		74.8150	-0.4618	-0.0124
OJ1548_F12.6	Putative Methyltransferase	At5g57280	Unknown Protein	0.2408	1.5710	3		51.0790	-0.1104	-0.0502
OJ1562_H01.5	Putative Cdc2 Protein Kinase	At5g10270	CDKC;1 (CYCLIN-DEPENDENT KINASE C;1); Kinase	0.1487	4.3894	3		50.8100	0.1979	-0.0505
OJ1634_H04.114	Putative DNA-Directed RNA Polymerase Iia	At5g51940	DNA-Directed RNA Polymerase II, Putative	0.1477	1.4128	3		46.2180	-0.2125	-0.0768
OJ1643_A10.33-1	Putative Carboxypeptidase D	At5g23210	Scpl34	0.3067	4.3214	3		85.1290	-0.5427	-0.0293
OJ991113_30.4	Unknown Protein	At5g03860	Malate Synthase, Putative	0.2050	4.4571	3		96.9580	-0.3966	-0.0369
OSJNBa0009C07.5	Unknown Protein	At1g64110	AAA-Type Atpase Family Protein	0.269	4.7809	3		50.7730	-0.2350	-0.0264

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OSJNBa0009H03.25	Putative Phosphoprotein Phosphatase	At5g55260	PPX2 (Protein Phosphatase X-2); Protein Serine/Threonine Phosphatase	0.0468	1.6778	3	42.2150	0.0135	-0.0658
OSJNBa0013D02.6	Putative Phosphate/Phosphoenolpyruvate	At5g05820	Phosphate Translocator-Related	0.1280	2.6135	3	73.7340	-0.5283	-0.0984
OSJNBa0014E22.8	ABA-Responsive Protein-Like	At5g13200	GRAM Domain-Containing Protein / ABA-Responsive Protein-Related	0.6978	3.8009	3	86.6970	-0.4374	-0.0690
OSJNBa0020H02.1	Putative Heat Shock Protein	At5g15450	APG6/CLPB-P/CLPB3 (ALBINO AND PALE GREEN 6); ATP Binding / Atpase	0.1391	4.8680	3	43.6870	-0.0188	-0.0338
OSJNBa0025J22.9	Unknown Protein	At3g57780	Unknown Protein	0.4561	4.5936	3	38.6190	0.2031	-0.0090
OSJNBa0026E05.37	Putative Beta-1,3-Glucanase	At5g58090	Glycosyl Hydrolase Family 17 Protein	0.3345	2.6407	3	62.4220	-0.2708	-0.0307
OSJNBa0026O12.11	Putative Esterase	At5g62930	GDSL-Motif Lipase/Hydrolase Family Protein	0.2353	1.4932	3	48.1980	-0.0827	-0.0661
OSJNBa0047E24.9	Phytochrome C	At5g35840	Phyc (Phytochrome Defective C)	0.3210	2.2289	3	58.7790	-0.6131	-0.0192
OSJNBa0058G03.4	Unknown Protein	At5g57580	Calmodulin-Binding Protein	0.3226	4.5580	3	43.4490	-0.0859	-0.0290
OSJNBa0059E14.19	Hypothetical Protein	At5g28150	Unknown Protein	0.2844	3.9411	3	70.1440	-0.3378	-0.0729
OSJNBa0061K21.20	Putative Histone H2A	At5g02560	Histone H2A, Putative	0.3919	3.4088	3	97.0150	-0.4244	-0.1288
OSJNBa0079L16.13	Putative Peptide Transport Protein	At5g46050	ATPTR3/PTR3 (PEPTIDE TRANSPORTER PROTEIN 3); Transporter	0.2643	4.5013	3	96.4290	-0.4089	-0.0257
OSJNBa0081C01.11	Unknown Protein	At5g10560	Glycosyl Hydrolase Family 3 Protein	0.3549	2.4647	3	55.2670	-0.3078	-0.0192
OSJNBa0081L15.14	Unknown Protein	At5g50320	ELO3 (ELONGATA 3); N-Acetyltransferase/ Catalytic/ Hydrogen Ion Transporting ATP Synthase, Rotational Mechanism / Hydrogen Ion Transporting Atpase, Rotational Mechanism / Iron Ion Binding	0.0772	2.4282	3	50.0940	-0.3105	-0.0609
OSJNBa0084K01.2	Unknown Protein	At5g20990	B73 (CHLORATE RESISTANT 6); Molybdenum Ion Binding	0.2682	1.9307	3	47.9300	-0.1315	-0.0404
OSJNBa0084K20.9	Unknown Protein	At5g14230	Ankyrin Repeat Family Protein	0.3866	7.4227	3	90.9950	-0.4383	-0.0145
OSJNBa0088A01.16	Unknown Protein	At5g56320	Atexpa14 (Arabidopsis Thaliana Expansin A14)	0.4622	3.8258	3	80.8000	-0.5291	-0.0405
OSJNBa0088H09.1	Unknown Protein	At5g41180	Leucine-Rich Repeat Protein Kinase, Putative	0.4089	1.3795	3	53.5890	-0.2284	-0.0636
OSJNBa0088H09.18	Unknown Protein	At5g03540	(EXOCYST SUBUNIT EXO70 FAMILY PROTEIN A1); Protein Binding	0.2462	1.7640	3	44.4440	0.2111	-0.0323
OSJNBa0088I06.10	Unknown Protein	At5g21170	AMP-Activated Protein Kinase	0.3696	1.8018	3	55.3900	-0.0764	-0.0534
OSJNBa0094J08.6	Putative Cinnamoyl-Coa Reductase	At5g58490	Cinnamoyl-Coa Reductase Family	0.2505	1.5614	3	77.9550	-0.3904	-0.0422
OSJNBb0013K01.36	Replication Protein A 70kda	At2g06510	Replication Protein, Putative	0.3052	2.2470	3	52.5970	-0.2212	-0.0309
OSJNBb0022E02.2	Unknown Protein	At1g18470	Zinc Finger (C3HC4-Type RING Finger) Family Protein	0.2698	1.4964	3	41.0840	-0.0436	-0.0307

OSJNBb0044B19.4	Putative Polyubiquitin	At5g20620	UBQ4 (Ubiquitin 4); Protein Binding	0.7612	1.7742	3	53.7220	-0.5510	-0.0466
OSJNBb0060J21.21	Expressed Protein	At3g03740	ATBPM4 (BTB-POZ AND MATH DOMAIN 4); Protein Binding	0.2857	4.3185	3	61.4430	-0.3481	-0.0595
OSJNBb0067G11.11	Unknown Protein	At5g55940	Emb2731 (Embryo Defective 2731)	0.3453	2.7703	3	75.7430	-0.4239	-0.0866
OSJNBb0067G11.14	Unknown Protein	At5g10480	Pas2 (Pasticcino 2)	0.3867	3.7394	3	64.7890	-0.3134	-0.0756
OSJNBb0095H08.30	Putative Tyrosine Decarboxylase	At2g20340	Tyrosine Decarboxylase, Putative	0.2091	2.4845	3	39.0660	0.1131	-0.0382
OSJNBb0106M04.24	Putative Allene Oxide Synthase	At5g42650	AOS (ALLENE OXIDE SYNTHASE); Hydro-Lyase/ Oxygen Binding	0.3538	4.3772	3	98.1560	-0.3914	-0.0518
P0003E08.5	Hypothetical Protein	At1g29820	Unknown Protein	0.3141	2.8095	3	45.8170	-0.1665	-0.0366
P0135D07.12	Dehydration-Responsive Family Protein-Like	At4g00750	Dehydration-Responsive Family Protein	0.3018	4.4865	3	89.6610	-0.5261	-0.0423
P0434A03.107	Putative Mannose-P-Dolichol Utilization Defect 1	At5g59470	PQ-Loop Repeat Family Protein / Transmembrane Family Protein	0.2644	1.8120	3	54.8940	-0.2697	-0.0566
P0446B05.2	Unknown Protein	At5g02190	PCS1 (PROMOTION OF CELL SURVIVAL1); Aspartic-Type Endopeptidase/ Peptidase	0.4436	4.3279	3	93.7790	-0.3942	-0.0090
P0458B05.10	ATP-Dependent Clp Protease ATP-Binding Subunit	At5g51070	ERD1 (EARLY RESPONSIVE TO DEHYDRATION 1); ATP Binding / Atpase	0.3137	1.8677	3	51.5050	-0.1980	-0.0225
P0471A11.31-1	Putative Poly(A) Binding Protein	At5g10350	Polyadenylate-Binding Protein Family Protein / PABP Family Protein	0.1841	3.6412	3	55.4970	-0.1473	-0.0538
P0478E02.11	Unknown Protein	At5g66090	Unknown Protein	0.3083	1.8750	3	59.7770	-0.3311	-0.1191
P0487D09.13	Ankyrin-Like Protein	At2g01680	Ankyrin Repeat Family Protein	0.3183	2.7478	3	55.2210	-0.4278	-0.0335
P0492G09.7	Pir7b Protein (Pseudomonas Inducible Protein)	At2g23600	ACL (ACETONE-CYANOHYDRIN LYASE); Hydrolase	0.5966	3.9185	3	81.6730	-0.3014	-0.0377
P0519E12.121	Putative Transmembrane Protein	At1g14010	Emp24/Gp25l/P24 Family Protein	0.3392	3.6759	3	88.3720	-0.4186	-0.0974
P0520B06.18	Unknown Protein	At1g68300	Universal Stress Protein (USP) Family Protein	0.4547	2.3231	3	73.4180	-0.2696	-0.1246
P0523B07.45	Putative Protein Kinase G11A	At5g47750	Protein Kinase, Putative	0.2414	4.5295	3	45.4030	-0.2261	-0.0152
P0544B02.10	Putative Glossy1 Protein	At5g57800	WAX2; Catalytic	0.2776	4.5247	3	85.8090	-0.3538	-0.0239
P0554D10.3	Putative Dihydrolipoamide Dehydrogenase	At1g48030	Dihydrolipoamide Dehydrogenase 1, Lipoamide Dehydrogenase 1 (MTLPD1)	0.1650	2.9238	3	56.2900	-0.3741	-0.0588
P0618H09.15	Putative Cytoplasmic Ribosomal Protein L18	At5g27850	60S Ribosomal Protein L18 (RPL18C)	0.1456	3.6868	3	77.2490	-0.5019	-0.0836
P0618H09.27	Putative Tyrosyl-Trna Synthetase	At1g28350	ATP Binding / Aminoacyl-Trna Ligase	0.4488	2.6622	3	39.3260	0.1528	-0.0392
P0628H02.1	Putative Crooked Neck Protein	At5g45990	Crooked Neck Protein, Putative / Cell Cycle Protein, Putative	0.2082	4.5769	3	58.3990	-0.5983	-0.0241
P0643A10.26	Unknown Protein	At1g23230	Unknown Protein	0.2685	2.5627	3	39.5080	0.0030	-0.0149
P0646B04.12	Putative DNA-Directed RNA Polymerase II	At2g15430	RBP36A (RNA Polymerase II 36 Kda Polypeptide A); DNA Binding / DNA-Directed RNA Polymerase	0.2055	4.0645	3	71.6170	-0.5641	-0.0755

P0669H03.9	Putative Cellulose Synthase-8	At4g39350	CESA2 (CELLULASE SYNTHASE 2); Cellulose Synthase/ Transferase, Transferring Glycosyl Groups	0.2038	2.9589	3	53.9360	-0.3479	-0.0190
P0676H03.17	Putative Cytochrome B5 Reductase	At5g17770	Atcbr (Nadh:Cytochrome B5 Reductase 1)	0.1780	2.1869	3	51.1280	-0.4032	-0.0907
P0679C12.4	Hypothetical Protein	At1g67190	F-Box Family Protein	0.2299	4.2321	3	43.7340	-0.2419	-0.0213
P0685G12.41	Sucrase-Like Protein	At5g55900	Sucrase-Related	0.4982	2.1026	3	58.7130	-0.5850	-0.0444
P0708H12.35	Trehalose-6-Phosphate Phosphatase	At5g51460	ATTPPA (Arabidopsis Thaliana Trehalose-6-Phosphate Phosphatase); Trehalose-Phosphatase	0.3425	2.1011	3	51.1490	-0.2106	-0.0461
B1012D10.2	MCT-1 Protein-Like	At1g09150	Pseudouridine Synthase And Archaeosine Transglycosylase (PUA) Domain-Containing Protein	0.0888	3.5418	4	43.0230	-0.3160	-0.0514
B1064G04.22	Asparaginyl Endopeptidase	At4g32940	GAMMA-VPE (Vacuolar Processing Enzyme Gamma); Cysteine-Type Endopeptidase	0.2579	2.5630	4	61.9960	-0.6738	-0.0397
B1064G04.27	Putative IAA-Ala Hydrolase	At1g51760	IAR3 (IAA-ALANINE RESISTANT 3); Metallopeptidase	0.3285	2.9616	4	59.0360	-0.4002	-0.0394
B1130G10.11	Putative GTP-Binding Protein Rab7a	At3g18820	Atrabg3f/Atrab7b (Arabidopsis Rab Gtpase Homolog G3f); GTP Binding	0.0674	1.9920	4	55.6700	-0.4732	-0.0883
B1151A10.18	Putativeethylene-Responsive Protein	At3g16050	A37 (PYRIDOXINE BIOSYNTHESIS 1.2); Protein Heterodimerization	0.3858	3.3005	4	91.8920	-0.5081	-0.1779
B1339H09.19	Putative Annexin	At1g68090	ANNAT5 (ANN5, ANNEXIN ARABIDOPSIS 5); Calcium Ion Binding / Calcium-Dependent Phospholipid Binding	0.3939	4.1168	4	43.7710	-0.2298	-0.0457
H0806H05.2	Cysteine Synthase	At3g61440	Atcysc1 (Beta-Substituted Ala Synthase 3;1)	0.2302	1.6436	4	56.3220	-0.2594	-0.0477
OJ000126_13.4	Unknown Protein	At2g27460	Sec23/Sec24 Transport Family Protein	0.3242	2.4150	4	47.5180	-0.0631	-0.0244
OJ1003_F04.28	Ubiquitin-Associated (UBA)/TS-N	At1g04850	Ubiquitin-Associated (UBA)/TS-N Domain-Containing Protein	0.1972	2.2242	4	58.2630	-0.4885	-0.0587
OJ1004_A05.39	Leucine-Rich Repeat-Like Protein	At1g15740	Leucine-Rich Repeat Family Protein	0.2932	4.5241	4	45.7500	-0.1257	-0.0196
OJ1004C08.14	Putative Ubiquitin Protein	At2g17190	Ubiquitin Family Protein	0.3417	2.3606	4	45.6650	-0.2586	-0.0454
OJ1005_H01.19	Putative Pectinesterase	At5g53370	Pectinesterase Family Protein	0.5744	4.4018	4	96.3300	-0.4251	-0.0144
OJ1006_A02.6	Putative Plastidic ATP/ADP Transporter	At1g80300	Chloroplast ADP, ATP Carrier Protein 1 / ADP, ATP Translocase 1 / Adenine Nucleotide Translocase 1 (AATP1)	0.2535	4.5973	4	68.6470	-0.3480	-0.0163
OJ1007_D04.18	Putative ATP Synthase	At2g21870	Unknown Protein	0.2772	1.7344	4	48.3570	-0.4238	-0.0833
OJ1065_B06.20	Putative Succinyl-Coa Ligase Alpha Subunit	At5g23250	Succinyl-Coa Ligase (GDP-Forming) Alpha-Chain, Putative / Succinyl-Coa Synthetase, Alpha Chain, Putative / SCS-Alpha, Putative	0.1268	1.8612	4	51.4470	-0.4194	-0.0767
OJ1077_A12.15	Putative Aspartate Transaminase	At2g30970	Asp1 (Aspartate Aminotransferase 1)	0.1639	1.8621	4	53.0560	0.0388	-0.0551
OJ1079_F11.26	Beta 1 Subunit Of 20S Proteasome	At4g31300	PBA1 (20S Proteasome Beta Subunit A 1); Peptidase	0.1411	1.9339	4	52.7430	-0.2279	-0.0780
OJ1097_A12.2	20S Proteasome Beta Subunit	At5g40580	PBB2 (20S Proteasome Beta Subunit B 2);	0.138	3.9845	4	50.3880	-0.2090	-0.0555

			Peptidase	3					
OJ1118_B06.10	Putative Peroxidase	At2g22420	Peroxidase 17 (PER17) (P17)	0.2669	4.0570	4	94.1350	-0.4448	-0.0489
OJ1118_D07.26-1	Putative Amino Acid Permease	At5g49630	AAP6 (AMINO ACID PERMEASE 6); Amino Acid Permease	0.2609	4.3706	4	84.4540	-0.4442	-0.0368
OJ1118_D07.29	Putative Oslrk1(Receptor-Type Protein Kinase)	At5g65700	BAM1 (Big Apical Meristem 1); ATP Binding / Kinase/ Protein Serine/Threonine Kinase	0.2379	4.9306	4	79.9380	-0.4455	-0.0184
OJ1118_F05.12	Unknown Protein	At1g15980	Hypothetical Protein	0.3499	4.3583	4	88.9140	-0.4389	-0.0247
OJ1119_D01.9	Helix-Loop-Helix-Like Protein	At5g54680	ILR3 (IAA-LEUCINE RESISTANT3); DNA Binding / Transcription Factor	0.3704	3.8504	4	61.4410	-0.3263	-0.0569
OJ1123_C12.123	Calcineurin-Like Phosphoesterase Family-Like	At1g13900	Calcineurin-Like Phosphoesterase Family Protein	0.3650	4.5803	4	63.9290	-0.5053	-0.0328
OJ1124_D06.18	Oligopeptidase A-Like	At5g65620	Peptidase M3 Family Protein / Thimet Oligopeptidase Family Protein	0.1675	2.4809	4	50.3530	-0.5489	-0.0058
OJ1145_F01.1	Unknown Protein	At1g21060	Unknown Protein	0.1302	2.1775	4	57.9710	-0.6306	-0.1528
OJ1172F09.5	Unknown Protein	At2g20370	MUR3 (MURUS 3); Catalytic	0.2574	4.4963	4	66.7270	-0.5166	-0.0398
OJ1175_B01.11	Putative GAMYB-Binding Protein	At1g77180	Chromatin Protein Family	0.2276	4.4529	4	60.0360	-0.1641	-0.0308
OJ1198_B10.9	Putative ABC Transporter	At3g47730	ATATH1 (ABC2 Homolog 1); Atpase, Coupled To Transmembrane Movement Of Substances	0.2642	3.9401	4	51.9610	-0.0750	-0.0227
OJ1200_C08.124-1	Calmodulin	At3g43810	CAM7 (CALMODULIN 7); Calcium Ion Binding	0.0084	3.3571	4	61.0690	-0.5805	-0.1221
OJ1211_G06.4	Putative Calcium-Dependent Protein Kinase	At1g18890	ATCDPK1; Calcium- And Calmodulin-Dependent Protein Kinase/ Kinase/ Protein Kinase	0.3591	4.3941	4	92.8030	-0.4147	-0.0412
OJ1234_B11.20	Putative Alcohol Oxidase	At4g28570	Alcohol Oxidase-Related	0.4174	4.7268	4	95.7180	-0.3943	-0.0269
OJ1288_G09.19	Putative Elicitor-Inducible Protein EIG-J7	At2g22170	Lipid-Associated Family Protein	0.4259	3.5359	4	94.1180	-0.3932	-0.0544
OJ1310_F05.15	Putative Poly(A)-Binding Protein	At4g34110	PAB2 (POLY(A)-BINDING PROTEIN 2); RNA Binding	0.2550	4.5353	4	53.1850	-0.4586	-0.0331
OJ1339_F05.125	Putative Receptor-Like Protein Kinase	At5g10020	Leucine-Rich Repeat Transmembrane Protein Kinase, Putative	0.4527	2.4806	4	56.7620	-0.3638	-0.0191
OJ1384D03.15	Putative CELL DIVISION CONTROL PROTEIN 2 HOMOLOG	At3g48750	CDC2/CDC2A/CDC2AAT/CDK2/CDKA;1 (CELL DIVISION CONTROL 2); Cyclin-Dependent Protein Kinase/ Kinase/ Protein Binding	0.1239	3.8828	4	47.5840	-0.2715	-0.0253
OJ1414_E05.17	Calcyclin Binding Protein-Like	At1g30070	SGS Domain-Containing Protein	0.3041	3.7721	4	62.0190	-0.4547	-0.1027
OJ1435_F07.31	Putative 60S Ribosomal Protein L9	At1g33140	60S Ribosomal Protein L9 (RPL90A/C)	0.1930	3.4459	4	84.3930	-0.5398	-0.0710
OJ1458_B07.103	Putative Adapter Protein ATH-55	At5g28740	Transcription-Coupled DNA Repair Protein-Related	0.2620	4.8811	4	60.5520	-0.5332	-0.0311
OJ1477_F01.114	Nucleoid DNA-Binding-Like Protein	At3g54400	Aspartyl Protease Family Protein	0.3566	4.2643	4	98.6520	-0.2871	-0.0528
OJ1479_B11.11	Putative Acyl Carrier Protein III, Chloroplast	At4g25050	Acp4 (Acyl Carrier Protein 4)	0.4908	1.9969	4	50.0000	-0.3442	-0.0790
OJ1513_F02.135	Casein Kinase II Alpha Subunit	At3g50000	CKA2 (Casein Kinase II Alpha Chain 2); Kinase	0.0501	1.7676	4	48.4080	-0.2314	-0.0408

OJ1612_A04.101	Putative Isopentenyl	At3g02780	IPP2 (ISOPENTENYL PYROPHOSPHATE:DIMETHYLLALLYL PYROPHOSPHATE ISOMERASE 2); Isopentenyl-Diphosphate Delta-Isomerase	0.1167	2.0255	4	63.2560	-0.5998	-0.1042
OJ1643_A10.34	Putative Ubiquitin-Conjugating Enzyme E2	At5g25760	PEX4 (PEROXIN4); Ubiquitin-Protein Ligase	0.0513	3.5102	4	46.0000	0.0450	-0.1000
OJ1666_A04.19	Putative F0 ATP Synthase D Chain	At3g52300	Atpq (Atp Synthase D Chain)	0.1463	1.9427	4	70.0680	-0.5554	-0.0976
OJ1669_F01.30	Putative GCPE Protein	At5g60600	Gcpe (CHLOROPLAST BIOGENESIS 4); 4-Hydroxy-3-Methylbut-2-En-1-Yl Diphosphate Synthase	0.1342	1.9124	4	43.4780	-0.3150	-0.0328
OJ1695_A02.24	Phosphatase 2A Regulatory A Subunit	At3g25800	PDF1 (65 KDA REGULATORY SUBUNIT OF PROTEIN PHOSPHATASE 2A); Protein Phosphatase Type 2A Regulator	0.0811	4.5071	4	41.8050	0.0415	-0.0211
OJ1705_E12.26	Putative Citrate Synthase, Glyoxysomal Precursor	At2g42790	CSY3 (CITRATE SYNTHASE 3); Citrate (SI)-Synthase	0.1459	2.2077	4	47.3680	-0.2610	-0.0180
OJ1741_B01.9	Voltage-Dependent Anion-Selective Channel (VDAC)	At5g15090	Porin, Putative / Voltage-Dependent Anion-Selective Channel Protein, Putative	0.3147	3.1489	4	58.9740	-0.4919	-0.0539
OJ1743_B12.5	Putative Serine Carboxypeptidase	At1g33540	SCPL18 (Serine Carboxypeptidase-Like 18); Serine Carboxypeptidase	0.5417	4.3229	4	54.2250	0.0360	-0.0379
OJ1743A09.16	Putative Leucine-Rich Repeat Transmembrane	At1g48480	RKL1 (Receptor-Like Kinase 1); ATP Binding / Kinase/ Protein Serine/Threonine Kinase	0.4197	4.5935	4	91.4060	-0.3512	-0.0370
OJ1754_E06.14	Chalcone Isomerase	At3g55120	TT5 (TRANSPARENT TESTA 5); Chalcone Isomerase	0.3907	3.8084	4	95.8530	-0.3182	-0.1021
OJ1754_E06.9	Putative Leukotriene A-4 Hydrolase	At5g13520	Peptidase M1 Family Protein	0.2466	2.9703	4	74.4680	-0.5526	-0.0327
OJ1789_C07.10	Putative Ribosomal Protein L17	At1g67430	60S Ribosomal Protein L17 (RPL17B)	0.1455	3.4379	4	66.0490	-0.4248	-0.0819
OJ1791_B03.41	Ankyrin Repeat-Like Protein	At3g01750	Ankyrin Repeat Family Protein	0.4735	4.6266	4	77.4850	-0.3816	-0.0318
OSJNBa0004N05.7	Unknown Protein	At2g33380	RD20 (RESPONSIVE TO DESSICATION 20); Calcium Ion Binding	0.2916	3.9006	4	69.4690	-0.1463	-0.1029
OSJNBa0005K07.2	Unknown Protein	At4g10440	Dehydration-Responsive Family Protein	0.2466	4.5532	4	74.2860	-0.4221	-0.0131
OSJNBa0006O14.4	Unknown Protein	At3g18350	Unknown Protein	0.3602	1.9524	4	41.4200	0.0221	-0.0205
OSJNBa0007H12.40	Putative Isocitrate Lyase	At3g21720	Isocitrate Lyase, Putative	0.1648	4.3341	4	94.6300	-0.4346	-0.0364
OSJNBa0008J01.24	Putative Avr9/Cf-9 Rapidly Elicited Protein 31	At4g20780	Calcium-Binding Protein, Putative	0.4200	3.5676	4	98.3520	-0.4602	-0.1122
OSJNBa0009C07.13	Putative Peroxisomal Ca-Dependent Solute	At4g01100	Substrate Carrier Family Protein	0.1285	1.8015	4	46.7460	-0.3602	-0.0524
OSJNBa0012L23.32	Putative Transcription Factor	At1g73230	Nascent Polypeptide-Associated Complex (NAC) Domain-Containing Protein	0.1700	2.4270	4	39.8690	-0.3040	-0.0713
OSJNBa0014G15.3	Putative Reductase	At5g37510	EMB1467 (EMBRYO DEFECTIVE 1467); NADH Dehydrogenase	0.1664	2.5521	4	51.1400	-0.2980	-0.0254
OSJNBa0015N08.12	Putative Transcription Factor	At1g17880	Nascent Polypeptide-Associated Complex (NAC) Domain-Containing Protein / BTF3b-Like Transcription Factor, Putative	0.1544	1.4554	4	65.7530	-0.6537	-0.1323
OSJNBa0015N08.9	Putative	At1g01630	SEC14 Cytosolic Factor, Putative /	0.370	3.6571	4	93.8780	-0.5178	-0.0487

			Phosphoglyceride Transfer Protein, Putative	3						
OSJNBa0017J22.12	Unknown Protein	At3g55070	Unknown Protein	0.2910	1.9599	4	66.4910	-0.4225	-0.0837
OSJNBa0017N12.8	Abscisic Acid-Inducible Protein Kinase	At1g78290	Serine/Threonine Protein Kinase, Putative	0.1536	4.0858	4	61.8750	-0.4606	-0.0523
OSJNBa0018H01.7	Putative Glutathione S-Transferase	At1g65820	Microsomal Glutathione S-Transferase, Putative	0.2772	3.4628	4	96.5030	-0.4431	-0.1061
OSJNBa0018H01.9	Putative Snrnp Protein	At2g33730	DEAD Box RNA Helicase, Putative	0.1771	4.5839	4	58.8760	-0.6310	-0.0245
OSJNBa0019K04.9	Unknown Protein	At5g51750	Subtilase Family Protein	0.3035	4.7927	4	85.8290	-0.4180	-0.0205
OSJNBa0026O12.9	Hypothetical Protein	At3g23300	Dehydration-Responsive Protein-Related	0.2294	4.4974	4	43.1510	0.1785	-0.0318
OSJNBa0029C15.2	Putative Thioredoxin-Like U5 Small	At5g08290	YLS8 (Yellow-Leaf-Specific Gene 8); Catalytic	0.0252	1.7657	4	77.4440	-0.4566	-0.1162
OSJNBa0032F06.12	Unknown Protein	At5g53470	Acbp1 (Acyl-Coa Binding Protein)	0.3900	3.2815	4	62.7010	-0.4970	-0.0655
OSJNBa0032F06.16	Unknown Protein	At2g45790	Eukaryotic Phosphomannomutase Family Protein	0.1181	3.8661	4	53.2470	-0.1900	-0.0661
OSJNBa0038J17.27	Hypothetical Protein	At1g15000	SCPL50 (Serine Carboxypeptidase-Like 50); Serine Carboxypeptidase	0.3981	4.2441	4	94.8660	-0.3733	-0.0452
OSJNBa0039C07.12	Unknown Protein	At5g13440	Ubiquinol-Cytochrome C Reductase Iron-Sulfur Subunit, Putative / Rieske Iron-Sulfur Protein, Putative	0.2519	4.0532	4	66.5410	-0.5280	-0.0752
OSJNBa0040D23.4	Putative Transmembrane Protein	At1g14530	(TOM THREE HOMOLOG); Virion Binding	0.1616	1.7838	4	59.4410	-0.0066	-0.0796
OSJNBa0041P03.2	Putative Signal Tranduction Protein	At1g15130	Hydroxyproline-Rich Glycoprotein Family Protein	0.2869	2.7907	4	56.5740	-0.4870	-0.0176
OSJNBa0042I09.17	Putative Receptor-Like Protein Kinase	At1g34300	Lectin Protein Kinase Family Protein	0.3695	4.7316	4	96.3500	-0.4025	-0.0330
OSJNBa0042I15.10	Unknown Protein	At1g08250	Prephenate Dehydratase Family Protein	0.2387	4.2158	4	95.9900	-0.4590	-0.0389
OSJNBa0042L16.3	Unknown Protein	At4g14110	Cop9 (Constitutive Photomorphogenic 9)	0.3526	3.6966	4	78.7230	-0.5161	-0.0520
OSJNBa0043A12.24	Unknown Protein	At1g49820	ATMTK; S-Methyl-5-Thioribose Kinase	0.2043	4.2184	4	63.7040	-0.3878	-0.0549
OSJNBa0053L11.37	Unknown Protein	At3g07090	Unknown Protein	0.3351	3.9196	4	94.8720	-0.3687	-0.0583
OSJNBa0054K20.22	Putative Initiation Factor 3g	At3g11400	EIF3G1 (Eukaryotic Translation Initiation Factor 3G1); RNA Binding / Translation Initiation Factor	0.2181	2.5048	4	63.0600	-0.5029	-0.0377
OSJNBa0056G17.13	Putative Ubiquinone Oxidoreductase Subunit	At3g03100	Oxidoreductase	0.2251	1.9021	4	64.3840	0.0205	-0.1038
OSJNBa0057L21.1	Putative Phragmoplastin	At3g60190	ADL4/ADLP2/DRP1E/EDR3 (DYNAMIN-LIKE PROTEIN 4); GTP Binding / Gtpase	0.1357	4.5400	4	45.2340	-0.3952	-0.0210
OSJNBa0067K08.8	Unknown Protein	At5g16250	Unknown Protein	0.3428	3.6324	4	96.2960	-0.3830	-0.1249
OSJNBa0070C17.12	Unknown Protein	At1g30630	Coatomer Protein Epsilon Subunit Family Protein / COPE Family Protein	0.1444	1.4927	4	59.9260	-0.4533	-0.0282
OSJNBa0070M12.12	Unknown Protein	At2g46860	Inorganic Pyrophosphatase, Putative (Soluble) / Pyrophosphate Phospho-Hydrolase, Putative /	0.1159	3.5795	4	49.2460	-0.5227	-0.0840

			Ppase, Putative							
OSJNBa0071I13.13	Unknown Protein	At2g18980	Peroxidase, Putative	0.4236	4.0568	4		95.4820	-0.4705	-0.0659
OSJNBa0072D21.14	Unknown Protein	At2g05170	ATVPS11 (Arabidopsis Thaliana Vacuolar Protein Sorting 11); Transporter	0.2154	1.7429	4		42.3340	-0.2702	-0.0182
OSJNBa0076F20.10	Putative Cytochrome	At5g53560	ATB5-A (Cytochrome B5 A)	0.2171	1.7427	4		59.6770	-0.3436	-0.1239
OSJNBa0076F20.4	Unknown Protein	At1g64980	Unknown Protein	0.2819	3.7767	4		97.1770	-0.5122	-0.0877
OSJNBa0078A17.8	Putative Splicing Factor	At5g06160	Splicing Factor-Related	0.2549	4.3714	4		51.3760	-0.3234	-0.0249
OSJNBa0078D06.37	Unknown Protein, 5'-Partial	At1g20980	SPL14 (SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 14); DNA Binding / Transcription Factor	0.8881	3.4762	4		48.6180	-0.2087	-0.0186
OSJNBa0081C13.10	Sec13p	At2g30050	Transducin Family Protein / WD-40 Repeat Family Protein	0.1381	4.0689	4		49.3200	-0.5617	-0.0344
OSJNBa0081C13.30	Putative Splicing Factor 3b, Subunit 3, 130kda	At3g55220	Splicing Factor, Putative	0.1423	2.7028	4		57.8630	-0.6003	-0.0179
OSJNBa0083F15.15	Putative Ubiquitin Conjugation Factor	At5g15400	U-Box Domain-Containing Protein	0.3100	4.9288	4		52.2870	-0.3540	-0.0224
OSJNBa0084A10.7	Unknown Protein	At1g21760	F-Box Family Protein	0.2911	1.7902	4		46.1040	-0.0778	-0.0363
OSJNBa0085I10.13	Unknown Protein	At5g09400	KUP7 (K+ Uptake Permease 7); Potassium Ion Transporter	0.3140	1.8195	4		50.1840	-0.1125	-0.0324
OSJNBa0087C10.9	Synaptobrevin-Like Protein	At1g04750	Vamp7b (Vesicle-Associated Membrane Protein 7b)	0.0807	3.6833	4		60.5770	-0.4406	-0.0918
OSJNBa0087O09.19	Putative Aldehyde Oxidase	At5g20960	Aao1 (Aldehyde Oxidase 1)	0.3822	5.1889	4		68.9790	-0.4263	-0.0066
OSJNBa0094J08.10	Unknown Protein	At3g11030	Steroid Hormone Receptor/ Transcription Factor	0.4330	4.1185	4		96.9700	-0.4475	-0.0357
OSJNBa0094J08.7	Putative Multiple Inositol Polyphosphate	At1g09870	Histidine Acid Phosphatase Family Protein	0.3409	1.9067	4		46.9600	-0.1985	-0.0162
OSJNBb0003H03.27	Putative ADP-Ribosylation Factor 3	At5g14670	ATARFA1B (ADP-Ribosylation Factor A1B); GTP Binding / Phospholipase Activator/ Protein Binding	0.3535	3.6135	4		55.5560	-0.2261	-0.1033
OSJNBb0004A17.1	Unknown Protein	At1g65840	ATPAO4 (POLYAMINE OXIDASE 4); Amine Oxidase	0.2635	2.4361	4		42.7960	-0.2003	-0.0317
OSJNBb0005G07.114	Putative WD Repeat Protein	At5g66240	Transducin Family Protein / WD-40 Repeat Family Protein	0.2447	4.0243	4		40.0000	-0.0480	-0.0472
OSJNBb0005J14.27	Cytochrome P450-Like Protein	At2g45510	CYP704A2 (Cytochrome P450, Family 704, Subfamily A, Polypeptide 2); Oxygen Binding	0.4234	4.3495	4		84.5530	-0.5040	-0.0404
OSJNBb0006O08.14	Putative Zinc Finger Protein	At5g46750	AGD8 (ARF-GAP DOMAIN 8); DNA Binding	0.2714	1.7079	4		50.7610	-0.1121	-0.0410
OSJNBb0007E22.7	Putative Serpin	At1g47710	Serpin, Putative / Serine Protease Inhibitor, Putative	0.3691	2.7209	4		64.9730	-0.5300	-0.0212
OSJNBb0009C07.2	Putative Transcription Initiation Factor	At4g12610	ATRAP74/RAP74; Transcription Initiation Factor	0.2875	4.3306	4		41.7190	0.1399	-0.0470
OSJNBb0014K18.8	Putative 1-Deoxy-D-Xylulose-5-Phosphate	At4g15560	Cla1 (Cloroplastos Alterados 1)	0.1447	4.7215	4		92.7010	-0.3547	-0.0307
OSJNBb0015I11.10	Putative Pollen Allergen	At3g45970	Atexla1 (Arabidopsis Thaliana Expansin-Like A1)	0.3861	3.9196	4		92.1350	-0.4659	-0.0415

OSJNBb0017F17.21	Putative Zinc Binding Protein	At2g40110	Yippee Family Protein	0.1774	2.2548	4	62.0970	-0.3583	-0.1519
OSJNBb0021P10.3	20S Proteasome Beta 4 Subunit	At4g14800	PBD2 (20S PROTEASOME BETA SUBUNIT 2); Peptidase	0.1840	3.7687	4	67.5000	-0.5239	-0.1080
OSJNBb0024K03.4	Putative Cullin 3	At1g26830	ATCUL3/ATCUL3A/CUL3/CUL3A (Cullin 3A); Protein Binding / Ubiquitin-Protein Ligase	0.1433	4.6644	4	50.7400	-0.3241	-0.0192
OSJNBb0027B08.34	Putative Isomerase	At4g15940	Fumarylacetoacetate Hydrolase Family Protein	0.2824	1.8897	4	57.5920	-0.2985	-0.0980
OSJNBb0028C01.32	Putative Arm Repeat Containing Protein	At2g45720	Binding	0.3069	4.5179	4	94.8050	-0.3912	-0.0235
OSJNBb0034G17.8	Unknown Protein	At3g57560	Aspartate/Glutamate/Uridylate Kinase Family Protein	0.3131	4.2349	4	82.9790	-0.4923	-0.0227
OSJNBb0040H10.15	Translocase Inner Membrane-Like Protein	At1g20350	ATTIM17-1 (Arabidopsis Thaliana Translocase Inner Membrane Subunit 17-1); Protein Translocase	0.3331	3.8248	4	95.7550	-0.4388	-0.0839
OSJNBb0041A22.12	Putative Inorganic Pyrophosphatase	At3g53620	Inorganic Pyrophosphatase, Putative (Soluble) / Pyrophosphate Phospho-Hydrolase, Putative / Ppase, Putative	0.1352	2.6949	4	49.0000	-0.3158	-0.0657
OSJNBb0043H09.9	Unknown Protein	At5g42150	Electron Carrier/ Protein Disulfide Oxidoreductase	0.3018	2.9607	4	54.8170	-0.1787	-0.0618
OSJNBb0048A17.11	Putative Serine Protease	At5g67360	ARA12; Subtilase	0.3101	4.7603	4	93.3960	-0.3481	-0.0309
OSJNBb0048A17.2	Translation Initiation Factor 5A	At1g69410	Eukaryotic Translation Initiation Factor 5A, Putative / Eif-5A, Putative	0.0858	1.5852	4	63.5760	-0.5594	-0.1081
OSJNBb0055I24.131	Chitinase III-Like Protein	At1g70800	C2 Domain-Containing Protein	0.4995	3.9547	4	68.0720	-0.4928	-0.0780
OSJNBb0058B20.19	Putative Transcription Initiation Factor IIE,	At4g20330	Transcription Initiation Factor-Related	0.2702	3.9883	4	52.2730	-0.3408	-0.0437
OSJNBb0062D12.129-2	Putative MAP4 Kinase	At3g15220	Protein Kinase, Putative	0.3681	4.5863	4	36.5510	-0.0208	-0.0392
OSJNBb0062P14.116-1	Putative ORMDL2	At1g01230	ORMDL Family Protein	0.1211	3.5619	4	72.2220	-0.2259	-0.1341
OSJNBb0064P21.2	Calcium-Dependent Protein Kinase	At2g17290	CPK6 (CALCIUM-DEPENDENT PROTEIN KINASE 6); Anion Channel/ Calcium- And Calmodulin-Dependent Protein Kinase/ Kinase	0.2776	4.4065	4	43.2050	0.0417	-0.0169
OSJNBb0064P21.3	Putative Sugar Transporter	At4g35300	TMT2 (TONOPLAST MONOSACCHARIDE TRANSPORTER2); Carbohydrate Transporter/ Sugar Porter	0.2206	4.5301	4	50.6440	-0.2655	-0.0319
OSJNBb0074M06.8	Putative Trypanothione-Dependent Peroxidase	At1g60420	DC1 Domain-Containing Protein	0.3818	2.3214	4	61.3590	-0.4616	-0.0466
OSJNBb0076N15.1	Putative Lipoxygenase	At1g72520	Lipoxygenase, Putative	0.2431	4.2542	4	82.8430	-0.2974	-0.0273
OSJNBb0079L11.8	Putative Isovaleryl-Coa Dehydrogenase	At3g45300	Ivd (Isovaleryl-Coa-Dehydrogenase)	0.1096	2.9922	4	57.8130	-0.4332	-0.0594
OSJNBb0081B07.12	Putative Peptide Transport Protein	At3g53960	Proton-Dependent Oligopeptide Transport (POT) Family Protein	0.3716	4.5140	4	93.5710	-0.4592	-0.0193
OSJNBb0081K01.19	Putative ABC (ATP-Binding Cassette) Transporter	At5g39040	ATTAP2 (Arabidopsis Thaliana Transporter Associated With Antigen Processing Protein 2); Atpase, Coupled To Transmembrane Movement Of Substances	0.1867	1.9282	4	46.0400	-0.1324	-0.0243

OSJNBb0084L07.12	Methylmalonate Semi-Aldehyde Dehydrogenase	At2g14170	ALDH6B2 (Aldehyde Dehydrogenase 6B2)	0.1960	2.6455	4	53.8460	-0.4857	-0.0345
OSJNBb0089A17.8	Putative Myb-Related Protein	At5g61620	Myb Family Transcription Factor	0.7889	4.0201	4	52.8240	-0.1363	-0.0585
OSJNBb0093E13.1	Unknown Protein	At3g22290	Unknown Protein	0.1626	3.9553	4	41.1590	-0.3184	-0.0340
OSJNBb0094K03.17	Putative ATP-Dependent RNA Helicase	At2g35920	Helicase Domain-Containing Protein	0.1800	4.7694	4	35.0180	0.1625	-0.0107
OSJNBb0103I08.15	Unknown Protein	At5g24380	YSL2 (YELLOW STRIPE LIKE 2); Oligopeptide Transporter	0.2681	4.6103	4	88.4850	-0.4334	-0.0330
OSJNBb0108E17.4	Putative Thioredoxin H-Type (TRX-H) (Trxta)	At5g42980	ATTRX3 (Thioredoxin H-Type 3); Thiol-Disulfide Exchange Intermediate	0.3101	1.1905	4	58.9290	-0.3696	-0.1545
OSJNBb0118P14.12	Unknown Protein	At5g36880	AMP Binding / Acetate-Coa Ligase/ Catalytic	0.1257	2.9558	4	54.3190	-0.2583	-0.0361
P0007D08.11	Putative Alcohol Dehydrogenase (Zn	At5g63620	Oxidoreductase, Zinc-Binding Dehydrogenase Family Protein	0.1891	1.6550	4	53.0150	-0.4716	-0.0282
P0018C07.117	Putative Placental Protein 6	At3g07950	Rhomboid Protein-Related	0.3763	1.6969	4	41.8060	-0.0727	-0.0756
P0025A05.6	Putative Glucosyltransferase IS5a,	At2g15480	UGT73B5 (UDP-Glucosyl Transferase 73B5); UDP-Glycosyltransferase/ Transferase, Transferring Glycosyl Groups	0.5424	4.3316	4	89.9140	-0.4394	-0.0255
P0034A04.112	26S Proteasome Regulatory Subunit 4 Homolog	At4g29040	RPT2A (Regulatory Particle Triple-A 2A); Atpase	0.0653	4.3653	4	59.8040	-0.5374	-0.0513
P0042D01.4	Putative Phenylalanine Ammonia-Lyase	At2g37040	PAL1 (PHE AMMONIA LYASE 1); Phenylalanine Ammonia-Lyase	0.2074	4.6178	4	92.1690	-0.4822	-0.0265
P0044F08.16	Putative WD40-Repeat Protein	At3g18060	Transducin Family Protein / WD-40 Repeat Family Protein	0.2474	2.6653	4	52.5600	-0.4573	-0.0364
P0046D03.133	Putative Prohibitin	At4g28510	Atphb1 (Prohibitin 1)	0.1500	2.5688	4	57.6210	-0.5074	-0.0789
P0047E05.15-1	Putative Ubiquitin Activating Enzyme	At1g05350	Thif Family Protein	0.2181	2.0408	4	44.1490	-0.0566	-0.0657
P0135D07.18	Membrane Bound O-Acyl Transferase-Like	At1g63050	Membrane Bound O-Acyl Transferase (MBOAT) Family Protein	0.2155	2.5321	4	53.6040	-0.0843	-0.0390
P0264G11.2-2	Putative Racd Protein	At4g35020	ARAC3/ATROP6/RHO1PS/ROP6 (Rho-Related Protein From Plants 6); GTP Binding / Gtpase	0.0515	2.6937	4	53.1250	-0.3843	-0.0853
P0408C03.13	Putative SLT1 Protein (Ion Homeostasis Related	At2g37570	Slt1 (Sodium- And Lithium-Tolerant 1)	0.3042	4.3542	4	65.6440	-0.3138	-0.0434
P0410E01.31	Putative Acetyl Transferase	At3g62160	Transferase Family Protein	0.6107	2.6075	4	72.9800	-0.5814	-0.0656
P0415A04.27	Disease Resistance Protein-Like	At5g43740	Disease Resistance Protein (CC-NBS-LRR Class), Putative	0.8145	4.8231	4	65.7750	-0.4451	-0.0087
P0421H07.20	Putative Farnesyl-Pyrophosphate Synthetase	At5g47770	FPS1 (FARNESYL DIPHOSPHATE SYNTHASE 1); Dimethylallyltranstransferase/ Geranyltranstransferase	0.2212	2.3733	4	50.7650	-0.3810	-0.0592
P0423A12.18	Putative Glutathione S-Transferase	At3g62760	ATGSTF13 (Arabidopsis Thaliana Glutathione S-Transferase (Class Phi) 13); Glutathione Transferase	0.4733	3.7309	4	95.7350	-0.4412	-0.0543
P0429B05.26	Putative Phosphoglycerate Dehydrogenase	At1g17740	Unknown Protein	0.2501	4.6744	4	82.0690	-0.4888	-0.0225
P0434B04.10	Putative Triose-Phosphate	At3g55440	ATCTIMC (CYTOSOLIC TRIOSE PHOSPHATE	0.139	1.5457	4	47.8810	-0.5111	-0.0534

	Isomerase		ISOMERASE); Triose-Phosphate Isomerase	2					
P0434E03.16-1	Putative Carrier Protein	At2g46320	Substrate Carrier Family Protein	0.3727	1.2615	4	47.6430	-0.0654	-0.0614
P0435B05.15	Putative Ribosomal Protein L18a, Cytosolic	At2g34480	60S Ribosomal Protein L18A (RPL18aB)	0.0746	3.2400	4	76.7440	-0.5411	-0.1343
P0439B06.7	Putative Acetoacyl-Coa-Thiolase	At5g47720	Acetyl-Coa C-Acetyltransferase	0.2001	1.5941	4	49.8760	-0.6124	-0.0262
P0439B07.4	Putative PHG1A Protein	At2g24170	Endomembrane Protein 70, Putative	0.1786	1.7161	4	52.7000	-0.4365	-0.0232
P0443G08.138	Putative Monodehydroascorbate Reductase	At1g63940	Monodehydroascorbate Reductase, Putative	0.2000	2.0147	4	39.2620	-0.1155	-0.0497
P0451H06.1	Putative Poly(A)-Binding Protein	At1g49760	PAB8 (POLY(A) BINDING PROTEIN 8); RNA Binding / Translation Initiation Factor	0.2651	4.5677	4	44.0890	-0.2869	-0.0418
P0453E05.118	Translation Initiation Factor 5A	At1g13950	EIF-5A (Eukaryotic Translation Initiation Factor 5A-1); Translation Initiation Factor	0.0628	3.4558	4	56.0000	-0.5699	-0.0981
P0455H11.118-1	Putative Pectinacetylesterase Precursor	At1g57590	Carboxylic Ester Hydrolase	0.3482	4.2050	4	47.9900	-0.1424	-0.0392
P0456F08.17	Putative Lipase	At2g42690	Lipase, Putative	0.4615	4.1134	4	93.6070	-0.4762	-0.0443
P0456F08.20	Putative Processing Peptidase Beta	At3g02090	MPPBETA; Metalloendopeptidase	0.3767	1.9509	4	57.6520	-0.4667	-0.0259
P0463G12.43-1	Putative Aminopropyl Transferase	At5g53120	Spds3 (Spermidine Synthase 3)	0.2075	3.1626	4	43.7160	-0.2421	-0.0244
P0470B03.25	Nitrate Reductase Apoenzyme	At1g77760	Nia1 (Nitrate Reductase 1)	0.2717	4.6950	4	96.6280	-0.4492	-0.0305
P0470G10.17	Putative Suppressor Of Actin 1	At5g66020	ATSAC1B/IBS2 (IMPAIRED IN BABA-INDUCED STERILITY 2); Phosphoinositide 5-Phosphatase	0.2912	4.4732	4	37.0370	0.2295	-0.0157
P0476C12.12	Putative 26S Proteasome Regulatory Particle	At5g58290	RPT3 (Root Phototropism 3); Atpase	0.0751	4.2666	4	58.3120	-0.6303	-0.0539
P0479C12.25-1	Putative Trehalose-6-Phosphate Synthase	At1g23870	ATTPS9 (Arabidopsis Thaliana Trehalose-Phosphatase/Synthase 9); Transferase, Transferring Glycosyl Groups / Trehalose-Phosphatase	0.4275	4.7492	4	84.0760	-0.4544	-0.0216
P0482D04.17	Unknown Protein	At1g27440	GUT2; Catalytic	0.1082	1.5669	4	58.0400	-0.2540	-0.0350
P0485G01.13	Ubiquitin-Conjugating Enzyme E2	At1g16890	UBC36; Ubiquitin-Protein Ligase	0.0183	1.7089	4	55.6340	-0.2397	-0.0673
P0492E07.128	Unknown Protein	At3g13930	Dihydrolipoamide S-Acetyltransferase, Putative	0.2719	4.5140	4	41.9160	-0.1579	-0.0250
P0493A04.9	Plastid (P)Ppgpp Synthase	At3g14050	RSH2 (RELA-SPOT HOMOLOG); Catalytic	0.2902	2.3970	4	63.0950	-0.5033	-0.0327
P0498H04.25	Unknown Protein	At1g08480	Unknown Protein	0.5265	3.3610	4	91.9120	-0.5085	-0.1063
P0504A05.24	Putative 4-Coumarate Coenzyme A Ligase	At1g51680	4cl1 (4-Coumarate:Coa Ligase 1)	0.2917	4.4406	4	88.5440	-0.5131	-0.0410
P0505D12.6	Putative Uricase	At2g26230	Uricase / Urate Oxidase / Nodulin 35, Putative	0.2723	4.0765	4	61.5920	-0.3101	-0.0577
P0506B12.12	Putative Respiratory Burst Oxidase Protein	At5g60010	Ferric Reductase-Like Transmembrane Component Family Protein	0.3537	4.7021	4	79.1980	-0.4443	-0.0218
P0506F02.114	Putative GTP-Binding Protein DRG	At4g39520	GTP-Binding Protein, Putative	0.071	1.9537	4	42.8990	-0.1423	-0.0241

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P0519E12.134	Unknown Protein	At4g08810	SUB1 (Short Under Blue Light 1)	0.3127	4.4229	4	75.3570	-0.5008	-0.0243
P0520B06.4	Oryza Sativa MAP Kinase Kinase 1	At5g56580	ATMKK6 (ARABIDOPSIS NQK1); Kinase	0.2327	2.6304	4	45.6460	-0.1235	-0.0421
P0523B07.38-1	Putative Polyphosphoinositide Binding Protein	At5g47730	SEC14 Cytosolic Factor, Putative / Polyphosphoinositide-Binding Protein, Putative	0.2896	2.6477	4	49.3670	-0.0065	-0.0648
P0528B09.18	Glyceraldehyde-3-Phosphate Dehydrogenase	At2g24270	ALDH11A3 (Aldehyde Dehydrogenase 11A3); 3-Chloroallyl Aldehyde Dehydrogenase	0.0852	3.7254	4	61.3250	-0.2104	-0.0236
P0530H10.9	Putative Ferrochelatase II	At2g30390	Ferrochelatase II	0.2157	4.4360	4	44.6060	-0.1211	-0.0236
P0544G09.31	Putative ER Lumen Protein-Retaining Receptor	At1g75760	ER Lumen Protein Retaining Receptor Family Protein	0.1217	1.6923	4	61.4230	-0.3848	-0.0706
P0576F08.10	Putative SINA2 Protein,Seven In Absentia	At3g58040	Seven In Absentia (SINA) Family Protein	0.2285	2.3717	4	60.7640	-0.3201	-0.0412
P0585B01.29-1	Putative HGA1	At3g57380	Unknown Protein	0.7417	4.2612	4	89.4970	-0.5192	-0.0398
P0594D10.134	Putative Protein Kinase Hvpkaba1(Abcisic	At4g33950	OST1 (OPEN STOMATA 1); Kinase/ Protein Kinase	0.2031	4.1253	4	58.4660	-0.4838	-0.0469
P0599F09.13	Putative Serine/Threonine-Protein Kinase 16	At5g08160	ATPK3 (Arabidopsis Thaliana Serine/Threonine Protein Kinase 3); Kinase	0.1742	2.8747	4	53.7740	-0.3408	-0.0668
P0610E02.33	Putative Glycinamide Ribonucleotide Synthetase	At1g09830	Phosphoribosylamine--Glycine Ligase (PUR2)	0.2671	1.9084	4	41.7340	-0.0490	-0.0400
P0617C02.124-2	Putative Glucose Transport Protein STP1	At1g11260	STP1 (SUGAR TRANSPORTER 1); Carbohydrate Transporter/ Sugar Porter	0.2393	4.0622	4	95.5800	-0.4091	-0.0476
P0627E03.33	Putative UDP-Glucose Glucosyltransferase1	At1g22360	UDP-Glycosyltransferase	0.3491	4.2661	4	92.0000	-0.4396	-0.0390
P0627E03.4	Putative Annexin P35	At5g10230	ANN7 (ANN7, ANNEXIN ARABIDOPSIS 7); Calcium Ion Binding / Calcium-Dependent Phospholipid Binding	0.3203	4.0829	4	68.0560	-0.1979	-0.0573
P0627E10.1	Putative Phosphoinositide-Specific Phospholipase	At3g08510	ATPLC2 (PHOSPHOLIPASE C 2); Phospholipase C	0.3371	4.4571	4	69.7180	-0.2317	-0.0283
P0643F09.35	Putative Potassium Channel Beta Subunit	At1g04690	KAB1 (POTASSIUM CHANNEL BETA SUBUNIT); Potassium Channel	0.1142	4.0505	4	78.3170	-0.5278	-0.0534
P0657H12.28	GL2-Type Homeobox Genes	At3g61150	HDG1 (HOMEODOMAIN GLABROUS1); DNA Binding / Transcription Factor	0.3565	4.7860	4	73.1030	-0.5154	-0.0228
P0665C04.32	Putative Glycyl-Trna Synthetase	At1g29880	Glycyl-Trna Synthetase / Glycine--Trna Ligase	0.1718	3.9667	4	54.4460	-0.3926	-0.0348
P0668H12.19	Putative 26S Proteasome Regulatory Subunit	At2g39990	EIF2 (Eukaryotic Translation Initiation Factor 2); Translation Initiation Factor	0.2090	1.9283	4	62.4540	-0.4157	-0.0423
P0673E01.19	Putative SNF2 Domain/Helicase Domain-Containing	At2g16390	DRD1 (DEFECTIVE IN RNA-DIRECTED DNA METHYLATION 1); ATP Binding / DNA Binding / Helicase/ Nucleic Acid Binding	0.5297	4.7376	4	37.3150	0.2257	-0.0095
P0676G05.13	Unknown Protein	At3g17020	Universal Stress Protein (USP) Family Protein	0.3694	1.9935	4	72.6110	-0.3973	-0.0539
P0676H02.3	Putative Purine Permease	At1g28220	ATPUP3 (Arabidopsis Thaliana Purine Permease 3); Purine Transporter	0.4255	4.1506	4	94.2360	-0.4214	-0.0573
P0676H03.26	Unknown Protein	At1g52890	ANAC019 (Arabidopsis NAC Domain Containing Protein 19); Transcription Factor	0.5865	3.9263	4	93.0690	-0.3425	-0.0522
P0679C08.10	Unknown Protein	At5g42090	Unknown Protein	0.239	4.2263	4	86.1110	-0.4920	-0.0445

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P0679C08.19	Rice Waxy Protein	At1g32900	Starch Synthase, Putative	0.3179	4.5634	4	82.6090	-0.5464	-0.0264
P0688A04.10	Putative Cytochrome P450	At3g14690	CYP72A15 (Cytochrome P450, Family 72, Subfamily A, Polypeptide 15); Oxygen Binding	0.3782	3.1487	4	53.8460	0.0232	-0.0528
P0691E06.15	Putative Latex-Abundant Protein	At1g79340	Latex-Abundant Protein, Putative (AMC7) / Caspase Family Protein	0.3491	4.1946	4	59.2880	-0.5299	-0.0453
P0691E06.20	Unknown Protein	At5g44860	Unknown Protein	0.4227	2.2377	4	86.0680	-0.4907	-0.0672
P0695H10.14	Putative Signal Recognition Particle 54K	At1g48900	Signal Recognition Particle 54 Kda Protein 3 / SRP54 (SRP-54C)	0.0945	4.2681	4	53.7310	-0.3921	-0.0532
P0695H10.9	Putative Transcription Initiation Factor	At1g75510	Transcription Initiation Factor IIF Beta Subunit (TFIIF-Beta) Family Protein	0.3376	3.9109	4	59.6710	-0.2542	-0.0590
P0700F06.17	Unknown Protein	At3g01780	Encodes TPLATE, A Cytokinesis Protein Targeted To The Cell Plate	0.2345	1.9064	4	54.7640	-0.3094	-0.0116
P0702H08.19	Putative Carboxymethylenebutenolidase	At2g32520	Dienelactone Hydrolase Family Protein	0.1720	2.1634	4	52.4340	-0.3031	-0.0214
P0705A05.111	Putative Iron Inhibited ABC Transporter 2	At5g60790	ATGCN1 (Arabidopsis Thaliana General Control Non-Repressible 1)	0.1083	4.4464	4	54.0000	-0.6337	-0.0360
P0712E02.8	Unknown Protein	At5g35460	Unknown Protein	0.2087	2.5368	4	61.8230	-0.3463	-0.0577
24K23.23	Putative Amylogenin	At3g08900	RGP3 (REVERSIBLY GLYCOSYLATED POLYPEPTIDE 3); Alpha-1,4-Glucan-Protein Synthase (UDP-Forming)	0.5406	2.7634	5	52.0680	-0.0975	-0.0254
B1026C12.3	Putative Ethylene-Inducible Protein	At5g01410	PDX1 (PYRIDOXINE BIOSYNTHESIS 1.3); Protein Heterodimerization/ Protein Homodimerization	0.0996	3.9587	5	94.6840	-0.5080	-0.0726
B1047A05.37	Putative 60S Ribosomal Protein L7	At3g13580	60S Ribosomal Protein L7 (RPL7D)	0.1541	3.7506	5	78.5710	-0.5678	-0.0698
B1080D07.15	Putative 33kda Oxygen Evolvingprotein Of	At3g50820	PSBO-2/PSBO2 (PHOTOSYSTEM II SUBUNIT O-2); Oxygen Evolving	0.1526	4.0490	5	88.7460	-0.4282	-0.0634
B1099H05.23	Putative Germin A	At5g39110	Germin-Like Protein, Putative	0.3232	3.1487	5	53.4250	-0.3020	-0.0398
B1112D09.3	Putative Root Hair Defective 3 (RHD3)	At3g13870	Rhd3 (Root Hair Defective 3)	0.2158	2.8438	5	39.8640	-0.0162	-0.0177
B1131G07.11	Putative Elongation Factor 1-Gamma	At1g57720	Translation Elongation Factor	0.1529	2.8276	5	53.4390	-0.4105	-0.0353
B1156H12.13	Putative DEAD BOX RNA Helicase	At5g11200	DEAD/DEAH Box Helicase, Putative	0.1378	2.3943	5	46.1150	-0.3229	-0.0415
B1215B07.34	Putative Adenosine Kinase	At5g03300	ADK2 (ADENOSINE KINASE 2); Kinase	0.1064	2.8493	5	49.6840	-0.4137	-0.0557
OJ1006F06.19	Unknown Protein	At1g21880	Peptidoglycan-Binding Lysm Domain-Containing Protein	0.9183	4.1376	5	78.6320	-0.3529	-0.0517
OJ1020_C02.26	Putative P18	At2g45640	SAP18 (SIN3 ASSOCIATED POLYPEPTIDE P18); Protein Binding / Transcription Regulator	0.2563	3.4497	5	49.2960	-0.0026	-0.1191
OJ1047_A06.117	Plasma Membrane Intrinsic Protein	At3g54820	PIP2;5/PIP2D (Plasma Membrane Intrinsic Protein 2;5); Water Channel	0.1399	3.8667	5	97.5350	-0.4102	-0.0521
OJ1065_B06.19-1	Putative Photosystem I Antenna Protein	At3g61470	LHCA2 (Photosystem I Light Harvesting Complex Gene 2); Chlorophyll Binding	0.1618	3.8001	5	94.0710	-0.4805	-0.0802
OJ1112_G07.32	Unknown Protein	At5g06270	Unknown Protein	0.5016	3.2746	5	98.3190	-0.3180	-0.0959

OJ1124_B05.4	Putative Osrad23	At5g38470	DNA Repair Protein RAD23, Putative	0.2741	1.4099	5	42.0630	-0.0210	-0.0429
OJ1124_H03.2	Cysteine Synthase	At4g14880	Oasa1 (O-Acetylserine (Thiol) Lyase (Oas-Tl) Isoform A1)	0.1509	1.8785	5	51.3330	-0.4202	-0.0434
OJ1131_E09.11	Putative Protein Kinase	At3g01090	AKIN10 (Arabidopsis SNF1 Kinase Homolog 10, SNF1-RELATED PROTEIN KINASE 1.1); Protein Kinase	0.1427	3.1375	5	39.6590	-0.3291	-0.0327
OJ1145_F01.6	Putative Cinnamyl-Alcohol Dehydrogenase	At4g34230	Cad5 (Cinnamyl Alcohol Dehydrogenase 5)	0.1962	4.1153	5	93.0840	-0.5033	-0.0523
OJ1150_A11.25	Monodehydroascorbate Reductase	At3g52880	ATMDAR1 (MONODEHYDROASCORBATE REDUCTASE 1); Monodehydroascorbate Reductase (NADH)	0.2054	1.5067	5	66.0100	-0.5749	-0.0437
OJ1163_G08.25	Putative Histidine Amino Acid Transporter	At5g40780	LHT1 (LYSINE HISTIDINE TRANSPORTER 1); Amino Acid Transporter	0.1749	4.3114	5	89.0160	-0.3391	-0.0407
OJ1191_A10.119	Putative 70 Kda Peptidylprolyl Isomerase	At3g25230	ROF1 (ROTAMASE FKBP 1); FK506 Binding / Calmodulin Binding / Peptidyl-Prolyl Cis-Trans Isomerase	0.1485	2.7183	5	47.6920	-0.3811	-0.0188
OJ1212_C05.3	Unknown Protein	At2g44310	Calcium-Binding EF Hand Family Protein	0.4002	3.3867	5	98.6490	-0.4632	-0.1120
OJ1225_F07.14	Unknown Protein	At5g12960	Catalytic	0.3930	3.7272	5	60.7230	-0.3751	-0.0304
OJ1225_F07.15	Putative Zinc-Finger Protein	At1g51200	DNA Binding / Zinc Ion Binding	0.3869	3.3106	5	75.7760	-0.7136	-0.0867
OJ1234_B11.27	Putative Protein Kinase (ADK1)	At1g03930	ADK1 (DUAL SPECIFICITY KINASE 1); Kinase	0.2332	4.3004	5	40.4550	0.2856	-0.0173
OJ1268_B08.8	GTP-Binding Nuclear Protein RAN-B1	At5g55190	RAN3; GTP Binding	0.0480	1.6293	5	52.6320	-0.5475	-0.0756
OJ1342_D02.8	Putative Oscttp	At5g26220	Chac-Like Family Protein	0.2986	2.2889	5	57.7890	-0.2370	-0.0671
OJ1343_D04.115	Putative Sex Determination Protein Tasselseed 2	At4g03140	Oxidoreductase	0.4987	3.9615	5	89.2720	-0.4387	-0.0667
OJ1351_C05.112	Probable Photosystem II Oxygen-Evolving Complex	At1g06680	PSBP-1 (OXYGEN-EVOLVING ENHANCER PROTEIN 2); Calcium Ion Binding	0.1826	3.8147	5	94.1910	-0.4061	-0.0555
OJ1359_D06.12	Putative Ribosomal Protein S4	At5g58420	40S Ribosomal Protein S4 (RPS4D)	0.0731	1.7769	5	67.1880	-0.6681	-0.0521
OJ1362_G11.23	Putative LEA Protein	At5g44310	Late Embryogenesis Abundant Domain-Containing Protein / LEA Domain-Containing Protein	0.8287	3.2982	5	93.9890	-0.5427	-0.0610
OJ1364E02.4	Putative LIM-Domain Protein	At2g39900	LIM Domain-Containing Protein	0.2007	1.9040	5	66.1290	-0.2475	-0.0990
OJ1371_D04.6	Putative Cysteine Proteinase 1 Precursor	At4g39090	RD19 (RESPONSIVE TO DEHYDRATION 19); Cysteine-Type Peptidase	0.2406	4.0585	5	75.7060	-0.5290	-0.0402
OJ1372_D06.35	Putative CER1 Protein	At1g02190	CER1 Protein, Putative	0.3912	2.8731	5	60.9800	-0.1280	-0.0291
OJ1457_D07.117	Putative Malate Dehydrogenase	At2g13560	Malate Oxidoreductase, Putative	0.1537	2.3151	5	47.7590	-0.0502	-0.0465
OJ1479_B11.3	Proteasome Alpha Subunit	At5g66140	PAD2 (20S Proteasome Alpha Subunit D2); Peptidase	0.0667	3.7241	5	91.1890	-0.5566	-0.0739
OJ1479_B11.9	Putative Peroxisome Type Ascorbate Peroxidase	At4g35000	APX3 (ASCORBATE PEROXIDASE 3); L-Ascorbate Peroxidase	0.1932	1.8655	5	47.9850	-0.3931	-0.0818
OJ1479_B12.23	Putative Diphosphate-Fructose-6-	At1g76550	Pyrophosphate--Fructose-6-Phosphate 1-	0.157	2.4030	5	46.8270	-0.3615	-0.0287

	Phosphate		Phosphotransferase Alpha Subunit, Putative / Pyrophosphate-Dependent 6-Phosphofructose-1-Kinase, Putative	0					
OJ1479_B12.9	Putative NADPH-Thioredoxin Reductase	At4g35460	NTR1 (NADPH-Dependent Thioredoxin Reductase 1)	0.1745	4.1540	5	85.0790	-0.5485	-0.0761
OJ1484_G09.129-1	Phosphoenolpyruvate Carboxylase	At1g53310	ATPPC1 (PHOSPHOENOLPYRUVATE CARBOXYLASE 1); Phosphoenolpyruvate Carboxylase	0.0864	2.2941	5	58.0140	-0.3406	-0.0188
OJ1540_H01.1	Heat Shock Protein 90	At4g24190	SHD (SHEPHERD); ATP Binding	0.1452	2.5735	5	62.8330	-0.5409	-0.0133
OJ1540_H01.4	Putative Protein Phosphatase	At3g51370	Protein Phosphatase 2C, Putative / PP2C, Putative	0.1776	4.2360	5	45.8450	-0.1749	-0.0355
OJ1559_F09.120	Cellulose Synthase-4	At5g05170	CESA3 (CELLULASE SYNTHASE 3); Cellulose Synthase/ Transferase, Transferring Glycosyl Groups	0.1334	2.0245	5	52.4320	-0.4130	-0.0191
OJ1582_D10.12	Histone H2A	At4g27230	Histone H2A, Putative	0.0843	3.3866	5	94.6150	-0.4840	-0.1133
OJ1611_C08.4	Putative Beta-1,3-Glucanase Precursor	At5g55180	Glycosyl Hydrolase Family 17 Protein	0.3268	4.2927	5	94.3040	-0.4131	-0.0365
OJ1613_G04.21	Putative Actin-Related Protein 4 (ARP4)	At1g18450	ATARP4 (ACTIN-RELATED PROTEIN 4); Structural Constituent Of Cytoskeleton	0.2060	1.7285	5	40.2440	0.0654	-0.0400
OJ1626_B09.4	Alpha 2 Subunit Of 20S Proteasome	At1g16470	PAB1 (20S Proteasome Alpha Subunit B1); Peptidase	0.0641	2.3265	5	48.4020	-0.1034	-0.0834
OJ1715_H01.42	Putative Ribosomal Protein L35A	At1g74270	60S Ribosomal Protein L35a (RPL35aC)	0.1155	2.9452	5	94.4950	-0.4771	-0.1777
OJ1789_C07.13	Moco Containing Protein(Osmcp)	At3g01910	Sox (Sulfite Oxidase)	0.1748	3.9918	5	42.4400	0.0569	-0.0506
OJ9003_G05.34	Putative Ribosomal Protein S14	At3g52580	40S Ribosomal Protein S14 (RPS14C)	0.0435	0.7864	5	46.4790	-0.3265	-0.0947
OJA1212_C06.25	Lactate Dehydrogenase	At4g17260	L-Lactate Dehydrogenase, Putative	0.2686	4.1675	5	96.3960	-0.4148	-0.0575
OJA1364E02.2	Putative Fructose-1,6-Biphosphotase, Chloroplast	At3g54050	Fructose-1,6-Bisphosphatase, Putative / D-Fructose-1,6-Bisphosphate 1-Phosphohydrolase, Putative / Fbpase, Putative	0.1624	4.1499	5	93.7340	-0.4550	-0.0404
OSJNAb0015J03.9	Putative Enolase (2-Phospho-D-Glycerate)	At2g36530	LOS2 (Low Expression Of Osmotically Responsive Genes 1); Phosphopyruvate Hydratase	0.1024	1.3938	5	53.6340	-0.4883	-0.0477
OSJNBa0006L06.7	60S Ribosomal Protein L17	At3g04400	EMB2171 (EMBRYO DEFECTIVE 2171); Structural Constituent Of Ribosome	0.0247	2.2510	5	82.6090	-0.6621	-0.0986
OSJNBa0007M04.13	Putative RNA Binding Protein	At5g04600	RNA Recognition Motif (RRM)-Containing Protein	0.3616	2.4572	5	58.8540	-0.4864	-0.0776
OSJNBa0013D02.10	Putative Ascorbate Peroxidase	At1g07890	Apx1 (Ascorbate Peroxidase 1, Maternal Effect Embryo Arrest 6)	0.1698	1.4244	5	70.9960	-0.6275	-0.0552
OSJNBa0013K16.2	Unknown Protein	At4g35310	CPK5 (CALMODULIN-DOMAIN PROTEIN KINASE 5); Calcium- And Calmodulin-Dependent Protein Kinase/ Kinase	0.1829	4.4998	5	60.3080	-0.3997	-0.0238
OSJNBa0017N12.5	Histone H3.2 Protein	At5g10980	Histone H3	0.0290	2.2588	5	60.0000	-0.6268	-0.0912
OSJNBa0018M05.20	Unknown Protein	At1g34130	STT3B (STAUROSPORIN AND TEMPERATURE SENSITIVE 3-LIKE B); Oligosaccharyl Transferase	0.1151	2.0262	5	61.0870	-0.3401	-0.0395
OSJNBa0020P07.11	Unknown Protein	At1g01090	PDH-E1 ALPHA (PYRUVATE DEHYDROGENASE	0.193	4.2599	5	61.6160	-0.6602	-0.0416

			E1 ALPHA); Pyruvate Dehydrogenase (Acetyl-Transferring)	2					
OSJNBa0024F18.3	Putative NAC-Domain Protein	At4g35580	No Apical Meristem (NAM) Family Protein	0.7197	3.9569	5	91.6110	-0.3877	-0.0354
OSJNBa0025J22.3	Putative Protein Kinase (KIPK)	At4g26610	Protein Kinase, Putative	0.7458	4.2308	5	95.7180	-0.3564	-0.0660
OSJNBa0027P10.3	Putative Peptide Methionine Sulfoxide Reductase	At4g25130	Peptide Methionine Sulfoxide Reductase, Putative	0.2002	3.6866	5	82.8130	-0.5371	-0.1288
OSJNBa0029H02.14	Unknown Protein	At5g48930	Transferase Family Protein	0.3006	4.3478	5	64.4550	-0.1996	-0.0430
OSJNBa0029P06.15	Putative Alpha-Mannosidase	At5g66150	Glycosyl Hydrolase Family 38 Protein	0.2815	2.7230	5	44.2830	0.1367	-0.0292
OSJNBa0032G08.18	Putative 40S Ribosomal Protein	At3g04770	RPSAB (40S Ribosomal Protein SA B); Structural Constituent Of Ribosome	0.1781	1.7562	5	64.6050	-0.5411	-0.0633
OSJNBa0032G11.5	Putative Late Embryogenesis Abundant Protein	At2g44060	Late Embryogenesis Abundant Family Protein / LEA Family Protein	0.2204	3.9874	5	88.0950	-0.5436	-0.0785
OSJNBa0032H19.8	Putative Ribosomal Protein S19	At5g61170	40S Ribosomal Protein S19 (RPS19C)	0.1770	1.7622	5	72.7270	-0.4670	-0.1096
OSJNBa0033P04.2	Putative Rubisco Subunit Binding-Protein Alpha	At2g28000	CPN60A (Chloroplast / 60 Kda Chaperonin Alpha Subunit); ATP Binding / Protein Binding / Unfolded Protein Binding	0.1615	2.1306	5	45.4210	-0.3317	-0.0163
OSJNBa0034D21.15	Putative Antifungal Zeamatin-Like Protein	At4g11650	Atosm34 (Osmotin 34)	0.3041	3.7167	5	96.0350	-0.4211	-0.0472
OSJNBa0035I03.10	Putative Inorganic Pyrophosphatase	At1g15690	AVP1 (Vacuolar-Type H+-Pumping Pyrophosphatase 1)	0.1124	1.6663	5	54.7430	-0.5982	-0.0218
OSJNBa0036B21.6	Unknown Protein	At1g15820	LHCB6 (LIGHT HARVESTING COMPLEX PSII); Chlorophyll Binding	0.1418	3.7990	5	97.5100	-0.4327	-0.0583
OSJNBa0040E01.8	Putative UDP-Glucose Dehydrogenase	At5g15490	UDP-Glucose 6-Dehydrogenase, Putative	0.0811	4.2243	5	96.9090	-0.4269	-0.0352
OSJNBa0042F15.2	Unknown Protein	At5g11560	Catalytic	0.3072	1.9131	5	34.7640	-0.0094	-0.0165
OSJNBa0042F21.13	Unknown Protein	At3g55800	SBPASE (Sedoheptulose-Bisphosphatase); Phosphoric Ester Hydrolase	0.1629	4.2551	5	73.7130	-0.5411	-0.0556
OSJNBa0043A12.14	Unknown Protein	At1g13640	Phosphatidylinositol 3- And 4-Kinase Family Protein	0.3416	3.3173	5	67.3800	-0.3496	-0.0279
OSJNBa0043A12.28	Unknown Protein	At5g43060	Cysteine Proteinase, Putative / Thiol Protease, Putative	0.3371	4.4060	5	70.1830	-0.4159	-0.0536
OSJNBa0043A12.6	Unknown Protein	At5g53300	UBC10 (Ubiquitin-Conjugating Enzyme 10); Ubiquitin-Protein Ligase	0.0369	3.3140	5	63.1940	-0.3698	-0.0932
OSJNBa0044E16.36	Type 1 Membrane Protein -Like	At3g24160	Pmp (Putative Type 1 Membrane Protein)	0.5882	2.1835	5	40.8570	-0.1942	-0.0243
OSJNBa0053L11.26-1	Glutathione Reductase	At3g24170	ATGR1; Glutathione-Disulfide Reductase	0.1931	2.1299	5	44.1810	-0.2226	-0.0264
OSJNBa0055P24.3	Cytoplasmic Malate Dehydrogenase	At5g43330	Malate Dehydrogenase, Cytosolic, Putative	0.0848	1.3959	5	52.7160	-0.5896	-0.0431
OSJNBa0058G03.7	Unknown Protein	At1g29150	ATS9 (19S PROTEOSOME SUBUNIT 9); Binding	0.1062	1.8837	5	47.1790	-0.3741	-0.0242
OSJNBa0059E14.17	Putative Ubiquinol-Cytochrome C Reductase	At5g25450	Ubiquinol-Cytochrome C Reductase Complex 14 Kda Protein, Putative	0.2344	3.3593	5	83.1930	-0.3921	-0.1056
OSJNBa0060K08.43	Putative BTB/POZ Domain-	At3g61600	ATPOB1 (Arabidopsis Thaliana POZ/BTB	0.325	4.4639	5	56.0930	-0.1853	-0.0344

	Containing Protein		Containing-Protein 1); Protein Binding	6					
OSJNBa0061E21.29	Putative TGF-Beta Receptor-Interacting Protein	At2g46280	TRIP-1 (TGF-BETA RECEPTOR INTERACTING PROTEIN 1); Nucleotide Binding	0.1495	4.0871	5	64.3090	-0.6411	-0.0512
OSJNBa0061K21.15	Putative Epimerase/Dehydratase	At5g28840	GME (GDP-D-MANNOSE 3',5'-EPIMERASE); GDP-Mannose 3,5-Epimerase/ NAD Binding / Catalytic	0.0601	4.0670	5	66.8600	-0.6483	-0.0270
OSJNBa0067K08.13	Unknown Protein	At5g16970	AT-AER (ALKENAL REDUCTASE); 2-Alkenal Reductase	0.2647	4.1193	5	94.7370	-0.4593	-0.0496
OSJNBa0067K08.23	Unknown Protein	At3g02470	Samdc (S-Adenosylmethionine Decarboxylase)	0.4242	1.9535	5	52.9890	-0.6404	-0.0384
OSJNBa0067N01.16	Tonoplast Intrinsic Protein	At2g36830	GAMMA-TIP (Tonoplast Intrinsic Protein (TIP) Gamma); Water Channel	0.1361	3.7966	5	96.7210	-0.4533	-0.0772
OSJNBa0068L06.2	Unknown Protein	At5g06900	CYP93D1 (Cytochrome P450, Family 93, Subfamily D, Polypeptide 1); Oxygen Binding	0.5877	4.3826	5	91.7570	-0.3658	-0.0273
OSJNBa0071I13.11	Unknown Protein	At4g30190	AHA2 (Arabidopsis H(+)-Atpase 2); Atpase	0.1041	1.4735	5	63.7800	-0.6890	-0.0130
OSJNBa0071I20.6	Putative Ribosomal Protein S10p/S20e	At3g47370	40S Ribosomal Protein S20 (RPS20B)	0.1558	3.2532	5	84.4260	-0.5319	-0.1823
OSJNBa0071M09.1	Hypothetical Protein	At3g11670	DGD1 (DIGALACTOSYL DIACYLGLYCEROL DEFICIENT 1); Galactolipid Galactosyltransferase	0.3843	4.3449	5	45.4120	-0.0278	-0.0443
OSJNBa0072F16.1	Unknown Protein	At1g12900	Gapa-2	0.1125	4.2114	5	96.9470	-0.4647	-0.0488
OSJNBa0075A22.29	Putative 3-Isopropylmalate Dehydrogenase	At1g80560	3-Isopropylmalate Dehydrogenase, Chloroplast, Putative	0.1885	1.5778	5	54.3310	-0.2059	-0.0248
OSJNBa0076F20.6	Putative Gamma-Lyase	At1g64660	ATMGL; Catalytic/ Methionine Gamma-Lyase	0.2687	4.1218	5	98.4130	-0.4154	-0.0207
OSJNBa0081L15.18	Unknown Protein	At5g40760	G6PD6 (GLUCOSE-6-PHOSPHATE DEHYDROGENASE 6); Glucose-6-Phosphate 1-Dehydrogenase	0.1673	3.9571	5	44.5400	0.1572	-0.0188
OSJNBa0084K11.2	Unknown Protein	At4g00430	TMP-C (Plasma Membrane Intrinsic Protein 1;4)	0.2602	3.9729	5	83.5710	-0.4486	-0.0688
OSJNBa0085K21.33	Tubulin Beta Chain	At5g62700	TUB3 (Tubulin Beta-3); Structural Molecule	0.0420	4.1371	5	82.0820	-0.5376	-0.0362
OSJNBa0087C10.23	Putative Vacuolar Protein Sorting-Associated	At1g75850	Unknown Protein	0.1562	2.1790	5	43.2470	0.0035	-0.0296
OSJNBa0087M10.1	Ribosomal Protein L15	At4g17390	60S Ribosomal Protein L15 (RPL15B)	0.0860	1.9825	5	76.7680	-0.5544	-0.0500
OSJNBa0088H09.11	Unknown Protein	At5g22250	CCR4-NOT Transcription Complex Protein, Putative	0.3923	3.8303	5	95.1920	-0.4293	-0.0246
OSJNBa0088H09.2	Unknown Protein	At3g48990	AMP-Dependent Synthetase And Ligase Family Protein	0.2376	4.4420	5	98.1480	-0.3761	-0.0347
OSJNBa0091C12.3	Unknown Protein	At4g38580	ATFP6 (FARNESYLATED PROTEIN 6); Metal Ion Binding	0.2748	3.3975	5	89.1160	-0.3922	-0.1000
OSJNBa0091J19.11	Putative Actin-Depolymerizing Factor	At2g31200	ADF6 (ACTIN DEPOLYMERIZING FACTOR 6); Actin Binding	0.1462	3.2694	5	54.4780	-0.2748	-0.1069
OSJNBa0094F01.1	Putative 40S Ribosomal Protein S15	At5g09510	40S Ribosomal Protein S15 (RPS15D)	0.0755	1.8193	5	79.4520	-0.4348	-0.1182
OSJNBa0094P09.18	Unknown Protein	At1g17200	Integral Membrane Family Protein	0.4381	3.7869	5	94.4720	-0.4082	-0.1160
OSJNBb0006N15.8	Unknown Protein	At5g02610	60S Ribosomal Protein L35 (RPL35D)	0.110	3.2154	5	92.3080	-0.5839	-0.1301

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OSJNBb0012A20.18	Putative NADPH-Dependent Oxidoreductase	At1g59960	Aldo/Keto Reductase, Putative	0.4133	4.0452	5	87.5000	-0.4524	-0.0664
OSJNBb0012E24.2	Unknown Protein	At3g47420	Glycerol-3-Phosphate Transporter, Putative / Glycerol 3-Phosphate Permease, Putative	0.2558	3.3000	5	63.3470	-0.3423	-0.0285
OSJNBb0015I02.14	Putative Helicase	At2g42520	DEAD Box RNA Helicase, Putative	0.1737	1.9436	5	42.8100	-0.1552	-0.0407
OSJNBb0015I02.15	Serine/Threonine Protein Phosphatase PP2A-2	At2g42500	PP2A-4 (Protein Phosphatase 2A-4); Protein Phosphatase Type 2A/ Protein Serine/Threonine Phosphatase	0.0442	4.0534	5	42.1050	0.1082	-0.0534
OSJNBb0015N08.10	Unknown Protein	At2g19330	Leucine-Rich Repeat Family Protein	0.3430	4.0683	5	89.4260	-0.4651	-0.0315
OSJNBb0020J19.1	Unknown Protein	At1g10940	ASK1 (ARABIDOPSIS SERINE/THREONINE KINASE 1); Kinase	0.1819	4.0459	5	88.4960	-0.5186	-0.0408
OSJNBb0020J19.10	Unknown Protein	At1g77610	Glucose-6-Phosphate/Phosphate Translocator-Related	0.1011	2.2928	5	54.2520	-0.2628	-0.0586
OSJNBb0021A09.5	Unknown Protein	At4g23630	Bti1 (Virb2-Interacting Protein 1)	0.2457	3.8163	5	68.0850	-0.5221	-0.0656
OSJNBb0022F16.7	Unknown Protein	At1g22920	AJH1 (COP9-Signalosome 5A)	0.1479	1.8409	5	60.1190	-0.3982	-0.0458
OSJNBb0024A20.12	Hypothetical Protein	At2g31670	Unknown Protein	0.6230	3.8550	5	96.3300	-0.3446	-0.0683
OSJNBb0024A20.19	Putative 40S Ribosomal Protein	At2g31610	40S Ribosomal Protein S3 (RPS3A)	0.1064	3.7976	5	67.7420	-0.6869	-0.0567
OSJNBb0024J04.9	Putative Dnaj Like Protein	At3g44110	ATJ3 (Arabidopsis Thaliana Dnaj Homologue 3)	0.1248	4.1461	5	70.6810	-0.6530	-0.0343
OSJNBb0036F07.3	Putative Histone H2 Protein	At3g54560	Histone H2A.F/Z	0.1107	2.5206	5	61.8320	-0.5825	-0.1336
OSJNBb0037J12.26	Putative Cytosolic Chaperonin Delta-Subunit	At3g18190	Chaperonin, Putative	0.1784	2.6095	5	61.2770	-0.7013	-0.0283
OSJNBb0042K11.1	Methylenetetrahydrofolate Reductase, 3-Partial	At3g59970	MTHFR1 (METHYLENETETRAHYDROFOLATE REDUCTASE 1); Methylenetetrahydrofolate Reductase (NADPH)	0.1221	4.1389	5	50.4250	-0.2912	-0.0297
OSJNBb0046O12.20	Glycerophosphoryl Diester Phosphodiesterase 2	At1g66980	Protein Kinase Family Protein / Glycerophosphoryl Diester Phosphodiesterase Family Protein	0.5296	3.4574	5	55.4740	-0.4094	-0.1529
OSJNBb0048E02.12	Unknown Protein	At1g24020	Bet V I Allergen Family Protein	0.4293	3.3237	5	98.6110	-0.4399	-0.1439
OSJNBb0048E02.7	Unknown Protein	At5g47000	Peroxidase, Putative	0.4240	4.0179	5	98.1600	-0.4034	-0.0600
OSJNBb0048O22.3	Putative Phosphoenolpyruvate Carboxykinase	At4g37870	ATP Binding / Phosphoenolpyruvate Carboxykinase (ATP)	0.1636	2.9707	5	51.1670	-0.1551	-0.0132
OSJNBb0056B16.16	Putative Vps52 / Sac2 Family Protein	At1g71270	Pok (Poky Pollen Tube)	0.1642	1.5171	5	45.4970	-0.2117	-0.0279
OSJNBb0060J21.1	Putative Ribosomal Protein S18A	At4g09800	RPS18C (S18 RIBOSOMAL PROTEIN); Structural Constituent Of Ribosome	0.0918	3.4261	5	86.3950	-0.5709	-0.0664
OSJNBb0060J21.19	Putative Beta-1,3 Glucanase	At2g19440	Glycosyl Hydrolase Family 17 Protein	0.2788	4.2997	5	95.6610	-0.4736	-0.0401
OSJNBb0062G19.5	Expressed Protein	At5g42960	Unknown Protein	0.4147	3.7170	5	88.5840	-0.4281	-0.0875
OSJNBb0072M01.9	Unknown Protein	At2g20450	60S Ribosomal Protein L14 (RPL14A)	0.122	1.6633	5	72.0930	-0.5995	-0.1299

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OSJNBb0076N15.12	Putative Fiddlehead-Like Protein	At2g26250	FDH (FIDDLEHEAD); Acyltransferase	0.2118	4.3563	5	93.4630	-0.4722	-0.0245
OSJNBb0076N15.5	Putative Alpha 1 Subunit Of 20S Proteasome	At2g05840	PAA2 (20S Proteasome Alpha Subunit A2); Peptidase	0.1072	2.6626	5	62.8820	-0.2311	-0.0606
OSJNBb0081B07.19	Putative Hsp70 Binding Protein	At3g53800	Armadillo/Beta-Catenin Repeat Family Protein	0.2900	3.0312	5	48.3050	-0.2537	-0.0433
OSJNBb0092C08.10	Putative Tawin2	At1g78300	GRF2 (GENERAL REGULATORY FACTOR 2); Protein Phosphorylated Amino Acid Binding	0.1490	3.8859	5	87.7640	-0.4239	-0.0265
P0004D12.9	Leaf Senescence Related Protein-Like	At4g25360	Unknown Protein	0.4876	2.1150	5	46.9730	-0.1197	-0.0502
P0005A05.14	Putative Isoflavone Reductase Homolog IRL	At1g75280	Isoflavone Reductase, Putative	0.3499	4.0188	5	93.9390	-0.4001	-0.0392
P0006C01.14	Beta-Adaptin-Like Protein A	At5g11490	Adaptin Family Protein	0.2000	1.9166	5	48.8110	-0.3061	-0.0243
P0010B10.27	Putative Vacuolar Protein Sorting-Associated	At4g21560	Vacuolar Protein Sorting-Associated Protein 28 Family Protein / VPS28 Family Protein	0.2365	3.7645	5	92.0000	-0.5279	-0.0977
P0018C10.31	Putative Stearoyl-Acyl Carrier Protein	At1g43800	Acyl-(Acyl-Carrier-Protein) Desaturase, Putative / Stearoyl-ACP Desaturase, Putative	0.2562	4.0839	5	96.3170	-0.4537	-0.0528
P0018C10.44	Unknown Protein	At1g21410	F-Box Family Protein	0.2803	3.5825	5	65.3950	-0.3621	-0.0420
P0026F07.24	Putative Caffeoyl-Coa O-Methyltransferase 1	At4g34050	Caffeoyl-Coa 3-O-Methyltransferase, Putative	0.3872	3.7638	5	95.7980	-0.3439	-0.0548
P0036E06.29	Putative Dnak-Type Molecular Chaperone Bip	At5g42020	BIP (LUMINAL BINDING PROTEIN); ATP Binding	0.0771	4.4757	5	70.2340	-0.6808	-0.0310
P0039H02.103	Putative Syntaxin-Related Protein	At5g08080	SYP132 (Syntaxin 132); T-SNARE	0.2776	1.9668	5	44.6430	-0.1556	-0.0525
P0039H02.138-1	Osrad6	At2g02760	ATUBC2 (UBIQUITING-CONJUGATING ENZYME 2); Ubiquitin-Protein Ligase	0.0303	2.9878	5	65.3060	-0.3329	-0.1000
P0410E03.13	Putative H+-Transporting Atpase	At4g32530	Vacuolar ATP Synthase, Putative / V-Atpase, Putative	0.0930	1.3681	5	58.9600	-0.4395	-0.0835
P0410E03.24	Unknown Protein	At5g11420	Unknown Protein	0.2693	4.1399	5	98.5880	-0.4053	-0.0686
P0413A11.18	Peroxisomal Fatty Acid Beta-Oxidation	At4g29010	AIM1 (ABNORMAL INFLORESCENCE MERISTEM); Enoyl-Coa Hydratase	0.2605	2.9296	5	42.7130	-0.0392	-0.0348
P0413C03.8	Putative Selenium Binding Protein	At4g14030	Selenium-Binding Protein, Putative	0.1998	2.6332	5	51.9650	-0.1639	-0.0413
P0413H11.35	Putative Chlorophyll A/B-Binding Protein	At3g47470	LHCA4 (Photosystem I Light Harvesting Complex Gene 4); Chlorophyll Binding	0.1643	3.8056	5	91.3790	-0.4747	-0.0627
P0415B12.4	RNA Binding Protein Rp120	At5g07350	Tudor Domain-Containing Protein / Nuclease Family Protein	0.2310	2.6851	5	40.3740	-0.1830	-0.0190
P0431A03.26	Ribonuclease	At1g26820	RNS3 (RIBONUCLEASE 3); Endoribonuclease	0.3802	3.7255	5	97.7170	-0.3816	-0.1371
P0440D10.18	Putative Tetrafunctional Protein Of Glyoxysomal	At3g06860	MFP2 (MULTIFUNCTIONAL PROTEIN); Enoyl-Coa Hydratase	0.1917	2.1858	5	39.1240	-0.1143	-0.0220
P0452F04.18-2	Putative Non-Transporter ABC Protein Abcf1	At1g64550	ATGCN3 (Arabidopsis Thaliana General Control Non-Repressible 3)	0.0915	2.0939	5	43.8360	-0.1047	-0.0325
P0453E03.111	Putative Translation Elongation Factor Eef-1	At5g19510	Elongation Factor 1B Alpha-Subunit 2 (Eef1balpha2)	0.2039	2.4060	5	60.5770	-0.3148	-0.0754
P0454H12.12	Putative 2,3-Bisphosphoglycerate-	At3g08590	2,3-Biphosphoglycerate-Independent	0.110	3.5077	5	44.8860	-0.4915	-0.0304

	Independent		Phosphoglycerate Mutase, Putative / Phosphoglyceromutase, Putative	2					
P0459B01.28	Putative 60S Ribosomal Protein L12	At2g37190	60S Ribosomal Protein L12 (RPL12A)	0.0937	3.4980	5	95.5130	-0.5168	-0.1175
P0461B08.25	Aquaporin	At4g23400	PIP1;5/PIP1D (Plasma Membrane Intrinsic Protein 1;5); Water Channel	0.0858	1.4407	5	77.5800	-0.5769	-0.0363
P0461D06.32	Putative Elongation Factor 2	At1g56075	Putative Elongation Factor	0.0638	1.9651	5	51.7330	-0.6069	-0.0155
P0468B07.27	Proteasome Subunit Alpha Type 3	At2g27020	PAG1 (20S Proteasome Alpha Subunit G1); Peptidase	0.0997	2.1817	5	44.3480	-0.3088	-0.0502
P0470D12.125	Putative Stress-Related Protein	At3g05500	Rubber Elongation Factor (REF) Family Protein	0.4700	2.7495	5	94.0930	-0.4109	-0.0416
P0482F12.1-1	Bax Inhibitor-1 (BI-1) (Osbi-1)	At5g47120	Atbi-1 (Arabidopsis Bax Inhibitor 1)	0.2048	3.9011	5	76.7630	-0.5884	-0.0743
P0483C08.42	Putative 40S Ribosomal Protein S8	At5g20290	40S Ribosomal Protein S8 (RPS8A)	0.1066	3.4509	5	62.0190	-0.4968	-0.0859
P0483D07.5	Putative Oligosaccharyl Transferase STT3	At5g19690	STT3A (STAUROSPORIN AND TEMPERATURE SENSITIVE 3-LIKE A); Oligosaccharyl Transferase	0.1375	1.7036	5	45.5150	-0.1423	-0.0304
P0485G01.26	Peroxiredoxin	At1g65970	TPX2 (THIOREDOXIN-DEPENDENT PEROXIDASE 2); Antioxidant	0.2080	3.6456	5	63.6360	-0.6066	-0.1698
P0487D09.8	Glutamine Synthetase Shoot Isozyme	At5g37600	ATGSR1 (Arabidopsis Thaliana Glutamine Synthase Clone R1); Glutamate-Ammonia Ligase	0.0859	4.0657	5	74.7750	-0.6509	-0.0309
P0489B03.15	Putative 60S Ribosomal Protein	At1g08360	60S Ribosomal Protein L10A (RPL10aA)	0.0885	3.4897	5	54.0820	-0.4188	-0.0418
P0497A05.15	Unknown Protein	At1g05690	BT3 (BTB And TAZ Domain Protein 3); Protein Binding / Transcription Regulator	0.6260	3.9244	5	92.0250	-0.5151	-0.0628
P0498H04.29	Putative Fructokinase	At4g10260	Pfkb-Type Carbohydrate Kinase Family Protein	0.2092	4.0458	5	94.9530	-0.5097	-0.0604
P0506B12.23	Unknown Protein	At5g18520	Unknown Protein	0.3216	4.2565	5	81.0870	-0.5108	-0.0350
P0506B12.36	40S Ribosomal Protein	At5g02960	40S Ribosomal Protein S23 (RPS23B)	0.0384	3.1279	5	59.2590	-0.5697	-0.1246
P0523B07.46	Putative Ribosomal Protein L17	At1g27400	60S Ribosomal Protein L17 (RPL17A)	0.1317	3.5172	5	60.8700	-0.5771	-0.0918
P0524G08.102	Putative Xylulose Kinase	At5g49650	Xylulose Kinase, Putative	0.2293	2.7379	5	48.7520	-0.1548	-0.0363
P0524G08.123	Transport Protein Particle Component Bet3-Like	At5g54750	Transport Protein Particle (TRAPP) Component Bet3, Putative	0.1060	1.9299	5	56.3950	-0.5312	-0.1118
P0534A03.127	Putative Vacuolar ATP Synthase Subunit H	At3g42050	Vacuolar ATP Synthase Subunit H Family Protein	0.1834	1.9300	5	46.9770	-0.2664	-0.0356
P0544H11.38	26S Proteasome Regulatory Particle Triple-A	At5g19990	ATSUG1; Atpase	0.0469	4.1880	5	51.1450	-0.4103	-0.0488
P0567H04.15	Chlorophyll A/B-Binding Protein	At5g01530	Chlorophyll A-B Binding Protein CP29 (LHCB4)	0.1253	3.8943	5	97.8100	-0.3769	-0.0645
P0582D05.130-1	60S Acidic Ribosomal Protein P0	At2g40010	60S Acidic Ribosomal Protein P0 (RPP0A)	0.1665	1.6637	5	68.1360	-0.6984	-0.0467
P0585B01.3	Putative Proteasome Subunit Alpha Type 1	At5g42790	PAF1 (Proteasome Alpha Subunit F1); Peptidase	0.2324	3.8695	5	73.0090	-0.5059	-0.1110
P0594D10.135	Putative 40S Ribosomal Protein S6	At5g10360	EMB3010 (EMBRYO DEFECTIVE 3010); Structural Constituent Of Ribosome	0.0862	2.0656	5	69.0380	-0.6865	-0.0464

P0616D06.101	Putative 60S Ribosomal Protein L27a	At1g23290	RPL27A (RIBOSOMAL PROTEIN L27A); Structural Constituent Of Ribosome	0.1504	3.2977	5	97.1830	-0.4953	-0.0925
P0616D06.117	Elongation Factor 1 Beta	At1g30230	Elongation Factor 1-Beta / EF-1-Beta	0.2082	2.2052	5	49.0570	-0.4194	-0.0498
P0617A09.16	Putative Potassium Transporter HAK2p	At5g14880	Potassium Transporter, Putative	0.2486	2.6821	5	57.8800	-0.3037	-0.0278
P0623F08.37	Putative Sorbitol Dehydrogenase	At5g51970	Sorbitol Dehydrogenase, Putative / L-Iditol 2-Dehydrogenase, Putative	0.1685	4.2522	5	92.6690	-0.3354	-0.0447
P0643F09.4	Alcohol Dehydrogenase Class III	At5g43940	ADH2 (ALCOHOL DEHYDROGENASE 2); Formaldehyde Dehydrogenase (Glutathione)	0.0705	1.4938	5	52.4860	-0.4040	-0.0580
P0654B04.16-2	WD-40 Repeat Protein-Like	At3g13340	WD-40 Repeat Family Protein	0.1988	3.7570	5	45.3740	-0.1349	-0.0338
P0663C08.13	Putative Vacuolar ATP Synthase Subunit C	At1g12840	Det3 (De-Etiolated 3)	0.1843	2.6392	5	55.4600	-0.5104	-0.0300
P0665C04.10	Putative Pyruvate Dehydrogenase E1 Beta Subunit	At5g50850	Pyruvate Dehydrogenase E1 Component Beta Subunit, PDHE1-B (PDH2)	0.1182	1.8640	5	43.1030	-0.2253	-0.0578
P0666G04.4	Putative Heat-Shock Protein	At1g79930	HSP91 (Heat Shock Protein 91)	0.1631	1.8775	5	48.3030	-0.4048	-0.0205
P0669G09.19	Putative Phosphoglycerate Kinase, Cytosolic	At1g79550	Pgk (Phosphoglycerate Kinase)	0.0984	1.9005	5	55.3190	-0.6038	-0.0289
P0672C09.22	Putative 1-Aminocyclopropane-1-Carboxylate	At2g19590	ACO1 (ACC OXIDASE 1); 1-Aminocyclopropane-1-Carboxylate Oxidase	0.4343	3.9172	5	95.9320	-0.4622	-0.0516
P0672D08.5	Putative 40S Ribosomal Protein S5	At2g37270	ATRPS5B (RIBOSOMAL PROTEIN 5B); Structural Constituent Of Ribosome	0.1292	3.5751	5	82.7230	-0.5882	-0.1050
P0676F10.7	Unknown Protein	At5g15890	Unknown Protein	0.4455	4.1849	5	95.3490	-0.3300	-0.0596
P0676H02.1	Putative Glutathione S-Transferase	At3g09270	ATGSTU8 (Arabidopsis Thaliana Glutathione S-Transferase (Class Tau) 8); Glutathione Transferase	0.4856	3.7358	5	92.1950	-0.5746	-0.0570
P0676H03_3	ADP-Ribosylation Factor	At2g47170	ARF1A1c (ADP-RIBOSYLATION FACTOR 1); GTP Binding / Phospholipase Activator/ Protein Binding	0.0281	2.5038	5	64.7060	-0.6360	-0.0641
P0679C08.30	40S Ribosomal Protein S20	At5g62300	40S Ribosomal Protein S20 (RPS20C)	0.1458	2.3864	5	77.2730	-0.5084	-0.1402
P0681F05.106-2	Putative Thiamine Biosynthesis Protein	At5g54770	Thi1 (Thiazole Requiring)	0.1987	4.0024	5	95.5480	-0.4598	-0.0490
P0683F02.22	Unknown Protein	At3g48410	Hydrolase, Alpha/Beta Fold Family Protein	0.4460	4.1532	5	87.3460	-0.4557	-0.0594
P0684A08.36	Putative Amino Acid Transport Protein	At4g38250	Amino Acid Transporter Family Protein	0.3663	4.2088	5	93.9610	-0.4665	-0.0382
P0690E03.3	Putative 12-Oxophytodienoate Reductase	At2g06050	Opr3 (Opda-Reductase 3)	0.2267	4.2639	5	65.1600	-0.4324	-0.0604
P0696G06.30	Putative 60S Ribosomal Protein L5	At5g39740	60S Ribosomal Protein L5 (RPL5B)	0.1740	1.7972	5	57.8570	-0.6181	-0.0415
P0698G06.1	Putative Sec61 Alpha Form 2	At2g34250	Protein Translocase	0.0609	1.5492	5	44.3960	-0.2436	-0.0398
P0700F06.14	Putative Tumor Differentially Expressed Protein	At1g16180	TMS Membrane Family Protein / Tumour Differentially Expressed (TDE) Family Protein	0.1657	1.5402	5	66.0850	-0.3529	-0.0657
P0701F11.5-1	Putative CBL-Interacting Protein Kinase	At5g10930	CIPK5 (CBL-INTERACTING PROTEIN KINASE 5); Kinase	0.3446	4.2106	5	94.7990	-0.4912	-0.0200
P0703C03.43	60S Ribosomal Protein L7A	At3g62870	60S Ribosomal Protein L7A (RPL7aB)	0.093	3.7805	5	74.0740	-0.6874	-0.0589

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P0706E03.4-1	Putative Eukaryotic Translation Initiation	At1g36730	Eukaryotic Translation Initiation Factor 5, Putative / Eif-5, Putative	0.2336	4.1915	5	52.1950	-0.6124	-0.0236
P0724B10.3-1	Putative Protein Kinase Yaka	At5g35980	Kinase	0.3884	2.9875	5	32.8220	0.3121	-0.0167
W455ERIPDK	Putative GTP-Binding Protein	At1g02130	ATRAB1B (Arabidopsis Thaliana Responsive To Abscisic Acid 1B); GTP Binding	0.0690	3.6432	5	52.8210	-0.2578	-0.0463

Supplementary Table 5: Details of rice-Arabidopsis tissue specific homologous gene-pairs with their corresponding short functional description. Dn represents non-synonymous substitution rates, Ds represents synonymous substitution rates, Exp_rank corresponds to expression rank for individual rice genes, GC_3 represents GC content at synonymous third codon position. wRn stands for error minimization values and FFE represents free folding energy of rice genes

Rice Tissue specific Gene ID	*Functional description*	*Arabidopsis Gene ID*	*Functional description*	*Dn*	*Ds*	*Exp_rank*	*GC_3*	*wRn*	*FFE*
B1029H08.10	Putative Thylakoid Lumenal 21.5 Kda Protein,	At4g15510	Calcium Ion Binding	0.2990	2.2258	1	68.5340	-0.2527	-0.1016
B1040D09.4	Putative RNA Helicase	At5g08610	DEAD Box RNA Helicase (RH26)	0.2765	2.2458	1	49.3670	-0.2445	-0.0345
B1063H10.8	Hypothetical Protein	At4g30410	Unknown Protein	0.7381	3.6047	1	92.4320	-0.4150	-0.1042
B1064G04.16	Similar To Membrane-Associated Salt-Inducible	At1g10910	Unknown Protein	0.4240	4.5767	1	50.9200	-0.0106	-0.0192
B1065E10.20	Putative Serine/Threonine Protein Kinase	At1g11050	Protein Kinase Family Protein	0.5110	4.5865	1	94.2220	-0.4435	-0.0351
B1070A12.16	Hypothetical Protein	At2g16030	Unknown Protein	0.6135	3.2827	1	85.7140	-0.4219	-0.1167
B1074C08.21	Putative RNA-Directed RNA Polymerase	At3g49500	RDR6 (RNA-DEPENDENT RNA POLYMERASE 6); Nucleic Acid Binding	0.3689	5.0978	1	64.4660	-0.1155	-0.0262
B1100D10.34	Putative Serine/Threonine Kinase	At4g27300	S-Locus Protein Kinase, Putative	0.5700	4.7054	1	39.9480	0.3214	-0.0118
B1120F06.101	Aspartate-Glutamate Carrier	At4g39460	SAMC1/SAMT1 (S-ADENOSYLMETHIONINE CARRIER 1, SAM TRANSPORTER1	0.2440	2.1642	1	29.6300	0.1555	-0.0444

			); S-Adenosylmethionine Transporter/ Binding						
B1121A12.18	Putative Auxin-Independent Growth Promoter	At5g15740	Unknown Protein	0.2267	2.2281	1	49.7930	0.0583	-0.0235
B1130G10.20	Unknown Protein	At4g18930	Cyclic Phosphodiesterase	0.5182	3.6360	1	80.0000	-0.3106	-0.1384
B1131B07.15	Putative Zinc Finger Protein	At5g20220	Zinc Knuckle (CCHC-Type) Family Protein	0.3287	3.8758	1	36.9650	0.2923	-0.0405
B1142C05.30	Rev Interacting Protein-Like	At5g08420	RNA Binding	0.2947	1.8766	1	57.5670	-0.5393	-0.0633
B1144D11.19	Putative Glutathione S-Transferase Osgstu4	At1g69920	ATGSTU12 (Arabidopsis Thaliana Glutathione S-Transferase (Class Tau) 12); Glutathione Transferase	0.5496	3.8498	1	96.1370	-0.3959	-0.1092
B1144D11.26	Putative Zinc Protease PQQL	At5g56730	Peptidase M16 Family Protein / Insulinase Family Protein	0.2114	1.9441	1	46.0870	-0.0042	-0.0297
B1147B12.16	Putative Sulfate Transporter-Like	At2g25680	Sulfate Transporter	0.3613	4.4098	1	91.1360	-0.4227	-0.0229
B1148D12.5	Putative Receptor Protein Kinase	At5g49760	Leucine-Rich Repeat Family Protein / Protein Kinase Family Protein	0.4936	4.7852	1	40.2950	0.0906	-0.0113
B1168F12.22	Transporter-Like Protein	At1g78130	UNE2 (Unfertilized Embryo Sac 2); Carbohydrate Transporter/ Sugar Porter	0.2823	3.4873	1	72.7820	-0.4031	-0.0290
B1234D02.6	Unknown Protein	At5g43410	Ethylene-Responsive Factor, Putative	0.5074	2.4717	1	85.7140	-0.1602	-0.1203
B1248C03.14	Unknown Protein	At4g21630	Subtilase Family Protein	0.5509	4.1884	1	54.0540	-0.0284	-0.0447
B1249D05.19	Putative	At1g50060	Pathogenesis-	0.5917	3.4806	1	93.3330	-0.2766	-0.1337

	Pathogenesis-Related Protein		Related Protein, Putative						
B1249D05.22	Putative Pathogenesis-Related Protein	At5g66590	Allergen V5/Tpx-1-Related Family Protein	0.7012	3.5266	1	95.8820	-0.2895	-0.1494
B1250G12.17	Putative Response Regulator	At5g24470	APRR5 (PSEUDO-RESPONSE REGULATOR 5); Transcription Regulator	0.8337	3.5593	1	82.0140	-0.1953	-0.1673
B1250G12.8	Unknown Protein	At3g01440	Oxygen Evolving Enhancer 3 (Psbq) Family Protein	0.7690	3.2583	1	87.9630	-0.5581	-0.1193
B1339H09.17	Putative Monoglyceride Lipase	At1g73480	Hydrolase, Alpha/Beta Fold Family Protein	0.2955	2.0306	1	38.6210	0.2568	-0.0539
B1342F01.34	Putative UDP-Glycosyltransferase 85A8	At1g22370	UDP-Glucoronosyl/UDP-Glucosyl Transferase Family Protein	0.3849	4.2901	1	95.6800	-0.3893	-0.0383
B1364A02.2	Putative LRR Receptor-Like Kinase	At1g17230	Leucine-Rich Repeat Family Protein / Protein Kinase Family Protein	0.3668	5.0467	1	71.1690	-0.4477	-0.0299
H0302E05.5	Putative Protein	At3g21610	Unknown Protein	0.4010	2.3592	1	48.7180	0.0869	-0.1485
OJ000126_13.7	Unknown Protein	At3g52600	ATCWINV2 (ARABIDOPSIS THALIANA CELL WALL INVERTASE 2); Hydrolase, Hydrolyzing O-Glycosyl Compounds	0.3544	4.3374	1	95.1610	-0.4505	-0.0401
OJ1001_G01.3	Putative Transmembrane Protein	At5g12130	Pde149 (Pigment Defective 149)	0.3452	1.7963	1	48.3330	-0.1912	-0.0504
OJ1003_H02.125	Putative RSH, Disease Resistance-Related	At1g54130	RSH3 (RELA/SPOT HOMOLOG 3); Catalytic	0.3900	4.5699	1	59.8920	-0.2779	-0.0402
OJ1004_A11.2	Lipase Class 3-	At5g67050	Lipase Class 3	0.4744	4.2971	1	89.4510	-0.3710	-0.0436

5	Like		Family Protein						
OJ1004_A11.27	Putative Flavonol Synthase	At5g08640	Fls (Flavonol Synthase)	0.3452	4.0410	1	94.7880	-0.3984	-0.0876
OJ1004C08.17	Putative Protein Kinase	At2g17220	Protein Kinase, Putative	0.3734	4.2889	1	86.1410	-0.3472	-0.0505
OJ1014_E02.13	Unknown Protein	At5g49410	Unknown Protein	0.3805	3.3226	1	91.4060	-0.4775	-0.1697
OJ1014_G12.22	Unknown Protein	At2g26690	Nitrate Transporter (NTP2)	0.2618	4.4843	1	99.0880	-0.4620	-0.0304
OJ1019_E02.23	Putative Lectin-Like Protein Kinase	At5g10530	Lectin Protein Kinase, Putative	0.5282	4.4905	1	86.1010	-0.4064	-0.0264
OJ1020_C02.24	Putative Pentatricopeptide (PPR)	At1g02060	Pentatricopeptide (PPR) Repeat-Containing Protein	0.6182	2.7819	1	67.4060	-0.4083	-0.0338
OJ1031_C12.26	Putative Kinetochore Protein	At1g75950	SKP1 (ARABIDOPSIS SKP1 HOMOLOGUE); Ubiquitin-Protein Ligase	0.3169	3.4511	1	84.3140	-0.4669	-0.0844
OJ1058_A12.123	Serine/Threonine Kinase Receptor Precursor-Like	At4g23280	Protein Kinase, Putative	0.6518	2.5898	1	64.8040	-0.3705	-0.0158
OJ1060_D03.125	Amino Acid Acetyltransferase(N-Acetylglutamate	At2g22910	GCN5-Related N-Acetyltransferase (GNAT) Family Protein / Amino Acid Kinase Family Protein	0.3974	1.9142	1	40.1870	-0.0275	-0.0426
OJ1063_D06.13	Putative DNA-Binding Protein	At3g61260	DNA-Binding Family Protein / Remorin Family Protein	0.4461	2.1011	1	68.1530	0.0122	-0.1128
OJ1081D05.5	Putative NADPH-Dependent Oxidoreductase	At1g59950	Aldo/Keto Reductase, Putative	0.3789	3.9622	1	94.6840	-0.5039	-0.0891
OJ1111_E05.24	Putative Latex Protein Allergen	At2g26560	PLP2 (PHOSPHOLIPASE A 2A); Nutrient Reservoir	0.3572	4.2113	1	93.4940	-0.4580	-0.0538
OJ1115_B01.19	Putative Cytochrome P450	At3g26210	CYP71B23 (Cytochrome P450, Family 71,	0.7027	4.4156	1	80.5500	-0.4504	-0.0298

			Subfamily B, Polypeptide 23); Oxygen Binding						
OJ1115_D04.1	Unknown Protein	At1g12790	Unknown Protein	0.3041	1.9592	1	40.2170	-0.1920	-0.0449
OJ1115_D04.4	Putative AAA-Type Atpase	At5g17760	AAA-Type Atpase Family Protein	0.4802	4.3012	1	83.4840	-0.5281	-0.0576
OJ1116_H09.4	Putative Potassium Channel	At5g46370	KCO2 (CA2+ ACTIVATED OUTWARD RECTIFYING K+ CHANNEL 2); Calcium Ion Binding / Outward Rectifier Potassium Channel	0.6365	2.4215	1	43.9680	0.2726	-0.0198
OJ1119_B04.18	Putative Hexose Transporter	At5g26250	Sugar Transporter, Putative	0.3202	4.3416	1	95.9760	-0.4039	-0.0439
OJ1119_D01.22	Putative Armadillo Repeat Containing Protein	At4g21350	B80; Binding / Ubiquitin-Protein Ligase	0.5942	4.2534	1	92.0590	-0.4196	-0.0612
OJ1123_C12.106	Hypothetical Protein	At3g55950	Protein Kinase Family Protein	1.2350	3.6084	1	58.0150	-0.2257	-0.1057
OJ1126_B10.14	Putative Cinnamoyl Coa Reductase	At5g14700	Cinnamoyl-Coa Reductase-Related	0.5448	3.4206	1	82.9550	-0.3744	-0.0478
OJ1135_F06.11	Putative Kelch Repeat-Containing F-Box Family	At1g55270	Kelch Repeat-Containing F-Box Family Protein	0.4664	4.3381	1	92.2550	-0.4442	-0.0253
OJ1135_F06.7	Unknown Protein	At2g25570	Binding	0.2665	2.5745	1	50.7410	-0.3501	-0.0919
OJ1150_A11.26	Two-Component Phosphorelay Mediator HP2	At1g03430	AHP5 (HISTIDINE-CONTAINING PHOSPHOTRANSFER FACTOR 5); Histidine Phosphotransfer Kinase	0.5441	3.4116	1	73.0500	-0.6471	-0.1000
OJ1159_D09.23	Lipase-Like Protein	At4g18550	Lipase Class 3 Family Protein	0.4252	2.4704	1	52.4930	-0.1688	-0.0405
OJ1165_F02.125	Putative ATP-Dependent Proteinase LON2	At5g26860	LON_ARA_ARA (Lon Protease Homolog Gene);	0.1768	3.7008	1	40.5380	-0.0639	-0.0268

			ATP Binding / ATP-Dependent Peptidase/ Serine-Type Peptidase						
OJ1167_G06.104	Hypothetical Protein	At3g56220	Unknown Protein	0.4583	3.0151	1	72.7270	-0.2636	-0.1401
OJ1202_E07.17	Zinc Finger-Like	At3g09320	Zinc Finger (DHHC Type) Family Protein	0.4871	1.8989	1	64.4190	-0.1588	-0.1114
OJ1212_A08.12	Unknown Protein	At1g73240	Unknown Protein	0.4315	1.8041	1	38.4620	0.0880	-0.0447
OJ1212_C01.15	Putative Lung Seven Transmembrane Receptor 1	At3g09570	Unknown Protein	0.4930	4.2668	1	93.8070	-0.4371	-0.0316
OJ1217_D10.10	Endo-1,3	At3g23570	Dienelactone Hydrolase Family Protein	0.5317	3.5968	1	40.2440	0.0420	-0.0671
OJ1217_D10.25	Putative Flavonol 3-Sulfotransferase	At1g28170	Sulfotransferase Family Protein	0.5955	4.0231	1	81.9770	-0.3902	-0.0458
OJ1217_D10.27	Putative Flavonol 3-Sulfotransferase	At5g43690	Sulfotransferase Family Protein	0.6635	4.0553	1	74.9240	-0.3660	-0.0451
OJ1224_G08.21	SWP1 Protein-Like	At3g04740	Swp (Struwwelpeter)	0.2845	1.9879	1	43.4570	-0.3176	-0.0365
OJ1268_B08.20	Hypothetical Protein	At2g12210	Transposable Element Gene	0.5226	4.6327	1	49.8880	0.1534	-0.0046
OJ1276_B06.28	Putative Alliinase	At4g24670	Alliinase Family Protein	0.4082	3.9088	1	85.3750	-0.5805	-0.0705
OJ1281_H05.8	'GTP Cyclohydrolase	At5g59750	Riboflavin Biosynthesis Protein, Putative	0.2806	2.1027	1	58.5460	-0.3866	-0.0155
OJ1288_G09.15	Putative Trehalose-6-Phosphate Phosphatase	At4g12430	Trehalose-6-Phosphate Phosphatase, Putative	0.4442	4.1137	1	85.5910	-0.3194	-0.0542
OJ1294_F06.14	Putative Cytochrome P450	At5g25120	CYP71B11 (Cytochrome P450, Family 71, Subfamily B, Polypeptide 11); Oxygen Binding	0.6537	3.0705	1	62.8850	-0.5002	-0.0324
OJ1311_D08.27	Putative Lysine-Ketoglutarate	At4g33150	Lkr (Saccharopine Dehydrogenase)	0.2280	1.5071	1	35.3490	-0.0257	-0.0877

OJ1323_A06.27	Putative Membrane Protein	At5g07250	Rhomboid Family Protein	0.3022	1.9341	1	63.2590	-0.4334	-0.0706
OJ1345_D02.3	Pentatricopeptide (PPR) Repeat-Containing	At2g44880	Pentatricopeptide (PPR) Repeat-Containing Protein	0.5234	1.9391	1	65.0990	-0.3756	-0.0571
OJ1349_D05.131	Putative Pentatricopeptide (PPR)	At4g02750	Pentatricopeptide (PPR) Repeat-Containing Protein	0.5665	4.5518	1	58.6620	-0.3938	-0.0160
OJ1349_D05.141	Putative Pectinesterase	At4g12420	SKU5 (Skewed 5); Copper Ion Binding	0.3471	3.4316	1	63.9320	-0.3653	-0.0447
OJ1365_D05.10	Putative Response Regulator Protein(Receiver	At3g04280	Arr22 (Arabidopsis Response Regulator 22)	0.6216	3.2661	1	89.1670	-0.3563	-0.1669
OJ1369_G08.6	Putative Polygalacturonase	At1g19170	Glycoside Hydrolase Family 28 Protein / Polygalacturonase (Pectinase) Family Protein	0.2397	1.6398	1	44.0300	-0.2695	-0.0260
OJ1435_F07.24-2	Unknown Protein	At5g45560	Pleckstrin Homology (PH) Domain-Containing Protein / Lipid-Binding START Domain-Containing Protein	0.3638	3.9107	1	50.5660	-0.0980	-0.0447
OJ1448_G06.11	Putative DNA-3-Methyladenine Glycosylase	At3g12040	DNA-3-Methyladenine Glycosylase (MAG)	0.3159	1.4716	1	64.3440	-0.3615	-0.0630
OJ1457_D07.114	GTP-Binding Protein Rab6	At2g44610	RAB6; GTP Binding	0.0637	1.7495	1	56.5660	-0.4178	-0.0740
OJ1477_F01.112	Putative Ferredoxin-Dependent Glutamate	At5g04140	Glu1 (Ferredoxin-Dependent Glutamate Synthase 1)	0.1437	2.2264	1	38.0360	0.0281	-0.0195
OJ1477_F01.115	Phosphatidylinositol-4-Phosphate 5-Kinase-Like	At3g56960	Phosphatidylinositol-4-Phosphate 5-Kinase Family	0.3262	4.6878	1	69.2210	-0.4287	-0.0271

			Protein						
OJ1479_B11.21	Putative Ripening Regulated Protein DDTFR18	At1g47530	Ripening-Responsive Protein, Putative	0.3962	4.3996	1	93.6630	-0.4529	-0.0289
OJ1486_E07.21	Unknown Protein	At2g23940	Unknown Protein	0.2910	3.5644	1	49.6930	-0.2119	-0.0609
OJ1489_G03.3	Putative NAD-/NADP-Dependent Oxidoreductase	At1g54870	Oxidoreductase	0.2297	3.9315	1	91.3790	-0.4119	-0.0282
OJ1489_G03.7	Unknown Protein	At4g15520	Trna/Rrna Methyltransferase (Spou) Family Protein	0.2793	1.7035	1	68.5990	-0.1788	-0.0634
OJ1493_H11.19-1	Putative Inner Membrane	At1g17530	ATTIM23-1; Protein Translocase	0.6001	3.7629	1	92.0630	-0.4373	-0.0714
OJ1513_F02.123	Pentatricopeptide (PPR) Repeat-Containing	At4g37380	Pentatricopeptide (PPR) Repeat-Containing Protein	0.4436	4.6032	1	81.6830	-0.5107	-0.0194
OJ1521_G02.9	Putative Resistance Gene Analog PIC27	At3g50950	Disease Resistance Protein (CC-NBS-LRR Class), Putative	0.8723	4.3586	1	49.6630	0.0424	-0.0393
OJ1524_D08.16	Putative Exopolygalacturonase Precursor	At3g14040	Exopolygalacturonase / Galacturan 1,4-Alpha-Galacturonidase / Pectinase	0.5913	4.2645	1	96.3860	-0.3964	-0.0581
OJ1524_D08.18	Putative 3-Oxoacyl Carrier Protein Synthase	At2g04540	3-Oxoacyl-(Acyl-Carrier-Protein) Synthase II, Putative	0.1710	1.7783	1	34.8210	0.2210	-0.0668
OJ1540_G08.30	Putative SKP1 Interacting Partner 1	At5g57900	Skip1 (Skp1 Interacting Partner 1)	0.4891	4.0102	1	68.3670	-0.2873	-0.0462
OJ1540_H01.10	Putative Receptor Protein Kinase	At1g75820	CLV1 (CLAVATA 1); ATP Binding / Kinase/ Protein Serine/Threonine Kinase	0.3722	4.8224	1	93.7960	-0.4107	-0.0005
OJ1562_B11.1	Unknown Protein	At5g19850	Hydrolase,	0.1777	1.5836	1	38.6500	-0.0719	-0.0707

04			Alpha/Beta Fold Family Protein						
OJ1568_B05.21	NBS-LRR Disease Resistance Protein-Like	At1g58400	Disease Resistance Protein (CC-NBS-LRR Class), Putative	1.0865	3.2697	1	73.2140	-0.3947	-0.1567
OJ1568_B05.26	Ubiquitin-Like Protein	At5g40630	Ubiquitin Family Protein	0.5315	3.4548	1	81.6460	-0.4887	-0.0929
OJ1568_B05.8	Putative Cytochrome P450	At5g63450	CYP94B1 (Cytochrome P450, Family 94, Subfamily B, Polypeptide 1); Oxygen Binding	0.6434	4.0769	1	96.5240	-0.3983	-0.0449
OJ1572_F02.9	Putative Ankyrin Repeat-Containing Protein	At5g20350	Tip1 (Tip Growth Defective 1)	0.2618	4.5170	1	42.2150	0.1878	-0.0312
OJ1575_B01.21	Putative Cyclic Nucleotide-Gated	At3g48010	ATCNGC16 (Cyclic Nucleotide Gated Channel 16); Calmodulin Binding / Cyclic Nucleotide Binding / Ion Channel	0.5364	2.7486	1	44.1500	0.2959	-0.0153
OJ1606_D04.114	Putative Protein Kinase Xa21, Receptor Type	At1g35710	Leucine-Rich Repeat Transmembrane Protein Kinase, Putative	0.8169	4.2544	1	47.6320	-0.1201	-0.0138
OJ1607A12.7	Hypothetical Protein	At3g23020	Pentatricopeptide (PPR) Repeat-Containing Protein	0.4425	2.4970	1	47.2220	-0.1058	-0.0117
OJ1653_D06.5	Putative Phosphoribosylglycinamide	At1g31220	Phosphoribosylglycinamide Formyltransferase	0.2518	1.6877	1	47.3210	-0.1996	-0.0744
OJ1655_B12.20	Putative Nuclear Protein P30	At5g16940	Carbon-Sulfur Lyase	0.3126	3.3507	1	98.6300	-0.4119	-0.1510
OJ1656_A11.6	Similar To Root Cap Protein	At5g54370	Late Embryogenesis Abundant Protein-Related / LEA Protein-Related	0.6601	3.8467	1	94.3570	-0.5042	-0.0840

OJ1657_H11.2	Putative Inosine-Uridine Preferring Nucleoside	At5g18860	Inosine-Uridine Preferring Nucleoside Hydrolase Family Protein	0.3381	4.8087	1	37.6580	0.0359	-0.0209
OJ1695_H09.19	Putative DEAD Box-Like RNA Helicase	At4g15850	ATRH1 (Arabidopsis Thaliana RNA Helicase 1); ATP-Dependent Helicase	0.3381	4.3361	1	40.5800	0.0002	-0.0435
OJ1699_E05.34	Unknown Protein	At5g55170	Sum3 (Small Ubiquitin-Like Modifier 3)	0.6035	3.0180	1	90.0990	-0.4648	-0.1127
OJ1705B08.11	Putative CAF Protein	At1g01040	DCL1 (DICER-LIKE1); ATP-Dependent Helicase/ Ribonuclease III	0.2175	3.1559	1	44.0230	-0.1051	-0.0067
OJ1717_A09.30	Putative Ring Finger Protein	At1g20823	Zinc Finger (C3HC4-Type RING Finger) Family Protein	0.5166	3.6417	1	94.9440	-0.3339	-0.0926
OJ1723_B06.130	Unknown Protein	At5g39650	Unknown Protein	0.7961	3.9040	1	89.6550	-0.4060	-0.0576
OJ1725_H08.12-2	Mechanosensitive Ion Channel Domain-Containing	At1g53470	Mechanosensitive Ion Channel Domain-Containing Protein / MS Ion Channel Domain-Containing Protein	0.4456	3.7614	1	64.6460	-0.4257	-0.0766
OJ1729_E01.2	Putative Serine/Threonine Kinase -Related	At4g05200	Protein Kinase Family Protein	0.6335	2.0929	1	69.4270	-0.4017	-0.0330
OJ1734_E02.41	Putative Atpase	At5g60730	Anion-Transporting Atpase Family Protein	0.3659	2.8799	1	57.6720	0.1217	-0.0638
OJ1734_E04.23	Unknown Protein	At1g25510	Aspartyl Protease Family Protein	1.0119	2.4530	1	56.1980	-0.1851	-0.1240
OJ1743_B12.18	Putative Cell Division Control Protein CDC91	At1g12730	Cell Division Cycle Protein-Related	0.3751	1.7188	1	43.7920	0.2310	-0.0669
OJ1743_B12.3	Putative	At1g49780	U-Box Domain-	0.8957	4.2571	1	94.6970	-0.3841	-0.0315

9	Immediate-Early Fungal Elicitor Protein		Containing Protein						
OJ1743A09.2	Putative Homocysteine S-Methyltransferase-1	At3g25900	ATHMT-1/HMT-1; Homocysteine S-Methyltransferase	0.2844	1.8052	1	73.6840	-0.2464	-0.0641
OJ1754_E06.32	Hypothetical Protein	At1g08070	Pentatricopeptide (PPR) Repeat-Containing Protein	0.5705	4.5878	1	62.8320	-0.5144	-0.0316
OJ1756_H07.55	Putative Pentatricopeptide (PPR)	At5g08490	Pentatricopeptide (PPR) Repeat-Containing Protein	0.5142	4.0506	1	49.0440	-0.2007	-0.0117
OJ1770_H02.15	PIN1-Like Auxin Transport Protein-Like	At5g15100	PIN8 (PIN-FORMED 8); Auxin:Hydrogen Symporter/ Transporter	0.6674	2.6612	1	90.1370	-0.3793	-0.0349
OJ1770_H02.17	Putative Proteasome Subunit Beta Type 1	At3g60820	PBF1 (20S Proteasome Beta Subunit F1); Peptidase	0.1982	3.7712	1	54.2860	-0.1324	-0.0849
OJ1773_H01.113	Putative Lysophospholipase Homolog	At1g11090	Hydrolase, Alpha/Beta Fold Family Protein	0.3428	3.9650	1	93.9100	-0.4392	-0.0731
OJ1791_B03.38	Putative Pentatricopeptide (PPR)	At3g04130	Binding	0.4250	4.2533	1	48.7180	-0.1804	-0.0282
OJ9003_G05.12	Putative Serine/Threonine Kinase	At5g07070	CIPK2 (CBL-INTERACTING PROTEIN KINASE 2); Kinase	0.2726	4.2267	1	40.1750	-0.0047	-0.0122
OJ991113_30.18	Unknown Protein	At1g06710	Pentatricopeptide (PPR) Repeat-Containing Protein	0.3381	4.5832	1	39.7990	-0.0179	-0.0196
OJ991113_30.3	Unknown Protein	At1g67600	Unknown Protein	0.2973	1.8419	1	48.6300	-0.0672	-0.1582
OJ991113_30.7	Unknown Protein	At1g27190	Leucine-Rich Repeat Transmembrane Protein Kinase, Putative	0.4390	4.5450	1	77.9460	-0.4370	-0.0146
OSJNBa0001K	Putative Alcohol	At4g19380	Alcohol Oxidase-	0.5666	4.5962	1	94.7220	-0.3846	-0.0295

12.13	Oxidase		Related						
OSJNBa0001K 12.5	Putative Alcohol Oxidase	At3g23410	Alcohol Oxidase-Related	0.4706	4.5977	1	93.0000	-0.3708	-0.0251
OSJNBa0001O 14.15	Hypothetical Protein	At5g04480	Unknown Protein	0.5140	2.3705	1	45.3490	-0.2114	-0.0244
OSJNBa0002I0 3.18	Putative Inositol Polyphosphate 5-Phosphatase	At1g47510	Endonuclease/Exonuclease/Phosphatase Family Protein	0.3978	4.0467	1	45.1100	0.0627	-0.0429
OSJNBa0002I0 3.19	Putative LIM Domain Containing Protein	At5g17890	LIM Domain-Containing Protein / Disease Resistance Protein-Related	0.5406	4.3180	1	35.8370	0.1783	-0.0152
OSJNBa0004A 10.16	Putative RNA-Binding Protein	At1g74230	GR-RBP5 (Glycine-Rich RNA-Binding Protein 5); RNA Binding	0.4243	2.4649	1	62.6090	-0.4815	-0.2008
OSJNBa0004B 24.15	Putative Cytochrome P450tyr	At2g22330	CYP79B3 (Cytochrome P450, Family 79, Subfamily B, Polypeptide 3); Oxygen Binding	0.4687	4.4092	1	93.5040	-0.4219	-0.0339
OSJNBa0004B 24.22	Putative Membrane-Associated Salt-Inducible	At5g08310	Pentatricopeptide (PPR) Repeat-Containing Protein	1.1074	4.7190	1	59.1410	-0.4854	-0.0251
OSJNBa0004E 08.12	Putative Receptor-Like Protein Kinase	At1g17750	Leucine-Rich Repeat Transmembrane Protein Kinase, Putative	0.7296	5.0219	1	62.4320	-0.2983	-0.0048
OSJNBa0005K 07.3	Putative Kinase	At2g46700	Calcium-Dependent Protein Kinase, Putative / CDPK, Putative	0.2535	4.5567	1	57.9930	-0.0869	-0.0123
OSJNBa0005K 07.4	Putative Serine Peptidase	At4g36190	Serine Carboxypeptidase S28 Family Protein	0.2823	2.5962	1	38.5210	0.1886	-0.0255
OSJNBa0006A 01.11	Unknown Protein	At5g01120	Unknown Protein	0.8548	1.9570	1	57.3770	-0.5178	-0.0326
OSJNBa0006B	Unknown Protein	At3g26540	Pentatricopeptide	0.5991	2.5949	1	57.6700	-0.4754	-0.0282

20.8			(PPR) Repeat-Containing Protein						
OSJNBa0006O15.16	Putative Lecithin-Cholesterol Acyl Transferase	At1g27480	Lecithin:Cholesterol Acyltransferase Family Protein / LACT Family Protein	0.6352	1.5751	1	62.6300	-0.1989	-0.0490
OSJNBa0009L15.1	Unknown Protein	At5g41880	DNA Primase Small Subunit Family	0.3158	2.5223	1	36.7740	-0.0541	-0.0536
OSJNBa0010D21.3	Unknown Protein	At1g74180	Leucine-Rich Repeat Family Protein	0.8845	4.7964	1	45.8700	0.3081	-0.0180
OSJNBa0010E04.19	Putative Ion Antiporter	At3g17630	ATCHX19 (CATION/H+ EXCHANGER 19); Monovalent Cation:Proton Antiporter	0.3302	4.8153	1	93.5830	-0.3694	-0.0259
OSJNBa0013A09.12	Expressed Protein	At1g69450	Unknown Protein	0.6359	2.0630	1	50.2110	-0.1278	-0.0145
OSJNBa0013M12.21	Hypothetical Protein	At5g61190	Zinc Finger Protein-Related	0.4629	3.7143	1	77.6540	-0.3950	-0.0922
OSJNBa0013M12.7	Putative Cytochrome P450-Related Protein	At2g46950	CYP709B2 (Cytochrome P450, Family 709, Subfamily B, Polypeptide 2); Oxygen Binding	0.4676	3.2371	1	58.9800	0.1779	-0.0571
OSJNBa0014M17.24	Putative Immediate-Early Fungal Elicitor	At3g52450	U-Box Domain-Containing Protein	0.5345	4.2818	1	96.3500	-0.3672	-0.0550
OSJNBa0015J15.13	Putative Lipid Transfer Protein	At4g12490	Protease Inhibitor/Seed Storage/Lipid Transfer Protein (LTP) Family Protein	0.3941	3.4583	1	87.6920	-0.4850	-0.0374
OSJNBa0016I09.14	Hypothetical Protein	At5g64700	Nodulin Mtn21 Family Protein	0.5239	4.2198	1	86.0270	-0.3873	-0.0423
OSJNBa0016I09.29	Putative 14-3-3-Like Protein	At1g26480	GRF12 (GENERAL REGULATORY FACTOR 12); Protein	0.3012	2.8247	1	43.6360	-0.3365	-0.0314

			Phosphorylated Amino Acid Binding						
OSJNBa0016N23.106	Putative Beta-Glucosidase Isozyme 2 Precursor	At2g44480	Glycosyl Hydrolase Family 1 Protein	0.4790	4.4086	1	80.3350	-0.4689	-0.0178
OSJNBa0017E08.18	Putative Membrane-Associated Protein	At1g12700	Helicase Domain-Containing Protein / Pentatricopeptide (PPR) Repeat-Containing Protein	1.0185	2.4323	1	48.7270	-0.2952	-0.0372
OSJNBa0018M05.13	Unknown Protein	At3g18620	Zinc Finger (DHHC Type) Family Protein	0.4612	2.0798	1	37.3210	0.1433	-0.0592
OSJNBa0018M05.16	Unknown Protein	At1g48930	Endo-1,4-Beta-Glucanase, Putative / Cellulase, Putative	0.3619	4.4959	1	96.3270	-0.4378	-0.0243
OSJNBa0018M05.21	Unknown Protein	At1g63070	Pentatricopeptide (PPR) Repeat-Containing Protein	1.0321	2.5115	1	68.3210	-0.4566	-0.0454
OSJNBa0018M05.8	Unknown Protein	At3g17670	Binding	0.6471	2.1730	1	70.0850	-0.4411	-0.0648
OSJNBa0019G23.8	Unknown Protein	At3g08980	Signal Peptidase I Family Protein	0.5189	2.5753	1	77.9870	-0.2808	-0.1134
OSJNBa0022H21.21	Unknown Protein	At5g50170	C2 Domain-Containing Protein / GRAM Domain-Containing Protein	0.4879	2.6491	1	54.5740	-0.1370	-0.0181
OSJNBa0023I13.30	Unknown Protein	At1g16080	Unknown Protein	0.2685	3.5275	1	42.8570	0.1912	-0.0965
OSJNBa0023I17.4	Putative Pentatricopeptide (PPR)	At2g36730	Pentatricopeptide (PPR) Repeat-Containing Protein	0.7495	2.7397	1	61.1480	-0.5280	-0.0712
OSJNBa0023I19.10	Putative Purple Acid Phosphatase	At1g14700	ATPAP3/PAP3 (Purple Acid Phosphatase 3)	0.3991	4.9680	1	63.4070	-0.3374	-0.0525
OSJNBa0024K	Expressed	At5g17830	Unknown Protein	0.9748	2.2696	1	47.6790	-0.2611	-0.0449

17.17	Protein								
OSJNBa0026E05.30	Putative Calcium Exchanger (CAX2)	At1g55730	ATCAX5 (Calcium Exchanger 5); Cation:Cation Antiporter	0.3156	1.7627	1	40.9300	0.2624	-0.0251
OSJNBa0027G07.7	Unknown Protein	At1g34580	Monosaccharide Transporter, Putative	0.4320	4.3328	1	96.0180	-0.4322	-0.0363
OSJNBa0027H06.5	Unknown Protein	At3g14540	Terpene Synthase/Cyclase Family Protein	0.9352	2.6798	1	55.6770	-0.1002	-0.0237
OSJNBa0027L23.3	Putative Plastid-Lipid Associated Protein	At2g35490	Plastid-Lipid Associated Protein PAP, Putative	0.4234	4.2449	1	67.6220	-0.4922	-0.0152
OSJNBa0027P08.8	Unknown Protein	At3g02850	SKOR (Stelar K+ Outward Rectifier); Cyclic Nucleotide Binding / Outward Rectifier Potassium Channel	0.3619	3.4666	1	73.8620	-0.3228	-0.0192
OSJNBa0028I23.24	Unknown Protein	At5g45370	Nodulin-Related / Integral Membrane Family Protein	0.9059	2.9090	1	66.0380	-0.2744	-0.0403
OSJNBa0029H02.19	Unknown Protein	At2g24240	Potassium Channel Tetramerisation Domain-Containing Protein	0.2504	4.2656	1	94.9770	-0.4297	-0.0308
OSJNBa0032F06.13	Unknown Protein	At3g59950	Autophagy 4b (APG4b)	0.4308	2.4290	1	45.1540	-0.0120	-0.0305
OSJNBa0032G08.1	Putative Dihydroflavonal-4-Reductase	At4g33360	Terpene Cyclase/Mutase-Related	0.3037	2.8546	1	62.3050	-0.1539	-0.0604
OSJNBa0032H19.14	Unknown Protein	At2g05640	Transposable Element Gene	0.5249	3.3394	1	42.9750	-0.2012	-0.0764
OSJNBa0032I19.1	Unknown Protein	At1g10810	Aldo/Keto Reductase Family Protein	0.3117	4.1613	1	65.6980	-0.5646	-0.0701
OSJNBa0033G16.6	Unknown Protein	At3g11680	Unknown Protein	0.5122	2.9992	1	70.6290	-0.2939	-0.0631
OSJNBa0033P	Putative DNA	At3g23240	ATERF1/ERF1	0.4575	3.4441	1	84.2110	-0.2080	-0.0687

04.20	Binding Protein		(ETHYLENE RESPONSE FACTOR 1); DNA Binding / Transcription Factor/ Transcriptional Activator						
OSJNBa0034B 05.21	Putative Protein Kinase	At1g50700	CPK33 (Calcium-Dependent Protein Kinase 33); Calcium- And Calmodulin-Dependent Protein Kinase/ Kinase	0.9411	4.0384	1	91.4750	-0.4678	-0.0684
OSJNBa0035H 01.10	Putative Cellulose Synthase	At3g03050	CSLD3 (CELLULOSE SYNTHASE-LIKE 3); Cellulose Synthase/ Transferase, Transferring Glycosyl Groups	0.1635	4.9102	1	94.0410	-0.4590	-0.0192
OSJNBa0035I2 4.3	Expressed Protein	At4g33700	CBS Domain-Containing Protein	0.2005	3.0946	1	47.1790	-0.2046	-0.0569
OSJNBa0035M 09.18	Unknown Protein	At4g25870	Unknown Protein	0.3533	1.7291	1	41.2090	0.1918	-0.0230
OSJNBa0038P 21.6	Unknown Protein	At1g62670	Pentatricopeptide (PPR) Repeat-Containing Protein	0.8685	2.4030	1	46.2050	-0.0405	-0.0279
OSJNBa0039K 24.10	Unknown Protein	At5g14130	Peroxidase, Putative	0.7242	4.0791	1	85.0610	-0.3939	-0.0704
OSJNBa0039N 21.16	Putative Transposon Protein	At1g34660	Transposable Element Gene	0.6798	4.2344	1	53.8810	-0.1939	-0.0294
OSJNBa0041A 02.25	Unknown Protein	At5g57550	XTR3 (XYLOGLUCAN ENDOTRANSGLYCOSYLASE 3); Hydrolase, Acting On Glycosyl Bonds	0.4292	3.8662	1	85.4610	-0.4835	-0.0724
OSJNBa0042E	Putative	At3g04260	PTAC3 (PLASTID	0.2771	3.5519	1	44.7490	-0.0644	-0.0048

19.39	Chloroplast RNA Processing Protein		TRANSCRIPTIONALLY ACTIVE3); DNA Binding						
OSJNBa0042H09.16	Hypothetical Protein	At2g45010	Unknown Protein	0.3243	2.5099	1	59.9080	-0.1426	-0.0953
OSJNBa0042I15.19	Unknown Protein	At5g22510	Beta-Fructofuranosidase, Putative / Invertase, Putative / Saccharase, Putative / Beta-Fructosidase, Putative	0.2412	4.4881	1	57.9040	-0.2914	-0.0456
OSJNBa0042L16.16	Unknown Protein	At1g49740	Phospholipase C	0.3360	4.1600	1	88.6930	-0.3997	-0.0559
OSJNBa0042P21.23	Putative Protein Kinase	At1g70520	Protein Kinase Family Protein	0.5403	3.4570	1	63.1080	-0.3361	-0.0308
OSJNBa0042P21.27	Putative Polygalacturonase	At3g26610	Polygalacturonase, Putative / Pectinase, Putative	0.4248	4.3027	1	75.7720	-0.2266	-0.0664
OSJNBa0043A12.38	Unknown Protein	At2g37250	ADK/ATPADK1 (ADENOSINE KINASE); Nucleotide Kinase	0.3151	2.7593	1	59.4590	-0.2424	-0.0902
OSJNBa0043L24.4	Unknown Protein	At3g24320	CHM (CHLOROPLAST MUTATOR); ATP Binding / Damaged DNA Binding	0.2514	2.9448	1	34.3070	0.2853	-0.0056
OSJNBa0045O17.6	Unknown Protein	At3g29732	Transposable Element Gene	0.7684	4.7600	1	52.7810	0.0399	-0.0153
OSJNBa0047A17.6	Putative Copine III	At5g07300	Bon2 (Bonzai 2)	0.3213	1.6959	1	43.1190	0.0423	-0.0527
OSJNBa0050F10.4	Putative Polynucleotide Phosphorylase	At3g03710	RIF10 (RESISTANT TO INHIBITION WITH FSM 10); 3'-5'-Exoribonuclease/ RNA Binding / Nucleic Acid Binding	0.2605	3.0016	1	39.0630	0.0144	-0.0127
OSJNBa0050F10.40	Galactose-1-Phosphate	At5g18200	UDP-Glucose:Hexose-	0.2954	3.6541	1	47.8020	-0.0743	-0.0764

	Uridylyltransferase-Like		1-Phosphate Uridylyltransferase						
OSJNBa0050H14.4	Hypothetical Protein	At1g72620	Hydrolase, Alpha/Beta Fold Family Protein	0.8940	3.9953	1	83.2240	-0.3573	-0.0524
OSJNBa0050N08.17	Putative Selenium-Binding Protein-Like	At2g22410	Pentatricopeptide (PPR) Repeat-Containing Protein	0.5227	2.7798	1	62.4800	-0.2300	-0.0065
OSJNBa0052K15.13-1	Putative Cyclic Nucleotide-Gated	At5g53130	CNGC1 (CYCLIC NUCLEOTIDE GATED CHANNEL 1); Calmodulin Binding / Cation Channel/ Cyclic Nucleotide Binding / Inward Rectifier Potassium Channel	0.2975	4.3827	1	32.5990	0.2101	-0.0263
OSJNBa0052O12.10	Putative Serine Palmitoyltransferase	At5g23670	LCB2 (Serine Palmitoyltransferase LCB2 (Long Chain Base) Subunit Gene); Serine C-Palmitoyltransferase	0.1522	2.5451	1	46.9080	-0.0669	-0.0370
OSJNBa0053B21.10	Unknown Protein	At1g36590	Transposable Element Gene	0.7337	4.4955	1	61.5110	-0.3045	-0.0284
OSJNBa0053C23.23	Hypothetical Protein	At5g52810	Ornithine Cyclodeaminase/ Mu-Crystallin Family Protein	0.5023	4.1148	1	94.0990	-0.4007	-0.0836
OSJNBa0053D03.12	Putative Flavonoid 3'-Hydroxylase	At5g07990	TT7 (TRANSPARENT TESTA 7); Flavonoid 3'-Monooxygenase/ Oxygen Binding	0.3625	2.5334	1	82.2000	-0.4948	-0.0314
OSJNBa0054K20.13	RING Zinc Finger Protein-Like	At4g32600	Zinc Finger (C3HC4-Type RING Finger) Family Protein	0.2349	2.9670	1	38.8300	0.0926	-0.0437

OSJNBa0054K20.23	Unknown Protein	At3g09250	DNA Binding / Nuclease	0.4344	3.8104	1	65.8990	-0.3093	-0.1087
OSJNBa0056A15.4	Putative Receptor-Like Protein Kinase	At4g00960	Protein Kinase Family Protein	0.6955	3.9823	1	35.4230	0.4354	-0.0283
OSJNBa0056E06.4	Expressed Protein	At1g79120	Unknown Protein	0.2978	4.0349	1	45.5090	-0.0938	-0.0306
OSJNBa0056E06.9	Expressed Protein	At1g31300	Unknown Protein	0.2765	1.5160	1	52.4900	-0.0857	-0.0451
OSJNBa0057L21.15	Hypothetical Protein	At5g46920	Intron Maturase, Type II Family Protein	0.3247	4.6750	1	69.6280	-0.3306	-0.0105
OSJNBa0057L21.19	Putative Peroxidase	At5g17820	Peroxidase 57 (PER57) (P57) (PRXR10)	0.5431	3.9463	1	94.6270	-0.4498	-0.0735
OSJNBa0058E19.16	Putative Disease Resistance Protein	At2g25790	Leucine-Rich Repeat Transmembrane Protein Kinase, Putative	0.7563	4.1433	1	57.1030	0.0756	-0.0261
OSJNBa0059G06.4	Putative Mate Efflux Family Protein	At4g22790	MATE Efflux Family Protein	0.4710	4.4554	1	93.1180	-0.3857	-0.0491
OSJNBa0059G06.5	Unknown Protein	At3g60810	Unknown Protein	0.3326	3.7342	1	60.7840	-0.3182	-0.0798
OSJNBa0060A14.12	Putative Glucosyltransferase	At5g03760	ATCSLA09 (RESISTANT TO AGROBACTERIUM TRANSFORMATION 4); Transferase, Transferring Glycosyl Groups	0.3193	2.5831	1	53.0170	-0.1821	-0.0334
OSJNBa0060G17.3	Hypothetical Protein	At5g07790	Unknown Protein	1.1964	3.4170	1	56.5890	-0.1391	-0.0907
OSJNBa0060K08.15	Putative Molybdenum Cofactor Biosynthesis	At2g31950	Molybdopterin Synthase (CNX2)	0.1204	3.9982	1	46.1130	-0.2152	-0.0519
OSJNBa0060M17.1	Putative Polygalacturonase	At3g57510	ADPG1 (Endo-Polygalacturonase 1); Polygalacturonase	0.5250	2.5159	1	75.3490	-0.2493	-0.0484
OSJNBa0060N	Unknown Protein	At5g20810	Calmodulin	0.6531	3.4401	1	95.0920	-0.4535	-0.0858

03.10			Binding						
OSJNBa0061E 21.13	Putative Phosphatidylinositol 3-Kinase	At1g60490	ATVPS34 (Arabidopsis Thaliana Vacuolar Protein Sorting 34); Phosphatidylinositol 3-Kinase	0.2955	2.4594	1	40.5680	0.2426	-0.0233
OSJNBa0062C 05.25	Putative PPR Repeat Containing Protein	At3g60050	Pentatricopeptide (PPR) Repeat-Containing Protein	0.4115	2.6963	1	62.3950	-0.2573	-0.0410
OSJNBa0063C 18.19	Unknown Protein	At1g62640	KAS III (3-KETOACYL-ACYL CARRIER PROTEIN SYNTHASE III); 3-Oxoacyl-[Acyl-Carrier-Protein] Synthase	0.3198	3.4367	1	43.0990	-0.0711	-0.0539
OSJNBa0064M 23.11	Unknown Protein	At3g02310	SEP2 (SEPALLATA2); DNA Binding / Transcription Factor	0.4594	3.5551	1	60.4350	-0.2450	-0.0341
OSJNBa0064M 23.14	Unknown Protein	At5g24530	Oxidoreductase, 2OG-Fe(II) Oxygenase Family Protein	0.2936	4.0773	1	82.9580	-0.5122	-0.0718
OSJNBa0065C 16.15	Putative Beta-Glucosidase	At1g26560	Glycosyl Hydrolase Family 1 Protein	0.2339	4.3712	1	56.7680	-0.0445	-0.0297
OSJNBa0068A 07.23	Putative Lipase	At1g28570	GDSL-Motif Lipase, Putative	0.5926	3.9771	1	90.9090	-0.4679	-0.0424
OSJNBa0068L 06.7	Unknown Protein	At1g58140	Transposable Element Gene; Copia-Like Retrotransposon Family,	0.7615	4.7407	1	41.2050	-0.1896	-0.0143
OSJNBa0070M 12.4	Unknown Protein	At2g35930	U-Box Domain-Containing Protein	0.4831	4.1621	1	95.5610	-0.3883	-0.0363
OSJNBa0070M 12.7	Unknown Protein	At3g15130	Pentatricopeptide (PPR) Repeat-Containing Protein	0.4786	4.7006	1	90.9940	-0.3997	-0.0370

OSJNBa0070N04.6	Putative Kinase	At1g49270	Protein Kinase Family Protein	0.3744	4.3066	1	94.3050	-0.3884	-0.0363
OSJNBa0070N04.9	Unknown Protein	At1g05070	Unknown Protein	0.3580	2.5749	1	62.5770	0.1026	-0.0913
OSJNBa0070O11.10	Unknown Protein	At5g10790	UBP22 (UBIQUITIN-SPECIFIC PROTEASE 22); Ubiquitin-Specific Protease	0.3480	4.1886	1	50.0000	-0.0315	-0.0338
OSJNBa0073A21.16	SAM-Dependent Methyltransferase-Like	At1g54310	RNA Binding	0.2447	2.1335	1	37.1950	-0.0021	-0.0237
OSJNBa0073L01.2	Putative Acetyl-Coa Carboxylase	At1g36160	ACC1 (ACETYL-COENZYME A CARBOXYLASE 1); Acetyl-Coa Carboxylase	0.2025	3.3011	1	39.0430	-0.1101	-0.0068
OSJNBa0073L20.5	Putative CDP-Diacylglycerol Synthetase	At4g26770	Phosphatidate Cytidylyltransferase, Putative / CDP-Diglyceride Synthetase, Putative	0.2169	2.0388	1	47.0170	-0.0969	-0.0309
OSJNBa0075N02.118	Tetratricopeptide Repeat (TPR)-Containing	At5g17270	Tetratricopeptide Repeat (TPR)-Containing Protein	0.4652	1.9954	1	47.0170	-0.0722	-0.0193
OSJNBa0076F20.9	Putative Retrotransposon Polyprotein	At4g21360	Transposable Element Gene	1.1693	2.3529	1	54.6390	-0.4360	-0.0837
OSJNBa0078D06.30	Putative Protein Phosphatase 2C	At3g17090	Protein Phosphatase Type 2C	0.3029	4.2242	1	67.8470	-0.4542	-0.0591
OSJNBa0078K05.12	Putative Sesquiterpene Cyclase	At3g14520	Terpene Synthase/Cyclase Family Protein	0.7611	1.5319	1	41.9350	0.0531	-0.0202
OSJNBa0079M09.14	Unknown Protein	At4g37940	AGL21 (AGAMOUS-LIKE 21); Transcription Factor	0.4859	1.6643	1	59.0240	-0.1139	-0.0405
OSJNBa0081C01.1	Unknown Protein	At2g20770	Lanthionine Synthetase C-Like Family Protein	0.3005	1.9045	1	58.8530	-0.3008	-0.0334
OSJNBa0081C01.5	Unknown Protein	At2g20750	Atexpb1 (Arabidopsis	0.2925	3.8990	1	91.8520	-0.3791	-0.0543

			Thaliana Expansin B1)						
OSJNBa0081P02.1	Hypothetical Protein	At1g25190	Unknown Protein	0.4764	1.9322	1	56.6100	-0.3655	-0.0502
OSJNBa0082M15.18	Putative	At1g63680	PDE316 (PIGMENT DEFECTIVE EMBRYO); ATP Binding / Ligase	0.3667	4.7662	1	64.7400	-0.5582	-0.0129
OSJNBa0083F15.12	Putative Sesquiterpene Synthase	At5g23960	Terpene Synthase/Cyclase Family Protein	0.7098	2.5178	1	34.3610	0.3895	-0.0178
OSJNBa0083M08.1	Putative Trna Synthetase	At5g26707	Unknown Protein	0.1758	4.2006	1	43.6090	-0.1668	-0.0186
OSJNBa0083M16.19	Putative Receptor Kinase	At1g68400	Leucine-Rich Repeat Transmembrane Protein Kinase, Putative	0.4219	4.6299	1	88.4900	-0.3624	-0.0369
OSJNBa0083N12.1	Unknown Protein	At1g21230	WAK5 (WALL ASSOCIATED KINASE 5); Kinase/ Protein Serine/Threonine Kinase	0.6262	3.2186	1	48.2860	-0.2433	-0.0139
OSJNBa0084K01.4	Unknown Protein	At5g03220	Transcriptional Co-Activator-Related	0.1854	2.6569	1	37.8050	0.1119	-0.0182
OSJNBa0084K11.9	Unknown Protein	At1g76040	CPK29 (Calcium-Dependent Protein Kinase 29); Calcium- And Calmodulin-Dependent Protein Kinase/ Kinase	0.2656	4.3867	1	69.3710	-0.2706	-0.0251
OSJNBa0085I10.3	Unknown Protein	At1g79350	EMB1135 (EMBRYO DEFECTIVE 1135); DNA Binding	0.2092	4.7516	1	33.5880	0.3051	-0.0125
OSJNBa0086F04.36	Putative Fertility Restorer Homologue	At5g01110	Pentatricopeptide (PPR) Repeat-Containing Protein	0.9791	2.8619	1	58.4850	-0.3178	-0.0168
OSJNBa0086F	Putative	At1g22990	Heavy-Metal-	0.4172	3.2495	1	93.7930	-0.4558	-0.1633

04.42	Farnesylated Protein		Associated Domain-Containing Protein / Copper Chaperone (CCH)-Related						
OSJNBa0086O06.1	Unknown Protein	At3g60160	ATMRP9 (Arabidopsis Thaliana Multidrug Resistance-Associated Protein 9)	0.2213	2.0701	1	39.9440	0.2245	-0.0134
OSJNBa0086O06.11	Unknown Protein	At3g19380	U-Box Domain-Containing Protein	0.8739	4.2490	1	95.1900	-0.4142	-0.0430
OSJNBa0087F21.31	Putative Plasma Membrane H+-Atpase	At2g18960	AHA1 (PLASMA MEMBRANE PROTON ATPASE); Atpase	0.1659	4.8311	1	93.2600	-0.4884	-0.0200
OSJNBa0088I06.20	Putative Nodulin Mtn21 Protein	At5g07050	Nodulin Mtn21 Family Protein	0.3066	4.1764	1	91.7950	-0.4655	-0.0490
OSJNBa0089K24.3	Hypothetical Protein	At1g24090	Rnase H Domain-Containing Protein	0.7929	3.7342	1	77.5400	-0.3191	-0.0608
OSJNBa0091C07.1	Unknown Protein	At1g74580	Pentatricopeptide (PPR) Repeat-Containing Protein	0.9212	4.6606	1	54.0100	-0.5227	-0.0271
OSJNBa0091C18.37	Putative Actin Related Protein 2	At3g27000	ARP2 (WURM); Structural Constituent Of Cytoskeleton	0.0801	2.6873	1	39.3940	0.0981	-0.0355
OSJNBa0091E13.20	Hypothetical Protein	At3g19540	Unknown Protein	0.2410	2.7686	1	62.0440	-0.7671	-0.0566
OSJNBa0091J19.10	Unknown Protein	At5g44450	Unknown Protein	0.3750	3.8228	1	54.9650	-0.4505	-0.0580
OSJNBa0091J19.14	Hypothetical Protein	At3g12870	Unknown Protein	0.3572	3.7184	1	88.9870	-0.4952	-0.1008
OSJNBa0091P11.22	Putative Pentatricopeptide Repeat Containing	At5g56310	Pentatricopeptide (PPR) Repeat-Containing Protein	0.6594	3.2606	1	67.7480	-0.3938	-0.0308
OSJNBa0091P11.24	Putative Auxin Independent Growth-Related	At2g03280	Unknown Protein	0.2962	2.3026	1	44.4190	-0.2024	-0.0408

OSJNBa0092N12.12	Putative Receptor-Like Protein Kinase	At2g01950	BRL2 (BRI1-LIKE 2); ATP Binding / Protein Serine/Threonine Kinase	0.3150	4.9436	1	94.2510	-0.3951	-0.0093
OSJNBa0093M23.10	Germin-Like Protein	At1g09560	GLP5 (GERMIN-LIKE PROTEIN 5); Manganese Ion Binding / Metal Ion Binding / Nutrient Reservoir	0.3281	3.7958	1	97.6960	-0.4295	-0.0653
OSJNBa0093O08.12	Unknown Protein	At4g14630	GLP9 (GERMIN-LIKE PROTEIN 9); Manganese Ion Binding / Metal Ion Binding / Nutrient Reservoir	0.3405	2.4558	1	72.7270	-0.4796	-0.0791
OSJNBa0093O08.13	Unknown Protein	At3g14580	Pentatricopeptide (PPR) Repeat-Containing Protein	0.5316	4.1602	1	58.5710	-0.0549	-0.0712
OSJNBa0093P23.1	Unknown Protein	At2g13610	ABC Transporter Family Protein	1.0592	3.5275	1	42.4660	0.4155	-0.0526
OSJNBa0094J08.18	Putative Amino Acid Transporter	At5g16740	Amino Acid Transporter Family Protein	0.9994	4.2511	1	93.5480	-0.4082	-0.0483
OSJNBa0095C07.6	Putative Protein Kinase	At5g46570	Protein Kinase Family Protein	0.1483	1.9808	1	62.3970	-0.4507	-0.0508
OSJNBa0096F01.8	Unknown Protein	At3g26290	CYP71B26 (Cytochrome P450, Family 71, Subfamily B, Polypeptide 26); Oxygen Binding	0.6773	4.4115	1	80.4260	-0.3003	-0.0152
OSJNBb0003E08.13	Putative Nitrate Transporter NRT1-5	At5g62680	Proton-Dependent Oligopeptide Transport (POT) Family Protein	0.5068	4.5568	1	94.6400	-0.4531	-0.0277
OSJNBb0003E08.15	Putative Thioredoxin	At5g39950	ATTRX2 (Arabidopsis Thioredoxin H2, Thioredoxin H-Type 1); Thiol-Disulfide	0.4250	3.3541	1	96.0320	-0.3162	-0.1790

			Exchange Intermediate						
OSJNBb0004A17.9	Unknown Protein	At3g50420	Pentatricopeptide (PPR) Repeat-Containing Protein	0.6063	2.1370	1	60.0290	-0.3675	-0.0334
OSJNBb0005B05.10	Unknown Protein	At2g44210	Unknown Protein	0.6302	3.5141	1	34.1460	0.2651	-0.0820
OSJNBb0008A05.2	Unknown Protein	At3g29240	Unknown Protein	0.4430	3.9997	1	97.1010	-0.2704	-0.0541
OSJNBb0008A05.25	Putative Beta-Galactosidase	At5g20710	BGAL7 (Beta-Galactosidase 7); Beta-Galactosidase	0.4552	4.7451	1	60.1020	-0.4655	-0.0301
OSJNBb0011A08.13	Putative Helicase	At3g30560	Transposable Element Gene	0.5831	5.1017	1	42.1950	0.5550	-0.0045
OSJNBb0011H13.3	Unknown Protein	At1g17870	Unknown Protein	0.2559	4.4868	1	93.7840	-0.3583	-0.0116
OSJNBb0011H15.39-1	Putative NADPH-Dependent Reductase	At4g35250	Vestitone Reductase-Related	0.1581	2.6484	1	61.8280	-0.5747	-0.0415
OSJNBb0011H15.4	Putative Auxin Induced Protein	At1g29430	Auxin-Responsive Family Protein	0.5491	3.3572	1	80.4510	-0.3758	-0.0930
OSJNBb0011N17.9	Unknown Protein	At3g01660	Methyltransferase	0.3195	3.9232	1	94.1410	-0.4144	-0.0914
OSJNBb0012E08.6	Unknown Protein	At1g37110	Transposable Element Gene; Copia-Like Retrotransposon Family,	0.3916	4.0005	1	35.0000	-0.2462	-0.0285
OSJNBb0012E08.8	Unknown Protein	At3g26680	Snm1 (Sensitive To Nitrogen Mustard 1)	0.3787	4.3107	1	52.0790	-0.4328	-0.0414
OSJNBb0012I09.11	Putative SKP1	At4g34210	ASK11 (ARABIDOPSIS SKP1-LIKE 11); Ubiquitin-Protein Ligase	0.4457	3.3207	1	94.6670	-0.4771	-0.1019
OSJNBb0012J10.19	Unknown Protein	At5g51170	Unknown Protein	0.3570	3.2835	1	36.0360	0.4106	-0.0750
OSJNBb0013J13.11	Unknown Protein	At5g35820	Transposable Element Gene	0.5140	4.3876	1	35.0550	-0.1401	-0.0292
OSJNBb0013K01.1	Putative Replication Factor C 36kda Subunit	At1g77470	Replication Factor C 36 Kda, Putative	0.1756	1.6978	1	52.5860	-0.1426	-0.0590

OSJNBb0013K01.4	Kinesin Motor Protein 1-Like	At5g06670	Kinesin Motor Protein-Related	0.2872	4.4751	1	48.0470	0.0042	-0.0410
OSJNBb0013K08.2	Putative Multidrug Efflux Protein	At3g26590	MATE Efflux Family Protein	0.4518	2.0788	1	83.0110	-0.4802	-0.0281
OSJNBb0014I10.10	Putative Apyrase	At5g18280	Atapy2 (Apyrase 2)	0.3016	1.9753	1	47.8170	-0.2405	-0.0564
OSJNBb0014I11.9	Putative Nitrate Transporter	At1g12110	NRT1.1 (Nitrate Transporter 1.1); Transporter	0.2965	4.4195	1	98.4350	-0.4536	-0.0318
OSJNBb0014K18.13	Unknown Protein	At2g40900	Nodulin Mtn21 Family Protein	0.3651	4.2176	1	96.0300	-0.4846	-0.0440
OSJNBb0015G09.5	Unknown Protein	At1g11410	S-Locus Protein Kinase, Putative	0.6676	4.7972	1	63.7150	-0.3346	-0.0117
OSJNBb0015I02.17	Putative Acyl-Activating Enzyme	At1g55320	Unknown Protein	0.2646	4.5166	1	34.5610	0.1390	-0.0158
OSJNBb0016D16.6	Unknown Protein	At1g19260	Hat Dimerisation Domain-Containing Protein	0.4720	4.4831	1	32.0570	0.0748	-0.0130
OSJNBb0016H12.23	Unknown Protein	At1g28010	PGP14 (P-GLYCOPROTEIN 14); Atpase, Coupled To Transmembrane Movement Of Substances	1.2824	3.5958	1	75.9260	-0.4890	-0.1069
OSJNBb0018A10.13	Unknown Protein	At1g44070	Transposable Element Gene; CACTA-Like Transposase Family (Tnp2/En/Spm),	0.6681	4.2066	1	52.0640	0.2250	-0.0233
OSJNBb0021C10.25	Hypothetical Protein	At1g51130	Unknown Protein	0.8198	3.6301	1	44.1180	0.1903	-0.0635
OSJNBb0022F23.3	Unknown Protein	At2g04780	Fla7 (Fla7)	0.5819	2.6489	1	90.7340	-0.3535	-0.0814
OSJNBb0022P19.1	Unknown Protein	At2g47800	ATMRP4 (Arabidopsis Thaliana Multidrug Resistance-Associated Protein 4)	0.4293	1.8483	1	61.1030	-0.4419	-0.0159
OSJNBb0024B	Putative Ran	At5g19820	EMB2734	0.2255	2.9683	1	51.2080	-0.1848	-0.0180

16.2	Binding Protein		(EMBRYO DEFECTIVE 2734); Lyase						
OSJNBb0024J04.2	Expressed Protein	At3g58520	Unknown Protein	0.9540	4.2017	1	75.3350	-0.4970	-0.0516
OSJNBb0031B09.22	Putative Lycopene Beta-Cyclase	At3g10230	Lyc (Lycopene Cyclase)	0.2684	4.3534	1	96.8020	-0.4378	-0.0104
OSJNBb0034I13.21	Unknown Protein	At5g39090	Transferase Family Protein	0.8927	4.2873	1	86.7010	-0.3929	-0.0301
OSJNBb0035N21.11	Unknown Protein, Contains Hat Family	At3g42170	Transposase	0.5417	2.5335	1	48.6410	-0.2476	-0.0168
OSJNBb0036F07.1	Hypothetical Protein	At3g04750	Pentatricopeptide (PPR) Repeat-Containing Protein	0.5914	3.0393	1	59.6570	-0.5919	-0.0343
OSJNBb0036F07.12	Putative Beige Protein	At1g03060	WD-40 Repeat Family Protein / Beige-Related	0.2548	3.7636	1	38.4890	-0.0909	-0.0041
OSJNBb0036G09.18	Cytochrome B245 Beta Chain Homolog Rboha	At1g64060	ATRBOH F (RESPIRATORY BURST OXIDASE PROTEIN F); NAD(P)H Oxidase	0.2361	4.8839	1	58.7440	-0.3287	-0.0306
OSJNBb0038A07.4	Putative Glutathione S-Transferase	At1g59700	ATGSTU16 (Arabidopsis Thaliana Glutathione S-Transferase (Class Tau) 16); Glutathione Transferase	0.5252	2.3655	1	91.5560	-0.4697	-0.0801
OSJNBb0040D15.1	Unknown Protein	At3g58670	Unknown Protein	0.3513	3.8478	1	35.9850	0.2652	-0.0712
OSJNBb0040H10.1	Alpha/Beta Hydrolase-Like Protein	At3g29770	Hydrolase, Alpha/Beta Fold Family Protein	0.2231	3.6094	1	49.0680	0.0171	-0.0895
OSJNBb0042J17.15	Putative Pentatricopeptide Repeat-Containing	At2g20540	Pentatricopeptide (PPR) Repeat-Containing Protein	0.4779	4.4861	1	84.8200	-0.3812	-0.0635
OSJNBb0043C10.13	Putative Lysine Decarboxylase-Like Protein	At3g53450	Unknown Protein	0.1840	4.9788	1	72.5890	-0.5280	-0.1114
OSJNBb0044B	Putative Casein	At3g23340	CKL10 (Casein	0.1140	3.9702	1	42.8570	0.2106	-0.0258

19.2	Kinase		Kinase I-Like 10); Casein Kinase I/Kinase						
OSJNBb0044B19.7	Hypothetical Protein	At1g03950	SNF7 Family Protein	0.1697	1.2751	1	44.6150	0.0219	-0.0599
OSJNBb0048A17.1	Casein Kinase II Alpha Subunit, 5'-Partial	At5g67380	CKA1 (CASEIN KINASE ALPHA 1); Kinase	0.0817	3.4936	1	34.2660	0.0230	-0.0867
OSJNBb0048A17.10	Unknown Protein	At1g77360	Pentatricopeptide (PPR) Repeat-Containing Protein	0.3383	3.1973	1	64.8350	-0.5059	-0.0401
OSJNBb0048D20.14	Alpha-Expansin	At2g03090	Atexpa15 (Arabidopsis Thaliana Expansin A15)	0.2272	3.9228	1	96.5910	-0.3839	-0.0356
OSJNBb0048I21.12	Putative GTP-Binding Protein	At4g02790	GTP-Binding Family Protein	0.3221	4.1907	1	49.5770	0.2859	-0.0555
OSJNBb0050N02.3	Unknown Protein	At3g49070	Unknown Protein	0.7074	4.2393	1	93.0360	-0.4330	-0.0359
OSJNBb0050O03.10	Unknown Protein	At3g17360	POK1 (PHRAGMOPLAST ORIENTING KINESIN 1); Microtubule Motor	1.0503	4.1549	1	57.5600	-0.2062	-0.0754
OSJNBb0050O03.15	Unknown Protein	At4g38890	Dihydrouridine Synthase Family Protein	0.3292	3.0839	1	43.5460	-0.2551	-0.0285
OSJNBb0053G03.3	Hypothetical Protein	At2g24970	Unknown Protein	0.5972	2.1761	1	83.4480	-0.3649	-0.1336
OSJNBb0054B09.7	Unknown Protein	At1g20390	Hypothetical Protein	0.7760	4.4139	1	65.3280	-0.4689	-0.0435
OSJNBb0058B20.9	Putative Disease Resistance Response Protein	At1g65870	Disease Resistance-Responsive Family Protein	0.8006	3.7264	1	92.8960	-0.2422	-0.1048
OSJNBb0059K02.9	Unknown Protein	At1g53920	GLIP5 (GDSL-Motif Lipase 5); Carboxylic Ester Hydrolase	1.0529	4.0704	1	86.9570	-0.5342	-0.0330
OSJNBb0060M15.2	Unknown Protein	At1g19920	Aps2 (Atp Sulfurylase Precursor)	0.1288	4.0923	1	53.5930	-0.3176	-0.0346
OSJNBb0061I18.14	Conserved Unknown Protein With Similarity	At1g72320	APUM23 (ARABIDOPSIS PUMILIO 23);	0.5316	2.0895	1	38.8170	-0.1610	-0.0186

	To		RNA Binding						
OSJNBb0061I18.20	Putative Red Chlorophyll Catabolite Reductase	At4g37000	Acd2 (Accelerated Cell Death 2)	0.7152	4.0063	1	96.7150	-0.3389	-0.0541
OSJNBb0062P14.106	Putative Cytochrome P450 77A3	At2g42250	CYP712A1 (Cytochrome P450, Family 712, Subfamily A, Polypeptide 1); Oxygen Binding	1.0301	4.4284	1	84.7110	-0.4178	-0.0190
OSJNBb0065J09.8	Unknown Protein	At3g53150	UGT73D1 (UDP-Glucosyl Transferase 73D1); UDP-Glycosyltransferase	0.6439	4.4016	1	88.0600	-0.4442	-0.0253
OSJNBb0070J16.2	Unknown Protein	At4g21760	BGLU47 (Beta-Glucosidase 47); Hydrolase, Hydrolyzing O-Glycosyl Compounds	0.4256	3.9844	1	72.6280	-0.1043	-0.0820
OSJNBb0070J16.3	Unknown Protein	At1g61820	BGLU46; Hydrolase, Hydrolyzing O-Glycosyl Compounds	0.4399	4.3845	1	68.3440	-0.2147	-0.0360
OSJNBb0072E24.15	Putative Ubiquitin Protein Ligase	At3g53090	UPL7 (Ubiquitin-Protein Ligase 7); Ubiquitin-Protein Ligase	0.3177	2.5911	1	35.4430	0.0602	-0.0141
OSJNBb0075O18.121	Osh45	At5g25220	Knat3 (Knotted1-Like Homeobox Gene 3)	0.1387	3.5543	1	50.9090	-0.0507	-0.0657
OSJNBb0079B02.9	Unknown Protein	At1g14340	RNA Recognition Motif (RRM)-Containing Protein	0.3574	1.8144	1	45.7260	-0.0638	-0.0359
OSJNBb0079B16.5	Putative Pentatricopeptide Repeat Protein	At5g66500	Pentatricopeptide (PPR) Repeat-Containing Protein	0.6206	2.3332	1	50.0000	-0.3571	-0.0214
OSJNBb0088C09.12	Unknown Protein	At1g43580	Unknown Protein	0.2729	1.8212	1	62.9290	-0.4464	-0.0508
OSJNBb0089B	Unknown Protein	At1g08550	Npq1 (Non-	0.3059	4.3424	1	58.7950	-0.2669	-0.0647

03.4			Photochemical Quenching 1)						
OSJNBb0089K 24.8	Unknown Protein	At1g58190	Leucine-Rich Repeat Family Protein	0.9577	1.8217	1	56.6000	-0.2787	-0.0390
OSJNBb0092C 08.31	Putative Glutamate/Malate Translocator	At5g64290	DCT/DIT2.1 (DICARBOXYLATE TRANSPORT); Oxoglutarate:Malate Antiporter	0.2048	1.9989	1	59.4500	-0.3029	-0.0319
OSJNBb0092E 21.11	Putative Gibberellin 20-Oxidase	At5g07200	YAP169 (Gibberellin 20 Oxidase 3); Gibberellin 20-Oxidase	0.4865	4.0783	1	95.1530	-0.3893	-0.0262
OSJNBb0096M 04.15	Putative Cytochrome P450	At3g26330	CYP71B37 (Cytochrome P450, Family 71, Subfamily B, Polypeptide 37); Oxygen Binding	0.5114	4.4232	1	92.9860	-0.4138	-0.0239
OSJNBb0099P 06.1	Unknown Protein	At3g17470	Rela/Spot Domain-Containing Protein / Calcium-Binding EF-Hand Family Protein	0.4391	4.4798	1	89.5720	-0.5496	-0.0448
OSJNBb0111K 12.10	Putative Beta-Glucosidase	At4g27820	Glycosyl Hydrolase Family 1 Protein	0.5010	2.1838	1	51.7860	-0.1429	-0.0264
OSJNBb0118P 14.5	Unknown Protein	At1g76130	AMY2/ATAMY2 (ALPHA-AMYLASE-LIKE 2); Alpha-Amylase	0.2144	3.4999	1	46.2720	-0.1488	-0.0282
P0003E08.6	Hypothetical Protein	At2g42960	Protein Kinase Family Protein	0.2998	4.3531	1	49.1340	-0.2276	-0.0244
P0010C01.19	Putative Beta-Expansin	At4g28250	Atexpb3 (Arabidopsis Thaliana Expansin B3)	0.3352	2.9874	1	86.2830	-0.4397	-0.0468
P0011G08.16	Putative Receptor-Like Protein Kinase	At5g61350	Protein Kinase Family Protein	0.5991	4.7836	1	85.9300	-0.3890	-0.0104
P0013B04.13	Unknown Protein	At3g50340	Unknown Protein	0.4029	4.3107	1	94.2710	-0.3337	-0.0573
P0013G02.12	Putative Ribosomal RNA	At1g55030	F-Box Family Protein	1.5032	4.3442	1	67.2490	-0.5123	-0.0399

	Apurinic Site Specific								
P0018C07.120	Pectin Methylesterase-Like Protein	At5g55590	QRT1 (QUARTET 1); Pectinesterase	0.7279	3.9485	1	88.6210	-0.4937	-0.0346
P0020C11.29-1	Putative Pentatricopeptide (PPR)	At1g09900	Pentatricopeptide (PPR) Repeat-Containing Protein	0.4125	4.4926	1	68.8340	-0.4089	-0.0283
P0020E09.15	Hypothetical Protein	At1g11290	Pentatricopeptide (PPR) Repeat-Containing Protein	0.6131	4.7305	1	62.0080	-0.6437	-0.0095
P0020E09.22	Putative Cinnamoyl-Coa Reductase	At2g02400	Cinnamoyl-Coa Reductase Family	0.3449	4.1213	1	88.6730	-0.4076	-0.0398
P0021G06.114	Putative IAA Amidohydrolase	At3g02875	ILR1 (IAA-LEUCINE RESISTANT 1); Metallopeptidase	0.4133	2.4076	1	76.1120	-0.3836	-0.0037
P0024C06.22	Putative Flavonol 3'-Sulfotransferase	At3g45070	Sulfotransferase Family Protein	0.6651	1.8422	1	67.5080	-0.3468	-0.0397
P0024C06.31	Putative Fatty Acyl Coa Reductase	At5g22500	Acyl Coa Reductase, Putative / Male-Sterility Protein, Putative	0.4335	2.8409	1	70.6520	-0.2922	-0.0274
P0026H03.15	Calcium-Binding EF Hand-Like Protein	At3g24110	Calcium-Binding EF Hand Family Protein	0.5677	3.7357	1	43.4780	0.3446	-0.0496
P0027G10.30-1	Acyl-Activating Enzyme 17-Like Protein	At5g23050	Acyl-Activating Enzyme 17 (AAE17)	0.3573	4.1399	1	45.1520	-0.2403	-0.0348
P0030D07.11	Putative Magnesium/Proton Exchanger	At2g47600	ATMHX (MAGNESIUM/PROTON EXCHANGER); Cation:Cation Antiporter	0.2699	1.9978	1	41.0190	-0.0538	-0.0305
P0031D02.12	Unknown Protein	At3g56290	Unknown Protein	0.3192	3.5581	1	70.0640	-0.1397	-0.0882
P0039H02.111	Putative Prolyl-Trna Synthetase	At5g52520	OVA6 (OVULE ABORTION 6); ATP Binding / Aminoacyl-Trna Ligase	0.1595	1.7451	1	54.0760	-0.2591	-0.0446

P0040H05.31	Unknown Protein	At1g79390	Unknown Protein	0.2044	3.3494	1	75.2000	-0.5147	-0.1445
P0048F12.11	Putative Phospholipid/Glycerol Acyltransferase	At1g02390	ATGPAT2/GPAT2 (GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE 2); Acyltransferase	0.5396	2.7952	1	73.8610	-0.4171	-0.0212
P0135D07.43	Putative CRT/DRE Binding Factor 1	At4g25470	CBF2 (FREEZING TOLERANCE QTL 4); DNA Binding / Transcription Factor/ Transcriptional Activator	0.4937	3.7501	1	84.4340	-0.2805	-0.1004
P0403C05.9	Putative Chorismate Mutase Precursor	At1g69370	CM3 (CHORISMATE MUTASE 3); Chorismate Mutase	0.3104	3.9937	1	52.4160	-0.0772	-0.0850
P0404D10.16	Stress Inducible Protein-Like	At1g22700	Binding	0.2131	2.3243	1	28.0990	0.0765	-0.0705
P0406E03.14-2	GDSL-Motif Lipase/Hydrolase-Like	At2g04570	GDSL-Motif Lipase/Hydrolase Family Protein	0.4251	4.0305	1	87.7250	-0.4969	-0.0659
P0406E03.15	SWIB Complex BAF60b Domain-Containing	At4g26810	SWIB Complex BAF60b Domain-Containing Protein	0.3175	2.0508	1	69.0000	-0.3056	-0.2206
P0406E03.33	Transcriptional Regulators Of Nagc/Xylr	At1g30540	Atpase, Badf/Badg/Bcra/Bcrd-Type Family	0.2924	1.4677	1	44.9850	-0.0889	-0.0824
P0408G07.2	Hypothetical Protein	At2g03880	Pentatricopeptide (PPR) Repeat-Containing Protein	0.6109	4.4426	1	94.9600	-0.4369	-0.0586
P0409B08.4	Putative Transcription Factor	At3g48670	XH/XS Domain-Containing Protein / XS Zinc Finger Domain-Containing Protein	0.5211	4.4044	1	56.1870	-0.4419	-0.0164
P0417F02.7	Hexokinase II	At1g47840	Hexokinase, Putative	0.3247	1.9558	1	56.0420	-0.2053	-0.0442
P0418E08.114	Putative UDP-	At3g11340	UDP-	0.5950	3.0420	1	74.8880	-0.2834	-0.0507

	Glucosyltransferase		Glucoronosyl/UDP-Glucosyl Transferase Family Protein						
P0419A09.30	Putative Ethylene Response Factor	At5g25390	SHN2 (SHINE2); DNA Binding / Transcription Factor	0.3818	3.6392	1	66.3160	-0.3618	-0.0795
P0419A09.34	Putative SPX (SYG1/Pho81/XPR1) Domain-Containing	At2g26660	SPX (SYG1/Pho81/XPR1) Domain-Containing Protein	0.3477	3.8856	1	89.6410	-0.4355	-0.0636
P0419H03.23	Phytosulfokine Receptor Precursor-Like	At1g17240	Leucine-Rich Repeat Family Protein	0.5748	1.8847	1	46.9110	-0.1208	-0.0219
P0431A03.1	Unknown Protein	At1g68660	Unknown Protein	0.2478	2.6488	1	63.3990	-0.3110	-0.1321
P0431B06.14	Pentatricopeptide (PPR) Repeat-Containing	At4g39620	EMB2453 (EMBRYO DEFECTIVE 2453); Binding	0.4204	3.6736	1	50.4950	0.0396	-0.0488
P0431B06.41	Putative Inositol Polyphosphate 5-Phosphatase I	At5g65090	BST1 (BRISTLED1); Hydrolase	0.3963	4.4277	1	77.0090	-0.3649	-0.0120
P0434E03.15	Putative Avr9 Elicitor Response Protein	At5g53340	Transferase, Transferring Hexosyl Groups	0.3069	2.2564	1	47.6490	0.1076	-0.0802
P0435E12.12	Putative 12-Oxophytodienoic Acid Reductase	At1g76680	OPR1 (12-Oxophytodienoate Reductase 1); 12-Oxophytodienoate Reductase	0.2880	1.4795	1	52.8360	-0.1958	-0.0510
P0435E12.43	Unknown Protein	At2g44090	Unknown Protein	0.4166	1.7416	1	58.0360	-0.3625	-0.0726
P0443H10.10	Unknown Protein	At1g51580	KH Domain-Containing Protein	0.9651	4.6378	1	38.1400	0.0070	-0.0361
P0446B05.22	Unknown Protein	At3g55580	Regulator Of Chromosome Condensation (RCC1) Family Protein	0.2971	2.1398	1	45.7560	0.2181	-0.0280
P0446F04.116	Putative 1-Aminocyclopropane-1-Carboxylate	At1g50960	ATGA2OX7 (GIBBERELLIN 2-OXIDASE 7); Gibberellin 2-	0.6198	4.0098	1	93.0380	-0.3436	-0.0305

			Beta-Dioxygenase/ Gibberellin 20-Oxidase						
P0446G09.124	Putative Pentatricopeptide (PPR)	At1g71490	Pentatricopeptide (PPR) Repeat-Containing Protein	0.4821	4.6773	1	58.1710	-0.1881	-0.0337
P0451A10.15	Putative Vacuolar ATP Synthase 16 Kda	At1g19910	AVA-P2 (Vacuolar-H+-Pumping Atpase 16 Kda Proteolipid Subunit 2); Atpase	0.0222	3.6451	1	83.6360	-0.4428	-0.1198
P0452F04.33-1	UDP-Glucoronosyl/UDP-Glucosyl Transferase Family	At1g64100	DNA Binding / Binding	1.0502	4.5225	1	70.1630	-0.4724	-0.0338
P0452F10.16	Hypothetical Protein	At3g24570	Peroxisomal Membrane 22 Kda Family Protein	0.3090	3.6896	1	60.0920	-0.3469	-0.1045
P0453E03.107	Pentatricopeptide (PPR)Repeat-Containing	At1g01970	Pentatricopeptide (PPR) Repeat-Containing Protein	0.5381	2.0914	1	58.7800	0.0113	-0.0280
P0453E03.113	Selenium-Binding Protein-Like	At2g29760	Pentatricopeptide (PPR) Repeat-Containing Protein	0.5190	4.4386	1	66.5360	-0.4547	-0.0268
P0453G03.27	Putative Geranylgeranyl Diphosphate Synthase	At4g36810	GGPS1 (GERANYLGERANYL PYROPHOSPHATE SYNTHASE 1); Farnesyltranstransferase	0.3711	4.2463	1	73.9130	-0.3809	-0.0232
P0453H10.11	Putative Protein Phosphatase 2A 48 Kda	At5g28900	Calcium-Binding EF Hand Family Protein	0.2547	2.5137	1	56.0780	-0.2710	-0.0444
P0454A11.10	NPK1-Related Protein Kinase-Like Protein	At3g07980	MAPKKK6 (MAP3K EPSILON PROTEIN	0.9203	4.2444	1	86.1970	-0.2337	-0.0829

			KINASE 2); Kinase						
P0454A11.19	Putative Flavonoid 3',5'-Hydroxylase	At5g44620	CYP706A3 (Cytochrome P450, Family 706, Subfamily A, Polypeptide 3); Oxygen Binding	0.4740	3.9937	1	86.1860	-0.4034	-0.0334
P0454H12.17	Hypothetical Protein	At5g09950	Pentatricopeptide (PPR) Repeat-Containing Protein	0.7937	2.3838	1	68.2290	-0.1151	-0.0467
P0454H12.5	Unknown Protein	At4g10360	Unknown Protein	0.4743	1.4764	1	53.7550	-0.0477	-0.0642
P0456A01.12	Putative Cytochrome P450	At3g14680	CYP72A14 (Cytochrome P450, Family 72, Subfamily A, Polypeptide 14); Oxygen Binding	0.4210	2.2910	1	58.1780	-0.0660	-0.0476
P0456A01.5	Subtilisin-Like Protease	At5g45650	Subtilase Family Protein	0.4191	4.8050	1	86.8980	-0.3687	-0.0063
P0456B03.116	Inositol Polyphosphate-5-Phosphatase-Like	At2g01900	Endonuclease/Exonuclease/Phosphatase Family Protein	0.4834	4.1946	1	90.6570	-0.4469	-0.0309
P0458A05.17	Hypothetical Protein	At1g74160	Unknown Protein	0.9873	3.3415	1	79.4390	-0.2559	-0.1082
P0458E05.31	Putative Rac Gtpase Activating Protein	At5g22400	Rac Gtpase Activating Protein, Putative	0.2956	3.9155	1	95.8330	-0.4599	-0.0578
P0458E05.6	Putative Chromosome Condensation Factor	At1g76950	Zinc Finger Protein (PRAF1) / Regulator Of Chromosome Condensation (RCC1) Family Protein	0.2964	4.8083	1	32.7630	0.1695	-0.0187
P0458H05.127	Putative Serine/Threonine Kinase Protein	At4g23140	Crk6 (Cysteine-Rich Rlk 6)	0.5849	4.6920	1	74.6330	-0.2366	-0.0232
P0461F06.19	Putative Dioscorin Class A Precursor	At1g08065	Carbonate Dehydratase/ Zinc Ion Binding	0.5500	3.9115	1	74.1440	-0.3246	-0.0462
P0462E11.7	Putative Ubiquinone	At2g47910	Crr6 (Chlororespiratory	0.3436	1.9902	1	57.1430	-0.2547	-0.0640

	Oxidoreductase Subunit 1		Reduction 6)						
P0462H08.5	Unknown Protein	At5g24860	Fpf1 (Flowering Promoting Factor 1)	0.2956	3.0384	1	94.3400	-0.3131	-0.0606
P0468B07.16	Hypothetical Protein	At3g56840	FAD-Dependent Oxidoreductase Family Protein	0.3059	2.2022	1	47.5410	-0.4364	-0.0677
P0468B07.18	Hypothetical Protein	At4g37510	Ribonuclease III Family Protein	0.2110	4.5281	1	69.3230	-0.2258	-0.0265
P0468B07.19	Putative Calmodulin	At3g56800	CAM3 (CALMODULIN 3); Calcium Ion Binding	0.0927	3.2784	1	89.0240	-0.5032	-0.1219
P0470G10.35	Putative DNA J Domain Protein	At1g76700	DNAJ Heat Shock N-Terminal Domain-Containing Protein	0.4352	4.1851	1	62.1780	-0.3525	-0.0440
P0471A11.50	Pentatricopeptide (PPR) Repeat-Containing	At1g73400	Pentatricopeptide (PPR) Repeat-Containing Protein	0.3356	4.3520	1	68.2690	-0.4509	-0.0227
P0475F05.7	Putative CTR1-Like Protein Kinase	At5g03730	CTR1 (CONSTITUTIVE TRIPLE RESPONSE 1); Kinase	0.3873	3.2872	1	56.1330	-0.3490	-0.0290
P0476H10.11	PDR-Like ABC Transporter	At3g53480	ATPDR9/PDR9 (PLEIOTROPIC DRUG RESISTANCE 9); Atpase, Coupled To Transmembrane Movement Of Substances	0.3374	5.2243	1	47.6540	0.0967	-0.0049
P0477A12.6	Putative Ubiquitin / Ribosomal Protein CEP52	At3g52590	UBQ1 (EARLY-RESPONSIVE TO DEHYDRATION 16, UBIQUITIN EXTENSION PROTEIN 1); Protein Binding	0.1585	3.1022	1	88.9710	-0.5644	-0.0972
P0477B05.11	Putative Nicotianamine	At5g36160	Aminotransferase-Related	0.3461	4.3023	1	87.5610	-0.3994	-0.0393

	Aminotransferase A								
P0477F03.101	Unknown Protein	At5g23040	CDF1 (CELL GROWTH DEFECT FACTOR 1); Heat Shock Protein Binding	0.2667	2.0451	1	41.8180	-0.1686	-0.1026
P0480C01.27	Putative MRP Protein (ATP/GTP-Binding Protein)	At3g24430	HCF101 (HIGH-CHLOROPHYLL-FLUORESCENCE 101); ATP Binding	0.1776	3.8105	1	46.9310	0.0507	-0.0311
P0481E12.30	Hypothetical Protein	At5g42660	Hypothetical Protein	0.3442	2.5835	1	50.8970	-0.0809	-0.0337
P0481E12.31	Putative Ribosomal Protein L13	At1g78630	EMB1473 (EMBRYO DEFECTIVE 1473); Structural Constituent Of Ribosome	0.2559	3.7932	1	58.4470	-0.2487	-0.0820
P0481F05.16	Putative Potential Copper-Transporting Atpase	At4g33520	PAA1 (Metal-Transporting P-Type Atpase 1)	0.3027	1.6860	1	43.2020	-0.1448	-0.0053
P0482C06.5	Putative Protein Kinase	At1g62400	HT1 (HIGH LEAF TEMPERATURE 1); Kinase/ Protein Threonine/Tyrosine Kinase	0.3443	3.8755	1	62.7310	-0.3634	-0.0495
P0487H05.39	Putative Importin 7<Ran-Binding Protein 7	At2g31660	SAD2 (SUPER SENSITIVE TO ABA AND DROUGHT2); Protein Transporter	0.2091	3.6953	1	32.4720	0.1583	-0.0160
P0489A01.13	Putative Cytochrome P450	At2g21910	CYP96A5 (Cytochrome P450, Family 96, Subfamily A, Polypeptide 5); Oxygen Binding	0.5709	4.4872	1	69.3110	-0.4408	-0.0129
P0491E01.9	Cyclin-Like	At3g21870	CYCP2;1 (Cyclin P2;1); Cyclin-	0.7696	3.7096	1	95.0250	-0.3632	-0.1071

			Dependent Protein Kinase						
P0492G09.26	Unknown Protein	At5g18630	Lipase Class 3 Family Protein	0.3442	2.6541	1	47.9090	0.0765	-0.0517
P0494D11.1	Putative 3-Glucanase	At4g31140	Glycosyl Hydrolase Family 17 Protein	0.3571	4.3719	1	94.4440	-0.4058	-0.0634
P0496D04.20-1	Putative Integral Membrane Protein	At2g32040	Integral Membrane Transporter Family Protein	0.1343	1.9764	1	35.6540	-0.0145	-0.0276
P0498E12.107	Putative Reticuline Oxidase Precursor	At5g44400	FAD-Binding Domain-Containing Protein	0.6328	4.4723	1	56.1170	-0.2573	-0.0098
P0498H04.1	Putative Bile Acid Beta-Glucosidase	At1g33700	Unknown Protein	0.3775	4.8851	1	79.1860	-0.2524	-0.0137
P0499G10.13-2	GEKO1-Like Protein	At2g03800	Gek1 (Geko1)	0.2580	2.0105	1	49.0910	-0.1768	-0.1369
P0501G01.15	Hypothetical Protein	At5g24030	C4-Dicarboxylate Transporter/Malic Acid Transport Family Protein	0.4539	4.4509	1	95.8130	-0.4178	-0.0220
P0501G04.9	Hydroperoxide Lyase	At4g15440	HPL1 (HYDROPEROXIDE LYASE 1); Heme Binding / Iron Ion Binding / Monooxygenase	0.4455	4.1595	1	97.1740	-0.4587	-0.0563
P0503E05.6	Putative Hydoxyethylthiazole Kinase	At3g24030	Hydroxyethylthiazole Kinase Family Protein	0.3738	1.8856	1	87.0370	-0.4586	-0.0689
P0504A05.25	Integral Membrane Protein-Like	At2g35760	Integral Membrane Family Protein	0.8628	3.7803	1	93.7500	-0.3035	-0.0821
P0506A10.22	Hypothetical Protein	At2g45750	Dehydration-Responsive Family Protein	0.6173	4.5562	1	63.7760	-0.3597	-0.0395
P0506B12.26	Unknown Protein	At3g12360	Ankyrin Repeat Family Protein	0.3265	1.8507	1	51.6540	0.0014	-0.0274
P0506E04.5	Hypothetical Protein	At3g25270	Unknown Protein	1.0674	3.9320	1	47.0390	-0.1026	-0.0271
P0506F02.124	Putative Receptor-Like Protein Kinase 4	At4g23160	Protein Kinase Family Protein	0.8328	3.3865	1	81.0340	-0.3920	-0.1048

P0510F09.22	SPP30 Homolog	At5g58030	Transport Protein Particle (TRAPP) Component Bet3 Family Protein	0.0518	1.7609	1	45.9770	-0.1724	-0.0885
P0515A04.36	Putative NBS-LRR Type Disease Resistance	At4g26090	Rps2 (Resistant To P. Syringae 2)	0.9176	2.6548	1	43.6770	0.1415	-0.0121
P0518C01.9	Putative Cysteine Proteinase	At1g20850	XCP2 (XYLEM CYSTEINE PEPTIDASE 2); Cysteine-Type Peptidase/ Peptidase	0.2831	4.0347	1	89.2540	-0.4046	-0.0425
P0518F01.24	Putative Cytochrome P450	At3g14630	CYP72A9 (Cytochrome P450, Family 72, Subfamily A, Polypeptide 9); Oxygen Binding	0.3703	1.9171	1	52.0450	0.2938	-0.0231
P0519E06.2	Unknown Protein	At2g44850	Unknown Protein	0.6753	2.2810	1	56.9770	-0.3872	-0.0423
P0523B07.7	Putative Flavonol 4'-Sulfotransferase	At5g07010	Sulfotransferase Family Protein	0.5858	2.0398	1	53.2080	-0.1745	-0.0361
P0524F03.3	Exostosin Family-Like Protein	At3g03650	EDA5 (Embryo Sac Development Arrest 5); Catalytic	0.4424	4.3347	1	88.0730	-0.4227	-0.0302
P0528B09.37	Putative Chorimate Mutase	At5g10870	ATCM2 (CHORISMATE MUTASE 2); Chorismate Mutase	0.4308	2.2157	1	62.8250	-0.1729	-0.0546
P0529E05.10	Hypothetical Protein	At3g09060	Pentatricopeptide (PPR) Repeat-Containing Protein	0.5486	1.9405	1	55.1110	-0.4657	-0.0165
P0543C11.29	Putative Nicotianamine Aminotransferase A	At5g53970	Aminotransferase, Putative	0.3871	3.1648	1	56.1610	-0.2139	-0.0372
P0543C11.42	Hypothetical Protein	At1g19480	Hhh-GPD Base Excision DNA Repair Family Protein	0.5812	4.0379	1	33.1150	0.1825	-0.0265
P0543D10.30	Putative	At3g58170	ATBS14A; Protein	0.2047	3.2664	1	43.8600	-0.1510	-0.1116

	Bet1/Sft1-Related SNARE (Atbs14a)		Transporter						
P0544B02.16	Putative Glutamine Amidotransferase Class-I	At2g23970	Defense-Related Protein, Putative	0.4408	3.8831	1	79.4960	-0.3230	-0.0625
P0544B02.31	Putative Protein Phosphatase Type-2C	At4g31860	Protein Phosphatase 2C, Putative / PP2C, Putative	0.1728	4.1245	1	39.4660	0.2585	-0.0315
P0544B02.5	Putative Dem Protein	At4g33400	Dem Protein-Related / Defective Embryo And Meristems Protein-Related	0.3254	4.5335	1	77.9030	-0.4282	-0.0265
P0544G09.25	Putative P450 Monooxygenase	At4g12310	CYP706A5 (Cytochrome P450, Family 706, Subfamily A, Polypeptide 5); Oxygen Binding	0.4686	4.1472	1	98.5760	-0.4223	-0.0520
P0544G09.37	Putative Armadillo Repeat Containing Protein	At5g66200	Armadillo/Beta-Catenin Repeat Family Protein	0.2858	4.3767	1	93.2450	-0.4626	-0.0223
P0544H11.26	Putative Cytochrome P450 Monooxygenase	At2g26710	BAS1 (PHYB ACTIVATION TAGGED SUPPRESSOR 1); Oxygen Binding	0.3495	4.4158	1	92.3810	-0.3448	-0.0118
P0554D10.26	Bromelain-Like Thiol Protaease	At2g34080	Cysteine Proteinase, Putative	0.5383	4.0060	1	96.1990	-0.3857	-0.0420
P0554F08.13	Putative Peptidyl-Trna Hydrolase (PTH)	At1g18440	Peptidyl-Trna Hydrolase Family Protein	0.2861	2.3858	1	47.7880	-0.2877	-0.0949
P0554F08.4	Putative P-Glycoprotein	At2g47000	PGP4 (P-GLYCOPROTEIN 4, P-GLYCOPROTEIN 4); Atpase, Coupled To Transmembrane Movement Of	0.2917	1.6845	1	60.0000	-0.1311	-0.0147

			Substances / Xenobiotic-Transporting Atpase						
P0567H04.24	Membrane Lipoprotein Lipid Attachment	At5g54240	Unknown Protein	0.3881	4.0103	1	98.0840	-0.3343	-0.1095
P0574F11.5	Pentatricopeptide (PPR) Repeat-Containing	At1g16480	Pentatricopeptide (PPR) Repeat-Containing Protein	0.7224	2.6175	1	52.5750	-0.3679	-0.0202
P0576F08.31	Hypothetical Protein	At5g17670	Hydrolase	0.2682	2.1029	1	58.1310	-0.2049	-0.0557
P0583G08.11	Putative Receptor-Like Kinase	At4g33430	BAK1 (BRI1-ASSOCIATED RECEPTOR KINASE); Kinase	0.5368	2.3323	1	49.9010	-0.1302	-0.0530
P0584E12.40-1	Unknown Protein	At5g15880	Unknown Protein	0.4298	1.5720	1	52.2290	-0.5154	-0.0681
P0599F09.21	Putative Strictosidine Synthase	At1g74000	Ss3 (Strictosidine Synthase 3)	0.7736	4.1223	1	92.8570	-0.3808	-0.0706
P0614D08.19	Hypothetical Protein	At3g10140	Reca Family Protein	0.4280	1.5978	1	40.5510	-0.3312	-0.0349
P0616D06.120	Putative Ids-4 Protein	At2g45130	SPX (SYG1/Pho81/XPR1) Domain-Containing Protein	0.3648	3.7552	1	94.1180	-0.3796	-0.0824
P0617H07.4	Putative MRP-Like ABC Transporter	At3g21250	ATMRP6 (Arabidopsis Thaliana Multidrug Resistance-Associated Protein 6)	0.3806	5.2207	1	72.1430	-0.2428	-0.0119
P0620H05.3	Putative Pentatricopeptide (PPR)	At4g31850	PGR3 (PROTON GRADIENT REGULATION 3); Binding	0.9458	4.6054	1	57.1670	-0.3725	-0.0257
P0625E02.103	Putative Triacylglycerol Lipase	At5g18640	Lipase Class 3 Family Protein	0.3862	2.1351	1	43.8810	-0.0890	-0.0364
P0625E02.108-2	DNA Polymerase Zeta Catalytic Subunit-Like	At1g67500	ATREV3 (Arabidopsis Thaliana Recovery Protein	0.2958	3.3039	1	61.8710	-0.2173	-0.1493

			3); DNA Binding						
P0627E03.1	Tetratricopeptide Repeat(TPR)-Containing	At5g65160	Tetratricopeptide Repeat (TPR)-Containing Protein	0.3944	3.7497	1	90.5470	-0.4410	-0.0894
P0627E03.18	Putative Histidine-Trna Ligase	At3g46100	ATHRS1 (HISTIDYL-TRNA SYNTHETASE 1); Histidine-Trna Ligase	0.3211	4.4335	1	49.5500	-0.1437	-0.0308
P0627E03.20	Disulfide Isomerase	At1g34780	ATAPRL4 (APR-LIKE 4); Electron Carrier/ Protein Disulfide Oxidoreductase	0.4675	1.7954	1	48.1230	-0.1838	-0.0572
P0643A10.51	Putative Caleosin	At1g70670	Caleosin-Related Family Protein	0.4615	2.6837	1	61.9510	-0.1105	-0.0217
P0643F09.7	Exoribonuclease-Like	At5g38890	Exoribonuclease-Related	0.2521	1.2540	1	58.4700	-0.3258	-0.0859
P0654B04.5	Putative Chloride Channel Protein	At1g55620	CLC-F (CHLORIDE CHANNEL F); Voltage-Gated Chloride Channel	0.3131	2.5397	1	44.4740	-0.0289	-0.0229
P0665C04.3	PHO85-Like Protein	At3g02040	SRG3 (SENESCENCE-RELATED GENE 3); Glycerophosphodiester Phosphodiesterase	0.4481	2.0401	1	55.9230	-0.2035	-0.0755
P0666G10.106	Putative Pentatricopeptide (PPR)	At3g12770	Pentatricopeptide (PPR) Repeat-Containing Protein	0.7389	4.5351	1	42.9600	-0.1521	-0.0198
P0669G09.17	Unknown Protein	At1g56180	Unknown Protein	0.2832	1.7115	1	57.6270	-0.3267	-0.0363
P0669G10.7	Putative Glyoxalase I	At1g67280	Lactoylglutathione Lyase, Putative / Glyoxalase I, Putative	0.1011	3.9967	1	77.7780	-0.4079	-0.0834
P0671B11.20	Putative 1-Aminocyclopropane-1-Carboxylic Acid	At4g26200	ACS7 (1-Amino-Cyclopropane-1-Carboxylate Synthase 7); 1-Aminocyclopropa	0.2668	4.2324	1	93.0180	-0.4451	-0.0605

			ne-1-Carboxylate Synthase						
P0671D01.4	Hypothetical Protein	At3g12470	Nucleic Acid Binding	0.7711	3.6192	1	92.3770	-0.4800	-0.1103
P0671F11.27	Putative 2-Oxoglutarate-Dependent Oxygenase	At2g30830	2-Oxoglutarate-Dependent Dioxygenase, Putative	0.4939	4.1230	1	94.4290	-0.4278	-0.0226
P0672D08.4	Hypothetical Protein	At5g16520	Unknown Protein	0.5278	2.6448	1	57.6170	-0.2781	-0.0372
P0676H02.7	Putative Ripening Regulated Protein DDTFR18	At5g65380	Ripening-Responsive Protein, Putative	0.3788	2.1739	1	77.8970	-0.5014	-0.0402
P0680F05.36	Phosphate/Phosphoenolpyruvate Translocator	At3g14410	Transporter-Related	0.2895	2.8635	1	50.8930	-0.1877	-0.0477
P0681F05.132	Hypothetical Protein	At4g05220	Harpin-Induced Protein-Related / HIN1-Related / Harpin-Responsive Protein-Related	0.5327	3.6284	1	97.9590	-0.4051	-0.1115
P0683B11.27	Hypothetical Protein	At3g12630	Zinc Finger (AN1-Like) Family Protein	0.5732	3.4184	1	91.4890	-0.3491	-0.1209
P0683F02.6	Putative 3-Deoxy-D-Manno-Octulosonic-Acid	At5g03770	3-Deoxy-D-Manno-Octulosonic Acid Transferase-Related	0.4411	2.5213	1	49.5390	-0.2339	-0.0659
P0684F11.21	Putative Avr9/Cf-9 Rapidly Elicited Protein 231	At1g70090	GATL9/LGT8 (Galacturonosyltransferase-Like 9); Polygalacturonate 4-Alpha-Galacturonosyltransferase/ Transferase, Transferring Glycosyl Groups / Transferase, Transferring Hexosyl Groups	0.3923	4.1644	1	88.7640	-0.2564	-0.0440
P0686H11.17	Zinc Finger	At2g04240	XERICO; Protein	0.6797	3.5189	1	97.5460	-0.3094	-0.1216

	Protein Family-Like		Binding / Zinc Ion Binding						
P0686H11.32	Unknown Protein	At5g56050	Unknown Protein	0.5488	3.8452	1	90.8700	-0.3290	-0.0358
P0689E12.32	Putative Energy Transfer Protein	At3g20240	Substrate Carrier Family Protein	0.2827	1.7759	1	54.5710	-0.4836	-0.0447
P0696F12.9	Putative Serine/Threonine-Specific Protein	At4g38830	Protein Kinase Family Protein	0.7124	4.6063	1	63.0650	-0.4643	-0.0274
P0698G06.3	Putative Histone Acetyltransferase HAT B	At5g56740	Histone Acetyltransferase Family Protein	0.4736	1.5480	1	50.8120	-0.4522	-0.0322
P0700F06.32	Translation Initiation Factor IF-3-Like	At2g24060	Translation Initiation Factor 3 (IF-3) Family Protein	0.3535	3.6323	1	39.1060	0.3236	-0.0640
P0701F11.30	Zinc Finger (C3HC4-Type RING Finger)-Like	At3g53690	Zinc Finger (C3HC4-Type RING Finger) Family Protein	0.5632	3.7242	1	90.0500	-0.3902	-0.0819
P0702F05.10	Unknown Protein	At4g23850	Long-Chain-Fatty-Acid--Coa Ligase / Long-Chain Acyl-Coa Synthetase	0.2688	2.6951	1	42.9280	0.0326	-0.0300
P0702G08.13	Unknown Protein	At5g46950	Invertase/Pectin Methylesterase Inhibitor Family Protein	1.3604	1.8347	1	94.2710	-0.4451	-0.0675
P0705A05.133	Putative SET1	At4g13460	SUVH9 (SU(VAR)3-9 HOMOLOG 9); Histone-Lysine N-Methyltransferase / Zinc Ion Binding	0.5581	4.4608	1	85.1920	-0.5063	-0.0148
P0706E03.9	Apospory-Associated Protein C-Like	At5g66530	Aldose 1-Epimerase Family Protein	0.2601	4.0678	1	49.5050	-0.0165	-0.0257
P0707D10.20	Unknown Protein	At5g11320	YUC4 (YUCCA4); Monooxygenase	0.3370	4.3215	1	80.4690	-0.4062	-0.0441
P0708B04.21	Putative Senescence-Associated Protein	At2g23810	Tet8 (Tetraspanin8)	0.4196	3.9273	1	97.0590	-0.4938	-0.0679
P0711F01.51	ATP-Binding Cassette Transporter	At3g47780	ATATH6 (ABC2 Homolog 6); Atpase, Coupled	0.5324	2.2736	1	38.1760	-0.1097	-0.0225

	Atabca1-Like		To Transmembrane Movement Of Substances						
PPR683	Hypothetical Protein	At1g63130	Pentatricopeptide (PPR) Repeat-Containing Protein	0.8473	3.0009	1	45.5400	-0.2258	-0.0341
PPR762	Hypothetical Protein	At1g62910	Pentatricopeptide (PPR) Repeat-Containing Protein	0.7729	4.1928	1	50.2080	-0.3626	-0.0290
B1120F06.107	Unknown Protein	At1g24310	Hypothetical Protein	0.3525	2.1657	3	60.2600	-0.3295	-0.0268
B1130G10.10	Putative Protein Kinase	At1g52290	Protein Kinase Family Protein	0.4517	3.9628	3	78.9300	-0.4641	-0.0675
B1130G10.4	Hypothetical Protein	At5g46020	Unknown Protein	0.2161	3.4128	3	49.3060	-0.4935	-0.1110
B1143G03.3	Hypothetical Protein	At5g42410	Auxin-Responsive Family Protein	0.8507	3.2963	3	84.9060	-0.2978	-0.1523
OJ1001_D02.30	Pentatricopeptide (PPR) Repeat-Containing	At5g39350	Pentatricopeptide (PPR) Repeat-Containing Protein	0.5998	1.9176	3	62.6960	-0.3983	-0.0169
OJ1005_D12.35	Unknown Protein	At4g33590	Hypothetical Protein	0.5292	4.2818	3	94.5880	-0.3473	-0.0365
OJ1007_D04.17	Putative Anthranilate Phosphoribosyltransferase	At1g70570	Anthranilate Phosphoribosyltransferase, Putative	0.2197	4.8227	3	49.1620	0.0356	-0.0455
OJ1058_A12.128-2	Contains EST(S): D22146(C10415)	At4g04500	Protein Kinase Family Protein	0.7759	1.9659	3	64.8370	-0.2772	-0.0286
OJ1112_G03.18	Unknown Protein	At5g23850	Unknown Protein	0.2688	4.1151	3	59.4900	-0.2643	-0.0603
OJ1115_A05.12-1	Putative RCH2 Protein	At3g21670	Nitrate Transporter (NTP3)	0.3310	4.5266	3	95.9040	-0.4463	-0.0338
OJ1118_C04.7	Putative SMC Protein	At5g48600	ATSMC3 (Arabidopsis Thaliana Structural Maintenance Of Chromosome 3); ATP Binding	0.2194	5.0077	3	39.8370	0.1103	-0.0231
OJ1123_G09.2	Hypothetical	At5g19020	Pentatricopeptide	0.5459	4.6292	3	53.5140	-0.3468	-0.0139

1	Protein		(PPR) Repeat-Containing Protein						
OJ1124_D06.17	Pentatricopeptide Repeat-Containing	At5g48910	Pentatricopeptide (PPR) Repeat-Containing Protein	0.7083	4.3994	3	95.7540	-0.4440	-0.0518
OJ1134F05.20	Hypothetical Protein	At2g48000	Pentatricopeptide (PPR) Repeat-Containing Protein	1.3081	1.8544	3	53.8670	-0.2206	-0.0738
OJ1177_E11.3	Putative Oxysterol Binding Protein	At4g22540	Oxysterol Binding	0.3898	4.6633	3	53.4020	-0.1002	-0.0187
OJ1200_C08.105	Carbonyl Reductase -Like Protein	At2g24190	Short-Chain Dehydrogenase/Reductase (SDR) Family Protein	0.4600	4.0531	3	57.1430	-0.1477	-0.0416
OJ1261C08.11	Hypothetical Protein	At2g39710	Aspartyl Protease Family Protein	0.4533	4.3068	3	93.6770	-0.3060	-0.0432
OJ1282_E10.12-2	Putative Na+/H+ Antiporter	At2g31910	Atchx21 (Cation/H+ Exchanger 21)	0.8865	4.6575	3	92.5100	-0.4363	-0.0172
OJ1282_E10.7	Pentatricopeptide (PPR) Repeat-Containing	At2g27610	Pentatricopeptide (PPR) Repeat-Containing Protein	0.9545	4.6821	3	84.8350	-0.4448	-0.0264
OJ1343_B12.129	Putative Kinetochore Protein	At1g20140	ASK4 (ARABIDOPSIS SKP1-LIKE 4); Ubiquitin-Protein Ligase	0.3149	3.2944	3	88.4620	-0.3027	-0.0895
OJ1351_C05.110	S-Receptor Kinase PK3 Precursor-Like Protein	At1g67000	Kinase	0.7942	4.2827	3	87.2040	-0.3680	-0.0164
OJ1372_D12.114	Putative PDR-Like ABC Transporter	At2g36380	ATPDR6/PDR6 (PLEIOTROPIC DRUG RESISTANCE 6); Atpase, Coupled To Transmembrane Movement Of Substances	0.3186	2.4556	3	48.2560	-0.1318	-0.0214
OJ1414_E05.8	Putative	At5g46240	KAT1 (K+ Atpase	0.2719	3.1662	3	76.4450	-0.3829	-0.0313

	Potassium Channel		1); Cyclic Nucleotide Binding / Inward Rectifier Potassium Channel						
OJ1477_F01.124	Putative Condensin Subunit 1	At3g57060	Binding	0.2889	2.6931	3	40.5890	0.0268	-0.0162
OJ1611_C08.25	Universal Stress Protein / Early Nodulin	At3g03270	Universal Stress Protein (USP) Family Protein / Early Nodulin ENOD18 Family Protein	0.3452	1.8193	3	62.1790	-0.2463	-0.1121
OJ1655_B12.16	Leaf Senescence Protein-Like	At5g64020	Hypothetical Protein	0.3087	2.9214	3	38.8590	0.1820	-0.0274
OJ1785_A05.14	Putative Pentatricopeptide Repeat Containing	At3g24000	Pentatricopeptide (PPR) Repeat-Containing Protein	0.6830	2.7939	3	56.3110	-0.4516	-0.0058
OJ1789_C07.21	Putative Microtubule-Associated Protein	At1g27920	Microtubule Associated Protein (MAP65/ASE1) Family Protein	0.4221	2.0963	3	42.6230	0.1610	-0.0254
OJ1793_E11.105	Putative 5-Alpha-Taxadienol-10-Beta-Hydroxylase	At5g36110	CYP716A1 (Cytochrome P450, Family 716, Subfamily A, Polypeptide 1); Oxygen Binding	0.6980	3.8609	3	56.7630	-0.2165	-0.0065
OJ2056_H01.9	Unknown Protein	At5g19630	Hypothetical Protein	0.3080	1.8037	3	70.5610	-0.4396	-0.0525
OSJNBa0009K15.12	Unknown Protein	At3g51970	Long-Chain-Alcohol O-Fatty-Acyltransferase Family Protein / Wax Synthase Family Protein	0.6762	4.0864	3	91.5660	-0.3875	-0.0459
OSJNBa0011F23.7	Unknown Protein	At1g73110	Ribulose Bisphosphate Carboxylase/Oxygenase Activase, Putative / Rubisco	0.2290	3.1429	3	52.4270	-0.0222	-0.0236

			Activase, Putative						
OSJNBa0011L 07.13	Unknown Protein	At3g58690	Protein Kinase Family Protein	0.8462	4.2227	3	90.5880	-0.3973	-0.0535
OSJNBa0019D 11.15	Unknown Protein	At3g62470	Pentatricopeptide (PPR) Repeat-Containing Protein	0.9104	4.2505	3	78.3720	-0.5512	-0.0448
OSJNBa0029C 04.10	Unknown Protein	At2g13000	Transposable Element Gene	0.7641	4.7261	3	48.5290	0.2625	-0.0071
OSJNBa0032F 06.15	Unknown Protein	At1g63220	C2 Domain-Containing Protein	0.3412	1.7293	3	69.2310	-0.3099	-0.1166
OSJNBa0032G 11.10	Putative Methyl Chloride Transferase	At2g43910	Thiol Methyltransferase, Putative	0.5013	1.9168	3	77.6820	-0.2582	-0.1114
OSJNBa0032G 11.16	Putative B' Regulatory Subunit Of Protein	At3g26020	Protein Phosphatase Type 2A Regulator	0.2468	4.4352	3	47.7990	0.0607	-0.0232
OSJNBa0035M 09.11	Unknown Protein	At2g15410	Transposable Element Gene	0.7111	2.0439	3	63.7840	-0.5432	-0.0279
OSJNBa0035M 09.16	Unknown Protein	At5g10620	Unknown Protein	0.2793	1.9371	3	48.2760	-0.2502	-0.0690
OSJNBa0035O 13.14	Unknown Protein	At3g62700	ATMRP10 (Arabidopsis Thaliana Multidrug Resistance-Associated Protein 10)	0.3956	2.1275	3	59.9590	-0.3867	-0.0129
OSJNBa0038P 21.9	Unknown Protein	At5g14770	Pentatricopeptide (PPR) Repeat-Containing Protein	1.0488	3.2343	3	55.6270	-0.4480	-0.0175
OSJNBa0041P 03.13	Putative Chloroplast RNA Processing Protein	At1g12300	Pentatricopeptide (PPR) Repeat-Containing Protein	0.7779	4.3344	3	57.8230	-0.3250	-0.0612
OSJNBa0042H 24.55-2	Leucine-Rich Repeat Protein Kinase-Like	At1g51860	Leucine-Rich Repeat Protein Kinase, Putative	0.5221	4.1025	3	36.3890	0.1355	-0.0274
OSJNBa0043L 24.12	Unknown Protein	At1g23360	Ubie/COQ5 Methyltransferase Family Protein	0.3155	1.6455	3	57.5880	-0.2614	-0.0985
OSJNBa0048K 16.23	Putative UDP-Glycosyltransfera	At1g22400	UGT85A1 (UDP-Glucosyl	0.5056	4.3534	3	88.6270	-0.4071	-0.0336

	se		Transferase 85A1); UDP-Glycosyltransferase/ Transferase, Transferring Glycosyl Groups / Transferase, Transferring Hexosyl Groups						
OSJNBa0049O 12.9	Hypothetical Protein	At5g60700	Glycosyltransferase Family Protein 2	0.2118	4.7708	3	97.0850	-0.4885	-0.0176
OSJNBa0052K 01.23	Putative Flap Endonuclease 1	At5g26675	Unknown Protein	0.1147	2.9234	3	46.0640	-0.0094	-0.0400
OSJNBa0052O 21.15	Unknown Protein	At1g05680	UDP-Glucoronosyl/UDP-Glucosyl Transferase Family Protein	0.6383	2.1295	3	77.1170	-0.2696	-0.0528
OSJNBa0053L 11.32	Putative LEUNIG	At2g32700	WD-40 Repeat Family Protein	0.2298	2.7809	3	42.2480	0.0412	-0.0133
OSJNBa0054K 20.1	Putative Pathogenesis-Related Protein PR-1	At4g30320	Allergen V5/Tpx-1-Related Family Protein	0.3922	3.4798	3	93.4910	-0.4502	-0.0703
OSJNBa0056E 06.20	Hypothetical Protein	At3g22540	Unknown Protein	0.2651	3.1321	3	76.6360	-0.2861	-0.1104
OSJNBa0061G 20.2	Unknown Protein	At4g27210	Transposable Element Gene	0.5512	4.4931	3	67.2970	-0.4843	-0.0269
OSJNBa0063E 14.35	Putative 68 Kda Protein HP68	At4g19210	ATRLI2 (Arabidopsis Thaliana Rnase L Inhibitor Protein 2)	0.1993	4.5077	3	40.4220	0.0952	-0.0281
OSJNBa0064E 16.9	Putative Transaminase	At4g33680	AGD2 (ABERRANT GROWTH AND DEATH 2); Transaminase	0.3002	4.3597	3	75.9910	-0.2198	-0.0205
OSJNBa0064H 22.17	Unknown Protein	At1g14140	Substrate Carrier Family Protein	0.3079	1.6900	3	61.6670	-0.2734	-0.0893
OSJNBa0064H 22.6	Unknown Protein	At2g02010	Glutamate Decarboxylase, Putative	0.2092	4.2869	3	95.4350	-0.4777	-0.0368
OSJNBa0064M 23.12	Unknown Protein	At3g61460	BRH1 (BRASSINOSTEROID-	0.8409	3.5471	3	90.9090	-0.4150	-0.1111

			RESPONSIVE RING-H2); Protein Binding / Zinc Ion Binding						
OSJNBa0067G20.8	Unknown Protein	At1g70080	Terpene Synthase/Cyclase Family Protein	0.8017	1.5817	3	42.3910	0.0731	-0.0178
OSJNBa0069E14.13	Putative Dehydrogenase	At3g03980	Short-Chain Dehydrogenase/Reductase (SDR) Family Protein	0.4656	4.0237	3	97.2330	-0.2339	-0.0951
OSJNBa0073A21.31	Putative High Affinity Potassium Transporter	At4g10310	HKT1 (HIGH-AFFINITY K+ TRANSPORTER 1); Sodium Ion Transporter	0.6445	2.7451	3	43.2490	0.0692	-0.0096
OSJNBa0078A17.13	Putative Transposase	At4g38180	FRS5 (FAR1-RELATED SEQUENCE 5); Zinc Ion Binding	0.6545	2.5694	3	38.9680	0.2398	-0.0139
OSJNBa0078N11.41	Transitional Endoplasmic Reticulum Atpase-Like	At1g50140	AAA-Type Atpase Family Protein	0.1887	4.3793	3	35.2400	0.0788	-0.0260
OSJNBa0087M10.16	Putative Pentatricopeptide Repeat Protein	At3g53700	MEE40 (Maternal Effect Embryo Arrest 40); Binding	0.4150	4.7031	3	53.1700	-0.4261	-0.0276
OSJNBa0092M19.3	Hypothetical Protein	At4g16010	Transposable Element Gene	1.2735	3.1324	3	52.9410	0.0650	-0.1250
OSJNBa0096I06.33	Putative Hydroxysteroiddehydrogenase	At3g29260	Short-Chain Dehydrogenase/Reductase (SDR) Family Protein	0.4120	3.9864	3	97.3780	-0.2893	-0.0529
OSJNBb0004A17.12	Unknown Protein	At1g10820	Unknown Protein	0.8018	2.3228	3	58.6090	-0.1236	-0.0601
OSJNBb0008D07.22	Hypothetical Protein, Similar To Oryza	At5g27370	Unknown Protein	0.5725	3.5517	3	88.9910	-0.3835	-0.0511
OSJNBb0011A08.1	Putative Rnase	At3g01410	Rnase H Domain-Containing Protein	0.5446	3.9029	3	40.5200	-0.0313	-0.0561
OSJNBb0011H13.18	Putative P-Type Atpase	At1g10130	ECA3 (ENDOPLASMIC RETICULUM-TYPE CALCIUM-	0.1643	2.1934	3	37.1630	0.1023	-0.0143

			TRANSPORTING ATPASE 3); Calcium-Transporting Atpase/ Calmodulin Binding						
OSJNBb0012J10.18	Putative ADH Glutamate Dehydrogenase	At5g07440	GDH2 (GLUTAMATE DEHYDROGENASE 2); Oxidoreductase	0.1299	3.2190	3	51.8130	-0.2238	-0.0589
OSJNBb0017F17.22	Putative ABC Transporter	At2g40090	ATATH9 (ABC2 Homolog 9)	0.3149	2.4366	3	48.6060	-0.1641	-0.0568
OSJNBb0032D24.14	Unknown Protein	At3g15310	Transposable Element Gene	0.4741	4.1066	3	34.8450	0.3295	-0.0216
OSJNBb0041A22.4	Unknown Protein	At2g35030	Pentatricopeptide (PPR) Repeat-Containing Protein	0.6934	4.5286	3	52.5980	-0.1280	-0.0248
OSJNBb0048A17.4	Putative Cytochrome P450	At4g37320	CYP81D5 (Cytochrome P450, Family 81, Subfamily D, Polypeptide 5); Oxygen Binding	0.5757	2.0872	3	74.6450	-0.3996	-0.0102
OSJNBb0050O03.5	Unknown Protein	At1g24470	Short-Chain Dehydrogenase/Reductase (SDR) Family Protein	0.6275	4.0481	3	94.1370	-0.4774	-0.0928
OSJNBb0055I24.101	Leaf Senescence Related Protein-Like	At2g14530	Unknown Protein	0.3338	1.7281	3	59.1370	-0.1939	-0.0729
OSJNBb0067H15.19	'Unknown Protein, Contains BURP Domain,	At5g25610	Rd22 (Responsive To Dessication 22)	0.4791	3.7247	3	96.0350	-0.3006	-0.0552
OSJNBb0070O09.3	Putative Protein Phosphatase 2A Regulatory	At3g09880	ATB' BETA (Arabidopsis Thaliana Serine/Threonine Protein Phosphatase 2A 55 Kda Regulatory Subunit B Prime	0.2614	4.4141	3	77.5550	-0.4695	-0.0404

			Beta); Protein Phosphatase Type 2A Regulator						
OSJNBb0108E 17.14	Unknown Protein	At3g04820	Pseudouridylate Synthase	0.4093	2.7146	3	50.3980	0.0739	-0.0573
P0019E03.1	Putative Purine Permease	At1g30840	ATPUP4 (Arabidopsis Thaliana Purine Permease 4); Purine Transporter	0.4735	4.1321	3	95.6160	-0.3167	-0.0952
P0030H07.20	Putative Aspartate--Trna Ligase	At4g33760	Trna Synthetase Class II (D, K And N) Family Protein	0.2854	2.0541	3	46.3700	-0.1510	-0.0108
P0042A10.14	Hypothetical Protein	At1g26310	CAL (CAULIFLOWER); DNA Binding / Transcription Factor	0.6855	3.4737	3	84.7460	-0.5213	-0.0495
P0406G08.10	Laccase	At5g60020	LAC17 (Laccase 17); Copper Ion Binding / Oxidoreductase	0.2231	4.5083	3	92.1570	-0.4861	-0.0177
P0409B11.10	Putative Phosphoadenylyl-Sulfate Reductase	At1g62180	Apr2 (5'adenylylphosphosulfate Reductase 2)	0.2538	4.3683	3	95.7490	-0.4706	-0.0234
P0432B10.6	Putative 60S Ribosomal Protein L30	At1g36240	60S Ribosomal Protein L30 (RPL30A)	0.1857	2.0897	3	62.8570	-0.6494	-0.1000
P0439E07.15	Putative Pectin Methylesterase	At5g19730	Pectinesterase Family Protein	0.2874	4.1362	3	93.4960	-0.3322	-0.0690
P0450B04.1	Putative P450	At2g30770	CYP71A13 (Cytochrome P450, Family 71, Subfamily A, Polypeptide 13); Oxygen Binding	0.7084	2.6279	3	64.1300	-0.4171	-0.0477
P0458G06.122	Leaf Senescence Related Protein-Like Protein	At4g01080	Unknown Protein	0.8621	4.2630	3	89.5730	-0.3290	-0.0275
P0462E11.12	Putative (+)-Delta-Cadinene Sythase	At3g14490	Terpene Synthase/Cyclase Family Protein	0.7065	4.2978	3	35.4460	0.4640	-0.0201

P0470D12.145	SKP1(S-Phase Kinase Associated Protein)	At4g29370	Kelch Repeat-Containing F-Box Family Protein	1.1023	4.2507	3	80.8220	-0.4787	-0.0327
P0489A05.5	Putative MADS-Box Protein	At2g42830	SHP2 (SHATTERPROOF 2); Transcription Factor	0.3080	3.7701	3	65.2170	-0.4327	-0.0287
P0496H05.25	Putative Peptidylprolyl Isomerase	At5g48570	Peptidyl-Prolyl Cis-Trans Isomerase, Putative / FK506-Binding Protein, Putative	0.6512	2.4098	3	49.0870	-0.0756	-0.0266
P0497A05.18	Proline Transport Protein-Like	At2g39890	Prot1 (PROLINE TRANSPORTER 1)	0.6254	4.3898	3	86.8180	-0.4570	-0.0506
P0498H04.26	Putative GDSL-Motif Lipase/Hydrolase Protein	At1g29670	GDSL-Motif Lipase/Hydrolase Family Protein	0.4624	4.1251	3	93.5140	-0.3526	-0.0483
P0520B06.15	Putative TATA Binding Protein-Associated Factor	At1g04950	TAFII59 (TATA Box Associated Factor II 59); Transcription Initiation Factor	0.3291	1.8677	3	46.2890	-0.0922	-0.0250
P0552F09.104	Disease Resistance Response Protein-Like	At5g42500	Disease Resistance-Responsive Family Protein	0.7883	3.5662	3	94.5780	-0.3593	-0.0931
P0556A11.20	Putative KH Domain Protein	At5g46190	KH Domain-Containing Protein	0.4177	4.2426	3	33.9710	-0.1440	-0.0229
P0582D05.138	Putative Pentatricopeptide (PPR)	At1g53600	Pentatricopeptide (PPR) Repeat-Containing Protein	0.5181	3.1832	3	55.9190	-0.2313	-0.0380
P0594D10.128	Putative Alcohol Dehydrogenase	At1g22440	Alcohol Dehydrogenase, Putative	0.3377	4.2273	3	83.7020	-0.4877	-0.0492
P0610E02.28	Hypothetical Protein	At1g50660	Unknown Protein	0.6467	3.0839	3	59.9660	-0.2673	-0.0153
P0616D06.103	Putative Exportin, Trna	At1g72560	Psd (Paused)	0.4658	2.6306	3	58.0260	-0.2557	-0.0208
P0643F09.13	Haloacid Dehalogenase-	At2g33250	Unknown Protein	0.3170	3.8673	3	64.5160	-0.3765	-0.1130

	Like Hydrolase-Like								
P0660F12.24	Unknown Protein	At2g01170	Amino Acid Permease Family Protein	0.2976	2.3526	3	78.1680	-0.4085	-0.0342
P0663C08.2	Unknown Protein	At5g28540	Luminal Binding Protein 1 (Bip-1) (BP1)	0.6617	4.2441	3	85.8510	-0.5413	-0.0540
P0665D10.14	Unknown Protein	At5g04560	Encodes A DNA Glycosylase DEMETER (DME)	0.2309	1.9326	3	30.7090	0.3743	-0.0237
P0680F05.51	Putative 33-Kda Secretory Protein	At1g63600	Protein Kinase-Related	0.9326	3.9181	3	74.7250	-0.2692	-0.0493
P0681F05.120	Putative ATP/GTP-Binding Protein	At4g21210	Encodes A PPDK Regulatory Protein That Has Both Protein Kinase And Protein Phosphatase Activities Towards PPDK (Pyruvate Orthophosphate Dikinase).	0.3471	3.0758	3	60.0000	-0.3437	-0.0410
P0700F06.15-1	Zinc Finger (CCCH-Type) Protein-Like	At2g24830	Zinc Finger (CCCH-Type) Family Protein / D111/G-Patch Domain-Containing Protein	0.3522	2.1380	3	41.8710	-0.1662	-0.0208
P0711F01.41	Putative FAE1	At4g34510	KCS2 (3-Ketoacyl-Coa Synthase 2); Acyltransferase	0.6034	4.3074	3	89.2470	-0.3336	-0.0367
P0724B10.43	Hydrolase, Alpha/Beta Fold Family-Like	At4g36530	Hydrolase, Alpha/Beta Fold Family Protein	0.3217	4.2614	3	86.6320	-0.4007	-0.0590
B1060H01.29	Putative 8-Amino-7-Oxononanoate Synthase	At5g04620	ATBIOF; 8-Amino-7-Oxononanoate Synthase/ Transaminase	0.3371	2.7422	4	45.6310	-0.1125	-0.0445
OJ1003C07.7	Putative Myo-Inositol-1-	At2g22240	Inositol-3-Phosphate	0.1125	4.3880	4	87.6570	-0.5150	-0.0363

	Phosphate Synthase		Synthase Isozyme 2 / Myo-Inositol-1-Phosphate Synthase 2 / MI-1-P Synthase 2 / IPS 2						
OJ1112_F06.15	Zinc Finger And C2 Domain Protein-Like	At1g48590	C2 Domain-Containing Protein	0.4489	3.4760	4	84.0760	-0.4016	-0.1163
OJ1214_E03.15	Unknown Protein	At1g28380	Nsl1 (Necrotic Spotted Lesions 1)	0.4405	4.6047	4	79.5680	-0.3992	-0.0096
OJ1435_F07.30	Putative Nodulin Mtn21	At4g01440	Nodulin Mtn21 Family Protein	0.5549	2.6334	4	55.4250	-0.1208	-0.0374
OJ1499_D04.8	Putative Leucine-Rich Repeat Receptor Kinase	At4g39270	Leucine-Rich Repeat Transmembrane Protein Kinase, Putative	0.6136	2.4230	4	58.7010	-0.2828	-0.0158
OJ1705B08.7	Putative Peroxidase	At1g05260	RCI3 (RARE COLD INDUCIBLE GENE 3); Peroxidase	0.5211	4.1006	4	85.7590	-0.3683	-0.0444
OJ9003_G05.21	Putative SNF2 Domain-Containing Protein	At3g54280	ATP Binding / DNA Binding / Helicase	0.3138	2.4169	4	36.4430	0.0509	-0.0064
OSJNBa0003O19.10	Putative Enoyl-Coa-Hydratase	At5g65940	Chy1 (Beta-Hydroxyisobutyryl-Coa Hydrolase 1)	0.2740	2.3934	4	37.3490	0.1424	-0.1098
OSJNBa0004N05.8	Unknown Protein	At4g16480	ATINT4 (INOSITOL TRANSPORTER 4); Carbohydrate Transporter/ Myo-Inositol:Hydrogen Symporter/ Sugar Porter	0.2928	2.1772	4	73.5990	-0.4689	-0.0224
OSJNBa0011K22.4	Unknown Protein	At3g02740	Aspartyl Protease Family Protein	0.5299	1.8691	4	43.3730	0.3516	-0.0348
OSJNBa0015J15.3	Putative Trehalose-6-Phosphate Phosphatase	At4g22590	Trehalose-6-Phosphate Phosphatase, Putative	0.3108	4.1612	4	43.1750	-0.2541	-0.0202
OSJNBa0019K	Unknown Protein	At4g25480	DREB1A	0.5328	3.7057	4	91.0450	-0.2750	-0.0858

04.2			(DEHYDRATION RESPONSE ELEMENT B1A); DNA Binding / Transcription Factor/ Transcriptional Activator						
OSJNBa0041M 21.2	Unknown Protein	At1g73040	Jacalin Lectin Family Protein	0.9585	1.7759	4	53.0200	-0.3439	-0.1073
OSJNBa0042H 24.55-1	Serine/Threonine -Specific Receptor Protein	At4g29990	Light Repressible Receptor Protein Kinase	0.6199	4.8359	4	41.3220	0.2891	-0.0149
OSJNBa0051D 19.17	Putative Tam3-Transposase	At1g42110	Transposable Element Gene; Hat-Like Transposase Family (Hobo/Ac/Tam3),	0.7290	4.3342	4	34.3510	-0.0631	-0.0167
OSJNBa0053E 05.18	Putative ATP-Dependent Clp Protease Subunit	At1g33360	ATP-Dependent Clp Protease ATP-Binding Subunit Clpx, Putative	0.3221	4.1807	4	36.2670	0.2343	-0.0355
OSJNBa0061E 21.10	Chloroplast RNA Processing Protein-Like Protein	At5g55840	Pentatricopeptide (PPR) Repeat-Containing Protein	1.0606	4.6601	4	51.0990	-0.0375	-0.0153
OSJNBa0087C 10.22	Unknow Protein	At5g23330	Riboflavin Biosynthesis Protein-Related	0.4760	4.1647	4	39.1980	0.1040	-0.0226
OSJNBa0087G 11.19	Putative 1,3-Beta-Glucanase	At5g20870	Glycosyl Hydrolase Family 17 Protein	0.3559	4.3104	4	97.7180	-0.4538	-0.0465
OSJNBa0091C 18.39	Hypothetical Protein	At5g25790	Transcription Factor	0.9292	2.9679	4	39.5350	0.0585	-0.0482
OSJNBa0092M 19.27	Putative Vacuolar Protein Sorting-Associated	At5g53530	Vacuolar Protein Sorting-Associated Protein 26, Putative / VPS26, Putative	0.2466	3.3884	4	39.4960	-0.0642	-0.1238
OSJNBb0006L 01.7	Unknown Protein	At1g59520	Cw7	0.3514	1.9920	4	38.8450	0.1749	-0.0462
OSJNBb0012A 20.13	Unknown Protein	At1g52200	Unknown Protein	0.7704	3.5258	4	86.5380	-0.2890	-0.1193

OSJNBb0013K08.9	Putative Nucleotide-Binding Protein	At4g19540	Unknown Protein	0.2837	1.0864	4	44.4040	-0.2397	-0.0531
OSJNBb0038F20.4	Putative NTGP4	At1g33970	GTP Binding	0.4886	1.6737	4	40.8160	-0.1734	-0.0364
OSJNBb0051N19.2	Unknown Protein	At2g23000	SCPL10 (Serine Carboxypeptidase-Like 10); Serine Carboxypeptidase	0.4658	1.9413	4	54.1760	-0.2370	-0.0463
OSJNBb0073N24.11	Putative Hypersensitivity-Related (Hsr)Protein	At5g17540	Transferase Family Protein	0.3893	4.3194	4	95.5850	-0.4116	-0.0345
OSJNBb0094O03.14	Putative Kinesin-Like Protein	At3g49650	Kinesin Motor Protein-Related	0.3355	4.7299	4	42.2430	-0.2218	-0.0278
OSJNBb0103I08.9	Unknown Protein	At3g45270	Transposable Element Gene	0.7196	3.2006	4	35.0880	-0.0329	-0.1114
P0012A04.17	Bola-Like Family Protein / Fe-S Metabolism	At4g26500	ATSUFE/CPSUFE/EMB1374 (EMBRYO DEFECTIVE 1374); Enzyme Activator/ Transcription Regulator	0.5502	4.2255	4	80.3570	-0.5093	-0.0377
P0035H10.13	Putative Knotted1-Type Homeobox Protein	At4g08150	KNAT1 (BREVIPEDICELLUS 1); Transcription Factor	0.5673	3.9221	4	83.4530	-0.3630	-0.0555
P0042A10.6	Similar To Phytochrome A Supressor	At1g53090	SPA4 (SPA1-RELATED 4); Signal Transducer	0.3885	4.7646	4	50.7340	0.1403	-0.0292
P0042A10.7	Hypothetical Protein	At1g28290	Pollen Ole E 1 Allergen And Extensin Family Protein	0.8329	2.0246	4	89.3490	-0.3990	-0.0657
P0430F03.13	Putative Glucosyltransferase	At2g18570	UDP-Glucoronosyl/UDP-Glucosyl Transferase Family Protein	0.7377	4.3351	4	96.0350	-0.3598	-0.0374
P0461B08.26	Putative MAP3K Alpha 1 Protein Kinase	At1g63700	YDA (YODA); Kinase	0.3808	4.7763	4	33.4110	0.1199	-0.0166

P0470F10.14	Putative Avr9 Elicitor Response Protein	At1g32930	Galactosyltransferase Family Protein	0.3312	2.2905	4	52.4590	-0.2272	-0.0840
P0483D07.18	'Unknown Protein, Contains Histidine-Containing	At3g16360	AHP4 (HPT PHOSPHOTRANSMITTER 4); Histidine Phosphotransfer Kinase/ Transferase, Transferring Phosphorus-Containing Groups	0.3495	3.3542	4	53.9570	-0.4345	-0.0651
P0496H05.17	Putative Cyt-P450 Monooxygenase	At2g45550	CYP76C4 (Cytochrome P450, Family 76, Subfamily C, Polypeptide 4); Oxygen Binding	0.6230	4.4066	4	95.2970	-0.4300	-0.0355
P0503D09.101	Unknown Protein	At5g46090	Unknown Protein	0.5524	3.7064	4	99.4680	-0.3325	-0.1080
P0524G08.110	Putative Calcium/Calmodulin-Dependent Protein	At2g41140	CRK1 (CDPK-RELATED KINASE 1); Calcium Ion Binding / Calcium-Dependent Protein Serine/Threonine Phosphatase/ Kinase	0.1645	4.5321	4	56.8350	-0.2631	-0.0278
P0524G08.134	Putative Transcription Factor APFI	At1g47260	APFI; Carbonate Dehydratase	0.1842	1.5381	4	50.9800	-0.2826	-0.0681
P0543D10.26	Putative SAP1 Protein	At3g04570	DNA-Binding Protein-Related	0.3132	3.9454	4	91.5560	-0.3796	-0.0681
P0643F09.26	Putative Myosin Subfamily XI Heavy Chain	At5g43900	Mya2 (Arabidopsis Myosin)	0.1990	5.1933	4	38.8770	0.0463	-0.0062
P0650H04.32	Putative White Pigment Protein	At2g39350	ABC Transporter Family Protein	0.6824	4.7121	4	85.7340	-0.4342	-0.0311
P0676H02.31-1	Putative Isoamylase-Type Starch Debranching	At4g09020	ATISA3/ISA3 (ISOAMYLASE 3); Alpha-Amylase	0.1843	2.1763	4	39.3020	-0.0251	-0.0103

P0680A05.37	Putative Hydrolase	At4g36610	Hydrolase, Alpha/Beta Fold Family Protein	0.3601	3.9562	4	92.7900	-0.4499	-0.0560
P0684F11.2	Putative Immediate-Early Fungal Elicitor Protein	At5g37490	U-Box Domain-Containing Protein	0.6936	4.2568	4	93.6020	-0.4303	-0.0442
B1090H08.30	Putative Cytochrome B-561	At5g38630	ACYB-1 (Arabidopsis Cytochrome B561-1); Carbon-Monoxide Oxygenase	0.3783	1.9794	5	68.5590	-0.2434	-0.1137
B1097D05.13	Putative Serine Threonine Kinase	At5g26150	Protein Kinase Family Protein	0.4472	4.6308	5	94.9350	-0.4037	-0.0207
OJ1001_C01.113	Putative GDP Dissociation Inhibitor	At2g44100	ATGDI1 (Arabidopsis Thaliana Guanosine Diphosphate Dissociation Inhibitor 1)	0.1352	2.9580	5	43.1600	0.0398	-0.0408
OJ1001_D02.31	Putative Anthranilate Phosphoribosyltransferase	At3g57880	C2 Domain-Containing Protein	0.4540	4.6964	5	91.1680	-0.4625	-0.0244
OJ1003_F05.11	Putative Flavonoid Glucosyl-Transferase	At2g36750	UGT72C1 (UDP-Glucosyl Transferase 72C1); UDP-Glycosyltransferase/ Transferase, Transferring Glycosyl Groups	0.5715	4.3665	5	89.4960	-0.3506	-0.0238
OJ1004_A05.35	Putative Emperature Stress-Induced Lipocalin	At5g58070	Lipocalin, Putative	0.2129	3.3779	5	98.9130	-0.4520	-0.0436
OJ1008_E02.21	Putative SEC14 Cytosolic Factor	At1g19650	SEC14 Cytosolic Factor, Putative / Phosphoglyceride Transfer Protein, Putative	0.4789	4.4936	5	45.3720	-0.1986	-0.0273
OJ1119_B04.4	Putative DD1A Protein	At1g55360	Unknown Protein	0.1983	4.1894	5	77.3780	-0.3961	-0.0613

OJ1124_H03.12	Hypothetical Protein	At1g05440	Unknown Protein	0.8574	4.0661	5	94.0980	-0.3799	-0.0548
OJ1159_D09.7	Lipase-Like Protein	At2g27360	Lipase, Putative	0.6232	2.5303	5	62.9920	-0.2983	-0.0670
OJ1200_C08.118	Unknown Protein	At1g08400	Chromosome Structural Maintenance Protein-Related	0.5736	4.5515	5	38.0420	0.0898	-0.0228
OJ1212_D02.8	Putative B-Keto Acyl Reductase	At1g67730	B-Keto Acyl Reductase, Putative (GLOSSY8)	0.3400	3.9013	5	81.7430	-0.4387	-0.1201
OJ1340_C08.132	Putative Thymidylate Kinase	At5g59440	Thymidylate Kinase Family Protein	0.2724	2.0266	5	42.7840	-0.3365	-0.1061
OJ1442_E05.31	UDP-Glucose Pyrophosphorylase	At5g17310	UTP--Glucose-1-Phosphate Uridylyltransferase, Putative / UDP-Glucose Pyrophosphorylase, Putative / Ugpase, Putative	0.1171	1.8506	5	61.5210	-0.2803	-0.0503
OJ1479_B11.10	Putative Glycosyl Hydrolase Family 35	At2g16730	BGAL13 (Beta-Galactosidase 13); Beta-Galactosidase	0.4147	4.6951	5	87.4060	-0.5294	-0.0320
OJ1532_D06.3	Unknown Protein	At1g32250	Calmodulin, Putative	0.6075	3.3311	5	97.2220	-0.4572	-0.1346
OJ1613_G04.20	Putative Polycomb Group Protein FIE2	At3g20740	FIE (FERTILIZATION-INDEPENDENT ENDOSPERM 1); Nucleotide Binding / Transcription Factor	0.2301	2.4023	5	50.2810	-0.1246	-0.0468
OJ1626_B09.8	Putative Nitrilase 2	At5g22300	Nit4 (Nitrilase 4)	0.2109	3.1311	5	47.3370	0.0449	-0.0492
OJ1679_B08.28	Avrrpt2-Induced Protein 2-Like	At2g24390	Unknown Protein	0.3517	1.6694	5	68.8890	-0.4062	-0.1196
OJ1743A09.9	Putative Topoisomerase	At1g22730	MA3 Domain-Containing Protein	0.3520	4.5722	5	91.4240	-0.4457	-0.0146
OJ1773_H01.102	Putative Lysine Ketoglutarate	At1g61240	Unknown Protein	0.3624	4.1083	5	39.5720	0.2493	-0.0192

	Reductase								
OSJNBa0005N02.7	Unknown Protein	At1g08430	ALMT1/ATALMT1 (AL-ACTIVATED MALATE TRANSPORTER 1); Malate Transporter	0.6846	4.3951	5	92.1320	-0.4193	-0.0402
OSJNBa0007M04.24	Putative Cell Division Cycle Protein	At3g53230	Cell Division Cycle Protein 48, Putative / CDC48, Putative	0.2788	4.6730	5	96.6710	-0.4506	-0.0226
OSJNBa0018M05.14	Unknown Protein	At1g65730	YSL7 (YELLOW STRIPE LIKE 7); Oligopeptide Transporter	0.2349	4.5978	5	91.0160	-0.3877	-0.0118
OSJNBa0018M05.19	Unknown Protein	At5g23240	DNAJ Heat Shock N-Terminal Domain-Containing Protein	0.5648	4.3741	5	84.4980	-0.4095	-0.0235
OSJNBa0020H14.13	Putative Plastid Division Protein Ftsz	At3g52750	FTSZ2-2 (Ftsz2-2); Structural Molecule	0.2535	2.8307	5	43.4000	-0.0585	-0.0318
OSJNBa0029C15.7	Anther-Specific Protein YY2	At1g02050	Chalcone And Stilbene Synthase Family Protein	0.3109	1.9675	5	57.6600	-0.5161	-0.0506
OSJNBa0033H08.6	Unknown Protein	At1g62940	4-Coumarate--Coa Ligase Family Protein / 4-Coumaroyl-Coa Synthase Family Protein	0.2975	4.5114	5	96.9110	-0.4160	-0.0272
OSJNBa0034E08.23	Putative Piwi Domain Containing Protein	At1g69440	Ago7 (Argonaute7)	0.3695	4.9166	5	53.7220	-0.1913	-0.0052
OSJNBa0036B21.20	Unknown Protein	At5g27870	Pectinesterase Family Protein	0.5375	4.3159	5	97.9590	-0.5238	-0.0255
OSJNBa0038F22.1	Receptor Protein Kinase-Like	At2g21480	Protein Kinase Family Protein	0.3126	4.7166	5	98.2650	-0.4691	-0.0425
OSJNBa0039C07.14	Unknown Protein	At5g45880	Pollen Ole E 1 Allergen And Extensin Family Protein	0.6195	3.5132	5	73.8560	-0.5475	-0.0655
OSJNBa0041A02.11	Unknown Protein	At1g31410	Putrescine-Binding	0.3654	1.5152	5	49.1180	-0.1631	-0.0261

			Periplasmic Protein-Related						
OSJNBa0041A02.24	Unknown Protein	At4g30160	VLN4 (ARABIDOPSIS THALIANA VILLIN 4); Actin Binding	0.2564	2.5275	5	38.7870	0.1219	-0.0136
OSJNBa0044E16.22	Carboxyl-Terminal Peptidase-Like	At5g18460	Hypothetical Protein	0.3878	4.2335	5	90.7800	-0.4427	-0.0795
OSJNBa0045C13.16	Putative Vacuolar Sorting Receptor Protein	At2g14740	Vacuolar Sorting Receptor, Putative	0.1825	2.7219	5	48.0540	0.0925	-0.0566
OSJNBa0052F07.11	Putative Argonaute Protein	At2g27880	Argonaute Protein, Putative / AGO, Putative	0.3546	4.9209	5	55.9000	-0.3816	-0.0323
OSJNBa0057M23.115	Unknown Protein	At2g16070	Pdv2 (Plastid Division2)	0.4777	3.9025	5	43.6120	-0.0443	-0.0393
OSJNBa0057M23.117	PRLI-Interacting Factor G-Like Protein	At3g50780	Unknown Protein	0.3777	4.3869	5	49.6960	-0.1151	-0.0254
OSJNBa0059E14.14	Unknown Protein	At1g55340	Unknown Protein	0.4568	3.6221	5	55.1020	0.1244	-0.0505
OSJNBa0060K08.30	Unknown Protein	At5g16730	Unknown Protein	1.2104	2.0750	5	37.7720	0.0330	-0.0322
OSJNBa0065J17.11	Putative Peroxidase	At5g66390	Peroxidase 72 (PER72) (P72) (PRXR8)	0.2304	4.0192	5	86.9300	-0.5267	-0.0202
OSJNBa0070N04.15	Hypothetical Protein	At2g22070	Pentatricopeptide (PPR) Repeat-Containing Protein	0.3651	2.4438	5	73.8790	-0.3854	-0.0367
OSJNBa0071K18.5	Putative WD Domain Containing Protein	At2g20330	Transducin Family Protein / WD-40 Repeat Family Protein	0.2423	4.5948	5	48.0070	-0.1445	-0.0413
OSJNBa0072H09.17	Extracellular Calcium Sensing Receptor	At5g23060	Unknown Protein	0.4030	5.7035	5	86.1700	-0.4210	-0.0625
OSJNBa0081C13.26	Putative WD Repeat Domain 11	At3g33530	Transducin Family Protein / WD-40 Repeat Family Protein	0.2324	2.3542	5	33.2350	0.1937	-0.0175
OSJNBa0084K11.20	Unknown Protein	At1g47670	Amino Acid Transporter Family Protein	0.3580	4.4975	5	89.0000	-0.4128	-0.0449

OSJNBa0084K20.5	Unknown Protein	At1g67530	Armadillo/Beta-Catenin Repeat Family Protein / U-Box Domain-Containing Family Protein	0.5083	2.2783	5	60.6800	-0.3404	-0.0119
OSJNBa0087O24.20	Unknown Protein	At5g65930	ZWI (ZWICHEL); Calmodulin Binding / Microtubule Motor	0.2004	5.0237	5	34.7370	0.3200	-0.0133
OSJNBa0088I22.12	Unknown Protein	At1g12740	CYP87A2 (Cytochrome P450, Family 87, Subfamily A, Polypeptide 2); Oxygen Binding	0.3558	2.4085	5	73.2760	-0.2150	-0.0583
OSJNBa0091P11.14	Putative Male Sterility Protein	At3g11980	Ms2 (Male Sterility 2)	0.4021	4.5342	5	77.1780	-0.2934	-0.0331
OSJNBa0095C07.6	Putative Protein Kinase	At4g35470	Leucine-Rich Repeat Family Protein	0.1708	4.1905	5	83.6600	-0.3691	-0.0430
OSJNBb0015I11.13	Protein Kinase-Like Protein	At4g35230	Protein Kinase Family Protein	0.2055	4.3608	5	59.1000	-0.3759	-0.0477
OSJNBb0023M11.20	Putative 1,4-Beta-Xylanase	At4g33830	Glycosyl Hydrolase Family 10 Protein	0.4472	4.3628	5	96.1540	-0.4356	-0.0407
OSJNBb0024B16.7	Putative Lipoxygenase	At3g22400	Lipoxygenase, Putative	0.3574	4.8361	5	62.4850	-0.3153	-0.0111
OSJNBb0038F03.4	Unknown Protein	At2g19170	SLP3 (Subtilisin-Like Serine Protease 3); Subtilase	0.6295	2.2780	5	60.0740	-0.1667	-0.0089
OSJNBb0039L24.1	Unknown Protein	At3g61220	Short-Chain Dehydrogenase/Reductase (SDR) Family Protein	0.4779	4.0425	5	77.2730	-0.3603	-0.0450
OSJNBb0039L24.7	Unknown Protein	At3g61230	LIM Domain-Containing Protein	0.2993	3.5704	5	78.7230	-0.3316	-0.0736
OSJNBb0088N06.16	Ubiquitin-Conjugating Enzyme	At4g27960	UBC9 (UBIQUITIN CONJUGATING ENZYME 9); Ubiquitin-Protein Ligase	0.0732	2.4790	5	72.6030	-0.3009	-0.0818
OSJNBb0091E	Unknown Protein	At3g07570	Membrane	0.5346	4.0781	5	95.7100	-0.4900	-0.0415

11.23			Protein, Putative						
OSJNBb0092C08.24	Putative Avr9/Cf-9 Rapidly Elicited Protein	At5g42340	Binding / Ubiquitin-Protein Ligase	0.4158	4.5732	5	94.4260	-0.4478	-0.0346
OSJNBb0094P23.29	Putative Acyl-[Acyl-Carrier Protein] Desaturase,	At3g02610	Acyl-[Acyl-Carrier-Protein] Desaturase	0.5136	4.2248	5	90.3140	-0.4423	-0.0259
OSJNBb0099O15.10	Putative Cation/Hydrogen Exchanger (CHX6a)	At2g13620	ATCHX15 (Cation/Hydrogen Exchanger 15); Monovalent Cation:Proton Antiporter	0.3565	4.8174	5	97.7270	-0.3991	-0.0252
P0028G04.28	Hypothetical Protein	At2g46930	Pectinacetylesterase, Putative	0.3852	4.2282	5	84.4830	-0.5329	-0.0474
P0034A04.127-2	Pyruvate Decarboxylase Isozyme 3	At4g33070	Pyruvate Decarboxylase, Putative	0.1567	4.4710	5	95.6990	-0.4660	-0.0264
P0039G05.11	Florfenicol Resistance Protein-Like	At1g60230	Radical SAM Domain-Containing Protein	0.2600	1.6006	5	52.6460	-0.4364	-0.0606
P0407A09.6-1	Transmembrane Protein-Like	At4g09810	Transporter-Related	0.1711	1.6252	5	42.1540	0.2981	-0.0511
P0407B12.19	Putative UTP-Glucose Glucosyltransferase	At1g01420	UDP-Glucoronosyl/UDP-Glucosyl Transferase Family Protein	0.5373	4.4233	5	93.7370	-0.4176	-0.0414
P0409B08.17	Putative Reductase	At1g68540	Oxidoreductase Family Protein	0.3293	4.1217	5	94.6710	-0.3801	-0.0546
P0413G02.1	Putative Cytokinin Oxidase	At1g75450	CKX5 (CYTOKININ OXIDASE 5); Cytokinin Dehydrogenase	0.2793	4.3985	5	93.4260	-0.4194	-0.0226
P0427G12.14	Putative Endoglucanase 1 Precursor	At1g02800	ATCEL2 (Arabidopsis Thaliana Cellulase 2); Hydrolase, Hydrolyzing O-Glycosyl Compounds	0.3392	4.3137	5	96.2750	-0.3729	-0.0289
P0434C04.32	Putative Seven	At4g02600	ATMLO1/MLO1	0.3093	3.4202	5	60.5430	-0.4304	-0.0424

	Transmembrane Protein		(MILDEW RESISTANCE LOCUS O 1); Calmodulin Binding						
P0453E05.113	Putative Cyclin-Dependent Kinase CDC2C	At1g18670	IBS1 (IMPAIRED IN BABA-INDUCED STERILITY 1); Kinase	0.4032	2.6483	5	47.7200	-0.1185	-0.0330
P0460E08.9	Ospk7	At4g18700	CIPK12 (CIPK12); Kinase	0.2945	4.3384	5	70.0410	-0.2381	-0.0521
P0461A06.15	Putative Germin Protein Type 1	At3g05950	Germin-Like Protein, Putative	0.3706	3.8827	5	54.7950	-0.1442	-0.0567
P0461B08.35	Putative Uracil Transport Protein	At5g03560	Nucleobase:Cation Symporter	0.3619	4.5189	5	89.9050	-0.3613	-0.0394
P0461D06.12	Putative High-Affinity Potassium Transporter	At2g30070	ATKT1 (Arabidopsis Thaliana K+ Uptake 1); Potassium Ion Transporter	0.5641	4.7169	5	90.2820	-0.3896	-0.0296
P0470A12.34	Putative Peptide Transporter	At1g69870	Proton-Dependent Oligopeptide Transport (POT) Family Protein	0.4563	3.0244	5	45.5030	0.1212	-0.0234
P0470A12.38	Putative Rho GDP-Dissociation Inhibitor	At3g07880	Rho GDP-Dissociation Inhibitor Family Protein	0.3598	3.6459	5	73.1580	-0.5763	-0.0516
P0475F05.16	Branching Enzyme-3 Precursor	At5g03650	Sbe2.2 (Starch Branching Enzyme 2.2)	0.1966	4.7038	5	41.9150	0.2122	-0.0298
P0476H10.22	Putative SNAP25	At1g13890	SNAP30 (Synaptosomal-Associated Protein 30)	0.4421	3.8509	5	77.6860	-0.5405	-0.0861
P0483C08.45	Putative O-Linked N-Acetyl Glucosamine	At3g04240	SEC (SECRET AGENT); Transferase, Transferring Glycosyl Groups	0.1785	4.8455	5	41.0850	-0.0188	-0.0291
P0487D09.19	Putative Myosin II Heavy Chain	At1g68060	ATMAP70-1 (MICROTUBULE-ASSOCIATED	0.1815	4.4790	5	40.9680	-0.0586	-0.0411

			PROTEINS 70-1); Microtubule Binding						
P0501G01.21	Putative Endopolygalacturonase	At3g59850	Polygalacturonase, Putative / Pectinase, Putative	0.4332	4.1676	5	89.6370	-0.3608	-0.0300
P0514G12.27	Unknown Protein	At3g53210	Nodulin Mtn21 Family Protein	0.8294	1.7145	5	55.5560	-0.0317	-0.0408
P0514H03.3	Hypothetical Protein	At4g21300	Pentatricopeptide (PPR) Repeat-Containing Protein	0.7948	4.6344	5	34.8110	0.1431	-0.0127
P0543C11.35	Putative Guanylate Binding Protein	At5g46070	GTP Binding / Gtpase	0.3787	2.9640	5	43.2570	-0.0816	-0.0239
P0554F08.6	Putative Phosphoethanolamine	At1g48600	Phosphoethanolamine N-Methyltransferase 2, Putative (NMT2)	0.1529	3.9837	5	51.5420	-0.3463	-0.0257
P0560B06.13	Putative DNA-Dependent Atpase	At3g06400	CHR11 (CHROMATIN-REMODELING PROTEIN 11); DNA-Dependent Atpase	0.1038	4.8524	5	44.0610	-0.2328	-0.0184
P0574F11.31	Putative Ubiquitin-Protein Ligase 1	At1g70320	UPL2 (UBIQUITIN-PROTEIN LIGASE 2); Ubiquitin-Protein Ligase	0.3653	5.8461	5	34.0440	0.1438	-0.0035
P0577B11.124	Putative CTP:Phosphorylcholine	At2g32260	Cholinephosphate Cytidylyltransferase, Putative / Phosphorylcholine Transferase, Putative / CTP:Phosphocholine Cytidylyltransferase, Putative	0.2389	3.9072	5	71.7050	-0.5077	-0.0701
P0585H11.109	Putative Phytosulfokine Receptor	At5g53890	Leucine-Rich Repeat Transmembrane	0.4063	4.9560	5	70.8850	-0.4180	-0.0141

			Protein Kinase, Putative						
P0613F08.1	Bet V I Allergen-Like	At5g53160	Unknown Protein	0.2047	3.6815	5	74.0540	-0.4529	-0.0451
P0622F08.20	Putative Fruit Protein	At1g15140	Oxidoreductase NAD-Binding Domain-Containing Protein	0.3412	1.5913	5	59.5670	-0.3263	-0.0199
P0663F07.43	Putative Serine/Threonine-Specific Protein	At2g33580	Protein Kinase Family Protein / Peptidoglycan-Binding Lysm Domain-Containing Protein	0.6364	3.7994	5	96.6940	-0.3791	-0.0584
P0669G09.12	Unknown Protein	At3g02070	OTU-Like Cysteine Protease Family Protein	0.3207	3.7041	5	43.2690	-0.0301	-0.0415
P0683F02.8	Putative Permease 1	At4g38050	Permease	0.5157	4.2338	5	48.2650	-0.0300	-0.0301
P0689H05.20	Putative Ent-Kaurene Synthase B	At1g79460	GA2 (GA REQUIRING 2); Ent-Kaurene Synthase	0.5764	1.8307	5	49.8690	0.1364	-0.0153
P0704D04.1	Hypothetical Protein	At1g66770	Nodulin Mtn3 Family Protein	0.5352	3.9456	5	90.3610	-0.5278	-0.0425

Supplementary Table 6: Details of Arabidopsis housekeeping highly expressed genes. GC$_3$ represents GC content at third codon position; wRn corresponds to error minimization values for individual Arabidopsis genes.

ARABIDOPSIS HOUSEKEEPING HIGHLY EXPRESSED GENE			
GENE ID	***Functional Description***	***GC$_3$***	***wRN***
At5g67360	ARA12; Subtilase	47.8740	-0.0903
At5g66140	PAD2 (20S Proteasome Alpha Subunit D2); Peptidase	51.9650	-0.5482
At5g65700	BAM1 (Big Apical Meristem 1); ATP Binding / Kinase/ Protein Serine/Threonine Kinase	45.5790	-0.0914
At5g62300	40S Ribosomal Protein S20 (RPS20C)	51.7240	-0.4076
At5g61170	40S Ribosomal Protein S19 (RPS19C)	51.0640	-0.4142
At5g58420	40S Ribosomal Protein S4 (RPS4D)	52.9880	-0.3444
At5g55180	Glycosyl Hydrolase Family 17 Protein	53.5560	-0.2769
At5g54770	Thi1 (Thiazole Requiring)	43.5820	-0.3474
At5g53300	UBC10 (Ubiquitin-Conjugating Enzyme 10); Ubiquitin-Protein Ligase	58.7410	-0.3385
At5g51750	Subtilase Family Protein	33.1990	0.3133
At5g50870	UBC27 (Ubiquitin-Conjugating Enzyme 26); Ubiquitin-Protein Ligase	39.4440	-0.1942
At5g50850	Pyruvate Dehydrogenase E1 Component Beta Subunit, PDHE1-B (PDH2)	34.6270	0.0028
At5g48930	Transferase Family Protein	41.6670	-0.3203
At5g47120	Atbi-1 (Arabidopsis Bax Inhibitor 1)	42.0830	0.0531
At5g45110	NPR3 (NPR1-LIKE PROTEIN 3); Protein Binding	34.0580	-0.2181
At5g43940	ADH2 (ALCOHOL DEHYDROGENASE 2); Formaldehyde Dehydrogenase (Glutathione)	40.8960	-0.3573
At5g43060	Cysteine Proteinase, Putative / Thiol Protease, Putative	45.7470	-0.1075
At5g42790	PAF1 (Proteasome Alpha Subunit F1); Peptidase	38.8890	0.0269
At5g42020	BIP (LUMINAL BINDING PROTEIN); ATP Binding	48.8370	-0.4166
At5g40810	Cytochrome C1, Putative	37.5440	0.1060
At5g39740	60S Ribosomal Protein L5 (RPL5B)	48.0140	-0.2558
At5g38470	DNA Repair Protein RAD23, Putative	35.0570	-0.1792
At5g37600	ATGSR1 (Arabidopsis Thaliana Glutamine Synthase Clone R1); Glutamate-Ammonia Ligase	45.8080	-0.1717
At5g33370	GDSL-Motif Lipase/Hydrolase Family Protein	47.0250	-0.2385
At5g27990	Unknown Protein	42.2620	-0.0204
At5g20890	Chaperonin, Putative	40.5800	-0.2958
At5g20720	CPN20 (CHAPERONIN 20); Calmodulin Binding	39.6620	-0.1372
At5g20290	40S Ribosomal Protein S8 (RPS8A)	52.8850	-0.3999
At5g20010	RAN-1 (Ras-Related GTP-Binding Nuclear Protein 1); GTP Binding	46.4110	-0.2164
At5g19690	STT3A (STAUROSPORIN AND TEMPERATURE SENSITIVE 3-LIKE A); Oligosaccharyl Transferase	41.1290	-0.2036
At5g19510	Elongation Factor 1B Alpha-Subunit 2 (Eef1balpha2)	46.7980	-0.4057
At5g15490	UDP-Glucose 6-Dehydrogenase, Putative	49.4480	-0.2707
At5g11560	Catalytic	39.6230	0.2041
At5g10360	EMB3010 (EMBRYO DEFECTIVE 3010); Structural Constituent Of Ribosome	51.4520	-0.3471
At5g09920	RPB15.9 (RNA Polymerase II 15.9)	39.4960	-0.1507
At5g09510	40S Ribosomal Protein S15 (RPS15D)	52.7780	-0.1652
At5g07350	Tudor Domain-Containing Protein / Nuclease Family Protein	36.3070	0.0209
At5g05170	CESA3 (CELLULASE SYNTHASE 3); Cellulose Synthase/ Transferase, Transferring Glycosyl Groups	40.4980	-0.1879

At5g03300	ADK2 (ADENOSINE KINASE 2); Kinase	50.1560	-0.2622
At5g02960	40S Ribosomal Protein S23 (RPS23B)	46.6670	-0.4041
At5g01530	Chlorophyll A-B Binding Protein CP29 (LHCB4)	56.8350	-0.2848
At4g38580	ATFP6 (FARNESYLATED PROTEIN 6); Metal Ion Binding	62.0690	-0.2886
At4g37870	ATP Binding / Phosphoenolpyruvate Carboxykinase (ATP)	43.0160	-0.1969
At4g35310	CPK5 (CALMODULIN-DOMAIN PROTEIN KINASE 5); Calcium- And Calmodulin-Dependent Protein Kinase/ Kinase	37.2590	-0.0488
At4g34230	Cad5 (Cinnamyl Alcohol Dehydrogenase 5)	46.1080	0.0111
At4g34200	EDA9 (Embryo Sac Development Arrest 9); NAD Binding / Amino Acid Binding / Cofactor Binding / Oxidoreductase, Acting On The CH-OH Group Of Donors, NAD Or NADP As Acceptor / Phosphoglycerate Dehydrogenase	47.7880	-0.4531
At4g34110	PAB2 (POLY(A)-BINDING PROTEIN 2); RNA Binding	46.7230	-0.3655
At4g32530	Vacuolar ATP Synthase, Putative / V-Atpase, Putative	40.9090	-0.1234
At4g30190	AHA2 (Arabidopsis H(+)-Atpase 2); Atpase	46.2230	-0.2945
At4g29010	AIM1 (ABNORMAL INFLORESCENCE MERISTEM); Enoyl-Coa Hydratase	40.8490	0.0881
At4g25130	Peptide Methionine Sulfoxide Reductase, Putative	46.3410	-0.1084
At4g24190	SHD (SHEPHERD); ATP Binding	46.7590	-0.2707
At4g23630	Bti1 (Virb2-Interacting Protein 1)	50.3940	-0.3516
At4g23400	PIP1;5/PIP1D (Plasma Membrane Intrinsic Protein 1;5); Water Channel	47.1220	-0.3019
At4g22310	Unknown Protein	41.9050	-0.1055
At4g15560	Cla1 (Cloroplastos Alterados 1)	33.5280	0.2790
At4g14880	Oasa1 (O-Acetylserine (Thiol) Lyase (Oas-Tl) Isoform A1)	38.2550	-0.0895
At4g14030	Selenium-Binding Protein, Putative	40.0430	0.0758
At4g13430	Aconitase Family Protein / Aconitate Hydratase Family Protein	37.5260	-0.0972
At4g10300	Unknown Protein	33.3330	0.1295
At4g09800	RPS18C (S18 RIBOSOMAL PROTEIN); Structural Constituent Of Ribosome	47.2970	-0.4091
At4g00360	CYP86A2 (ABERRANT INDUCTION OF TYPE THREE GENES 1); Oxygen Binding	63.2380	-0.2474
At3g62870	60S Ribosomal Protein L7A (RPL7aB)	57.5000	-0.5135
At3g61470	LHCA2 (Photosystem I Light Harvesting Complex Gene 2); Chlorophyll Binding	53.0120	-0.1664
At3g59970	MTHFR1 (METHYLENETETRAHYDROFOLATE REDUCTASE 1); Methylenetetrahydrofolate Reductase (NADPH)	41.6520	-0.2335
At3g55800	SBPASE (Sedoheptulose-Bisphosphatase); Phosphoric Ester Hydrolase	41.8920	0.0384
At3g54820	PIP2;5/PIP2D (Plasma Membrane Intrinsic Protein 2;5); Water Channel	55.6740	-0.4304
At3g54050	Fructose-1,6-Bisphosphatase, Putative / D-Fructose-1,6-Bisphosphate 1-Phosphohydrolase, Putative / Fbpase, Putative	50.7650	0.0448
At3g52580	40S Ribosomal Protein S14 (RPS14C)	39.8600	-0.2305
At3g50820	PSBO-2/PSBO2 (PHOTOSYSTEM II SUBUNIT O-2); Oxygen Evolving	56.4520	-0.2746
At3g47470	LHCA4 (Photosystem I Light Harvesting Complex Gene 4); Chlorophyll Binding	53.5860	-0.0590
At3g47370	Structural Constituent Of Ribosome	50.8770	-0.5380
At3g45640	ATMPK3 (MITOGEN-ACTIVATED PROTEIN KINASE 3); MAP Kinase/ Kinase/ Protein Kinase	38.3290	-0.0705
At3g44890	RPL9 (Ribosomal Protein L9); Structural Constituent Of Ribosome	47.5410	-0.1589
At3g44110	ATJ3 (Arabidopsis Thaliana Dnaj Homologue 3)	45.9950	-0.2160
At3g42050	Vacuolar ATP Synthase Subunit H Family Protein	47.4450	-0.2314
At3g25800	PDF1 (65 KDA REGULATORY SUBUNIT OF PROTEIN PHOSPHATASE 2A); Protein Phosphatase Type 2A Regulator	38.3490	-0.0963
At3g24420	Hydrolase, Alpha/Beta Fold Family Protein	54.8260	-0.1356
At3g24170	ATGR1; Glutathione-Disulfide Reductase	37.4460	-0.0596
At3g24160	Pmp (Putative Type 1 Membrane Protein)	36.5500	-0.0116
At3g22890	APS1 (ATP Sulfurylase 3)	44.4700	-0.1700
At3g18190	Chaperonin, Putative	45.4370	-0.3706
At3g13580	60S Ribosomal Protein L7 (RPL7D)	53.6040	-0.2321
At3g13080	ATMRP3 (Arabidopsis Thaliana Multidrug Resistance-Associated Protein 3)	40.0980	0.0430
At3g08590	2,3-Biphosphoglycerate-Independent Phosphoglycerate Mutase, Putative / Phosphoglyceromutase, Putative	37.9960	-0.1936

At3g04400	EMB2171 (EMBRYO DEFECTIVE 2171); Structural Constituent Of Ribosome	45.6520	-0.2888
At3g04090	Sip1;1 (Small And Basic Intrinsic Protein 1a)	51.6810	-0.3683
At3g02570	MEE31 (Maternal Effect Embryo Arrest 31); Mannose-6-Phosphate Isomerase	42.1050	0.0478
At3g02470	Samdc (S-Adenosylmethionine Decarboxylase)	58.6310	-0.3948
At3g01910	Sox (Sulfite Oxidase)	49.7310	-0.4106
At3g01090	AKIN10 (Arabidopsis SNF1 Kinase Homolog 10, SNF1-RELATED PROTEIN KINASE 1.1); Protein Kinase	44.7700	-0.1081
At2g47170	ARF1A1c (ADP-RIBOSYLATION FACTOR 1); GTP Binding / Phospholipase Activator/ Protein Binding	53.8010	-0.3439
At2g46280	TRIP-1 (TGF-BETA RECEPTOR INTERACTING PROTEIN 1); Nucleotide Binding	44.0890	-0.2934
At2g44310	Calcium-Binding EF Hand Family Protein	47.6920	0.2155
At2g44060	Late Embryogenesis Abundant Family Protein / LEA Family Protein	49.0000	-0.2071
At2g42500	PP2A-4 (Protein Phosphatase 2A-4); Protein Phosphatase Type 2A/ Protein Serine/Threonine Phosphatase	45.7630	-0.1276
At2g39570	ACT Domain-Containing Protein	38.0100	0.1217
At2g37270	ATRPS5B (RIBOSOMAL PROTEIN 5B); Structural Constituent Of Ribosome	48.7310	-0.4586
At2g37190	60S Ribosomal Protein L12 (RPL12A)	46.1040	-0.1340
At2g37040	PAL1 (PHE AMMONIA LYASE 1); Phenylalanine Ammonia-Lyase	44.9400	-0.0754
At2g36830	GAMMA-TIP (Tonoplast Intrinsic Protein (TIP) Gamma); Water Channel	56.0980	-0.3465
At2g36530	LOS2 (Low Expression Of Osmotically Responsive Genes 1); Phosphopyruvate Hydratase	49.5150	-0.4091
At2g34250	Protein Translocase	47.5880	-0.3743
At2g31610	40S Ribosomal Protein S3 (RPS3A)	40.0000	-0.2799
At2g28000	CPN60A (Chloroplast / 60 Kda Chaperonin Alpha Subunit); ATP Binding / Protein Binding / Unfolded Protein Binding	37.9370	-0.3967
At2g27600	AAA-Type Atpase Family Protein / Vacuolar Sorting Protein-Related	36.9350	-0.2239
At2g27020	PAG1 (20S Proteasome Alpha Subunit G1); Peptidase	40.7890	-0.2541
At2g21130	Peptidyl-Prolyl Cis-Trans Isomerase / Cyclophilin (CYP2) / Rotamase	50.3030	-0.1829
At2g20450	60S Ribosomal Protein L14 (RPL14A)	57.4800	-0.4520
At2g06050	Opr3 (Opda-Reductase 3)	43.5830	0.0591
At2g05840	PAA2 (20S Proteasome Alpha Subunit A2); Peptidase	38.5960	0.1300
At2g02760	ATUBC2 (UBIQUITING-CONJUGATING ENZYME 2); Ubiquitin-Protein Ligase	43.5370	0.1853
At1g80300	Chloroplast ADP, ATP Carrier Protein 1 / ADP, ATP Translocase 1 / Adenine Nucleotide Translocase 1 (AATP1)	50.8360	-0.1783
At1g79550	Pgk (Phosphoglycerate Kinase)	47.4800	-0.3617
At1g77760	Nia1 (Nitrate Reductase 1)	52.1080	-0.0684
At1g77610	Glucose-6-Phosphate/Phosphate Translocator-Related	43.9020	-0.1577
At1g74270	60S Ribosomal Protein L35a (RPL35aC)	65.1380	-0.2521
At1g73060	Unknown Protein	42.9430	-0.1932
At1g72750	ATTIM23-2 (Arabidopsis Thaliana Translocase Inner Membrane Subunit 23-2); Protein Translocase	41.4360	-0.2267
At1g69530	Atexpa1 (Arabidopsis Thaliana Expansin A1)	45.6000	0.0696
At1g58290	HEMA1; Glutamyl-Trna Reductase	35.8870	-0.0853
At1g54690	Histone H2A, Putative	33.8240	0.0708
At1g51200	DNA Binding / Zinc Ion Binding	48.7800	0.0585
At1g49760	PAB8 (POLY(A) BINDING PROTEIN 8); RNA Binding / Translation Initiation Factor	37.0700	-0.1372
At1g43800	Acyl-(Acyl-Carrier-Protein) Desaturase, Putative / Stearoyl-ACP Desaturase, Putative	56.0440	-0.1322
At1g32210	Atdad1 (Defender Against Apoptotic Death 1)	45.1330	-0.3585
At1g30230	Elongation Factor 1-Beta / EF-1-Beta	42.4660	-0.4372
At1g24020	Bet V I Allergen Family Protein	53.5210	-0.5308
At1g23290	RPL27A (RIBOSOMAL PROTEIN L27A); Structural Constituent Of Ribosome	55.2450	-0.3662
At1g17200	Integral Membrane Family Protein	43.8780	-0.4203
At1g16860	Merozoite Surface Protein-Related	36.2260	0.0091
At1g16180	TMS Membrane Family Protein / Tumour Differentially Expressed (TDE) Family Protein	43.1820	-0.2575
At1g15820	LHCB6 (LIGHT HARVESTING COMPLEX PSII); Chlorophyll Binding	58.7040	-0.3353

At1g15690	AVP1 (Vacuolar-Type H+-Pumping Pyrophosphatase 1)	43.5140	-0.4351
At1g12840	Det3 (De-Etiolated 3)	39.7660	-0.2275
At1g10940	ASK1 (ARABIDOPSIS SERINE/THREONINE KINASE 1); Kinase	43.6920	-0.0887
At1g09620	ATP Binding / Aminoacyl-Trna Ligase	41.4760	-0.2421
At1g07890	Apx1 (Ascorbate Peroxidase 1, Maternal Effect Embryo Arrest 6)	47.6600	-0.2690
At1g06680	PSBP-1 (OXYGEN-EVOLVING ENHANCER PROTEIN 2); Calcium Ion Binding	50.1990	-0.0944
At1g02130	ATRAB1B (Arabidopsis Thaliana Responsive To Abscisic Acid 1B); GTP Binding	40.3140	-0.1864
At1g01090	PDH-E1 ALPHA (PYRUVATE DEHYDROGENASE E1 ALPHA); Pyruvate Dehydrogenase (Acetyl-Transferring)	48.1010	-0.3322

Supplementary Table 7: Details of Arabidopsis housekeeping lowly expressed genes. GC_3 represents GC content at synonymous third codon position; wRn corresponds to error minimization values for Arabidopsis genes.

ARABIDOPSIS HOUSEKEEPING LOWLY EXPRESSED GENES			
GENE ID	***Functional description***	***GC3***	***wRN***
At1g03010	Phototropic-Responsive NPH3 Family Protein	39.1600	0.0848
At1g05690	BT3 (BTB And TAZ Domain Protein 3); Protein Binding / Transcription Regulator	41.4720	0.1309
At1g14130	2-Oxoglutarate-Dependent Dioxygenase, Putative	43.0070	0.2457
At1g18450	ATARP4 (ACTIN-RELATED PROTEIN 4); Structural Constituent Of Cytoskeleton	44.4720	-0.1354
At1g21410	F-Box Family Protein	44.0920	-0.0160
At1g34130	STT3B (STAUROSPORIN AND TEMPERATURE SENSITIVE 3-LIKE B); Oligosaccharyl Transferase	43.6260	-0.0577
At1g34300	Lectin Protein Kinase Family Protein	43.7740	-0.1373
At1g54940	Glycogenin Glucosyltransferase (Glycogenin)-Related	45.3510	0.2623
At1g56130	Leucine-Rich Repeat Family Protein / Protein Kinase Family Protein;	39.1480	0.2365
At1g79930	HSP91 (Heat Shock Protein 91)	45.3330	-0.4120
At2g19330	Leucine-Rich Repeat Family Protein	47.0590	-0.0967
At2g19440	Glycosyl Hydrolase Family 17 Protein	38.5780	0.0586
At2g19490	Reca Family Protein	34.7700	0.0312
At2g22370	Unknown Protein	29.1260	0.0135
At2g45240	MAP1A (METHIONINE AMINOPEPTIDASE 1A); Methionyl Aminopeptidase	34.2250	0.1409
At3g05320	Unknown Protein	37.8310	0.2822
At3g50360	ATCEN2 (CENTRIN2); Calcium Ion Binding	35.0990	0.2606
At3g58490	Phosphatidic Acid Phosphatase Family Protein / PAP2 Family Protein	44.6650	-0.1181
At4g02730	Transducin Family Protein / WD-40 Repeat Family Protein	42.7690	-0.2505
At4g08620	SULTR1;1 (Sulfate Transporter 1;1); Sulfate Transporter	49.5990	-0.1519
At4g10440	Dehydration-Responsive Family Protein	36.6720	0.1449
At4g22330	ATCES1 (ATCES1); Catalytic	49.4620	0.0090
At4g26610	Protein Kinase, Putative	39.8730	-0.0267
At4g27070	TSB2 (TRYPTOPHAN SYNTHASE BETA-SUBUNIT); Tryptophan Synthase	48.1900	-0.1929
At4g39830	L-Ascorbate Oxidase, Putative	49.1010	0.1367
At5g10930	CIPK5 (CBL-INTERACTING PROTEIN KINASE 5); Kinase	54.6130	0.2554
At5g11200	DEAD/DEAH Box Helicase, Putative	45.2690	-0.1607
At5g16970	AT-AER (ALKENAL REDUCTASE); 2-Alkenal Reductase	41.5380	-0.0824
At5g19530	Acl5 (Acaulis 5)	44.8390	-0.3001
At5g24940	Protein Phosphatase 2C, Putative / PP2C, Putative	34.9280	0.0759
At5g25450	Ubiquinol-Cytochrome C Reductase Complex 14 Kda Protein, Putative	40.1710	-0.0991
At5g35220	EGY1 (ETHYLENE-DEPENDENT GRAVITROPISM-DEFICIENT AND YELLOW-GREEN 1); Sterol Regulatory Element-Binding Protein Site 2 Protease	35.5340	0.1468
At5g40850	UPM1 (UROPHORPHYRIN METHYLASE 1); Uroporphyrin-III C-Methyltransferase	33.2370	0.1009
At5g42960	Unknown Protein	46.5690	-0.3561
At5g54750	Transport Protein Particle (TRAPP) Component Bet3, Putative	42.6900	-0.2300

Supplementary Table 8: Details of Arabidopsis tissue specific highly expressed genes. GC_3 represents GC content at synonymous third codon position; wRn corresponds to error minimization values for individual Arabidopsis genes.

ARABIDOPSIS TISSUE SPECIFIC HIGHLY EXPRESSED GENES			
Arabidopsis	***Functional description***	GC_3	***wRN***
At1g05010	EFE (Ethylene Forming Enzyme)	54.9830	-0.3395
At1g08380	Psao (Photosystem I Subunit O)	55.7970	0.2920
At1g11680	Cyp51g1 (Cytochrome P450 51); Oxygen Binding	45.1750	-0.0887
At1g12200	Flavin-Containing Monooxygenase Family Protein	49.7690	0.0329
At1g15130	Hydroxyproline-Rich Glycoprotein Family Protein	44.1480	-0.3099
At1g15690	Avp1 (Vacuolar-Type H+-Pumping Pyrophosphatase 1)	43.5140	-0.4351
At1g21720	Pbc1 (20s Proteasome Beta Subunit C1); Peptidase	42.9320	-0.2086
At1g29670	Gdsl-Motif Lipase/Hydrolase Family Protein	45.9380	0.1159
At1g48410	Ago1 (Argonaute 1)	36.7840	-0.0058
At1g55360	Unknown Protein	42.2220	-0.0436
At1g61720	Ban (Banyuls)	49.6790	0.1455
At1g67730	B-Keto Acyl Reductase, Putative (Glossy8)	39.4290	-0.0211
At1g70660	Mmz2 (Mms Zwei Homologe 2); Ubiquitin-Protein Ligase	40.9720	-0.0310
At1g74520	Athva22a (Arabidopsis Thaliana Hva22 Homologue A)	40.1200	-0.1931
At2g05990	Mod1 (Mosaic Death 1); Enoyl-[Acyl-Carrier-Protein] Reductase (Nadh)/ Oxidoreductase	37.3330	0.1768
At2g17190	Ubiquitin Family Protein	41.4870	-0.2281
At2g21270	Ubiquitin Fusion Degradation Ufd1 Family Protein	37.6270	-0.0407
At2g22330	Cyp79b3 (Cytochrome P450, Family 79, Subfamily B, Polypeptide 3); Oxygen Binding	48.2040	-0.1121
At2g33730	Dead Box Rna Helicase, Putative	41.0410	-0.3078
At2g44100	Atgdi1 (Arabidopsis Thaliana Guanosine Diphosphate Dissociation Inhibitor 1)	41.7270	-0.2253
At3g01910	Sox (Sulfite Oxidase)	49.7310	-0.4106
At3g08030	Unknown Protein	43.0640	-0.3687
At3g09250	Dna Binding / Nuclease	41.3330	0.0622
At3g13920	Eif4a1 (Eukaryotic Translation Initiation Factor 4a-1)	49.8710	-0.4750
At3g18190	Chaperonin, Putative	45.4370	-0.3706
At3g18410	Nadh-Ubiquinone Oxidoreductase-Related	53.1910	-0.2896
At3g20050	Attcp-1 (Arabidopsis Thaliana T-Complex Protein 1 Alpha Subunit); Atp Binding / Protein Binding / Unfolded Protein Binding	42.4060	-0.1059
At3g24170	Atgr1; Glutathione-Disulfide Reductase	37.4460	-0.0596
At3g25800	Pdf1 (65 Kda Regulatory Subunit Of Protein Phosphatase 2a); Protein Phosphatase Type 2a Regulator	38.3490	-0.0963
At3g45640	Atmpk3 (Mitogen-Activated Protein Kinase 3); Map Kinase/ Kinase/ Protein Kinase	38.3290	-0.0705
At3g45970	Atexla1 (Arabidopsis Thaliana Expansin-Like A1)	42.8570	0.0118
At3g50820	Psbo-2/Psbo2 (Photosystem Ii Subunit O-2); Oxygen Evolving	56.4520	-0.2746
At3g51240	F3h (Transparent Testa 6); Naringenin 3-Dioxygenase	51.5150	-0.2120
At3g52850	Atelp1 (Vacuolar Sorting Receptor Homolog)	41.2270	-0.0762
At3g54210	Ribosomal Protein L17 Family Protein	43.9610	-0.1139
At3g58610	Ketol-Acid Reductoisomerase	45.2420	-0.2699
At3g63140	Mrna-Binding Protein, Putative	57.0310	-0.4050
At4g21110	G10 Family Protein	45.0380	0.3328
At4g25130	Peptide Methionine Sulfoxide Reductase, Putative	46.3410	-0.1084

At4g29480	Atp Synthase G Subunit Family Protein	53.9820	-0.0532
At4g30210	Atr2 (Arabidopsis P450 Reductase 2)	36.5440	-0.0431
At4g35260	Idh1 (Isocitrate Dehydrogenase 1); Isocitrate Dehydrogenase (Nad+)	47.2300	-0.1616
At4g37390	Ydk1 (Auxin Upregulated1, Yadokari 1); Indole-3-Acetic Acid Amido Synthetase	50.5400	0.1042
At4g37930	Shm1 (Serine Hydroxymethyltransferase 1); Glycine Hydroxymethyltransferase	39.0400	-0.2133
At4g38130	Hd1 (Histone Deacetylase 19, Histone Deacetylase19)	44.0860	-0.4026
At5g01750	Unknown Protein	62.0850	-0.1003
At5g05200	Abc1 Family Protein	39.4510	0.0374
At5g14040	Phosphate Transporter	47.7900	-0.3445
At5g15490	Udp-Glucose 6-Dehydrogenase, Putative	49.4480	-0.2707
At5g23740	Rps11-Beta (Ribosomal Protein S11-Beta); Structural Constituent Of Ribosome	47.7420	-0.3773
At5g24710	Unknown Protein	34.7590	0.0256
At5g26360	Chaperonin, Putative	37.4760	-0.2310
At5g27640	Tif3b1 (Eukaryotic Translation Initiation Factor 3b); Nucleic Acid Binding / Translation Initiation Factor	47.4700	-0.4395
At5g35630	Gs2 (Glutamine Synthetase 2)	40.8980	-0.1428
At5g47500	Pectinesterase Family Protein	50.9860	-0.0380
At5g53300	Ubc10 (Ubiquitin-Conjugating Enzyme 10); Ubiquitin-Protein Ligase	58.7410	-0.3385
At5g53560	Atb5-A (Cytochrome B5 A)	44.1860	-0.1322
At5g55280	Ftsz1-1 (Ftsz1-1); Structural Molecule	35.0120	0.0521
At5g58420	40s Ribosomal Protein S4 (Rps4d)	52.9880	-0.3444
At5g66140	Pad2 (20s Proteasome Alpha Subunit D2); Peptidase	51.9650	-0.5482

Supplementary Table 9: Details of Arabidopsis tissue specific lowly expressed genes. GC_3 represents GC content at third codon position; wRn corresponds to error minimization values for individual Arabidopsis genes.

ARABIDOPSIS TISSUE SPECIFIC LOWLY EXPRESSED GENES			
GENE ID	***Functional Description***	***GC_3***	***wRN***
At1g03010	Phototropic-Responsive NPH3 Family Protein	39.1600	0.0848
At1g11800	Endonuclease/Exonuclease/Phosphatase Family Protein	44.3910	0.0301
At1g13580	Lag13 (Lag1 Longevity Assurance Homolog 3)	41.3790	0.1075
At1g13920	Remorin Family Protein	39.2280	0.0335
At1g18800	NRP2 (NAP1-RELATED PROTEIN 2); DNA Binding / Chromatin Binding / Histone Binding	44.6510	0.0515
At1g28010	PGP14 (P-GLYCOPROTEIN 14); Atpase, Coupled To Transmembrane Movement Of Substances	39.3710	0.3670
At1g34130	STT3B (STAUROSPORIN AND TEMPERATURE SENSITIVE 3-LIKE B); Oligosaccharyl Transferase	43.6260	-0.0577
At1g47550	Unknown Protein	38.0050	0.2038
At1g49180	Protein Kinase Family Protein	38.2750	-0.0489
At1g49910	WD-40 Repeat Family Protein / Mitotic Checkpoint Protein, Putative	34.4720	0.1891
At1g56130	Leucine-Rich Repeat Family Protein / Protein Kinase Family Protein;	39.1480	0.2365
At1g62310	Transcription Factor Jumonji (Jmjc) Domain-Containing Protein	36.0410	0.3533
At1g62860	Hypothetical Protein	43.4870	-0.2307
At1g69440	Ago7 (Argonaute7)	39.9350	-0.0015
At1g74110	CYP78A10 (Cytochrome P450, Family 78, Subfamily A, Polypeptide 10); Oxygen Binding	51.0890	-0.3194
At2g01900	Endonuclease/Exonuclease/Phosphatase Family Protein	41.4140	0.3752
At2g03620	Magnesium Transporter Cora-Like Family Protein (MRS2-5)	39.7440	0.0368
At2g05910	Unknown Protein	44.6240	0.3134
At2g07698	ATP Synthase Alpha Chain	40.6640	0.0452
At2g16730	BGAL13 (Beta-Galactosidase 13); Beta-Galactosidase	44.3870	-0.0698
At2g17140	Binding	40.8820	0.2452
At2g19440	Glycosyl Hydrolase Family 17 Protein	38.5780	0.0586
At2g20750	Atexpb1 (Arabidopsis Thaliana Expansin B1)	56.2260	-0.1472
At2g21480	Protein Kinase Family Protein	41.1120	0.0209
At2g21960	Unknown Protein	41.7680	-0.0834
At2g26350	PEX10 (Peroxin 10); Protein Binding / Zinc Ion Binding	35.0340	0.2080
At2g30530	Unknown Protein	39.7630	-0.1942
At2g35720	DNAJ Heat Shock N-Terminal Domain-Containing Protein	39.1130	0.2766
At2g41670	GTP-Binding Family Protein	38.9190	-0.0936
At2g44525	Unknown Protein	40.3730	0.0284
At2g46050	Pentatricopeptide (PPR) Repeat-Containing Protein	39.4970	0.1114
At3g02330	Pentatricopeptide (PPR) Repeat-Containing Protein	41.1470	0.2699
At3g03420	Ku70-Binding Family Protein	33.7020	0.3163
At3g05640	Protein Phosphatase 2C, Putative / PP2C, Putative	47.4780	0.1426
At3g08620	KH Domain-Containing Protein	37.2090	0.2269
At3g12040	DNA-3-Methyladenine Glycosylase (MAG)	34.7280	-0.0331
At3g20300	Extracellular Ligand-Gated Ion Channel	44.9310	-0.1784
At3g27470	Unknown Protein	41.9790	0.0677

At3g45070	Sulfotransferase Family Protein	39.9330	0.0545
At3g46340	Leucine-Rich Repeat Protein Kinase, Putative	35.0540	0.2975
At3g50100	Exonuclease Family Protein	34.2250	0.3060
At3g53090	UPL7 (Ubiquitin-Protein Ligase 7); Ubiquitin-Protein Ligase	34.7660	0.1938
At3g56220	Unknown Protein	37.3240	0.0383
At3g57910	D111/G-Patch Domain-Containing Protein	36.9860	-0.0687
At4g19460	Glycosyl Transferase Family 1 Protein	48.0210	0.1767
At4g21300	Pentatricopeptide (PPR) Repeat-Containing Protein	35.3300	0.0537
At4g23160	Protein Kinase Family Protein	51.1540	-0.0192
At5g03030	DNAJ Heat Shock N-Terminal Domain-Containing Protein	35.1850	-0.1943
At5g04500	Glycosyltransferase Family Protein 47	40.9900	-0.0596
At5g10620	Unknown Protein	40.9840	-0.0462
At5g14670	ATARFA1B (ADP-Ribosylation Factor A1B); GTP Binding / Phospholipase Activator/ Protein Binding	51.6850	-0.3622
At5g15300	Pentatricopeptide (PPR) Repeat-Containing Protein	37.8660	-0.0196
At5g17270	Tetratricopeptide Repeat (TPR)-Containing Protein	39.4380	0.0669
At5g18390	Pentatricopeptide (PPR) Repeat-Containing Protein	44.6760	-0.2984
At5g19020	Pentatricopeptide (PPR) Repeat-Containing Protein	44.2700	-0.1441
At5g24940	Protein Phosphatase 2C, Putative / PP2C, Putative	34.9280	0.0759
At5g26860	LON_ARA_ARA (Lon Protease Homolog Gene); ATP Binding / ATP-Dependent Peptidase/ Serine-Type Peptidase	39.7890	-0.0031
At5g42990	UBC18 (Ubiquitin-Conjugating Enzyme 16); Ubiquitin-Protein Ligase	38.3120	0.1699
At5g54170	Unknown Protein	38.6850	0.0030
At5g57110	ACA8 (AUTOINHIBITED CA2+ -ATPASE, ISOFORM 8); Calmodulin Binding	33.5080	0.1082
At5g57890	Anthranilate Synthase Beta Subunit, Putative	39.5260	-0.0315