

Supplemental table 2.

Description	Species	Accession	localization	spot ID	PLGS Score	Cov/Pep	Theoretical	
							MW/pi	Exp MW/pi
01 Metabolism								
01.01 Amino Acids								
Hydroxypyruvate reductase	Chlamydomonas reinhardtii	A8IP17	?	443	110.56	8.4/2	44.7/8.4	33/6.4
Aminopeptidase	Micromonas sp strain RCC299	C1EA64	plastid	25	119.46	2.6/4	63.0/7.7	105/6.3
Aminopeptidase	Micromonas sp strain RCC299	C1EA64	plastid	83	53.95	5.1/4	63.0/7.7	90/6.4
Aminopeptidase	Micromonas sp strain RCC299	C1EA64	plastid	73	166.29	2.6/4	63.0/7.7	92/7.0
Aspartate aminotransferase	Gossypium hirsutum	H2D5S4	cytoplasm	376	157.64	7.9/6	44.0/7.8	45/7.2
Ketol acid reductoisomerase chloroplastic	Spinacia oleracea	Q01292	plastid	183	1926.64	28.9/23	63.7/6.6	70/6.3
Ketol acid reductoisomerase chloroplastic	Spinacia oleracea	Q01292	plastid	186	75.57	4.5/2	63.7/6.6	69/6.3
Acetolactate synthase	Amaranthus sp Iowa	Q38795	plastid	47	45.40	8.7/3	72.4/6.8	101/6.1
Ferredoxin dependent glutamate synthase chloroplastic	Spinacia oleracea	Q43155	cytoplasm	537	48.87	2.0/3	165.3/5.8	26/6.1
Ferredoxin dependent glutamate synthase chloroplastic	Spinacia oleracea	Q43155	cytoplasm	468	41.94	1.0/3	165.3/5.8	31/6.8
phosphoglycerate dehydrogenase (92%)	Gossypium hirsutum	B9HS53	cytoplasm	164	143.52	10.9/5	57.2/5.7	73/6.3
Adenosylhomocysteinase	Beta vulgaris	Q4H1G1	cytoplasm	226	333.89	25.7/12	53.4/5.8	64/6.3
Glutamine synthetase	Beta vulgaris	Q9AXD1	cytoplasm	371	2056.95	21.3/8	39.1/5.1	46/6.0
Pollen allergen MetE Fragment	Amaranthus retroflexus	E3VW74	cytoplasm	55	289.36	16.0/9	83.7/6.1	95/6.7
Pollen allergen MetE Fragment	Amaranthus retroflexus	E3VW74	cytoplasm	57	122.61	7.4/4	83.7/6.1	95/6.7
Pollen allergen MetE Fragment	Amaranthus retroflexus	E3VW74	cytoplasm	58	809.11	27.7/22	83.7/6.1	94/6.7
Pollen allergen MetE Fragment	Amaranthus retroflexus	E3VW74	cytoplasm	60	880.33	16.1/9	83.7/6.1	94/6.8
Sal k 3 pollen allergen Fragment	Salsola kali	C1KEU0	cytoplasm	59	237.60	13.6/9	83.5/5.9	94/6.9
01.03 Nucleotides								
Nucleoside diphosphate kinase 1	Spinacia oleracea	Q02254	cytoplasm	616	1303.43	23.0/4	16.3/6.5	12/6.8
RelA homolog	Suaeda japonica	Q84KS9	plastid	369	83.67	6.4/3	79.1/6.4	46/5.7
01.05 Sugars								
Glucose 1 phosphate adenyltransferase Fragment	Spinacia oleracea	Q43152	plastid	280	43.28	6.8/2	49.0/5.0	58/6.0
similar to xylose isomerase-like (99%)	Vitis vinifera	A5B1E9	cytoplasm	245	489.85	16.0/12	51.6/5.4	61/6.3
L-iditol 2-dehydrogenase (100%)	Populus trichocarpa	B9I4E5	cytoplasm	358	369.48	31.0/11	39.2/5.9	48/6.6
Sucrose synthase Fragment	Prunus persica	Q946X3	?	53	105.94	27.3/3	23.5/7.3	95/6.2
01.06 Lipids								
Enoyl ACP reductase Fragment	Dimocarpus longan	E9NVZ3	mitochondrial	426	599.44	24.6/11	35.9/10.0	38/5.7
Glycerol 3 phosphate acyltransferase chloroplastic	Spinacia oleracea	Q43869	plastid	365	48.36	8.3/3	52.1/5.6	46/6.6
Delta12 oleic acid desaturase	Euphorbia lagascae	Q6RXX0	cytoplasm	581	107.24	16.0/2	44.2/8.9	18/6.2
01.07.Cofactors								
L-idonate 5-dehydrogenase (100%)	Vitis vinifera	A5AIP9	cytoplasm	341	134.29	13.0/5	37.4/6.3	50/6.5
similar to GDP-mannose 3,5-epimerase 1 (95%)	Zea mays	I1I416	cytoplasm	318	300.08	19.3/5	42.8/5.9	53/6.6
02 Energy								
02.01 Glycolysis								
Glyceraldehyde 3 phosphate dehydrogenase	Beta vulgaris	A3FMH0	cytoplasm	416	3569.20	28.5/21	36.6/6.9	39/7.5

Glyceraldehyde 3 phosphate dehydrogenase Fragment	Spinacia oleracea	D7SA11	cytoplasm	401	2014.29	33.2/6	21.2/8.2	38/7.3
Glyceraldehyde 3 phosphate dehydrogenase Fragment	Spinacia oleracea	D7SA11	cytoplasm	408	551.87	24.3/3	21.2/8.2	40/7.0
Glyceraldehyde 3 phosphate dehydrogenase Fragment	Spinacia oleracea	D7SA11	cytoplasm	409	130.40	14.4/2	21.2/8.2	40/7.1
Glyceraldehyde 3 phosphate dehydrogenase Fragment	Spinacia oleracea	D7SA11	cytoplasm	411	1844.96	27.7/4	21.2/8.2	38/7.3
Glyceraldehyde 3 phosphate dehydrogenase	Beta vulgaris	A3FMH0	cytoplasm	417	873.9	24.3/3	36.6/6.9	38/7.4
6 phosphofructokinase	Medicago truncatula	G7L7C5	cytoplasm	212	69.70	7.3/2	39.1/6.6	67/6.7
Fructose bisphosphate aldolase cytoplasmic isozyme	Spinacia oleracea	P29356	cytoplasm	400	1391.08	10.1/9	38.4/5.9	40/6.9
Phosphoglycerate kinase putative	Arabidopsis thaliana	Q8LFV7	cytoplasm	352	427.82	14.7/4	42.1/5.3	50/6.0
Phosphoglycerate kinase putative	Arabidopsis thaliana	Q8LFV7	cytoplasm	343	1125.09	18.0/6	42.1/5.3	50/6.2
Enolase	Spinacia oleracea	Q9LEE0	cytoplasm	163	1417.87	29.7/8	48.1/5.4	74/6.4
Enolase	Spinacia oleracea	Q9LEE0	cytoplasm	215	4092.60	36.9/17	48.1/5.4	67/6.1
Enolase	Spinacia oleracea	Q9LEE0	cytoplasm	228	8783.77	41.9/22	48.1/5.4	63/6.2
Enolase	Spinacia oleracea	Q9LEE0	cytoplasm	232	117.05	14.0/4	48.1/5.4	63/5.9
Pyruvate dehydrogenase E1 alpha subunit	Beta vulgaris	Q852R9	mitochondrial	166	47.8	7.6/2	43.7/8.2	73/6.6
<i>02.02 Gluconeogenesis</i>								
Malic enzyme	Ricinus communis	B9RKI6	cytoplasm	138	318.92	6.1/3	65.1/5.9	79/6.8
Malate dehydrogenase Fragment	Pinus sylvestris	E3V248	mitochondrial	435	4634.14	19.7/6	14.5/9.8	36/6.8
Malate dehydrogenase	Glycine max	I1LXZ7	ER	388	460.05	10.2/3	41.0/6.1	43/6.9
Malate dehydrogenase Fragment	Hyparrhenia rufa	Q2MG94	cytoplasm	310	265.64	9.1/2	38.2/5.3	54/6.3
Malate dehydrogenase cytoplasmic	Beta vulgaris	Q9SML8	cytoplasm	387	5307.80	38.9/20	35.4/5.8	43/6.7
<i>02.07 Pentose Phosphate</i>								
Transketolase chloroplastic	Spinacia oleracea	O20250	plastid	84	66.97	3.2/2	80.2/6.2	90/6.3
Transketolase chloroplastic	Spinacia oleracea	O20250	plastid	87	82.30	7.7/3	80.2/6.2	89/6.5
Transketolase chloroplastic	Spinacia oleracea	H6ULZ6	plastid	314	68.07	12.7/2	24.9/9.3	54/6.9
6 phosphogluconate dehydrogenase decarboxylating	Spinacia oleracea	Q94KU1	cytoplasm?	287	284.64	26.9/12	53.2/6.0	57/6.8
6 phosphogluconate dehydrogenase decarboxylating	Spinacia oleracea	Q94KU2	plastid	271	267.99	11.0/4	58.3/5.4	58/6.6
CP12 (100%)	Spinacia oleracea	O24360	plastid	225	57.39	12.1/3	13.6/4.6	63/6.1
<i>02.10 TCA pathway</i>								
Putative aconitase	Capsicum chinense	B1Q486	?	40	342.13	16.5/22	108.3/7.1	103/6.7
Cytosolic aconitase	Pyrus pyrifolia	G3BMW4	plastid	39	52.76	12.0/6	97.9/5.9	104/6.6
Isocitrate dehydrogenase NADP	Pyrus pyrifolia	G3BMV7	cytoplasm	309	208.66	12.1/7	46.2/6.6	54/6.6
Isocitrate dehydrogenase NADP	Arabidopsis thaliana	Q8RYD5	cytoplasm	301	192.85	15.9/6	45.7/6.1	55/6.4
<i>02.13 Respiration</i>								
ATP synthase subunit alpha Fragment	Celosia cristata	E5DK56	cytoplasm	207	103.52	13.5/4	37.3/7.2	68/6.7
ATP synthase subunit alpha	Beta vulgaris	E6ZE62	cytoplasm	213	8658.62	50.8/69	55.0/5.9	66/6.7
ATP synthase subunit alpha	Beta vulgaris	E8ZCA7	cytoplasm	206	987.37	34.0/16	55.0/5.9	68/6.5
ATP synthase subunit beta mitochondrial	Hevea brasiliensis	P29685	mitochondrial	220	1926.87	43.2/56	60.2/5.9	65/5.7
probable ATP synthase 24 kDa subunit, mitochondrial-like (100%)	Vitis vinifera	D7SW76	mitochondrial	527	97.45	6.3/3	27.7/9.7	26/6.6
ATP synthase subunit alpha	Beta vulgaris	E6ZE62	cytoplasm	24	116.7	9.3/3	55/5.9	106/6.6
<i>02.16 Fermentation</i>								
Pyruvate decarboxylase	Gossypium hirsutum	D2D327	cytoplasm	142	134.04	7.4/3	60.4/6.2	77/6.8

Alcohol dehydrogenase 1 Fragment	Spinacia oleracea	E1A4D0	cytoplasm	322	230.65	17.8/11	35.8/6.6	53/6.8
Alcohol dehydrogenase 1 Fragment	Spinacia oleracea	E1A4D0	cytoplasm	346	634.02	22.9/13	35.8/6.6	50/6.7
Alcohol dehydrogenase 1 Fragment	Spinacia oleracea	E1A4D0	cytoplasm	347	574.52	17.8/22	35.8/6.6	49/6.8
<i>02.20 E-transport</i>								
NADH ubiquinone oxidoreductase putative	Ricinus communis	B9T118	mitochondrial	79	74.25	5.6/3	80.7/6.6	91/6.2
<i>02.30 Photosynthesis</i>								
Photosystem II 22 kDa protein	Arabidopsis thaliana	F4IEG8	plastid	519	158.82	12.7/3	22.0/10.0	27/7.1
Ribulose biphosphate carboxylase large chain Fragment	Atriplex patula	G8D4D3	cytoplasm	487	129.71	27.2/4	22.4/5.4	29/5.7
Ribulose biphosphate carboxylase large chain Fragment	Forchhammeria watsonii	Q5VGZ2	cytoplasm	425	95.63	12.0/2	32.1/5.9	38/6.1
Ribulose biphosphate carboxylase large subunit Fragment	Manocharisma albicans	A2VA68	cytoplasm	64	43.61	17.9/3	27.6/6.2	90/7.3
Ribulose biphosphate carboxylase small chain 2 chloroplastic	Amaranthus hypochondriacus	Q9XGX5	plastid	185	113.44	23.9/3	20.4/8.8	68/7.2
03 Cell growth/division								
<i>03.22 Cell cycle</i>								
Cyclin d putative	Ricinus communis	B9SG00	cytoplasm	35	75.18	18.1/2	31.7/9.3	104/6.6
Cystatin	Amaranthus hypochondriacus	Q0GPA4	ER	539	10411.60	56.3/44	27.7/5.6	25/6.5
Cystatin	Amaranthus hypochondriacus	Q0GPA4	ER	540	524.04	17.0/3	27.7/5.6	25/6.6
cyclin-D2-1-like (100%)	Brachypodium distachyon	I1IPV4	cytoplasm	51	67.61	15.5/2	35.2/4.8	96/7.0
<i>03.30 seed maturation</i>								
Late embryogenesis abundant protein	Vigna radiata	A4VBF1	cytoplasm	611	277.62	17.9/3	12.2/9.1	13/6.4
<i>03.99 Others</i>								
Maturase K 2	Anacampseros vulcanensis	Q5J2V7	cytoplasm	375	78.04	3.0/2	60.9/10.0	46/6.5
04 Transcription								
Helicase	Cucumis melo	E5GB87	cytoplasm	257	835.83	34.4/12	46.9/5.2	60/6.0
similar to transcription factor MYB3 (93%)	Arabidopsis thaliana	D7KLT8	cytoplasm	552	56.29	7.8/4	29.3/8.2	22/5.8
similar to transcription factor MYB3 (93%)	Arabidopsis thaliana	D7KLT8	cytoplasm	428	250.36	14.8/4	29.3/8.2	38/6.9
similar to transcription factor MYB3 (93%)	Arabidopsis thaliana	D7KLT8	cytoplasm	361	163.52	7.8/4	29.3/8.2	47/5.9
similar to transcription factor MYB3 (93%)	Arabidopsis thaliana	D7KLT8	cytoplasm	364	149.34	7.8/3	29.3/8.2	47/7.0
similar to agamous-like MADS-box protein AGL18-like (96%)	Glycine max	I1JGA3	cytoplasm	265	134.33	5.7/3	29.9/5.7	59/6.4
MPF1-like-A (100%)	Withania sp. W009	C9X3L8	?	382	56.32	14.9/3	22.3/9.6	44/6.0
05 Protein synthesis								
<i>05.01 Ribosomal proteins</i>								
Ribosomal protein S12 Fragment	Celosia cristata	G0YEE8	mitochondrial	619	224.31	25.9/3	6.4/11.4	11/5.7
Ribosomal protein S12 Fragment	Celosia cristata	G0YEE8	mitochondrial	130	223.50	25.9/3	6.4/11.4	80/6.5
Ribosomal protein S12	Beta vulgaris	Q5U6C5	cytoplasm	621	206.88	16.8/4	14.2/12.0	11/6.5
Ribosomal protein S12	Beta vulgaris	Q5U6C5	cytoplasm	615	133.06	12.0/3	14.2/12.0	12/6.6
Ribosomal protein S12 Fragment	Celosia cristata	G0YEE8	plastid	372	121.19	25.9/3	6.4/11.4	46/6.2
50S ribosomal protein L2 chloroplastic	Spinacia oleracea	P06509	plastid	499	49.27	8.1/2	29.8/11.6	28/5.6
50S ribosomal protein L15 chloroplastic Fragments	Spinacia oleracea	P22798	plastid	31	35.11	29.7/2	9.8/10.3	104/6.4
Ribosomal protein L16 Fragment	Nymphaea sp Bergthorsson	Q5IA34	cytoplasm	596	63.37	10.3/4	18.2/11.0	16/6.3
Putative 60S acidic ribosomal protein P0 Fragment	Zinnia elegans	Q8LNX8	cytoplasm	414	673.30	11.8/2	21.9/10.0	39/5.9
50S ribosomal protein L23-like (100%)	Glycine max	I1K4J4	plastid	194	114.84	35.1/2	11.1/10.3	67/7.4

Ribosomal protein L22p/L17e family protein (100%)	Arabidopsis thaliana	Q8LDU0	mitochondrial	386	141.26	11.4/4	30.4/11.3	43/6.1
<i>05.04 Translation factors</i>								
Eukaryotic translation initiation factor 5A	Medicago truncatula	G7JWN5	cytoplasm	594	345.30	24.1/3	15.5/5.8	16/6.6
<i>05.10 tRNA synthase</i>								
Arginyl tRNA synthetase putative	Ricinus communis	B9RKG2	cytoplasm	159	88.97	12.5/5	66.8/5.8	76/6.5
glycyl-tRNA synthetase 1, mitochondrial-like (100%)	Vitis vinifera	D7SH83	cytoplasm	90	165.26	10.8/9	76.3/5.8	89/6.6
<i>05.99 Others</i>								
Elongation factor Tu	Glycine max	I1N9E6	mitochondrial	344	56.07	7.5/4	49.1/6.4	49/6.6
Elongation factor Tu	Glycine max	I1N9E6	mitochondrial	353	565.74	13.7/10	49.1/6.4	49/6.6
Elongation factor 2	Beta vulgaris	O23755	cytoplasm	36	116.62	8.1/7	93.7/5.9	104/6.8
Elongation factor 2	Beta vulgaris	O23755	cytoplasm	37	2150.85	27.5/42	93.7/5.9	103/6.8
Elongation factor 1 alpha	Salsola komarovii	Q8H9A9	cytoplasm	167	162.36	23.0/15	49.3/9.4	73/5.9
06. Protein storage and destination								
<i>06.01 Folding and stability</i>								
Heat shock 70 protein	Spinacia oleracea	O50047	mitochondrial	104	290.91	26.4/11	72.3/5.4	86/5.8
Chaperonin 60kD ch60 putative	Ricinus communis	B9RWQ2	mitochondrial	151	215.31	10.8/8	61.3/5.7	77/5.9
T complex protein 1 subunit epsilon	Arabidopsis thaliana	F4IAR7	cytoplasm	154	288.18	16.6/13	51.1/5.2	76/5.8
TCP 1 cpn60 chaperonin family protein	Arabidopsis thaliana	F4J7H2	cytoplasm	160	1575.05	21.8/16	59.5/6.2	76/6.6
putative TCP-1/cpn60 chaperonin family protein (100%)	Zea mays	C0P530	plastid	145	257.19	11.7/8	61.7/5.2	76/5.7
20 kDa chaperonin, chloroplastic-like (100%)	Vitis vinifera	D7SIZ7	plastid	548	208.45	13.1/3	26.3/9.8	24/5.9
<i>06.13 Proteolysis</i>								
Proteasome subunit alpha type 3	Spinacia oleracea	O24362	cytoplasm	497	483.56	22.9/11	27.3/6.1	28/6.2
similar to Proteasome component (PCI) domain protein	Theobroma cacao	A9PB47	cytoplasm	296	48.5	10.3/3	45.2/4.9	55/5.7
ClpC protease	Spinacia oleracea	O98447	plastid	44	44.42	10.2/6	99.4/9.0	102/6.0
26S protease regulatory subunit 7	Spinacia oleracea	Q41365	cytoplasm	250	275.49	18.1/9	47.7/6.1	61/6.7
F box protein (100%)	Medicago truncatula	G7JM44	cytoplasm	370	57.23	18.3/4	28.0/9.2	46/6.1
26S proteasome ATPase subunit Fragment	Pisum sativum	Q6GX77	cytoplasm	250	185.64	23.7/4	23.6/6.9	61/6.7
mitochondrial-processing peptidase subunit alpha (100%)	Vitis vinifera	D7TBD9	mitochondrial	241	238.06	18.6/7	54.4/5.6	62/5.8
<i>06.20 Storage proteins</i>								
11S globulin	Amaranthus hypochondriacus	A2I9A6	ER	466	248.63	12.9/11	55.0/6.5	31/6.2
11S globulin	Amaranthus hypochondriacus	A2I9A6	ER	467	2191.87	12.3/5	55.0/6.5	30/6.3
11S globulin	Amaranthus hypochondriacus	A2I9A6	ER	490	636.82	12.5/18	55.0/6.5	29/6.3
High molecular weight glutenin subunit y10	Triticum aestivum	A9ZMG8	ER	109	89.55	10.5/3	69.7/7.3	84/6.1
11S globulin seed storage protein Fragment	Amaranthus hypochondriacus	Q38712	ER	496	1227.99	16.6/25	56.6/6.7	28/6.4
11S globulin seed storage protein Fragment	Amaranthus hypochondriacus	Q38712	ER	562	1736.64	19.0/22	56.6/6.7	20/7.6
11S globulin seed storage protein Fragment	Amaranthus hypochondriacus	Q38712	ER	564	668.96	8.2/6	56.6/6.7	20/7.5
11S globulin seed storage protein Fragment	Amaranthus hypochondriacus	Q38712	ER	568	1219.89	30.3/27	56.6/6.7	20/6.4
11S globulin seed storage protein Fragment	Amaranthus hypochondriacus	Q38712	ER	464	1434.79	16.2/26	56.6/6.7	29/6.4
11S globulin seed storage protein Fragment	Amaranthus hypochondriacus	Q38712	ER	469	300.33	4.4/6	56.6/6.7	29/6.6
11S globulin seed storage protein Fragment	Amaranthus hypochondriacus	Q38712	ER	470	856.27	17.6/21	56.6/6.7	30/6.5
11S globulin seed storage protein Fragment	Amaranthus hypochondriacus	Q38712	ER	473	114.37	6.8/6	56.6/6.7	30/6.9

11S globulin seed storage protein Fragment	Amaranthus hypochondriacus	Q38712	ER	477	137.85	9.2/9	56.6/6.7	30/6.7
11S globulin seed storage protein Fragment	Amaranthus hypochondriacus	Q38712	ER	485	453.90	6.8/16	56.6/6.7	29/6.1
11S globulin seed storage protein Fragment	Amaranthus hypochondriacus	Q38712	ER	495	96.53	6.8/4	56.6/6.7	28/6.3
Agglutinin	Amaranthus hypochondriacus	Q38719	cytoplasm	395	6593.93	61.5/40	34.9/6.7	41/7.2
Agglutinin	Amaranthus hypochondriacus	Q38719	cytoplasm	397	1121.79	55.6/13	34.9/6.7	39/7.2
Agglutinin	Amaranthus hypochondriacus	Q38719	cytoplasm	404	174.89	18.8/6	34.9/6.7	40/6.9
Agglutinin	Amaranthus hypochondriacus	Q38719	cytoplasm	444	441.90	15.8/4	34.9/6.7	34/6.5
Agglutinin	Amaranthus hypochondriacus	Q38719	cytoplasm	449	1457.26	42.1/14	34.9/6.7	33/6.6
Agglutinin	Amaranthus hypochondriacus	Q38719	cytoplasm	451	7806.66	61.5/47	34.9/6.7	33/6.7
Agglutinin	Amaranthus hypochondriacus	Q38719	cytoplasm	460	6729.44	53.6/44	34.9/6.7	32/7.3
Agglutinin	Amaranthus hypochondriacus	Q38719	cytoplasm	461	6316.09	61.5/27	34.9/6.7	32/7.4
Agglutinin	Amaranthus caudatus	Q6YNX3	cytoplasm	446	9215.30	54.3/43	34.9/6.7	33/7.1
Agglutinin	Amaranthus caudatus	Q6YNX3	cytoplasm	442	7614.45	54.6/38	34.9/6.7	33/6.8
Seed protein AmA1	Amaranthus hypochondriacus	Q8S390	cytoplasm	427	590.33	34.2/10	34.9/6.2	38/6.9
Seed protein AmA1	Amaranthus hypochondriacus	Q8S390	cytoplasm	440	2807.27	50.0/22	34.9/6.2	34/6.6
Seed protein AmA1	Amaranthus hypochondriacus	Q8S390	cytoplasm	441	6548.20	27.0/26	34.9/6.2	33/7.0
Seed protein AmA1	Amaranthus hypochondriacus	Q8S390	cytoplasm	450	2113.28	50.0/24	34.9/6.2	33/6.7
<i>06.21 Allergens</i>								
allergen Pru p 1 06C	Prunus dulcis x Prunus persica	B6CQT1	cytoplasm	588	110.77	23.8/2	17.3/4.8	16/6.1
07 Transporters								
similar to magnesium transporter NIPA2-like (98%)	Glycine max	C6TK16 plasm/membrane		128	80.20	29.2/2	14.4/10.1	80/7.2
similar to magnesium transporter NIPA2-like (98%)	Glycine max	C6TK16 plasm/membrane		174	108.80	29.2/2	14.4/10.1	72/6.6
08 Intracellular transport								
<i>08.07 Vesicular</i>								
guanosine nucleotide diphosphate dissociation inhibitor 1 (100%)	Arabidopsis thaliana	B9DFX1	cytoplasm	243	738.43	23.7/21	48.4/6.0	61/6.1
09 Cell structure								
<i>09.04 Cytoskeleton</i>								
Actin Fragment	Suaeda maritima	B9VNV6	cytoplasm	320	6003.79	56.8/26	21.8/5.1	52/5.9
similar to kinesin light chain-like (99%)	Brachypodium distachyon	I1H7X6	mitochondrial	571	134.94	5.1/2	60.0/8.2	19/6.3
<i>09.07 ER/Golgi</i>								
Luminal binding protein	Spinacia oleracea	Q42434	ER	303	1826.52	19.8/13	73.5/4.8	55/6.4
<i>09.16 Mitochondrion</i>								
Voltage dependent anion channel protein	Spinacia oleracea	Q41368	cytoplasm	526	103.52	6.2/3	29.6/6.7	26/6.7
<i>09.99 Others</i>								
Aquaporin	Atriplex canescens	H2DPZ8	cytoplasm	249	52.01	18.4/2	30.2/9.2	60/7.4
10 Signal Transduction								
<i>10.0404 Kinases</i>								
Non receptor serine threonine protein kinase	Medicago truncatula	G7IUD9	cytoplasm	379	88.87	18.1/4	43.4/8.1	45/6.9
Flowering locus T like protein FT1 Fragment	Beta vulgaris	E5KIA6	?	281	76.61	61.7/2	7.1/9.9	57/6.2
11 Disease/defence								
<i>11.05 Stress responses</i>								

Stress induced protein sti1 like protein	Atriplex canescens	H9B3R7	cytoplasm	112	93.85	8.1/4	51.3/5.4	83/6.3
Stress induced protein sti1 like protein	Atriplex canescens	H9B3R7	cytoplasm	113	179.66	16.8/7	51.3/5.4	83/6.4
Salt tolerance protein 2	Beta vulgaris	Q711N3	cytoplasm	502	59.99	5.3/2	38.4/5.2	27/6.4
Heat shock protein 83 Fragment	Beta vulgaris	Q1H8M1	cytoplasm	50	317.10	12.6/6	39.9/4.8	98/5.6
Heat shock protein 101	Triticum durum	Q334I0	cytoplasm	23	96.47	11.9/8	101.0/5.8	105/6.6
Cytosolic heat shock 70 protein	Spinacia oleracea	Q41374	cytoplasm	91	1678.54	33.8/23	70.8/5.0	88/5.7
Cytosolic heat shock 70 protein	Spinacia oleracea	Q41374	cytoplasm	94	3024.86	30.0/28	70.8/5.0	87/5.8
17 67 kDa heat shock protein	Helianthus annuus	Q8VXJ4	cytoplasm	603	337.96	23.9/7	17.7/6.2	14/6.8
Putative thioredoxin dependent peroxidase	Citrus hybrid cultivar	A1ECJ6	cytoplasm	585	158.88	10.5/3	17.3/5.0	17/6.2
Glutathione reductase chloroplastic Fragment	Spinacia oleracea	Q43154	plastid	198	170.59	14.5/5	52.6/5.4	69/6.5
Glutathione reductase chloroplastic Fragment	Spinacia oleracea	Q43154	plastid	189	70.5	12.7/3	52.6/5.4	68/6.3
Inducer of CBF expression	Medicago truncatula	G7IR54	cytoplasm	578	276,9012	17.3/2	17.2/7.2	18/6.4
11.06 Detoxification								
Putative lactoylglutathione lyase	Brassica campestris	A8CF50	cytoplasm	421	424.59	10.2/5	31.9/5.2	38/6.2
Putative lactoylglutathione lyase	Brassica campestris	A8CF50	cytoplasm	438	495.07	7.8/2	31.9/5.2	36/6.3
Gamma class glutathione transferase EF1Bgamma2	Populus trichocarpa	A9PE52	cytoplasm	258	580.81	12.1/9	47.8/5.7	59/6.4
NAD P H quinone oxidoreductase	Amaranthus hybridus	A7U3X0	cytoplasm	626	219.91	28.9/2	15.1/5.9	10/6.1
NAD P H quinone oxidoreductase	Amaranthus spinosus	A7U3X1	cytoplasm	418	113.60	28.9/2	15.0/5.9	39/6.4
13 PUF								
Brother of FT AND TFL1 like protein BFT1	Beta vulgaris	E3UKE9	cytoplasm	52	45.94	23.0/2	19.5/8.5	96/6.1
Fgenesh protein 60	Beta vulgaris	Q1ZY19	cytoplasm	351	52.94	5.3/2	56.2/6.4	49/6.1
Putative GTP binding protein	Oryza sativa	Q7EZT3	cytoplasm	229	126.02	1.7/2	50.3/6.2	65/6.2
Putative GTP binding protein	Oryza sativa	Q7EZT3	cytoplasm	127	149.42	6.1/3	50.3/6.2	80/7.1
Putative TAG factor protein	Lupinus angustifolius	Q8GSE7	cytoplasm	471	88.51	24.1/5	32.2/6.3	31/7.0
Uncharacterized protein	Beta vulgaris	A2I5E8	cytoplasm	625	45.67	11.7/6	24.5/4.3	11/7.0
Uncharacterized protein	Beta vulgaris	A2I5E8	cytoplasm	56	185.54	14.4/7	24.5/4.3	94/6.5
Uncharacterized protein	Beta vulgaris	A2I5E8	cytoplasm	67	50.01	14.4/3	24.5/4.3	92/6.1
Uncharacterized protein	Beta vulgaris	A2I5E8	cytoplasm	261	92.92	9.5/2	24.5/4.3	59/5.8
Uncharacterized protein	Vitis vinifera	A5C2S6	cytoplasm	125	416.11	14.8/12	59.8/5.7	81/6.6
Uncharacterized protein	Picea sitchensis	A9NQ96	mitochondrial	475	139.94	16.8/2	17.5/8.2	30/5.9
Uncharacterized protein	Picea sitchensis	A9NV22	plastid	146	154.58	15.4/7	65.5/5.5	77/5.7
Uncharacterized protein	Zea mays	B4FQH5	plastid	398	163.28	41.4/2	10.8/11.5	41/6.0
Uncharacterized protein	Ricinus communis	B9SEC8	mitochondrial	402	110.34	38.8/2	7.5/11.1	40/6.1
Uncharacterized protein	Sorghum bicolor	C5WZR7	cytoplasm	359	47.50	4.7/4	36.6/9.1	48/6.0
Uncharacterized protein	Sorghum bicolor	C5X4W3	plastid	560	65.56	3.9/3	81.0/4.7	21/6.1
Uncharacterized protein	Sorghum bicolor	C5Y1I3	cytoplasm	687	185.16	72.0/2	5.7/5.5	68/7.3
Uncharacterized protein	Sorghum bicolor	C5YX72	cytoplasm	251	54.87	18.4/2	18.3/8.7	61/6.6
Uncharacterized protein	Sorghum bicolor	C5Z454	cytoplasm	522	92.43	4.6/3	54.4/6.2	27/6.5
Uncharacterized protein	Sorghum bicolor	C5Z454	cytoplasm	373	57.74	4.6/3	54.4/6.2	46/6.0
Uncharacterized protein	Sorghum bicolor	C5Z589	?	348	68.08	10.2/2	53.0/5.2	50/7.0
Uncharacterized protein	Glycine max	C6SWF7	cytoplasm	614	105.43	21.9/3	12.7/5.7	12/6.4

Uncharacterized protein	Glycine max	C6TLM7	plastid	187	86.94	9.1/2	24.9/6.6	68/7.1
Uncharacterized protein	Arabidopsis lyrata	D7L4A9	mitochondrial	152	264.98	11.1/11	61.3/5.4	76/5.9
Uncharacterized protein	Arabidopsis lyrata	D7LVQ4	ER	589	41.10	7.1/2	37.7/8.7	16/7.0
Uncharacterized protein	Arabidopsis lyrata	D7MBZ4	cytoplasm	179	66.84	7.3/2	36.8/9.1	71/6.1
Uncharacterized protein	Vitis vinifera	D7SS45	?	510	237.47	22.7/4	7.5/10.0	27/6.7
Uncharacterized protein	Volvox carteri	D8UJQ0	mitochondrial	541	54.83	15.3/2	15.0/10.4	25/7.2
Uncharacterized protein	Chlorella variabilis	E1ZLY5	mitochondrial	117	273.09	4.6/3	19.4/10.9	83/7.0
Uncharacterized protein	Chlorella variabilis	E1ZLY5	mitochondrial	345	236.22	12.1/4	19.4/10.9	50/6.7
Uncharacterized protein	Chlorella variabilis	E1ZU40	ER	70	680.11	10.0/4	33.7/9.1	92/5.8
Uncharacterized protein	Beta vulgaris	F4NCI9	cytoplasm	535	59.70	7.8/2	49.6/6.4	26/6.3
Uncharacterized protein	Beta macrocarpa	G2XLR9	cytoplasm	136	42.52	15.7/2	17.1/9.3	79/6.6
Uncharacterized protein	Aegilops longissima	G8CNC3	cytoplasm	315	2372.37	34.6/22	30.3/4.7	53/6.3
Uncharacterized protein	Ceratopteris richardii	H8WFA4	cytoplasm	325	50.88	13.7/2	20.6/7.3	53/6.8
Uncharacterized protein	Coccomyxa subellipsoidea	I0Z1T9	cytoplasm	407	63.82	6.6/4	42.7/6.4	40/6.7
Uncharacterized protein	Brachypodium distachyon	I1H9T4	cytoplasm	457	69.58	31.4/3	21.7/4.1	32/6.0
Uncharacterized protein	Brachypodium distachyon	I1I2G4	ER	81	91.75	23.3/3	13.5/12.2	91/6.6
Uncharacterized protein	Brachypodium distachyon	I1IF68	?	63	56.93	38.5/3	13.0/5.2	92/7.2
Uncharacterized protein	Glycine max	I1L6W0	cytoplasm	135	269.16	10.4/10	60.8/5.4	79/6.2
Uncharacterized protein	Glycine max	I1MIA6	?	156	262.74	2.9/3	61.4/7.3	76/6.0
Uncharacterized protein	Medicago truncatula	I3S6L5	cytoplasm	357	413.23	21.6/4	10.6/8.9	49/6.5
Uncharacterized protein	Oryza brachyantha	J3LIK1	cytoplasm	237	136.03	30.2/4	13.4/9.8	59/7.2
Uncharacterized protein	Oryza brachyantha	J3N8C8	cytoplasm	71	50.66	11.5/2	47.6/7.9	91/7.2
Uncharacterized protein	Beta vulgaris	Q0PEL5	cytoplasm	356	67.62	12.0/2	29.8/10.9	49/6.5
Predicted protein	Ostreococcus lucimarinus	A4RXT4	cytoplasm	203	291.79	59.4/2	11.1/7.4	68/7.5
Predicted protein	Chlamydomonas reinhardtii	A8HPZ7	mitochondrial	584	98.22	26.6/2	30.0/9.2	17/7.1
Predicted protein	Physcomitrella patens	A9RGW9	cytoplasm	267	190.69	5.1/3	18.8/9.9	59/5.9
Predicted protein	Physcomitrella patens	A9SJE6	mitochondrial	686	208.99	7.0/3	46.3/5.9	68/7.1
Predicted protein	Physcomitrella patens	A9T1X4	cytoplasm	92	209.15	10.7/3	12.4/10.0	89/6.1
Predicted protein	Populus trichocarpa	B9HNC0	cytoplasm	248	402.52	19.4/4	17.9/7.4	60/6.6
Predicted protein	Populus trichocarpa	B9IGY9	cytoplasm	137	566.57	16.6/14	61.1/5.3	79/6.1
Predicted protein	Populus trichocarpa	B9N2L3	ER	465	199.24	2.4/2	55.9/6.0	31/6.1
uncharacterized protein	Ostreococcus tauri	Q00Y82	cytoplasm	308	333.58	49.6/3	13.7/10.6	54/7.0
expressed protein (100%)	Chlorella variabilis	E1Z287	ER	542	152.57	3.0/5	55.0/9.1	24/6.7
expressed protein (100%)	Chlorella variabilis	E1Z287	ER	577	94.62	3.0/3	55.0/9.1	19/5.6
RING-H2 finger protein ATL8-like (100%)	Brachypodium distachyon	I1IE86	ER	288	67.51	30.1/2	16.0/5.5	57/6.5
DUF185-domain-containing protein (100%)	Coccomyxa subellipsoidea	I0YJQ5	cytoplasm	316	200.97	8.9/2	97.0/5.5	54/7.1
zinc finger CCCH domain-containing protein 37-like (100%)	Glycine max	I1KW27	cytoplasm	32	174.92	1.6/2	55.1/7.5	104/6.4
20 Secondary metabolism								
Gibberellin 20 oxidase 1	Gossypium hirsutum	Q2QCX5	cytoplasm	530	62.49	12.8/2	41.4/5.2	26/6.5
Delta aminolevulinic acid dehydratase chloroplastic	Spinacia oleracea	P24493	plastid	105	73.26	9.0/2	47.3/5.8	86/6.5
Betaine aldehyde dehydrogenase	Halostachys caspica	A4LAP2	cytoplasm	169	405.85	18.8/9	54.5/5.1	73/5.9

Betaine aldehyde dehydrogenase	Amaranthus hypochondriacus	O22477	cytoplasm	170	630.49	21.6/8	54.4/5.2	72/6.0
Betaine aldehyde dehydrogenase	Amaranthus hypochondriacus	O22477	cytoplasm	173	95.55	13.0/4	54.4/5.2	71/6.1
Choline monooxygenase	Atriplex nummularia	Q7XZR0	plastid	153	76.13	9.6/2	48.7/6.1	76/6.1
Choline monooxygenase	Atriplex nummularia	Q7XZR0	plastid	273	44.65	14.4/4	48.7/6.1	57/6.9
Choline monooxygenase chloroplastic	Atriplex hortensis	Q9LKN0	plastid	149	41.09	9.6/2	48.7/6.1	77/6.2
Choline monooxygenase chloroplastic	Atriplex hortensis	Q9LKN0	plastid	239	54.79	9.6/3	48.7/6.1	62/7.0
Choline monooxygenase chloroplastic	Atriplex hortensis	Q9LKN0	plastid	200	43.69	9.6/3	48.7/6.1	67/7.4
Choline monooxygenase chloroplastic	Atriplex hortensis	Q9LKN0	plastid	398	42.57	9.6/3	48.7/6.1	41/6.0
Choline monooxygenase	Atriplex nummularia	Q7XZR0	plastid	293	56	9.6/2	48.7/6.1	55/6.7
Glutamate 1 semialdehyde aminotransferase Fragment	Amaranthus tricolor	Q9AVF5	cytoplasm	472	57.44	15.8/2	32.9/4.9	30/6.8