

Isolation and identification of ubiquitin-related proteins from *Arabidopsis* seedlings

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Supplementary data

Figure S1. Respective SDS-PAGE images of proteins immunopurified with FK2 obtained from three independent experiments (Ex1, Ex2, and Ex3). The staining pattern of the purified proteins was reproducible.

Table S1. Ub-related proteins identified from *Arabidopsis* seedlings.

Table S2. Proteins containing potential ubiquitination-targeting signal motifs for Ub/proteasome-dependent proteolysis.

Fig. S1

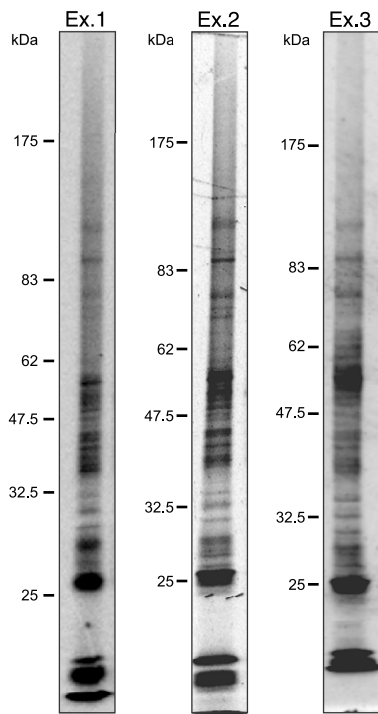


Table S1 : Ub-related proteins identified from *Arabidopsis* seedlings.

Protein number	Score	At number	Description	Peptide sequence	Charge state	Modification	Gel pieces	Motifs
1^a	325	At1g13440 At3g04120	GAPC-2; glyceraldehyde-3-phosphate dehydrogenase GAPC; glyceraldehyde-3-phosphate dehydrogenase C subunit	K.LTGMSFR.V	2+	Oxidation (M)	4	-
				R.IGINGFGR.I	2+			
				R.AASFNIPSSSTGAAK.A	2+			
				K.TLLFGKEKPTVFGIR.N	3+			
				K.DAPMFVGVNEHEYK.S	3+			
				R.FGIVEGLMTTVHSITATQK.T	3+			
				K.GILGYTEDDVVSTDFVGDNR.S	3+			
K.KVVISAPSK.D	2+							
2^b	316	At2g04030	CR88 (EMBRYO DEFECTIVE 1956); ATP binding	R.EETDPDNL.R	2+	Oxidation (M)	1	+
				R.ELVSNASDALDK.L	2+			
				K.SGETEVVEPSEVR.A	2+			
				K.GVVDSDDLPLNVS.R	2+			
				K.AQALGDTSSLEFMR.G	2+			
				R.TIEVEDEPVEKEGEEGEPK.K	3+			
				R.VLATLYEK.D	2+			
K.VLFDSPRK.V	2+							
3	292	At2g47730	Glutathione S-transferase 6, chloroplast precursor	K.DLQFELIPVDMR.A	2+	Oxidation (M)	6	+
				K.VLDVYEAR.L	2+			
				K.VHGVPMSSTATMR.V	3+			
				R.AITQYLAEYSEK.G	2+			
				K.GMFGMTTDPAAVQLEGK.L	3+			
				K.SEVLDFIR.S	2+			
				R.YLYPHFR.F	2+			
4	269	At4g24820	Probable 26S proteasome non-ATPase regulatory subunit 6, RPN7	K.VVDAPEILTVLGK.I	2+	Oxidation (M)	1	+
				K.VAGVLETNRPDAK.N	3+			
				K.LFLTLHPDVPDIEK.V	3+			
				K.AFGVSVDFIDQELSR.F	2+			
				K.DTDILAAFR.V	2+			
				R.ESTLGFVDLLR.D	2+			
				K.LTYTYPEYETK.D	2+			
5	264	AtCG00490	Ribulosebiphosphate carboxylase	K.TFQGPPIHQVER.D	3+	Oxidation (M)	17	-
				R.ESTLGFVDLLRDDYVEK.D	3+			
				R.GGLDFTKDDENVNSQPFMR.W	3+			
				K.AAQEALYVR.C	2+			
				R.NLNAMNQLK.T	2+			
				K.ANSEATLGTYK.G	2+			
				K.VSPEVIAEHTVR.A	3+			
6^b	247	At3g52930	Fructose biphosphate aldolase-like protein	K.RLASINVENVETNR.R	3+	Oxidation (M)	7	-
				R.TVPAVPAIVFLSGGQSEEEATR.N	3+			
				K.LFVDILK.E	2+			
				K.GILAADESTGTIGK.R	2+			
				K.YYEAGAR.F	2+			
				K.FADELIANAAYIGTPGK.G	2+			
				R.NLLSVAYK.N	2+			
7	245	At4g09000	14-3-3-like protein GF14 chi	K.DSTLIMQLLR.D	2+	Oxidation (M)	4	-
				R.IISSIEQKEESR.G	3+			
				K.LLDTILVPAASGDSK.V	2+			
				K.AAQDIANSELAPTHPIR.L	3+			
				K.EAAPAAAKPADEQQS.-	2+			
				K.VLDVYEAR.L	2+			
				K.LAFEQIFK.S	2+			
8	231	At4g02520	Glutathione S-transferase PM24	R.NPFGQVPFEDGDLK.L	2+	Oxidation (M)	6	-
				K.SIYGLTTDEAVVAEEEA.K.L	2+			
				K.SLSMVYNR.K	2+			
				K.YLEAGTLPTAK.E	2+			
				K.GLGLYTVISVGK.K	2+			
				R.ALQESLASELAAR.M	2+			
				K.ITGEILEIVAGANAQV.-	2+			
9	213	At4g04640	ATP synthase gamma chain	K.NVSLYQFR.N	2+	Oxidation (M)	7	+
				R.VQFTEYVQK.N	2+			
				R.LVIAPPNFVIK.I	2+			
				R.NGIPLSTAAANFTR.G	2+			
				K.LVAASGEPGDR.V	2+			
				R.GELATALR.K	2+			
				K.VAINGFGR.I	2+			
10	201	At4g14800	Proteasome subunit beta type-2-B	K.IIQVSVNR.N	2+	Oxidation (M)	2	-
				K.TFAEEVNAAFR.D	2+			
				R.KDSPLDIIAINDTGGVK.Q	3+			
				K.YSEGYPGAR.Y	2+			
				K.FAQTLMER.G	2+			
				K.VLEAVHIASNK.N	2+			
				K.AYQEQVLSNSAK.F	2+			
11	191	At4g37930	Glycine hydroxymethyltransferase like protein	R.HYYSIAINYR.K	2+	Oxidation (M)	1	-
				R.SINPQITMLGQEP.R.Q	2+			
				K.TNEQTVQEMLSLAAK.Y	2+			
				R.AGVPMVEMGLMLGEFVDEYTVR.V	3+			
				R.AVAVVVDPIQSVK.G	2+			
				K.VVIDAFR.S	2+			
				K.WTDGLTLR.R	2+			
12	187	At5g23540	26S proteasome subunit RPN11	K.AVQEEDELSPEK.L	2+	3 Oxidation (M)	3	+
				R.AVLSSSGFQADV.K.A	2+			
				R.MSTGYSILSR.D	2+			
				R.FEETLYGTSR.L	2+			
				R.YTGGMVPDVNQIVK.E	2+			
				K.GFPGTHEFLLDDEGK.W	3+			
				K.LTGITGGDQVAAMGIYGP.R.T	3+			
13	185	At3g60820	PBF1 (20S proteasome beta subunit F1)	K.LLSVVSGLNR.G	2+	Oxidation (M)	1	+
				R.LLYSSAFSSR.S	2+			
				R.GLVASVDDLER.A	2+			
				R.YTGGMVPDVNQIVK.E	2+			
				K.GFPGTHEFLLDDEGK.W	3+			
				K.LTGITGGDQVAAMGIYGP.R.T	3+			
				K.LTGGMVPDVNQIVK.E	2+			
14^a	181	At3g55800	Sedoheptulose-bisphosphatase precursor	R.FEETLYGTSR.L	2+	Oxidation (M)	1	+
				R.YTGGMVPDVNQIVK.E	2+			
				K.GFPGTHEFLLDDEGK.W	3+			
				K.LTGITGGDQVAAMGIYGP.R.T	3+			
				K.LLSVVSGLNR.G	2+			
				R.LLYSSAFSSR.S	2+			
				R.GLVASVDDLER.A	2+			
15	181	At3g23400	Harpin binding protein 1	K.LLSVVSGLNR.G	2+	Oxidation (M)	1	+
				R.LLYSSAFSSR.S	2+			
				R.GLVASVDDLER.A	2+			
				R.YTGGMVPDVNQIVK.E	2+			
				K.GFPGTHEFLLDDEGK.W	3+			
				K.LTGITGGDQVAAMGIYGP.R.T	3+			
				K.LTGGMVPDVNQIVK.E	2+			
16	181	At3g23400	Harpin binding protein 1	R.LLYSSAFSSR.S	2+	Oxidation (M)	1	+
				R.GLVASVDDLER.A	2+			
				R.YTGGMVPDVNQIVK.E	2+			
				K.GFPGTHEFLLDDEGK.W	3+			
				K.LTGITGGDQVAAMGIYGP.R.T	3+			
				K.LTGGMVPDVNQIVK.E	2+			
				R.LLYSSAFSSR.S	2+			

17	178	At2g30200	Binding / catalytic/ transferase	R.LEAALAATEIR.S K.SAMVSIIGLDSEK.V K.LRGEAMQAAADAAS.S	2+ 2+ 3+	Oxidation (M) Oxidation (M)	1	+
18	176	At1g32060	Ribulose-5-phosphate kinase	K.FYGEVTQGMK.H R.ANDFDLMYEQVK.A K.HADFPGSNNGTGLFQTIVGLK.I	2+ 2+ 3+	Oxidation (M) Oxidation (M)	1	+
19	172	At2g39730	Rubisco activase	R.GLAYDTSDDQDITR.G R.EGPPVFEQPEPTYEK.L K.LMEYGNMLVMEQENVKR.V R.VQLAETYLSQLAALGDANADAIGR.G	2+ 2+ 3+ 3+	Oxidation (M) 3 Oxidation (M)	2	+
20	163	At1g30630	Coatomer protein epsilon subunit family protein	K.ESTISL.R.E R.AASAEDNFER.A K.LLAMYLSSPENK.E K.LSHPEHLVLR	2+ 2+ 2+ 2+	Oxidation (M)	4	+
21	163	At5g43010	26S proteasome RPT4A	R.TAAVSEYR.K K.VVSSAIDK.Y K.GVLLYGPPGTGK.T R.AIASNIDANFLK.V K.SLQSVGQIIGEVLRPLDNER.L R.VLDMTTLTIMR.A	2+ 2+ 2+ 2+ 3+ 2+	2 Oxidation (M)	2	+
22	162	At4g14880	Cysteine synthase	R.YLSTVLFDAIR.K K.LFVAIFPSFGER.Y K.IDGFVSGIGTGTITGAGK.Y	2+ 2+ 2+		2	+
23	162	At1g35160	RF4 (General regulatory factor 4)	K.DSTLIMQLLR.D R.KDAAEHTLTAYK.A R.YEEMVEFMEK.V K.AAQDIANAELAPTHPIR.L	2+ 3+ 2+ 3+	Oxidation (M) 2 Oxidation (M)	2	+
24	162	At1g78300	GRF2; protein phosphorylated amino acid binding	R.NLLSVAYK.N K.DSTLIMQLLR.D R.IISIEQKEESR.G K.SAQDIANAELAPTHPIR.L	2+ 2+ 3+ 2+	Oxidation (M)	2	-
25	162	At5g14740	beta carbonic anhydrase 2	R.NIANMVPPFDK.V K.ITAELQAASSDSK.S M.GNESYEDAIEALK.L	2+ 2+ 3+	Oxidation (M)	2	+
26 ^b	162	At4g14960 At1g50010 At1g04820	Tubulin alpha-6 chain TUA2 (tubulin alpha-2 chain) tubulin alpha-2/alpha-4 chain	R.LVSVQVISSLTASLR.F R.AVFVLDLEPTVIDEVR.T R.IHFMLSSYAPVISAER.A K.DVNAAVGTIK.T	3+ 2+ 3+ 2+	Oxidation (M)	4	+
27	159	At1g45000	26S proteasome regulatory complex subunit p42D, putative	R.TAAVTDYR.K K.VVSSAIDK.Y K.GVLLYGPPGTGK.T R.VLDMTTLTIMR.A R.AIASNIDANFLK.V K.SLQSVGQIIGEVLRPLDNER.L	2+ 2+ 2+ 2+ 2+ 3+	2 Oxidation (M)	2	+
28 ^b	155	At1g78900	Vacuolar-type H+-ATPase subunit A	R.LASFYER.A K.LYDDLNAGFR.A K.LAADTPLL TGQR.V R.VGHDNLIGEIR.L K.YSTALESFYEK.F R.LAEMPADSGYPAYLAAR.L R.EDDLNEIVQLVGK.D R.TTLVANTSNMPPVAAR.E	2+ 2+ 2+ 3+ 2+ 2+ 2+	Oxidation (M) Oxidation (M)	2	+
29	152	At3g11630	2-cys peroxiredoxin, chloroplast (BAS1)	K.AQADDLPLVGNK.A K.EGVQIHSTINNLGIGR.S K.SGGLGDLNLYPLISDVTK.S	2+ 3+ 2+		1	+
30	150	At3g60750	Transketolase	K.TPSLALS.R.Q K.VTTTIGYGSFNK.A R.NLSQQCLNALAK.V K.ALPTYTPESPGDATR.N K.ESVLPDVSAR.V	2+ 2+ 2+ 2+ 2+		4	+
31	149	At1g20620	CAT3 (CATALASE 3); catalase	R.DEEINYPSPK.F K.VPTPTNSVTGIR.T R.HMEGFGVHTYTLIAK.S R.DGIQFPDVVHALKPNPK.T	2+ 2+ 3+ 2+	Oxidation (M)	1	+
32	148	At2g27020	PAG1 (20S proteasome alpha subunit G1)	K.AVDNSGTVVGIK.C K.MMLPGSNR.R R.SYESVYGDVAVPK.E	2+ 2+ 2+		3	-
33	147	AtMg01190	ATP synthase subunit alpha, mitochondrial	R.GIRPAINVGLSVSR.V R.NFYANFQVDEIGR.V K.AILNSVKPELLQALK.G R.EVAFAQFGSDLDAAATQALLNR.G K.AVDSLVPIGR.G K.SVHEPMQTGLK.A	3+ 2+ 3+ 3+ 2+ 3+		4	-
34	145	At3g02090	Putative mitochondrial processing peptidase	R.VSDADVTR.A R.IDAVDASTVK.R R.EDLQNYIK.T	2+ 2+ 2+		1	+
35	142	At3g14420	Glycolate oxidase/ oxidoreductase	K.AIALTVDTPLR.L R.IPVFLDGGVR.R R.FTLPPNLT.LK.N K.MAHPDGEYATAR.A	2+ 2+ 2+ 3+	Oxidation (M)	1	-
36	141	At4g38970	Putative fructose-bisphosphate aldolase	R.ATPEQVAAYTLK.L R.LDSIGLENTAANR.Q	2+ 2+		2	-
37	140	At4g09320	Nucleoside diphosphate kinase 1	R.NVIHGSDSVESAR.K K.IIGATNPAASEPGTIR.G	2+ 2+		3	-
38	140	At1g16470 At1g79210	Proteasome subunit alpha type-2-A 20S proteasome alpha subunit B, putative	K.EGFEGEISSK.N K.KLPSILVDEASVQK.I	2+ 3+		2	-
39	138	AtCG00120	ATPase alpha subunit	R.ELIIGDR.Q R.VINALANPIDGR.G R.LIESPAPGIIISR.R K.EGIIQEQLER.F K.IAQIPVSEAYLGR.V	2+ 2+ 2+ 2+ 2+		4	-
40	137	At2g31610	40S ribosomal protein S3 (RPS3A)	K.TPLPDVVIHAPK.D R.ELAEDGYSYGVVVR.V K.FKDGVMVSSGGPTK.E	3+ 2+ 3+	Oxidation (M)	1	+

41	134	At2g28000	60-kDa chaperonin-60 alpha-polypeptide	R.NVVDEFGSPK.V K.TVQGLIEELQK.K K.DIIPILEK.T K.VVNDGVTIAR.A	2+ 2+ 2+ 2+		2	+
42	130	At2g42600	ATPPC2 (PHOSPHOENOLPYRUVATE CARBOXYLASE 2)	R.VTPEVTR.D K.NIGINER.V R.TPPTPODEMRA R.EIQAAFR.T R.LATPELEYGR.M R.FVEYFRL	2+ 2+ 2+ 2+ 2+ 2+		3	+
43	129	At5g20720	Cpn21 protein	K.DGSNYIALR.A K.EKPSIGTVIAGPGSLDEEGK.I	2+ 3+		1	-
44	129	At1g21720	Putative 20S proteasome beta subunit PBC2	R.DMKPETFASLVSAILYK.R R.VFIGLSGLATDVQTLTYQR.L	2+ 2+	Oxidation (M)	2	+
45	128	At3g28300	AT14A (At14a-2 integrin - like protein)	K.ITSMNLNAV.K K.DATEDGANEVDTK.Q	2+ 2+	Oxidation (M)	1	+
46	126	At2g05840	PAA2 (20S PROTEASOME SUBUNIT PAA2)	K.ATEIEVGVVRA K.YLGLLATGMTADSR.S	2+ 2+	Oxidation (M)	1	+
47	125	At3g62030	Peptidyl-prolyl cis-trans isomerase CYP20-3	K.FEDENFTLK.H R.IVMGLFGEVVPK.T K.HVVFQGVIEGMK.L	2+ 2+ 2+	Oxidation (M) Oxidation (M)	1	-
48	123	At5g38420	Ribulose biphosphate carboxylase small chain 2B	K.EVDYLLR.N R.IIGFDNTR.Q K.KFETLSYLPDLSDELAK.E	2+ 2+ 3+		6	+
49	122	At5g09900	26S proteasome subunit RPN5a	K.SMIGGSLGDK.A K.HLSEMVVSK.A K.IAFILEQVR.L K.TLNNVSAGK.I K.NLSEIPDFK.M K.IAFILEQVR.L K.YKDEFEK.E	2+ 2+ 2+ 2+ 2+ 2+ 2+	Oxidation (M) Oxidation (M)	3	-
50	122	At2g47510	FUM1 (FUMARASE 1); fumarate hydratase	R.LIADASASFEK.N R.SLQNFIEIGGER.E K.VNMEYGLDPTIGK.A	2+ 2+ 2+	Oxidation (M)	1	+
51	122	At2g43750	Cysteine synthase, chloroplast/chromoplast precursor	K.LIAVVFPSFGER.Y R.AFGAELVLTTEPAK.G	2+ 2+		2	+
52 ^a	122	At3g58700 At4g18730 At5g45775 At2g42740	Ribosomal protein L16 60S ribosomal protein L11 (RPL11D) RPL16A (ribosomal protein large subunit 16A)	K.YEGVILNK.S K.AMQLLESGLK.V K.VLEQLSGQTPVFSK.A	2+ 2+ 2+	Oxidation (M)	1	-
53	121	At1g04410	Malate dehydrogenase/ oxidoreductase	R.LSVPVSDVK.N K.MELIDAAFPLK.G K.MDLTAEELKEEK.D	2+ 2+ 3+	Oxidation (M) Oxidation (M)	1	-
54	120	At2g20580	26S proteasome subunit RPN1a	K.TPEDIYK.A R.NLSSYYK.D R.TCNYLTSAAAR.Y K.AFHETMADSDLKK.Y K.VQDLLAQCGHELEK.G	2+ 2+ 2+ 3+ 3+	Oxidation (M)	1	-
55	119	At4g02770	Putative photosystem I reaction center subunit II precursor	K.TDSSAAAAAAPATK.E R.VFPNGEVQYLHPK.D	2+ 3+		4	-
56	115	At1g64520	26S proteasome subunit RPN12	K.TEDQDAFER.D R.DIYEHAVVLSVK.T K.AYDYVSISDAR.Q	2+ 3+ 2+		5	+
57	112	At1g29150	26S proteasome subunit RPN6a	R.LAALLMENK.E K.LRPFSLIPK.A K.AGLQYVGPDLAMK.A K.EYVEALALLSTLVK.E	2+ 3+ 2+ 2+	Oxidation (M) Oxidation (M)	2	+
58	110	At1g09100 At3g05530	RPT5B (26S proteasome AAA-ATPase subunit RPT5B) RPT5A (regulatory particle triple-A 5A)	R.FDSEVSGDR.E R.STDDFNQAQLK.A K.QIQELVEAIVLPMTHK.E	2+ 2+ 3+	Oxidation (M)	1	+
59	109	At2g30860	ATGSTF9; glutathione transferase	R.ALVTIEK.G R.SQGPDLLGK.T K.LAGVLDVYEAHLSK.S	2+ 2+ 3+		1	-
60 ^b	108	At2g01250	Structural constituent of ribosome / transcription regulator	R.IALTDNSIVEQALGK.H	2+		1	+
61	107	At1g07890	APX1; L-ascorbate peroxidase	R.TGGPFGTMR.F K.EGLLQLVSDK.A R.EDKPPPPPEGR.L K.ALLDDPVFRPLVEK.Y	2+ 2+ 3+ 3+	Oxidation (M)	1	-
62	106	At4g28750	Photosystem I subunit PSI-E-like protein	R.AAEDPAPASSSK.D K.NVGSVVAVDQDPK.T	2+ 2+		2	+
63	104	At5g35590	PAA1 (20S proteasome alpha subunit A1)	K.TAGITSIGVR.G K.EQEAVNFLEK.K	2+ 2+		2	+
64	102	At3g22630	Proteasome subunit beta type-2-A	K.NVSLYKFR.N R.VQFTEYVQK.N	2+ 2+		1	+
65	102	At2g36160	40S ribosomal protein S14 (RPS14A)	K.TPGPGAQSALR.A K.VDVVTLGFSVR.E	2+ 2+		3	+
66 ^b	99	At4g20360	Elongation factor Tu precursor	K.VGETVDLVGLR.E	2+		2	-
67 ^a	98	At5g10860	Uncharacterized protein At5g10860, mitochondrial precursor	K.LITVTPETK.V K.VGDMTEENK.L	2+ 2+		4	+
68	96	At3g13120	30S ribosomal protein S10, chloroplast, putative	R.FHFEIR.T K.TMGPVPLPTK.K	2+ 2+		2	+
69 ^b	96	At3g17390	MTO3; methionine adenosyltransferase	K.ANVDYEQIVR.K K.IPDKEILEIVK.E R.FVIGGPHGDAGLTGR.K K.SIVASGLAR.R	2+ 3+ 3+ 2+		8	-
70	96	At5g19990 At5g20000	26S proteasome AAA-ATPase subunit Similar to 26S proteasome AAA-ATPase subunit RPT6a	K.GVLLYGGPPGTGK.T K.HPELFESLGIAPK.G	2+ 3+		1	+
71	95	At1g65930	Isocitrate dehydrogenase (NADP+)-oxidoreductase	R.LIDDMVAYALK.S K.LITPFVELDIK.Y R.AFADASMNTAYEK.K	2+ 2+ 2+	Oxidation (M)	1	-
72	94	At3g20820	Leucine-rich repeat family protein	R.VADINLR.G R.LSAITADWK.G R.LAVLNVADNR.I	2+ 2+ 2+		2	+

				R.IPESLTNIYR.L	2+			
73	94	At4g25100	FSD1 (FE SUPEROXIDE DISMUTASE 1); iron superoxide dismutase	K.TFMTNLVSWAVSAR.L	2+	Oxidation (M)	1	-
74	92	At5g04590	Sulfite reductase	R.NVLAPAAPYVK.K K.VGLDYDESIVIR.V	2+ 2+		1	+
75	92	At1g05190	EMB2394; structural constituent of ribosome	K.MQIPDSLK.V R.TLTDNMVVGVS.K.G	2+ 2+	Oxidation (M) Oxidation (M)	1	+
76	92	At2g21330	Fructose-bisphosphate aldolase, putative	K.ANSLAQLGK.Y K.AAQDILLAR.A	2+ 2+		1	-
77	91	At5g36790	Putative p-nitrophenylphosphatase	K.ISDFLSPK.A K.VYVIGEEGILK.E	2+ 2+		1	-
78	91	At1g47250	PAF2 (20S proteasome alpha subunit F2)	R.ETLQGETLK.S	2+		2	+
		At5g42790	PAF1; endopeptidase/ peptidase/ threonine endopeptidase	K.VDDHIGVAIAGLTADGR.V	3+			
79	90	At5g58290	26S proteasome AAA-ATPase subunit RPT3 (RPT3)	R.FDAQTGADR.E R.VVGSEFVQK.Y	2+ 2+		1	+
80	90	At5g14320	30S ribosomal protein S13, chloroplast precursor	R.HIQGLPCR.G R.VGGVEIPANK.R	2+ 2+		2	+
81	89	At5g04140	Ferredoxin-dependent glutamate synthase	K.LVAAEAGIGTVASGVAK.G K.VAQGAKPGEQGLPGK.K R.ICHTNNCPVGVASQR.E	2+ 3+ 3+		2	+
82	88	At1g12840	DET3 (DE-ETIOLATED 3)	R.GQLNAINR.K K.LVQDQESLR.S R.VAEYNNIR.G	2+ 2+ 2+		2	+
83	88	At3g07090	Unknown protein	K.LEAAETSTATEK.V	2+		1	-
84	87	At1g68010	HPR (Hydroxyppyruvate reductase)	K.FVTAYGQFLK.A R.EGMATLAALNVLGR.V	2+ 2+	Oxidation (M)	1	-
85 ^b	86	At5g02870	60S ribosomal protein-like	R.MSLLAEASR.V K.LESIYGSFEKPESEK.K	2+ 3+	Oxidation (M)	1	+
86	85	At3g54050	Fructose-bisphosphatase	R.TLLYGGIYGYPR.D R.VLDIQPTEIHQR.V	2+ 3+		1	-
87	84	At1g50200	Alanyl t-RNA synthetase	K.LATEAAESAASDGK.T	2+		1	+
88 ^a	84	At2g26080	Glycine dehydrogenase (decarboxylating)	K.IAILNANYMAK.R	2+	Oxidation (M)	1	-
		At4g33010	P-Protein-like protein	K.NTAGIEPEDVAK.R	2+			
89	83	At2g30870	ATGSTF10; glutathione transferase	R.SQGPDLLGK.T K.LAEVLDVYEAQLSK.N	2+ 2+		1	-
90	83	At4g38630	26S proteasome regulatory subunit S5A	K.KALEIVGK.R K.ELLASLPDESK.R K.DGDTASASQETVAR.T R.VLTPPTSDLGKI K.DKDGDTASASQETVAR.T	2+ 2+ 2+ 2+ 3+		4	-
91	82	At2g38230	ATPDX1.1 (Pyridoxine biosynthesis 1.1)	K.IAAPYDLVQTK.E	2+		1	-
92	82	At4g13940	Adenosylhomocysteinase	K.AGIIVLAEGR.L	2+		1	-
93	82	At5g63310	Nucleoside diphosphate kinase II	K.TDPLQAEPTIR.G R.NIVHGSDSPENKGR.E	2+ 3+		3	+
94	81	At2g05990	MOD1; enoyl-[acyl-carrier-protein] reductase (NADH)/ oxidoreductase	R.VNTISAGPLGSR.A R.IPGYGGGMSAK.A R.VLPDGLMEIK.K	2+ 2+ 2+	Oxidation (M) Oxidation (M)	2	+
95	80	At3g51260	Proteasome subunit alpha type-7-A	R.YIAGLQKQ.Y	2+		5	-
		At5g66140	Proteasome subunit alpha type-7-B	R.ALLEVVESGGK.N R.LTLEDPVTVEYITR.Y	2+ 2+			
96 ^b	80	At3g58610	Ketol-acid reductoisomerase	K.VSLAGYEEYIVR.G	2+		2	+
97	79	At1g69740	Porphobilinogen synthase	K.TYQMNPNANYR.E R.AGADVSPSPMDMDGR.V	2+ 2+	Oxidation (M) Oxidation (M)	1	+
98	79	At3g26520	TIP2 (Tonoplast intrinsic protein2)	R.NIAGGVQEEVYHPNALR.A	3+		1	+
99 ^a	78	At5g01410	Pyridoxal biosynthesis protein PDX1.3	K.VGLAQLMR.G R.TKGEAGTGNIEAVR.H	2+ 3+	Oxidation (M)	3	-
100 ^b	77	At5g42980	Thioredoxin H-type 3	R.FIAPVFADLAK.K K.VQAMPTFIFMK.E	2+ 2+	2 Oxidation (M)	1	-
101 ^b	76	At1g58380 At1g59359 At2g41840 At3g57490	40S ribosomal protein S2 homolog	K.VLQFAGIDDVFTSSR.G	2+		1	-
102	75	At2g36530	Enolase	K.LAMQEFMILPVGAASF.K.E K.IVLPVPFNFVINGGSHAGNK.L	3+ 3+	2 Oxidation (M)	2	-
103 ^b	75	At5g20010 At5g20020 At5g55190	Atran1; GTP binding Atran2; GTP binding Atran3; GTP binding	K.LVIVDGGTGK.T	2+		1	-
104	75	At1g19550 At1g19570	Glutathione dehydrogenase (ascorbate)	R.VSAVDLSLAPK.L	2+		1	-
105 ^b	74	At3g44310	Nitrilase I	K.LMPTSLER.C R.KLMPTSLER.C K.GAELVLFPEGFIGGYPR.G K.YIVEAASK.G	2+ 2+ 2+ 2+	Oxidation (M) Oxidation (M)	3	+
106 ^a	73	At5g48300	ADP glucose pyrophosphorylase small subunit	K.IINSDNVQEAAR.E	2+		1	-
107	72	At3g27430 At5g40580	PBB1 (20S proteasome beta subunit B1) 20S proteasome beta subunit PBB2	R.ATEGPVADK.N R.NYMEPNPR.T	2+ 2+		2	-
108	70	At3g14310	ATPME3 (Arabidopsis thaliana pectin methylesterase 3)	R.IGATSDLQSVK.G K.TVAAAVAAAPENSINKR.Y	2+ 3+		1	+
109	70	At3g19950	Zinc finger (C3HC4-type RING finger) family protein	K.SAIDALPTVK.V R.SSGTHFEFVIENHPSDPGNR.M K.SIQQNFQSDAPDPIIFLQNHILQILK R.SQGSQGSQSGDQGSVEGQQT.PR.F	2+ 3+ 3+ 3+		7	+
110	69	At1g13060	Proteasome precursor, beta subunit	R.ASMGGYISSQSVK.K	2+	Oxidation (M)	1	-
111	69	At1g32470	Glycine cleavage system H protein, mitochondrial, putative	K.VKPSSPAELEALMGPK.E	3+	Oxidation (M)	1	-
112	69	At5g60600	GcpE; 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	R.GMVESAFEFAR.I	2+	Oxidation (M)	1	+
113	69	At5g67590	FRO1 (Frostbite1)	K.KPNTPLLK.V K.VSGPIPEEHLR.K	2+ 3+		2	-
114	68	At3g49010	60S ribosomal protein L13-1	K.KLAPTIGIADVDR.R	3+		2	-
115	67	At3g15950	TSA1-LIKE	R.NSMLEAFER.E R.EFEAVTESFK.Q	2+ 2+	Oxidation (M)	2	+
116 ^b	67	At5g52640 At5g56000 At5g56010	Heat shock protein 83 Heat shock protein Heat shock protein 90A	R.ELISSSDALDK.I	2+		2	+
117	65	At2g41530	ATSF6H; Arabidopsis thaliana S-formylglutathione hydrolase	K.LLSENFSQLDITTK.A	2+		1	-
118 ^b	64	At1g49240	ACT8 (ACTIN 8)	K.EITALAPSSMK.I	2+	Oxidation (M)	2	+

		At3g18780	ACT2 (ACTIN 2)	K.AEYDEAGPGVHR.K	3+		
119	64	At3g02540	RAD23-3; PUTATIVE DNA REPAIR PROTEIN RAD23-3	R.AAFNNPER.A	2+	1	+
		At5g38470	DNA repair protein RAD23, putative	R.NSQQFQALR.A	2+		
120	64	At3g23990	Chaperonin hsp60	K.SVAAGMNAMDLR.R	2+	2 Oxidation (M)	+
121 ^a	64	At3g47520	Malate dehydrogenase, chloroplast precursor	R.ANTFVFSQK.K K.LFGVTTLDVVR.A	2+	1	+
122	64	At3g61820	Putative uncharacterized protein F15G16.210	R.VAYDLVGSR.V R.GGLSFPSQTK.N	2+	1	+
123	63	At2g37270 At3g11940	ATRPS5B (Ribosomal protein 5B); structural constituent of ribosome ATRPS5A (Ribosomal protein 5A); structural constituent of ribosome	R.VNOAIFLLTTGAR.E	2+	1	-
124	63	At5g25980 At5g26000	TGG2 (glucoside glucosylase 2) TGG1 (Thioglucoside glucosylase 1)	R.GYALGTDAPGR.C	2+	2	+
125 ^b	62	At1g53240	Mitochondrial NAD-dependent malate dehydrogenase	K.ALEGADLVIIIPAGVPR.K	2+	2	+
126	62	At2g21580	40S ribosomal protein S25 (RPS25B)	K.LITPSILSDR.M R.MVSAHSSQIYTR.A	2+ 3+	2	-
127	62	At3g22230	60S ribosomal protein L27 (RPL27B)	K.EVATLDALKSK.D	2+	1	+
128	62	At3g25530	Gamma-hydroxybutyrate dehydrogenase (ATGHBHDH)	K.KPAEDGQLIILAAGDK.A	3+	1	+
129	62	At3g63140	mRNA binding	K.STEQPPHVEGDAVK.A R.AVPIPGSGLQLTNISHVR.D	3+ 3+	1	+
130	62	At4g15000	60S ribosomal protein L27-3	K.EVATLDALQSK.D	2+	1	+
131 ^a	61	At1g20260 At1g76030 At4g38510	Vacuolar ATP synthase subunit B3 Vacuolar ATP synthase subunit B1 Probable H ⁺ -transporting ATPase	K.SAIEGEMTR.K K.HVLVLTDMSSYADALR.E	2+ 2+	Oxidation (M)	+
132	61	At1g32990	PRPL11 (Plastid ribosomal protein L11)	K.VGVITDQLR.T	2+	1	-
133	61	At2g45640	SAP18 (SIN3 associated polypeptide P18)	K.SGGHHTSEDIYAVR.G	3+	2	-
134 ^a	60	At3g45970	Expansin-like A1 precursor	R.VPTGAIQFR.F	2+	1	-
135 ^b	59	At3g04840	40S ribosomal protein S3A (RPS3aA)	K.LMVDVHGDIYSAEDVGVK.V	3+	Oxidation (M)	+
136	59	At1g14320 At1g26910 At1g66580	Structural constituent of ribosome	K.ENVSSEALEAAR.I	2+	1	-
137 ^{ab}	59	At1g20010 At1g75780 At2g29550 At4g20890 At5g12250 At5g23860 At5g44340 At5g62690 At5g62700	TUB5 (tubulin beta-5 chain) TUB1 (tubulin beta-1 chain) TUB7 (tubulin beta-7 chain) Tubulin beta-9 chain TUB6 (BETA-6 TUBULIN) TUB8 (tubulin beta-8) TUB4 (tubulin beta-4 chain) Putative tubulin beta-2/beta-3 chain Tubulin beta-2/beta-3	K.LAVNLIPFPR.L	2+	3	-
138	58	At1g11910	Aspartyl protease family protein	K.FDGLLGLFQIEISVGK.A	2+	1	+
139	58	At3g27830 At3g27850	50S ribosomal protein L12-1 50S ribosomal protein L12-3	R.LIVDYLQDK.F	2+ 2+	2	-
140	58	At4g31300	PBA1 (20S proteasome beta subunit A 1)	R.TVINSEGVTR.N R.TSTGMVYANR.A	2+ 2+	2	+
141	57	At5g19440	Alcohol dehydrogenase	R.VVVTSSMAAVGYNGKPR.T	3+	Oxidation (M)	+
142	56	At1g10840	Eukaryotic initiation factor 3H1 subunit	R.VVQIEGLAVLK.I	2+	1	+
143	56	At1g76790	O-methyltransferase	R.TGFSVAVLK.K	2+	1	+
144 ^b	56	At2g09990 At5g18380	40S ribosomal protein S16 (RPS16A) 40S ribosomal protein S16 (RPS16C)	R.VNGGGHTSQVYAIR.Q	3+	1	+
145	56	At2g17390 At4g35450	AKR2B; protein binding / transcription regulator AKR2 (Ankyrin repeat-containing protein 2)	K.AALASGGNKDEEDSEGR.T	3+	4	-
146	55	At4g39260	Glycine-rich RNA-binding protein 8	R.TFSQFDVIDSK.I	2+	1	-
147	54	At1g78370	Arabidopsis thaliana Glutathione S-transferase (class tau) 20	K.SPILLQSNPIHK.K	3+	1	-
148	54	At3g05560	60S ribosomal protein L22-2 (RPL22B)	K.AGALGDSVTITR.E	2+	1	+
149	54	At5g26260 At5g26280 At5g26320	Meprin and TRAF homology domain-containing protein	K.IVITISFSVIK.G K.YLTVTDGLVK.R	2+ 2+	2	-
150	53	At1g58270	ZW9, biological process unknown	R.FLSFADIK.N	2+	1	-
151	53	At4g37800	Endo-xyloglucan transferase-like protein	R.SGQPYTVQTNVFAHGK.G	3+	1	-
152	53	At5g52960	Unknown protein	K.SGPGNLER.D	2+	2	+
153	52	At1g07770	Ribosomal protein S15A	K.FLIVMQK.H R.ISVLNDALK.S	2+ 2+	Oxidation (M)	-
154	52	At1g20200	26S proteasome subunit RPN3a	R.IGDLELFR.T	2+	1	+
155 ^b	52	At1g54270 At1g72730 At3g13920	Eukaryotic translation initiation factor 4A-2 RNA helicase (eukaryotic translation initiation factor 4A, putative) Eukaryotic translation initiation factor 4A-1	K.RDELTLEGIK.Q	2+	1	-
156	51	At1g11580	ATMPEPCRA	K.TVNEAVAAAPENSNTY.Y	2+	1	+
157	51	At1g29250	Nucleic acid binding	K.NNGFAVEK.K K.IMTSTVDIK.D	2+ 2+	2	-
158	51	At3g01500	Carbonic anhydrase, chloroplast precursor	K.AFDPVETIK.Q R.NIANMVPPFDK.V	2+ 2+	2	-
159	51	At4g19006 At5g45620	26S proteasome subunit RPN9b 26S proteasome subunit RPN9a	R.VLGIPIQIK.S K.LSIEDVEHLLMK.S	2+ 3+	1	+
160	51	At5g10540 At5g65620	Peptidase M3 family protein	K.TQVIPPLPEDR.F	2+	1	+
161	50	At1g28410	Similar to myosin heavy chain-related	K.SGLPLVQKR.T	2+	Phospho (STY)	+
162	50	At2g33800	Ribosomal protein S5 family protein	R.IVLEMAGVENALGK.Q	2+	Oxidation (M)	+
163	49	At3g01340	Protein transport protein SEC13 family protein	K.ITGVSNSSGGSQHLATLTGHR.G	3+	1	-
164	49	At1g79550	Phosphoglycerate kinase	K.FAAGTEAVAK.Q	2+	1	-
165	48	At2g21170	Triose-phosphate isomerase	K.VASPPQQAQEVHVAVR.G	3+	1	-
166	48	At4g29350	Profilin-2	K.YMVVQGEAGAVIR.G	2+	Oxidation (M)	-
167	48	At5g37510	EMB1467; NADH dehydrogenase	R.YEAMVNAR.I	2+	Oxidation (M)	+
168	47	At1g63940	Disulfide oxidoreductase/ oxidoreductase	K.EAYAPYERPALTK.A R.TSTPGIFAGDVAAPFLK.I	3+ 2+	1	-
169	47	At3g24503	ALDH2C4; aldehyde dehydrogenase/ oxidoreductase	R.VFVQEGYDK.V	2+	1	+
170	47	At3g52960	Peroxisome oxidoreductase, chloroplast precursor	R.YAILADDGVVK.V	2+	1	-
171	47	At4g39200	40S ribosomal protein S25-4	R.MVAAHSSQIYTR.A	3+	Oxidation (M)	-
172	46	At1g02560	ATP-dependent Clp protease proteolytic subunit 5	R.FQSIQSLFQYR.I	2+	1	+
173	46	At1g24510	T-complex protein 1 epsilon subunit, putative putative	K.AVLAVADLER.R	2+	1	+
174	46	At2g10450	14-3-3 protein, putative / grf15, putative	K.DSTLIMKILR.D	2+	Oxidation (M)	-
175	46	At2g43030	Ribosomal protein L3 family protein	R.LTNIIEGFEPNQK.L	2+	1	-
176	46	At2g43160 At2g43170	Putative clathrin binding protein (epsin) Epsin like protein	R.VIDEIRER.A	2+	3	+
177	46	At3g45030	40S ribosomal protein S20-1	R.VIDLFSSPDDVK.Q	2+	1	+

		At3g47370	40S ribosomal protein S20-2					
		At5g62300	40S ribosomal protein S20 (RPS20C)					
178	45	At3g56910	Ribosomal protein, chloroplast	K.TVVAVPVVK.L	2+		2	+
179^b	44	At1g23310	Alanine-2-oxoglutarate aminotransferase 1	K.LVLLGDEVYQQNIYQDERPFISSK.K	3+		1	+
		At1g70580	Alanine-2-oxoglutarate aminotransferase 2					
180	44	At1g66200	ATGSR2: glutamate-ammonia ligase	R.TLPGPVTDP SK.L	2+		1	-
181	44	At1g70200	RNA recognition motif (RRM)-containing protein	K.RDDNLLK.G	2+		4	+
182	44	At2g35370	GDCH (Glycine decarboxylase complex H)	K.VKPSSPAELESIMGPK.E	3+		1	-
183	44	At4g11010	Nucleoside diphosphate kinase III	R.GLISEIISR.F	2+		1	-
184	44	At4g24770	RNA-binding protein	R.AEFPEPSEEA.K.L	2+		1	+
185	43	At1g11430	Plastid developmental protein DAG, putative	R.DGPPPPEQR.K	2+		4	-
186	43	At1g54100	Putative aldehyde dehydrogenase	R.VGSMVQQTVNAR.S	2+	Oxidation (M)	1	+
187	43	At3g20250	APUM5 (ARABIDOPSIS PUMILIO 5)	K.LELSDIAGR.V	2+		1	+
188	43	At5g66510	APUM12 (ARABIDOPSIS PUMILIO 12)	K.VLSALSSK.K	2+	GlyGly (K)	1	+
				K.KVLSALSSK.K	2+	GlyGly (K)		
189	42	At1g60970	Clathrin adaptor complex small chain family protein	K.NILLDSEGR.K	2+		2	+
		At4g08520	Clathrin adaptor complex small chain family protein					
190^b	42	At1g79920	Heat shock protein 70, putative	K.TNVPLSELVYGALK.T	2+		1	+
		At1g79930	HSP91 (Heat shock protein 91)					
191^b	42	At2g37190	60S ribosomal protein L12 (RPL12A)	K.IGPLGLAPK.K	2+		3	-
		At3g53430	60S ribosomal protein L12 (RPL12B)					
		At5g60670	60S ribosomal protein L12 (RPL12C)					
192	42	At3g07110	Structural constituent of ribosome	K.VFEGVPTPYDK.I	2+		1	-
193	42	At3g22110	PAC1 (20S proteasome alpha subunit C1)	R.TTIFSP EGR.L	2+		2	-
194	42	At3g51600	Non-specific lipid transfer protein 5	R.ISYPISAR.T	2+		3	-
195	42	At5g16130	40S ribosomal protein S7-3	K.LETMVG VYR.K	2+	Oxidation (M)	1	+
196	41	At4g24690	Putative uncharacterized protein F22K18.110	R.KPVNLNEPTGAH SK.T	3+		1	+

Gel pieces; number of gel pieces containing the identified protein

a, b; proteins referenced in (a)Manzano et al. (2008) and (b)Maor et al. (2007)

Locus	putative D-box	putative KEN-Box	putative PEST motif
At1g02560	IRDDLO	-	-
At1g04820	CRRSL(S)(213-218)	-	-
At1g09100	AREDL(A)(421-426)	-	-
At1g10840	QRTNLD(43-48)	KENQ(66-60)	-
	ARSLF(Q)(5-10)	-	SAGEEPLPEEDPSNPFI(278-292)
	SRL(Y)T(328-331)	-	-
At1g11580	ARDL(K)(210-215)	-	-
	DRKLE(E)(230-235)	-	-
At1g11910	ERVQL(K)(31-36)	DKENA(365-369)	-
	PRGPL(W)(474-479)	-	-
At1g12840	JRGQL(N)(146-151)	-	-
	LRSSLL(274-279)	-	-
	MRYGL(P)(307-312)	-	-
	VRSILE(I)(330-335)	-	-
At1g20200	LRQKLT(57-62)	-	-
At1g20260	ERVTL(F)(232-237)	-	-
	PRIAL(T)(252-257)	-	-
At1g20620	-	KKENN(423-427)	-
At1g21720	FRHKLY(69-74)	-	-
	DRDCL(S)(175-180)	-	-
At1g22310	VRGEL(Y)(22-27)	-	-
At1g24510	LRSSL(Q)(4-9)	KENI(478-482)	-
At1g28410	EREKLI(66-71)	-	-
	QRKHL(P)(185-190)	-	-
At1g29150	LRKLL(T)(63-68)	-	-
	KRTFL(R)(118-123)	-	-
At1g30630	ERDCL(V)(41-46)	-	-
	LRWLA(Q)(94-99)	-	-
At1g32060	LRVRL(I)(259-264)	-	-
At1g35160	-	-	DNLTLWTSDDMODESPEEI(235-252)
At1g42970	NRDPL(K)(159-164)	-	-
At1g45000	TRVVL(D)(102-107)	-	-
At1g47250	IRETL(Q)(195-200)	-	-
At1g49240	KRGIL(T)(63-68)	-	-
At1g50010	CRRSL(S)(213-218)	-	-
	AREDL(A)(421-426)	-	-
At1g50200	LRRLR(L)(377-382)	-	FSSSSSTSSSVAVMPGSEPEIQWPA(36-21)
	ERGLL(V)(483-488)	-	-
	ERRLI(I)(637-642)	-	-
At1g53240	FRSML(V)(2-7)	-	-
	TRDDL(F)(114-119)	-	-
At1g54100	LRSKLD(I)(91-96)	-	-
	TRIPLV(235-240)	-	-
	ARSLV(F)(285-290)	-	-
	CRRL(L)(303-308)	-	-
At1g60970	BRLLH(H)(304-309)	-	-
	KREAL(D)(109-114)	-	-
	AREHL(T)(167-172)	-	-
At1g64520	ARQML(I)(203-208)	-	-
At1g69740	GRNLI(V)(45-50)	-	-
At1g70200	-	-	SGDSVIVSDDDEEDDEWGEFDGEDEGEEEEEDEGEFLPMD(73-115)/LPYSGLEGDSSADVVEEVLLGSGEEFSDSSEEEVDE(295-330)/LDDQESEFAVETLLNDELGGDEEEVAEDNLEPLNSSLSSSEEN/308-442
At1g70580	VRGELY(22-27)	-	-
At1g76030	ERVTL(F)(231-236)	-	-
	PRIAL(T)(251-256)	-	-
At1g76790	CRYFL(K)(111-116)	-	-
At1g78900	KRTVL(V)(310-315)	-	FEDPAEGEDTLVE(690-602)
At1g79920	RRAVL(D)(153-158)/ERAKL(K)(476-481)/VRLNLH(484-489)/MRNKL(S)(633-638)	-	DTSDATGTDNGVPESAE(645-661)
At1g79930	RRAVL(D)(153-158)/ERAKL(K)(476-481)/VRLNLH(484-489)/MRNKL(S)(633-638)	-	DTSDATGTDNGVPESAE(645-661)
At2g01250	QRIAL(T)(159-164)	-	-
At2g04030	FRSIL(Y)(376-381)/SREIL(Q)(440-445)/MRKRL(I)(453-458)/GRRILE(671-676)	-	SGETVVEPSEV(760-771)
At2g05840	ERGPL(L)(146-151)	MKENP(163-187)	-
At2g05990	DRTL(L)(116-121)	-	-
At2g09990	DRTL(L)(116-121)	-	-
At2g28000	SBAAL(Q)(57-62)/RAPLL(L)(287-292)/LRGVL(N)(311-316)/TRCALQ(548-551)	-	-
At2g30200	MRSLL(H)(-6)/HRTILL(6-11)/VRTSL(S)(20-25)	-	-
At2g31610	VBHVL(L)(172-177)	-	-
At2g33800	-	-	ASSTDTEIFFEDETPEITANVFDPPAPEGVSPYPPYDEGSDETEIEIATFEELYGPAYSGESMLG(50-118)
At2g36160	GRETL(V)(48-53)	-	JEDVTPIDTST(128-139)
At2g39730	NRAPLS(12-17)/KRVQLA(408-413)	-	-
At2g42600	VRRSL(L)(177-182)/RRSL(L)(178-183)/RDCL(T)(188-193)/YRAILG(364-369)/VRDKLY(371-376)/382-287)	-	-
At2g43160	GRGGL(Q)(273-378)	-	DGGETPQVTPGAASPPPOVAAPAEASPTGTINTANTITAFVNESPSQ(308-358)/AFTSTDDTSTPQONFASFPPTTAFVNES(463-493)
At2g43750	ERRVL(L)(174-179)/RRVLLR(175-180)	-	YETTGPEIWD(228-239)
At2g47730	ARLPL(F)(6-11)	-	-
At3g02090	RRLFL(T)(15-20)/GRTL(G)(248-253)/GRQLL(T)(465-470)	-	-
At3g02540	-	-	SSSSFAIDSVPASASPTALSPPPP(25-49)
At3g04840	GRNLV(L)(93-98)	-	PPPPAPTTPAPVAATETVITPPEVPTATSSSTPAPDSAPVGSQGDVYGOAASNLAAAGSNLESTIQOILDMGGGTWD(125-203)
At3g05560	VRDWH(R)(2-7)	-	-
At3g11630	RSSSL(S)(1-5)	-	-
At3g13120	JRIKL(R)(95-100)	-	VFAVPDTLDPTEILDPEASEVPSSSISVDAD(56-87)
At3g14310	DRRL(Q)(269-274)	-	-

A13q15950	TRAKLL(657-662)	-	-	-
A13q18780	KRGILT(63-689)	-	-	-
A13q19950	-	-	-	FELPTDDPDYEN(258-269)
A13q20250	KRNRLD(43-49)JLRNLLK(74-79)IRSSLH(154-159)SRRTAL(161-166)	-	-	EEPEDEASSGEGQQSYASLAG(170-189)ETDLSSSDAIASEDPFTDILASQSFTNAOTE(253-283)
A13q20820	DRRALL(24-29)IRRALLA(25-30)FRSALH(31-36)LRNLLI(182-187)SRALLS(202-207)SRNLLQ(278-283)IRACLK(359-364)	-	-	-
A13q22230	TRYTL(83-88)	-	-	-
A13q22630	TRGELA(84-89)IRSNLV(161-171)	-	-	-
A13q24400	SRGCLP(156-160)DRGELR(274-279)	-	-	NLAANSSLVEVSGGSEDPSSSSGGGDD(52-81)
A13q23090	CRPLI(274-279)IRRTALV(531-536)	-	-	-
A13q24503	ERAKL(82-87)ITRGSLEF(146-151)	-	-	-
A13q25530	MRLALA(240-245)	-	-	-
A13q26520	LBAALA(21-26)JRGILY(102-107)	-	-	-
A13q28300	-	-	-	SKENM(4-8)DKEND(139-143)
A13q44310	FRFGLA(75-80)NRMPLY(189-194)YRTALY(194-199)ARAKLY(301-306)	-	-	-
A13q45030	IRITLS(25-30)DRFELR(83-88)	-	-	-
A13q47370	IRITLS(23-28)DRFELR(81-86)	-	-	-
A13q47520	TRODDF(167-172)	-	-	-
A13q51260	HRLTLE(95-100)JREFLE(170-175)IRALLE(191-196)	-	-	-
A13q55800	SRGILP(9-14)JLRTLM(93-98)	-	-	-
A13q56910	NRVSL(45-50)RRRRLV(121-126)	-	-	-
A13q58610	LRDSL(138-143)VRPELR(582-587)	-	-	-
A13q60750	QRSSLP(26-30)TRNLLG(352-357)SRQKLP(597-602)	-	-	ALPTYTPESGDAT(420-433)
A13q60920	DRAVLS(54-59)	-	-	-
A13q61820	QRDSL(88-93)GRGGLS(265-270)	-	-	-
A13q63140	HRESLP(29-34)	-	-	-
A13q64640	FRSVLK(26-31)	-	-	-
A13q68520	AREHLA(171-176)ARSLT(176-181)	-	-	-
A13q14800	TRGELA(84-89)IRSNLV(166-171)	-	-	-
A13q14880	RRILL(105-110)	-	-	-
A13q14960	CRRSLN(213-218)ARFEDA(421-426)	-	-	-
A13q15000	TRYTL(83-88)	-	-	-
A13q19006	TRINL(68-73)	-	-	-
A13q24690	TRPKL(372-377)SRFVLD(378-383)	-	-	EKENL(554-558)
A13q24770	GRINLP(48-53)SRVSL(57-62)	-	-	SPFVFAQTSQDWAEEGEGSVAVEETENSLESQQVSEGESEGDASEGVSEGESEQDVEGAVSE(72-139)
A13q24920	DRVSLK(230-235)	-	-	-
A13q27150	-	-	-	AAEDPAPASSS(45-56)
A13q31300	VRVYELH(71-76)	-	-	-
A13q38510	ERVTLF(232-237)PRIALT(252-257)	-	-	-
A13q02870	ERLNL(240-245)KRAVLK(317-322)	-	-	-
A13q04140	TRRRL(42-47)ARETL(898-903)LRDLE(969-974)ERVILR(1224-1229)OREELR(1281-1286)VRGILA(1307-1312)GRTELL(1324-1329)VRNSLA(1511-1516)	-	-	KENS(555-559)
A13q04590	IRYPLN(82-92)NRNVA(202-207)	-	-	-
A13q10540	ARQRLV(131-136)YRAYLS(249-254)HRDRLM(525-530)	-	-	-
A13q10860	HREELQ(191-196)	-	-	-
A13q14320	SRNTLA(26-31)ARQILV(76-81)	-	-	-
A13q14740	HRLSL(39-44)	-	-	-
A13q16130	TRYRLD(141-146)	-	-	-
A13q18380	DRTLLV(116-121)	-	-	-
A13q19440	ERHLF(58-63)GRYCLV(249-254)	-	-	TPDVTVDWTFWSPPELCEAS(142-161)
A13q19990	TRVALR(124-129)	-	-	-
A13q20000	TRVALR(124-129)	-	-	-
A13q23540	-	-	-	AVOEEDLSPE(267-267)
A13q25980	LRSSLP(532-537)DRKSLT(542-547)	-	-	PEEETCEENVPFTCSQYTD(30-48)
A13q26000	DRKSLA (534-539)	-	-	-
A13q35590	-	-	-	MKENP (183-187)
A13q37510	KRQRLS(340-345)WRDAL(361-366)	-	-	PELQSPESAASVEPEPTQILPP(34-56)
A13q42790	SREDL(183-188)VRTELQ(195-200)	-	-	-
A13q43010	TRVVD(102-107)	-	-	-
A13q48300	VRQYLW(193-198)	-	-	-
A13q52840	TRKKLN(331-336)SRETLO(376-381)	-	-	KKENE(233-237)
A13q52960	RRKPLT(53-58)	-	-	EISDDEDEPE (222-232)JLGLSIDENVEEDGMPLEEDAEES(672-699)
A13q56000	SRETLO(370-375)	-	-	-
A13q56010	SRETLO(370-375)	-	-	LGLSIEDDAVEADAEMPLEDDADAEGS(665-693)
A13q56510	QRKLC(158-163)GRWLQ(246-251)	-	-	LGLSIDDDVVEADAEMPLEDDADAEGS(665-693)
A13q58200	NRKLL(110-115)	-	-	-
A13q60600	IRVSLT(341-346)YRNVLH(404-409)ARLAK(465-470)HRDELV(585-590)	-	-	YSLTEPPEEIDPC(343-356)
A13q62300	IRITLS(25-30)DREELR(83-88)	-	-	-
A13q63310	FRTALA(37-42)SRRLR(57-62)	-	-	-
A13q65620	SRASLN(8-13)ARQRLV(219-224)YRAYLS(337-342)HRDRLM(613-618)	-	-	ESPDWSSLS(209-219)
A13q66140	HRLTLE(95-100)JREFLE(170-175)IRALLE(191-196)	-	-	-