

Supplemental Table II – Top 200 ESTs

	LEAVES	TC		Leaf	P(leaf)
		Total			
		Singleton			
		Counted			
				32789	32789
				3777	3777
				29012	29012
1	TC35585: chlorophyll a/b binding protein {Medicago sativa}			464	15.993382
2	TC31882: photosystem ii p680 chlorophyll a apoprotein (cp-47 protein) {Nicotiana tabacum}□SP P06411 PSBB_TOBA			434	14.959327
3	TC28295: RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (EC 4.1.1.39) (RUBISCO SMALL SUBUNIT). [Alfa			381	13.132497
4	TC31883: cytochrome B6 {Lotus japonicus}			356	12.270785
5	TC31885: chlorophyll a-b binding protein of lhci type ii precursor (cab-215) (lhcp) {Pisum sativum}□SP P2752			273	9.4098994
6	TC28334: lipoygenase {Pisum sativum}□GP 541746 emb CAA53730.1 X76124 lipoygenase {Pisum sativum}□PIR S5665			213	7.3417896
7	TC31888: oxygen-evolving enhancer protein 1 precursor (oe1) (33 kDa subunit of oxygen evolving system of pho			204	7.0315731
8	TC39344: plastidic aldolase NPALDP1 {Nicotiana paniculata}			190	6.5490142
9	TC39351: chlorophyll a/b-binding protein-like {Arabidopsis thaliana}□GP 7267731 emb CAB78157.1 AL161517 chlo			182	6.2732662
10	TC35679: BETA-AMYLASE (EC 3.2.1.2) (1,4-ALPHA-D-GLUCAN MALTOHYDROLASE). [Alfalfa] {Medicago sativa}□GP 255900			157	5.4115538
11	TC28300: RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (EC 4.1.1.39) (RUBISCO SMALL SUBUNIT). [Alfa			156	5.3770853
12	TC31902: carbonic anhydrase, chloroplast precursor dehydratase) {Pisum sativum}□SP P17067 CAHC_PEA CARBONIC A			148	5.1013374
13	TC35584: photosystem II type I chlorophyll a/b-binding protein {Glycine max}□GP 506629 gb AAA50172.1 U01964			148	5.1013374
14	TC31884: chlorophyll a/b-binding protein {Pisum sativum}□GP 20671 emb CAA49149.1 X69215 chlorophyll a/b-bind			146	5.0324004
15	TC35608: photosystem I subunit XI precursor {Arabidopsis thaliana}			145	4.9979319
16	TC31891: caffeic acid ortho-methyltransferase {Pinus radiata}			144	4.9634634
17	TC35642: PHOTOSYSTEM II 10 KDA POLYPEPTIDE PRECURSOR. [Tomato] {Lycopersicon esculentum}□GP 1217642 emb CAA65			143	4.9289949
18	TC39364: oxygen-evolving enhancer protein 2 precursor (oe2) (23 kDa subunit of oxygen evolving system of pho			142	4.8945264
19	TC39377: Type II chlorophyll a/b binding protein from photosystem I {Pisum sativum}□GP 602359 emb CAA57492.1			121	4.170688
20	TC39365: glyceraldehyde 3-phosphate dehydrogenase a precursor, chloroplast {Pisum sativum}□SP P12858 G3PA_PEA			120	4.1362195
21	TC31931: PSI light-harvesting antenna chlorophyll a/b-binding protein {Pisum sativum}□PIR T51616 T51616 chlor			117	4.032814
22	TC28314: light harvesting protein {Pisum sativum}□GP 309673 gb AAA84545.1 L19651 light harvesting protein {P			117	4.032814
23	TC28344: ribulose 1,5-bisphosphate carboxylase small subunit {Cicer arietinum}			112	3.8604715
24	TC31932: photosystem II 22 kDa protein precursor {Spinacia oleracea}□SP Q02060 PSBS_SPIOL PHOTOSYSTEM II 22 K			98	3.3779126
25	TC28301: ribulose-1,5-bisphosphate carboxylase/oxygenase activase {Malus domestica}□SP Q40281 RCA_MALDO RIBUL			98	3.3779126
26	TC39376: glycolate oxidase {Cucurbita sp.}□PIR T10242 T10242 (S)-2-hydroxy-acid oxidase (EC 1.1.3.15) - cucur			97	3.3434441

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27	TC39330: acid phosphatase {Glycine max}□PIR T07086 T07086 acid phosphatase (EC 3.1.3.-) - soybean	95	3.2745071
28	TC28324: elongation factor 1-alpha 1; EF-1-alpha1 {Lilium longiflorum}	94	3.2400386
29	TC39394: photosystem i reaction centre subunit ii precursor (photosystem i 20 kDa protein) (psi-d) (ps i subu	91	3.1366331
30	TC39302: glyceraldehyde 3-phosphate dehydrogenase, cytosolic {Pisum sativum}□SP P34922 G3PC_PEA GLYCERALDEHYD	91	3.1366331
31	TC28285: ribulose bisphosphate carboxylase small subunit 3a precursor {Pisum sativum}□SP P07689 RBS3_PEA RIBU	89	3.0676961
32	TC35571: lipoxygenase {Phaseolus vulgaris}□PIR T11852 T11852 lipoxygenase (EC 1.13.11.12) - kidney bean	85	2.9298221
33	TC31853: S-adenosylmethionine synthetase {Brassica juncea}	85	2.9298221
34	TC31960: plastocyanin precursor {Pisum sativum}□SP P16002 PLAS_PEA PLASTOCYANIN PRECURSOR. [Garden pea] {Pisu	82	2.8264167
35	TC39424: chlorophyll a/b-binding protein CP24 precursor {Vigna radiata}	80	2.7574797
36	TC35711: putative serine-glyoxylate aminotransferase {Fritillaria agrestis}	80	2.7574797
37	TC31890: THIAZOLE BIOSYNTHETIC ENZYME, CHLOROPLAST PRECURSOR. [Sweet orange] {Citrus sinensis}□GP 2582665 emb	77	2.6540742
38	TC39366: cysteine protease {Pisum sativum}□GP 1134882 emb CAA92583.1 Z68291 cysteine protease {Pisum sativum	76	2.6196057
39	TC31961: photosystem ii reaction centre w protein precursor (psii 61 kDa protein) {Spinacia oleracea}□SP Q413	75	2.5851372
40	TC35562: aquaporin-like transmembrane channel protein {Medicago sativa}□PIR T09260 T09260 aquaporin-like tran	74	2.5506687
41	TC39325: 5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.14) (VITAMIN-B12-IND	74	2.5506687
42	TC32005: ATP synthase a subunit precursor {Pisum sativum}□SP P06452 ATPI_PEA ATP SYNTHASE A CHAIN PRECURSOR (71	2.4472632
43	TC35586: photosystem II type I chlorophyll a/b-binding protein {Glycine max}□GP 506629 gb AAA50172.1 U01964	70	2.4127947
44	TC31977: ATP synthase gamma subunit, chloroplast precursor {Pisum sativum}□SP P28552 ATPG_PEA ATP SYNTHASE GA	68	2.3438577
45	TC39425: photosystem I light-harvesting chlorophyll a/b-binding protein {Nicotiana tabacum}□GP 493723 emb CAA	64	2.2059837
46	TC39380: transketolase-like protein {Arabidopsis thaliana}□PIR T47886 T47886 transketolase-like protein - Ara	62	2.1370467
47	TC35743: OXYGEN-EVOLVING ENHANCER PROTEIN 3-1, CHLOROPLAST PRECURSOR (OEE3) (16 KDA SUBUNIT OF OXYGEN EVOLVIN	61	2.1025782
48	TC39426:	61	2.1025782
49	TC39416: chloroplast phosphoglycerate kinase {Populus nigra}	59	2.0336413
50	TC35739: serine hydroxymethyltransferase, mitochondrial precursor (serine methylase) (glycine hydroxymethyltr	58	1.9991728
51	TC39293: cysteine proteinase 15a precursor protein 15a) {Pisum sativum}□SP P25804 CYSP_PEA CYSTEINE PROTEINAS	56	1.9302358
52	TC28336: chlorophyll a/b binding protein CP29 {Vigna radiata}	55	1.8957673
53	TC35686: 2,4-D inducible glutathione S-transferase {Glycine max}□PIR T06239 T06239 probable glutathione trans	55	1.8957673
54	TC39445: photosystem i reaction centre subunit iv b precursor (psi-e b) {Nicotiana sylvestris}□SP Q41229 PSE2	54	1.8612988
55	TC39450: lectin-related polypeptide {Robinia pseudoacacia}	54	1.8612988
56	TC35732: CPRD46 protein {Vigna unguiculata}□GP 1853970 dbj BAA13542.1 D88122 CPRD46 protein {Vigna unguicula	52	1.7923618
57	TC28337: elongation factor 1-alpha 1; EF-1-alpha1 {Lilium longiflorum}	52	1.7923618
58	TC28287: lipoxygenase {Pisum sativum}□PIR T06827 T06827 lipoxygenase (EC 1.13.11.12) - garden pea	51	1.7578933

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59	TC35761:	50	1.7234248
60	TC35583: photosystem II type I chlorophyll a/b-binding protein {Glycine max}□GP 506629 gb AAA50172.1 U01964	50	1.7234248
61	TC31981: ferredoxin i precursor {Pisum sativum}□SP P09911 FER1_PEA FERREDOXIN I PRECURSOR. [Garden pea] {Pisu	50	1.7234248
62	TC35751: PHOTOSYSTEM I REACTION CENTRE SUBUNIT N PRECURSOR (PSI-N). [Mouse-ear cress] {Arabidopsis thaliana}□	49	1.6889563
63	TC28357: ascorbate peroxidase {Pisum sativum}□GP 20648 emb CAA43992.1 X62077 L-ascorbate peroxidase {Pisum s	49	1.6889563
64	TC35795: similar to PSI-K subunit of photosystem I from barley {Medicago sativa}	48	1.6544878
65	TC35630: S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (EC 4.1.1.50) (ADOMETDC) (SAMDC) [CONTAINS: S-ADENOSYLM	48	1.6544878
66	TC35613: type 1 metallothionein {Medicago sativa}□GP 6164920 gb AAF04584.1 AF189766_1 AF189766 type 1 metallo	48	1.6544878
67	TC32020: photosystem I psaH protein {Nicotiana sylvestris}□GP 397555 emb CAA43841.1 X61664 photosystem I psa	47	1.6200193
68	TC31849: TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP). [Alfalfa] {Medicago sativa}□GP 1419685 emb	47	1.6200193
69	TC35698: putative dTDP-glucose 4-6-dehydratase {Arabidopsis thaliana}□GP 13605497 gb AAK32742.1 AF361574_1 AF	46	1.5855508
70	TC35790: NADP-DEPENDENT GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (EC 1.2.1.9) (NON-PHOSPHORYLATING GLYCERALDE	45	1.5510823
71	TC32050:	45	1.5510823
72	TC39353: UDP-galactose-4-epimerase {Pisum sativum}□SP Q43070 GAE1_PEA UDP-GLUCOSE 4-EPIMERASE (EC 5.1.3.2) (G	45	1.5510823
73	TC39470: mRNA binding protein precursor-like {Arabidopsis thaliana}□PIR T48103 T48103 mRNA binding protein CS	43	1.4821453
74	TC39441: RNA-binding protein-like {Arabidopsis thaliana}□GP 14532488 gb AAK63972.1 AY039868 AT5g50250/K6A12_	43	1.4821453
75	TC39446: ferredoxin--NADP reductase precursor {Vicia faba}□SP P41346 FENR_VICFA FERREDOXIN--NADP REDUCTASE PR	43	1.4821453
76	TC35776: hypothetical protein {Arabidopsis thaliana}□GP 2191138 gb AAB61025.1 AF007269 A_IG002N01.18 gene pr	42	1.4476768
77	TC35746: unknown protein {Arabidopsis thaliana}□PIR G84494 G84494 hypothetical protein At2g10940 [imported] -	41	1.4132083
78	TC31887: cationic peroxidase {Cicer arietinum}	41	1.4132083
79	TC35723: nod factor binding lectin-nucleotide phosphohydrolase {Medicago sativa}	40	1.3787398
80	TC28345: vcCyP {Vicia faba}□PIR T50770 T50770 peptidylprolyl isomerase (EC 5.2.1.8) vcCyP [similarity] - fava	40	1.3787398
81	TC35706: triosephosphate isomerase, cytosolic {Coptis japonica}□SP P21820 TPIS_COPJA TRIOSEPHOSPHATE ISOMERAS	39	1.3442713
82	TC35696: adenosine kinase {Arabidopsis thaliana}□GP 7378610 emb CAB83286.1 AL162751 adenosine kinase-like pr	39	1.3442713
83	TC31915: cysteine proteinase precursor {Phaseolus vulgaris}□PIR T12041 T12041 cysteine proteinase (EC 3.4.22.	39	1.3442713
84	TC39475: Lhcb4:3 protein {Arabidopsis thaliana}□GP 4895259 gb AAD32843.1 AC007658_2 AC007658 putative chlorop	38	1.3098028
85	TC35810:	38	1.3098028
86	TC39464: 29kD A ribonucleoprotein {Nicotiana sylvestris}□SP Q08935 ROC1_NICSY 29 KDA RIBONUCLEOPROTEIN A, CHL	38	1.3098028
87	TC39538: fructose-bisphosphate aldolase, cytoplasmic isozyme 1 {Pisum sativum}□SP P46256 ALF1_PEA FRUCTOSE-BI	37	1.2753343
88	TC35561: plasma membrane integral protein ZmPIP2-7 {Zea mays}	37	1.2753343
89	TC35606: 14-3-3-like protein {Pisum sativum}	36	1.2408658
90	TC35864: Germin-like protein {Pisum sativum}	35	1.2063974

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91	TC39497: chloroplast translation elongation factor {Pisum sativum}□SP O24310 EFTU_PEA ELONGATION FACTOR TU,	35	1.2063974
92	TC35844: photosystem I subunit V precursor {Arabidopsis thaliana}□GP 11908046 gb AAG41452.1 AF326870_1 AF3268	34	1.1719289
93	TC32054: FtsH-like protein Pff precursor {Nicotiana tabacum}	34	1.1719289
94	TC39326: aquaporin	34	1.1719289
95	TC35847: glycine cleavage system h protein precursor {Pisum sativum}□SP P16048 GCSH_PEA GLYCINE CLEAVAGE SYST	33	1.1374604
96	TC39556: protochlorophyllide reductase (EC 1.3.1.33) precursor - garden pea	33	1.1374604
97	TC39577: photosystem I reaction center subunit III {Vigna radiata}	32	1.1029919
98	TC35702: myo-inositol-1-phosphate synthase {Glycine max}	32	1.1029919
99	TC39386: pathogenesis-related protein 4A {Pisum sativum}	32	1.1029919
100	TC31954: gene_id:MCO15.7~pir T04808~strong similarity to unknown protein {Arabidopsis thaliana}	32	1.1029919
101	TC35588: photosystem II type I chlorophyll a/b-binding protein {Glycine max}□GP 506629 gb AAA50172.1 U01964	31	1.0685234
102	TC35815: phosphoribulokinase {Pisum sativum}□GP 1885326 emb CAA72118.1 Y11248 phosphoribulokinase {Pisum sat	31	1.0685234
103	TC35763: putative alanine aminotransferase; 91367-88744 {Arabidopsis thaliana}□GP 12325053 gb AAG52480.1 AC01	31	1.0685234
104	TC35753:	31	1.0685234
105	TC28402: ribulose 1,5-bisphosphate carboxylase small subunit {Cicer arietinum}	30	1.0340549
106	TC39401:	30	1.0340549
107	TC39491: putative 1-deoxy-D-xylulose 5-phosphate reductoisomerase {Zea mays}	30	1.0340549
108	TC31998: hypothetical protein {Citrus x paradisi}	30	1.0340549
109	TC39474: chloroplast triose phosphate translocator precursor (ctpt) (p36) (e30) {Pisum sativum}□SP P21727 CPT	30	1.0340549
110	TC39348: enolase {Lupinus luteus}	30	1.0340549
111	TC39399: abscisic acid and environmental stress inducible protein {Medicago falcata}□SP Q09134 GRPA_MEDFA ABS	29	0.9995864
112	TC39534: cytochrome b6-f complex iron-sulfur subunit precursor (rieske iron-sulfur protein) (risp) {Pisum sat	29	0.9995864
113	TC35587: photosystem II type I chlorophyll a/b-binding protein {Glycine max}□GP 506629 gb AAA50172.1 U01964	29	0.9995864
114	TC32074: glycine dehydrogenase (decarboxylating) precursor (glycine decarboxylase) (glycine cleavage system p	29	0.9995864
115	TC28479:	28	0.9651179
116	TC31886: initiation factor 5A-2 (EIF-5A) (EIF-4D) {Nicotiana plumbaginifolia}□SP P24922 IF52_NICPL INITIATION	28	0.9651179
117	TC31918: proline oxidase precursor {Arabidopsis thaliana}	28	0.9651179
118	TC28483: ESTs gb T20589, gb T04648, gb AA597906, gb T04111, gb R84180, gb R65428, gb T44439, gb T76570, gb R9	27	0.9306494
119	TC35722: putative apyrase [Medicago truncatula]	27	0.9306494
120	TC31852: CHALCONE SYNTHASE (EC 2.3.1.74) (NARINGENIN-CHALCONE SYNTHASE). [White birch, Betula pendula] {Betul	27	0.9306494
121	TC35767: Similar to Populus balsamifera subsp. trichocarpa X Populus deltoides vegetative storage protein. (L	27	0.9306494
122	TC39591:	26	0.8961809

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123	TC32113: glutamine synthetase precursor {Medicago sativa}	26	0.8961809
124	TC35593: VuP5CS {Vigna unguiculata}	26	0.8961809
125	TC28375: ribulose 1,5-bisphosphate carboxylase small subunit {Cicer arietinum}	25	0.8617124
126	TC39620: geranylgeranyl hydrogenase {Glycine max}	25	0.8617124
127	TC35900: malate dehydrogenase, glyoxysomal precursor {Cucumis sativus}□SP P46488 MDHG_CUCSA MALATE DEHYDROGEN	25	0.8617124
128	TC35733: CPRD46 protein {Vigna unguiculata}□GP 1853970 dbj BAA13542.1 D88122 CPRD46 protein {Vigna unguicula	25	0.8617124
129	TC39570: leucine zipper-containing protein AT103 {Arabidopsis thaliana}□PIR T47754 T47754 leucine zipper-cont	25	0.8617124
130	TC28290: contains similarity to receptor protein kinase~gene_id:MLD14.4 {Arabidopsis thaliana}	25	0.8617124
131	TC28353: ribulose 1,5-bisphosphate carboxylase small subunit {Cicer arietinum}	24	0.8272439
132	TC32038: AMINOMETHYLTRANSFERASE, MITOCHONDRIAL PRECURSOR (EC 2.1.2.10) (GLYCINE CLEAVAGE SYSTEM T PROTEIN) (G	24	0.8272439
133	TC32111: Ca ²⁺ /H ⁺ exchanger {Vigna radiata}□PIR T07821 T07821 Ca ²⁺ /H ⁺ -exchanging protein - mung bean	24	0.8272439
134	TC39455: granule-bound glycogen (starch) synthase {Astragalus membranaceus}	24	0.8272439
135	TC32252: germin-like protein precursor {Arabidopsis thaliana}□GP 4154285 gb AAD05223.1 AF090733 germin-like	23	0.7927754
136	TC32196: fructose-1,6-bisphosphatase {Pisum sativum}	23	0.7927754
137	TC39400: dormancy-associated protein {Pisum sativum}□PIR T06256 T06256 dormancy-associated protein 2 - garden	23	0.7927754
138	TC28473: glycine dehydrogenase (decarboxylating) precursor (glycine decarboxylase) (glycine cleavage system p	23	0.7927754
139	TC39594:	23	0.7927754
140	TC32084: Putative GSH-dependent dehydroascorbate reductase {Arabidopsis thaliana}□GP 14517510 gb AAK62645.1	23	0.7927754
141	TC35752: poly(A)-binding protein {Cucumis sativus}	23	0.7927754
142	TC31913: At1g56070/T6H22_13 {Arabidopsis thaliana}	23	0.7927754
143	TC39355: heat shock cognate protein 80 {Lycopersicon esculentum}□SP P36181 HS80_LYCES HEAT SHOCK COGNATE PROT	23	0.7927754
144	TC31865: aquaporin-like protein PIP2 [Medicago truncatula]	23	0.7927754
145	TC39299: glyceraldehyde-3-phosphate dehydrogenase {Nicotiana tabacum}	23	0.7927754
146	TC39623:	22	0.7583069
147	TC32122: nClpP5 {Arabidopsis thaliana}□GP 8569101 gb AAF76446.1 AC015445_13 AC015445 Identical to nClpP5 from	22	0.7583069
148	TC35846: carboxytransferase beta subunit {Lotus japonicus}	22	0.7583069
149	TC32121: oxoglutarate malate translocator {Solanum tuberosum}□GP 1486472 emb CAA68164.1 X99853 oxoglutarate	22	0.7583069
150	TC39428: ankyrin-repeat protein HBP1 {Nicotiana tabacum}	22	0.7583069
151	TC31994: calmodulin {Daucus carota}□EGAD 125658 134028 calmodulin {Lilium longiflorum}□EGAD 125658 134029 cal	22	0.7583069
152	TC28293: histone H3 variant H3.3 {Lycopersicon esculentum}□EGAD 131603 140441 histone H3 {Lolium temulentum}□	22	0.7583069
153	TC39298: cell wall proline-rich protein	22	0.7583069
154	TC39690:	21	0.7238384

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155	TC28539: Identical to gb Y10557 g5bf gene from Arabidopsis thaliana. ESTs gb R30578, gb R90475, gb T22384, g	21	0.7238384
156	TC32156:	21	0.7238384
157	TC32064: chloroplast ribosomal protein L2 {Nicotiana tabacum}□SP P06379 RK2_TOBAC CHLOROPLAST 50S RIBOSOMAL P	21	0.7238384
158	TC31992: metallothionein - soybean	21	0.7238384
159	TC28289: hydroxyproline-rich glycoprotein precursor {Phaseolus vulgaris}□GP 727264 gb AAA87902.1 U18791 hydr	21	0.7238384
160	TC35697: L3 Ribosomal protein {Medicago sativa subsp. x varia}	21	0.7238384
161	TC28359: S-adenosyl-L-homocystein hydrolase; SAH {Mesembryanthemum crystallinum}□SP P93253 SAHH_MESCR ADENOSY	21	0.7238384
162	TC39277: PR10-1 protein	21	0.7238384
163	TC32282:	20	0.6893699
164	TC28566: ESTs gb R65052, gb AA712146, gb H76533, gb H76282, gb AA650771, gb H76287, gb AA650887, gb N37383, g	20	0.6893699
165	TC35921: FtsH protease {Medicago sativa}	20	0.6893699
166	TC35974: ATP synthase beta chain precursor (subunit II) {Arabidopsis thaliana}□GP 2864617 emb CAA16964.1 AL0	20	0.6893699
167	TC32104: 2-Cys peroxiredoxin {Pisum sativum}	20	0.6893699
168	TC39288: cystathionine-gamma-synthase precursor {Glycine max}	20	0.6893699
169	TC39317: polyubiquitin(ubiquitin) {maize, Peptide, 533 aa} [Zea mays]□GP 248339 gb AAB21994.1 S94466 polyubi	20	0.6893699
170	TC39427: UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (EC 2.7.7.9) (UDP-GLUCOSE PYROPHOSPHORYLASE) (UDPGP) (U	20	0.6893699
171	TC28387: adenine nucleotide translocator {Lupinus albus}	20	0.6893699
172	TC32235: unknown protein {Arabidopsis thaliana}□PIR T02683 T02683 hypothetical protein At2g46820 [imported] -	19	0.6549014
173	TC32222: thioredoxin m {Pisum sativum}	19	0.6549014
174	TC35965: CP12 protein {Pisum sativum}□GP 1617206 emb CAA96570.1 Z72489 CP12 {Pisum sativum}□PIR T06562 T0656	19	0.6549014
175	TC39676: ABC transporter protein 1-like {Arabidopsis thaliana}	19	0.6549014
176	TC35942: ATP synthase delta subunit, chloroplast precursor {Pisum sativum}□SP Q02758 ATPD_PEA ATP SYNTHASE DE	19	0.6549014
177	TC28521: hydroxypyruvate reductase {Bruguiera gymnorhiza}	19	0.6549014
178	TC39530: rubisco subunit binding-protein alpha subunit precursor (60 kDa chaperonin alpha subunit) (cpn-60 al	19	0.6549014
179	TC39469: chaperonin precursor {Pisum sativum}□SP P08927 RUBB_PEA RUBISCO SUBUNIT BINDING-PROTEIN BETA SUBUNIT	19	0.6549014
180	TC32006: sulfate adenylyltransferase {Solanum tuberosum}□GP 479090 emb CAA55655.1 X79053 sulfate adenylyltra	19	0.6549014
181	TC39407: b2 protein {Daucus carota}□SP P37707 B2_DAUCA B2 PROTEIN. [Carrot] {Daucus carota}□GP 297889 emb CAA	19	0.6549014
182	TC35684: GTP-binding protein {Cicer arietinum}	19	0.6549014
183	TC35555: aquaporin 2 {Samanea saman}	19	0.6549014
184	TC35710: putative Hs1pro-1 homolog {Pisum sativum}	19	0.6549014
185	TC39291: fructose-bisphosphate aldolase, cytoplasmic isozyme 2 {Pisum sativum}□SP P46257 ALF2_PEA FRUCTOSE-BI	19	0.6549014
186	TC32107: PROBABLE MANNITOL DEHYDROGENASE (EC 1.1.1.255) (NAD-DEPENDENT MANNITOL DEHYDROGENASE). [Strawberry]	18	0.6204329

Supplemental Table II – Top 200 ESTs

187	TC28463: thaumatin-like protein 1 - apple tree	18	0.6204329
188	TC35984: hypothetical protein; 69776-68193 {Arabidopsis thaliana}□PIR F96552 F96552 hypothetical protein F5D2	18	0.6204329
189	TC32130: Putative membrane related protein {Arabidopsis thaliana}□PIR D96670 D96670 probable membrane related	18	0.6204329
190	TC39493:	18	0.6204329
191	TC35604: vf14-3-3c protein {Vicia faba}	18	0.6204329
192	TC39439: 60S ribosomal protein L6 {Cicer arietinum}	18	0.6204329
193	TC39295: single-stranded nucleic acid binding protein {Triticum aestivum}□GP 974605 gb AAA75104.1 U32310 sin	18	0.6204329
194	TC39431: elongation factor 1 beta' {Triticum aestivum}□PIR S35501 S35501 translation elongation factor eEF-1	18	0.6204329
195	TC31927:	17	0.5859644
196	TC39757: ribosomal protein L15, chloroplast precursor (cl15) {Pisum sativum}□SP P31165 RK15_PEA 50S RIBOSOMAL	17	0.5859644
197	TC39718: Unknown protein {Arabidopsis thaliana}□GP 14423502 gb AAK62433.1 AF386988_1 AF386988 Unknown protein	17	0.5859644
198	TC39662: ESTs gb AI992412, gb AI994629 come from this gene. {Arabidopsis thaliana}□GP 12083328 gb AAG48823.1	17	0.5859644
199	TC39387: NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP). [Chickpea, Garbanzo] {Cicer arietinum}□GP 263217	17	0.5859644
200	TC32018: putative chitinase	17	0.5859644

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	STEMS	TC	Stem	P(stem)
		Total	10314	10314
		Singleton	1569	1569
		Counted	8745	8745
1	TC39325: 5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.14) (VITAMIN-B12-IND		130	12.604227
2	TC28324: elongation factor 1-alpha 1; EF-1-alpha1 {Lilium longiflorum}		98	9.5016482
3	TC28337: elongation factor 1-alpha 1; EF-1-alpha1 {Lilium longiflorum}		74	7.174714
4	TC28334: lipoxygenase {Pisum sativum}□GP 541746 emb CAA53730.1 X76124 lipoxygenase {Pisum sativum}□PIR S5665		64	6.205158
5	TC28318: adenosylhomocysteinase {Medicago sativa}□SP P50246 SAHH_MEDSA ADENOSYLHOMOCYSTEINASE (EC 3.3.1.1) (S		55	5.3325577
6	TC31923: tubulin alpha subunit {Prunus dulcis}□SP P33629 TBA_PRUDU TUBULIN ALPHA CHAIN. [Almond, Prunus amygd		46	4.4599573
7	TC31853: S-adenosylmethionine synthetase {Brassica juncea}		42	4.072135
8	TC31891: caffeic acid ortho-methyltransferase {Pinus radiata}		39	3.7812682
9	TC31890: THIAZOLE BIOSYNTHETIC ENZYME, CHLOROPLAST PRECURSOR. [Sweet orange] {Citrus sinensis}□GP 2582665 emb		38	3.6843126
10	TC39355: heat shock cognate protein 80 {Lycopersicon esculentum}□SP P36181 HS80_LYCES HEAT SHOCK COGNATE PROT		35	3.3934458
11	TC28287: lipoxygenase {Pisum sativum}□PIR T06827 T06827 lipoxygenase (EC 1.13.11.12) - garden pea		24	2.3269343
12	TC31889: thiamin biosynthetic enzyme {Glycine max}		24	2.3269343
13	TC39380: transketolase-like protein {Arabidopsis thaliana}□PIR T47886 T47886 transketolase-like protein - Ara		23	2.2299787
14	TC31913: At1g56070/T6H22_13 {Arabidopsis thaliana}		23	2.2299787
15	TC35585: chlorophyll a/b binding protein {Medicago sativa}		23	2.2299787
16	TC35726: malate oxidoreductase dependent malic enzyme) (NADP-me) {Vitis vinifera}□SP P51615 MAOX_VITVI NADP-D		22	2.1330231
17	TC28387: adenine nucleotide translocator {Lupinus albus}		21	2.0360675
18	TC32117: beta-glucosidase {Polygonum tinctorium}		20	1.9391119
19	TC39427: UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (EC 2.7.7.9) (UDP-GLUCOSE PYROPHOSPHORYLASE) (UDPGP) (U		20	1.9391119
20	TC35696: adenosine kinase {Arabidopsis thaliana}□GP 7378610 emb CAB83286.1 AL162751 adenosine kinase-like pr		20	1.9391119
21	TC39348: enolase {Lupinus luteus}		20	1.9391119
22	TC39481: PHOSPHOGLUCOMUTASE, CYTOPLASMIC (EC 5.4.2.2) (GLUCOSE PHOSPHOMUTASE) (PGM). [Garden pea] {Pisum sati		19	1.8421563
23	TC39409: KETOL-ACID REDUCTOISOMERASE PRECURSOR (EC 1.1.1.86) (ACETOHYDROXY-ACID REDUCTOISOMERASE) (ALPHA-KETO		19	1.8421563
24	TC39302: glyceraldehyde 3-phosphate dehydrogenase, cytosolic {Pisum sativum}□SP P34922 G3PC_PEA GLYCERALDEHYD		19	1.8421563
25	TC32214: hypothetical protein {Medicago sativa}□GP 537313 gb AAB41813.1 L36159 unknown protein {Medicago sat		18	1.7452007

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26	TC32111: Ca ²⁺ /H ⁺ exchanger { <i>Vigna radiata</i> }□PIR T07821 T07821 Ca ²⁺ /H ⁺ -exchanging protein - mung bean	18	1.7452007
27	TC39412: receptor-like protein kinase homolog RK20-1 { <i>Phaseolus vulgaris</i> }	18	1.7452007
28	TC39344: plastidic aldolase NPALDP1 { <i>Nicotiana paniculata</i> }	17	1.6482451
29	TC35860: unknown protein { <i>Arabidopsis thaliana</i> }	16	1.5512895
30	TC28359: S-adenosyl-L-homocystein hydrolase; SAH { <i>Mesembryanthemum crystallinum</i> }□SP P93253 SAHH_MESCR ADENOSY	16	1.5512895
31	TC28321: hypothetical protein { <i>Cicer arietinum</i> }	16	1.5512895
32	TC31908:	16	1.5512895
33	TC31862: S-adenosyl-L-methionine synthetase { <i>Elaeagnus umbellata</i> }	16	1.5512895
34	TC28378: putative protein { <i>Arabidopsis thaliana</i> }□GP 7269521 emb CAB79524.1 AL161565 putative protein { <i>Arabid</i>	15	1.4543339
35	TC39446: ferredoxin--NADP reductase precursor { <i>Vicia faba</i> }□SP P41346 FENR_VICFA FERREDOXIN--NADP REDUCTASE PR	15	1.4543339
36	TC39430: Contains similarity to gb D13630 KIAA0005 gene from <i>Homo sapiens</i> . ESTs gb T45345, gb T21086, gb R90	15	1.4543339
37	TC31918: proline oxidase precursor { <i>Arabidopsis thaliana</i> }	15	1.4543339
38	TC31977: ATP synthase gamma subunit, chloroplast precursor { <i>Pisum sativum</i> }□SP P28552 ATPG_PEA ATP SYNTHASE GA	15	1.4543339
39	TC35698: putative dTDP-glucose 4-6-dehydratase { <i>Arabidopsis thaliana</i> }□GP 13605497 gb AAK32742.1 AF361574_1 AF	15	1.4543339
40	TC31887: cationic peroxidase { <i>Cicer arietinum</i> }	15	1.4543339
41	TC28357: ascorbate peroxidase { <i>Pisum sativum</i> }□GP 20648 emb CAA43992.1 X62077 L-ascorbate peroxidase { <i>Pisum s</i>	15	1.4543339
42	TC28556: D-3-PHOSPHOGLYCERATE DEHYDROGENASE PRECURSOR (EC 1.1.1.95) (PGDH). [Mouse-ear cress] { <i>Arabidopsis th</i>	14	1.3573783
43	TC32116: cell division cycle protein 48 homolog (valosin containing protein homolog) (vcp) { <i>Glycine max</i> }□SP P	14	1.3573783
44	TC35676: ATP synthase beta subunit, mitochondrial precursor { <i>Zea mays</i> }□SP P19023 ATP2_MAIZE ATP SYNTHASE BETA	14	1.3573783
45	TC35562: aquaporin-like transmembrane channel protein { <i>Medicago sativa</i> }□PIR T09260 T09260 aquaporin-like tran	14	1.3573783
46	TC39585: unnamed protein product { <i>Brassica napus</i> }	13	1.2604227
47	TC39530: rubisco subunit binding-protein alpha subunit precursor (60 kDa chaperonin alpha subunit) (cpn-60 al	13	1.2604227
48	TC39510: methylenetetrahydrofolate reductase MTHFR2 { <i>Arabidopsis thaliana</i> }	13	1.2604227
49	TC39514: AT3g52990/F8J2_160 { <i>Arabidopsis thaliana</i> }	13	1.2604227
50	TC31975:	13	1.2604227
51	TC39366: cysteine protease { <i>Pisum sativum</i> }□GP 1134882 emb CAA92583.1 Z68291 cysteine protease { <i>Pisum sativum</i>	13	1.2604227
52	TC35606: 14-3-3-like protein { <i>Pisum sativum</i> }	13	1.2604227
53	TC39291: fructose-bisphosphate aldolase, cytoplasmic isozyme 2 { <i>Pisum sativum</i> }□SP P46257 ALF2_PEA FRUCTOSE-BI	13	1.2604227
54	TC36269: methionine synthase { <i>Mesembryanthemum crystallinum</i> }□SP P93263 METE_MESCR 5-METHYLTETRAHYDROPTEROYLTR	12	1.1634671
55	TC32261: putative Na ⁺ dependent ileal bile acid transporter { <i>Arabidopsis thaliana</i> }□PIR T02645 T02645 hypothet	12	1.1634671
56	TC39503: unknown protein { <i>Arabidopsis thaliana</i> }□PIR F86442 F86442 unknown protein [imported] - <i>Arabidopsis th</i>	12	1.1634671
57	TC28398: UDP-glucose dehydrogenase { <i>Glycine max</i> }□SP Q96558 UGDH_SOYBN UDP-GLUCOSE 6-DEHYDROGENASE (EC 1.1.1.2	12	1.1634671

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58	TC31935: tubulin beta-2 chain - garden pea (fragment)	12	1.1634671
59	TC35729: UDP-glucose dehydrogenase {Glycine max} □SP Q96558 UGDH_SOYBN UDP-GLUCOSE 6-DEHYDROGENASE (EC 1.1.1.2	12	1.1634671
60	TC28301: ribulose-1,5-bisphosphate carboxylase/oxygenase activase {Malus domestica} □SP Q40281 RCA_MALDO RIBUL	12	1.1634671
61	TC39365: glyceraldehyde 3-phosphate dehydrogenase a precursor, chloroplast {Pisum sativum} □SP P12858 G3PA_PEA	12	1.1634671
62	TC39351: chlorophyll a/b-binding protein-like {Arabidopsis thaliana} □GP 7267731 emb CAB78157.1 AL161517 chlo	12	1.1634671
63	TC36096:	11	1.0665115
64	TC28618: F10A5.13 {Arabidopsis thaliana} □GP 14532628 gb AAK64042.1 AY039938 unknown protein {Arabidopsis tha	11	1.0665115
65	TC28439: ELONGATION FACTOR 1-GAMMA (EF-1-GAMMA) (EEF-1B GAMMA). [Cherry] {Prunus avium} □GP 10444415 gb AAG179	11	1.0665115
66	TC32143: gb AAF02137.1~gene_id:MHF15.9~strong similarity to unknown protein {Arabidopsis thaliana}	11	1.0665115
67	TC35695: MALATE DEHYDROGENASE, CYTOPLASMIC (EC 1.1.1.37). [Alfalfa] {Medicago sativa} □GP 2827082 gb AAB99756.	11	1.0665115
68	TC35752: poly(A)-binding protein {Cucumis sativus}	11	1.0665115
69	TC39416: chloroplast phosphoglycerate kinase {Populus nigra}	11	1.0665115
70	TC31915: cysteine proteinase precursor {Phaseolus vulgaris} □PIR T12041 T12041 cysteine proteinase (EC 3.4.22.	11	1.0665115
71	TC31888: oxygen-evolving enhancer protein 1 precursor (oeo1) (33 kDa subunit of oxygen evolving system of pho	11	1.0665115
72	TC32417:	10	0.9695559
73	TC36086: diphenol oxidase {Nicotiana tabacum} □GP 4756886 emb CAB42313.1 A68085 unnamed protein product {unid	10	0.9695559
74	TC28407: putative phytochelatin synthetase {Arabidopsis thaliana} □PIR T51392 T51392 probable phytochelatin sy	10	0.9695559
75	TC35735: hydroxymethyltransferase {Arabidopsis thaliana} □GP 2244749 emb CAB10172.1 Z97335 hydroxymethyltrans	10	0.9695559
76	TC31922: tubulin alpha-1 subunit {Pisum sativum} □SP P46259 TBA1_PEA TUBULIN ALPHA-1 CHAIN. [Garden pea] {Pisu	10	0.9695559
77	TC39539: unnamed protein product {Arabidopsis thaliana} □GP 4049343 emb CAA22568.1 AL034567 cellulose synthas	10	0.9695559
78	TC31966: caffeic acid 3-o-methyltransferase methionine:caffeic acid 3-o-methyltransferase) (comt) {Medicago s	10	0.9695559
79	TC39474: chloroplast triose phosphate translocator precursor (cpt) (p36) (e30) {Pisum sativum} □SP P21727 CPT	10	0.9695559
80	TC31984: eukaryotic initiation factor 4a-11 (eif-4a-11) {Nicotiana tabacum} □SP Q40465 IF4V_TOBAC EUKARYOTIC I	10	0.9695559
81	TC39373: reversibly glycosylated polypeptide-2 (AtRGB) {Arabidopsis thaliana} □GP 14532444 gb AAK63950.1 AY03	10	0.9695559
82	TC35739: serine hydroxymethyltransferase, mitochondrial precursor (serine methylase) (glycine hydroxymethyltr	10	0.9695559
83	TC31894: phosphoglyceromutase {Mesembryanthemum crystallinum} □SP Q42908 PMGI_MESCR 2,3-BISPHOSPHOGLYCERATE-IN	10	0.9695559
84	TC40030: putative protein {Arabidopsis thaliana} □GP 7269804 emb CAB79664.1 AL161574 putative protein {Arabid	9	0.8726003
85	TC32570: alpha-glucosidase {Solanum tuberosum subsp. tuberosum}	9	0.8726003
86	TC36170: putative chloroplast nucleoid DNA-binding protein {Arabidopsis thaliana} □PIR T02706 T02706 hypotheti	9	0.8726003
87	TC28720: aminopeptidase-like protein {Arabidopsis thaliana} □GP 7270256 emb CAB80026.1 AL161582 aminopeptidas	9	0.8726003
88	TC35902: phospholipase D {Vigna unguiculata} □SP O04865 PLD_VIGUN PHOSPHOLIPASE D PRECURSOR (EC 3.1.4.4) (PLD)	9	0.8726003
89	TC32132: ABC transporter {Arabidopsis thaliana}	9	0.8726003

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90	TC35831: putative post-transcriptional gene silencing protein { <i>Arabidopsis thaliana</i> }	9	0.8726003
91	TC32113: glutamine synthetase precursor { <i>Medicago sativa</i> }	9	0.8726003
92	TC35814: beta-tubulin { <i>Cicer arietinum</i> }□SP Q39445 TBB_CICAR TUBULIN BETA CHAIN. [Chickpea, Garbanzo] { <i>Cicer a</i>	9	0.8726003
93	TC35727: phenylalanine ammonia-lyase { <i>Stylosanthes humilis</i> }□SP P45732 PALY_STYHU PHENYLALANINE AMMONIA-LYASE	9	0.8726003
94	TC39293: cysteine proteinase 15a precursor protein 15a { <i>Pisum sativum</i> }□SP P25804 CYSP_PEA CYSTEINE PROTEINAS	9	0.8726003
95	TC32528: permease 1 { <i>Arabidopsis thaliana</i> }	8	0.7756448
96	TC35991: putative protein kinase { <i>Arabidopsis thaliana</i> }□GP 7269998 emb CAB79814.1 AL161578 putative protein	8	0.7756448
97	TC39706: putative O-linked GlcNAc transferase { <i>Arabidopsis thaliana</i> }	8	0.7756448
98	TC39286: nuM1 protein { <i>Medicago sativa</i> }□GP 1279563 emb CAA61298.1 X88845 nuM1 { <i>Medicago sativa</i> }□PIR T09648 T	8	0.7756448
99	TC32188: endo-1,4-beta-glucanase { <i>Lycopersicon esculentum</i> }□GP 206553 gb AAC49704.1 U78526 endo-1,4-beta-glu	8	0.7756448
100	TC28455: AT5g62000/mtg10_20 { <i>Arabidopsis thaliana</i> }	8	0.7756448
101	TC32068: F20B24.11 { <i>Arabidopsis thaliana</i> }	8	0.7756448
102	TC28471: nucleolar protein { <i>Arabidopsis thaliana</i> }□GP 11878189 gb AAG40838.1 AF302492_1 AF302492 NOP56-like pr	8	0.7756448
103	TC35856: fiber annexin { <i>Gossypium hirsutum</i> }□PIR T31428 T31428 fiber annexin - upland cotton	8	0.7756448
104	TC39523: Identical to atranbp1a from <i>Arabidopsis thaliana</i> gb X97377. It contains a RanBP1 domain PF 00638.	8	0.7756448
105	TC32100: endoplasmic homolog precursor (grp94 homolog) { <i>Catharanthus roseus</i> }□SP P35016 ENPL_CATRO ENDOPLASMIN	8	0.7756448
106	TC35794: GDP dissociation inhibitor { <i>Cicer arietinum</i> }□GP 3175990 emb CAA06731.1 AJ005836 GDP dissociation in	8	0.7756448
107	TC35797: dTDP-glucose 4-6-dehydratase homolog D18 { <i>Arabidopsis thaliana</i> }□PIR T48072 T48072 dTDP-glucose 4-6-d	8	0.7756448
108	TC28290: contains similarity to receptor protein kinase-gene_id:MLD14.4 { <i>Arabidopsis thaliana</i> }	8	0.7756448
109	TC32024: mitochondrial processing peptidase beta subunit { <i>Cucumis melo</i> }	8	0.7756448
110	TC35734: hydroxymethyltransferase { <i>Arabidopsis thaliana</i> }□GP 2244749 emb CAB10172.1 Z97335 hydroxymethyltrans	8	0.7756448
111	TC35740: isocitrate dehydrogenase (NADP), chloroplast precursor { <i>Medicago sativa</i> }□SP Q40345 IDHP_MEDSA ISOCIT	8	0.7756448
112	TC39371: Contains similarity to a basic endochitinase from <i>Arabidopsis thaliana</i> gb AB023448, and contains a Ch	8	0.7756448
113	TC39313: polyubiquitin(ubiquitin) {maize, Peptide, 533 aa} [Zea mays]□GP 248339 gb AAB21994.1 S94466 polyubi	8	0.7756448
114	TC35630: S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (EC 4.1.1.50) (ADOMETDC) (SAMDC) [CONTAINS: S-ADENOSYLM	8	0.7756448
115	TC28314: light harvesting protein { <i>Pisum sativum</i> }□GP 309673 gb AAA84545.1 L19651 light harvesting protein {P	8	0.7756448
116	TC31884: chlorophyll a/b-binding protein { <i>Pisum sativum</i> }□GP 20671 emb CAA49149.1 X69215 chlorophyll a/b-bind	8	0.7756448
117	TC39298: cell wall proline-rich protein	8	0.7756448
118	TC31885: chlorophyll a-b binding protein of lhci type ii precursor (cab-215) (lhcp) { <i>Pisum sativum</i> }□SP P2752	8	0.7756448
119	TC31882: photosystem ii p680 chlorophyll a apoprotein (cp-47 protein) { <i>Nicotiana tabacum</i> }□SP P06411 PSBB_TOBA	8	0.7756448
120	TC40245:	7	0.6786892
121	TC36546:	7	0.6786892

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122	TC36421: coatomer complex subunit, putative; 33791-27676 { <i>Arabidopsis thaliana</i> }□PIR G96563 G96563 probable co	7	0.6786892
123	TC28763: hypothetical protein { <i>Arabidopsis thaliana</i> }□PIR E84724 E84724 hypothetical protein At2g31740 [import	7	0.6786892
124	TC36277: basic chitinase { <i>Arabidopsis thaliana</i> }	7	0.6786892
125	TC32398: whitefly-induced gp91-phox { <i>Lycopersicon esculentum</i> }□GP 8131890 gb AAF73124.1 AF148534_1 AF148534 wh	7	0.6786892
126	TC36147: 2-oxoglutarate dehydrogenase, E1 subunit-like protein { <i>Arabidopsis thaliana</i> }□PIR T47680 T47680 proba	7	0.6786892
127	TC32477: polygalacturonase inhibitor-like protein { <i>Arabidopsis thaliana</i> }	7	0.6786892
128	TC28709: eukaryotic initiation factor 4, eIF4-like protein { <i>Arabidopsis thaliana</i> }	7	0.6786892
129	TC28721: ferulate-5-hydroxylase { <i>Populus balsamifera</i> subsp. <i>trichocarpa</i> }	7	0.6786892
130	TC28531: unknown { <i>Malus x domestica</i> }	7	0.6786892
131	TC39643: PROBABLE VACUOLAR ATP SYNTHASE SUBUNIT H (EC 3.6.1.34) (V-ATPASE H SUBUNIT) (VACUOLAR PROTON PUMP H	7	0.6786892
132	TC28597: VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (EC 3.6.1.34) (V-ATPASE A SUBUNIT) (VACUOLAR PROTON PUMP A	7	0.6786892
133	TC32230: contains ESTs AU032141(R3625),AU162501(R3625),AU108768(C50986)~similar to <i>Arabidopsis thaliana</i> chrom	7	0.6786892
134	TC28492: putative RNA-binding protein { <i>Arabidopsis thaliana</i> }□PIR T02113 T02113 probable RNA-binding protein A	7	0.6786892
135	TC39653: aconitate hydratase, cytoplasmic (aconitase) { <i>Cucurbita maxima</i> }□SP P49608 ACOC_CUCMA ACONITATE HYDRA	7	0.6786892
136	TC28374:	7	0.6786892
137	TC28513: delta-tonoplast intrinsic protein { <i>Gossypium hirsutum</i> }□GP 1439609 gb AAB04557.1 U62778 delta-tonopl	7	0.6786892
138	TC31997: unnamed protein product { <i>Brassica napus</i> }	7	0.6786892
139	TC39582: sucrose carrier { <i>Ricinus communis</i> }□GP 468562 emb CAA83436.1 Z31561 sucrose carrier { <i>Ricinus communi</i>	7	0.6786892
140	TC39600: nucleoid DNA-binding protein cnd41-like protein { <i>Arabidopsis thaliana</i> }□PIR T50786 T50786 nucleoid DN	7	0.6786892
141	TC35899: putative vacuolar proton-ATPase subunit 1 { <i>Arabidopsis thaliana</i> }□PIR H84600 H84600 probable vacuolar	7	0.6786892
142	TC32151: putative ubiquitin-conjugating enzyme { <i>Arabidopsis thaliana</i> }□PIR H84545 H84545 probable ubiquitin-co	7	0.6786892
143	TC32133: 26S proteasome p55 protein-like { <i>Arabidopsis thaliana</i> }□GP 14334434 gb AAK59415.1 AY034908 putative	7	0.6786892
144	TC35724: trans-cinnamate 4-monooxygenase 4-hydroxylase (ca4h) (p450c4h) { <i>Medicago sativa</i> }□SP P37114 TCMO_MED	7	0.6786892
145	TC39525: putative aminopeptidase; 4537-10989 { <i>Arabidopsis thaliana</i> }	7	0.6786892
146	TC32052: 60S ribosomal protein L1 { <i>Prunus armeniaca</i> }	7	0.6786892
147	TC39520: gene_id:K21H1.1~unknown protein { <i>Arabidopsis thaliana</i> }	7	0.6786892
148	TC32039: phospho-2-dehydro-3-deoxyheptonate aldolase 1 precursor (phospho-2-keto-3-deoxyheptonate aldolase 1)	7	0.6786892
149	TC39307: hexameric polyubiquitin { <i>Nicotiana glauca</i> }□GP 170352 gb AAA34123.1 M74101 hexameric polyubiquit	7	0.6786892
150	TC39288: cystathionine-gamma-synthase precursor { <i>Glycine max</i> }	7	0.6786892
151	TC39461: Putative histidine decarboxylase { <i>Arabidopsis thaliana</i> }□GP 13430642 gb AAK25943.1 AF360233_1 AF3602	7	0.6786892
152	TC31987: vacuolar ATP synthase subunit b isoform 1 subunit { <i>Gossypium hirsutum</i> }□SP Q43432 VAT1_GOSHI VACUOLA	7	0.6786892
153	TC35763: putative alanine aminotransferase; 91367-88744 { <i>Arabidopsis thaliana</i> }□GP 12325053 gb AAG52480.1 AC01	7	0.6786892

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154	TC39317: polyubiquitin(ubiquitin) {maize, Peptide, 533 aa} [Zea mays]□GP 248339 gb AAB21994.1 S94466 polyubi	7	0.6786892
155	TC35746: unknown protein {Arabidopsis thaliana}□PIR G84494 G84494 hypothetical protein At2g10940 [imported] -	7	0.6786892
156	TC39314: ubiquitin precursor - common sunflower (fragment)	7	0.6786892
157	TC39421: glucosyltransferase-like protein {Arabidopsis thaliana}	7	0.6786892
158	TC35600: S6 ribosomal protein {Asparagus officinalis}	7	0.6786892
159	TC35731: glutamine synthetase	7	0.6786892
160	TC35706: triosephosphate isomerase, cytosolic {Coptis japonica}□SP P21820 TPIS_COPJA TRIOSEPHOSPHATE ISOMERAS	7	0.6786892
161	TC39369:	7	0.6786892
162	TC40521: laccase {Liriodendron tulipifera}□GP 1621467 gb AAB17194.1 U73106 laccase {Liriodendron tulipifera}	6	0.5817336
163	TC29213: arbutin synthase {Rauvolfia serpentina}	6	0.5817336
164	TC29249:	6	0.5817336
165	TC40139:	6	0.5817336
166	TC36352: beta tubulin {Arabidopsis thaliana}	6	0.5817336
167	TC36379: CDPK-related kinase 1 {Arabidopsis thaliana}□GP 3402722 gb AAD12016.1 AC004261 CPDK-related protein	6	0.5817336
168	TC36390: CRYPTOCHROME 2 APOPROTEIN (BLUE LIGHT PHOTORECEPTOR). [Mouse-ear cress] {Arabidopsis thaliana}□GP 18	6	0.5817336
169	TC39948: lipoxygenase {Nicotiana tabacum}□GP 899344 emb CAA58859.1 X84040 lipoxygenase {Nicotiana tabacum}□P	6	0.5817336
170	TC28788:	6	0.5817336
171	TC28789: 4-alpha-glucanotransferase {Arabidopsis thaliana}□PIR T00748 T00748 4-alpha-glucanotransferase homol	6	0.5817336
172	TC39764: Identical to MEK kinase from Arabidopsis thaliana gb U58918 and contains protein kinase PF 00069 dom	6	0.5817336
173	TC32453: thiosulfate sulfurtransferase {Datisca glomerata}	6	0.5817336
174	TC35766: 60S acidic ribosomal protein p0 {Glycine max}□SP P50346 RLA0_SOYBN 60S ACIDIC RIBOSOMAL PROTEIN P0.	6	0.5817336
175	TC28643: protein transport protein Sec23 {Arabidopsis thaliana}	6	0.5817336
176	TC32370: phosphoethanolamine N-methyltransferase {Spinacia oleracea}	6	0.5817336
177	TC36067: Similar to beta-glucosidase BGQ60 precursor gb L41869 from Hordeum vulgare. {Arabidopsis thaliana}□P	6	0.5817336
178	TC36092: CYTOCHROME P450 98A2 (EC 1.14.-.-). [Soybean] {Glycine max}□GP 2738998 gb AAB94587.1 AF022458 CYP98	6	0.5817336
179	TC39780: pyrophosphatase {Vigna radiata}□PIR T10841 T10841 inorganic pyrophosphatase (EC 3.6.1.1) - mung bean	6	0.5817336
180	TC35931: unknown protein {Arabidopsis thaliana}□PIR D84453 D84453 hypothetical protein At2g03890 [imported] -	6	0.5817336
181	TC32290: serine palmitoyltransferase {Arabidopsis thaliana}	6	0.5817336
182	TC28436: NADH dehydrogenase {Arabidopsis thaliana}	6	0.5817336
183	TC39687: calcium dependent protein kinase {Vigna radiata}□PIR S71770 S71770 calcium-dependent protein kinase	6	0.5817336
184	TC31933: tubulin beta-1 subunit {Pisum sativum}□SP P29500 TBB1_PEA TUBULIN BETA-1 CHAIN. [Garden pea] {Pisum	6	0.5817336
185	TC35950: RNA helicase {Vigna radiata}	6	0.5817336

Supplemental Table II – Top 200 ESTs

186	TC39608: zinc metalloprotease (insulinase family) {Arabidopsis thaliana}	6	0.5817336
187	TC28477: putative protein {Arabidopsis thaliana}□GP 7268912 emb CAB79115.1 AL161554 putative protein {Arabid	6	0.5817336
188	TC39652: endo-beta-1,4-glucanase {Fragaria x ananassa}	6	0.5817336
189	TC39619: 26s protease regulatory subunit 6 homolog {Solanum tuberosum}□SP P54778 PRS6_SOLTU 26S PROTEASE REGU	6	0.5817336
190	TC28485: TUBULIN BETA CHAIN. [Rice] {Oryza sativa}□GP 493708 dbj BAA06381.1 D30716 beta-tubulin {Oryza sativ	6	0.5817336
191	TC28500: putative protein {Arabidopsis thaliana}□GP 7268555 emb CAB78805.1 AL161547 putative protein {Arabid	6	0.5817336
192	TC28313: Similar to dTDP-D-glucose 4,6-dehydratase {Arabidopsis thaliana}□GP 14596091 gb AAK68773.1 AY042833	6	0.5817336
193	TC28454: Hypothetical protein {Arabidopsis thaliana}□PIR C96597 C96597 Rubisco subunit binding-protein beta s	6	0.5817336
194	TC35901: AtSUG1 {Arabidopsis thaliana}	6	0.5817336
195	TC39513: T-COMPLEX PROTEIN 1, EPSILON SUBUNIT (TCP-1-EPSILON) (CCT-EPSILON). [Mouse-ear cress] {Arabidopsis t	6	0.5817336
196	TC28473: glycine dehydrogenase (decarboxylating) precursor (glycine decarboxylase) (glycine cleavage system p	6	0.5817336
197	TC39571: xylosidase {Arabidopsis thaliana}	6	0.5817336
198	TC39372: reversibly glycosylatable polypeptide {Pisum sativum}□GP 2130521 gb AAB88408.1 U31565 reversibly gl	6	0.5817336
199	TC39522: arbutin synthase {Rauvolfia serpentina}	6	0.5817336
200	TC35829: hypothetical protein {Arabidopsis thaliana}□PIR B84652 B84652 hypothetical protein At2g25740 [import	6	0.5817336

Supplemental Table II – Top 200 ESTs

	ROOTS	TC	Root	P(root)
		Total	72858	72858
		Singleton	9228	9228
		Counted	63630	63630
1	TC35566: leghemoglobin		380	5.9720258
2	TC39326: aquaporin		295	4.6361779
3	TC28324: elongation factor 1-alpha 1; EF-1-alpha1 {Lilium longiflorum}		292	4.5890303
4	TC39325: 5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.14) (VITAMIN-B12-IND		279	4.3847242
5	TC39277: PR10-1 protein		230	3.6146472
6	TC28337: elongation factor 1-alpha 1; EF-1-alpha1 {Lilium longiflorum}		223	3.5046362
7	TC39299: glyceraldehyde-3-phosphate dehydrogenase {Nicotiana tabacum}		207	3.2531825
8	TC28357: ascorbate peroxidase {Pisum sativum}□GP 20648 emb CAA43992.1 X62077 L-ascorbate peroxidase {Pisum s		203	3.190319
9	TC31853: S-adenosylmethionine synthetase {Brassica juncea}		198	3.1117397
10	TC39298: cell wall proline-rich protein		190	2.9860129
11	TC35562: aquaporin-like transmembrane channel protein {Medicago sativa}□PIR T09260 T09260 aquaporin-like tran		186	2.9231495
12	TC39302: glyceraldehyde 3-phosphate dehydrogenase, cytosolic {Pisum sativum}□SP P34922 G3PC_PEA GLYCERALDEHYD		175	2.750275
13	TC31849: TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP). [Alfalfa] {Medicago sativa}□GP 1419685 emb		170	2.6716957
14	TC31865: aquaporin-like protein PIP2 [Medicago truncatula]		163	2.5616847
15	TC35561: plasma membrane integral protein ZmPIP2-7 {Zea mays}		155	2.4359579
16	TC31899: sucrose synthase		154	2.420242
17	TC35563: putative plasma membrane intrinsic protein {Pisum sativum}		151	2.3730945
18	TC31887: cationic peroxidase {Cicer arietinum}		146	2.2945152
19	TC39292: T3P18.7 {Arabidopsis thaliana}□PIR B96651 B96651 protein T3P18.7 [imported] - Arabidopsis thaliana		138	2.1687883
20	TC39348: enolase {Lupinus luteus}		132	2.0744932
21	TC35590: MtN12		125	1.9644822
22	TC31941: beta glucosidase-like protein [Medicago truncatula]		125	1.9644822
23	TC31862: S-adenosyl-L-methionine synthetase {Elaeagnus umbellata}		125	1.9644822
24	TC39291: fructose-bisphosphate aldolase, cytoplasmic isozyme 2 {Pisum sativum}□SP P46257 ALF2_PEA FRUCTOSE-BI		116	1.8230394
25	TC35681:		114	1.7916077

Supplemental Table II – Top 200 ESTs

26	TC39353: UDP-galactose-4-epimerase {Pisum sativum}□SP Q43070 GAE1_PEA UDP-GLUCOSE 4-EPIMERASE (EC 5.1.3.2) (G	113	1.7758919
27	TC39293: cysteine proteinase 15a precursor protein 15a {Pisum sativum}□SP P25804 CYSP_PEA CYSTEINE PROTEINAS	106	1.6658809
28	TC31924:	104	1.6344492
29	TC28387: adenine nucleotide translocator {Lupinus albus}	103	1.6187333
30	TC31908:	103	1.6187333
31	TC31894: phosphoglyceromutase {Mesembryanthemum crystallinum}□SP Q42908 PMGI_MESCR 2,3-BISPHOSPHOGLYCERATE-IN	101	1.5873016
32	TC31930: isoflavone reductase	98	1.540154
33	TC28338: ubiquitin conjugating enzyme E2 {Lycopersicon esculentum}	98	1.540154
34	TC35606: 14-3-3-like protein {Pisum sativum}	97	1.5244382
35	TC28321: hypothetical protein {Cicer arietinum}	95	1.4930064
36	TC39369:	93	1.4615747
37	TC35719: pathogen-inducible alpha-dioxygenase {Nicotiana attenuata}	91	1.430143
38	TC39381: AT4g27450/F27G19_50 {Arabidopsis thaliana}□GP 15028057 gb AAK76559.1 AY045885 unknown protein {Arab	89	1.3987113
39	TC31874: MtN22	85	1.3358479
40	TC39313: polyubiquitin(ubiquitin) {maize, Peptide, 533 aa} [Zea mays]□GP 248339 gb AAB21994.1 S94466 polyubi	83	1.3044162
41	TC31915: cysteine proteinase precursor {Phaseolus vulgaris}□PIR T12041 T12041 cysteine proteinase (EC 3.4.22.	81	1.2729844
42	TC39414: proline-rich 14 kDa protein {Phaseolus vulgaris}□GP 1420885 gb AAC49369.1 U34333 proline-rich 14 kD	80	1.2572686
43	TC35736: fructokinase {Beta vulgaris}□GP 1052973 gb AAA80675.1 U37838 fructokinase {Beta vulgaris}□PIR T1454	77	1.210121
44	TC28345: vcCyP {Vicia faba}□PIR T50770 T50770 peptidylprolyl isomerase (EC 5.2.1.8) vcCyP [similarity] - fava	76	1.1944052
45	TC39412: receptor-like protein kinase homolog RK20-1 {Phaseolus vulgaris}	74	1.1629734
46	TC28355: vcCyP {Vicia faba}□PIR T50770 T50770 peptidylprolyl isomerase (EC 5.2.1.8) vcCyP [similarity] - fava	73	1.1472576
47	TC35731: glutamine synthetase	73	1.1472576
48	TC39361: asparagine synthase (glutamine-hydrolysing) {Pisum sativum}□PIR S11443 AJPMN2 asparagine synthase (g	73	1.1472576
49	TC39417: ribosomal protein L9 (gibberellin-regulated protein ga) {Pisum sativum}□SP P30707 RL9_PEA 60S RIBOSO	73	1.1472576
50	TC35613: type 1 metallothionein {Medicago sativa}□GP 6164920 gb AAF04584.1 AF189766_1 AF189766 type 1 metallo	73	1.1472576
51	TC32012: early nodule-specific protein	72	1.1315417
52	TC39319: extensin-like protein {Vigna unguiculata}□GP 791146 emb CAA60020.1 X86028 extensin-like protein {Vi	72	1.1315417
53	TC35676: ATP synthase beta subunit, mitochondrial precursor {Zea mays}□SP P19023 ATP2_MAIZE ATP SYNTHASE BETA	72	1.1315417
54	TC39415: zinc finger transcription factor-like protein {Arabidopsis thaliana}	70	1.10011
55	TC28359: S-adenosyl-L-homocystein hydrolase; SAH {Mesembryanthemum crystallinum}□SP P93253 SAHH_MESCR ADENOSY	70	1.10011
56	TC31937: Sali3-2 {Glycine max}□GP 2317900 gb AAB66369.1 U89693 Sali3-2 {Glycine max}□PIR T08896 T08896 Sali3	69	1.0843942
57	TC39429: cytochrome P450 {Cicer arietinum}	68	1.0686783

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58	TC31871: aba-responsive protein abr17 {Pisum sativum}□SP Q06931 AB17_PEA ABA-RESPONSIVE PROTEIN ABR17. [Garde	68	1.0686783
59	TC31978: SAH7 protein {Arabidopsis thaliana}	68	1.0686783
60	TC35710: putative Hs1pro-1 homolog {Pisum sativum}	68	1.0686783
61	TC35697: L3 Ribosomal protein {Medicago sativa subsp. x varia}	68	1.0686783
62	TC39335: peroxidase {Medicago sativa}□GP 537317 gb AAB41811.1 L36157 peroxidase {Medicago sativa}□PIR T09665	67	1.0529624
63	TC35600: S6 ribosomal protein {Asparagus officinalis}	66	1.0372466
64	TC31975:	66	1.0372466
65	TC35557: peroxidase {Glycine max}	65	1.0215307
66	TC31904: actin depolymerizing factor 1 (ADF1) {Arabidopsis thaliana}□GP 1408471 gb AAB03696.1 U48938 actin d	64	1.0058149
67	TC39421: glucosyltransferase-like protein {Arabidopsis thaliana}	64	1.0058149
68	TC31913: At1g56070/T6H22_13 {Arabidopsis thaliana}	64	1.0058149
69	TC28294: cytochrome P450 like_TBP {Nicotiana tabacum}□GP 1545805 dbj BAA10929.1 D64052 cytochrome P450 like_	62	0.9743832
70	TC39355: heat shock cognate protein 80 {Lycopersicon esculentum}□SP P36181 HS80_LYCES HEAT SHOCK COGNATE PROT	61	0.9586673
71	TC31958: 60S ribosomal protein L13a {Arabidopsis thaliana}	60	0.9429514
72	TC39423: putative ribosomal protein L19 {Arabidopsis thaliana}□GP 14423512 gb AAK62438.1 AF386993_1 AF386993	60	0.9429514
73	TC35593: VuP5CS {Vigna unguiculata}	60	0.9429514
74	TC39438:	59	0.9272356
75	TC35730: PNDKN1 {Pisum sativum}	59	0.9272356
76	TC31994: calmodulin {Daucus carota}□EGAD 125658 134028 calmodulin {Lilium longiflorum}□EGAD 125658 134029 cal	58	0.9115197
77	TC35686: 2,4-D inducible glutathione S-transferase {Glycine max}□PIR T06239 T06239 probable glutathione trans	57	0.8958039
78	TC35729: UDP-glucose dehydrogenase {Glycine max}□SP Q96558 UGDH_SOYBN UDP-GLUCOSE 6-DEHYDROGENASE (EC 1.1.1.2	56	0.880088
79	TC28318: adenosylhomocysteinase {Medicago sativa}□SP P50246 SAHH_MEDSA ADENOSYLHOMOCYSTEINASE (EC 3.3.1.1) (S	56	0.880088
80	TC35565: leghemoglobin {Medicago sativa}□PIR S21375 S21375 leghemoglobin - alfalfa	55	0.8643722
81	TC35788:	55	0.8643722
82	TC39449: putative 14-kDa proline-rich protein {Cicer arietinum}	55	0.8643722
83	TC32032: CPRD49 {Vigna unguiculata}	55	0.8643722
84	TC39339: peroxidase1B {Medicago sativa}□GP 971560 emb CAA62226.1 X90693 peroxidase1B {Medicago sativa}□PIR J	55	0.8643722
85	TC28331: lipoxygenase {Pisum sativum}□PIR T06827 T06827 lipoxygenase (EC 1.13.11.12) - garden pea	55	0.8643722
86	TC31935: tubulin beta-2 chain - garden pea (fragment)	55	0.8643722
87	TC35555: aquaporin 2 {Samanea saman}	55	0.8643722
88	TC35706: triosephosphate isomerase, cytosolic {Coptis japonica}□SP P21820 TPIS_COPJA TRIOSEPHOSPHATE ISOMERAS	55	0.8643722
89	TC31875: leghemoglobin	54	0.8486563

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90	TC31949: ripening related protein {Glycine max}	54	0.8486563
91	TC39409: KETOL-ACID REDUCTOISOMERASE PRECURSOR (EC 1.1.1.86) (ACETOHYDROXY-ACID REDUCTOISOMERASE) (ALPHA-KETO	54	0.8486563
92	TC39314: ubiquitin precursor - common sunflower (fragment)	53	0.8329404
93	TC28293: histone H3 variant H3.3 {Lycopersicon esculentum}□EGAD 131603 140441 histone H3 {Lolium temulentum}□	53	0.8329404
94	TC35677: nodulin 25ssnodulin 25 [Medicago truncatula]	52	0.8172246
95	TC35796: leghemoglobin 29 {Vicia faba}□SP P93848 LGB9_VICFA LEGHEMOGLOBIN 29. [Broad bean] {Vicia faba}□GP 15	52	0.8172246
96	TC35754:	52	0.8172246
97	TC39310: polyubiquitin(ubiquitin) {maize, Peptide, 533 aa} [Zea mays]□GP 248339 gb AAB21994.1 S94466 polyubi	52	0.8172246
98	TC35742: hypothetical protein {Citrus x paradisi}	52	0.8172246
99	TC35684: GTP-binding protein {Cicer arietinum}	52	0.8172246
100	TC31889: thiamin biosynthetic enzyme {Glycine max}	52	0.8172246
101	TC35696: adenosine kinase {Arabidopsis thaliana}□GP 7378610 emb CAB83286.1 AL162751 adenosine kinase-like pr	52	0.8172246
102	TC39330: acid phosphatase {Glycine max}□PIR T07086 T07086 acid phosphatase (EC 3.1.3.-) - soybean	52	0.8172246
103	TC32070: auxin down regulated {Glycine max}□EGAD 124785 158383 auxin down regulated {Glycine max}□GP 296445 e	51	0.8015087
104	TC39362: asparagine synthetase {Medicago sativa}	51	0.8015087
105	TC35611: type 1 metallothionein {Medicago sativa}□GP 6164920 gb AAF04584.1 AF189766_1 AF189766 type 1 metallo	51	0.8015087
106	TC39285:	50	0.7857929
107	TC35745: acetyl-CoA C-acetyltransferase {Arabidopsis thaliana}	50	0.7857929
108	TC28315: Carbonic anhydrase {Medicago sativa}□GP 1938227 emb CAA63712.1 X93312 Carbonic anhydrase {Medicago	49	0.770077
109	TC39358: 1-aminocyclopropane-1-carboxylate oxidase (acc oxidase) (ethylene- forming enzyme) (efe) {Pisum sati	49	0.770077
110	TC32015: ribosomal protein S8 {Oryza sativa}□SP P49199 RS8_ORYSA 40S RIBOSOMAL PROTEIN S8. [Rice] {Oryza sati	48	0.7543612
111	TC39395: 40S RIBOSOMAL PROTEIN S18. [Mouse-ear cress] {Arabidopsis thaliana}□GP 405613 emb CAA80684.1 Z23165	48	0.7543612
112	TC35744: isocitrate dehydrogenase (NAD+) {Solanum tuberosum}	48	0.7543612
113	TC35740: isocitrate dehydrogenase (NADP), chloroplast precursor {Medicago sativa}□SP Q40345 IDHP_MEDSA ISOCIT	48	0.7543612
114	TC35737: CYP83D1p {Glycine max}□PIR T05940 T05940 cytochrome P450 83D1p - soybean (fragment)	47	0.7386453
115	TC39442: B12D protein {Ipomoea batatas}	47	0.7386453
116	TC32003: 60S RIBOSOMAL PROTEIN L15. [Mouse-ear cress] {Arabidopsis thaliana}□GP 7268422 emb CAB78714.1 AL161	47	0.7386453
117	TC35620: ribosomal protein S4 {Arabidopsis thaliana}□PIR T48480 T48480 ribosomal protein S4 - Arabidopsis tha	47	0.7386453
118	TC31923: tubulin alpha subunit {Prunus dulcis}□SP P33629 TBA_PRUDU TUBULIN ALPHA CHAIN. [Almond, Prunus amygd	47	0.7386453
119	TC39366: cysteine protease {Pisum sativum}□GP 1134882 emb CAA92583.1 Z68291 cysteine protease {Pisum sativum	47	0.7386453
120	TC39443: chalcone--flavanone isomerase 1 {Medicago sativa}□SP P28012 CFI1_MEDSA CHALCONE--FLAVONONE ISOMERASE	46	0.7229294
121	TC35703: heat shock protein 70 {Cucumis sativus}	46	0.7229294

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122	TC35755: DnaJ-like protein {Medicago sativa}□GP 2370312 emb CAA04447.1 AJ000995 DnaJ-like protein {Medicago	46	0.7229294
123	TC39331: ubiquitin extension protein {Lupinus albus}□GP 438111 emb CAA80334.1 Z22613 ubiquitin extension pro	46	0.7229294
124	TC39370: ribosomal protein L33 {Castanea sativa}	46	0.7229294
125	TC35637: ADP-ribosylation factor {Oryza sativa}	46	0.7229294
126	TC32101: basic blue protein {Medicago sativa subsp. x varia}	45	0.7072136
127	TC32043: germin-like protein {Pisum sativum}	45	0.7072136
128	TC39462: unknown {Prunus armeniaca}	45	0.7072136
129	TC28291: 40S RIBOSOMAL PROTEIN S14. [Yellow lupine] {Lupinus luteus}□GP 2565340 gb AAB81972.1 AF026079 ribos	45	0.7072136
130	TC35636: ADP-ribosylation factor {Oryza sativa}□GP 1132483 dbj BAA04607.1 D17760 ADP-ribosylation factor {Or	45	0.7072136
131	TC39388: dehydrin-cognate {Pisum sativum}□GP 18375 emb CAA78515.1 Z14145 dehydrin-cognate {Pisum sativum}□PI	45	0.7072136
132	TC39407: b2 protein {Daucus carota}□SP P37707 B2_DAUCA B2 PROTEIN. [Carrot] {Daucus carota}□GP 297889 emb CAA	45	0.7072136
133	TC31886: initiation factor 5A-2 (EIF-5A) (EIF-4D) {Nicotiana plumbaginifolia}□SP P24922 IF52_NICPL INITIATION	45	0.7072136
134	TC35698: putative dTDP-glucose 4-6-dehydratase {Arabidopsis thaliana}□GP 13605497 gb AAK32742.1 AF361574_1 AF	45	0.7072136
135	TC32103: lectin-related polypeptide {Robinia pseudoacacia}	44	0.6914977
136	TC35581: MtN4	44	0.6914977
137	TC35787: glutamine synthetase	44	0.6914977
138	TC28373: EF-1 alpha {Oryza sativa}□GP 2662345 dbj BAA23659.1 D63582 EF-1 alpha {Oryza sativa}□GP 2662347 dbj	44	0.6914977
139	TC35693: cytosolic malate dehydrogenase {Cicer arietinum}	44	0.6914977
140	TC32007: protein disulfide isomerase precursor (pdi) diphosphooligosaccharide-protein glycotransferase (glyco	44	0.6914977
141	TC35741: S-adenosyl-L-methionine:trans-caffeoyl-CoA 3-O-methyltransferase {Medicago sativa}□GP 684942 gb AAC2	44	0.6914977
142	TC39371: Contains similarity to a basic endochitinase from Arabidopsis thaliana gb AB023448, and contains a Ch	44	0.6914977
143	TC35830:	43	0.6757819
144	TC39480: Putative ribosomal protein L19 {Arabidopsis thaliana}□PIR G86157 G86157 probable ribosomal protein L	43	0.6757819
145	TC35734: hydroxymethyltransferase {Arabidopsis thaliana}□GP 2244749 emb CAB10172.1 Z97335 hydroxymethyltrans	43	0.6757819
146	TC39447: gb AAD10646.1~gene_id:MRP15.12~strong similarity to unknown protein {Arabidopsis thaliana}	43	0.6757819
147	TC39295: single-stranded nucleic acid binding protein {Triticum aestivum}□GP 974605 gb AAA75104.1 U32310 sin	43	0.6757819
148	TC39431: elongation factor 1 beta' {Triticum aestivum}□PIR S35501 S35501 translation elongation factor eEF-1	43	0.6757819
149	TC35630: S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (EC 4.1.1.50) (ADOMETDC) (SAMDC) [CONTAINS: S-ADENOSYLM	43	0.6757819
150	TC32066: unknown protein {Arabidopsis thaliana}	42	0.660066
151	TC35756: 40S ribosomal protein S19 {Arabidopsis thaliana}	42	0.660066
152	TC31950: 40S ribosomal protein S2 homolog {Arabidopsis thaliana}□PIR T46185 T46185 ribosomal protein S2, cyto	42	0.660066
153	TC32006: sulfate adenylyltransferase {Solanum tuberosum}□GP 479090 emb CAA55655.1 X79053 sulfate adenylyltra	42	0.660066

Supplemental Table II – Top 200 ESTs

154	TC35726: malate oxidoreductase dependent malic enzyme) (NADP-me) {Vitis vinifera}□SP P51615 MAOX_VITVI NADP-D	42	0.660066
155	TC31918: proline oxidase precursor {Arabidopsis thaliana}	42	0.660066
156	TC32109: tonoplast intrinsic protein, root-specific rb7-5a (rt-tip) {Nicotiana tabacum}□SP P21653 TIP1_TOBAC	41	0.6443501
157	TC31864: unknown protein {Arabidopsis thaliana}□GP 14517502 gb AAK62641.1 AY039586 At2g38310/T19C21.20 {Arab	41	0.6443501
158	TC35709: ribosomal protein L11 (L5) {Medicago sativa}□SP P46287 RL11_MEDSA 60S RIBOSOMAL PROTEIN L11 (L5). [A	41	0.6443501
159	TC39410: 60S ribosomal protein L10 {Euphorbia esula}	41	0.6443501
160	TC35690: 40S ribosomal protein S9 {Arabidopsis thaliana}	41	0.6443501
161	TC35727: phenylalanine ammonia-lyase {Stylosanthes humilis}□SP P45732 PALY_STYHU PHENYLALANINE AMMONIA-LYASE	41	0.6443501
162	TC39430: Contains similarity to gb D13630 KIAA0005 gene from Homo sapiens. ESTs gb T45345, gb T21086, gb R90	41	0.6443501
163	TC31973: 40S RIBOSOMAL PROTEIN S11-ALPHA. [Mouse-ear cross] {Arabidopsis thaliana}□GP 6522573 emb CAB62017.1	40	0.6286343
164	TC39404: chalcone reductase {Medicago sativa}□GP 537298 gb AAB41556.1 U13925 chalcone reductase {Medicago sa	40	0.6286343
165	TC28366: ubiquitin conjugating protein {Avicennia marina}	40	0.6286343
166	TC32040: cytochrome P450-like {Arabidopsis thaliana}	40	0.6286343
167	TC39389:	40	0.6286343
168	TC39392: thaumatin-like protein PR-5b {Cicer arietinum}	40	0.6286343
169	TC39528:	39	0.6129184
170	TC39287: disease resistance response protein pi49 {Pisum sativum}□SP P14710 DRR3_PEA DISEASE RESISTANCE RESPO	39	0.6129184
171	TC32065: putative protein {Arabidopsis thaliana}□GP 6457331 gb AAF09479.1 AF188329_1 AF188329 phytoalexin-def	39	0.6129184
172	TC39444: 40S RIBOSOMAL PROTEIN SA (P40). [Chickpea, Garbanzo] {Cicer arietinum}□GP 3204099 emb CAA07226.1 AJ	39	0.6129184
173	TC39428: ankyrin-repeat protein HBP1 {Nicotiana tabacum}	39	0.6129184
174	TC28429: ENOD20	38	0.5972026
175	TC35803: NAD(p)h dependent 6'-deoxychalcone synthase {Glycine max}□SP P26690 6DCS_SOYBN NAD(P)H DEPENDENT 6'-	38	0.5972026
176	TC32029: putative protein {Arabidopsis thaliana}□GP 13605728 gb AAK32857.1 AF361845_1 AF361845 AT5g10860/T30N	38	0.5972026
177	TC35689: 40S ribosomal protein S9 {Arabidopsis thaliana}	38	0.5972026
178	TC39337: peroxidase1B {Medicago sativa}□GP 971560 emb CAA62226.1 X90693 peroxidase1B {Medicago sativa}□PIR J	37	0.5814867
179	TC32033: MtN5	37	0.5814867
180	TC35597: ribosomal protein S27 {Arabidopsis thaliana}□GP 4193382 gb AAD10029.1 AF083336 ribosomal protein S2	37	0.5814867
181	TC39356: cellulose synthase isolog {Arabidopsis thaliana}	37	0.5814867
182	TC32023: MAP kinase 3 {Pisum sativum}	37	0.5814867
183	TC35759: 6-phosphogluconate dehydrogenase {Medicago sativa}□GP 603221 gb AAB41553.1 U18239 6-phosphogluconat	37	0.5814867
184	TC28289: hydroxyproline-rich glycoprotein precursor {Phaseolus vulgaris}□GP 727264 gb AAA87902.1 U18791 hydr	37	0.5814867
185	TC35564: leghemoglobin {Medicago sativa}□SP P28010 LGB4_MEDSA LEGHEMOGLOBIN. [Alfalfa] {Medicago sativa}□GP 1	36	0.5657709

Supplemental Table II – Top 200 ESTs

186	TC35635: ADP-ribosylation factor {Capsicum annuum}□PIR T52339 T52339 ADP-ribosylation factor [imported] - pep	36	0.5657709
187	TC32051:	36	0.5657709
188	TC32094: mevalonate diphosphate decarboxylase {Arabidopsis thaliana}□GP 3250736 emb CAA76803.1 Y17593 mevalo	36	0.5657709
189	TC32069: putative 60S ribosomal protein L18 {Arabidopsis thaliana}□GP 14335090 gb AAK59824.1 AY037224 AT3g05	36	0.5657709
190	TC35791: unnamed protein product {unidentified}□GP 13899097 gb AAK48970.1 AF370543_1 AF370543 Unknown protein	36	0.5657709
191	TC35627: ribosomal protein L23 {Spinacia oleracea}	36	0.5657709
192	TC39448: RNA Binding Protein 45 {Nicotiana plumbaginifolia}	36	0.5657709
193	TC35875:	35	0.550055
194	TC28356: lipoxygenase {Vicia faba}□GP 2143422 emb CAA97845.1 Z73498 lipoxygenase {Vicia faba}□PIR T12142 T12	35	0.550055
195	TC32090: O-diphenol-O-methyl transferase {Medicago sativa subsp. x varia}	35	0.550055
196	TC35579: cell wall proline-rich protein	35	0.550055
197	TC35838: nucleotide sugar epimerase-like protein {Arabidopsis thaliana}□PIR A85356 A85356 nucleotide sugar ep	35	0.550055
198	TC31969: 60S ribosomal protein L21 {Oryza sativa}	35	0.550055
199	TC35801: Strong similarity to gb AF099906 J8 gene from Arabidopsis thaliana and contains PF 00226 DnaJ domain	35	0.550055
200	TC39289: calnexin {Glycine max}□SP Q39817 CALX_SOYBN CALNEXIN HOMOLOG PRECURSOR. [Soybean] {Glycine max}□GP 6	35	0.550055

Supplemental Table II – Top 200 ESTs

	FLOWERS	TC	Flower	P(flower)
		Total	3404	3404
		Singleton	442	442
		Counted	2962	2962
1	TC35571: lipoxygenase {Phaseolus vulgaris}□PIR T11852 T11852 lipoxygenase (EC 1.13.11.12) - kidney bean		18	6.076975
2	TC31882: photosystem ii p680 chlorophyll a apoprotein (cp-47 protein) {Nicotiana tabacum}□SP P06411 PSBB_TOBA		13	4.3889264
3	TC39330: acid phosphatase {Glycine max}□PIR T07086 T07086 acid phosphatase (EC 3.1.3.-) - soybean		12	4.0513167
4	TC35606: 14-3-3-like protein {Pisum sativum}		12	4.0513167
5	TC35767: Similar to Populus balsamifera subsp. trichocarpa X Populus deltoides vegetative storage protein. (L		11	3.713707
6	TC31981: ferredoxin i precursor {Pisum sativum}□SP P09911 FER1_PEA FERREDOXIN I PRECURSOR. [Garden pea] {Pisu		11	3.713707
7	TC39325: 5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.14) (VITAMIN-B12-IND		11	3.713707
8	TC39527: endoxyloglucan transferase {Cicer arietinum}		10	3.3760972
9	TC39386: pathogenesis-related protein 4A {Pisum sativum}		10	3.3760972
10	TC31975:		10	3.3760972
11	TC31960: plastocyanin precursor {Pisum sativum}□SP P16002 PLAS_PEA PLASTOCYANIN PRECURSOR. [Garden pea] {Pisu		10	3.3760972
12	TC39370: ribosomal protein L33 {Castanea sativa}		9	3.0384875
13	TC28337: elongation factor 1-alpha 1; EF-1-alpha1 {Lilium longiflorum}		9	3.0384875
14	TC28522:		8	2.7008778
15	TC31954: gene_id:MCO15.7~pir T04808~strong similarity to unknown protein {Arabidopsis thaliana}		8	2.7008778
16	TC39394: photosystem i reaction centre subunit ii precursor (photosystem i 20 kDa protein) (psi-d) (ps i subu		8	2.7008778
17	TC39365: glyceraldehyde 3-phosphate dehydrogenase a precursor, chloroplast {Pisum sativum}□SP P12858 G3PA_PEA		8	2.7008778
18	TC31887: cationic peroxidase {Cicer arietinum}		8	2.7008778
19	TC39302: glyceraldehyde 3-phosphate dehydrogenase, cytosolic {Pisum sativum}□SP P34922 G3PC_PEA GLYCERALDEHYD		8	2.7008778
20	TC35562: aquaporin-like transmembrane channel protein {Medicago sativa}□PIR T09260 T09260 aquaporin-like tran		8	2.7008778
21	TC31885: chlorophyll a-b binding protein of lhci type ii precursor (cab-215) (lhcp) {Pisum sativum}□SP P2752		8	2.7008778
22	TC39326: aquaporin		8	2.7008778
23	TC28295: RIBULOSE BIPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (EC 4.1.1.39) (RUBISCO SMALL SUBUNIT). [Alfa		8	2.7008778
24	TC31905: actin-depolymerizing factor 2 {Petunia x hybrida}□GP 14906210 gb AAK72616.1 AY038062 actin-depolyme		7	2.3632681
25	TC35689: 40S ribosomal protein S9 {Arabidopsis thaliana}		7	2.3632681

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26	TC35703: heat shock protein 70 {Cucumis sativus}	7	2.3632681
27	TC31961: photosystem ii reaction centre w protein precursor (psii 61 kDa protein) {Spinacia oleracea}□SP Q413	7	2.3632681
28	TC31923: tubulin alpha subunit {Prunus dulcis}□SP P33629 TBA_PRUDU TUBULIN ALPHA CHAIN. [Almond, Prunus amygd	7	2.3632681
29	TC31932: photosystem II 22 kDa protein precursor {Spinacia oleracea}□SP Q02060 PSBS_SPIOL PHOTOSYSTEM II 22 K	7	2.3632681
30	TC31888: oxygen-evolving enhancer protein 1 precursor (oeo1) (33 kDa subunit of oxygen evolving system of pho	7	2.3632681
31	TC28324: elongation factor 1-alpha 1; EF-1-alpha1 {Lilium longiflorum}	7	2.3632681
32	TC39387: NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP). [Chickpea, Garbanzo] {Cicer arietinum}□GP 263217	6	2.0256583
33	TC28509:	6	2.0256583
34	TC39613: histone H3 variant H3.3 {Lycopersicon esculentum}□EGAD 131603 140441 histone H3 {Lolium temulentum}□	6	2.0256583
35	TC39486: nascent polypeptide associated complex alpha chain, putative; 85450-84199 {Arabidopsis thaliana}□GP	6	2.0256583
36	TC35697: L3 Ribosomal protein {Medicago sativa subsp. x varia}	6	2.0256583
37	TC39381: AT4g27450/F27G19_50 {Arabidopsis thaliana}□GP 15028057 gb AAK76559.1 AY045885 unknown protein {Arab	6	2.0256583
38	TC31891: caffeic acid ortho-methyltransferase {Pinus radiata}	6	2.0256583
39	TC35877: ripening-related protein-like; contains similarity to pectinesterase {Arabidopsis thaliana}	5	1.6880486
40	TC35952:	5	1.6880486
41	TC39605: serine protease-like protein {Arabidopsis thaliana}	5	1.6880486
42	TC35814: beta-tubulin {Cicer arietinum}□SP Q39445 TBB_CICAR TUBULIN BETA CHAIN. [Chickpea, Garbanzo] {Cicer a	5	1.6880486
43	TC32064: chloroplast ribosomal protein L2 {Nicotiana tabacum}□SP P06379 RK2_TOBAC CHLOROPLAST 50S RIBOSOMAL P	5	1.6880486
44	TC39373: reversibly glycosylated polypeptide-2 (AtRGB) {Arabidopsis thaliana}□GP 14532444 gb AAK63950.1 AY03	5	1.6880486
45	TC28366: ubiquitin conjugating protein {Avicennia marina}	5	1.6880486
46	TC35627: ribosomal protein L23 {Spinacia oleracea}	5	1.6880486
47	TC35756: 40S ribosomal protein S19 {Arabidopsis thaliana}	5	1.6880486
48	TC39439: 60S ribosomal protein L6 {Cicer arietinum}	5	1.6880486
49	TC31935: tubulin beta-2 chain - garden pea (fragment)	5	1.6880486
50	TC28338: ubiquitin conjugating enzyme E2 {Lycopersicon esculentum}	5	1.6880486
51	TC39376: glycolate oxidase {Cucurbita sp.}□PIR T10242 T10242 (S)-2-hydroxy-acid oxidase (EC 1.1.3.15) - cucur	5	1.6880486
52	TC31915: cysteine proteinase precursor {Phaseolus vulgaris}□PIR T12041 T12041 cysteine proteinase (EC 3.4.22.	5	1.6880486
53	TC31884: chlorophyll a/b-binding protein {Pisum sativum}□GP 20671 emb CAA49149.1 X69215 chlorophyll a/b-bind	5	1.6880486
54	TC31865: aquaporin-like protein PIP2 [Medicago truncatula]	5	1.6880486
55	TC31849: TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP). [Alfalfa] {Medicago sativa}□GP 1419685 emb	5	1.6880486
56	TC28334: lipoxygenase {Pisum sativum}□GP 541746 emb CAA53730.1 X76124 lipoxygenase {Pisum sativum}□PIR S5665	5	1.6880486
57	TC31853: S-adenosylmethionine synthetase {Brassica juncea}	5	1.6880486

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58	TC31883: cytochrome B6 { <i>Lotus japonicus</i> }	5	1.6880486
59	TC35585: chlorophyll a/b binding protein { <i>Medicago sativa</i> }	5	1.6880486
60	TC28689: serine carboxypeptidase ii-2 precursor { <i>Hordeum vulgare</i> }□SP P55748 CP22_HORVU SERINE CARBOXYPEPTIDAS	4	1.3504389
61	TC32490: T23E23.17 { <i>Arabidopsis thaliana</i> }	4	1.3504389
62	TC36134: dehydrogenase-like protein { <i>Arabidopsis thaliana</i> }	4	1.3504389
63	TC35721: putative apyrase { <i>Medicago truncatula</i> }	4	1.3504389
64	TC39334: ubiquitin extension protein { <i>Lupinus albus</i> }□GP 438111 emb CAA80334.1 Z22613 ubiquitin extension pro	4	1.3504389
65	TC39628: histone H2A { <i>Euphorbia esula</i> }	4	1.3504389
66	TC32060: 60S RIBOSOMAL PROTEIN L37A. [Upland cotton] { <i>Gossypium hirsutum</i> }□GP 4741896 gb AAD28753.1 AF127042_1	4	1.3504389
67	TC35906: 40S ribosomal protein S16 { <i>Euphorbia esula</i> }	4	1.3504389
68	TC28328: poly(A)-binding protein { <i>Daucus carota</i> }	4	1.3504389
69	TC31995: GTP-BINDING PROTEIN SAR1A. [Mouse-ear cress] { <i>Arabidopsis thaliana</i> }□GP 7268592 emb CAB80701.1 AL161	4	1.3504389
70	TC39532: eukaryotic initiation factor 4a-10 (eif-4a-10) { <i>Nicotiana tabacum</i> }□SP P41382 IF4U_TOBAC EUKARYOTIC I	4	1.3504389
71	TC39584: putative expansin { <i>Arabidopsis thaliana</i> }□PIR C84444 C84444 probable expansin [imported] - Arabidopsi	4	1.3504389
72	TC35848: 40S ribosomal protein S25 { <i>Arabidopsis thaliana</i> }□GP 15081638 gb AAK82474.1 AY048211 At2g21580/F2G1.	4	1.3504389
73	TC39523: Identical to atranbp1a from <i>Arabidopsis thaliana</i> gb X97377. It contains a RanBP1 domain PF 00638.	4	1.3504389
74	TC31855: 40S ribosomal protein S3 { <i>Arabidopsis thaliana</i> }	4	1.3504389
75	TC39433: putative aspartic protease { <i>Ipomoea batatas</i> }	4	1.3504389
76	TC39437: putative 21kD protein precursor { <i>Medicago sativa</i> }□GP 1871577 emb CAA72315.1 Y11553 putative 21kD pr	4	1.3504389
77	TC39474: chloroplast triose phosphate translocator precursor (cptp) (p36) (e30) { <i>Pisum sativum</i> }□SP P21727 CPT	4	1.3504389
78	TC39395: 40S RIBOSOMAL PROTEIN S18. [Mouse-ear cress] { <i>Arabidopsis thaliana</i> }□GP 405613 emb CAA80684.1 Z23165	4	1.3504389
79	TC32003: 60S RIBOSOMAL PROTEIN L15. [Mouse-ear cress] { <i>Arabidopsis thaliana</i> }□GP 7268422 emb CAB78714.1 AL161	4	1.3504389
80	TC32020: photosystem I psaH protein { <i>Nicotiana sylvestris</i> }□GP 397555 emb CAA43841.1 X61664 photosystem I psa	4	1.3504389
81	TC35637: ADP-ribosylation factor { <i>Oryza sativa</i> }	4	1.3504389
82	TC39423: putative ribosomal protein L19 { <i>Arabidopsis thaliana</i> }□GP 14423512 gb AAK62438.1 AF386993_1 AF386993	4	1.3504389
83	TC35730: PNDKN1 { <i>Pisum sativum</i> }	4	1.3504389
84	TC39417: ribosomal protein L9 (gibberellin-regulated protein ga) { <i>Pisum sativum</i> }□SP P30707 RL9_PEA 60S RIBOSO	4	1.3504389
85	TC31918: proline oxidase precursor { <i>Arabidopsis thaliana</i> }	4	1.3504389
86	TC28293: histone H3 variant H3.3 { <i>Lycopersicon esculentum</i> }□EGAD 131603 140441 histone H3 { <i>Lolium temulentum</i> }□	4	1.3504389
87	TC35555: aquaporin 2 { <i>Samanea saman</i> }	4	1.3504389
88	TC35676: ATP synthase beta subunit, mitochondrial precursor { <i>Zea mays</i> }□SP P19023 ATP2_MAIZE ATP SYNTHASE BETA	4	1.3504389
89	TC39355: heat shock cognate protein 80 { <i>Lycopersicon esculentum</i> }□SP P36181 HS80_LYCES HEAT SHOCK COGNATE PROT	4	1.3504389

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90	TC28345: vcCyP { <i>Vicia faba</i> }□PIR T50770 T50770 peptidylprolyl isomerase (EC 5.2.1.8) vcCyP [similarity] - faba	4	1.3504389
91	TC39291: fructose-bisphosphate aldolase, cytoplasmic isozyme 2 { <i>Pisum sativum</i> }□SP P46257 ALF2_PEA FRUCTOSE-BI	4	1.3504389
92	TC39353: UDP-galactose-4-epimerase { <i>Pisum sativum</i> }□SP Q43070 GAE1_PEA UDP-GLUCOSE 4-EPIMERASE (EC 5.1.3.2) (G	4	1.3504389
93	TC39348: enolase { <i>Lupinus luteus</i> }	4	1.3504389
94	TC39299: glyceraldehyde-3-phosphate dehydrogenase { <i>Nicotiana tabacum</i> }	4	1.3504389
95	TC28357: ascorbate peroxidase { <i>Pisum sativum</i> }□GP 20648 emb CAA43992.1 X62077 L-ascorbate peroxidase { <i>Pisum s</i>	4	1.3504389
96	TC31942: non-cyanogenic beta-glucosidase precursor { <i>Trifolium repens</i> }□SP P26204 BGLS_TRIRP NON-CYANOGENIC BET	3	1.0128292
97	TC33978: Is a member of the PF 00955 Anion exchanger family. { <i>Arabidopsis thaliana</i> }	3	1.0128292
98	TC34306: CEL I mismatch endonuclease { <i>Apium graveolens</i> }	3	1.0128292
99	TC28585: pectate lyase { <i>Fragaria x ananassa</i> }	3	1.0128292
100	TC32542: elicitor inducible chitinase Nt-SubE76 { <i>Nicotiana tabacum</i> }	3	1.0128292
101	TC35772: endo-xyloglucan transferase { <i>Vigna angularis</i> }□PIR A49539 A49539 xyloglucan endo-1,4-beta-D-glucanase	3	1.0128292
102	TC40805:	3	1.0128292
103	TC29385: CYTOCHROME P450 77A3 (EC 1.14.-.-). [Soybean] { <i>Glycine max</i> }□GP 2739010 gb AAB94593.1 AF022464 CYP77	3	1.0128292
104	TC28380: unknown protein; 7482-9019 { <i>Arabidopsis thaliana</i> }□GP 14517393 gb AAK62587.1 AY039531 At1g75110/F9E1	3	1.0128292
105	TC32925: unknown protein { <i>Arabidopsis thaliana</i> }	3	1.0128292
106	TC36614: putative chloroplast initiation factor 3 { <i>Arabidopsis thaliana</i> }□PIR B84632 B84632 probable chloropla	3	1.0128292
107	TC39385: NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP). [Chickpea, Garbanzo] { <i>Cicer arietinum</i> }□GP 263217	3	1.0128292
108	TC29135: xyloglucan endotransglycosylase 1 { <i>Fagus sylvatica</i> }	3	1.0128292
109	TC36532: 60S ribosomal protein L37, putative; 56921-57860 { <i>Arabidopsis thaliana</i> }□GP 13877907 gb AAK44031.1 AF	3	1.0128292
110	TC40188: F22C12.5 { <i>Arabidopsis thaliana</i> }	3	1.0128292
111	TC29030: predicted protein of unknown function { <i>Arabidopsis thaliana</i> }□GP 4982479 gb AAD36947.1 AF069441_7 AF0	3	1.0128292
112	TC32672: stearoyl-acyl carrier protein desaturase { <i>Glycine max</i> }□SP Q42807 STAD_SOYBN ACYL-[ACYL-CARRIER PROTE	3	1.0128292
113	TC36357: unknown protein { <i>Arabidopsis thaliana</i> }□PIR E84812 E84812 hypothetical protein At2g39050 [imported] -	3	1.0128292
114	TC32577: H ⁺ -ATPase	3	1.0128292
115	TC32583: contains similarity to unknown protein~gb AAF35411.1~gene_id:F5N5.2 { <i>Arabidopsis thaliana</i> }	3	1.0128292
116	TC36251: annexin { <i>Medicago truncatula</i> }	3	1.0128292
117	TC40031: SBT1 { <i>Lycopersicon esculentum</i> }□GP 3687305 emb CAA06999.1 AJ006378 subtilisin-like protease { <i>Lycoper</i>	3	1.0128292
118	TC32561: homeobox-leucine zipper protein ATHB-12 { <i>Arabidopsis thaliana</i> }□PIR T47981 T47981 homeobox-leucine zi	3	1.0128292
119	TC36224: putative alpha7 proteasome subunit { <i>Nicotiana tabacum</i> }	3	1.0128292
120	TC36234: unknown protein { <i>Arabidopsis thaliana</i> }	3	1.0128292
121	TC39984: cytochrome P450, putative { <i>Arabidopsis thaliana</i> }□PIR F86441 F86441 probable cytochrome P450 [importe	3	1.0128292

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122	TC32509: putative ribonucleoprotein { <i>Arabidopsis thaliana</i> }□GP 3924594 gb AAC79095.1 AF069442 putative ribonu	3	1.0128292
123	TC36144: similar to wpk4 protein kinase { <i>Arabidopsis thaliana</i> }	3	1.0128292
124	TC39923: T7N9.14 { <i>Arabidopsis thaliana</i> }□PIR E86397 E86397 protein T7N9.14 [imported] - <i>Arabidopsis thaliana</i>	3	1.0128292
125	TC28717: putative protein { <i>Arabidopsis thaliana</i> }□GP 7269622 emb CAB81418.1 AL161571 putative protein { <i>Arabid</i>	3	1.0128292
126	TC28643: protein transport protein Sec23 { <i>Arabidopsis thaliana</i> }	3	1.0128292
127	TC28654: 60S ribosomal protein L7 { <i>Arabidopsis thaliana</i> }□GP 14532552 gb AAK64004.1 AY039900 AT3g13580/K20M4_	3	1.0128292
128	TC28706: SUPEROXIDE DISMUTASE [CU-ZN], CHLOROPLAST PRECURSOR (EC 1.15.1.1). [Alfalfa] { <i>Medicago sativa</i> }□GP 30	3	1.0128292
129	TC32424: unknown protein { <i>Arabidopsis thaliana</i> }	3	1.0128292
130	TC39781: unknown protein { <i>Arabidopsis thaliana</i> }□GP 14532908 gb AAK64136.1 AY040078 unknown protein { <i>Arabidop</i>	3	1.0128292
131	TC32075: ribosomal protein L27 homolog { <i>Pisum sativum</i> }□PIR T06426 T06426 ribosomal protein L27 - garden pea	3	1.0128292
132	TC32362: ESTs gb N38288.gb T43486.gb AA395242 come from this gene. { <i>Arabidopsis thaliana</i> }□GP 13878003 gb AAK4	3	1.0128292
133	TC36097: peroxidase { <i>Medicago sativa</i> }□GP 537319 gb AAB41812.1 L36158 peroxidase { <i>Medicago sativa</i> }□PIR T09667	3	1.0128292
134	TC28651: hypothetical protein { <i>Lotus japonicus</i> }	3	1.0128292
135	TC39312: ubiquitin precursor - common sunflower (fragment)	3	1.0128292
136	TC28611: putative DNA-binding protein { <i>Arabidopsis thaliana</i> }□GP 13878167 gb AAK44161.1 AF370346_1 AF370346 pu	3	1.0128292
137	TC32246: putative xyloglucan endotransglycosylase { <i>Arabidopsis thaliana</i> }□GP 4262149 gb AAD14449.1 AC005275 p	3	1.0128292
138	TC39733: ribosomal protein L34 { <i>Pisum sativum</i> }□SP P40590 RL34_PEA 60S RIBOSOMAL PROTEIN L34. [Garden pea] {Pi	3	1.0128292
139	TC32314: hydroxyproline-rich glycoprotein { <i>Arabidopsis thaliana</i> }	3	1.0128292
140	TC28523: non-cyanogenic beta-glucosidase precursor (<i>Trifolium repens</i>)□SP P26204 BGLS_TRIRP NON-CYANOGENIC BET	3	1.0128292
141	TC32059: 60S RIBOSOMAL PROTEIN L37A. [Upland cotton] { <i>Gossypium hirsutum</i> }□GP 4741896 gb AAD28753.1 AF127042_1	3	1.0128292
142	TC36017: unknown protein { <i>Arabidopsis thaliana</i> }□PIR F84788 F84788 hypothetical protein At2g37110 [imported] -	3	1.0128292
143	TC32281: ribosomal protein S27 { <i>Arabidopsis thaliana</i> }□GP 4193382 gb AAD10029.1 AF083336 ribosomal protein S2	3	1.0128292
144	TC35975: osmotin-like protein precursor { <i>Lycopersicon esculentum</i> }□SP Q41350 OLP1_LYCES OSMOTIN-LIKE PROTEIN P	3	1.0128292
145	TC28528: putative vacuolar proton-ATPase 16 kDa proteolipid { <i>Arabidopsis thaliana</i> }□PIR E84650 E84650 hypothet	3	1.0128292
146	TC35857: vesicle-associated membrane protein 7B; synaptobrevin 7B { <i>Arabidopsis thaliana</i> }	3	1.0128292
147	TC39418: putative 60S ribosomal protein L10A { <i>Arabidopsis thaliana</i> }	3	1.0128292
148	TC39602: proline-rich protein { <i>Phaseolus vulgaris</i> }□GP 21046 emb CAA42942.1 X60391 proline-rich protein { <i>Phas</i>	3	1.0128292
149	TC32159: chloroplast outer envelope protein 34 { <i>Pisum sativum</i> }□GP 510190 emb CAA82196.1 Z28341 chloroplast o	3	1.0128292
150	TC35934: fatty acid 9-hydroperoxide lyase { <i>Cucumis melo</i> }	3	1.0128292
151	TC39632: putative homeodomain transcription factor { <i>Arabidopsis thaliana</i> }□PIR H84774 H84774 probable homeodom	3	1.0128292
152	TC32195: 26S proteasome beta subunit { <i>Spinacia oleracea</i> }□SP O24361 PRCE_SPIOL PROTEASOME EPSILON CHAIN PRECUR	3	1.0128292
153	TC35883: ATP synthase delta subunit, mitochondrial precursor (oligomycin sensitivity conferral protein) (oscp	3	1.0128292

Supplemental Table II – Top 200 ESTs

154	TC39595: EIL2 {Lycopersicon esculentum}	3	1.0128292
155	TC28455: AT5g62000/mtg10_20 {Arabidopsis thaliana}	3	1.0128292
156	TC35733: CPRD46 protein {Vigna unguiculata} □ GP 1853970 dbj BAA13542.1 D88122 CPRD46 protein {Vigna unguiculata}	3	1.0128292
157	TC39591:	3	1.0128292
158	TC35587: photosystem II type I chlorophyll a/b-binding protein {Glycine max} □ GP 506629 gb AAA50172.1 U01964	3	1.0128292
159	TC35839: unknown {Prunus armeniaca} □ PIR T51098 T51098 hypothetical protein p85RF [imported] - Prunus armeniaca	3	1.0128292
160	TC39561: putative RNA polymerase B transcription factor 3 {Arabidopsis thaliana} □ GP 12324314 gb AAG52123.1 AC	3	1.0128292
161	TC28433: omega-6 fatty acid desaturase, endoplasmic reticulum isozyme 2 {Glycine max} □ SP P48631 FD62_SOYBN OM	3	1.0128292
162	TC32130: Putative membrane related protein {Arabidopsis thaliana} □ PIR D96670 D96670 probable membrane related	3	1.0128292
163	TC32124: Cu/Zn-superoxide dismutase {Pisum sativum} □ PIR T06570 T06570 superoxide dismutase (EC 1.15.1.1) (Cu-	3	1.0128292
164	TC39535: gb AAF27127.1~gene_id:T6J22.19~similar to unknown protein {Arabidopsis thaliana}	3	1.0128292
165	TC32014: ribosomal protein S26 {Pisum sativum} □ PIR T50822 T50822 ribosomal protein S26, cytosolic [imported]	3	1.0128292
166	TC39521: pyrophosphate--fructose 6-phosphate 1-phosphotransferase alpha subunit (pfp) {Ricinus communis} □ SP Q	3	1.0128292
167	TC35716: calreticulin {Ricinus communis} □ EGAD 125720 134100 calreticulin {Ricinus communis} □ SP P93508 CRTC_RI	3	1.0128292
168	TC39501:	3	1.0128292
169	TC32042: nodulin homologous to narbonin {Vicia faba} □ GP 1143617 emb CAA87009.1 Z46911 nodulin homologous to	3	1.0128292
170	TC32100: endoplasmic homolog precursor (grp94 homolog) {Catharanthus roseus} □ SP P35016 ENPL_CATRO ENDOPLASMIN	3	1.0128292
171	TC39289: calnexin {Glycine max} □ SP Q39817 CALX_SOYBN CALNEXIN HOMOLOG PRECURSOR. [Soybean] {Glycine max} □ GP 6	3	1.0128292
172	TC28363: 40S ribosomal protein S7 homolog, putative {Arabidopsis thaliana} □ GP 12597817 gb AAG60128.1 AC073555	3	1.0128292
173	TC35824: 40S RIBOSOMAL PROTEIN S15. [Mouse-ear cress] {Arabidopsis thaliana} □ GP 313152 emb CAA80679.1 Z23161	3	1.0128292
174	TC35801: Strong similarity to gb AF099906 J8 gene from Arabidopsis thaliana and contains PF 00226 DnaJ domain	3	1.0128292
175	TC32069: putative 60S ribosomal protein L18 {Arabidopsis thaliana} □ GP 14335090 gb AAK59824.1 AY037224 AT3g05	3	1.0128292
176	TC35597: ribosomal protein S27 {Arabidopsis thaliana} □ GP 4193382 gb AAD10029.1 AF083336 ribosomal protein S2	3	1.0128292
177	TC39469: chaperonin precursor {Pisum sativum} □ SP P08927 RUBB_PEA RUBISCO SUBUNIT BINDING-PROTEIN BETA SUBUNIT	3	1.0128292
178	TC35791: unnamed protein product {unidentified} □ GP 13899097 gb AAK48970.1 AF370543_1 AF370543 Unknown protein	3	1.0128292
179	TC39475: Lhcb4:3 protein {Arabidopsis thaliana} □ GP 4895259 gb AAD32843.1 AC007658_2 AC007658 putative chlorop	3	1.0128292
180	TC32054: FtsH-like protein Pff precursor {Nicotiana tabacum}	3	1.0128292
181	TC35758: 60S RIBOSOMAL PROTEIN L5. [Mouse-ear cress] {Arabidopsis thaliana} □ GP 10177974 dbj BAB11380.1 AB016	3	1.0128292
182	TC39455: granule-bound glycogen (starch) synthase {Astragalus membranaceus}	3	1.0128292
183	TC31950: 40S ribosomal protein S2 homolog {Arabidopsis thaliana} □ PIR T46185 T46185 ribosomal protein S2, cyto	3	1.0128292
184	TC35776: hypothetical protein {Arabidopsis thaliana} □ GP 2191138 gb AAB61025.1 AF007269 A_IG002N01.18 gene pr	3	1.0128292
185	TC39444: 40S RIBOSOMAL PROTEIN SA (P40). [Chickpea, Garbanzo] {Cicer arietinum} □ GP 3204099 emb CAA07226.1 AJ	3	1.0128292

Supplemental Table II – Top 200 ESTs

186	TC32007: protein disulfide isomerase precursor (pdi) diphosphooligosaccharide-protein glycotransferase (glyco	3	1.0128292
187	TC35742: hypothetical protein {Citrus x paradisi}	3	1.0128292
188	TC39371: Contains similarity to a basic endochitinase from Arabidopsis thaliana gb AB023448, and contains a Ch	3	1.0128292
189	TC28287: lipoxygenase {Pisum sativum}□PIR T06827 T06827 lipoxygenase (EC 1.13.11.12) - garden pea	3	1.0128292
190	TC31958: 60S ribosomal protein L13a {Arabidopsis thaliana}	3	1.0128292
191	TC35600: S6 ribosomal protein {Asparagus officinalis}	3	1.0128292
192	TC39361: asparagine synthase (glutamine-hydrolysing) {Pisum sativum}□PIR S11443 AJPMN2 asparagine synthase (g	3	1.0128292
193	TC35698: putative dTDP-glucose 4-6-dehydratase {Arabidopsis thaliana}□GP 13605497 gb AAK32742.1 AF361574_1 AF	3	1.0128292
194	TC39369:	3	1.0128292
195	TC35696: adenosine kinase {Arabidopsis thaliana}□GP 7378610 emb CAB83286.1 AL162751 adenosine kinase-like pr	3	1.0128292
196	TC35630: S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (EC 4.1.1.50) (ADOMETDC) (SAMDC) [CONTAINS: S-ADENOSYLM	3	1.0128292
197	TC28314: light harvesting protein {Pisum sativum}□GP 309673 gb AAA84545.1 L19651 light harvesting protein {P	3	1.0128292
198	TC35681:	3	1.0128292
199	TC39366: cysteine protease {Pisum sativum}□GP 1134882 emb CAA92583.1 Z68291 cysteine protease {Pisum sativum	3	1.0128292
200	TC31908:	3	1.0128292

Supplemental Table II – Top 200 ESTs

	SEED POD	TC	Seed-Pod	P(seed-pod)
		Total	4587	4587
		Singleton	484	484
		Counted	4103	4103
1	TC35639: glycinin {Glycine max}		96	20.92871158
2	TC35641: legumin (minor small) {Pisum sativum}□PIR T06453 T06453 probable legumin B - garden pea		54	11.77240026
3	TC35777: legumin a2 precursor {Pisum sativum}□SP P15838 LEG2_PEA LEGUMIN A2 PRECURSOR. [Garden pea] {Pisum sa		54	11.77240026
4	TC35640: legumin; legumin-related high molecular weight polypeptide {Vicia faba}□GP 403336 emb CAA81262.1 Z2		52	11.33638544
5	TC35672: vicilin 47kD protein {Pisum sativum}□GP 297170 emb CAA47814.1 X67429 vicilin 47kD protein {Pisum sa		49	10.6823632
6	TC35671: vicilin 47kD protein {Pisum sativum}□GP 297170 emb CAA47814.1 X67429 vicilin 47kD protein {Pisum sa		46	10.02834096
7	TC35825: convicilin {Pisum sativum}		45	9.810333551
8	TC35673: provicilin precursor {Pisum sativum}□SP P13918 VCLC_PEA VICILIN PRECURSOR. [Garden pea] {Pisum sativ		40	8.72029649
9	TC31882: photosystem ii p680 chlorophyll a apoprotein (cp-47 protein) {Nicotiana tabacum}□SP P06411 PSBB_TOBA		39	8.502289078
10	TC31887: cationic peroxidase {Cicer arietinum}		36	7.848266841
11	TC35922:		29	6.322214955
12	TC39325: 5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.14) (VITAMIN-B12-IND		29	6.322214955
13	TC35675: convicilin precursor {Vicia narbonensis}		25	5.450185306
14	TC32306: embryonic abundant protein precursor (clone usp lambda vf301) {Vicia faba}□SP P21745 EA30_VICFA EMBR		22	4.79616307
15	TC28324: elongation factor 1-alpha 1; EF-1-alpha1 {Lilium longiflorum}		20	4.360148245
16	TC31853: S-adenosylmethionine synthetase {Brassica juncea}		19	4.142140833
17	TC39862:		16	3.488118596
18	TC31908:		16	3.488118596
19	TC31877: nodulin		15	3.270111184
20	TC31879: nodulin {Medicago truncatula}□GP 437310 gb AAA62850.1 L23504 nodulin {Medicago truncatula}		14	3.052103772
21	TC35674: provicilin precursor {Pisum sativum}□SP P13918 VCLC_PEA VICILIN PRECURSOR. [Garden pea] {Pisum sativ		14	3.052103772
22	TC31883: cytochrome B6 {Lotus japonicus}		14	3.052103772
23	TC31880: nodulin {Medicago truncatula}□GP 437310 gb AAA62850.1 L23504 nodulin {Medicago truncatula}		13	2.834096359
24	TC32501: putative oleosin protein {Arabidopsis thaliana}□PIR A84654 A84654 probable oleosin protein [imported		13	2.834096359
25	TC28651: hypothetical protein {Lotus japonicus}		12	2.616088947

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26	TC31862: S-adenosyl-L-methionine synthetase {Elaeagnus umbellata}	12	2.616088947
27	TC28337: elongation factor 1-alpha 1; EF-1-alpha1 {Lilium longiflorum}	12	2.616088947
28	TC39960:	11	2.398081535
29	TC39293: cysteine proteinase 15a precursor protein 15a {Pisum sativum}□SP P25804 CYSP_PEA CYSTEINE PROTEINAS	11	2.398081535
30	TC39348: enolase {Lupinus luteus}	11	2.398081535
31	TC35562: aquaporin-like transmembrane channel protein {Medicago sativa}□PIR T09260 T09260 aquaporin-like tran	11	2.398081535
32	TC32064: chloroplast ribosomal protein L2 {Nicotiana tabacum}□SP P06379 RK2_TOBAC CHLOROPLAST 50S RIBOSOMAL P	10	2.180074123
33	TC39317: polyubiquitin(ubiquitin) {maize, Peptide, 533 aa} [Zea mays]□GP 248339 gb AAB21994.1 S94466 polyubi	10	2.180074123
34	TC28318: adenosylhomocysteinase {Medicago sativa}□SP P50246 SAHH_MEDSA ADENOSYLHOMOCYSTEINASE (EC 3.3.1.1) (S	10	2.180074123
35	TC31917: germin-like protein {Pisum sativum}	9	1.96206671
36	TC35561: plasma membrane integral protein ZmPIP2-7 {Zea mays}	9	1.96206671
37	TC35585: chlorophyll a/b binding protein {Medicago sativa}	9	1.96206671
38	TC31878: nodulin {Medicago truncatula}□GP 437310 gb AAA62850.1 L23504 nodulin {Medicago truncatula}	8	1.744059298
39	TC31954: gene_id:MCO15.7~pir T04808~strong similarity to unknown protein {Arabidopsis thaliana}	8	1.744059298
40	TC28345: vcCyP {Vicia faba}□PIR T50770 T50770 peptidylprolyl isomerase (EC 5.2.1.8) vcCyP [similarity] - fava	8	1.744059298
41	TC39291: fructose-bisphosphate aldolase, cytoplasmic isozyme 2 {Pisum sativum}□SP P46257 ALF2_PEA FRUCTOSE-BI	8	1.744059298
42	TC39302: glyceraldehyde 3-phosphate dehydrogenase, cytosolic {Pisum sativum}□SP P34922 G3PC_PEA GLYCERALDEHYD	8	1.744059298
43	TC33035: lipoxygenase {Pisum sativum}	7	1.526051886
44	TC36678:	7	1.526051886
45	TC36775:	7	1.526051886
46	TC39898: Putative cytochrome P450 {Arabidopsis thaliana}□GP 14334810 gb AAK59583.1 AY035078 putative cytochr	7	1.526051886
47	TC28620: UDP-D-glucuronate carboxy-lyase {Pisum sativum}	7	1.526051886
48	TC35850: hypothetical protein {Arabidopsis thaliana}□PIR G84809 G84809 hypothetical protein At2g38820 [import	7	1.526051886
49	TC35846: carboxytransferase beta subunit {Lotus japonicus}	7	1.526051886
50	TC39510: methylenetetrahydrofolate reductase MTHFR2 {Arabidopsis thaliana}	7	1.526051886
51	TC39296: hydroxyproline rich glycoprotein PsHRGP1 {Pisum sativum}□PIR T06789 T06789 hydroxyproline-rich glyco	7	1.526051886
52	TC39358: 1-aminocyclopropane-1-carboxylate oxidase (acc oxidase) (ethylene- forming enzyme) (efe) {Pisum sati	7	1.526051886
53	TC32007: protein disulfide isomerase precursor (pdi) diphosphooligosaccharide-protein glycotransferase (glyco	7	1.526051886
54	TC31992: metallothionein - soybean	7	1.526051886
55	TC39371: Contains similarity to a basic endochitinase from Arabidopsis thaliana gb AB023448, and contains a Ch	7	1.526051886
56	TC39409: KETOL-ACID REDUCTOISOMERASE PRECURSOR (EC 1.1.1.86) (ACETOHYDROXY-ACID REDUCTOISOMERASE) (ALPHA-KETO	7	1.526051886
57	TC35697: L3 Ribosomal protein {Medicago sativa subsp. x varia}	7	1.526051886

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58	TC39364: oxygen-evolving enhancer protein 2 precursor (oee2) (23 kDa subunit of oxygen evolving system of pho	7	1.526051886
59	TC36920:	6	1.308044474
60	TC40650: putative GDSL-motif lipase/acylhydrolase {Arabidopsis thaliana}	6	1.308044474
61	TC28721: ferulate-5-hydroxylase {Populus balsamifera subsp. trichocarpa}	6	1.308044474
62	TC36086: diphenol oxidase {Nicotiana tabacum}□GP 4756886 emb CAB42313.1 A68085 unnamed protein product {unid	6	1.308044474
63	TC36057: PHENYLALANINE AMMONIA-LYASE 2 (EC 4.3.1.5). [Chickpea, Garbanzo] {Cicer arietinum}□GP 6433808 emb CA	6	1.308044474
64	TC28407: putative phytochelatin synthetase {Arabidopsis thaliana}□PIR T51392 T51392 probable phytochelatin sy	6	1.308044474
65	TC32031: vacuolar processing enzyme precursor b) {Vicia sativa}□SP P49044 VPE_VICSA VACUOLAR PROCESSING ENZYM	6	1.308044474
66	TC32045: anthranilate N-benzoyltransferase {Arabidopsis thaliana}	6	1.308044474
67	TC39435: Skp1 {Medicago sativa}	6	1.308044474
68	TC35741: S-adenosyl-L-methionine:trans-caffeoyl-CoA 3-O-methyltransferase {Medicago sativa}□GP 684942 gb AAC2	6	1.308044474
69	TC39376: glycolate oxidase {Cucurbita sp.}□PIR T10242 T10242 (S)-2-hydroxy-acid oxidase (EC 1.1.3.15) - cucur	6	1.308044474
70	TC31915: cysteine proteinase precursor {Phaseolus vulgaris}□PIR T12041 T12041 cysteine proteinase (EC 3.4.22.	6	1.308044474
71	TC28636: Sali3-2 {Glycine max}□GP 2317900 gb AAB66369.1 U89693 Sali3-2 {Glycine max}□PIR T08896 T08896 Sali3	5	1.090037061
72	TC29733:	5	1.090037061
73	TC35699: p24 oleosin isoform a (p89) {Glycine max}□SP P29530 OLE1_SOYBN P24 OLEOSIN ISOFORM A (P89). [Soybean	5	1.090037061
74	TC37004: emb CAB85555.1~gene_id:MZN1.2~similar to unknown protein {Arabidopsis thaliana}	5	1.090037061
75	TC40811: putative cytochrome P450 {Arabidopsis thaliana}□PIR T00404 T00404 probable cytochrome P450 At2g44890	5	1.090037061
76	TC40919:	5	1.090037061
77	TC40222: aquaporin 2 {Samanea saman}	5	1.090037061
78	TC36251: annexin {Medicago truncatula}	5	1.090037061
79	TC39884: CATIONIC PEROXIDASE 1 PRECURSOR (EC 1.11.1.7). [Peanut] {Arachis hypogaea}□GP 1491776 gb AAB06183.1	5	1.090037061
80	TC28600: PROTEASOME SUBUNIT ALPHA TYPE 5 (EC 3.4.99.46) (20S PROTEASOME ALPHA SUBUNIT E) (20S PROTEASOME SUBU	5	1.090037061
81	TC35963: hypothetical protein {Arabidopsis thaliana}□PIR G86459 G86459 hypothetical protein AAG26075.1 [impor	5	1.090037061
82	TC32249: SCARECROW like protein {Arabidopsis thaliana}□PIR C71441 C71441 probable SCARECROW - Arabidopsis tha	5	1.090037061
83	TC39621: putative bZIP DNA-binding protein {Capsicum chinense}	5	1.090037061
84	TC39594:	5	1.090037061
85	TC28398: UDP-glucose dehydrogenase {Glycine max}□SP Q96558 UGDH_SOYBN UDP-GLUCOSE 6-DEHYDROGENASE (EC 1.1.1.2	5	1.090037061
86	TC32085: F21M12.5 gene product {Arabidopsis thaliana}□PIR D86230 D86230 hypothetical protein [imported] - Ara	5	1.090037061
87	TC32039: phospho-2-dehydro-3-deoxyheptonate aldolase 1 precursor (phospho-2-keto-3-deoxyheptonate aldolase 1)	5	1.090037061
88	TC35695: MALATE DEHYDROGENASE, CYTOPLASMIC (EC 1.1.1.37). [Alfalfa] {Medicago sativa}□GP 2827082 gb AAB99756.	5	1.090037061
89	TC35700: myo-inositol-1-phosphate synthase {Glycine max}	5	1.090037061

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90	TC39455: granule-bound glycogen (starch) synthase {Astragalus membranaceus}	5	1.090037061
91	TC35734: hydroxymethyltransferase {Arabidopsis thaliana}□GP 2244749 emb CAB10172.1 Z97335 hydroxymethyltrans	5	1.090037061
92	TC39331: ubiquitin extension protein {Lupinus albus}□GP 438111 emb CAA80334.1 Z22613 ubiquitin extension pro	5	1.090037061
93	TC39426:	5	1.090037061
94	TC35729: UDP-glucose dehydrogenase {Glycine max}□SP Q96558 UGDH_SOYBN UDP-GLUCOSE 6-DEHYDROGENASE (EC 1.1.1.2	5	1.090037061
95	TC35555: aquaporin 2 {Samanea saman}	5	1.090037061
96	TC31923: tubulin alpha subunit {Prunus dulcis}□SP P33629 TBA_PRUDU TUBULIN ALPHA CHAIN. [Almond, Prunus amygd	5	1.090037061
97	TC35630: S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (EC 4.1.1.50) (ADOMETDC) (SAMDC) [CONTAINS: S-ADENOSYLM	5	1.090037061
98	TC39353: UDP-galactose-4-epimerase {Pisum sativum}□SP Q43070 GAE1_PEA UDP-GLUCOSE 4-EPIMERASE (EC 5.1.3.2) (G	5	1.090037061
99	TC39351: chlorophyll a/b-binding protein-like {Arabidopsis thaliana}□GP 7267731 emb CAB78157.1 AL161517 chlo	5	1.090037061
100	TC31849: TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP). [Alfalfa] {Medicago sativa}□GP 1419685 emb	5	1.090037061
101	TC31885: chlorophyll a-b binding protein of lhci type ii precursor (cab-215) (lhcp) {Pisum sativum}□SP P2752	5	1.090037061
102	TC28403: light harvesting protein {Pisum sativum}□GP 309673 gb AAA84545.1 L19651 light harvesting protein {P	4	0.872029649
103	TC29849: dessication-related protein, putative; 70055-71849 {Arabidopsis thaliana}□PIR B96520 B96520 hypothet	4	0.872029649
104	TC30166: BURP domain-containing protein {Bruguiera gymnorhiza}	4	0.872029649
105	TC33884:	4	0.872029649
106	TC35778: legumin A precursor {Vicia narbonensis}□PIR S49877 S49877 legumin A precursor - Vicia narbonensis	4	0.872029649
107	TC37356: CPRD2 {Vigna unguiculata}	4	0.872029649
108	TC39899: Putative cytochrome P450 {Arabidopsis thaliana}□GP 14334810 gb AAK59583.1 AY035078 putative cytochr	4	0.872029649
109	TC40581: hypothetical protein; 19613-17891 {Arabidopsis thaliana}□PIR G96708 G96708 hypothetical protein T26J	4	0.872029649
110	TC29463: peroxidase {Glycine max}	4	0.872029649
111	TC40684: apocytochrome f precursor {Vicia faba}□SP P06669 CYF_VICFA APOCYTOCHROME F PRECURSOR. [Broad bean] {	4	0.872029649
112	TC28587: pectate lyase {Vitis vinifera}	4	0.872029649
113	TC36790: pectinacetylsterase precursor {Vigna radiata}□PIR S68805 S68805 pectin acetylsterase (EC 3.1.1.-)	4	0.872029649
114	TC40464: F28K19.27 {Arabidopsis thaliana}	4	0.872029649
115	TC40476:	4	0.872029649
116	TC28945: fructokinase, putative {Arabidopsis thaliana}□GP 12324405 gb AAG52172.1 AC020665_17 AC020665 fructok	4	0.872029649
117	TC32694: cysteine proteinase (EC 3.4.22.-) - kidney bean	4	0.872029649
118	TC36314: putative myosin heavy chain {Arabidopsis thaliana}□PIR F84730 F84730 probable myosin heavy chain [im	4	0.872029649
119	TC32141: acyl carrier protein {Casuarina glauca}□GP 1838961 emb CAA71885.1 Y10994 acyl carrier protein {Casu	4	0.872029649
120	TC36266: hypothetical protein {Pisum sativum}□SP P12227 RPOD_PEA DNA-DIRECTED RNA POLYMERASE BETA' CHAIN (EC	4	0.872029649
121	TC39962: cellulose synthase {Gossypium hirsutum}□GP 1706958 gb AAB37767.1 U58284 cellulose synthase {Gossypi	4	0.872029649

Supplemental Table II – Top 200 ESTs

122	TC35853: putative extracellular dermal glycoprotein {Cicer arietinum}	4	0.872029649
123	TC36151: flavanone 3 beta-hydroxylase - garden petunia (fragment)	4	0.872029649
124	TC36160:	4	0.872029649
125	TC31861: S-adenosyl-L-methionine synthetase 1 {Catharanthus roseus}□SP Q96551 METK_CATRO S-ADENOSYLMETHIONINE	4	0.872029649
126	TC32262: hypothetical protein {Cicer arietinum}	4	0.872029649
127	TC31898: sucrose synthase isoform 3 {Pisum sativum}	4	0.872029649
128	TC28454: Hypothetical protein {Arabidopsis thaliana}□PIR C96597 C96597 Rubisco subunit binding-protein beta s	4	0.872029649
129	TC32205: putative glutamate decarboxylase {Arabidopsis thaliana}□GP 13605710 gb AAK32848.1 AF361836_1 AF36183	4	0.872029649
130	TC35885: calmodulin {Glycine max}□EGAD 125651 134022 calmodulin {Glycine max}□GP 170070 gb AAA34013.1 L01430	4	0.872029649
131	TC39589:	4	0.872029649
132	TC35595: S6 ribosomal protein {Asparagus officinalis}	4	0.872029649
133	TC35812: sugar epimerase BlmG {Streptomyces verticillus}	4	0.872029649
134	TC28415:	4	0.872029649
135	TC32117: beta-glucosidase {Polygonum tinctorium}	4	0.872029649
136	TC31996: GTP-BINDING PROTEIN SAR1A. [Mouse-ear cross] {Arabidopsis thaliana}□GP 7268592 emb CAB80701.1 AL161	4	0.872029649
137	TC32084: Putative GSH-dependent dehydroascorbate reductase {Arabidopsis thaliana}□GP 14517510 gb AAK62645.1	4	0.872029649
138	TC35810:	4	0.872029649
139	TC31952: similar to ribosomal protein S2 {Arabidopsis thaliana}□PIR T52466 T52466 hypothetical protein RF12 [4	0.872029649
140	TC32025: G protein beta subunit-like {Medicago sativa}□SP O24076 GBLP_MEDSA GUANINE NUCLEOTIDE-BINDING PROTEI	4	0.872029649
141	TC39447: gb AAD10646.1~gene_id:MRP15.12~strong similarity to unknown protein {Arabidopsis thaliana}	4	0.872029649
142	TC35690: 40S ribosomal protein S9 {Arabidopsis thaliana}	4	0.872029649
143	TC35752: poly(A)-binding protein {Cucumis sativus}	4	0.872029649
144	TC28336: chlorophyll a/b binding protein CP29 {Vigna radiata}	4	0.872029649
145	TC32005: ATP synthase a subunit precursor {Pisum sativum}□SP P06452 ATPI_PEA ATP SYNTHASE A CHAIN PRECURSOR (4	0.872029649
146	TC35726: malate oxidoreductase dependent malic enzyme) (NADP-me) {Vitis vinifera}□SP P51615 MAOX_VITVI NADP-D	4	0.872029649
147	TC39427: UTP--GLUCOSE-1-PHOSPHATE URIDYLTRANSFERASE (EC 2.7.7.9) (UDP-GLUCOSE PYROPHOSPHORYLASE) (UDPGP) (U	4	0.872029649
148	TC35684: GTP-binding protein {Cicer arietinum}	4	0.872029649
149	TC39415: zinc finger transcription factor-like protein {Arabidopsis thaliana}	4	0.872029649
150	TC28359: S-adenosyl-L-homocystein hydrolase; SAH {Mesembryanthemum crystallinum}□SP P93253 SAHH_MESCR ADENOSY	4	0.872029649
151	TC39355: heat shock cognate protein 80 {Lycopersicon esculentum}□SP P36181 HS80_LYCES HEAT SHOCK COGNATE PROT	4	0.872029649
152	TC35696: adenosine kinase {Arabidopsis thaliana}□GP 7378610 emb CAB83286.1 AL162751 adenosine kinase-like pr	4	0.872029649
153	TC35686: 2,4-D inducible glutathione S-transferase {Glycine max}□PIR T06239 T06239 probable glutathione trans	4	0.872029649

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154	TC39299: glyceraldehyde-3-phosphate dehydrogenase {Nicotiana tabacum}	4	0.872029649
155	TC28357: ascorbate peroxidase {Pisum sativum}□GP 20648 emb CAA43992.1 X62077 L-ascorbate peroxidase {Pisum s	4	0.872029649
156	TC28295: RIBULOSE BIPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR (EC 4.1.1.39) (RUBISCO SMALL SUBUNIT). [Alfa	4	0.872029649
157	TC30341:	3	0.654022237
158	TC30602:	3	0.654022237
159	TC30670: gene_id:MNA5.1~unknown protein {Arabidopsis thaliana}	3	0.654022237
160	TC34089:	3	0.654022237
161	TC34210:	3	0.654022237
162	TC34346:	3	0.654022237
163	TC34352:	3	0.654022237
164	TC34425:	3	0.654022237
165	TC35572: seed lipoxygenase-3 {Pisum sativum}□SP P09918 LOX3_PEA SEED LIPOXYGENASE-3 (EC 1.13.11.12). [Garden	3	0.654022237
166	TC37398: putative protein {Arabidopsis thaliana}□PIR T48179 T48179 hypothetical protein F7A7.100 - Arabidopsi	3	0.654022237
167	TC37667: tonoplast intrinsic protein alpha - kidney bean	3	0.654022237
168	TC38045:	3	0.654022237
169	TC38138: unknown protein {Arabidopsis thaliana}□PIR D86405 D86405 unknown protein [imported] - Arabidopsis th	3	0.654022237
170	TC41508:	3	0.654022237
171	TC37380: gene_id:MWI23.5~unknown protein {Arabidopsis thaliana}	3	0.654022237
172	TC37435: P54 protein {Pisum sativum}□PIR T06459 T06459 62K sucrose-binding protein homolog - garden pea	3	0.654022237
173	TC37510: amine oxidase {Canavalia lineata}	3	0.654022237
174	TC33507:	3	0.654022237
175	TC35688: 2,4-D inducible glutathione S-transferase {Glycine max}□PIR T06239 T06239 probable glutathione trans	3	0.654022237
176	TC37005: putative tetracycline transporter protein {Arabidopsis thaliana}□PIR G84546 G84546 probable tetracyc	3	0.654022237
177	TC40506: epoxide hydrolase {Nicotiana tabacum}□GP 1354849 gb AAB02006.1 U57350 epoxide hydrolase {Nicotiana	3	0.654022237
178	TC40890: allergen Gly m Bd 28K {Glycine max}	3	0.654022237
179	TC29162: hypothetical protein {Arabidopsis thaliana}□PIR T00518 T00518 hypothetical protein At2g23140 [import	3	0.654022237
180	TC29581: UDP-glucuronyltransferase-like protein {Arabidopsis thaliana}	3	0.654022237
181	TC33136: Unknown protein {Arabidopsis thaliana}□PIR F96756 F96756 hypothetical protein F3N23.30 [imported] -	3	0.654022237
182	TC36885: putative protein {Arabidopsis thaliana}□PIR T45666 T45666 hypothetical protein F14P22.50 - Arabidops	3	0.654022237
183	TC40443: sucrolytic enzyme/ferredoxin homolog {Solanum tuberosum=potatoes, cv. Cara, leaf, Peptide, 322 aa}□P	3	0.654022237
184	TC28468: protein phosphatase type 2C {Lotus japonicus}	3	0.654022237
185	TC40192: knotted1-like homeobox protein {Malus domestica}□SP O04136 HKL3_MALDO HOMEBOX PROTEIN KNOTTED-1 LIK	3	0.654022237

Supplemental Table II – Top 200 ESTs

186	TC40407: putative protein {Arabidopsis thaliana}□GP 9758990 dbj BAB09517.1 AB020752 gb AAD14519.1~gene_id:MT	3	0.654022237
187	TC35728: phenylalanine ammonia-lyase {Medicago sativa}□SP P27990 PALY_MEDSA PHENYLALANINE AMMONIA-LYASE (EC 4	3	0.654022237
188	TC32747: hypothetical protein {Lotus japonicus}	3	0.654022237
189	TC36434: phosphatidylinositol transfer-like protein III {Lotus japonicus}	3	0.654022237
190	TC32601: alpha-galactosidase-like protein {Arabidopsis thaliana}	3	0.654022237
191	TC36362: contains similarity to unknown protein~gene_id:MDA7.1~pir T08924 {Arabidopsis thaliana}	3	0.654022237
192	TC39985: unknown protein {Arabidopsis thaliana}	3	0.654022237
193	TC39995: DNA-binding protein GBP16 {Oryza sativa}□PIR T02069 T02069 probable DNA-binding protein GBP16 - rice	3	0.654022237
194	TC39859: unknown protein {Arabidopsis thaliana}	3	0.654022237
195	TC28866: F1N21.10 {Arabidopsis thaliana}□PIR E96696 E96696 protein F1N21.10 [imported] - Arabidopsis thaliana	3	0.654022237
196	TC36194:	3	0.654022237
197	TC36215: methionine S-methyltransferase {Arabidopsis thaliana}	3	0.654022237
198	TC39559: histone h1 {Pisum sativum}□SP P08283 H1_PEA HISTONE H1. [Garden pea] {Pisum sativum}□GP 20762 emb CA	3	0.654022237
199	TC28426: putative protein {Arabidopsis thaliana}□GP 7268881 emb CAB79085.1 AL161553 putative protein {Arabid	3	0.654022237
200	TC32476: HYPOTHETICAL MO25-LIKE PROTEIN AT5G47540. [Mouse-ear cress] {Arabidopsis thaliana}□GP 9758782 dbj BA	3	0.654022237

Supplemental Table II – Top 200 ESTs

	CELL CULTURE	TC	Elicited_cell	P(cell)
		Total	8926	8926
		Singleton	1275	1275
		Counted	7651	7651
1	TC31847: chalcone synthase 8 {Medicago sativa}□SP P30076 CHS8_MEDSA CHALCONE SYNTHASE 8 (EC 2.3.1.74) (NARING		104	13.592994
2	TC39358: 1-aminocyclopropane-1-carboxylate oxidase (acc oxidase) (ethylene- forming enzyme) (efe) {Pisum sati		70	9.1491308
3	TC32021: patatin-like protein 1 {Nicotiana tabacum}		50	6.5350935
4	TC28324: elongation factor 1-alpha 1; EF-1-alpha1 {Lilium longiflorum}		40	5.2280748
5	TC35807: (+)-delta-cadinene synthase {Gossypium hirsutum}		38	4.966671
6	TC39404: chalcone reductase {Medicago sativa}□GP 537298 gb AAB41556.1 U13925 chalcone reductase {Medicago sa		38	4.966671
7	TC35574: putative chalcone synthase		36	4.7052673
8	TC39277: PR10-1 protein		35	4.5745654
9	TC35724: trans-cinnamate 4-monooxygenase 4-hydroxylase (ca4h) (p450c4h) {Medicago sativa}□SP P37114 TCMO_MED		31	4.0517579
10	TC39536: acidic glucanase {Medicago sativa}□GP 862931 gb AAB41551.1 U27179 acidic glucanase {Medicago sativa		30	3.9210561
11	TC39298: cell wall proline-rich protein		29	3.7903542
12	TC31854: chalcone synthase 2 {Medicago sativa}□SP P30074 CHS2_MEDSA CHALCONE SYNTHASE 2 (EC 2.3.1.74) (NARING		27	3.5289505
13	TC39287: disease resistance response protein pi49 {Pisum sativum}□SP P14710 DRR3_PEA DISEASE RESISTANCE RESPO		27	3.5289505
14	TC31930: isoflavone reductase		25	3.2675467
15	TC31853: S-adenosylmethionine synthetase {Brassica juncea}		23	3.006143
16	TC35837: unnamed protein product {unidentified}		21	2.7447392
17	TC39463:		21	2.7447392
18	TC31846: CHALCONE SYNTHASE 9 (EC 2.3.1.74) (NARINGENIN-CHALCONE SYNTHASE 9). [Alfalfa] {Medicago sativa}□GP 1		19	2.4833355
19	TC39292: T3P18.7 {Arabidopsis thaliana}□PIR B96651 B96651 protein T3P18.7 [imported] - Arabidopsis thaliana		19	2.4833355
20	TC28337: elongation factor 1-alpha 1; EF-1-alpha1 {Lilium longiflorum}		19	2.4833355
21	TC32033: MtN5		18	2.3526336
22	TC31979: EDGP precursor {Daucus carota}□GP 285741 dbj BAA03413.1 D14550 EDGP precursor {Daucus carota}□PIR T		17	2.2219318
23	TC32351: auxin-responsive GH3 product {Glycine max}□GP 18591 emb CAA42636.1 X60033 auxin-responsive GH3 prod		16	2.0912299
24	TC39755: heme activated protein {Arabidopsis thaliana}		16	2.0912299
25	TC28373: EF-1 alpha {Oryza sativa}□GP 2662345 dbj BAA23659.1 D63582 EF-1 alpha {Oryza sativa}□GP 2662347 dbj		16	2.0912299

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26	TC28357: ascorbate peroxidase {Pisum sativum}□GP 20648 emb CAA43992.1 X62077 L-ascorbate peroxidase {Pisum s	16	2.0912299
27	TC35576: CHALCONE SYNTHASE 4 (EC 2.3.1.74) (NARINGENIN-CHALCONE SYNTHASE 4) (CHS12-1). [Alfalfa] {Medicago sa	15	1.960528
28	TC35818: Similar to gb X77136 HSR203J protein from Nicotiana tabacum and is a member of the PF 00135 Carboxyl	15	1.960528
29	TC39437: putative 21kD protein precursor {Medicago sativa}□GP 1871577 emb CAA72315.1 Y11553 putative 21kD pr	15	1.960528
30	TC39443: chalcone--flavanone isomerase 1 {Medicago sativa}□SP P28012 CFI1_MEDSA CHALCONE--FLAVONONE ISOMERASE	15	1.960528
31	TC35737: CYP83D1p {Glycine max}□PIR T05940 T05940 cytochrome P450 83D1p - soybean (fragment)	15	1.960528
32	TC35727: phenylalanine ammonia-lyase {Stylosanthes humilis}□SP P45732 PALY_STYHU PHENYLALANINE AMMONIA-LYASE	15	1.960528
33	TC35710: putative Hs1pro-1 homolog {Pisum sativum}	15	1.960528
34	TC39366: cysteine protease {Pisum sativum}□GP 1134882 emb CAA92583.1 Z68291 cysteine protease {Pisum sativum}	15	1.960528
35	TC32218: putative protein {Arabidopsis thaliana}□PIR T08454 T08454 hypothetical protein F22O6.170 - Arabidops	14	1.8298262
36	TC28496: PR-1	14	1.8298262
37	TC31871: aba-responsive protein abr17 {Pisum sativum}□SP Q06931 AB17_PEA ABA-RESPONSIVE PROTEIN ABR17. [Garde	14	1.8298262
38	TC28293: histone H3 variant H3.3 {Lycopersicon esculentum}□EGAD 131603 140441 histone H3 {Lolium temulentum}□	14	1.8298262
39	TC31849: TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP). [Alfalfa] {Medicago sativa}□GP 1419685 emb	14	1.8298262
40	TC28703: monosaccharide transporter {Arabidopsis thaliana}	13	1.6991243
41	TC31848: CHALCONE SYNTHASE 9 (EC 2.3.1.74) (NARINGENIN-CHALCONE SYNTHASE 9). [Alfalfa] {Medicago sativa}□GP 1	13	1.6991243
42	TC36008: 4-coumarate:CoA ligase 3 {Populus balsamifera subsp. trichocarpa x Populus deltoides}	13	1.6991243
43	TC35925: l-asparaginase (l-asparagine amidohydrolase) {Arabidopsis thaliana}	13	1.6991243
44	TC35835: contains similarity to chalcone-flavonone isomerase (chalcone isomerase)~gene_id:K18123.7 {Arabidops	13	1.6991243
45	TC32110: SNAP25A protein {Arabidopsis thaliana}□GP 5731764 emb CAB52583.1 X92420 SNAP25AB protein {Arabidops	13	1.6991243
46	TC35726: malate oxidoreductase dependent malic enzyme) (NADP-me) {Vitis vinifera}□SP P51615 MAOX_VITVI NADP-D	13	1.6991243
47	TC32582: patatin-like protein 1 {Nicotiana tabacum}	12	1.5684224
48	TC35575: CHALCONE SYNTHASE 4 (EC 2.3.1.74) (NARINGENIN-CHALCONE SYNTHASE 4) (CHS12-1). [Alfalfa] {Medicago sa	12	1.5684224
49	TC39790: putative heat shock transcription factor {Arabidopsis thaliana}□PIR T00825 T00825 probable heat shoc	12	1.5684224
50	TC39655: cinnamoyl CoA reductase-like protein {Arabidopsis thaliana}□PIR T48643 T48643 cinnamoyl CoA reductas	12	1.5684224
51	TC35861: putative WRKY DNA binding protein {Oryza sativa}	12	1.5684224
52	TC39524:	12	1.5684224
53	TC28360:	12	1.5684224
54	TC39392: thaumatin-like protein PR-5b {Cicer arietinum}	12	1.5684224
55	TC39407: b2 protein {Daucus carota}□SP P37707 B2_DAUCA B2 PROTEIN. [Carrot] {Daucus carota}□GP 297889 emb CAA	12	1.5684224
56	TC39353: UDP-galactose-4-epimerase {Pisum sativum}□SP Q43070 GAE1_PEA UDP-GLUCOSE 4-EPIMERASE (EC 5.1.3.2) (G	12	1.5684224
57	TC36112:	11	1.4377206

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58	TC39641: bispecific caffeic acid / 5-hydroxyferulic acid o-methyltransferase {Populus tremuloides}□SP Q00763	11	1.4377206
59	TC35884: non-symbiotic hemoglobin {Medicago sativa}	11	1.4377206
60	TC39337: peroxidase1B {Medicago sativa}□GP 971560 emb CAA62226.1 X90693 peroxidase1B {Medicago sativa}□PIR J	11	1.4377206
61	TC32039: phospho-2-dehydro-3-deoxyheptonate aldolase 1 precursor (phospho-2-keto-3-deoxyheptonate aldolase 1)	11	1.4377206
62	TC31913: At1g56070/T6H22_13 {Arabidopsis thaliana}	11	1.4377206
63	TC35630: S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (EC 4.1.1.50) (ADOMETDC) (SAMDC) [CONTAINS: S-ADENOSYLM	11	1.4377206
64	TC31868: aba-responsive protein abr17 {Pisum sativum}□SP Q06931 AB17_PEA ABA-RESPONSIVE PROTEIN ABR17. [Garde	10	1.3070187
65	TC40019: Strong similarity to gb D14550 extracellular dermal glycoprotein (EDGP) precursor from Daucus carota	10	1.3070187
66	TC32449: 6a-hydroxymaackiain methyltransferase {Pisum sativum}□GP 1568637 gb AAC49856.1 U69554 6a-hydroxymaa	10	1.3070187
67	TC39785: chitinase {Trifolium repens}	10	1.3070187
68	TC39701: glucose-6-phosphate dehydrogenase {Medicago sativa}□SP Q42919 G6PD_MEDSA GLUCOSE-6-PHOSPHATE 1-DEHYD	10	1.3070187
69	TC35930:	10	1.3070187
70	TC39612: triacylglycerol lipase like protein {Arabidopsis thaliana}□GP 2245036 emb CAB10455.1 Z97342 triacyl	10	1.3070187
71	TC32163:	10	1.3070187
72	TC28453: putative heat shock protein {Arabidopsis thaliana}□PIR H84453 H84453 probable heat shock protein [im	10	1.3070187
73	TC35713: pectinesterase {Pisum sativum}□PIR T06468 T06468 pectinesterase (EC 3.1.1.11) precursor - garden pea	10	1.3070187
74	TC35803: NAD(p)h dependant 6'-deoxychalcone synthase {Glycine max}□SP P26690 6DCS_SOYBN NAD(P)H DEPENDENT 6'-	10	1.3070187
75	TC32035: ubiquitin-conjugating enzyme UBC7 {Arabidopsis thaliana}□GP 992704 gb AAC49321.1 U33757 UBC7 {Arabi	10	1.3070187
76	TC32023: MAP kinase 3 {Pisum sativum}	10	1.3070187
77	TC35557: peroxidase {Glycine max}	10	1.3070187
78	TC39355: heat shock cognate protein 80 {Lycopersicon esculentum}□SP P36181 HS80_LYCES HEAT SHOCK COGNATE PROT	10	1.3070187
79	TC39348: enolase {Lupinus luteus}	10	1.3070187
80	TC32726:	9	1.1763168
81	TC39855: unnamed protein product {Asparagus officinalis}	9	1.1763168
82	TC28595: putative protein {Arabidopsis thaliana}□GP 7269230 emb CAB81299.1 AL161560 putative protein {Arabid	9	1.1763168
83	TC32294: putative protein {Arabidopsis thaliana}□GP 7269272 emb CAB79332.1 AL161561 putative protein {Arabid	9	1.1763168
84	TC35953: putative membrane protein {Solanum tuberosum}	9	1.1763168
85	TC28440: phenylalanine ammonia-lyase {Medicago sativa}□SP P27990 PALY_MEDSA PHENYLALANINE AMMONIA-LYASE (EC 4	9	1.1763168
86	TC32152: ASPARTATE AMINOTRANSFERASE 1 (EC 2.6.1.1) (TRANSAMINASE A). [Alfalfa] {Medicago sativa}□GP 777386 gb	9	1.1763168
87	TC39533: unnamed protein product {Medicago sativa}□GP 4469288 emb CAA65771.1 X97059 ferritin {Medicago sativ	9	1.1763168
88	TC28392: serine/threonine protein kinase-like protein {Arabidopsis thaliana}□PIR T50802 T50802 serine/threoni	9	1.1763168
89	TC39335: peroxidase {Medicago sativa}□GP 537317 gb AAB41811.1 L36157 peroxidase {Medicago sativa}□PIR T09665	9	1.1763168

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90	TC39409: KETOL-ACID REDUCTOISOMERASE PRECURSOR (EC 1.1.1.86) (ACETOHYDROXY-ACID REDUCTOISOMERASE) (ALPHA-KETO	9	1.1763168
91	TC35697: L3 Ribosomal protein {Medicago sativa subsp. x varia}	9	1.1763168
92	TC39381: AT4g27450/F27G19_50 {Arabidopsis thaliana}□GP 15028057 gb AAK76559.1 AY045885 unknown protein {Arab	9	1.1763168
93	TC29053: peroxidase {Nicotiana tabacum}	8	1.045615
94	TC40169: germin-like protein {Pisum sativum}	8	1.045615
95	TC32145: 12-oxophytodienoate reductase OPR2 {Arabidopsis thaliana}□GP 6143903 gb AAF04449.1 AC010718_18 AC010	8	1.045615
96	TC36078: probable glutathione s-transferase para protein para (str246c protein) {Nicotiana tabacum}□SP P2531	8	1.045615
97	TC39971: immediate-early fungal elicitor protein CMPG1 {Petroselinum crispum}□GP 14582202 gb AAK69402.1 AF274	8	1.045615
98	TC28797: beta-fructofuranosidase precursor hydrolase (invertase) {Pisum sativum}□SP Q43089 INV1_PEA BETA-FRU	8	1.045615
99	TC39873: unknown protein {Arabidopsis thaliana}	8	1.045615
100	TC36002: disease resistance response protein-like {Arabidopsis thaliana}	8	1.045615
101	TC32057: SRG1 {Arabidopsis thaliana}□GP 5734767 gb AAD50032.1 AC007651_27 AC007651 SRG1 Protein {Arabidopsis	8	1.045615
102	TC31970: gb AAD56319.1~gene_id:MYC6.4~similar to unknown protein {Arabidopsis thaliana}	8	1.045615
103	TC28575: EMBRYONIC ABUNDANT PROTEIN USP92 PRECURSOR. [Broad bean] {Vicia faba}□GP 22051 emb CAA31602.1 X1321	8	1.045615
104	TC28560:	8	1.045615
105	TC39549: alcohol dehydrogenase 1 {Pisum sativum}□SP P12886 ADH1_PEA ALCOHOL DEHYDROGENASE 1 (EC 1.1.1.1). [Ga	8	1.045615
106	TC39615:	8	1.045615
107	TC39596: Elicitor inducible gene product Nt-SubE80 {Nicotiana tabacum}	8	1.045615
108	TC32016: EREBP-4 like protein {Arabidopsis thaliana}□GP 2245108 emb CAB10530.1 Z97343 EREBP-4 like protein {	8	1.045615
109	TC35840: glutathione S-transferase GST 8 {Glycine max}	8	1.045615
110	TC31980: EDGP precursor {Daucus carota}□GP 285741 dbj BAA03413.1 D14550 EDGP precursor {Daucus carota}□PIR T	8	1.045615
111	TC39540: AUXIN-RESPONSIVE PROTEIN IAA7 (INDOLEACETIC ACID-INDUCED PROTEIN 7). [Mouse-ear cress] {Arabidopsis	8	1.045615
112	TC32045: anthranilate N-benzoyltransferase {Arabidopsis thaliana}	8	1.045615
113	TC32043: germin-like protein {Pisum sativum}	8	1.045615
114	TC39449: putative 14-kDa proline-rich protein {Cicer arietinum}	8	1.045615
115	TC28338: ubiquitin conjugating enzyme E2 {Lycopersicon esculentum}	8	1.045615
116	TC35606: 14-3-3-like protein {Pisum sativum}	8	1.045615
117	TC31865: aquaporin-like protein PIP2 [Medicago truncatula]	8	1.045615
118	TC39299: glyceraldehyde-3-phosphate dehydrogenase {Nicotiana tabacum}	8	1.045615
119	TC39302: glyceraldehyde 3-phosphate dehydrogenase, cytosolic {Pisum sativum}□SP P34922 G3PC_PEA GLYCERALDEHYD	8	1.045615
120	TC39326: aquaporin	8	1.045615
121	TC39325: 5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (EC 2.1.1.14) (VITAMIN-B12-IND	8	1.045615

Supplemental Table II – Top 200 ESTs

122	TC28441: phenylalanine ammonia-lyase {Pisum sativum}□EGAD 138222 147409 phenylalanine ammonia-lyase {Pisum sa	7	0.9149131
123	TC29059: F21D18.18 {Arabidopsis thaliana}□PIR C96521 C96521 protein F21D18.18 [imported] - Arabidopsis thalia	7	0.9149131
124	TC36479: emb CAB45066.1~gene_id:MIL23.12~similar to unknown protein {Arabidopsis thaliana}	7	0.9149131
125	TC28917: unknown protein {Arabidopsis thaliana}□PIR E84423 E84423 hypothetical protein At2g01340 [imported] -	7	0.9149131
126	TC39952: whitefly-induced gp91-phox {Lycopersicon esculentum}□GP 8131890 gb AAF73124.1 AF148534_1 AF148534 wh	7	0.9149131
127	TC28616: immediate-early fungal elicitor protein CMPG1 {Petroselinum crispum}□GP 14582202 gb AAK69402.1 AF274	7	0.9149131
128	TC39878: putative chitinase	7	0.9149131
129	TC32332: putative phi-1-like phosphate-induced protein {Arabidopsis thaliana}□GP 4325369 gb AAD17365.1 AF128	7	0.9149131
130	TC32418: putative protein {Arabidopsis thaliana}□GP 7269279 emb CAB79339.1 AL161561 putative protein {Arabid	7	0.9149131
131	TC36085: allene oxide synthase {Lycopersicon esculentum}	7	0.9149131
132	TC36094: strong similarity to similar to pectinesterase~Contains Pectinesterase signatures AA407-414~contains	7	0.9149131
133	TC28569: Putative ABC transporter {Arabidopsis thaliana}□PIR A86289 A86289 probable ABC transporter [imported	7	0.9149131
134	TC35853: putative extracellular dermal glycoprotein {Cicer arietinum}	7	0.9149131
135	TC28553: heat shock factor protein hsf24 (heat shock transcription factor 24) (hsf 24) (heat stress transcri	7	0.9149131
136	TC35979: trehalose-6-phosphate phosphatase-like protein {Arabidopsis thaliana}□GP 7269105 emb CAB79214.1 AL1	7	0.9149131
137	TC32206: acyl-CoA synthetase {Brassica napus}□GP 1617270 emb CAA64327.1 X94624 acyl-CoA synthetase {Brassica	7	0.9149131
138	TC32123: putative mitochondrial dicarboxylate carrier protein {Arabidopsis thaliana}□GP 13877659 gb AAK43907.	7	0.9149131
139	TC39378: transketolase (EC 2.2.1.1) precursor - potato (fragment)	7	0.9149131
140	TC35805: auxin-induced atb2 {Arabidopsis thaliana}	7	0.9149131
141	TC32099: peroxidase 3 precursor {Phaseolus vulgaris}	7	0.9149131
142	TC39532: eukaryotic initiation factor 4a-10 (eif-4a-10) {Nicotiana tabacum}□SP P41382 IF4U_TOBAC EUKARYOTIC I	7	0.9149131
143	TC32044: putative RNA binding protein {Nicotiana tabacum}□PIR T01932 T01932 RNA binding protein homolog - com	7	0.9149131
144	TC32051:	7	0.9149131
145	TC39461: Putative histidine decarboxylase {Arabidopsis thaliana}□GP 13430642 gb AAK25943.1 AF360233_1 AF3602	7	0.9149131
146	TC39454: ARG10 {Vigna radiata}□PIR T07820 T07820 hypothetical protein ARG10 - mung bean	7	0.9149131
147	TC31950: 40S ribosomal protein S2 homolog {Arabidopsis thaliana}□PIR T46185 T46185 ribosomal protein S2, cyto	7	0.9149131
148	TC39429: cytochrome P450 {Cicer arietinum}	7	0.9149131
149	TC35740: isocitrate dehydrogenase (NADP), chloroplast precursor {Medicago sativa}□SP Q40345 IDHP_MEDSA ISOCIT	7	0.9149131
150	TC39415: zinc finger transcription factor-like protein {Arabidopsis thaliana}	7	0.9149131
151	TC28321: hypothetical protein {Cicer arietinum}	7	0.9149131
152	TC28345: vcCyP {Vicia faba}□PIR T50770 T50770 peptidylprolyl isomerase (EC 5.2.1.8) vcCyP [similarity] - fava	7	0.9149131
153	TC35613: type 1 metallothionein {Medicago sativa}□GP 6164920 gb AAF04584.1 AF189766_1 AF189766 type 1 metallo	7	0.9149131

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154	TC35563: putative plasma membrane intrinsic protein {Pisum sativum}	7	0.9149131
155	TC31862: S-adenosyl-L-methionine synthetase {Elaeagnus umbellata}	7	0.9149131
156	TC39293: cysteine proteinase 15a precursor protein 15a {Pisum sativum}□SP P25804 CYSP_PEA CYSTEINE PROTEINAS	7	0.9149131
157	TC29559:	6	0.7842112
158	TC32890:	6	0.7842112
159	TC29078: Nt-gh3 deduced protein {Nicotiana tabacum}	6	0.7842112
160	TC32773: hypothetical protein {Arabidopsis thaliana}□GP 2244866 emb CAB10288.1 Z97337 hypothetical protein {	6	0.7842112
161	TC29051:	6	0.7842112
162	TC32055: SRG1-like protein {Arabidopsis thaliana}□GP 7269381 emb CAB81341.1 AL161563 SRG1-like protein {Arab	6	0.7842112
163	TC32647: WIZZ {Nicotiana tabacum}	6	0.7842112
164	TC39750:	6	0.7842112
165	TC40065: F1E22.7 {Arabidopsis thaliana}	6	0.7842112
166	TC28923: GmMYB29A2 {Glycine max}	6	0.7842112
167	TC32578: allergen bet v iii {Betula verrucosa}□SP P43187 ALL3_BETVE CALCIUM-BINDING ALLERGEN BET V 3 (BET V I	6	0.7842112
168	TC32607: putative carbonic anhydrase {Arabidopsis thaliana}□PIR B84682 B84682 probable carbonic anhydrase [im	6	0.7842112
169	TC39684: putative RING-H2 zinc finger protein ATL6 {Arabidopsis thaliana}	6	0.7842112
170	TC39967: syntaxin-related protein At-SYR1 {Arabidopsis thaliana}□GP 6671938 gb AAF23198.1 AC016795_11 AC01679	6	0.7842112
171	TC28674: beta-1,3-glucanase {Glycine max}□EGAD 124928 133257 beta-1,3-glucanase {Glycine max}□EGAD 124928 145	6	0.7842112
172	TC28781: contains similarity to RNA-binding protein~gene_id:MPL12.3 {Arabidopsis thaliana}	6	0.7842112
173	TC31858: CATIONIC PEROXIDASE 1 PRECURSOR (EC 1.11.1.7). [Peanut] {Arachis hypogaea}□GP 1491776 gb AAB06183.1	6	0.7842112
174	TC39630: arbutin synthase {Rauvolfia serpentina}	6	0.7842112
175	TC39842: F5O11.14 {Arabidopsis thaliana}□PIR F86258 F86258 protein F5O11.14 [imported] - Arabidopsis thaliana	6	0.7842112
176	TC28520: unknown protein; 9323-8826 {Arabidopsis thaliana}□PIR D96749 D96749 unknown protein T10D10.2 [import	6	0.7842112
177	TC39646: putative protein kinase {Arabidopsis thaliana}□GP 7268664 emb CAB78872.1 AL161549 putative protein	6	0.7842112
178	TC31933: tubulin beta-1 subunit {Pisum sativum}□SP P29500 TBB1_PEA TUBULIN BETA-1 CHAIN. [Garden pea] {Pisum	6	0.7842112
179	TC39573: AP47/50p {Arabidopsis thaliana}□GP 2271477 gb AAB88283.1 AF009631 AP47/50p {Arabidopsis thaliana}	6	0.7842112
180	TC32184: Similar to gb Z48431 DNA-binding protein from Avena fatua. {Arabidopsis thaliana}□PIR A96841 A96841	6	0.7842112
181	TC39599:	6	0.7842112
182	TC28463: thaumatin-like protein 1 - apple tree	6	0.7842112
183	TC35882: cinnamyl-alcohol dehydrogenase {Medicago sativa}□SP P31656 CADH_MEDSA CINNAMYL-ALCOHOL DEHYDROGENASE	6	0.7842112
184	TC28458: DNA-binding protein WRKY3 {Avena sativa}	6	0.7842112
185	TC32156:	6	0.7842112

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186	TC28342: E2 ubiquitin-conjugating-like enzyme Ahus5 {Arabidopsis thaliana}□GP 1174162 gb AAA86642.1 U44976 u	6	0.7842112
187	TC35685: GTP-binding protein {Cicer arietinum}	6	0.7842112
188	TC32131: chitinasesputative chitinase	6	0.7842112
189	TC39537: transcription factor {Vicia faba}□GP 2104681 emb CAA66481.1 X97907 transcription factor {Vicia faba	6	0.7842112
190	TC39495: In2-1 protein {Glycine max}	6	0.7842112
191	TC31966: caffeic acid 3-o-methyltransferase methionine:caffeic acid 3-o-methyltransferase) (comt) {Medicago s	6	0.7842112
192	TC39486: nascent polypeptide associated complex alpha chain, putative; 85450-84199 {Arabidopsis thaliana}□GP	6	0.7842112
193	TC35785: Unknown (protein for MGC:12025) {Mus musculus}□GP 13543234 gb AAH05782.1 AAH05782 BC005782 Unknown (6	0.7842112
194	TC35794: GDP dissociation inhibitor {Cicer arietinum}□GP 3175990 emb CAA06731.1 AJ005836 GDP dissociation in	6	0.7842112
195	TC39410: 60S ribosomal protein L10 {Euphorbia esula}	6	0.7842112
196	TC35734: hydroxymethyltransferase {Arabidopsis thaliana}□GP 2244749 emb CAB10172.1 Z97335 hydroxymethyltrans	6	0.7842112
197	TC32025: G protein beta subunit-like {Medicago sativa}□SP O24076 GBLP_MEDSA GUANINE NUCLEOTIDE-BINDING PROTEI	6	0.7842112
198	TC32015: ribosomal protein S8 {Oryza sativa}□SP P49199 RS8_ORYSA 40S RIBOSOMAL PROTEIN S8. [Rice] {Oryza sati	6	0.7842112
199	TC32007: protein disulfide isomerase precursor (pdi) diphosphooligosaccharide-protein glycotransferase (glyco	6	0.7842112
200	TC39310: polyubiquitin(ubiquitin) {maize, Peptide, 533 aa} [Zea mays]□GP 248339 gb AAB21994.1 S94466 polyubi	6	0.7842112