Supplemental Table 3. Transcripts with differential expression patterns in elevated (E) and ambient (A) carbon dioxide concentration ([CO_2]). Annotations are based first on the BLASTX hit of the 3′ end EST if sequence information was available, and second on the 5′ end EST.

Clone ID	Annotation	F	p	E/A
Gm-r1070-4675	60S ribosomal protein L21 [Oryza sativa]	56.63	0.0003	0.673
Gm-r1070-1059	No hits	11.74	0.0140	0.678
Gm-r1070-1071	No hits	17.40	0.0059	0.682
Gm-r1070-481	No hits	13.12	0.0111	0.698
Gm-r1070-1301	No hits	16.04	0.0071	0.700
Gm-r1070-588	No hits	6.16	0.0477	0.700
Gm-r1070-883	No hits	13.61	0.0102	0.704
Gm-r1070-1505	pectin methylesterase isoform alpha [Vigna radiata]	11.48	0.0147	0.709
Gm-r1070-4055	PAC motif-containing protein [Arabidopsis thaliana]	7.48	0.0340	0.710
Gm-r1070-107	ribosomal protein L31	7.18	0.0366	0.711
Gm-r1070-2402	No hits	29.36	0.0016	0.711
Gm-r1070-825	No hits	8.69	0.0257	0.718
Gm-r1070-1257	60S ribosomal protein L7A [Arabidopsis thaliana]	11.60	0.0144	0.719
Gm-r1070-509	unknown protein [Oryza sativa]	8.01	0.0299	0.725
Gm-r1070-1299	No hits	6.05	0.0491	0.726
Gm-r1070-1061	No hits	26.92	0.0020	0.728
Gm-r1070-868	No hits	11.16	0.0156	0.731
Gm-r1070-1217	No hits	8.67	0.0258	0.732
Gm-r1070-1249	No hits	11.16	0.0156	0.733
Gm-r1070-701	No hits	10.27	0.0185	0.741
Gm-r1070-881	No hits	13.30	0.0108	0.746
Gm-r1070-1269	No hits	9.33	0.0224	0.751
Gm-r1070-2597	No hits	9.28	0.0226	0.753
Gm-r1070-4491	No hits	12.35	0.0126	0.753
Gm-r1070-1070	No hits	23.55	0.0028	0.753
Gm-r1070-871	No hits	14.55	0.0088	0.755
Gm-r1070-1455	unknown protein [Arabidopsis thaliana]	7.47	0.0340	0.755
Gm-r1070-608	No hits	6.38	0.0449	0.757
Gm-r1088-8100	unknown [Zea mays]	6.23	0.0372	0.757
Gm-r1070-101	trypsin inhibitor subtype A [Glycine max]	8.67	0.0258	0.760
Gm-r1070-907	No hits	11.72	0.0141	0.760
Gm-r1070-1459	No hits	7.30	0.0355	0.771

Gm-r1070-1375	No hits	7.85	0.0311	0.771
Gm-r1070-1687	glycinin A5A4B3 precursor - soybean (fragment)	8.18	0.0288	0.771
Gm-r1070-2928	No hits	10.66	0.0172	0.772
Gm-r1070-1137	unknown protein [Arabidopsis thaliana]	16.17	0.0069	0.779
Gm-r1088-2139	putative nitrate transporter [Arabidopsis thaliana]	9.43	0.0153	0.780
Gm-r1070-4052	No hits	6.51	0.0435	0.780
Gm-r1070-3033	putative acyl-CoA synthetase [Capsicum annuum]	6.91	0.0392	0.782
Gm-r1070-1503	hypothetical protein [Capsicum chinense]	8.16	0.0289	0.783
Gm-r1070-1267	No hits	11.82	0.0138	0.786
Gm-r1070-1270	No hits	14.42	0.0090	0.791
Gm-r1070-3931	No hits	7.93	0.0305	0.793
Gm-r1070-309	alpha' subunit of beta-conglycinin [Glycine max]	6.74	0.0409	0.794
Gm-r1070-4163	No hits	6.62	0.0422	0.796
Gm-r1070-4875	No hits	11.24	0.0154	0.797
Gm-r1070-1083	No hits	9.11	0.0235	0.797
Gm-r1070-1268	AKIN beta3 [Medicago truncatula] (5')	14.07	0.0095	0.797
Gm-r1070-703	putative protein kinase C inhibitor [Arabidopsis thaliana]	8.85	0.0248	0.797
Gm-r1070-2922	No hits	17.18	0.0060	0.800
Gm-r1070-905	No hits	10.54	0.0175	0.800
Gm-r1070-933	unknown protein [Arabidopsis thaliana]	6.26	0.0463	0.804
Gm-r1070-3112	No hits	7.68	0.0324	0.805
Gm-r1070-2806	No hits	17.61	0.0057	0.805
Gm-r1070-1507	U3-55K-like protein 2 [Arabidopsis thaliana]	6.70	0.0413	0.806
Gm-r1070-927	expressed protein [Arabidopsis thaliana]	6.68	0.0416	0.806
Gm-r1070-5180	No hits	11.16	0.0156	0.806
Gm-r1070-1068	putative endosomal protein [Arabidopsis thaliana]	14.46	0.0089	0.809
Gm-r1070-1395	No hits	10.09	0.0192	0.809
Gm-r1070-1101	allene-oxide cyclase [Medicago truncatula]	8.65	0.0259	0.811
Gm-r1070-1021	putative small nuclear ribonucleoprotein polypeptide F [Oryza sativa]	10.41	0.0180	0.811
Gm-r1070-1399	annexin [Cicer arietinum]	8.81	0.0250	0.814
Gm-r1070-2191	B-gal alpha peptide [Shuttle vector pMQ61]	6.86	0.0397	0.814
Gm-r1070-1373	No hits	6.43	0.0443	0.814
Gm-r1070-2555	apyrase GS52 [Glycine soja]	20.92	0.0038	0.818
Gm-r1070-1281	ribosomal protein S19	31.70	0.0013	0.822
Gm-r1070-1139	No hits	8.59	0.0262	0.822
Gm-r1070-3423	acid phosphatase [Glycine max]	8.21	0.0286	0.824
Gm-r1070-1073	No hits	6.12	0.0482	0.827
Gm-r1070-1710	Adenylate kinase B (ATP-AMP transphosphorylase)	12.21	0.0129	0.832

Gm-r1088-4235	glycosyl hydrolase family 17 protein [Arabidopsis thaliana]	7.03	0.0292	0.838
Gm-r1070-4149	thylakoid lumen protein, chloroplast precursor [Arabidopsis thaliana]	8.53	0.0266	0.839
Gm-r1070-511	No hits	8.12	0.0292	0.841
Gm-r1070-1074	No hits	9.23	0.0228	0.842
Gm-r1070-1481	truncated copper-binding protein CUTA (CUTA) [Arabidopsis thaliana]	7.88	0.0308	0.846
Gm-r1088-1813	N-acetylglucosamine-phosphate mutase [Arabidopsis thaliana]	7.62	0.0247	0.849
Gm-r1088-4493	non-repetitive/WGA-negative nucleoporin family protein [Arabidopsis thaliana]	8.30	0.0205	0.851
Gm-r1070-4147	AT5g55940/MYN21_5 [Arabidopsis thaliana]	7.22	0.0362	0.852
Gm-r1070-1473	C2 domain-containing protein [Cicer arietinum]	26.28	0.0022	0.856
Gm-r1088-2433	helicase-like protein [Arabidopsis thaliana]	5.97	0.0403	0.857
Gm-r1088-5814	ATP binding / ATP-dependent helicase/ RNA helicase/ helicase/ [Arabidopsis thaliana]	8.74	0.0182	0.859
Gm-r1070-6272	No hits	7.62	0.0329	0.861
Gm-r1070-2668	No hits	6.42	0.0444	0.861
Gm-r1070-3036	No hits	8.19	0.0288	0.865
Gm-r1070-4157	Chain 1, Bean Pod Mottle Virus (Bpmv), Top Component	6.92	0.0390	0.867
Gm-r1070-874	triosephosphate isomerase [Glycine max]	8.43	0.0272	0.902
Gm-r1088-5244	unnamed protein product [Arabidopsis thaliana]	8.57	0.0191	0.904
Gm-r1088-6769	unnamed protein product [Arabidopsis thaliana]	5.37	0.0491	0.909
Gm-r1088-2199	Putative phospatase 2A inhibitor [Arabidopsis thaliana]	6.02	0.0398	0.921
Gm-r1088-4763	unknown protein [Arabidopsis thaliana]	5.88	0.0415	1.114
Gm-r1088-4646	ubiquitin-conjugating enzyme E2 [Gossypium raimondii]	6.33	0.0360	1.116
Gm-r1070-8546	No hits	8.65	0.0259	1.120
Gm-r1070-6993	hypothetical protein Tfus02000823 [Thermobifida fusca]	8.80	0.0250	1.129
Gm-r1070-7416	LEC1-like protein [Phaseolus coccineus]	6.36	0.0452	1.136
Gm-r1070-5991	F28K19.29 [Arabidopsis thaliana]	6.74	0.0409	1.139
Gm-r1070-5341	unknown protein [Arabidopsis thaliana]	6.62	0.0422	1.140
Gm-r1070-4232	No hits	8.23	0.0285	1.141
Gm-r1070-5429	cytosolic phosphoglycerate kinase [Pisum sativum]	10.60	0.0173	1.142
Gm-r1070-3469	omega-3 fatty acid desaturase (EC 1.14.99.-) GMD [similarity] - soybean	7.02	0.0380	1.145
Gm-r1070-8622	hypothetical protein [Cicer arietinum]	6.22	0.0470	1.153
Gm-r1070-7398	putative RING zinc finger protein [Arabidopsis thaliana]	7.60	0.0330	1.162
Gm-r1070-5320	expressed protein [Arabidopsis thaliana]	6.46	0.0439	1.165
Gm-r1070-9038	putative urease accessory protein G [Oryza sativa]	7.46	0.0342	1.167
Gm-r1070-4318	F1-ATP synthase delta subunit [Ipomoea batatas]	6.08	0.0488	1.168
Gm-r1070-5274	unnamed protein product [Arabidopsis thaliana]	12.29	0.0127	1.170
Gm-r1070-7785	cytosolic malate dehydrogenase [Glycine max]	9.77	0.0205	1.171

Gm-r1070-8883	nucleoid DNA-binding-like protein [Arabidopsis thaliana]	8.30	0.0280	1.173
Gm-r1088-839	unnamed protein product [Arabidopsis thaliana]	7.38	0.0264	1.178
Gm-r1070-7820	Similar to SOUL Protein [Arabidopsis thaliana]	7.02	0.0380	1.181
Gm-r1070-8504	Proteasome subunit alpha type 3	6.39	0.0448	1.187
Gm-r1070-5372	No hits	15.10	0.0081	1.187
Gm-r1070-8855	putative splicing factor [Cicer arietinum]	17.41	0.0059	1.189
Gm-r1070-8885	aspartyl protease family protein [Arabidopsis thaliana]	7.72	0.0321	1.192
Gm-r1070-6484	ATP synthase (gamma subunit) [Pisum sativum]	18.97	0.0048	1.193
Gm-r1070-6964	putative peroxisomal membrane protein PEX11-1 [Arabidopsis thaliana]	8.52	0.0267	1.194
Gm-r1070-7855	AT4g18710 [Arabidopsis thaliana], shaggy-like protein kinase etha (EC 2.7.1.-)	6.60	0.0424	1.195
Gm-r1070-6065	hydrogen-transporting ATPase, rotational mechanism [Arabidopsis thaliana]	6.16	0.0476	1.198
Gm-r1070-5853	unknown protein [Arabidopsis thaliana]	6.21	0.0470	1.204
Gm-r1070-5896	No hits	7.20	0.0364	1.207
Gm-r1070-8315	photosystem I reaction center subunit III [Vigna radiata]	7.50	0.0338	1.208
Gm-r1070-6966	transcription factor EIL1 [Vigna radiata]	22.66	0.0031	1.208
Gm-r1070-3700	cyclophilin [Cucumis sativus]	6.49	0.0436	1.210
Gm-r1070-6442	enolase, isoform 2 [Hevea brasiliensis]	10.73	0.0169	1.214
Gm-r1070-5659	responce reactor 4 [Arabidopsis thaliana]	7.72	0.0321	1.215
Gm-r1070-7015	No hits	6.79	0.0403	1.216
Gm-r1070-7800	L-galactose-1-phosphate phosphatase [Actinidia deliciosa]	8.82	0.0250	1.217
Gm-r1070-5026	No hits	25.17	0.0024	1.217
Gm-r1070-7770	hypothetical protein [Nicotiana tabacum]; DNA binding [Arabidopsis thaliana]	17.97	0.0054	1.218
Gm-r1070-7399	unknown protein [Arabidopsis thaliana]; GO: response to stress	7.48	0.0340	1.219
Gm-r1070-8647	core protein [Pisum sativum]	6.71	0.0412	1.222
Gm-r1070-4830	Peptidase C1A, papain; Somatotropin hormone [Medicago truncatula]	7.61	0.0329	1.223
Gm-r1070-1714	homogentisate phytylprenyltransferase [Glycine max]	14.87	0.0084	1.224
Gm-r1070-6056	BEL1-related homeotic protein 29 [Solanum tuberosum]	6.25	0.0465	1.225
Gm-r1070-7337	unknown protein [Arabidopsis thaliana]	11.13	0.0157	1.227
Gm-r1070-5742	putative PRT1 protein [Arabidopsis thaliana]	7.01	0.0381	1.227
Gm-r1070-7935	Dc3 promoter-binding factor-3 [Helianthus annuus]	7.38	0.0348	1.228
Gm-r1070-6613	eukaryotic initiation factor 4, eIF4-like protein [Arabidopsis thaliana]	7.89	0.0308	1.228
Gm-r1070-6635	unknown protein [Arabidopsis thaliana]	10.53	0.0176	1.230
Gm-r1070-6474	structural molecule [Arabidopsis thaliana] chloroplast	6.68	0.0416	1.230
Gm-r1070-3096	transcription factor EIL2 [Vigna radiata]	7.90	0.0307	1.231
Gm-r1070-6672	hyuC-like protein [Arabidopsis thaliana]	7.29	0.0356	1.235

Gm-r1088-8748	amidohydrolase family [Arabidopsis thaliana]	5.48	0.0473	1.236
Gm-r1070-3954	myb family transcription factor [Arabidopsis thaliana]	6.41	0.0446	1.237
Gm-r1070-6086	unknown protein [Oryza sativa]	26.71	0.0021	1.238
Gm-r1070-7963	Tubulin beta-3 chain (Beta-3 tubulin)	9.87	0.0200	1.239
Gm-r1070-6564	Phosphofructokinase [Medicago truncatula]	13.13	0.0111	1.241
Gm-r1070-7604	At1g36050 [Arabidopsis thaliana]	8.63	0.0260	1.242
Gm-r1070-5241	unnamed protein product [Arabidopsis thaliana]	11.87	0.0137	1.242
Gm-r1070-5439	In2-1 protein [Glycine max]	11.30	0.0152	1.243
Gm-r1070-4852	glyceraldehyde 3-phosphate dehydrogenase [Solanum tuberosum]	11.27	0.0153	1.244
Gm-r1070-5473	acyl-CoA thioesterase [Arabidopsis thaliana]	6.27	0.0462	1.244
Gm-r1070-5823	ubiquitin-specific protease 16 [Arabidopsis thaliana]	13.62	0.0102	1.244
Gm-r1070-9031	chlorophyll a/b-binding protein CP24 precursor [Vigna radiata]	6.49	0.0437	1.246
Gm-r1070-3891	No hits	9.25	0.0227	1.247
Gm-r1088-1409	No hits	5.56	0.0461	1.247
Gm-r1070-5847	UVB-resistance protein UVR8 [Arabidopsis thaliana]	11.70	0.0141	1.248
Gm-r1070-4236	cysteine proteinase [Glycine max]	8.19	0.0287	1.250
Gm-r1070-5463	No hits	6.81	0.0402	1.250
Gm-r1070-9041	expressed protein [Arabidopsis thaliana]	7.49	0.0339	1.250
Gm-r1070-7752	33 kDa polypeptide of water-oxidizing complex of photosystem II [Nicotiana tabacum]	8.32	0.0279	1.251
Gm-r1070-5457	At1g64520/F1N19_10 proteasome regulatory subunit [Arabidopsis thaliana]	6.99	0.0384	1.258
Gm-r1070-4599	putative nitrate transporter NRT1-3 [Glycine max]	6.73	0.0410	1.259
Gm-r1070-8505	hypothetical protein [Arabidopsis thaliana]	9.24	0.0228	1.260
Gm-r1070-5593	L-galactose-1-phosphate phosphatase [Actinidia deliciosa]	6.09	0.0486	1.261
Gm-r1070-6948	ferritin [Malus xiaojinensis]	9.61	0.0211	1.262
Gm-r1070-7584	enoyl-ACP reductase [Nicotiana tabacum]	7.71	0.0321	1.263
Gm-r1070-8125	HMG-1 like protein gene [Glycine max]	6.32	0.0456	1.263
Gm-r1070-3898	unknown protein [Oryza sativa]	12.61	0.0121	1.264
Gm-r1070-5874	unknown protein [Arabidopsis thaliana]	29.59	0.0016	1.264
Gm-r1070-4035	Sali3-2 [Glycine max]	9.48	0.0217	1.265
Gm-r1070-6421	protein kinase family protein [Arabidopsis thaliana]	11.95	0.0135	1.266
Gm-r1070-5796	putative NAD dependent epimerase [Arabidopsis thaliana]	18.47	0.0051	1.268
Gm-r1070-2576	unknown protein [Arabidopsis thaliana]	7.42	0.0344	1.268
Gm-r1070-5646	No hits	18.21	0.0053	1.268
Gm-r1070-6170	NAM-like protein [Prunus persica] (5')	11.64	0.0143	1.272
Gm-r1070-5852	No hits	10.22	0.0187	1.273
Gm-r1070-6989	nucleic acid binding / transcription factor [Arabidopsis thaliana]	7.06	0.0377	1.276

Gm-r1070-4068	No hits	11.29	0.0152	1.281
Gm-r1070-5468	MYB transcription factor [Arabidopsis thaliana]	43.60	0.0006	1.282
Gm-r1070-5107	At1g32230/F3C3_1 [Arabidopsis thaliana]	12.67	0.0119	1.284
Gm-r1070-5291	No hits	10.91	0.0163	1.284
Gm-r1070-6647	AT4g36780/C7A10_580 brassinosteroid signalling positive regulator-related (5')	7.25	0.0359	1.285
Gm-r1070-3503	At3g03150 [Arabidopsis thaliana]	6.80	0.0403	1.286
Gm-r1070-8143	pentameric polyubiquitin	9.91	0.0199	1.287
Gm-r1070-7595	LHY protein [Phaseolus vulgaris]	11.64	0.0143	1.287
Gm-r1070-8741	OSJNBb0065L13.14 [Oryza sativa (japonica cultivar-group)]	7.86	0.0310	1.288
Gm-r1070-6109	lipoxygenase [Phaseolus vulgaris]	25.18	0.0024	1.293
Gm-r1070-3139	gigantea [Arabidopsis thaliana]	11.62	0.0143	1.294
Gm-r1070-5792	vacuolar ATPase subunit E [Phaseolus acutifolius]	10.96	0.0162	1.294
Gm-r1070-8122	No hits	19.44	0.0045	1.302
Gm-r1070-4646	UDP-D-apiose/UDP-D-xylose synthase [Arabidopsis thaliana]	8.61	0.0261	1.303
Gm-r1070-3489	cullin 1C [Nicotiana tabacum]	9.85	0.0201	1.304
Gm-r1070-5877	unknown [Arabidopsis thaliana]	10.88	0.0164	1.304
Gm-r1070-4694	NAD dependent epimerase/dehydratase family [Oryza sativa]	6.71	0.0412	1.306
Gm-r1070-9006	palmitoyl-acyl carrier protein thioesterase [Gossypium hirsutum]	18.55	0.0051	1.308
Gm-r1088-3426	unknown protein [Arabidopsis thaliana]	6.94	0.0300	1.309
Gm-r1070-4312	putative Mob1-like protein [Oryza sativa]	19.24	0.0046	1.310
Gm-r1070-6762	hypothetical protein [Oryza sativa]	12.75	0.0118	1.312
Gm-r1070-8950	Helicase, C-terminal; Zinc finger, CCHC-type [Medicago truncatula] (5')	25.16	0.0024	1.313
Gm-r1070-8759	Chain A, Crystal Structure Of Soybean Beta-Amylase Mutant (M51t) With Increased Ph Optimum	14.97	0.0083	1.313
Gm-r1070-5278	Ser/Thr protein kinase [Lotus corniculatus]	12.58	0.0121	1.313
Gm-r1070-5848	malate dehydrogenase precursor [Medicago sativa]	9.60	0.0212	1.313
Gm-r1070-2400	AT4g15470/dl3775w [Arabidopsis thaliana]	20.91	0.0038	1.314
Gm-r1070-3491	chloroplast photosystem I reaction center V [Camellia sinensis]	8.20	0.0287	1.315
Gm-r1070-8169	Skp1 [Medicago sativa]	10.24	0.0186	1.315
Gm-r1070-8564	mRNA-binding protein precursor [Nicotiana tabacum]	24.43	0.0026	1.316
Gm-r1070-8635	chloroplast RNA binding protein [Phaseolus vulgaris]	9.96	0.0197	1.316
Gm-r1070-6262	putative protein [Arabidopsis thaliana]	9.22	0.0229	1.316
Gm-r1070-7587	putative protein [Arabidopsis thaliana]	12.78	0.0117	1.316
Gm-r1070-3509	thioredoxin [Glycine max]	8.32	0.0279	1.316
Gm-r1070-7756	putative pyruvate dehydrogenase E1 beta subunit isoform 1 protein [Oryza sativa]	7.03	0.0379	1.322
Gm-r1070-6300	No hits	14.93	0.0083	1.323

Gm-r1070-6633	heat shock protein 70 [Nicotiana benthamiana]	6.40	0.0447	1.324
Gm-r1070-7983	At5g19590 [Arabidopsis thaliana]	20.69	0.0039	1.325
Gm-r1070-6974	translation initiation factor [Arabidopsis thaliana]	7.31	0.0354	1.326
Gm-r1070-7889	unknown [Arabidopsis thaliana]	7.14	0.0369	1.326
Gm-r1070-3522	putative caffeic acid methyl transferase [Arachis hypogaea]	8.15	0.0290	1.327
Gm-r1070-6244	glutamine synthetase precursor [Glycine max]	8.98	0.0241	1.328
Gm-r1070-7002	DnaJ-like protein [Medicago sativa]	18.17	0.0053	1.328
Gm-r1070-4274	No hits	7.84	0.0311	1.334
Gm-r1070-2347	putative RNA recognition motif (RRM)-containing protein [Oryza sativa]	10.27	0.0185	1.338
Gm-r1088-1518	metal-dependent hydrolase-like protein [Oryza sativa (japonica cultivar-group)]	6.22	0.0373	1.338
Gm-r1070-2941	vacuolar H+-ATPase c subunit [Citrus unshiu]	10.53	0.0176	1.339
Gm-r1070-1976	DNA-binding protein 4 [Nicotiana tabacum] (5')	8.24	0.0284	1.340
Gm-r1070-6615	hypothetical protein [Solanum tuberosum]	7.43	0.0344	1.341
Gm-r1070-7605	Unknown protein [Arabidopsis thaliana]	17.66	0.0057	1.343
Gm-r1070-1672	unnamed protein product [Arabidopsis thaliana]	13.51	0.0104	1.345
Gm-r1070-6309	hypothetical protein [Cicer arietinum]	7.11	0.0372	1.345
Gm-r1070-6616	cellulose synthase (EC 2.4.1.-) catalytic chain celA2 - upland cotton (fragment)	8.64	0.0260	1.346
Gm-r1070-3733	1-deoxy-D-xylulose 5-phosphate reductoisomerase [Pueraria montana var. lobata]	9.01	0.0240	1.347
Gm-r1070-5787	microsomal omega-3 fatty acid desaturase [Glycine max]	6.82	0.0400	1.348
Gm-r1070-4104	No hits	11.81	0.0139	1.349
Gm-r1070-6809	unknown protein [Arabidopsis thaliana]	7.04	0.0378	1.349
Gm-r1088-2089	cation diffusion facilitator 9 [Stylosanthes hamata]	5.36	0.0494	1.349
Gm-r1070-9107	synaptobrevin 1 [Oryza sativa (japonica cultivar-group)]	18.95	0.0048	1.349
Gm-r1070-7510	phosphoglycerate mutase [Ricinus communis]	10.75	0.0169	1.352
Gm-r1088-1727	alpha-mannosidase precursor [Arabidopsis thaliana]	5.35	0.0494	1.353
Gm-r1070-9047	receptor-like protein kinase [Nicotiana tabacum]	11.79	0.0139	1.354
Gm-r1070-5454	No hits	8.48	0.0269	1.354
Gm-r1070-1970	No hits	12.28	0.0128	1.354
Gm-r1070-8292	homeodomain-leucine zipper protein 56 [Glycine max]	6.41	0.0445	1.355
Gm-r1070-3650	unknown protein [Arabidopsis thaliana]	11.93	0.0136	1.357
Gm-r1070-5070	beta-amylase [Glycine max]	16.41	0.0067	1.360
Gm-r1070-7887	malate synthase	8.27	0.0282	1.364
Gm-r1070-5461	NAC3 protein [Glycine max]	8.98	0.0241	1.365
Gm-r1070-5835	transducin family protein / WD-40 repeat family protein [Arabidopsis thaliana]	17.15	0.0061	1.366

Gm-r1070-8862	expressed protein [Arabidopsis thaliana]	14.03	0.0096	1.368
Gm-r1070-4141	SEU3B protein [Antirrhinum majus]	9.40	0.0221	1.370
Gm-r1070-7027	cryptochrome 2A apoprotein [Pisum sativum]	11.96	0.0135	1.372
Gm-r1070-3547	putative purple acid phosphatase precursor [Phaseolus vulgaris]	7.13	0.0370	1.373
Gm-r1070-2965	Ca2+/H+-exchanging protein - mung bean	51.02	0.0004	1.373
Gm-r1070-3546	unknown protein [Oryza sativa (japonica cultivar-group)]	9.64	0.0210	1.373
Gm-r1070-2547	No hits	10.93	0.0163	1.375
Gm-r1070-8913	auxin response factor-like protein [Mangifera indica]	15.32	0.0079	1.376
Gm-r1070-6975	No hits	11.73	0.0141	1.376
Gm-r1070-7793	membrane related protein CP5, putative [Arabidopsis thaliana]	8.15	0.0290	1.376
Gm-r1070-1954	histone H2B [Cicer arietinum]	11.68	0.0142	1.379
Gm-r1070-3342	L-galactose-1-phosphate phosphatase [Actinidia deliciosa]	14.75	0.0086	1.381
Gm-r1070-8717	putative chlorophyll a/b-binding protein [Arabidopsis thaliana]	14.07	0.0095	1.384
Gm-r1070-7007	Tubulin alpha-3 chain (Alpha-3 tubulin)	10.12	0.0190	1.387
Gm-r1070-4114	No hits	10.57	0.0174	1.387
Gm-r1070-1738	dehydrin [Glycine max]	7.47	0.0340	1.389
Gm-r1070-4704	double WRKY type transfactor [Solanum tuberosum]	8.38	0.0275	1.389
Gm-r1070-6997	remorin [Solanum tuberosum]	13.30	0.0107	1.389
Gm-r1070-1903	No hits	7.57	0.0332	1.390
Gm-r1088-1149	outer envelope protein [Pisum sativum]	5.35	0.0494	1.390
Gm-r1070-6232	No hits	7.60	0.0330	1.391
Gm-r1070-8148	peptide methionine sulfoxide reductase; cPMSR [Gossypium barbadense]	10.00	0.0195	1.395
Gm-r1070-8484	Chain A, Crystal Structure Of Soybean Beta-Amylase Mutant (M51t) With Increased Ph Optimum	11.88	0.0137	1.401
Gm-r1070-8567	putative NAD synthetase [Oryza sativa]	13.77	0.0100	1.403
Gm-r1070-5887	At1g69340/F10D13.28 [Arabidopsis thaliana]	6.50	0.0436	1.403
Gm-r1070-5647	No hits	14.29	0.0092	1.405
Gm-r1088-2099	indole-3-glycerol phosphate synthase [Arabidopsis thaliana]	5.49	0.0472	1.409
Gm-r1088-2285	unnamed protein product [Arabidopsis thaliana]	8.24	0.0208	1.411
Gm-r1070-1927	photosystem II protein Z [Glycine max] (5')	6.60	0.0424	1.412
Gm-r1070-5797	P-Protein precursor [Solanum tuberosum]	15.94	0.0072	1.417
Gm-r1070-4563	seed specific protein Bn15D1B [Brassica napus]	11.19	0.0155	1.417
Gm-r1070-5188	subtilisin-like protease C1 [Glycine max]	9.21	0.0229	1.418
Gm-r1070-5594	vacuolar H+-ATPase B subunit [Citrus unshiu]	27.29	0.0020	1.424
Gm-r1070-3597	phosphoenolpyruvate carboxykinase [Flaveria pringlei]	10.79	0.0167	1.429
Gm-r1070-5613	beta-amylase [Glycine max]	15.39	0.0078	1.434
Gm-r1070-8296	putative cinnamoyl-CoA reductase [Solanum demissum]	7.62	0.0328	1.439
Gm-r1070-5904	putative glycerophosphoryl diester phosphodiesterase family protein	11.20	0.0155	1.439

	[Nicotiana tabacum]			
Gm-r1070-7310	unknown protein [Arabidopsis thaliana]	13.58	0.0103	1.444
Gm-r1070-1668	No hits	7.61	0.0329	1.453
Gm-r1088-7077	phosphogluconate dehydrogenase (decarboxylating) (EC 1.1.1.44) - soybean	6.54	0.0338	1.454
Gm-r1070-5440	plasma membrane polypeptide [Nicotiana tabacum]	6.23	0.0467	1.454
Gm-r1070-3821	putative von Hippel-Lindau binding protein [Arabidopsis thaliana]	11.63	0.0143	1.459
Gm-r1070-5817	malate dehydrogenase (NADP+) [Pisum sativum]	9.20	0.0230	1.465
Gm-r1070-8919	Formate--tetrahydrofolate ligase	63.54	0.0002	1.472
Gm-r1088-4414	Ferritin 3, chloroplast precursor (SFerH-3)	6.97	0.0297	1.473
Gm-r1088-2301	adventitious rooting related oxygenase [Malus x domestica]	5.92	0.0410	1.475
Gm-r1088-2682	alpha-galactosidase preproprotein [Cyamopsis tetragonoloba]	5.85	0.0419	1.476
Gm-r1088-183	No hits	6.89	0.0304	1.476
Gm-r1070-7330	copper chaperone homolog CCH [Glycine max]	20.05	0.0042	1.495
Gm-r1070-1866	hypothetical protein [Arabidopsis thaliana]	8.48	0.0269	1.496
Gm-r1088-555	No hits	6.02	0.0397	1.498
Gm-r1070-8298	adenosine 5'-phosphosulfate reductase [Glycine max]	18.72	0.0049	1.504
Gm-r1070-3980	putative protein [Arabidopsis thaliana]	15.27	0.0079	1.514
Gm-r1070-7908	probable aminopeptidase F24D7.4 [imported] - Arabidopsis thaliana	41.24	0.0007	1.516
Gm-r1088-2863	hydroxymethylbilane synthase [Arabidopsis thaliana]	7.52	0.0254	1.533
Gm-r1070-3592	cysteine proteinase [Glycine max]	8.71	0.0256	1.536
Gm-r1088-2667	putative inorganic pyrophosphatase [Arabidopsis thaliana]	6.36	0.0357	1.559
Gm-r1070-2003	unknown protein [Arabidopsis thaliana]	8.91	0.0245	1.571
Gm-r1088-1725	No hits	9.94	0.0135	1.573
Gm-r1070-3539	No hits	13.24	0.0108	1.574
Gm-r1070-1814	No hits	11.80	0.0139	1.576
Gm-r1070-2666	No hits	11.66	0.0142	1.582
Gm-r1088-1920	ADP, ATP carrier-like protein [Arabidopsis thaliana]	5.75	0.0433	1.600
Gm-r1070-5393	Ca2+/H+-exchanging protein - mung bean	40.58	0.0007	1.616
Gm-r1070-5236	No hits	6.60	0.0424	1.617
Gm-r1070-8413	dehydroascorbate reductase [Glycine max]	11.08	0.0158	1.620
Gm-r1088-1712	No hits	6.96	0.0298	1.621
Gm-r1070-5643	No hits	11.73	0.0141	1.627
Gm-r1070-5151	transcription factor EIL1 [Vigna radiata]	7.63	0.0327	1.632
Gm-r1088-2878	bZIP DNA-binding protein [Antirrhinum majus]	8.12	0.0215	1.643
Gm-r1070-9139	unknown protein [Oryza sativa]	19.83	0.0043	1.653
Gm-r1070-3635	AT3g15840 [Arabidopsis thaliana]	12.52	0.0122	1.655
Gm-r1088-4020	myo-inositol-1-phosphate synthase [Glycine max]	6.21	0.0375	1.668

Gm-r1070-7203	At1g54990/F14C21_5 [Arabidopsis thaliana]	11.62	0.0143	1.683
Gm-r1070-5201	Inositol-3-phosphate synthase [Glycine max]	7.01	0.0382	1.714
Gm-r1070-6113	putative nitrate transporter NRT1-3 [Glycine max]	8.90	0.0245	1.734
Gm-r1088-3446	DnaJ domain family [Arabidopsis thaliana]	6.79	0.0313	1.805
Gm-r1070-7748	granule-bound starch synthase Ib precursor [Phaseolus vulgaris]	10.60	0.0173	1.829
Gm-r1088-3448	No hits	5.41	0.0484	1.836
Gm-r1088-3248	plastidial phosphoglucomutase [Pisum sativum]	6.49	0.0343	1.901
Gm-r1088-3648	aquaporin [Vitis vinifera]	9.82	0.0139	1.998