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Supplementary Figure Captions：

Supplementary Fig. S1 Hierarchical clustering analysis of the relative abundance profiles in broccoli sprouts with different functions. Abundance changes were made based on the log2 conversion expression ratios of the proteins applying Gene Cluster 3.0 software. Visualize results using JAVA Treeview software. a: $ZnSO_4$ vs CK; b: Melatonin vs CK; c: $ZnSO_4$+Melatonin vs $ZnSO_4$; d: $ZnSO_4$+Melatonin vs melatonin.

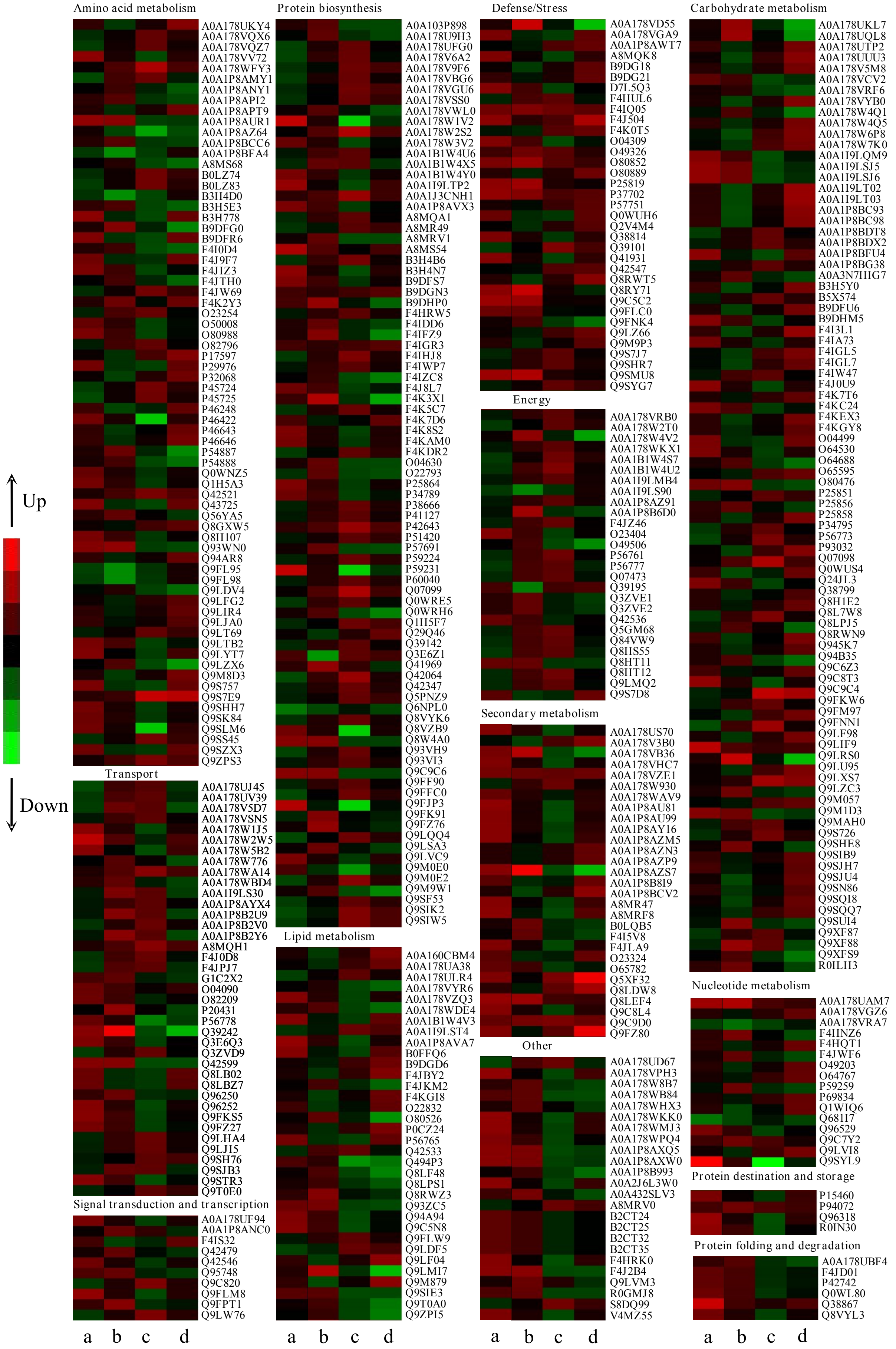
Supplementary Fig. S2 Mass spectrogram of different fractions.

Supplementary Table Captions：

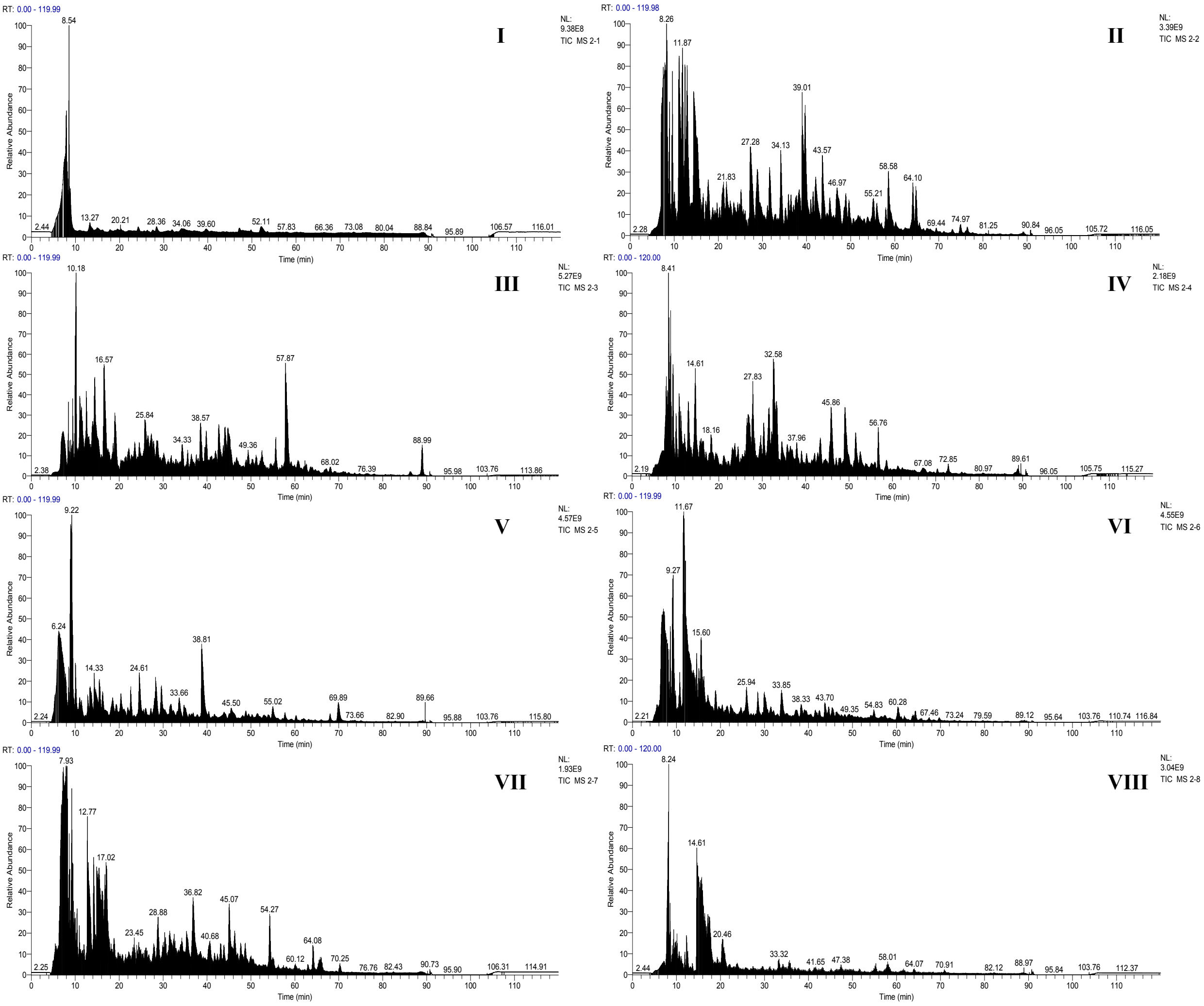
Supplementary Table S1 The primer sequence of ITCs metabolism genes in broccoli sprouts.

Supplementary Table S2 Mass spectrometric data of eight fractions.

Supplementary Table S3 Differentially abundant proteins in broccoli sprouts under different treatments.



Supplementary Fig. S1



Supplementary Fig. S2

Supplementary Table S1. The primer sequence of ITCs metabolism genes in broccoli sprouts

Primer	Sequences (5’-3’)
UGT74B1	**F:** CAAAGACGATAAAGGCTACGGC
	R: TCCCAAAGGAACCAAACGAA
ST5b	**F:** CCGACACTACCTTACCGAACCA
	R: CGTGAGGAAAAGAGGCGATG
OX	**F:** GTGGACATTATACCGAACCTTACG
	R: TGTGGACTTCTTTGGCGACCT
MYR	**F:** AAGGTCATCAGGGAGAAGGGTG
	R: TGTTTGGCAGGGTTCTTAGTGG
MYB28	**F:** AGACTGCGATGGACTAACTACCTAAA
	R: CCGACCACTTGTTTCCACGA
CYP83A1	**F:** CTGCGGCGGTTGTATGGG
	R: AAGGTTCTTCACGTCGTCTTCAGT
ESP	**F:** ACATTTGGGACCAGGGACG
	R: TTTCCATACACGGTGGCAGTC
AOP2	**F:** GAGTAACGGAAAGAAAGAAGACAAGG
	R: ATAAGCGTGAAGAGTAGAACGAGGT
BoSAT1	**F:** ATATCCATCCAGCAGCGAAG
	R: CTGTCTCCGCAAGCTTTACC
BoHMT1	**F:** TTCAGGAATGCCTTGAAACC
	R: TTAGCTTTTCCGTCCCACAC
Actin	**F:** CTGTTCCAATCTACGAGGGTTTCT
	R: GCTCGGCTGTGGTGGTGAA

F: forward primer sequence, R: reverse primer sequence

Supplementary Table S2. Mass spectrometric data of eight fractions

RT/min	Compound Name	Cas	Area %
Fraction I			
9.64	Cyclohexasiloxane, dodecamethyl	540-97-6	0.45
18.44	5'-Fluoro-2'-hydroxy-4-methylchalcone	498535-04-9	0.01
19.71	Sulfamethizole	144-82-1	0.11
20.22	Glycan Galacto-N-biose	20972-29-6	0.34
29.22	Apigenin 7-glucoside	578-74-5	0.01
30.14	20-HETE ethanolamide	942069-11-6	0.03
35.91	Stigmasta-4,6,22-trienol	96737-58-5	0.04
40.39	Lorazepam	846-49-1	0.01
49.08	2-Butanol, 3-methylol	598-75-4	0.05
50.58	Trandolapril	87679-37-6	0.01
51.12	Fluvastatin	93957-55-2	0.01
58.38	Arachidonoylglycine	179113-91-8	0.01
59.07	N-Acetyl-L-tyrosine	537-55-3	0.01
Fraction II			
5.83	L-Alanine, N-[N-[N-(3-pyridinylmethylene)-L-valyl]-L-isoleucyl]	37580-32-8	0.01
6.58	Indican	487-60-5	0.03
8.50	Nifedipine	21829-25-4	0.01
9.84	6-Methoxyluteolin	520-11-6	0.01
11.10	Palmitelaidic acid	10030-73-6	8.04
12.19	Docosatetraenoyl ethanolamide	150314-35-5	0.01
16.31	Monolauryl phosphate	2627-35-2	0.16
20.30	Cyproterone acetate	427-51-0	0.21
20.56	N-[4-(6-Methyl-2-benzothiazolyl)phenyl]-4-nitrobenzenesulfonamide	339223-67-5	0.01
21.45	6H-[1,3]Dioxolo[5,6]benzofuro[3,2-c][1]benzopyran-3-ol, 4-(3,7-dimethyl-2,6-octadienyl)-6a,12a-dihydrocis	66446-94-4	0.01
22.30	Tricyclo[3.3.1.13,7]decane, 1-(2-chloro-3,5-dinitrophenyl)	71466-68-7	0.01
22.69	(+)-Abscisic acid	21293-29-8	0.28
29.68	Rosmarinic acid	20283-92-5	0.03
29.88	(+)-Abscisic acid	21293-29-8	0.04
31.14	N-[Tris(hydroxymethyl)methyl]-3-aminopropanesulfonic acid	29915-38-6	0.19
33.46	Urs-20-en-16-one, 3-hydroxy	42482-69-9	0.04
34.59	Bestatin	58970-76-6	0.01
36.19	9-Oxo-prosta-10,12Z,14E-trienoic acid	573951-20-9	0.01
39.42	1,2,3,4-Phenazinetetrol, 7-methylol	23774-08-5	0.01
42.65	R-1 Methanandamide phosphate	649569-33-5	0.02
42.78	R-1 Methanandamide phosphate	649569-33-5	0.01
43.57	Fenamifos sulfoxide	31972-43-7	1.36
44.30	Pamoic acid	130-85-8	0.01
44.36	Benzethonium	10172-60-8	0.01
48.17	Fenamifos sulfoxide	31972-43-7	0.01
49.32	Oxamflatin	151720-43-3	0.01
49.59	s-Triazolo[4,3-a]pyrazine, 3-methyl-5,6-diphenyl	33709-78-3	0.42

52.50	9-Oxo-prosta-10,12Z,14E-trienoic acid	573951-20-9	0.01
53.11	N-Lauroylsarcosine	97-78-9	0.10
53.45	Glycerol 1-stearate	123-94-4	0.01
54.39	Dodecylbenzenesulfonic acid	27176-87-0	0.01
54.46	9-Oxo-prosta-10,12Z,14E-trienoic acid	573951-20-9	0.01
57.36	Trioctylmethylammonium cation	22061-11-6	0.01
58.58	4-Methylumbelliferyl, D-glucuronide	6160-80-1	1.02
59.39	Indican	487-60-5	0.02
Fraction III			
2.19	Aminopyralid	150114-71-9	0.10
4.03	Glycan Chitobiose	577-76-4	0.17
4.51	3-Hydroxy-4'-methoxy-6-methylflavone	6971-17-1	0.01
5.35	1-Hexadecanoyl-sn-glycerol	542-44-9	0.10
11.79	Sorbitan monopalmitate	26266-57-9	0.03
13.39	N-2-Hydroxyethylpiperazine-N-3-propanesulfonic acid	16052-06-5	0.22
13.91	2'-Deoxyguanosine 5'-diphosphate	3493-09-2	0.83
15.64	Prostaglandin	551-11-1	0.01
17.22	Cholest-4-en-26-oic acid, 7-hydroxyoxo	1246298-65-6	0.01
17.28	HC Toxin	83209-65-8	0.01
18.65	Cholest-4-en-26-oic acid, 7-hydroxy-3-oxo	1246298-65-6	0.32
19.67	Hydrocortisone 21-acetate	50-03-3	0.01
20.40	9-Octadecenamide	301-02-0	0.59
21.26	Olean-12-en-1-one, 3-hydroxy	66088-17-3	0.09
22.22	Tetradecylphosphonate	4671-75-4	0.68
22.81	Cephalothin	153-61-7	0.15
23.20	Stigmasta-4,6,22-trienol	96737-58-5	0.02
24.01	Cyclohexasiloxane, dodecamethyl	540-97-6	0.02
24.94	Dinor-12-oxophytodienoic Acid	197247-23-7	0.07
25.55	3,3'-Dihydroxy-5,5'-dimethoxy-7,7'-dimethyl-2,2'-binaphthalene-1,1',4,4'-tetrone	88381-91-3	0.04
26.88	Mefloquine	53230-10-7	0.01
27.38	Naphthalene, 3-methoxy-1-nitro-2-(pentachlorophenyl)	57187-61-8	0.77
27.87	4(5)-EpDPE methyl ester	121818-29-9	0.46
28.18	Decanedioic acid, bis(2-ethylhexyl) ester	122-62-3	0.01
28.25	N-Arachidonoyltaurine	119959-65-8	0.01
30.49	Diisodecyl phthalate	26761-40-0	0.07
30.74	HC Toxin	83209-65-8	0.01
31.19	Palmitelaidic acid	10030-73-6	0.22
31.38	Carbaprostacyclin	69552-46-1	0.04
31.50	Aloenin	38412-46-3	0.01
32.38	Tribenzylamine N-oxide	6852-46-6	0.09
32.89	13-Docosenamide	112-84-5	0.28
33.74	8-iso-Prostaglandin A2	474391-66-7	0.06
34.33	Bezafibrate	41859-67-0	1.27
35.94	4,4'-Sulfonylbisphenol	80-09-1	0.01
36.47	Guanosine 5'-diphosphate	146-91-8	0.79

40.46	Lactitol	585-86-4	0.01
40.52	9-Oxo-prosta-10,12Z,14E-trienoic acid	573951-20-9	0.01
41.03	Mono-tert-butyl carbonotrithioate	68060-10-6	0.13
41.55	Adenosine 3',5'-cyclic monophosphate	60-92-4	0.02
41.62	Dinor-12-oxophytodienoic Acid	197247-23-7	0.01
42.34	Dodecylbenzenesulfonic acid	27176-87-0	0.01
43.06	9-Oxo-prosta-10,12Z,14E-trienoic acid	573951-20-9	0.01
44.02	17,20,21-Trihydroxypregn-1-ene-3,11-dione	147202-58-2	1.17
46.00	Picrotoxinin	17617-45-7	0.01
47.08	Cytidine 2',3'-cyclic monophosphoric acid	15718-51-1	0.23
49.09	2-Phenylacetamide	103-81-1	0.01
49.36	Ampicillin	69-53-4	0.59
50.25	N-Propyl-L-arginine	137361-05-8	0.32
51.58	9-Oxo-prosta-10,12Z,14E-trienoic acid	573951-20-9	0.01
52.52	17-Phenyl trinor prostaglandin E2	38315-43-4	0.78
53.12	17-Phenyl trinor prostaglandin E2	38315-43-4	0.04
53.40	9-Oxo-prosta-10,12Z,14E-trienoic acid	573951-20-9	0.03
53.60	Isodeoxycholic acid	566-17-6	0.04
53.87	Deoxycholic acid	83-44-3	0.05
54.00	Prostaglandin E1	745-65-3	0.01
54.34	Dodecylbenzenesulfonic acid	27176-87-0	0.12
54.75	Thymidine 5'-monophosphate	365-07-1	0.08
55.23	4-Benzyloxy-2',3,4',6'-tetramethoxychalcone	1017900-43-4	0.09
56.18	Dodecylbenzenesulfonic acid	27176-87-0	0.01
56.24	5S,12R-Dihydroxy-6Z,8E,10E,14Z-eicosatetraene-1,20-dioic acid	80434-82-8	0.01
56.58	D-myo-Inositol-1,3,4-triphosphate	93133-76-7	0.06
56.99	Estradiol 3-(D-glucuronide)	15270-30-1	0.13
57.33	Corticosterone	50-22-6	0.01
57.46	2'-Deoxyguanosine 5'-diphosphate	3493-09-2	0.02
58.13	Quercetin 3,5,7,3',4'-pentamethyl ether	1247-97-8	3.68
58.67	Olean-12-en-1-one, 3-hydroxy	66088-17-3	0.05
59.19	Dodecylbenzenesulfonic acid	27176-87-0	0.19
59.53	9-Deoxy-9-methylene-16,16-dimethyl Prostaglandin E2	61263-35-2	0.01
59.94	3-Amino-4-hydroxyphenyl sulfone	7545-50-8	0.10
Fraction IV			
7.16	Neomenthyldiphenylphosphine oxide	43077-30-1	0.29
15.28	5-Methoxytryptophan	28052-84-8	0.01
27.18	3-Methoxyprostaglandin	54432-43-8	0.96
29.08	Adenosine 3',5'-cyclic monophosphate	60-92-4	0.01
30.87	Lovastatin hydroxy acid	75225-51-3	0.01
40.69	Guanosine 3',5'-cyclic monophosphate	7665-99-8	0.01
43.88	5S,12R-Dihydroxy-6Z,8E,10E,14Z-eicosatetraene-1,20-dioic acid	80434-82-8	0.01
47.69	4-(2-Hydroxyethyl)piperazine-1-ethanesulfonic acid	7365-45-9	0.28
49.73	Dodecylbenzenesulfonic acid	27176-87-0	0.01
50.54	Thymidine 5'-monophosphate	365-07-1	0.07
51.97	2-(Cyclohexylamino)ethanesulfonic acid	103-47-9	0.02

52.24	2-(Cyclohexylamino)ethanesulfonic acid	103-47-9	0.01
52.58	Dodecylbenzenesulfonic acid	27176-87-0	0.75
53.54	1-Hexadecanoyl-sn-glycerol	542-44-9	0.01
54.09	Inosine 5'-monophosphate	131-99-7	0.09
54.77	2-(Cyclohexylamino)ethanesulfonic acid	103-47-9	0.01
55.16	20a,20b-Dihomo-9-oxo-11R,15S-dihydroxy-5Z,13E-prostadienoic acid	37492-24-3	0.13
55.30	Prostaglandin	551-11-1	0.06
56.83	Val-Leu	3989-97-7	2.12
58.06	8-iso-Prostaglandin A2	474391-66-7	0.01
59.91	5S,12R-Dihydroxy-6Z,8E,10E,14Z-eicosatetraene-1,20-dioic acid	80434-82-8	0.01
Fraction V			
4.60	Enrofloxacin	93106-60-6	0.01
6.09	Pyrazol-5(4H)-one, 4-(2,5-dimethoxybenzylideno)-3-methyl-1-phenylol	67866-56-2	30.28
6.58	Oleoyl ethylamide	85075-82-7	14.35
7.27	9-Borabicyclo[3.3.1]nonane, 9,9'-selenobis	116951-81-6	7.04
7.54	Clopidogrel	113665-84-2	2.69
8.04	3',5'-Cyclic Inosine monophosphate	3545-76-4	0.01
8.49	Oleoyl ethylamide	85075-82-7	0.59
9.63	Calcipotriol	112828-00-9	0.01
10.49	Cholestanone oxime acetate	26988-10-3	0.01
10.55	Dichotine, 2-deoxy-2,21-epoxy	29474-91-7	0.01
10.68	15-Ketobimatoprost	1163135-96-3	0.01
11.02	7-Hydroxyflavanone	6515-36-2	0.49
11.89	Vomicine	125-15-5	0.01
12.30	Fluvastatin	93957-55-2	0.03
13.49	Neomenthyldiphenylphosphine oxide	43077-30-1	0.92
14.33	Aristolochic acid	313-67-7	1.05
15.24	17-Phenyl trinor prostaglandin cyclopropyl methyl amide	1138395-10-4	0.01
17.70	3-Hydroxy-2',4,4',6'-tetramethoxychalcone	97080-85-8	0.01
17.84	Aristolochic acid	313-67-7	0.01
17.91	Fosamax	121268-17-5	0.01
19.36	HC Toxin	83209-65-8	0.40
20.03	Bimatoprost diethylamide	1176637-26-5	0.01
20.77	N-[Tris(hydroxymethyl)methyl]-3-amino-2-hydroxypropanesulfonic acid	68399-81-5	0.09
21.16	N-Lauroylsarcosine	97-78-9	0.09
21.44	Glycodeoxycholic acid	360-65-6	0.06
21.97	Thiamine monophosphate	495-23-8	0.24
23.05	Fluvastatin	93957-55-2	0.01
23.11	4-(4-tert-Butyl-benzylidene)-2-(3-iodo-phenyl)-4H-oxazol-5-one	331667-84-6	0.01
23.45	Arachidonic acid methyl ester	2566-89-4	0.07
23.73	2-Phenyl-4,6-di(4-acetylaminophenyl)pyrimidine	136009-76-2	0.01
23.80	Sulfaphenazole	526-08-9	0.01
24.07	3-Amino-4-hydroxyphenyl sulfone	7545-50-8	0.02
24.27	Phytanic acid	14721-66-5	0.01
25.34	N-Desmethylverapamil	77326-93-3	0.01
26.01	Cholest-5-enediol	17320-10-4	0.29

26.42	3,7,14,18-Tetrathiatricyclo[18.2.2.2(9,12)]hexacosa-9,11,20,22,23,25-hexaene	26822-25-3	0.01
26.83	Phytanic acid	14721-66-5	0.01
26.89	Thiamine monophosphate	495-23-8	0.01
27.63	Norfloxacin	70458-96-7	0.01
27.76	Isoxathion	18854-01-8	0.01
28.89	Guanosine 5'-diphosphate	146-91-8	0.01
28.96	Cytidine 5'-diphosphate	63-38-7	0.01
29.23	Adrenosterone	382-45-6	0.01
29.30	Hexylglutathione	24425-56-7	0.01
29.96	Dodecyldimethylphosphine oxide	871-95-4	0.01
30.10	Glycerol 1-myristate	589-68-4	0.01
30.44	Stigmasta-4,6,22-trienol	96737-58-5	0.05
30.98	Cytidine 2',3'-cyclic monophosphoric acid	15718-51-1	0.01
31.31	Egtazic acid	67-42-5	0.01
31.79	Diisodecyl phthalate	26761-40-0	0.50
32.11	Prosulfuron	94125-34-5	0.01
32.38	9-Octadecenamide	301-02-0	0.06
34.20	2'-Deoxyguanosine 5'-diphosphate	3493-09-2	0.01
34.33	2'-Deoxyguanosine 5'-diphosphate	3493-09-2	0.01
34.47	9-Oxo-prosta-10,12Z,14E-trienoic acid	573951-20-9	0.01
34.74	Prostaglandin B2	13367-85-6	0.46
35.01	Flufenamic acid	530-78-9	0.35
35.67	Cholest-4-en-26-oic acid, 7-hydroxy-3-oxo	1246298-65-6	0.01
35.95	cis-9-Hexadecenoic acid	373-49-9	0.08
36.22	Estriol	50-27-1	0.01
36.50	Fluroxypyr	69377-81-7	0.07
37.24	2'-Deoxycytidine 5'-diphosphate	800-73-7	0.01
38.20	Dinor-12-oxophytodienoic Acid	197247-23-7	0.01
38.47	Estriol	50-27-1	0.01
38.53	D-myo-Inositol-1,2,6-triphosphate	28841-62-5	0.01
39.47	Diisooctyl phthalate	131-20-4	0.01
39.54	Uridine 5'-monophosphate	58-97-9	0.01
39.80	Uridine 5'-monophosphate	58-97-9	0.01
39.87	5-Iodouridine	1024-99-3	0.01
39.94	Salicin	138-52-3	0.01
40.41	Salicin	138-52-3	0.17
40.75	Cholic acid	81-25-4	0.01
40.82	Bestatin	58970-76-6	0.01
40.96	Prostaglandin B2	13367-85-6	0.01
41.71	Normorphine	466-97-7	0.13
42.46	Uridine 5'-monophosphate	58-97-9	0.01
43.20	Dodecylbenzenesulfonic acid	27176-87-0	0.01
43.40	Thymidine 3',5'-cyclic monophosphate	6453-60-7	0.01
44.14	Dodecylbenzenesulfonic acid	27176-87-0	0.11
45.97	Flufenamic acid	530-78-9	0.01

46.18	4-Androsten-17-olone sulfate	651-45-6	0.05
46.44	9-Octadecenamide	301-02-0	0.02
46.72	5-Iodouridine	1024-99-3	0.01
46.79	Dodecylbenzenesulfonic acid	27176-87-0	0.01
49.19	5-Iodouridine	1024-99-3	0.01
49.87	9-Octadecenamide	301-02-0	0.01
49.94	Dodecylbenzenesulfonic acid	27176-87-0	0.01
50.01	Dodecylbenzenesulfonic acid	27176-87-0	0.01
50.21	Thymidine 3',5'-cyclic monophosphate	6453-60-7	0.09
50.49	Cyclophosphamide	50-18-0	0.03
50.69	Dexamethasone	50-02-2	0.01
50.82	5-Iodouridine	1024-99-3	0.01
51.51	Neomenthyldiphenylphosphine oxide	43077-30-1	0.20
52.11	Dodecylbenzenesulfonic acid	27176-87-0	0.02
52.38	Benzethonium	10172-60-8	0.01
52.44	Dodecylbenzenesulfonic acid	27176-87-0	0.01
52.57	N6-(4-Methoxybenzoyl)adenosine	56883-05-7	0.01
54.13	Metolazone	17560-51-9	0.09
55.56	Monolauryl phosphate	2627-35-2	0.01
55.63	Dodecylbenzenesulfonic acid	27176-87-0	0.01
56.11	D-myo-Inositol-1,4-diphosphate	74465-19-3	0.02
56.25	Cytidine 5'-monophosphate	63-37-6	0.02
56.59	9-Oxo-prosta-10,12Z,14E-trienoic acid	573951-20-9	0.01
56.66	Dodecylbenzenesulfonic acid	27176-87-0	0.01
56.73	Phlorizin	60-81-1	0.01
57.20	3',5'-Cyclic Inosine monophosphate	3545-76-4	0.04
58.16	N-Acetyl-D-lactosamine	32181-59-2	0.01
58.30	Prostaglandin B1	13345-51-2	0.01
58.37	N-Acetylglucosaminylasparagine	2776-93-4	0.01
59.82	1,4-Piperazinediethanesulfonic acid	5625-37-6	0.01
Fraction VI			
4.15	Propaquizafop	111479-05-1	0.13
6.16	Glycan N-Acetyllactosamine	32181-59-2	0.06
7.28	Kenpaullone	142273-20-9	4.20
11.21	2,3,3',4,5-Pentachloro-1,1'-biphenyl	70424-69-0	0.01
14.09	D-Mannitol 1-phosphate	15806-48-1	0.42
14.27	Cobalt,bis[(1,2,3,4,5,6-1-phenylboratabenzene]	36534-31-3	0.19
16.07	3-[N,N-Bis(2-hydroxyethyl)amino]-2-hydroxypropanesulfonic acid	68399-80-4	0.30
19.60	Isoconazole	27523-40-6	0.10
21.01	20-Hydroxy-(5Z,8Z,11Z,14Z)-eicosatetraenoic acid	79551-86-3	0.03
22.02	2,4-Di-tert-butyl-6-(5-chloro-2H-benzotriazol-2-yl)phenol	3864-99-1	0.01
22.30	3'-Hydroxy-D-sepiapterin	41230-32-4	0.39
23.24	Butorphanol	42408-82-2	0.05
30.60	Neomenthyldiphenylphosphine oxide	43077-30-1	0.01
31.00	Neomenthyldiphenylphosphine oxide	43077-30-1	0.01
31.07	Dodecyldimethylphosphine oxide	871-95-4	0.01

32.56	D-Glucose 6-phosphate	56-73-5	0.01
34.59	Melibiose	585-99-9	0.01
34.66	Tioconazole	65899-73-2	0.01
36.30	Aldosterone	52-39-1	0.02
36.71	Dodecylbenzenesulfonic acid	27176-87-0	0.01
38.06	Glycerol 1-myristate	589-68-4	0.01
40.23	N-Lauroylsarcosine	97-78-9	0.01
41.12	Melibiose	585-99-9	0.01
42.15	Neomenthyldiphenylphosphine oxide	43077-30-1	0.01
43.16	Flurandrenolide	1524-88-5	0.01
44.17	Methaqualone	72-44-6	0.01
45.05	N6-(4-Methoxybenzoyl)adenosine	56883-05-7	0.01
45.40	Dodecylbenzenesulfonic acid	27176-87-0	0.14
47.16	Thymidine 3',5'-cyclic monophosphate	6453-60-7	0.01
49.83	Epitestosterone	481-30-1	0.03
51.40	Cholic acid	81-25-4	0.01
51.88	Dodecylbenzenesulfonic acid	27176-87-0	0.03
52.43	N-Tris(hydroxymethyl)methyl-4-aminobutanesulfonic acid	54960-65-5	0.01
52.98	Butanoic acid, heptafluoro, lithium salt	4146-76-3	0.01
53.40	5-Iodouridine	1024-99-3	0.01
55.24	Metolazone	17560-51-9	0.01
55.99	Xanthosine	146-80-5	0.01
56.20	Dodecylbenzenesulfonic acid	27176-87-0	0.01
59.61	Monolauryl phosphate	2627-35-2	0.01
Fraction VII			
0.77	4-Amino-6-[[3,4-dichlorophenyl]sulfonyl]quinazoline	52979-19-8	0.01
4.48	Thioridazine	50-52-2	0.01
4.93	Tebufenozide	112410-23-8	0.06
6.27	S-Methyl-L-thiocitrulline	209589-59-3	0.02
6.34	1,3,5(10)-Estratriendiol 17-glucosiduronate	1806-98-0	0.01
9.19	Fipronil	120068-37-3	2.59
11.36	16,16-Dimethylprostaglandin E2	39746-25-3	0.01
11.69	D-myo-Inositol-1,2-diphosphate	208584-51-4	0.16
15.82	Quercetin 3,5,7,3',4'-pentamethyl ether	1247-97-8	0.01
16.75	Niflumic acid	4394-00-7	2.76
20.19	9-Oxo-prosta-10,12Z,14E-trienoic acid	573951-20-9	0.12
21.48	Glycoursodeoxycholic acid	64480-66-6	0.18
22.77	Cholic acid	81-25-4	0.01
23.45	Tetradecylphosphonate	4671-75-4	0.54
26.16	Fosamax	121268-17-5	0.11
28.27	Calcitriol	32222-06-3	0.01
28.41	Cholesta-5,8(9)-dienol	70741-38-7	0.01
29.49	Decanedioic acid, bis(2-ethylhexyl) ester	122-62-3	0.02
30.04	Uridine 5'-monophosphate	58-97-9	0.10
30.57	Roquefortine	58735-64-1	0.30
30.84	N-[Tris(hydroxymethyl)methyl]-3-amino-2-hydroxypropanesulfonic acid	68399-81-5	0.01

31.39	6-Phosphogluconic acid	921-62-0	0.19
31.52	Pentasiloxane, dodecamethyl	141-63-9	0.35
31.78	Pentasiloxane, dodecamethyl	141-63-9	0.22
32.19	Uridine 5'-monophosphate	58-97-9	0.01
33.06	Normorphine	466-97-7	0.04
33.40	Pregn-16-en-20-one, 3,18-bis(acetyloxy)-14,15-epoxy	30344-58-2	0.05
35.89	Decanedioic acid, bis(2-ethylhexyl) ester	122-62-3	0.01
36.28	19(20)-EpDPE	155073-47-5	0.01
36.82	5a,6-Anhydrotetracycline	1665-56-1	1.83
37.28	Apigenin 7-glucoside	578-74-5	0.01
37.35	Abrine	526-31-8	0.02
37.96	Limaprost	74397-12-9	0.01
39.18	Dodecylbenzenesulfonic acid	27176-87-0	0.06
39.59	Urs-20-enone	66965-53-5	0.07
40.07	Lactulose	4618-18-2	0.01
40.56	3,2'-Dihydroxychalcone	36574-83-1	0.84
41.02	D-Glucosamine 1-phosphate	2152-75-2	0.01
42.39	Dodecylbenzenesulfonic acid	27176-87-0	0.17
42.73	Dinor-12-oxophytodienoic Acid	197247-23-7	0.01
43.13	Dinor-12-oxophytodienoic Acid	197247-23-7	0.48
43.47	Hexylglutathione	24425-56-7	0.01
44.28	Mebeverine	3625-06-7	0.01
44.68	Dodecylbenzenesulfonic acid	27176-87-0	0.01
44.74	N-Arachidonoyltaurine	119959-65-8	0.01
45.07	Ethanediamide, N-(1-methylpropyl)-N'-(3-pyridinylmethyl)	339241-94-0	1.63
45.68	Octadecanamide	124-26-5	0.02
45.82	Cytidine 2',3'-cyclic monophosphoric acid	15718-51-1	0.01
46.29	Geranyl pyrophosphate	763-10-0	0.56
46.69	Dodecylbenzenesulfonic acid	27176-87-0	0.01
47.65	Palmitamide	629-54-9	0.41
48.12	Estriol	50-27-1	0.03
49.01	5-Iodouridine	1024-99-3	0.01
49.08	Bestatin	58970-76-6	0.01
49.28	Glycerol 1-myristate	589-68-4	0.02
50.85	N-[Tris(hydroxymethyl)methyl]-3-aminopropanesulfonic acid	29915-38-6	0.01
50.92	5-Iodo-2'-deoxyuridine	54-42-2	0.01
51.46	Cystine, N,N'-dicarboxy, N-N'-diethyl dimethyl ester	21026-91-5	0.01
51.87	5-Iodouridine	1024-99-3	0.07
52.96	5-Iodouridine	1024-99-3	0.03
53.65	5-Iodouridine	1024-99-3	0.01
54.27	2'-Deoxycytidine 5'-diphosphate	800-73-7	1.37
55.22	Polythiazide	346-18-9	0.11
55.50	Capsaicin	404-86-4	0.01
55.77	Estriol	50-27-1	0.01
56.26	Prostaglandin D1	17968-82-0	0.10
56.81	(4-Methyl-1-naphthalenyl)(1-pentyl-1H-indol-3-yl)methanone	619294-47-2	0.01

57.15	Thromboxane B2	54397-85-2	0.02
57.97	16,16-Dimethyl-6-ketoprostaglandin E1	75874-32-7	0.03
58.18	Jatrorrhizine cation	3621-38-3	0.03
58.38	(+)-Abscisic acid	21293-29-8	0.01
58.59	Dodecylbenzenesulfonic acid	27176-87-0	0.01
Fraction VIII			
22.02	5H,13H-Dibenzo[c,h]dipyrrolonaphthyridine, 6,7,7a,8,14,15-hexahydro-7,15-dimethylol	16739-54-1	0.07
40.26	Uridine 5'-monophosphate	58-97-9	0.11
40.48	Guanosine 3',5'-cyclic monophosphate	7665-99-8	0.03
47.86	Enterodiol	80226-00-2	0.02
50.01	N-(3-Furanylmethyl)-5Z,8Z,11Z,14Z-eicosatetraenamide	390824-20-1	0.02
50.50	N-(3-Furanylmethyl)-5Z,8Z,11Z,14Z-eicosatetraenamide	390824-20-1	0.02
51.06	Picrotoxinin	17617-45-7	0.02
54.26	Inosine 5'-diphosphate	42599-71-3	0.01

Supplementary Table S3. Differentially abundant proteins in broccoli sprouts under different treatments

Accession No.	Description	Zn/ CK	MT/ CK	ZM/ Zn	ZM/ MT	Cove	MW (kDa)	TpId	EmPAI	Unique Peptides
Carbohydrate metabolism										
A0A178UKL7	Malate synthase	1.13	2.06	0.83	0.45	53	63.846	7.94	3.15	13
A0A178UQL8	6-phosphogluconate dehydrogenase, decarboxylating	1.08	2.15	0.97	0.49	5	53.284	5.8	0.43	2
A0A178UTP2	L-lactate dehydrogenase	1.31	0.81	1.09	1.77	2	37.927	6.55	0.26	2
A0A178UUU3	Glucose-6-phosphate isomerase	1.07	0.71	1.28	1.93	2	67.006	5.69	0.11	2
A0A178V5M8	Phosphoglycerate kinase	1.21	0.80	1.17	1.76	30	50.081	6.24	1.37	5
A0A178VCV2	APS1	1.58	1.36	0.70	0.80	6	51.427	6.81	0.59	2
A0A178VRF6	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial	1.11	1.25	0.74	0.66	9	69.319	6.27	0.44	4
A0A178VYB0	IDH2	1.15	0.71	1.17	1.90	4	39.124	6.33	0.78	1
A0A178W4Q1	Phosphoglycerate kinase	0.93	1.45	0.87	0.56	21	49.908	8.27	0.75	3
A0A178W4Q5	Glyceraldehyde-3-phosphate dehydrogenase	1.25	0.80	1.14	1.79	89	36.89	7.18	9.00	10
A0A178W6P8	Pyruvate kinase	0.93	0.69	1.37	1.84	2	62.575	7.81	0.14	2
A0A178W7K0	Isocitrate dehydrogenase [NADP]	0.96	0.77	1.44	1.79	12	45.717	6.57	1.33	8
A0A1I9LQM9	Mannose-binding lectin superfamily protein	1.89	1.40	0.68	0.92	1	31.964	5.55	0.18	1
A0A1I9LSJ5	Citrate synthase	2.04	1.74	0.70	0.82	2	46.811	6.29	0.25	1
A0A1I9LSJ6	Citrate synthase	2.04	1.74	0.68	0.80	4	52.374	6.67	0.45	1
A0A1I9LT02	UDP-GLUCOSE PYROPHOSPHORYLASE 1	1.23	0.70	1.19	2.09	18	52.822	6.24	0.81	6
A0A1I9LT03	UDP-GLUCOSE PYROPHOSPHORYLASE 1	1.23	0.70	1.19	2.09	18	51.084	6.48	0.84	6
A0A1P8BC93	UDP-glucose pyrophosphorylase 2	1.24	0.69	1.09	1.96	21	37.212	7.05	1.51	6
A0A1P8BC98	UDP-glucose pyrophosphorylase 2	1.26	0.70	1.06	1.90	22	42.871	6.46	1.56	7
A0A1P8BDT8	Phosphoenolpyruvate carboxykinase 2	0.74	1.16	1.61	1.03	18	76.513	6.54	0.46	1
A0A1P8BDX2	Phosphoenolpyruvate carboxykinase 2	0.87	1.16	1.61	1.20	18	62.857	6.95	0.59	1
A0A1P8BFU4	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial	1.99	0.90	0.69	1.54	4	24.623	8.62	0.54	2
A0A1P8BG38	Glucose-6-phosphate isomerase	0.90	1.18	1.56	1.18	3	58.073	6.67	0.23	2
A0A3N7HIG7	Nitrilase/cyanide hydratase and apolipoprotein N-acyltransferase family protein (Fragment)	1.13	1.57	0.84	0.70	12	19.441	5.66	1.15	2
B3H5Y0	Aconitate hydratase	1.31	0.71	0.97	1.79	42	86.491	6.61	2.25	9
B5X574	At5g65690	0.86	1.16	1.62	1.21	18	72.845	6.42	0.48	1
B9DFU6	AT3G08590 protein	1.17	0.72	1.08	1.75	10	60.726	5.85	0.67	7
B9DHM5	Pyruvate, phosphate dikinase	1.92	1.35	0.73	1.03	15	95.332	5.52	0.70	7
F4I3L1	Phosphoglycerate kinase	1.26	0.71	1.17	2.07	21	42.589	5.54	0.98	3
F4IA73	Glutathione S-transferase U21	1.76	1.15	0.77	1.19	3	25.629	5.5	0.36	1
F4IGL5	Fructose-bisphosphate aldolase	0.97	0.75	1.39	1.80	18	41.781	6.28	2.51	2
F4IGL7	Fructose-bisphosphate aldolase	0.97	0.73	1.25	1.66	13	33.302	6.8	2.16	2

F4IW47	Transketolase-2, chloroplastic	0.90	1.38	1.55	1.02	5	79.872	6.58	0.26	3
F4J0U9	Dicarboxylate diiron protein, putative (Crd1)	1.96	1.18	0.71	1.17	1	39.154	6.44	0.11	1
F4K7T6	1-deoxy-D-xylulose 5-phosphate reductoisomerase	1.17	0.91	1.24	1.59	1	54.194	7.25	0.07	1
F4KC24	Xylose isomerase	1.83	1.44	0.74	0.94	8	32.387	7.75	1.34	6
F4KEX3	Malate dehydrogenase	1.23	0.75	1.07	1.76	6	36.368	5.07	0.47	4
F4KGY8	UDP-glucose pyrophosphorylase 2	1.23	0.82	1.05	1.57	22	43.722	7.84	1.40	7
O04499	2,3-bisphosphoglycerate-independent phosphoglycerate mutase 1	1.83	0.81	0.76	1.71	5	60.542	5.53	0.30	3
O64530	Thiosulfate/3-mercaptopyruvate sulfurtransferase 1, mitochondrial	1.83	1.14	0.73	1.18	3	41.867	6.39	0.29	3
O64688	Pyruvate dehydrogenase E1 component subunit beta-3, chloroplastic	1.14	1.47	0.75	0.59	1	43.987	5.8	0.15	1
O65595	Probable pyruvate kinase, cytosolic isozyme	0.99	0.87	1.46	1.67	1	54.284	7.9	0.07	1
O80476	Methylesterase 2	1.72	1.90	0.76	0.69	4	29.647	5.34	0.36	1
P25851	Fructose-1,6-bisphosphatase 1, chloroplastic	0.83	1.01	1.56	1.28	6	45.134	5.4	0.87	4
P25856	Glyceraldehyde-3-phosphate dehydrogenase GAPA1, chloroplastic	1.24	1.59	0.95	0.74	22	42.463	7.75	2.46	7
P25858	Glyceraldehyde-3-phosphate dehydrogenase GAPC1, cytosolic	1.21	0.77	1.15	1.81	89	36.891	7.12	9.00	10
P34795	Glucose-6-phosphate isomerase, cytosolic	0.76	1.18	1.57	1.01	3	61.679	6.65	0.22	2
P56773	Cytochrome b6	0.72	1.10	1.81	1.18	1	24.137	8.76	0.29	1
P93032	Isocitrate dehydrogenase [NAD] regulatory subunit 2, mitochondrial	1.03	0.72	1.33	1.90	4	39.565	6.55	0.78	1
Q07098	Serine/threonine-protein phosphatase PP2A-2 catalytic subunit	1.04	1.45	2.32	1.37	1	34.912	4.89	0.13	1
Q0WUS4	Malate dehydrogenase	1.32	0.69	0.87	1.67	14	37.442	7.96	0.93	4
Q24JL3	Thiosulfate/3-mercaptopyruvate sulfurtransferase 2	1.86	1.35	0.72	0.99	1	37.389	6.13	0.11	1
Q38799	Pyruvate dehydrogenase E1 component subunit beta-1, mitochondrial	1.21	0.82	0.98	1.44	10	39.151	5.83	1.45	6
Q8H1E2	Malate dehydrogenase [NADP], chloroplastic	1.21	0.89	1.20	1.63	6	48.286	6.16	0.35	4
Q8L7W8	FUC95A	0.76	1.29	1.83	1.09	1	93.628	7.12	0.05	1
Q8LPJ5	Isocitrate dehydrogenase [NADP], chloroplastic/mitochondrial	0.85	1.47	1.07	0.62	3	54.162	7.97	0.23	1
Q8RWN9	Dihydrolipoyllysine-residue acetyltransferase component 2 of pyruvate dehydrogenase complex, mitochondrial	1.37	0.76	1.00	1.80	3	58.431	7.65	0.15	2
Q945K7	Isocitrate dehydrogenase [NAD] catalytic subunit 5, mitochondrial	1.17	0.81	1.09	1.57	2	40.599	6.79	0.26	2
Q94B35	4-hydroxy-3-methylbut-2-enyl diphosphate reductase, chloroplastic	1.17	1.46	0.74	0.59	3	52.748	6.07	0.22	3

Q9C6Z3	Pyruvate dehydrogenase E1 component subunit beta-2, chloroplastic	1.38	0.91	1.07	1.62	1	44.216	6.35	0.15	1
Q9C8T3	Ribulose-phosphate 3-epimerase	2.02	1.20	0.67	1.13	1	24.095	6.1	0.33	1
Q9C9C4	Enolase 1, chloroplastic	0.84	0.94	2.56	2.29	1	51.442	6.13	0.08	1
Q9FKW6	Ferredoxin--NADP reductase, leaf isozyme 1, chloroplastic	0.87	1.33	1.61	1.06	3	40.301	8.13	0.27	3
Q9FM97	Pyruvate kinase	0.97	0.76	1.36	1.74	1	54.376	6.86	0.07	1
Q9FNN1	Pyruvate kinase	0.68	1.34	2.15	1.09	1	54.941	6.29	0.07	1
Q9LF98	Fructose-bisphosphate aldolase 8, cytosolic	1.12	0.76	1.21	1.78	34	38.516	6.46	8.01	7
Q9LIF9	Beta-glucosidase 19	2.53	1.45	1.28	1.38	1	59.977	6.65	0.08	1
Q9LRS0	(S)-2-hydroxy-acid oxidase GLO2	1.15	2.66	0.91	0.40	18	40.281	8.97	2.31	3
Q9LU95	Pyruvate kinase	1.05	0.79	1.38	1.84	1	53.741	7.39	0.07	1
Q9LXS7	Citrate synthase 1, peroxisomal	1.06	1.21	2.21	1.93	3	52.862	7.96	0.25	1
Q9LZC3	Malate synthase (Fragment)	1.14	1.72	0.83	0.75	30	36.438	7.28	2.36	7
Q9M057	Pyruvate kinase	0.98	0.90	1.48	1.61	1	54.946	6.09	0.08	1
Q9M1D3	Citrate synthase 5, mitochondrial	1.90	1.73	0.70	0.77	4	51.692	6.67	0.47	1
Q9MAH0	Phosphoenolpyruvate carboxylase 1	0.86	1.39	1.62	1.00	7	110.217	6.06	0.27	5
Q9S726	Probable ribose-5-phosphate isomerase 3, chloroplastic	0.80	1.17	1.76	1.19	2	29.287	6.02	0.12	1
Q9SHE8	Photosystem I reaction center subunit III, chloroplastic	1.08	1.76	0.98	0.71	6	24.158	9.54	0.93	2
Q9SIB9	Aconitate hydratase 3, mitochondrial	1.29	0.90	1.13	1.62	83	108.133	7.17	3.77	15
Q9SJH7	Citrate synthase 3, peroxisomal	1.39	0.87	0.99	1.57	9	56.14	7.66	0.93	3
Q9SJU4	Fructose-bisphosphate aldolase 1, chloroplastic	1.09	0.70	1.06	1.64	19	42.904	6.58	2.68	2
Q9SN86	Malate dehydrogenase, chloroplastic	1.23	0.77	0.95	1.52	12	42.379	8.51	0.98	5
Q9SQI8	Dihydrolipoyllysine-residue acetyltransferase component 4 of pyruvate dehydrogenase complex, chloroplastic	1.07	0.72	1.11	1.65	4	50.049	8.37	0.45	1
Q9SQQ7	Pyruvate kinase	0.97	0.80	1.31	1.59	1	55.255	5.99	0.07	1
Q9SUI4	Photosystem I reaction center subunit XI, chloroplastic	0.92	1.92	0.81	0.70	1	23.037	9.85	0.23	1
Q9XF87	Chlorophyll a-b binding protein 2.4, chloroplastic	0.77	1.27	1.56	0.94	9	28.784	5.9	1.85	1
Q9XF88	Chlorophyll a-b binding protein CP29.2, chloroplastic	0.84	2.09	1.60	0.71	7	31.174	6.24	0.31	0
Q9XFS9	1-deoxy-D-xylulose 5-phosphate reductoisomerase, chloroplastic	1.01	1.45	0.80	0.56	1	51.931	7.05	0.08	1
R0ILH3	Glyceraldehyde 3-phosphate dehydrogenase A (Fragment)	1.24	1.69	0.98	0.72	10	8.168	4.25	16.78	3
Amino acid metabolism										
A0A178UKY4	Aspartate aminotransferase	1.27	0.76	1.14	1.91	11	48.923	9.29	1.21	4
A0A178VQX6	Phenylalanine ammonia-lyase	0.81	1.06	1.61	1.23	1	78.676	6.3	0.06	1
A0A178VQZ7	S-formylglutathione hydrolase	0.74	1.09	1.61	1.10	2	31.635	6.37	0.33	2
A0A178VV72	Glycine cleavage system H protein	1.99	1.14	0.69	1.21	2	17.936	5.34	0.52	1
A0A178WFY3	Serine/threonine-protein phosphatase	1.04	1.45	2.33	1.43	1	35.019	5.01	0.12	1

A0A1P8AMY1	3-phosphoserine phosphatase	0.70	1.38	1.70	0.87	1	31.004	6.96	0.14	1
A0A1P8ANY1	Semialdehyde dehydrogenase family protein	1.02	1.34	0.85	0.65	5	33.218	7.58	1.03	2
A0A1P8API2	Serine protease inhibitor (SERPIN) family protein	1.25	1.52	0.78	0.71	2	45.785	5.74	0.20	2
A0A1P8APT9	Aspartate aminotransferase	1.19	0.80	1.15	1.71	2	37.273	6.27	0.27	1
A0A1P8AUR1	Class I glutamine amidotransferase-like superfamily protein	2.02	1.96	0.73	0.75	1	40.336	7.05	0.13	1
A0A1P8AZ64	Glutamate decarboxylase	1.10	0.71	0.45	0.69	2	61.999	7.53	0.16	1
A0A1P8BCC6	Probable alanine--tRNA ligase, chloroplastic	1.20	1.52	0.76	0.72	1	111.006	5.97	0.03	1
A0A1P8BFA4	Glutathione S-transferase family protein	0.76	0.49	0.75	1.15	1	31.141	5.4	0.12	1
A8MS68	Dihydrolipoyl dehydrogenase 1, chloroplastic	1.01	1.20	0.70	0.59	5	66.62	8.41	0.40	4
B0LZ74	Phenylalanine ammonia-lyase (Fragment)	0.80	1.08	1.74	1.30	1	21.744	6.61	0.26	1
B0LZ83	Phenylalanine ammonia-lyase (Fragment)	0.75	1.08	1.74	1.21	1	21.543	6.61	0.26	1
B3H4D0	Glutathione S-transferase family protein	0.78	0.49	0.71	1.12	1	31.113	5.24	0.13	1
B3H5E3	Delta 1-pyrroline-5-carboxylate synthase 2	1.26	1.45	0.71	0.62	2	67.649	7.39	0.06	1
B3H778	Arginosuccinate synthase family	1.97	0.84	0.70	1.64	2	48.998	7.72	0.16	2
B9DFG0	AT2G39800 protein	1.16	1.89	0.85	0.52	2	66.718	5.94	0.06	1
B9DFR6	Cysteine synthase	1.87	0.79	0.70	1.66	3	46.086	8.37	0.29	2
F4I0D4	Aspartate aminotransferase	1.20	1.34	0.69	0.62	2	44.573	6.73	0.21	1
F4J9F7	Cysteine synthase	1.74	0.82	0.79	1.69	3	46.058	9.06	0.28	2
F4JIZ3	Phospho-2-dehydro-3-deoxyheptonate aldolase	1.83	1.35	0.71	0.96	2	38.626	7.55	0.23	0
F4JTH0	Aspartate aminotransferase	1.01	1.40	0.84	0.61	13	49.293	7.87	1.31	10
F4JW69	Phenylalanine ammonia-lyase	0.80	1.08	1.74	1.30	1	76.626	6.51	0.05	1
F4K2Y3	Alpha/beta-Hydrolases superfamily protein	1.20	1.70	0.96	1.68	1	81.255	5.8	0.06	1
O23254	Serine hydroxymethyltransferase 4	0.85	1.42	1.65	0.98	4	51.685	7.23	0.41	3
O50008	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase 1	1.66	1.24	0.72	0.96	64	84.304	6.51	2.31	8
O80988	Glycine dehydrogenase (decarboxylating) 2, mitochondrial	1.83	1.35	0.72	0.97	2	113.703	6.65	0.05	1
O82796	Phosphoserine phosphatase, chloroplastic	0.87	1.37	1.61	1.02	1	32.298	6.38	0.12	1
P17597	Acetolactate synthase, chloroplastic	1.06	0.79	1.41	1.89	1	72.539	6.65	0.08	1
P29976	Phospho-2-dehydro-3-deoxyheptonate aldolase 1, chloroplastic	1.76	0.79	0.72	1.62	5	57.942	8.06	0.37	3
P32068	Anthranilate synthase alpha subunit 1, chloroplastic	1.06	0.73	1.20	1.74	1	66.269	6.49	0.06	1
P45724	Phenylalanine ammonia-lyase 2	0.74	1.07	1.75	1.22	1	77.811	6.46	0.05	1
P45725	Phenylalanine ammonia-lyase 3	0.70	1.07	1.72	1.13	1	76.193	6.51	0.06	1
P46248	Aspartate aminotransferase, chloroplastic	1.35	0.71	0.85	1.62	13	49.799	8.15	1.31	10

P46422	Glutathione S-transferase F2	1.75	1.15	0.37	1.22	11	24.114	6.35	1.51	3
P46643	Aspartate aminotransferase, mitochondrial	1.27	0.76	1.00	1.67	20	47.727	8.19	2.43	9
P46646	Aspartate aminotransferase, cytoplasmic isozyme 2	1.29	0.80	1.09	1.76	2	44.33	6.55	0.21	1
P54887	Delta-1-pyrroline-5-carboxylate synthase A	1.16	1.69	0.83	0.51	2	77.654	6.29	0.05	1
P54888	Delta-1-pyrroline-5-carboxylate synthase B	1.14	1.40	0.70	0.57	2	78.822	6.81	0.05	1
Q0WNZ5	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase 3, chloroplastic	1.65	1.16	0.78	1.10	22	90.537	8.05	0.50	1
Q1H5A3	Glutamate dehydrogenase	1.77	1.25	0.75	1.07	3	44.496	6.86	0.30	3
Q42521	Glutamate decarboxylase 1	1.15	1.39	1.80	1.49	2	57.03	5.53	0.18	1
Q43725	Cysteine synthase, mitochondrial	1.87	0.81	0.71	1.64	3	45.786	8.18	0.29	2
Q56YA5	Serine--glyoxylate aminotransferase	1.22	1.61	1.02	0.77	3	44.18	7.83	0.35	3
Q8GXW5	Glutamine synthetase cytosolic isozyme 1-5	1.07	0.93	1.36	1.57	4	38.883	6.65	0.54	1
Q8H107	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex 2, mitochondrial	1.80	1.32	0.76	1.04	1	50.028	9.09	0.10	1
Q93WN0	Selenium-binding protein 2	1.91	2.02	0.74	0.70	1	53.903	6.19	0.09	1
Q94AR8	3-isopropylmalate dehydratase large subunit, chloroplastic	1.27	0.83	1.08	1.65	4	54.979	7.84	0.39	4
Q9FL95	At5g45020/K21C13_21	0.73	0.50	0.78	1.13	1	37.319	6.33	0.11	1
Q9FL98	Glutathione S-transferase family protein	0.74	0.50	0.77	1.13	1	40.587	5.59	0.10	1
Q9LDV4	Alanine aminotransferase 2, mitochondrial	0.97	1.19	0.72	0.59	2	59.473	6.38	0.15	2
Q9LFG2	Diaminopimelate epimerase, chloroplastic	1.07	0.85	1.22	1.54	3	38.959	5.68	0.35	3
Q9LIR4	Dihydroxy-acid dehydratase, chloroplastic	1.23	0.87	1.14	1.61	4	64.872	6.23	0.32	3
Q9LJA0	Putative inactive cysteine synthase 2	1.28	0.92	1.09	1.51	5	19.625	7.93	1.15	3
Q9LT69	D-3-phosphoglycerate dehydrogenase 3, chloroplastic	0.86	1.06	1.62	1.32	1	62.083	8.24	0.07	1
Q9LTB2	Methionine S-methyltransferase	1.80	1.41	0.72	0.92	4	118.641	5.63	0.18	4
Q9LYT7	3-isopropylmalate dehydratase small subunit 2	1.87	1.01	0.74	1.37	1	27.191	6.87	0.14	1
Q9LZX6	4-hydroxy-tetrahydrodipicolinate synthase 1, chloroplastic	1.01	1.47	0.69	0.48	1	40.595	7.14	0.12	1
Q9M8D3	Probable phosphoribosylformylglycinamidine synthase, chloroplastic/mitochondrial	1.18	0.75	1.12	1.76	1	153.856	5.36	0.03	1
Q9S757	Bifunctional L-3-cyanoalanine synthase/cysteine synthase C1, mitochondrial	1.83	0.79	0.72	1.66	5	39.902	8.54	0.67	2
Q9S7E9	Glutamate--glyoxylate aminotransferase 2	1.23	1.32	2.66	2.46	8	53.41	6.58	0.66	2

Q9SHH7	Glutathione S-transferase U25	1.76	1.15	0.74	1.13	3	25.574	5.3	0.29	1
Q9SK84	Phospho-2-dehydro-3-deoxyheptonate aldolase	1.70	1.18	0.75	1.09	2	58.29	8.32	0.15	0
Q9SLM6	Glutathione S-transferase F3	1.74	1.12	0.37	1.24	12	24.106	6.74	1.93	4
Q9SS45	Phenylalanine ammonia-lyase 4	0.79	1.08	1.76	1.30	1	76.871	6.27	0.06	1
Q9SZX3	Argininosuccinate synthase, chloroplastic	1.70	0.81	0.75	1.59	2	53.812	6.67	0.14	2
Q9ZPS3	Glutamate decarboxylase 4	1.10	1.38	1.82	1.46	2	55.97	6.34	0.18	1
Lipid metabolism										
A0A160CBM4	Acyl-[acyl-carrier-protein] desaturase	1.15	0.75	1.23	1.88	6	45.675	6.4	0.56	4
A0A178UA38	Acyl-coenzyme A oxidase	1.04	0.81	1.32	1.69	1	77.432	8.29	0.05	1
A0A178ULR4	Biotin carboxyl carrier protein of acetyl-CoA carboxylase	0.73	1.04	1.58	1.11	3	26.911	9.54	0.64	3
A0A178VYR6	CAC3	1.02	1.18	0.71	0.61	2	85.253	5.82	0.10	2
A0A178VZQ3	Non-specific lipid-transfer protein	1.92	1.20	0.72	1.15	5	11.747	8.95	1.68	1
A0A178WDE4	Acyl-coenzyme A oxidase	1.22	1.48	0.72	0.59	4	75.629	7.99	0.24	2
A0A1B1W4V3	Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta, chloroplastic	1.92	0.90	0.75	1.59	3	55.574	6.24	0.26	2
A0A1I9LST4	3-hydroxyacyl-CoA dehydrogenase family protein	0.78	0.89	1.66	1.46	2	25.764	6.54	0.36	2
A0A1P8AVA7	Saposin-like aspartyl protease family protein	2.05	1.24	0.68	1.12	5	52.741	6.95	0.41	2
B0FFQ6	AccD (Fragment)	1.92	0.91	0.72	1.51	2	12.468	8.62	0.93	1
B9DGD6	Acetyl-coenzyme A synthetase, chloroplastic/glyoxysomal	1.10	0.87	1.35	1.71	4	81.837	6.09	0.26	3
F4JBY2	Transketolase	1.14	0.77	1.26	1.87	24	79.789	6.43	1.04	10
F4JKM2	Cinnamyl alcohol dehydrogenase 5	1.03	1.40	0.83	0.61	1	38.691	5.44	0.12	1
F4KGI8	Acyl-coenzyme A oxidase	1.14	0.74	1.08	1.66	1	72.216	8.46	0.05	1
O22832	Stearoyl-[acyl-carrier-protein] 9-desaturase 7, chloroplastic	1.34	0.77	0.93	1.62	6	45.664	6.48	0.53	4
O80526	ATP-citrate synthase alpha chain protein 3	1.05	1.59	0.86	0.48	2	46.916	5.26	0.22	1
P0CZ24	Putative acyl-coenzyme A oxidase At3g06690	1.17	0.81	1.26	1.81	3	21.024	5.63	0.87	1
P56765	Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta, chloroplastic	1.76	0.79	0.73	1.61	3	55.6	6.24	0.26	2
Q42533	Biotin carboxyl carrier protein of acetyl-CoA carboxylase 1, chloroplastic	0.81	1.40	1.61	0.93	3	29.594	9.06	0.64	3
Q494P3	At3g17770	1.44	1.24	0.49	0.56	1	61.882	5.14	0.07	1
Q8LF48	3-ketoacyl-CoA thiolase 1, peroxisomal	1.05	1.44	0.71	0.52	7	46.582	8.29	0.47	1
Q8LPS1	Long chain acyl-CoA synthetase 6, peroxisomal	1.12	1.35	0.79	0.65	1	76.555	7.93	0.06	1
Q8RWZ3	Probable acyl-CoA dehydrogenase IBR3	1.24	1.90	0.93	0.81	2	91.655	8.32	0.09	2
Q93ZC5	Allene oxide cyclase 4, chloroplastic	1.70	1.79	0.73	0.70	2	27.792	9.07	0.16	1

Q94A94	Diaminopimelate decarboxylase 2, chloroplastic	1.87	1.35	0.69	0.96	2	54.13	6.67	0.16	2
Q9C5N8	GDSL esterase/lipase At1g54020	1.90	1.36	0.69	0.96	1	41.774	7.94	0.11	1
Q9FLW9	Plastidial pyruvate kinase 2	0.89	1.23	1.57	1.14	3	63.481	7.03	0.22	3
Q9LDF5	3-hydroxyacyl-CoA dehydrogenase family protein	0.72	0.85	1.66	1.41	2	31.669	7.09	0.31	2
Q9LF04	Stearoyl-[acyl-carrier-protein] 9-desaturase 1, chloroplastic	1.27	0.74	1.16	1.99	3	44.99	6.55	0.19	2
Q9LMI7	Putative acyl-coenzyme A oxidase 3.2, peroxisomal	1.19	2.36	0.79	0.40	2	75.852	7.85	0.11	1
Q9M879	Stearoyl-[acyl-carrier-protein] 9-desaturase 5, chloroplastic	1.27	0.69	1.08	1.99	3	45.274	6.23	0.19	2
Q9SIE3	At2g22230/T26C19.11	1.55	1.54	0.70	0.70	1	24.226	8.48	0.23	1
Q9T0A0	Long chain acyl-CoA synthetase 4	1.07	1.37	0.72	0.56	1	74.46	5.87	0.07	1
Q9ZPI5	Peroxisomal fatty acid beta-oxidation multifunctional protein MFP2	0.99	1.30	0.72	0.55	17	78.79	9.17	0.73	9
Nucleotide metabolism										
A0A178UAM7	ADK1	2.17	2.37	1.43	1.31	6	26.915	7.36	0.62	1
A0A178VGZ6	Dihydrolipoyl dehydrogenase	1.21	0.91	1.21	1.62	5	60.719	8.09	0.47	4
A0A178VRA7	MORF6	0.73	0.58	0.73	0.91	1	26.351	8.9	0.19	1
F4HNZ6	Glyceraldehyde 3-phosphate dehydrogenase A subunit 2	1.24	1.79	0.99	0.68	20	34.311	6.64	3.64	5
F4HQT1	Glyceraldehyde-3-phosphate dehydrogenase C2	1.26	0.84	1.12	1.68	78	33.885	7.21	6.08	8
F4JWF6	DEAD/DEAH box RNA helicase family protein	1.13	1.61	0.85	0.70	6	55.429	5.92	0.39	5
O49203	Nucleoside diphosphate kinase III, chloroplastic/mitochondrial	1.21	0.81	1.08	1.62	4	25.718	9.23	0.29	1
O64767	AICARFT/IMPCHase bienzyme family protein	1.13	0.90	1.30	1.63	4	59.434	6.3	0.24	3
P59259	Histone H4	0.93	1.70	0.82	0.71	9	11.402	11.47	13.68	5
P69834	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase, chloroplastic	1.15	0.90	1.28	1.63	1	33.916	6.16	0.14	1
Q1WIQ6	NADP-dependent glyceraldehyde-3-phosphate dehydrogenase	1.21	0.71	0.97	1.65	15	53.026	6.64	1.26	9
Q681I7	Uncharacterized protein At4g09040	0.56	0.71	0.90	0.71	1	33.997	7.59	0.18	1
Q96529	Adenylosuccinate synthetase, chloroplastic	1.81	1.28	0.72	1.01	8	52.931	7.14	0.40	5
Q9C7Y2	Multiple organellar RNA editing factor 5, chloroplastic/mitochondrial	1.36	1.72	1.43	1.13	1	26.008	9.11	0.19	1
Q9LVI8	Glutamine synthetase cytosolic isozyme 1-3	1.09	0.82	1.35	1.79	15	38.57	6.06	1.74	3
Q9SYL9	50S ribosomal protein L13, chloroplastic	4.28	1.30	0.26	0.86	2	26.772	9.92	0.18	1
Energy										
A0A178VRB0	Chlorophyll a-b binding protein, chloroplastic	0.89	1.27	1.58	1.10	7	28.036	5.44	1.15	1
A0A178W2T0	Chlorophyll a-b binding protein, chloroplastic	0.76	1.00	1.58	1.20	5	28.209	5.43	0.78	0
A0A178W4V2	ACLA-1	1.05	2.01	0.86	0.45	3	46.649	5.5	0.33	1

A0A178WKX1	Chlorophyll a-b binding protein, chloroplastic	0.89	1.30	1.57	1.08	5	28.223	5.66	0.78	0
A0A1B1W4S7	Photosystem II protein D1	0.76	1.08	1.72	1.20	1	38.911	5.25	0.21	1
A0A1B1W4U2	Photosystem I P700 chlorophyll a apoprotein A2	0.78	1.37	1.88	1.07	4	82.423	7.4	0.62	2
A0A1I9LMB4	Chlorophyll a-b binding protein, chloroplastic	0.89	1.27	1.57	1.10	9	32.567	6.23	1.85	1
A0A1I9LS90	Photosystem II subunit T	0.75	0.53	0.78	1.12	4	15.623	9.63	1.00	1
A0A1P8AZ91	Chlorophyll a-b binding protein, chloroplastic	0.89	1.26	1.57	1.11	9	35.131	7.02	1.15	1
A0A1P8B6D0	Photosystem I subunit l	0.93	2.18	0.81	0.73	1	30.422	10.14	0.18	1
F4JZ46	Ferredoxin--NADP reductase	0.86	1.38	1.63	1.02	3	29.665	6.15	0.37	3
O23404	Pyruvate, phosphate dikinase 1, chloroplastic	1.89	1.35	0.74	1.03	15	105.071	6.38	0.60	7
O49506	Peroxisomal (S)-2-hydroxy-acid oxidase GLO5	1.01	1.40	0.70	0.51	12	40.456	8.31	1.46	1
P56761	Photosystem II D2 protein	0.82	1.37	1.72	1.02	3	39.522	5.74	0.87	3
P56777	Photosystem II CP47 reaction center protein	0.77	1.42	1.57	0.85	1	56.001	6.89	0.12	1
Q07473	Chlorophyll a-b binding protein CP29.1, chloroplastic	0.82	1.41	1.59	0.92	8	31.12	6.14	0.59	1
Q39195	Photosystem II 5 kDa protein, chloroplastic	1.40	0.54	1.38	1.45	4	11.021	9.48	1.37	1
Q3ZVE1	ATPase alpha subunit (Fragment)	1.21	1.62	0.88	0.75	13	19.75	5.55	2.98	4
Q3ZVE2	ATPase alpha subunit (Fragment)	1.21	1.62	0.88	0.77	13	19.663	5.55	2.98	4
Q42536	Protochlorophyllide reductase A, chloroplastic	1.65	1.36	0.83	1.02	31	43.836	9.36	3.13	3
Q5GM68	Phosphoenolpyruvate carboxylase 2	0.85	1.41	1.65	1.00	3	109.684	5.8	0.10	2
Q84VW9	Phosphoenolpyruvate carboxylase 3	0.81	1.40	1.61	0.93	7	110.091	6.04	0.25	5
Q8HS55	Photosystem II CP47 reaction center protein (Fragment)	0.77	1.42	1.57	0.85	1	51.951	6.61	0.14	1
Q8HT11	Photosystem II CP43 reaction center protein (Fragment)	1.63	1.66	0.77	0.76	1	43.973	7.59	0.19	1
Q8HT12	Photosystem II D2 protein (Fragment)	0.82	1.38	1.72	1.01	3	35.22	5.91	1.15	3
Q9LMQ2	Chlorophyll a-b binding protein, chloroplastic	0.82	1.34	1.58	0.97	10	27.505	7.4	1.89	3
Q9S7D8	ATP sulfurylase 4, chloroplastic	1.54	0.76	0.83	1.67	4	52.093	8.87	0.33	1
Defense/Stress										
A0A178VD55	GOX2	1.15	2.69	0.91	0.39	17	40.908	8.76	2.02	3
A0A178VGA9	SOX	1.82	0.84	0.74	1.60	4	43.302	8.68	0.32	3
A0A1P8AWT7	Catalase 3	0.99	0.89	1.46	1.63	61	63.519	8.9	3.25	7
A8MQK8	60S acidic ribosomal protein family	1.85	1.06	0.72	1.25	1	9.994	4.36	0.59	1
B9DG18	AT1G20620 protein	1.05	0.75	1.13	1.59	61	55.932	7.64	4.41	7
B9DG21	Aspartate aminotransferase	1.28	0.91	1.15	1.62	13	50.942	7.53	1.31	10
D7L5Q3	JR1	1.89	1.38	0.73	1.00	1	48.491	5.33	0.11	1
F4HUL6	Catalase 3	0.83	1.41	1.56	0.92	58	48.867	6.8	4.88	6
F4IQ05	Peroxidase	1.72	1.87	1.69	1.56	1	33.25	7.68	0.14	1
F4J504	Superoxide dismutase	1.97	1.23	1.44	2.31	3	25.33	8.48	0.70	3
F4K0T5	Anthranilate synthase alpha subunit 1	0.91	0.83	1.51	1.65	1	69.63	6.44	0.06	1

O04309	Jacalin-related lectin 35	1.88	1.40	0.69	0.93	1	48.467	5.26	0.11	1
O49326	Nitrile-specifier protein 2	1.35	1.71	1.53	1.21	2	51.18	5.76	0.16	1
O80852	Glutathione S-transferase F9	1.82	2.10	1.53	1.33	20	24.13	6.65	6.74	3
O80889	Alpha/beta-Hydrolases superfamily protein	1.21	0.84	1.19	1.71	2	25.905	5.47	0.43	2
P25819	Catalase-2	1.99	2.17	1.17	1.07	77	56.9	7.12	4.74	6
P37702	Myrosinase 1	2.05	1.91	1.44	1.54	15	61.09	5.92	0.32	1
P57751	UTP--glucose-1-phosphate uridylyltransferase 1	1.12	0.95	1.32	1.56	23	51.887	6.01	1.25	8
Q0WUH6	Catalase	1.67	0.82	0.76	1.56	33	56.726	7.42	3.18	4
Q2V4M4	Catalase 3	1.02	0.81	1.21	1.52	25	43.921	7.61	3.49	7
Q38814	Thiamine thiazole synthase, chloroplastic	1.83	1.15	0.77	1.22	11	36.641	6.23	1.15	3
Q39101	Ferritin (Fragment)	0.75	1.00	1.86	1.40	4	5.787	4.88	1.15	1
Q41931	1-aminocyclopropane-1-carboxylate oxidase 2	1.91	1.11	0.73	1.26	4	36.16	5.12	0.62	3
Q42547	Catalase-3	0.99	0.95	1.48	1.55	61	56.66	7.64	4.41	7
Q8RWT5	AICARFT/IMPCHase bienzyme family protein	1.19	0.75	1.22	1.93	4	64.866	6.92	0.21	3
Q8RY71	Epithiospecifier protein	1.97	2.67	1.11	0.82	7	36.99	5.86	0.30	2
Q9C5C2	Myrosinase 2	2.14	2.10	1.06	1.08	11	62.69	7.44	0.35	1
Q9FLC0	Peroxidase 52	1.68	1.65	0.96	0.98	2	34.19	8.31	0.36	1
Q9FNK4	Ornithine aminotransferase, mitochondrial	1.09	1.42	0.75	0.58	1	52.145	7.44	0.08	1
Q9LZ66	Assimilatory sulfite reductase (ferredoxin), chloroplastic	1.07	0.87	1.36	1.68	4	71.905	8.31	0.32	4
Q9M9P3	UTP--glucose-1-phosphate uridylyltransferase 2	1.19	0.81	1.07	1.57	18	51.706	6.13	0.81	6
Q9S7J7	Chlorophyll a-b binding protein 2.2, chloroplastic	0.83	1.24	1.57	1.05	9	28.602	5.43	1.85	1
Q9SHR7	Chlorophyll a-b binding protein 2.1, chloroplastic	0.89	1.25	1.57	1.12	9	28.631	5.43	1.85	1
Q9SMU8	Peroxidase 34	2.15	2.37	1.17	1.06	1	38.81	7.64	0.12	1
Q9SYG7	Aldehyde dehydrogenase family 7 member B4	0.87	1.08	1.60	1.30	1	54.174	5.54	0.08	1
Protein biosynthesis										
A0A103P898	Ribosomal protein PO (Fragment)	1.19	1.54	0.71	0.70	2	8.648	9.64	2.16	1
A0A178U9H3	Probable alanine--tRNA ligase, chloroplastic	0.98	1.60	0.80	0.71	1	107.764	5.59	0.04	1
A0A178UFG0	40S ribosomal protein S4	0.73	1.16	1.64	1.03	12	29.855	10.17	2.16	7
A0A178V6A2	60S ribosomal protein L13	0.72	1.26	1.67	0.95	4	23.488	10.55	0.36	1
A0A178V9F6	Histone H2B	0.78	0.96	1.71	1.39	3	16.426	10.02	0.59	2
A0A178VBG6	40S ribosomal protein S3a	0.75	1.15	1.66	1.08	4	29.832	9.76	0.54	1
A0A178VGU6	Histone H2B	0.82	0.99	1.71	1.41	3	15.902	10.02	0.59	2
A0A178VSS0	EMB2296	0.78	1.00	1.66	1.30	12	27.842	10.9	1.45	1
A0A178VWL0	RPL16A	1.06	1.51	0.92	0.68	4	20.818	9.92	0.87	3
A0A178W1V2	Ribosomal protein	2.60	1.18	0.36	0.80	2	24.409	9.88	0.36	2
A0A178W2S2	Serine/threonine-protein phosphatase	1.02	1.48	2.36	1.43	1	34.912	4.96	0.12	1
A0A178W3V2	UGGT	1.65	1.19	0.69	0.96	1	181.818	5.83	0.02	1

A0A1B1W4U6	30S ribosomal protein S4, chloroplastic	0.89	1.37	1.57	1.02	3	23.226	10.33	0.78	2
A0A1B1W4X5	30S ribosomal protein S19, chloroplastic	0.82	1.62	1.56	0.79	1	10.602	10.77	0.59	1
A0A1B1W4Y0	50S ribosomal protein L14, chloroplastic	1.81	1.26	0.76	1.09	3	13.573	9.29	0.59	2
A0A1I9LTP2	Cysteine synthase C1	2.07	1.07	0.69	1.34	3	36.296	8.28	0.33	1
A0A1J3CNH1	GF14 protein chi chain (Fragment)	1.24	1.42	2.12	1.35	8	10.402	4.41	1.68	1
A0A1P8AVX3	EMS-MUTAGENIZED BRI1 SUPPRESSOR 1	1.82	1.37	0.74	0.98	1	186.297	5.91	0.02	1
A8MQA1	60S ribosomal protein L13	0.82	1.27	1.58	1.02	5	23.525	11	0.70	2
A8MR49	Ribosomal protein L31e family protein	0.78	0.90	1.55	1.33	1	9.758	9.01	0.78	1
A8MRV1	Histone H4	1.09	1.60	0.69	0.70	8	9.388	11.21	9.00	4
A8MS54	RNA-binding (RRM/RBD/RNP motifs) family protein	2.33	1.49	1.02	1.39	1	27.686	8.97	0.21	1
B3H4B6	Ribosomal protein S25 family protein	0.78	1.30	1.79	1.08	4	11.918	10.68	2.16	2
B3H4N7	60S acidic ribosomal protein family	2.00	1.14	0.69	1.20	2	11.757	4.51	0.78	1
B9DFS7	AT4G00810 protein	1.85	1.35	0.78	1.07	1	11.3	4.32	0.59	1
B9DGN3	AT2G27710 protein	1.37	1.23	1.37	1.52	1	11.437	4.68	0.47	1
B9DHP0	AT4G27090 protein	1.39	2.08	0.91	0.61	6	15.496	10.04	2.16	3
F4HRW5	Ribosomal protein L22p/L17e family protein	0.89	1.25	1.57	1.12	8	14.758	10.04	4.62	4
F4IDD6	tRNA synthetase beta subunit family protein	1.18	1.61	0.83	0.71	1	65.918	5.49	0.06	1
F4IFZ9	Delta-1-pyrroline-5-carboxylate synthase	1.17	1.89	0.84	0.52	2	77.389	6.24	0.05	1
F4IGR3	60S acidic ribosomal protein family	1.38	1.24	1.38	1.53	1	10.237	4.68	0.47	1
F4IHJ8	Ribosomal protein S25 family protein	0.76	1.21	1.85	1.16	3	11.934	10.68	1.15	1
F4IWP7	Breast basic conserved 1	0.90	1.26	1.55	1.11	5	17.737	10.55	1.15	2
F4IZC8	Alpha-soluble NSF attachment protein 2	1.01	1.30	0.69	0.54	4	27.232	5.33	0.62	4
F4J8L7	Aha1 domain-containing protein	1.69	1.39	0.74	0.89	2	35.772	5.71	0.27	1
F4K3X1	Ubiquitin-specific protease 12	1.32	2.38	0.79	0.44	1	115.079	5.68	0.04	1
F4K5C7	40S ribosomal protein S4	0.78	1.19	1.67	1.09	12	27.69	9.99	2.36	7
F4K7D6	S-(hydroxymethyl)glutathione dehydrogenase	1.42	0.87	0.98	1.60	3	42.016	6.95	0.23	2
F4K8S2	RmlC-like cupins superfamily protein	1.85	1.15	0.72	1.16	9	31.626	8.81	0.36	1
F4KAM0	60S acidic ribosomal protein family	1.78	1.14	0.76	1.18	2	8.939	5.29	0.78	1
F4KDR2	Ribosomal L29 family protein	0.75	0.97	1.61	1.24	1	17.011	10.56	0.29	1
O04630	Threonine--tRNA ligase, mitochondrial 1	1.14	1.61	0.71	0.70	2	80.885	6.98	0.11	2
O22793	MORF2	0.79	1.57	0.72	0.68	1	24.699	8.24	0.21	1
P25864	50S ribosomal protein L9, chloroplastic	1.86	1.26	0.74	1.09	5	22.12	9.67	1.15	3
P34789	40S ribosomal protein S28-2	1.73	1.35	0.72	0.93	1	7.336	11.17	0.59	1
P38666	60S ribosomal protein L24-2	0.85	1.21	1.65	1.15	5	18.62	10.78	3.22	3
P41127	60S ribosomal protein L13-1	0.89	1.27	1.58	1.10	5	23.752	11.02	0.70	2
P42643	14-3-3-like protein GF14 chi	1.24	1.44	2.10	1.46	21	29.913	4.81	2.16	1
P51420	60S ribosomal protein L31-3	0.89	1.10	1.57	1.27	1	13.795	9.95	0.59	1

P57691	60S acidic ribosomal protein P0-3	1.10	1.62	0.71	0.69	10	34.369	5.15	2.73	4
P59224	40S ribosomal protein S13-2	0.84	1.15	1.66	1.22	5	17.074	10.39	2.16	4
P59231	60S ribosomal protein L10a-3	2.63	1.18	0.36	0.79	2	24.516	9.82	0.36	2
P60040	60S ribosomal protein L7-2	0.87	1.19	1.61	1.18	14	28.153	9.94	2.16	3
Q07099	Serine/threonine-protein phosphatase PP2A-1 catalytic subunit	1.04	1.47	2.32	1.37	1	34.938	4.96	0.12	1
Q0WRE5	Ribosomal protein L17-like protein	0.76	1.26	1.58	0.95	8	19.842	10.11	2.98	4
Q0WRH6	60S ribosomal protein L22-like	1.11	1.47	0.69	0.52	1	14.038	9.55	0.33	1
Q1H5F7	Histone H2B OS=Arabidopsis thaliana PE=2 SV=1	0.83	0.99	1.70	1.41	3	15.723	10.05	0.59	2
Q29Q46	At3g56190	1.05	0.77	1.20	1.64	4	32.734	5.33	0.45	4
Q39142	Chlorophyll a-b binding protein, chloroplastic	0.82	1.24	1.58	1.05	7	28.152	5.27	1.31	1
Q3E6Z1	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	1.42	0.48	1.59	1.38	2	16.703	5.86	0.47	2
Q41969	Eukaryotic translation initiation factor 2 subunit beta	1.25	2.04	1.30	0.79	2	30.644	7.2	0.31	2
Q42064	60S ribosomal protein L8-3	0.69	1.29	2.12	1.14	13	27.931	10.83	1.78	1
Q42347	60S ribosomal protein L24-1	0.84	1.19	1.66	1.18	5	18.838	10.7	4.18	3
Q5PNZ9	At1g22780	0.86	1.06	1.63	1.32	3	17.534	10.54	1.00	3
Q6NPL0	At4g09040	0.56	0.70	0.90	0.72	1	34.011	7.59	0.18	1
Q8VYK6	40S ribosomal protein S4-3	0.79	1.18	1.65	1.10	10	29.797	10.21	1.51	6
Q8VZB9	60S ribosomal protein L10a-1	1.74	1.18	0.36	1.12	2	24.453	9.88	0.36	2
Q8W4A0	Eukaryotic translation initiation factor 3 subunit M	1.94	1.95	0.73	0.73	1	46.755	5.12	0.09	1
Q93VH9	40S ribosomal protein S4-1	0.72	1.18	1.67	1.02	12	29.784	10.17	2.16	7
Q93VI3	60S ribosomal protein L17-1	0.89	1.24	1.57	1.13	8	19.885	10.11	2.98	4
Q9C9C6	60S ribosomal protein L6-2	1.94	1.91	0.72	0.73	3	25.992	10.17	0.44	2
Q9FF90	60S ribosomal protein L13-3	0.83	1.25	1.57	1.04	9	23.471	11	1.89	4
Q9FFC0	Histone H2B	0.70	0.99	1.72	1.21	3	15.765	10.05	0.59	2
Q9FJP3	50S ribosomal protein L29, chloroplastic	2.39	0.89	0.35	0.95	2	19.365	10.51	0.78	2
Q9FK91	Poly [ADP-ribose] polymerase 3	0.83	1.87	0.98	0.87	4	91.347	5.22	0.21	1
Q9FZ76	60S ribosomal protein L6-1	1.08	2.04	0.96	0.82	1	26.136	10.1	0.12	1
Q9LQQ4	Histone H2B.1	0.70	0.99	1.71	1.21	3	16.392	10.05	0.67	2
Q9LSA3	60S ribosomal protein L30-3	1.05	1.68	0.93	0.74	4	12.271	9.69	1.37	3
Q9LVC9	60S acidic ribosomal protein P3-2	1.83	1.14	0.75	1.19	2	11.856	4.51	0.78	1
Q9M0E0	40S ribosomal protein S15a-5	1.42	0.80	0.48	0.86	1	14.907	9.82	0.39	1
Q9M0E2	60S ribosomal protein L28-2	0.71	1.15	1.97	1.21	1	15.901	11.05	0.33	1
Q9M9W1	60S ribosomal protein L22-2	1.09	1.47	0.69	0.51	5	14.009	9.55	2.16	3
Q9SF53	60S ribosomal protein L35-1	0.75	0.97	1.61	1.23	2	14.276	10.92	0.93	2
Q9SIK2	40S ribosomal protein S25-2	0.69	0.90	1.88	1.44	3	12.062	10.7	1.15	1
Q9SIW5	40S ribosomal protein S25-1	0.75	0.97	1.88	1.45	3	12.119	10.58	1.15	1
Protein destination and storage										
P15460	SESA4	1.82	1.04	0.76	1.32	3	19.17	7.5	0.52	1
P94072	Germin-like protein subfamily 3 member 3	1.40	1.72	1.46	1.35	4	21.822	6.76	1.37	2
Q96318	12S seed storage protein CRC	2.09	1.14	0.68	1.25	24	58.199	6.99	0.74	4

R0IN30	Putative germin	2.02	1.35	0.68	1.02	1	23.474	8.25	0.23	1
Protein folding and degradation										
A0A178UBF4	Peptidyl-prolyl cis-trans isomerase SV=1	1.29	1.52	0.80	0.68	4	21.947	9.06	0.70	1
F4JD01	Proteasome subunit beta type	1.60	1.41	0.81	0.92	2	24.669	7.81	0.39	2
P42742	Proteasome subunit beta type-1	1.60	1.42	0.80	0.91	2	24.628	7.4	0.39	2
Q0WL80	UDP-glucose:glycoprotein glucosyltransferase	1.70	1.39	0.77	0.94	1	181.69	5.83	0.02	1
Q38867	Peptidyl-prolyl cis-trans isomerase CYP19-3	2.69	1.39	1.17	1.47	2	18.908	7.81	0.39	2
Q8VYL3	Aspartic proteinase A2	1.75	1.18	0.73	1.09	5	55.713	6.34	0.37	2
Secondary metabolism										
A0A178US70	Phospho-2-dehydro-3-deoxyheptonate aldolase	1.89	1.21	0.69	1.07	3	56.113	8.78	0.23	1
A0A178V3B0	CAD5	0.95	0.72	1.42	1.88	1	38.718	5.67	0.12	1
A0A178VB36	MTO1	1.79	2.42	0.72	0.53	1	59.881	6.87	0.08	1
A0A178VHC7	GSA2	1.86	1.16	0.69	1.12	10	50.109	7.39	1.08	6
A0A178VZE1	IPMI2	1.77	1.67	1.61	1.71	2	27.026	6.11	0.33	2
A0A178W930	Protein disulfide-isomerase	0.84	1.29	1.68	1.09	4	56.329	5	0.30	4
A0A178WAV9	ASA1	1.65	1.20	0.88	1.21	2	53.604	6.61	0.15	1
A0A1P8AU81	Rhodanese homologue 2	2.02	1.13	0.70	1.24	1	32.126	6.8	0.12	1
A0A1P8AU99	Rhodanese homologue 2	1.90	1.13	0.69	1.16	1	29.433	5.8	0.14	1
A0A1P8AY16	Ferredoxin thioredoxin reductase catalytic beta chain family protein	1.94	1.15	0.73	1.24	1	10.17	6.76	0.33	1
A0A1P8AZM5	Alpha/beta-Hydrolases superfamily protein	1.93	1.04	0.72	1.32	1	24.316	5.6	0.21	1
A0A1P8AZN3	Alpha/beta-Hydrolases superfamily protein	1.21	0.90	1.21	1.62	2	34.699	6.81	0.26	2
A0A1P8AZP9	Alpha/beta-Hydrolases superfamily protein	1.21	0.90	1.21	1.62	2	30.018	6.55	0.31	2
A0A1P8AZS7	Thioredoxin reductase	1.93	3.33	0.69	0.40	1	38.234	8.12	0.12	1
A0A1P8B8I9	Pseudouridine synthase/archaeosine transglycosylase-like family protein	1.54	0.82	0.89	1.67	5	57.49	8.51	0.40	1
A0A1P8BCV2	Acetyl-coenzyme A synthetase	1.17	0.72	1.22	1.99	4	67.555	5.27	0.33	3
A8MR47	Sulfurtransferase	1.91	1.04	0.73	1.34	3	31.69	7.39	0.47	3
A8MRF8	Sulfite oxidase	1.97	0.90	0.70	1.53	2	26.628	5.44	0.33	2
B0LQB5	Malate synthase (Fragment)	1.14	1.68	0.83	0.76	30	36.466	7.28	2.36	7
F4I5V8	ATP-citrate lyase A-1	1.05	1.61	0.85	0.73	3	49.018	5.59	0.32	1
F4JLA9	Cruciferin 3	1.87	1.10	0.70	1.19	24	50.031	7.14	0.96	4
O23324	ATP-sulfurylase 3, chloroplastic	1.54	0.82	0.88	1.64	5	51.997	7.4	0.51	1
O65782	Cytochrome P450 83B1	1.61	1.34	0.75	0.90	1	56.81	8.37	0.07	1
Q5XF32	3-isopropylmalate dehydrogenase	1.85	1.03	1.82	3.27	3	44.134	6.01	0.39	1
Q8LDW8	Probable hydroxyacylglutathione hydrolase 2, chloroplastic	1.24	0.89	1.59	2.23	1	36.602	8.12	0.14	1
Q8LEF4	3-isopropylmalate dehydrogenase	2.07	2.15	1.37	1.32	4	43.27	6.06	0.45	2
Q9C8L4	Persulfide dioxygenase ETHE1 homolog, mitochondrial	1.90	1.14	0.72	1.21	4	32.312	7.01	0.72	3
Q9C9D0	Cytosolic sulfotransferase 16	1.62	1.77	1.84	1.68	1	39.194	5.62	0.11	1

Q9FZ80	Cytosolic sulfotransferase 17	1.88	0.92	1.55	3.16	1	39.887	6.47	0.10	1
Signal transduction and transcription										
A0A178UF94	SUPO1	1.80	1.15	0.73	1.14	4	43.482	6.46	0.43	4
A0A1P8ANC0	Hydroxypyruvate reductase	1.05	1.63	1.28	0.82	1	39.736	8.03	0.10	1
F4IS32	Acyl-[acyl-carrier-protein] desaturase	1.37	0.72	0.84	1.60	6	45.622	6.64	0.53	4
Q42479	Calcium-dependent protein kinase 3	1.11	1.62	0.95	0.79	1	59.299	6.37	0.08	1
Q42546	SAL1 phosphatase	1.71	1.15	0.76	1.13	4	37.541	5.17	0.59	4
Q95748	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3	1.46	1.65	0.85	0.75	3	22.865	7.44	0.59	2
Q9C820	Ras-related protein RABG3d	0.75	1.17	1.86	1.19	3	23.054	5.33	0.54	3
Q9FLM8	DNA-directed RNA polymerases II, IV and V subunit 12	2.05	1.19	0.70	1.20	1	5.893	8.18	1.15	1
Q9FPT1	Ubiquitin carboxyl-terminal hydrolase 12	1.31	1.94	0.80	0.91	1	130.525	5.77	0.04	1
Q9LW76	Ras-related protein RABG3c	0.75	1.16	1.86	1.21	3	22.951	5.52	0.54	3
Transport										
A0A178UJ45	NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	0.70	1.34	1.52	0.78	2	53.415	8.16	0.16	2
A0A178UV39	Plasma membrane ATPase	0.75	1.43	1.58	0.83	7	104.335	6.99	0.29	2
A0A178V5D7	Plasma membrane ATPase	0.75	1.68	1.54	0.68	3	105.453	6.84	0.15	1
A0A178VSN5	Plasma membrane ATPase	0.89	1.35	1.57	1.03	9	104.158	6.7	0.40	4
A0A178W1J5	MEE4	1.96	1.20	0.71	1.15	1	16.115	9.2	0.26	1
A0A178W2W5	Ferredoxin	2.52	1.49	0.84	1.43	2	15.53	4.49	0.93	1
A0A178W5B2	Sulfurtransferase	1.93	0.98	0.68	1.35	1	34.695	5.27	0.13	1
A0A178W776	Plasma membrane ATPase	0.99	1.52	1.05	0.69	2	104.749	6.43	0.10	1
A0A178WA14	VHP1	1.16	1.49	1.93	1.41	1	80.768	5.26	0.08	1
A0A178WBD4	CURT1C	1.22	1.61	0.87	0.72	1	16.935	9.04	0.26	1
A0A1I9LS30	Plasma membrane ATPase	0.88	1.84	1.55	0.74	3	105.439	6.84	0.15	1
A0A1P8AYX4	Plasma membrane ATPase	0.89	1.35	1.57	1.03	9	96.797	7.12	0.45	4
A0A1P8B2U9	Plasma membrane ATPase	0.90	1.91	1.56	0.73	3	102.597	7.5	0.14	1
A0A1P8B2V0	Plasma membrane ATPase	0.78	1.20	1.67	1.08	2	76.458	9.03	0.12	0
A0A1P8B2Y6	Plasma membrane ATPase	0.90	1.96	1.54	0.70	3	109.823	7.27	0.13	1
A8MQH1	Inorganic H pyrophosphatase family protein	1.16	1.44	1.93	1.43	1	67.663	5.17	0.10	1
F4J0D8	V-type proton ATPase subunit	0.78	1.37	1.67	0.95	2	40.019	5.05	0.27	2
F4JPJ7	Plasma membrane ATPase	0.76	1.48	1.59	0.81	5	108.247	7.14	0.18	2
G1C2X2	Nad9	1.42	1.59	0.88	0.78	3	22.674	7.5	0.59	2
O04090	Ferredoxin-1, chloroplastic	1.68	1.38	1.05	1.28	2	15.887	4.54	0.93	1
O82209	Copia-like retroelement pol polyprotein	1.69	1.35	0.83	1.04	1	13.838	9.04	0.23	1
P20431	ATPase 3, plasma membrane-type	1.01	2.02	1.03	0.72	5	104.384	7.18	0.24	1
P56778	Photosystem II CP43 reaction center protein	1.66	1.19	0.54	0.75	1	51.835	7.2	0.16	1
Q39242	Thioredoxin reductase 2	1.93	3.32	0.70	0.41	1	40.61	6.7	0.12	1
Q3E6Q3	Ras-related small GTP-binding family protein	1.85	1.32	0.72	1.02	5	13.817	5.07	1.37	1
Q3ZVD9	ATPase beta subunit (Fragment)	0.74	1.19	1.63	1.01	15	16.677	8.76	4.01	4
Q42599	NADH dehydrogenase [ubiquinone]	1.90	1.92	0.69	0.69	2	25.487	5.41	0.27	2

	iron-sulfur protein 8-A, mitochondrial									
Q8LB02	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit 2, mitochondrial	1.69	0.81	0.76	1.57	4	31.121	8.62	0.39	2
Q8LBZ7	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit 1, mitochondrial	1.66	0.81	0.76	1.55	4	31.151	8.44	0.39	2
Q96250	ATP synthase subunit gamma, mitochondrial	1.29	1.68	0.81	0.85	6	35.426	8.9	0.73	5
Q96252	ATP synthase subunit delta', mitochondrial	1.92	1.22	0.70	1.10	1	21.534	6.7	0.29	1
Q9FKS5	Cytochrome c1 2, heme protein, mitochondrial	1.94	1.36	0.73	1.04	3	33.669	6.18	0.59	1
Q9FZ27	Germin-like protein subfamily 2 member 2	1.79	1.35	0.72	0.96	1	23.426	8.56	0.23	1
Q9LHA4	V-type proton ATPase subunit d2	0.84	1.28	1.67	1.09	2	40.761	5.11	0.26	2
Q9LJI5	V-type proton ATPase subunit d1	0.85	1.28	1.65	1.09	2	40.765	5.16	0.26	2
Q9SH76	ATPase 6, plasma membrane-type	0.89	1.00	1.58	1.40	4	104.946	6.19	0.20	0
Q9SJB3	ATPase 5, plasma membrane-type	0.86	1.62	1.59	0.84	3	104.673	7.23	0.14	1
Q9STR3	Copia-like retroelement pol polyprotein	1.93	1.36	0.68	0.96	1	13.86	9.03	0.26	1
Q9T0E0	Putative ATPase, plasma membrane-like	0.83	1.00	1.56	1.30	1	90.381	6.8	0.05	1
Other										
A0A178UD67	RPS10B	0.71	1.43	1.68	0.83	3	19.721	9.73	0.87	2
A0A178VPH3	DJ1A	2.04	1.03	0.71	1.39	2	41.831	5.41	0.23	1
A0A178W8B7	SERPIN1	1.25	1.57	0.78	0.71	2	42.613	5.08	0.22	2
A0A178WB84	SDH6	1.49	1.57	0.70	0.69	1	15.803	6.8	0.29	1
A0A178WHX3	RACK1A_AT	1.16	1.57	1.02	0.75	15	35.725	7.71	2.33	5
A0A178WKK0	Sulfurtransferase	2.02	1.11	0.70	1.26	3	35.606	5.25	0.39	3
A0A178WMJ3	GSTU21	1.99	1.14	0.72	1.26	3	25.787	5.52	0.36	1
A0A178WPQ4	COX6B	1.87	1.30	0.71	1.02	1	21.182	4.34	0.26	1
A0A1P8AXQ5	Acetone-cyanohydrin lyase	1.95	1.82	0.70	0.75	4	31.379	5.74	0.31	1
A0A1P8AXW0	Acetone-cyanohydrin lyase	1.95	1.82	0.72	0.77	4	20.818	6.42	0.52	1
A0A1P8B993	Aldolase-type TIM barrel family protein	1.05	1.34	0.75	0.59	11	28.96	8.65	2.16	1
A0A2J6L3W0	4-methyl-5(B-hydroxyethyl)-thiazole monophosphate biosynthesis protein (Fragment)	1.96	1.06	0.71	1.32	2	14.445	8.43	0.59	1
A0A432SLV3	Glyceraldehyde-3-phosphate dehydrogenase (Fragment)	1.34	1.79	0.92	0.68	9	14.226	5.01	9.00	3
A8MRV0	RNA binding Plectin/S10 domain-containing protein	0.83	1.00	1.68	1.40	2	14.344	9.74	0.93	1
B2CT24	APS1 (Fragment)	1.57	1.34	0.84	0.99	3	16.904	6.33	1.00	2
B2CT25	APS1 (Fragment)	1.57	1.34	0.84	0.99	3	16.918	6.81	1.00	2
B2CT32	APS1 (Fragment)	1.57	1.34	0.84	0.99	3	16.89	6.33	1.00	2
B2CT35	APS1 (Fragment)	1.57	1.34	0.84	0.99	3	16.919	6.33	1.00	2
F4HRK0	Glyoxalase II 3	1.91	1.04	0.68	1.24	3	32.338	7.01	0.50	2
F4J2B4	Proteasome component (PCI) domain protein	1.93	1.97	0.70	0.69	1	41.13	5.07	0.10	1
Q9LVM3	YCF54	1.12	1.67	1.20	0.80	3	24.089	8.1	0.19	1

R0GMJ8	SDH6	1.45	1.62	0.73	0.72	1	18.659	6.92	0.33	1
S8DQ99	TAT-binding protein homolog (Fragment)	0.80	1.06	1.75	1.32	1	7.631	5.45	0.59	1
V4MZ55	GSTF3	1.84	1.14	0.70	1.13	12	26.578	6.81	1.58	4