






































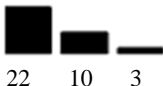

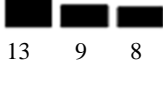
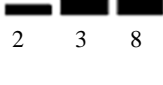
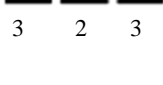
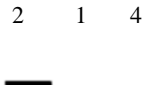
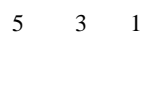






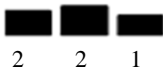


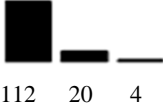

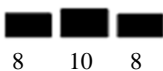
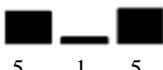
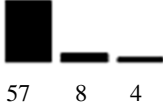





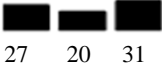
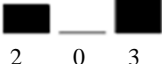

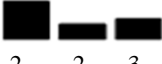
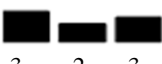










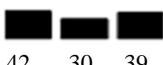
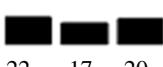










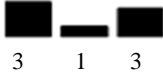
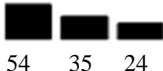
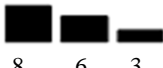
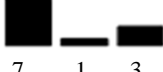









Protein	Top Hit			Expression		
	Organism	Acc No	% Coverage	N	O	H
<b>Amino acid synthesis</b>						
5-methyltetrahydropteroyltriglutamate-homocysteine methyltransferase	Mesembryanthemum crystallinum	P93263	14.25	 39	 61	 42
Cysteine synthase, chloroplastic/chromoplastic	Spinacia oleracea	P32260	13.58	 10	 8	 5
Serine hydroxymethyltransferase, mitochondrial	Arabidopsis thaliana	Q9SZJ5	9.86	 2	 3	 3
Glutamine synthetase leaf isozyme, chloroplastic	Medicago sativa	Q9XQ94	7.01	 3	 2	 4
Adenosylhomocysteinase	Triticum aestivum	P32112	5.15	 7	 16	 14
Aspartate aminotransferase, cytoplasmic	Daucus carota	P28734	4.44	 20	 13	 8
Ferredoxin-dependent glutamate synthase, chloroplastic	Spinacia oleracea	Q43155	1.91	 0	 4	 1
<b>Carbohydrate metabolism</b>						
Glyceraldehyde-3-phosphate dehydrogenase, cytosolic	Antirrhinum majus	P25861	32.94	 122	 58	 88
Malate dehydrogenase, cytoplasmic	Beta vulgaris	Q9SML8	28.01	 87	 49	 71
Enolase 2	Saccharomyces cerevisiae	P00925	24.03	 42	 14	 29
Phosphoglycerate kinase, chloroplastic	Nicotiana tabacum	Q42961	19.13	 13	 9	 10
Phosphoglycerate kinase, cytosolic	Nicotiana tabacum	Q42962	19.02	 20	 19	 18
Fructose-bisphosphate aldolase 1, chloroplastic (Fragment)	Pisum sativum	Q01516	18.26	 23	 15	 24






Protein	Top Hit			Expression			
	Organism	Acc No	% Coverage	N	O	H	
Triosephosphate isomerase, cytosolic	Oryza sativa subsp. japonica	P48494	17.39		22	10	3
Phosphoglucomutase, cytoplasmic	Populus tremula	Q9ZSQ4	10.31		8	3	5
Transketolase, chloroplastic	Spinacia oleracea	O20250	9.72		13	9	8
UTP--glucose-1-phosphate uridylyltransferase	Pyrus pyrifolia	O64459	8.49		2	3	8
Sedoheptulose-1,7-bisphosphatase, chloroplastic	Arabidopsis thaliana	P46283	6.87		3	2	3
UDP-arabinopyranose mutase 1	Arabidopsis thaliana	Q9SRT9	6.16		2	1	4
Glucose-1-phosphate adenylyltransferase small subunit, chloroplastic/amyloplastic	Hordeum vulgare	P55238	5.85		5	3	1
Phosphoenolpyruvate carboxylase 1	Zea mays	P04711	4.02		44	30	12
Granule-bound starch synthase 1, chloroplastic/amyloplastic	Pisum sativum	Q43092	3.98		10	2	3
Pyruvate kinase 1	Saccharomyces cerevisiae	P00549	20.2		15	5	15
Pyruvate decarboxylase isozyme 1	Saccharomyces cerevisiae	P06169	12.43		20	9	18
Isocitrate dehydrogenase [NADP], chloroplastic (Fragment)	Medicago sativa	Q40345	6.47		3	2	3
Cofactor/ Coenzyme synthesis							
S-adenosylmethionine synthase 1	Atriplex nummularia	Q7XZR1	35.35		69	81	117

Protein	Top Hit			Expression			
	Organism	Acc No	% Coverage	N	O	H	
Thiamine-phosphate pyrophosphorylase	Streptococcus suis	A4W0K4	15.28		2	3	4
Thiazole biosynthetic enzyme, chloroplastic	Arabidopsis thaliana	Q38814	9.74		2	2	1
4-hydroxythreonine-4-phosphate dehydrogenase	Geobacter lovleyi	B3E252	11.9		5	4	4
Defense							
Putative germin-like protein subfamily 1 member 9	Arabidopsis thaliana	Q9FMB0	13.96		5	2	1
Detoxifying and antioxidant							
Glutathione S-transferase class-mu 26 kDa isozyme	Schistosoma japonicum	P08515	29.36		112	20	4
Thioredoxin H-type 1	Nicotiana tabacum	P29449	17.46		2	3	1
Peroxisomal (S)-2-hydroxy-acid oxidase GLO1	Arabidopsis thaliana	Q9LRR9	6.27		8	10	8
Catalase-3	Arabidopsis thaliana	Q42547	5.08		5	1	5
DNA modifying							
Probable histone H2A.1	Medicago truncatula	Q2HU68	35.14		57	8	4
Histone H4	Xenopus borealis	P62798	33.01		15	1	0
Histone H2B.5	Triticum aestivum	Q43216	19.12		17	6	0
Energy production and conversion							
ATP synthase subunit beta, chloroplastic	Magnolia tripetala	Q9MU41	54.82		149	154	133
ATP synthase epsilon chain, chloroplastic	Eucalyptus globulus subsp. globulus	Q49KZ2	24.06		5	6	7

Protein	Top Hit			Expression		
	Organism	Acc No	% Coverage	N	O	H
ATP synthase subunit alpha, chloroplastic	Silene latifolia	Q589B3	19.72	 42 52 44		
V-type proton ATPase subunit B2	Arabidopsis thaliana	Q9SZN1	8.21	 27 20 31		
Alcohol dehydrogenase class-3	Zea mays	P93629	7.87	 2 0 3		
ADP,ATP carrier protein 1, mitochondrial	Triticum aestivum	Q41629	7.55	 5 2 4		
ATP synthase gamma chain 1, chloroplastic	Arabidopsis thaliana	Q01908	6.7	 2 2 3		
Formate--tetrahydrofolate ligase	Spinacia oleracea	P28723	5.81	 3 2 3		
<b>Photosynthesis</b>						
Alanine aminotransferase 2	Hordeum vulgare	P52894	14.11	 18 18 19		
Glutamate-1-semialdehyde 2,1-aminomutase	Synechococcus sp.	Q3AWP4	6.54	 2 4 7		
NAD(P)H-quinone oxidoreductase subunit I, chloroplastic	Spinacia oleracea	Q9M3I7	21.18	 5 2 4		
Pyruvate, phosphate dikinase, chloroplastic	Flaveria trinervia	P22221	14.48	 99 67 42		
Ferredoxin--NADP reductase, leaf isozyme 1, chloroplastic	Arabidopsis thaliana	Q9FKW6	13.06	 13 8 11		
Photosystem I iron-sulfur center	Illicium oligandrum	A6MMZ6	51.85	 32 21 18		
Ribulose biphosphate carboxylase large chain	Daphniphyllum sp.	P28397	51.61	 364 380 373		

Protein	Top Hit			Expression			
	Organism	Acc No	% Coverage	N	O	H	
Chlorophyll a-b binding protein 21, chloroplastic	Nicotiana tabacum	P27493	36.6		23	36	27
Photosystem I reaction center subunit II, chloroplastic	Spinacia oleracea	P12353	35.85		35	24	26
Photosystem I reaction center subunit IV, chloroplastic	Spinacia oleracea	P12354	26.4		5	9	5
Carbonic anhydrase, chloroplastic	Arabidopsis thaliana	P27140	21.61		42	30	39
Apocytochrome f	Nicotiana tabacum	P06449	20.62		22	17	20
Oxygen-evolving enhancer protein 2, chloroplastic	Solanum tuberosum	P93566	18.85		8	16	11
Oxygen-evolving enhancer protein 1, chloroplastic	Spinacia oleracea	P12359	16.57		70	49	50
Cytochrome b6-f complex iron-sulfur subunit, chloroplastic	Spinacia oleracea	P08980	13.04		2	2	3
Oxygen-evolving enhancer protein 3-1, chloroplastic	Zea mays	Q41048	9.22		8	7	12
Geranylgeranyl diphosphate reductase, chloroplastic	Arabidopsis thaliana	Q9CA67	6.85		5	2	3
Photosystem II CP43 chlorophyll apoprotein	Nicotiana sylvestris	Q3C1I3	6.51		12	5	5
RuBisCO large subunit-binding protein subunit beta, chloroplastic	Brassica napus	P21241	4.25		2	6	4
Post translational modification and signal transduction							
Peptidyl-prolyl cis-trans isomerase CYP20-3, chloroplastic	Arabidopsis thaliana	P34791	10.77		5	2	3

Protein	Top Hit			Expression			
	Organism	Acc No	% Coverage	N	O	H	
ATP-dependent Clp protease ATP-binding subunit clpA homolog	Populus euphratica	P84565	37.5		3	1	3
Heat shock cognate 70 kDa protein 1	Solanum lycopersicum	P24629	20.92		54	35	24
Luminal-binding protein 5	Nicotiana tabacum	Q03685	10.63		8	6	3
Alcohol dehydrogenase 1	Saccharomyces cerevisiae	P00330	7.18		7	1	3
Cell division cycle protein 48 homolog	Capsicum annuum	Q96372	7.08		5	8	10
Chaperone protein ClpC1, chloroplastic	Arabidopsis thaliana	Q9FI56	4.31		5	1	1
Chaperone protein DnaK	Sphingomonas wittichii	A5V5P9	3.81		3	4	4
GTP-binding protein ypt71	Schizosaccharomyces pombe	Q9HDY0	25		15	2	0
Transcription and translation							
Elongation factor Tu, chloroplastic	Arabidopsis thaliana	P17745	7.35		2	2	0
40S ribosomal protein S12	Saccharomyces cerevisiae	P48589	31.47		5	1	1
60S ribosomal protein L12-3	Arabidopsis thaliana	Q9FF52	26.51		8	7	11
Elongation factor 1-alpha	Saccharomyces cerevisiae	P02994	19.65		174	62	144
31 kDa ribonucleoprotein, chloroplastic	Nicotiana sylvestris	P19683	15.56		5	6	4

Protein	Top Hit			Expression		
	Organism	Acc No	% Coverage	N	O	H
Aspartyl-tRNA synthetase 1	Syntrophus aciditrophicus	Q2LPW5	4.43	 2    2    1		
Elongation factor 2	Saccharomyces cerevisiae	P32324	4.28	 13    0    4		
<b>Transport and structural</b>						
Tubulin alpha-2/alpha-4 chain	Arabidopsis thaliana	P29510	19.78	 10    13    18		
Actin-46 (Fragment)	Solanum tuberosum	P93586	7.74	 8    8    7		
Tubulin beta-1 chain (Fragment)	Avena sativa	P25862	34.97	 18    16    15		