Genes changed in expression in BLR-OX in the same direction in all 3 replicates with an average of >1.5-fold change, arranged in order of spot confidence

Upregulated genes

SPOTNUMBER	BLOCK	NAME	AG ID	BLR-OX (1)	Col-0 (1)	BLR-OX (2)	Col-0 (2)	BLR-OX (3)	Col-0 (3)	Mean Ratio (BLR-OX:Col-0)	Spot Confidence
3912	7	expressed protein similar to hypothetical protein GB:CAB80917 GI:7267605 from [Arabidopsis thaliana]	At1g01430	1787.80183	1147.219	1552.76854	1034.998	2896.35392	1655.476	1.602733601	0.803712
261	1	trypsin inhibitor, putative similar to SP|P26780 Trypsin inhibitor 2 precursor (MTI-2) {Sinapis alba}	At2g43520	2623.64804	1356.269	2447.05036	1903.594	1752.37643	1232.123	1.547397015	0.778414
13777	22	expressed protein weak similarity to SP|P53809 Phosphatidylcholine transfer protein (PC-TP) {Rattus norvegicus}	At1g64720	5778.65146	4729.678	3573.64263	2901.194	5432.67396	2605.493	1.512884545	0.76076
143	1	band 7 family protein strong similarity to hypersensitive-induced response protein [Zea mays] GI:7716466; contains Pfam profile PF01145: SPFH domain / Band 7 family	At1g69840	934.878854	463.826	433.947088	365.051	1183.55169	682.818	1.645881681	0.743728
5793	9	expressed protein similar to unknown protein (pir||S76207)	At5g51020	789.769087	559.846	560.420118	483.709	890.795804	460.651	1.501018393	0.73692
27	1	thioredoxin family protein contains Pfam profile: PF00085 Thioredoxin; similar to ESTs gb|T46281, gb|R83933, gb|N65879, emb|F14466, gb|N96726, gb|AA042340, and emb|Z18150	At1g08570	1353.88436	662.757	1128.70825	799.401	936.390775	737.109	1.575035001	0.735816
11720	19	UDP-glucose transferase (UGT75B2) similar to UDP-glucose:indole-3-acetate beta-D-glucosyltransferase GI:2149127 from (Arabidopsis thaliana); identical to cDNA UDP-glucosyltransferase (UGT75B2) GI:13661274	At1g05560	985.290944	765.769	852.459289	673.083	2681.85157	861.069	1.889242905	0.72891
23208	36	MERI-5 protein (MERI-5) (MERI5B) / endo-xyloglucan transferase / xyloglucan endo-1,4-beta-D-glucanase (SEN4) identical to endo-xyloglucan transferase gi:944810, SP|P24806 MERI-5 protein precursor (Endo-xyloglucan transferase) (Xyloglucan endo-1,4-beta-D-glucanase) {Arabidopsis thaliana}	At4g30270	1472.93189	555.304	1890.00339	564.614	3446.82975	447.573	4.567020224	0.72864
29856	46	expressed protein	At5g56550	953.785661	467.624	805.732384	579.965	2182.90695	1098.222	1.805531167	0.728376
13384	21	alkaline alpha galactosidase, putative similar to alkaline alpha galactosidase II [Cucumis melo] GI:29838631; contains Pfam profile PF05691: Raffinose synthase or seed imbibition protein Sip1	At3g57520	1275.32972	747.599	1160.01461	514.271	1283.00576	1123.01	1.701339916	0.7209
23377	36	ripening-responsive protein, putative similar to ripening regulated protein DDTFR18 [Lycopersicon esculentum] GI:12231296; contains Pfam profile PF01554: Uncharacterized membrane protein family	At5g65380	892.259659	638.703	891.633662	729.42	626.72106	308.31	1.55071222	0.72036
251	1	yippee family protein similar to mdgl-1 [Mus musculus] GI:10441648, Yippee protein [Drosophila melanogaster] GI:5713279; contains Pfam profile PF03226: Yippee putative zinc-binding protein	At2g40110	769.61837	374.016	603.829645	533.64	937.675344	601.399	1.582800619	0.7128
3038	5	26S proteasome regulatory subunit, putative (RPN9) similar to 26S proteasome subunit p40.5 [Homo sapiens] gi|3618343|dbj|BAA33214	At4g19006	1072.05668	623.653	803.869745	572.546	1417.85042	565.897	1.876171324	0.71253
11064	18	methylcrotonyl-CoA carboxylase alpha chain, mitochondrial / 3-methylcrotonyl-CoA carboxylase 1 (MCCA) nearly identical to SP|Q42523 Methylcrotonyl-CoA carboxylase alpha chain, mitochondrial precursor (EC 6.4.1.4) (3-Methylcrotonyl-CoA carboxylase 1) (MCCase alpha subunit) (3-methylcrotonyl-CoA:carbon dioxi	At1g03090	910.623123	429.567	700.803189	352	3579.37332	1203.481	2.361654827	0.712356
18415	29	sinapoylglucose:malate sinapoyltransferase (SNG1) similar to serine carboxypeptidase I precursor (SP:P37890) [Oryza sativa]; contains Pfam profile PF00450: Serine carboxypeptidase; identical to cDNA sinapoylglucose:malate sinapoyltransferase (SNG1) GI:8699618	At2g22990	4085.189	2704	2941.75071	1695.299	4667.97208	1862.184	1.917584609	0.711822
767	2	expressed protein	At1g60010	9712.49188	4649.268	7498.23099	6174.497	9932.44589	5086.816	1.752003388	0.700245
2815	5	sinapoylglucose:malate sinapoyltransferase (SNG1) similar to serine carboxypeptidase I precursor (SP:P37890) [Oryza sativa]; contains Pfam profile PF00450: Serine carboxypeptidase; identical to cDNA sinapoylglucose:malate sinapoyltransferase (SNG1) GI:8699618	At2g22990	5398.73235	3458.197	3257.97392	2537.054	3825.25791	2175.012	1.534675553	0.693966
4203	7	serine carboxypeptidase S10 family protein contains Pfam profile: PF00450 serine carboxypeptidase; similar to serine carboxypeptidase I precursor (SP:P37890) [Oryza sativa]	At3g12230	2776.2309	1719.291	1840.89122	1297.522	2964.02162	1506.091	1.667183616	0.68904
13379	21	strictosidine synthase family protein similar to strictosidine synthase [Rauvolfia serpentina][SP|P15324]	At3g57020	1033.37886	687.06	607.430641	503.934	1121.54599	422.16	1.788707045	0.68904
18180	28	expressed protein similar to hypothetical protein GB:CAB80917 GI:7267605 from [Arabidopsis thaliana]	At1g01431	3364.08697	1830.95	2369.03522	1743.529	3672.4817	1682.677	1.903980553	0.688344
14032	22	trypsin inhibitor, putative similar to SP|P26780 Trypsin inhibitor 2 precursor (MTI-2) {Sinapis alba}	At2g43521	3465.72434	1873.31	2429.35368	1790.431	3767.31092	1721.287	1.908170305	0.68714
24315	38	expressed protein weak similarity to SP|P53809 Phosphatidylcholine transfer protein (PC-TP) {Rattus norvegicus}	At1g74960	3567.36171	1915.67	2489.67215	1837.332	3862.14015	1759.898	1.912360057	0.681384
19018	30	zinc finger (B-box type) family protein similar to zinc finger protein GI:3618316 from [Oryza sativa]	At1g78600	1324.91289	1124.333	1727.28459	1456.649	1702.24939	675.64	1.627884801	0.68034
14659	23	asparagine synthetase 1 [glutamine-hydrolyzing] / glutamine-dependent asparagine synthetase 1 (ASN1) identical to SP|P49078 Asparagine synthetase [glutamine-hydrolyzing] (EC 6.3.5.4) (Glutamine- dependent asparagine synthetase) {Arabidopsis thaliana}	At3g47340	1266.23944	777.959	1643.81796	1443.662	3379.26308	799.412	2.331157781	0.67983
11918	19	ABC transporter family protein similar to PDR5-like ABC transporter GI:1514643 from [Spirodela polyrhiza]	At2g26910	1151.06161	957.544	1331.99403	960.898	1786.05976	913.899	1.514208158	0.679272
2796	5	UDP-glucoronosyl/UDP-glucosyl transferase family protein contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase	At2g15490	656.863125	339.012	416.066391	367.222	767.000909	243.693	2.072665894	0.673552
29144	45	polyubiquitin (UBQ4) identical to GI:17677	At5g20620	10704.5532	7731.081	9411.38114	7622.13	10895.6971	5629.167	1.518311976	0.66928
27282	42	xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative similar to endo-xyloglucan transferase GI:2244732 from [Gossypium hirsutum]	At5g65730	1070.29724	769.445	1416.30991	780.267	1646.2892	1065.555	1.583721976	0.665364
22655	35	bZIP transcription factor family protein similar to seed storage protein opaque-2(bZIP family)GI:168428 from Zea mays; contains Pfam profile PF00170: bZIP transcription factor; identical to cDNA bZIP protein BZO2H3 GI:10954098	At5g28770	763.301483	376.854	781.707687	273.982	742.346675	668.329	1.996447438	0.66521
28563	44	copper transporter 1 (COPT1) nearly identical to SP|Q39065 Copper transporter 1 (COPT1) {Arabidopsis thaliana}	At5g59030	826.422216	702.949	812.083521	663.591	763.877119	281.286	1.705027132	0.663872
15283	24	expressed protein	At3g27770	395.281354	304.093	973.10221	696.513	1153.14679	618.696	1.520269932	0.66339
25923	40	chaperone protein dnaJ-related similar to Chaperone protein dnaJ (SP:Q9WZV3) [Thermotoga maritima]	At5g43260	528.72638	449.406	748.030409	561.464	754.241823	325.448	1.608778507	0.658416
22572	35	pectinesterase family protein contains Pfam profile: PF01095 pectinesterase	At4g33220	955.217817	691.288	721.054807	589.872	685.08749	340.709	1.538318815	0.657888
18068	28	alpha-glucosidase 1 (AGLU1) identical to alpha-glucosidase 1 [Arabidopsis thaliana] GI:2323344	At5g11720	1126.01333	633.312	1204.73069	690.89	832.977841	410.758	1.84987238	0.657888
8444	13	importin alpha-1 subunit, putative similar to importin alpha-1 subunit (Karyopherin alpha-1 subunit, KAP alpha) [Arabidopsis thaliana] SWISS-PROT:Q96321	At1g32880	1117.83218	660.835	1114.45882	683.742	727.509185	453.906	1.641420208	0.65772
17151	27	zinc finger (CCCH-type) family protein contains Pfam domain, PF00642: Zinc finger C-x8-C-x5-C-x3-H type (and similar) and Pfam domain, PF00023: Ankyrin repeat	At2g40140	3845.94522	1852.075	4059.06325	2057.915	3265.53442	1333.214	2.166115211	0.657443
21322	33	nodulin family protein similar to nodulin-like protein [Arabidopsis thaliana] GI:3329368, nodule-specific protein Nlj70 [Lotus japonicus] GI:3329366	At5g14120	2639.33543	1674.732	2729.70304	1558.574	3226.09631	1527.239	1.813252343	0.65736
9639	15	raffinose synthase family protein / seed imbibition protein, putative (din10) similar to seed imbibition protein GB:AAA32975 GI:167100 from [Hordeum vulgare]; contains nonconsensus AT donor splice site at intron 1; contains Pfam profile PF05691: Raffinose synthase or seed imbibition protein Sip1; identical to cDNA see	At5g20250	3425.05727	1433.546	3229.69654	735.179	7815.1468	5532.069	2.731664712	0.65736
13322	21	glycolipid transfer protein-related contains weak similarity to Glycolipid transfer protein (GLTP) (Swiss-Prot:P17403) [Sus scrofa]	At3g21260	877.663223	512.159	897.580085	682.184	858.984687	396.788	1.731414697	0.6561
6014	10	wound-responsive protein, putative similar to wound-responsive protein 14.05 (GI:16506638) [Castanea sativa]	At1g77310	4025.0866	2583.169	3413.43337	2548.594	3432.41495	1992.317	1.540120888	0.653883
7854	13	12-oxophytodienoate reductase, putative similar to OPR1 [GI:3882355] and OPR2 [GI:3882356]	At1g18020	2821.39995	1819.391	1602.53398	1018.547	2975.52294	1339.871	1.781614984	0.64989
5043	8	homeodomain protein (BELLRINGER) several homeodomain proteins;	At5g02030	1997.31154	633.566	2116.11884	540.4	3408.33392	946.186	3.556837127	0.649194
5461	9	trypsin inhibitor, putative similar to SP|P26780 Trypsin inhibitor 2 precursor (MTI-2) {Sinapis alba}	At2g43510	616.755282	425.664	658.437313	505.848	1171.86273	200.919	2.861029648	0.648
26220	41	CBL-interacting protein kinase 3 (CIPK3) identical to CBL-interacting protein kinase 3 [Arabidopsis thaliana] gi|9280638|gb|AAF86507	At2g26980	802.937645	449.692	560.38347	322.618	1524.53354	814.292	1.798245101	0.64792
3836	6	glycosyl hydrolase family 3 protein	At5g49360	2157.03913	629.007	1057.0803	381.654	3101.16737	1940.799	2.598964415	0.645606
1931	3	asparagine synthetase 2 (ASN2) identical to asparagine synthetase (ASN2) [Arabidopsis thaliana] GI:3859536	At5g65010	2723.47645	1608.764	2191.69992	1841.95	7634.68655	2981.252	1.814559866	0.64328
17040	27	UbiE/COQ5 methyltransferase family protein low similarity to SP|Q05197 Phosphatidylethanolamine N-methyltransferase (EC 2.1.1.17) [Rhodopseudomonas sphaeroides] {Rhodobacter sphaeroides}; contains Pfam profile PF01209: methlytransferase, UbiE/COQ5 family	At1g69526	1608.70751	708.456	1481.00356	1057.31	917.274826	647.485	1.696041525	0.642936
28816	45	serine carboxypeptidase S10 family protein similar to serine carboxypeptidase I precursor (SP:P37890) [Oryza sativa]	At2g23000	3089.55744	2281.431	2883.53886	2045.557	2347.01627	1084.925	1.642392258	0.642816
29215	45	xyloglucan:xyloglucosyl transferase / xyloglucan endotransglycosylase / endo-xyloglucan transferase (TCH4) identical to xyloglucan endotransglycosylase TCH4 protein GI:886116	At5g57560	486.388482	186.933	705.078176	250.232	1814.01923	1263.888	2.284969009	0.642005
9042	14	pyridoxamine 5'-phosphate oxidase-related contains weak similarity to Pyridoxamine 5'-phosphate oxidase (EC 1.4.3.5) (PNP/PMP oxidase) (PNPOx). (Swiss-Prot:P28225) [Shigella flexneri]	At5g49970	868.588983	764.514	677.917745	596.381	848.37617	254.988	1.866657792	0.639821
27738	43	glutathione S-transferase-related contains weak hit to Pfam profile PF00043: Glutathione S-transferase, C-terminal domain	At4g19880	1322.62508	1030.956	1816.56857	1602.899	1337.73086	601.011	1.547338063	0.638664
25005	39	cytochrome P450, putative similar to GB:Q05047 from [Catharanthus roseus]	At3g14690	3411.44163	2466.579	3114.7228	2416.425	3480.86979	1371.652	1.736588841	0.63648
23654	37	ACT domain-containing protein contains Pfam ACT domain PF01842	At2g39570	547.189315	311.386	586.720134	266.541	557.954367	317.346	1.90556578	0.63597
25128	39	monooxygenase, putative (MO1) similar to GI:3426062	At4g15760	1479.21241	864.126	2302.10869	1345.038	1117.17474	743.609	1.641908964	0.63495
7793	12	thioesterase family protein contains Pfam profile PF03061: thioesterase family protein	At1g35250	1424.72633	950.977	1076.10663	658.437	993.025202	699.994	1.517041917	0.63495
5550	9	nitrilase 2 (NIT2) identical to SP|P32962 Nitrilase 2 (EC 3.5.5.1) {Arabidopsis thaliana}	At3g44300	6358.29049	5358.119	5582.12357	4930.994	5720.70807	2614.229	1.502336489	0.63468
13062	21	expressed protein similar to TolB protein precursor (SP:Q9ZDM5) {Rickettsia prowazekii}; ESTs gb|N96028, gb|F14286, gb|T20680, gb|F14443, gb|AA657300 and gb|N65244 come from this gene	At1g21680	2892.84943	1900.774	1354.90178	956.867	2643.44028	1226.645	1.697642008	0.63427
29968	47	expressed protein	At1g25275	5657.46693	3620.371	6573.76134	4679.333	5921.55853	3568.766	1.542266502	0.63168
246	1	expressed protein contains Pfam profile PF04749: Protein of unknown function, DUF614	At2g37110	2673.23977	1647.646	1384.2961	1248.984	2677.62053	1054.476	1.756695975	0.628488
15886	25	expressed protein identical to unknown protein GB:AAF30301 from [Arabidopsis thaliana]	At3g06080	652.093908	427.992	701.649263	402.293	1036.22836	487.223	1.798180812	0.628227
25059	39	asparagine synthetase 1 [glutamine-hydrolyzing] / glutamine-dependent asparagine synthetase 1 (ASN1) identical to SP|P49078 Asparagine synthetase [glutamine-hydrolyzing] (EC 6.3.5.4) (Glutamine- dependent asparagine synthetase) {Arabidopsis thaliana}	At3g47340	1628.7962	1342.263	1730.76289	1449.36	2885.29178	1270.729	1.559402279	0.627792
5430	9	BTB/POZ domain-containing protein contains Pfam PF00651: BTB/POZ domain; contains Interpro IPR000210/ PS50097: BTBB/POZ domain; similar to MigA (GI:1841872) [Dictyostelium discoideum]	At2g30600	2238.72762	1095.847	1404.06015	506.57	4232.00637	1728.942	2.420787815	0.627264
11863	19	auxin efflux carrier family protein contains auxin efflux carrier domain, Pfam:PF03547	At1g76530	686.151188	587.824	729.69401	559.437	1050.10706	489.085	1.539564837	0.62656
13360	21	expressed protein	At3g47295	2500.44736	2025.918	2629.8726	1903.631	3391.93145	1649.575	1.557326107	0.624624
22354	35	expressed protein similar to GI:7572912 (At3g56140)[Arabidopsis thaliana]	At2g40400	712.019832	539.166	598.714956	463.586	627.558195	315.125	1.534513027	0.620928
2689	5	expressed protein	At1g42550	459.282344	288.533	323.004549	262.13	423.468479	233.077	1.546958565	0.620928
30909	48	LOB domain protein 38 / lateral organ boundaries domain protein 38 (LBD38) identical to SP|Q9SN23 LOB domain protein 38 {Arabidopsis thaliana}	At3g49940	1131.1323	579.119	586.868317	383.556	1580.78445	1221.565	1.59244398	0.620508
19258	30	expressed protein	At4g08555	2331.85623	1282.003	3549.66574	1989.898	4761.426	929.918	2.907674595	0.619875
29310	46	glycosyl transferase family 20 protein / trehalose-phosphatase family protein contains Pfam profile: PF02358 trehalose-phosphatase	At1g23870	530.708295	232.296	609.951338	214.063	885.509072	694.22	2.136522422	0.6188
25908	40	jacalin lectin family protein similar to myrosinase-binding protein homolog [Arabidopsis thaliana] GI:2997767; contains Pfam profile PF01419 jacalin-like lectin domain	At5g35940	764.796744	523.723	1371.68784	704.988	555.249143	268.065	1.82577338	0.61659
13435	21	expressed protein	At4g18740	798.067889	616.031	892.212052	602.189	1128.38328	458.989	1.745174834	0.613524
30816	48	F-box family protein contains Pfam:PF00646 F-box domain	At2g16365	689.173796	576.787	558.286607	385.442	875.750061	361.51	1.688586685	0.613008
22036	34	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein contains Pfam protease inhibitor/seed storage/LTP family domain PF00234	At5g48485	1041.74825	928.492	1409.61142	932.325	1861.36064	700.336	1.763906988	0.612765
15503	24	expressed protein similar to PGPS/D12 [Petunia x hybrida] GI:4105794; contains Pfam profile PF04749: Protein of unknown function, DUF614	At5g35525	970.484873	519.39	891.281529	596.649	905.596179	496.564	1.72868204	0.61236
16016	25	major intrinsic family protein / MIP family protein contains Pfam profile: MIP PF00230	At4g10380	561.530123	332.347	551.787288	267.291	832.227307	635.403	1.687907313	0.61232
2091	4	glutamate:glyoxylate aminotransferase 2 (GGT2) identical to glutamate:glyoxylate aminotransferase 2 [Arabidopsis thaliana] GI:24461829; similar to alanine aminotransferase from Panicum miliaceum [SP|P34106], GI:4730884 from Oryza sativa; contains Pfam profile PF00155: aminotransferase, classes I and II	At1g70580	1605.87743	1219.415	1435.76963	1288.218	3091.5197	1461.668	1.515508881	0.61194
27784	43	DNAJ heat shock N-terminal domain-containing protein (J11) identical to dnaJ heat shock protein J11 [Arabidopsis thaliana] GI:9843641; contains Pfam profile PF00226 DnaJ domain	At4g36040	6067.5704	2534.588	5921.10156	3749.741	6056.10834	2940.255	2.010899862	0.611064
10690	17	glutathione S-transferase, putative similar to glutathione transferase GB:CAA71784 [Glycine max]	At3g09270	2258.40451	1211.734	898.477148	728.693	766.04006	380.263	1.703759315	0.60588
11218	18	nitrate reductase 1 (NR1) identical to SP|P11832 Nitrate reductase 1 (formerly EC 1.6.6.1) (NR1){Arabidopsis thaliana}	At1g77760	892.354851	558.081	702.104964	506.615	2472.81121	860.714	1.952607191	0.605734
16695	26	RWP-RK domain-containing protein similar to nodule inception protein [Lotus japonicus] GI:6448579; contains Pfam profile: PF02042 RWP-RK domain	At4g24020	502.406377	315.936	322.330557	240.203	662.688984	301.09	1.711030352	0.60544
2513	4	proline oxidase, putative / osmotic stress-responsive proline dehydrogenase, putative similar to proline oxidase, mitochondrial precursor (Osmotic stress- induced proline dehydrogenase) [Arabidopsis thaliana] SWISS-PROT:P92983	At5g38710	744.11231	447.057	912.673994	303.915	1992.80109	1199.205	2.109764596	0.60544
201	1	expressed protein similar to myo-inositol oxygenase [Sus scrofa] gi|17432544|gb|AAL39076	At2g19800	1100.58535	323.853	1620.5055	364.496	3592.97779	1413.754	3.461911706	0.60291
820	2	phosphoribulokinase/uridine kinase-related	At1g80380	1104.01974	540.526	664.823504	559.588	1859.54204	844.766	1.81060047	0.601996
19351	30	monooxygenase, putative (MO3) similar to GI:3426064; identical to cDNA monooxygenase 3, partial GI:3426065	At5g05320	1097.7296	735.625	1046.35858	895.174	1208.16262	429.485	1.824726284	0.598347
23175	36	disease resistance protein (TIR-NBS class), putative domain signature TIR-NBS exists, suggestive of a disease resistance protein.	At4g16990	926.48807	704.352	1186.26045	810.076	433.654305	243.966	1.519092536	0.596687
7233	12	thioesterase family protein contains Pfam profile PF03061: thioesterase family protein	At1g35250	2695.23656	1734.294	2208.22786	1380.021	2557.77625	1644.243	1.569939551	0.591948
3690	6	26.5 kDa class P-related heat shock protein (HSP26.5-P) contains Pfam profile: PF00011 Hsp20/alpha crystallin family: identified in Scharf, K-D., et al,Cell Stress & Chaperones (2001) 6: 225-237.	At4g21870	411.455407	302.512	435.143702	267.889	1679.07973	666.477	1.83460295	0.59168
17266	27	nonspecific lipid transfer protein 5 (LTP5) identical to SP|Q9XFS7 Nonspecific lipid-transfer protein 5 (LTP 5) {Arabidopsis thaliana}	At3g51600	5398.66818	3712.602	5251.07732	2785.961	8282.53804	3761.998	1.84687157	0.5916
4067	7	multi-copper oxidase type I family protein similar to pollen-specific BP10 protein [SP|Q00624][Brassica napus]; contains Pfam profile: PF00394 Multicopper oxidase	At1g76160	1004.03945	662.054	694.085579	434.87	1614.59355	1059.801	1.545371902	0.59136
25231	39	NADP-dependent oxidoreductase, putative (P1) identical to probable NADP-dependent oxidoreductase P1, zeta-crystallin homolog [SP|Q39172][gi:886428], Arabidopsis thaliana; similar to allyl alcohol dehydrogenase [Nicotiana tabacum] GI:6692816; contains Pfam profile PF00107: oxidoreductase, zinc-binding dehydro	At5g16970	1258.61233	1026.281	1327.2729	1195.558	1170.273	444.763	1.655926778	0.590132
852	2	expressed protein contains Pfam profile PF04720: Protein of unknown function (DUF506)	At2g20670	7021.44911	2262.284	4264.07304	2138.008	4283.63037	3673.593	2.088057782	0.588588
19682	31	PAC motif-containing protein similar to nonphototropic hypocotyl 1 [Zea mays] GI:2687358; contains Pfam profile PF00785: PAC motif	At2g02710	465.756457	269.216	890.092882	459.015	585.394238	430.888	1.6759202	0.58548
14916	23	heat shock protein-related contains similarity to 101 kDa heat shock protein; HSP101 [Triticum aestivum] gi|11561808|gb|AAC83689	At5g57710	494.176028	206.402	949.611289	606.69	694.172257	477.264	1.804652129	0.583596
27705	43	methionine sulfoxide reductase domain-containing protein / SelR domain-containing protein low similarity to pilin-like transcription factor [Homo sapiens] GI:5059062; contains Pfam profile PF01641: SelR domain	At4g04840	2827.81417	1731.896	3598.1294	2170.1	1472.39407	999.544	1.587966245	0.582505
2310	4	peroxidase, putative identical to peroxidase [Arabidopsis thaliana] gi|405611|emb|CAA50677	At3g49120	2553.5783	1525.549	1342.45763	970.142	3740.34854	1999.258	1.642839235	0.580041
1084	2	DREPP plasma membrane polypeptide family protein contains Pfam profile: PF05558 DREPP plasma membrane polypeptide	At4g20260	5287.99753	2748.755	3717.97883	3141.819	7308.2927	3419.365	1.74816261	0.578676
14464	23	gibberellin-regulated protein 1 (GASA1) / gibberellin-responsive protein 1 identical to SP|P46689 Gibberellin-regulated protein 1 precursor {Arabidopsis thaliana}; supporting cDNA gi|887938|gb|U11766.1|ATU11766	At1g75750	5861.81702	3176.735	6384.73137	1882.801	20423.8565	2863.992	4.122523109	0.578676
27218	42	transferase family protein similar to anthocyanin 5-aromatic acyltransferase from Gentiana triflora GI:4185599, malonyl CoA:anthocyanin 5-O-glucoside-6'''-O-malonyltransferase from Perilla frutescens GI:17980232, Salvia splendens GI:17980234; contains Pfam profile PF02458 transferase family	At5g39080	1258.34066	1078.81	1292.97102	1042.073	1155.63758	514.806	1.550661904	0.578
6207	10	transferase family protein similar to hypersensitivity-related hsr201 protein - Nicotiana tabacum,PIR2:T03274; contains Pfam transferase family domain PF00248	At3g48720	761.248977	448.328	575.080632	325.308	475.657433	387.899	1.564005754	0.57749
21674	34	superoxide dismutase [Cu-Zn], chloroplast (SODCP) / copper/zinc superoxide dismutase (CSD2) identical to GP:3273753:AF061519	At2g28190	313.944758	267.414	359.487735	264.551	818.942434	226.895	2.047402668	0.57749
63	1	gibberellin-responsive protein, putative similar to SP|P46688 Gibberellin-regulated protein 2 precursor {Arabidopsis thaliana}; contains Pfam profile PF02704: Gibberellin regulated protein	At1g22690	5772.83085	2874.644	5339.29694	3178.644	15275.8227	2733.033	3.092420026	0.577125
26376	41	expressed protein	At3g54880	1286.65006	997.735	1616.9523	969.385	691.337133	425.018	1.52806545	0.57596
12653	20	beta-galactosidase, putative / lactase, putative similar to beta-galactosidase precursor SP:P48980 from [Lycopersicon esculentum]	At3g13750	857.001251	486.281	951.026193	378.085	1687.11292	1428	1.819728797	0.5742
9601	15	myb family transcription factor contains PFAM profile: PF00249 myb-like DNA binding domain	At5g02840	744.669556	565.468	529.04684	418.472	2038.59194	673.221	1.869753373	0.57239
1826	3	expressed protein	At5g14730	492.986665	328.463	494.859686	411.892	607.691711	331.521	1.511787184	0.57154
14606	23	expressed protein	At3g14760	1544.33431	1337.916	1612.01129	1289.866	1983.62148	899.683	1.536278294	0.57104
12657	20	UDP-glucoronosyl/UDP-glucosyl transferase family protein contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase	At3g16520	581.170655	521.563	1253.30271	742.82	912.17779	528.493	1.509169025	0.570459
21744	34	no apical meristem (NAM) family protein similar to to NAC2 (GI:645671) [Arabidopsis thaliana]; contains Pfam PF02365: No apical meristem (NAM) protein	At3g10500	445.316955	291.904	258.444748	217.953	820.77547	285.681	1.861463497	0.570459
14831	23	NADP-dependent oxidoreductase, putative strong similarity to probable NADP-dependent oxidoreductase (zeta-crystallin homolog) P1 [SP|Q39172][gi:886428] and P2 [SP|Q39173][gi:886430], Arabidopsis thaliana	At5g16990	1482.49065	1121.556	1702.94281	1283.197	2004.54572	673.611	1.874915444	0.565812
7999	13	expressed protein	At2g15960	3528.16819	2192.825	4258.06766	2915.838	6097.55269	4166.397	1.510930464	0.56416
29896	46	nitrate reductase 2 (NR2) identical to SP|P11035 Nitrate reductase 2 (formerly EC 1.6.6.1) (NR2) {Arabidopsis thaliana}	At1g37130	405.684002	238.987	847.123123	461.811	1291.66783	628.869	1.861939641	0.56406
19332	30	cytochrome P450, putative similar to cytochrome p450 SP:O65790 from [Arabidopsis thaliana]	At4g37410	4505.88764	2571.39	1162.9209	720.054	2973.00947	1622.195	1.733356846	0.56232
14542	23	mitochondrial transcription termination factor-related / mTERF-related contains Pfam profile PF02536: mTERF	At2g36000	1518.72451	1077.916	1799.00176	1203.792	2296.61086	847.979	1.870575141	0.561946
12379	20	Toll-Interleukin-Resistance (TIR) domain-containing protein domain signature TIR exists, suggestive of a disease resistance protein.	At1g09665	1178.21695	819.22	1466.46573	790.368	1562.95101	1084.63	1.578212894	0.5607
24710	39	CBL-interacting protein kinase 9 (CIPK9) identical to CBL-interacting protein kinase 9 [Arabidopsis thaliana] gi|13249117|gb|AAK16684; contains Pfam profiles PF00069: Protein kinase domain and PF03822: NAF domain; identical to cDNA CBL-interacting protein kinase 9 (CIPK9) GI:13249116	At1g01140	366.797609	190.738	843.810525	634.072	537.240439	322.433	1.640010835	0.558012
3517	6	expressed protein	At3g01060	365.107687	244.047	265.425262	229.759	712.572724	296.043	1.686092929	0.557345
29336	46	nitrate reductase 2 (NR2) identical to SP|P11035 Nitrate reductase 2 (formerly EC 1.6.6.1) (NR2) {Arabidopsis thaliana}	At1g37130	1854.17192	1181.382	2816.58743	1785.798	3742.2558	1800.756	1.741622386	0.55695
3151	5	expressed protein	At5g24570	1356.1818	1112.696	1278.52561	927.392	3056.17447	961.797	1.925005653	0.554648
1616	3	expressed protein contains similarity to phosphoserine aminotransferase GB:P19689 from [Yersinia enterocolitica]	At3g19030	9302.09642	4095.432	7341.59404	4669.33	10661.4232	8966.762	1.677543217	0.554625
9036	14	expressed protein similar to unknown protein (emb|CAB82953.1)	At5g49340	382.345963	300.529	580.035985	525.189	1502.93711	662.291	1.548658742	0.552464
22001	34	meprin and TRAF homology domain-containing protein / MATH domain-containing protein low similarity to ubiquitin-specific protease 12 [Arabidopsis thaliana] GI:11993471; contains Pfam profile PF00917: MATH domain	At5g26280	8915.87968	5256.638	8054.98956	5988.278	6168.55655	3543.909	1.593950834	0.552188
13189	21	hypothetical protein	At2g07190	391.964615	318.068	438.306524	270.641	497.798201	281.419	1.54024284	0.551286
24740	39	thioredoxin family protein similar to thioredoxin H-type from Arabidopsis thaliana SP|P29448, Nicotiana tabacum SP|Q07090; contains Pfam profile: PF00085 Thioredoxin	At1g11530	1670.44957	1041.457	1192.56219	1029.736	2247.91684	737.502	1.936697739	0.55112
17891	28	proline oxidase, mitochondrial / osmotic stress-responsive proline dehydrogenase (POX) (PRO1) (ERD5) nearly identical to SP|P92983 Proline oxidase, mitochondrial precursor (EC 1.5.3.-) (Osmotic stress- induced proline dehydrogenase) [Arabidopsis thaliana]; identical to cDNA proline oxidase precursor GI:1817543	At3g30775	480.0855	339.703	333.84259	161.152	686.283397	581.604	1.554945108	0.549753
24478	38	inositol polyphosphate 5-phosphatase II (IP5PII) nearly identical to inositol polyphosphate 5-phosphatase II [Arabidopsis thaliana] GI:10444263 isoform contains an AT-acceptor splice site at intron 6	At4g18010	397.649385	295.372	345.692416	259.001	994.738648	192.747	2.613944157	0.549626
7929	13	cytochrome P450, putative similar to cytochrome P450 89A2 (CYPLXIX) (SP:Q42602) [Arabidopsis thaliana];similar to cytochrome P450 (GI:438242) [Solanum melongena]	At1g64950	2162.92819	1937.22	1307.91675	1120.768	2172.53349	766.966	1.705375786	0.548049
6292	10	major latex protein-related / MLP-related low similarity to major latex protein {Papaver somniferum}[GI:294060] ; contains Pfam profile PF00407: Pathogenesis-related protein Bet v I family	At4g23680	1587.32465	1149.128	2177.954	1582.808	2074.41966	878.866	1.705890944	0.54735

23616	37	serine carboxypeptidase S10 family protein similar to serine carboxypeptidase I precursor (SP:P37890) [Oryza sativa]	At2g23010	2219.22613	1714.013	1558.14294	1089.417	1655.6482	776.794	1.618798308	0.54675
17720	28	kelch repeat-containing F-box family protein similar to SP|Q9ER30 Kelch-related protein 1 (Sarcosin) {Rattus norvegicus}; contains Pfam profiles PF01344: Kelch motif, PF00646: F-box domain	At1g80440	1633.70874	799.598	1404.23224	695.271	1358.92933	930.799	1.840937714	0.543576
20757	32	beta-galactosidase, putative / lactase, putative similar to beta-galactosidase precursor GI:3869280 from [Carica papaya]	At5g56870	1105.20055	282.977	625.728798	158.689	797.939839	353.94	3.367727681	0.54264
9464	15	broad-spectrum mildew resistance RPW8 family protein contains Pfam PF05659: Arabidopsis broad-spectrum mildew resistance protein RPW8	At3g50480	360.167339	287.909	339.943569	213.493	1154.47672	619.095	1.569350423	0.539616
7603	12	no apical meristem (NAM) family protein (RD26) contains Pfam PF02365: No apical meristem (NAM) domain; Arabidopsis thaliana nap gene,PID:e1234813; identical to cDNA RD26 mRNA for NAM-like protein GI:15375403	At4g27410	481.018166	226.394	403.5362	241.324	1187.5456	787.157	1.768507455	0.537516
19112	30	autophagy 8e (APG8e) identical to autophagy 8e [Arabidopsis thaliana] GI:19912159; contains Pfam profile PF02991: Microtubule associated protein 1A/1B, light chain 3	At2g45170	3948.08497	1914.459	3520.42119	1728.483	3589.19418	2378.754	1.869270657	0.536844
7090	11	acetyl-CoA C-acyltransferase, putative / 3-ketoacyl-CoA thiolase, putative strong similarity to Acetoacetyl-coenzyme A thiolase (E.C. 2.3.1.9) [Raphanus sativus] GI:1542941; contains InterPro accession IPR002155: Thiolase	At5g48230	9105.54671	6615.708	9926.00169	6688.256	9330.33164	5592.62	1.509592001	0.536256
5078	8	DNAJ heat shock N-terminal domain-containing protein similar to SP|P30725 Chaperone protein dnaJ Clostridium acetobutylicum; contains Pfam profile PF00226: DnaJ domain	At5g16650	920.516655	549.73	841.125712	496.199	2114.64954	1656.558	1.548719559	0.535952
9826	16	xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative (XTR4) identical to N-terminal partial sequence of xyloglucan endotransglycosylase-related protein XTR4 GI:1244754 from [Arabidopsis thaliana]; similar to endoxyloglucan transferase [Arabid	At1g32170	690.767456	326.462	464.565113	339.227	1196.5149	741.13	1.699949402	0.530868
16210	25	CER1 protein, putative (WAX2) similar to maize glossy1 homolog GI:2213643 from [Oryza sativa]; contains Pfam profile PF01598: Sterol desaturase	At5g57800	589.737919	436.21	476.88498	312.251	395.676021	206.007	1.599966567	0.525888
16458	26	auxin-responsive protein, putative similar to small auxin-up regulated protein SAUR (GI:3043536) [Raphanus sativus]	At2g21210	3059.90893	2400.28	2294.50995	1361.066	5561.07103	2381.446	1.765265773	0.524477
19045	30	hypothetical protein	At2g18200	485.523199	332.983	503.782508	449.31	399.989533	206.195	1.506399487	0.522144
10575	17	CBS domain-containing protein low similarity to SP|Q9MYP4 5'-AMP-activated protein kinase, gamma-3 subunit (AMPK gamma-3 chain) (AMPK gamma3) {Sus scrofa}; contains Pfam profile PF00571: CBS domain	At1g80090	608.623334	410.415	485.739288	310.224	716.525401	428.664	1.573415737	0.52164
1856	3	NAD-dependent epimerase/dehydratase family protein similar to sugar epimerase BlmG from Streptomyces verticillus GI:9937230; contains Pfam profile PF01370 NAD dependent epimerase/dehydratase family	At5g28840	1705.07158	1129.764	1832.47509	1384.063	3840.62325	1753.779	1.674374477	0.5214
30422	47	auxin-responsive GH3 family protein similar to auxin-responsive GH3 product [Glycine max] GI:18591; contains Pfam profile PF03321: GH3 auxin-responsive promoter	At5g13370	703.037575	459.113	309.642623	223.267	870.360234	224.832	2.263108296	0.520828
26958	42	jacalin lectin family protein similar to SP|Q9SAV1 Myrosinase binding protein-like At1g52030 {Arabidopsis thaliana}; contains Pfam profile: PF01419 jacalin-like lectin domain	At3g16450	5265.29268	3223.773	3956.07158	2886.038	4635.42692	2485.196	1.62308275	0.518868
19859	31	asparagine synthetase 1 [glutamine-hydrolyzing] / glutamine-dependent asparagine synthetase 1 (ASN1) identical to SP|P49078 Asparagine synthetase [glutamine-hydrolyzing] (EC 6.3.5.4) (Glutamine- dependent asparagine synthetase) {Arabidopsis thaliana}	At3g47340	467.39397	229.677	1138.86274	363.042	2087.82618	251.607	4.48999031	0.516516
28616	45	no apical meristem (NAM) family protein contains Pfam PF02365: No apical meristem (NAM) domain; similar to NAC domain protein NAM GB:AAD17313 GI:4325282 from [Arabidopsis thaliana]	At1g01720	1770.37531	1473.838	2360.17554	1886.714	1994.4135	736.52	1.720011192	0.515592
26965	42	expressed protein	At3g19660	625.628443	403.134	630.426027	542.109	447.485584	213.821	1.602543437	0.514796
8630	14	glycine-rich protein (GRP3S) identical to cDNA glycine-rich protein 3 short isoform (GRP3S) GI:4206766	At2g05380	16050.1899	11608.78	19018.8094	14729.65	22993.2763	11367.69	1.565489883	0.511758
8647	14	gibberellin-responsive protein, putative similar to SP|P46689 Gibberellin-regulated protein 1 precursor {Arabidopsis thaliana}; contains Pfam profile PF02704: Gibberellin regulated protein	At2g18420	1057.91695	633.314	793.422077	330.877	7259.93477	753.934	4.5659288	0.50949
18034	28	PQ-loop repeat family protein / transmembrane family protein similar to SP|Q10482 Seven transmembrane protein 1 {Schizosaccharomyces pombe}; contains Pfam profile PF04193: PQ loop repeat	At4g36850	501.480129	235.461	352.387719	216.48	657.870305	358.637	1.863983296	0.508956
30661	48	cytochrome P450, putative similar to SP:Q42569 from [Arabidopsis thaliana]	At1g55940	407.874483	294.335	411.931619	214.958	589.757236	198.995	2.088587738	0.5031
28560	44	expressed protein	At5g58650	357.609994	308.912	440.540416	281.895	558.471906	281.798	1.567413985	0.502824
16701	26	expressed protein	At4g27040	526.340167	458.305	412.291719	358.861	1756.02601	548.857	1.832254275	0.500976
29704	46	expressed protein	At4g28080	2882.50989	2039.285	1681.74155	1171.269	2740.74791	1469.623	1.57141724	0.50049
26951	42	2-oxoisovalerate dehydrogenase / 3-methyl-2-oxobutanoate dehydrogenase / branched-chain alpha-keto acid dehydrogenase E1 beta subunit (DIN4) identical to branched chain alpha-keto acid dehydrogenase E1 beta subunit [Arabidopsis thaliana] GI:7021286	At3g13450	852.767889	542.894	1126.64007	851.199	942.310513	487.554	1.609034662	0.49662
13215	21	sinapoylglucose:malate sinapoyltransferase (SNG1) similar to serine carboxypeptidase I precursor (SP:P37890) [Oryza sativa]; contains Pfam profile PF00450: Serine carboxypeptidase; identical to cDNA sinapoylglucose:malate sinapoyltransferase (SNG1) GI:8699618	At2g22990	4727.50061	3288.406	3052.85896	2231.705	5543.61904	2696.614	1.620448761	0.494586
19842	31	cytochrome P450 family protein contains Pfam profile: PF00067 cytochrome P450	At3g28740	1948.39578	1355.407	429.514358	290.052	532.469184	176.831	1.976497567	0.492328
23827	37	integral membrane family protein contains TIGRFAM TIGR01569 : plant integral membrane protein TIGR01569; contains Pfam PF04535 : Domain of unknown function (DUF588)	At4g15610	1586.89575	916.54	2537.11031	1541.72	4948.5091	753.343	3.315255864	0.489288
16063	25	expressed protein	At4g29905	4001.74107	1703.996	3897.2192	1590.37	4709.83912	3853.931	2.007014386	0.489216
23835	37	expressed protein	At4g18740	311.151039	235.378	297.515553	198.571	441.761727	156.103	1.883380368	0.489168
13750	22	expressed protein similar to PGPS/D12 [Petunia x hybrida] GI:4105794; contains Pfam profile PF04749: Protein of unknown function, DUF614	At1g52200	640.665542	290.882	256.532714	157.974	522.615325	426.776	1.68365026	0.485112
29083	45	catalase 2 identical to catalase 2 SP:P25819, GI:17865693 from [Arabidopsis thaliana]	At4g35090	3341.16332	2392.986	2266.62135	1832.177	3628.38487	1650.253	1.610678359	0.483807
8916	14	UDP-glucoronosyl/UDP-glucosyl transferase family protein contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase	At4g34135	1117.30488	803.638	977.613015	816.577	3149.57684	1020.532	1.891242683	0.482856
1525	3	WRKY family transcription factor	At2g30250	447.30101	289.577	546.162723	274.967	576.682677	316.847	1.783673898	0.47712
13977	22	hydrolase, alpha/beta fold family protein low similarity to 3-oxoadipate enol-lactone hydrolase [Pseudomonas sp. B13] GI:17736948, B-ketoadipate enol-lactone hydrolase [Bradyrhizobium japonicum] GI:2239060; contains Pfam profile:PF00561 abhydrolase:alpha/beta hydrolase fold	At3g24420	302.286434	267.16	392.623271	335.09	607.63604	187.542	1.847725218	0.472685
12855	20	glutamate dehydrogenase 2 (GDH2) identical to glutamate dehydrogenase 2 (GDH 2) [Arabidopsis thaliana] SWISS-PROT:Q38946	At5g07440	3403.08079	1891.486	4092.93332	2626.374	5715.37392	2574.548	1.859168873	0.471077
17967	28	major latex protein-related / MLP-related low similarity to major latex protein {Papaver somniferum}[GI:294060] ; contains Pfam profile PF00407: Pathogenesis-related protein Bet v I family	At4g14060	1882.7776	827.188	326.956084	242.282	1673.64866	1007.612	1.762202956	0.47073
20031	31	NADP-dependent oxidoreductase, putative strong similarity to probable NADP-dependent oxidoreductase (zeta-crystallin homolog) P1 [SP|Q39172][gi:886428] and P2 [SP|Q39173][gi:886430], Arabidopsis thaliana	At5g16980	1698.63063	1260.975	1798.39469	1346.834	2344.18527	754.096	1.930318696	0.46215
9509	15	arginase, putative similar to Swiss-Prot:P46637 arginase (EC 3.5.3.1) [Arabidopsis thaliana]	At4g08870	351.727354	217.176	480.012748	193.88	629.201536	169.979	2.599005516	0.46136
24028	37	no apical meristem (NAM) family protein contains Pfam PF02365: No apical meristem (NAM) domain; contains similarity to NAC-domain protein	At5g63790	2459.29669	1768.805	2794.274	2441.158	3595.37166	1332.859	1.744170418	0.459648
1107	2	villin, putative similar to villin 2 (VLN2) [Arabidopsis thaliana] GI:3415115, villin 3 (VLN3) [Arabidopsis thaliana] GI:3415117; contains Pfam profiles PF00626: Gelsolin repeat, PF02209: Villin headpiece domain	At4g30160	2998.03746	1838.975	2274.20734	2042.05	2388.26886	1256.566	1.548198727	0.45864
4701	8	integral membrane protein, putative strong similarity to integral membrane protein GI:1209756 from [Beta vulgaris]; contains Pfam profile PF00083: major facilitator superfamily protein	At1g75220	371.320825	280.851	237.052283	157.326	970.818453	494.454	1.597433685	0.458575
6345	10	expressed protein	At5g01280	275.14607	222.294	340.233561	267.169	281.825709	102.195	1.75631983	0.457884
6431	10	26S proteasome regulatory subunit, putative (RPN9) contains similarity to 26S proteasome subunit p40.5 GI:3618343 from [Homo sapiens]	At5g45620	3773.09139	2160.17	3908.15443	2364.345	5128.658	1324.07	2.424340819	0.454674
23977	37	serine protease inhibitor, potato inhibitor I-type family protein similar to SP|P24076 Glu S.griseus protease inhibitor (BGIA) {Momordica charantia}; contains Pfam profile PF00280: Potato inhibitor I family	At5g43570	337.278519	178.679	515.343935	245.868	1205.27389	118.804	4.709567618	0.452709
15199	24	calcium-transporting ATPase 4, plasma membrane-type / Ca2+-ATPase, isoform 4 (ACA4) identical to SP|O22218 Calcium-transporting ATPase 4, plasma membrane-type (EC 3.6.3.8) (Ca(2+)-ATPase isoform 4) {Arabidopsis thaliana}	At2g41560	192.19977	160.194	634.176798	385.475	840.213077	450.361	1.570206671	0.451704
427	1	expressed protein contains Pfam PF05421: Protein of unknown function (DUF751)	At4g16410	3138.19404	2127.783	2157.76133	1849.897	4777.5563	2437.021	1.533898802	0.451269
16397	26	expressed protein contains Pfam profile: PF00561 alpha/beta hydrolase fold	At1g73750	266.902886	221.55	453.82586	306.23	344.47266	149.997	1.661071567	0.44982
23615	37	sinapoylglucose:malate sinapoyltransferase (SNG1) similar to serine carboxypeptidase I precursor (SP:P37890) [Oryza sativa]; contains Pfam profile PF00450: Serine carboxypeptidase; identical to cDNA sinapoylglucose:malate sinapoyltransferase (SNG1) GI:8699618	At2g22990	4646.76191	3162.665	2679.82447	1874.187	2844.85158	1174.999	1.773422406	0.449064
1223	2	metalloendopeptidase identical to chloroplast processing enzyme metalloendopeptidase [Arabidopsis thaliana] gi|2827039|gb|AAC39482	At5g42390	566.642672	381.22	474.633561	330.218	777.102197	466.981	1.529274978	0.44772
10371	16	MA3 domain-containing protein low similarity to programmed cell death 4 protein [Gallus gallus] GI:12958564; contains Pfam profile PF02847: MA3 domain	At5g63190	282.490814	222.888	425.366839	308.637	830.606647	439.573	1.511732801	0.443111
17007	27	AP2 domain-containing protein RAP2.12 (RAP2.12) identical to AP2 domain containing protein GI:2281649 from [Arabidopsis thaliana]	At1g53910	9939.20029	5701.513	9052.98485	5221.677	8509.22008	4206.881	1.833226287	0.43282
16082	25	senescence-associated protein (SEN1) identical to senescence-associated protein GI:1046270 from [Arabidopsis thaliana]	At4g35770	1619.12941	532.436	2529.72031	1262.767	3030.33876	1823.453	2.235389202	0.42768
2147	4	zinc finger (C3HC4-type RING finger) family protein contains Pfam PF00097: Zinc finger, C3HC4 type (RING finger) domain; similar to RING-H2 finger protein RHA3a (GI:3790573) [Arabidopsis thaliana]; similar to ReMembR-H2 protein JR700 (GI:6942147) [Arabidopsis thaliana]	At2g17730	308.399033	220.022	360.196781	253.047	889.758664	455.032	1.593495967	0.42435
24134	38	expressed protein	At1g36640	525.304823	314.184	290.499984	237.34	304.733507	148.833	1.647811369	0.420036
10014	16	cytochrome P450 family protein	At2g45560	830.47482	674.413	866.672069	687.117	1274.76019	605.184	1.533040509	0.41888
13860	22	protein phosphatase 2C, putative / PP2C, putative	At2g25070	926.889159	796.283	926.928202	765.436	4095.28538	1062.742	2.076169664	0.418656
4730	8	glycine-rich protein	At2g05540	1613.71952	1076.313	1011.26639	816.128	3507.71377	1439.974	1.7247874	0.41624
2368	4	xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative (XTR7) almost identical to xyloglucan endotransglycosylase-related protein XTR7 GI:1244760 from [Arabidopsis thaliana], one amino acid difference	At4g14130	281.026572	187.022	233.985063	149.863	722.432768	481.665	1.521277049	0.413859
14592	23	kelch repeat-containing F-box family protein contains F-box domain Pfam:PF00646 and Kelch motif Pfam:PF01344	At3g08810	461.047136	413.146	303.399835	245.941	916.167582	405.024	1.537193019	0.411514
11761	19	proton-dependent oligopeptide transport (POT) family protein contains Pfam profile: PF00854 POT family	At1g22570	460.559412	278.783	343.691154	156.559	758.808949	429.133	1.871851576	0.411348
22790	36	expressed protein	At1g13245	2381.87472	1554.505	3464.5213	1934.383	1832.80528	863.746	1.815062525	0.4004
30114	47	serine carboxypeptidase S10 family protein similar to serine carboxypeptidase I precursor (SP:P37890) [Oryza sativa]	At2g22920	3879.00245	2734.365	3100.55463	2327.008	3346.39008	1877.564	1.511112355	0.396198
19164	30	expressed protein	At3g20340	420.77351	192.322	372.258524	200.668	674.580007	158.394	2.767276519	0.394548
13306	21	cytochrome P450, putative similar to GB:Q05047 from [Catharanthus roseus]	At3g14650	3853.598	2869.309	3350.94016	2435.775	4273.35175	2061.368	1.597274873	0.386384
2664	5	AP2 domain-containing transcription factor family protein similar to TINY GB:CAA64359 GI:1246403 from [Arabidopsis thaliana]	At1g21910	282.811686	147.737	339.299852	159.379	530.056751	444.412	1.745297696	0.368456
14355	23	myb family transcription factor contains Pfam profile: PF00249 myb-like DNA-binding domain	At1g18330	454.650032	375.744	309.62669	209.463	1202.42433	225.533	2.673223554	0.366244
25069	39	ABC transporter family protein PDR5-like ABC transporter, Spirodela polyrrhiza, EMBL:Z70524	At3g53480	636.548763	355.69	585.404018	460.738	578.895104	357.851	1.559298132	0.365625
6650	11	serine carboxypeptidase S10 family protein similar to serine carboxypeptidase I precursor (SP:P07519) [Hordeum vulgare]; glucose acyltransferase GB:AAD01263 [Solanum berthaultii]; contains Pfam profile: PF00450 Serine carboxypeptidase	At1g73310	2326.95118	1283.12	2132.77265	1358.711	5151.48744	2317.878	1.868571556	0.35945
19303	30	nodulin MtN21 family protein similar to MtN21 GI:2598575 (root nodule development) from [Medicago truncatula]	At4g28040	593.187285	496.581	247.275287	192.144	358.141048	154.41	1.600295311	0.346566
5954	10	leucine-rich repeat protein kinase, putative smilar to light repressible receptor protein kinase [Arabidopsis thaliana] gi|1321686|emb|CAA66376; contains leucine rich repeat (LRR) domains, Pfam:PF00560; contains protein kinase domain, Pfam:PF00069	At1g51790	379.877393	214.591	159.72488	116.154	311.624404	168.475	1.665009876	0.337041
20824	33	Ras-related protein (ARA-1) (ARA) / small GTP-binding protein, putative nearly identical to SP:P19892 Ras-related protein ARA-1 [Arabidopsis thaliana] (Gene 76:313-319(1989))	At1g05810	479.503653	341.611	364.677312	262.713	512.231557	284.621	1.530490517	0.33264
27380	43	FAD-binding domain-containing protein similar to SP|P30986 reticuline oxidase precursor (Berberine-bridge-forming enzyme) (BBE) (Tetrahydroprotoberberine synthase) [Eschscholzia californica]; contains PF01565 FAD binding domain	At1g30700	320.699099	161.485	245.450889	222.655	244.880442	162.622	1.531381845	0.330398
23912	37	lysine decarboxylase family protein contains Pfam profile PF03641: lysine decarboxylase family	At5g06300	268.537191	174.359	298.095536	195.356	195.868889	116.307	1.583372256	0.32718
27732	43	expressed protein	At4g16840	231.253015	194.71	254.94254	214.939	281.555599	126.651	1.532292432	0.32376
6855	11	ABC transporter family protein AbcA, Dictyostelium discoideum, DDU66526	At3g47730	154.589375	107.213	162.683751	125.007	353.530622	175.89	1.584413426	0.3192
1605	3	expressed protein	At3g15440	435.322884	271.467	429.566939	376.145	285.605187	156.448	1.523726272	0.313235
12847	20	basic helix-loop-helix (bHLH) family protein contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain; PMID: 12679534	At5g04150	1127.06044	383.614	442.31064	379.482	214.980714	182.967	1.759513546	0.311904
20736	32	bZIP family transcription factor similar to bZIP transcription factor GI:1769891 from [Arabidopsis thaliana]	At5g49450	519.021093	164.954	472.903171	154.894	373.155862	305.427	2.47376236	0.3042
17727	28	MATE efflux family protein contains Pfam profile: PF01554 uncharacterized membrane protein family	At2g04040	362.53216	310.934	464.550773	208.78	267.678958	149.194	1.7283953	0.303408
7680	12	expressed protein	At5g18490	199.263216	148.491	162.361893	98.205	484.131875	265.623	1.605948197	0.292077
5365	9	expressed protein	At1g76660	528.718893	287.58	243.428913	134.603	563.519456	206.492	2.12533987	0.2805
9888	16	myb family transcription factor similar to MybHv5 GI:19055 from [Hordeum vulgare]	At1g71030	1632.94934	1304.886	2115.07519	878.746	2151.91235	1258.082	1.789602186	0.27805
4722	8	major latex protein-related / MLP-related low similarity to major latex protein {Papaver somniferum}[GI:169000] contains Pfam profile PF00407: Pathogenesis-related protein Bet v I family	At2g01520	1710.02584	806.227	168.781544	75.301	2199.02488	1518.703	1.936803404	0.274512
8885	14	protein kinase family protein contains Pfam domain PF00069: Protein kinase domain	At4g21400	241.240669	198.283	239.55386	197.95	555.065634	240.868	1.577086978	0.27376
19538	31	S-locus lectin protein kinase family protein contains Serine/Threonine protein kinases active-site signature, PROSITE:PS00108	At1g11350	278.248896	218.101	319.61069	188.756	250.989875	146.863	1.559344905	0.273296
4895	8	expressed protein	At3g45730	195.581753	98.185	305.879105	92.474	453.034178	269.74	2.326408123	0.25704
27966	44	transferase family protein similar to anthranilate N-hydroxycinnamoyl/benzoyltransferase from Dianthus caryophyllus [gi:2239091]; contains Pfam transferase family domain PF002458	At1g03390	504.571189	456.776	450.632765	368.443	369.452675	134.606	1.690802032	0.25675
14578	23	TCP family transcription factor, putative similar to transcription factor PCF6 [Oryza sativa (japonica cultivar-group)] GI:20975255; contains Pfam profile PF03634: TCP family transcription factor	At3g02150	222.931753	153.754	180.183635	122.827	371.438293	156.826	1.761789912	0.253232
6759	11	electron transfer flavoprotein-ubiquinone oxidoreductase family protein contains Pfam profile: PF05187 Electron transfer flavoprotein-ubiquinone oxidoreductase	At2g43400	154.70061	114.185	125.53454	85.073	500.2828	221.002	1.698045507	0.24424
16388	26	expressed protein	At1g70100	266.592711	146.222	304.529528	217.766	366.122694	218.501	1.632413924	0.2431
1985	4	UDP-glucose 4-epimerase / UDP-galactose 4-epimerase / Galactowaldenase identical to SP|Q42605 [GB:CAA90941] from [Arabidopsis thaliana] (Arch. Biochem. Biophys. 327 (1), 27-34 (1996))	At1g12780	193.341002	89.166	200.448001	115.056	325.503106	205.264	1.832094033	0.23408
21290	33	zinc finger (B-box type) family protein salt-tolerance protein - Arabidopsis thaliana, PID:e224078	At4g39070	318.620923	200.383	354.242391	177.46	1723.97159	567.156	2.208639741	0.230912
707	2	expressed protein	At1g22890	396.402265	127.147	185.728532	82.632	760.070837	281.064	2.689863405	0.221312
3019	5	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein contains protease inhibitor/seed storage/LTP family domain, Pfam:PF00234	At4g12545	1342.94693	659.652	81.3745396	57.294	778.172327	573.613	1.604251615	0.218592
15023	24	expressed protein	At1g31835	222.811961	196.172	298.731287	201.572	265.427355	132.29	1.541404045	0.21105
19331	30	cytochrome P450 family protein Similar to Cytochrome P450 91A1 (SP:Q9FG65) [Arabidopsis thaliana];	At4g37340	298.921564	214.81	345.094905	257.478	174.660103	85.095	1.594794081	0.185334
7092	11	expressed protein low similarity to extracellular dermal glycoprotein EDGP precursor [Daucus carota] GI:285741, SP|P13917 Basic 7S globulin precursor {Glycine max}; expression supported by MPSS	At5g48430	125.391156	79.284	153.807137	128.296	174.09514	94.504	1.540862947	0.177444
30678	48	RNA polymerase sigma subunit SigA (sigA) / sigma factor 1 (SIG1) identical to sigma factor SigA [Arabidopsis thaliana] GI:5478439, sigma factor 1 [Arabidopsis thaliana] GI:2353171, plastid RNA polymerase sigma-subunit [Arabidopsis thaliana] GI:2398851; contains Pfam profiles PF04545: Sigma-70, region 4, PF0453	At1g64860	444.002453	398.77	528.632566	471.259	2450.04362	657.832	1.986532231	0.172773
19954	31	xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative (XTR6) identical to xyloglucan endotransglycosylase-related protein GI:1244758 from [Arabidopsis thaliana]	At4g25810	187.630562	130.358	279.254042	135.973	222.797407	133.686	1.719889006	0.171564
14434	23	expressed protein	At1g65490	180.55535	119.296	222.597312	110.992	238.422546	189.514	1.592368804	0.167586
123	1	beta-fructosidase (BFRUCT3) / beta-fructofuranosidase / invertase, vacuolar identical to beta-fructosidase GB:CAA67560 GI:1429209 [Arabidopsis thaliana]; supported by full-length cDNA GI:14517549; identical to cDNA Beta-fructosidase GI:3115854	At1g62660	414.706903	192.382	87.8419919	79.833	207.394954	137.509	1.588064332	0.14742
10377	16	glycosyl hydrolase family 38 protein similar to lysosomal alpha-mannosidase SP:O09159 from [Mus musculus]	At5g66150	123.856322	102.031	96.0366476	79.121	363.110246	161.006	1.560987498	0.14616
10686	17	expressed protein identical to unknown protein GB:AAF30301 from [Arabidopsis thaliana]	At3g06080	296.527864	206.547	170.926208	71.515	152.931716	103.876	1.765990367	0.145299
24447	38	F-box family protein contains Pfam PF00646: F-box domain; similar to F-box protein FBL2 (GI:6063090) [Homo sapiens]	At4g02740	90.913535	73.114	158.085312	126.713	558.177053	108.442	2.546091711	0.1431
12700	20	isovaleryl-CoA-dehydrogenase (IVD) identical to isovaleryl-CoA-dehydrogenase precursor [Arabidopsis thaliana] GI:5596622	At3g45300	113.734971	83.831	210.060747	132.539	308.877942	126.223	1.79623209	0.142662
24474	38	UDP-glucoronosyl/UDP-glucosyl transferase family protein contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase	At4g15260	215.860819	120.235	157.564283	97.867	190.50999	70.418	2.036908059	0.125097
23460	37	2-oxoisovalerate dehydrogenase, putative / 3-methyl-2-oxobutanoate dehydrogenase, putative / branched-chain alpha-keto acid dehydrogenase E1 alpha subunit, putative similar to branched-chain alpha-keto acid dehydrogenase E1-alpha subunit [Gallus gallus] GI:12964598; contains Pfam profile PF00676: Dehydroge	At1g21400	191.387965	160.939	158.963254	88.597	148.576967	32.607	2.513340448	0.12432
7632	12	mannitol transporter, putative similar to mannitol transporter [Apium graveolens var. dulce] GI:12004316; contains Pfam profile PF00083: major facilitator superfamily protein	At4g36670	112.887871	98.146	108.195585	59.694	290.174375	164.606	1.575183012	0.12096
16385	26	zinc finger (MYND type) family protein / F-box family protein	At1g67340	199.491035	167.752	224.560333	199.557	1523.11494	472.638	1.845692936	0.102524
11260	18	expressed protein	At2g24100	148.071409	91.743	140.089892	81.536	354.648176	82.893	2.536833671	0.100674
29006	45	expressed protein	At4g03565	304.951805	227.613	126.568631	70.46	129.768242	74.544	1.625642799	0.091008
27809	43	expressed protein	At5g06980	145.872371	107.082	188.966241	126.804	179.74683	48.624	2.18304706	0.090801
5902	10	plant defensin-fusion protein, putative (PDF1.4) plant defensin protein family member, personal communication, Bart Thomma (Bart.Thomma@agr.kuleuven.ac.be); similar to SWISS-PROT:P30224, Cysteine-rich antifungal protein 1 precursor (AFP1)[Arabidopsis thaliana]	At1g19610	127.988075	87.367	105.445444	61.466	237.60603	58.843	2.406140667	0.088972
11444	18	expansin, putative (EXP17) similar to alpha-expansin precursor GI:4027891 from [Nicotiana tabacum]; alpha-expansin gene family, PMID:11641069	At4g01630	154.683497	78.963	124.715552	65.441	208.434156	121.889	1.858246615	0.0861
3832	6	disease resistance protein (TIR-NBS-LRR class), putative domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.	At5g46450	133.379782	80.603	92.110606	69.425	116.553474	74.746	1.513621956	0.074777
4751	8	dehydrin family protein contains Pfam domain, PF00257: Dehydrin	At2g21490	299.250992	271.422	173.591901	151.61	792.620116	308.184	1.606475201	0.072427
1342	3	MATE efflux family protein similar to ripening regulated protein DDTFR18 [Lycopersicon esculentum] GI:12231296; contains Pfam profile PF01554: Uncharacterized membrane protein family	At1g15170	241.007503	149.997	242.603552	199.854	404.459749	198.136	1.620658873	0.065934
28034	44	thioesterase family protein contains Pfam profile PF03061: thioesterase family protein	At1g35290	255.519442	156.529	340.381744	204.181	216.158063	113.586	1.734167612	0.063375
24694	38	expressed protein	At1g36640	196.970056	87.243	91.2501911	72.034	121.776286	91.646	1.617750441	0.06048
1896	3	expressed protein similar to unknown protein (gb|AAB68039.1)	At5g51390	353.015117	158.742	217.624432	160.463	507.408754	385.188	1.632453006	0.060291
25229	39	myb family transcription factor (MYB9) contains Pfam profile: PF00249 Myb-like DNA-binding domain	At5g16770	195.125046	154.436	220.057494	178.994	832.864437	378.07	1.565272822	0.058464
3426	6	pentatricopeptide (PPR) repeat-containing protein contains Pfam profile PF01535: PPR repeat	At2g01860	113.957442	73.512	83.3216268	41.731	230.556367	110.876	1.875410621	0.0539
25123	39	xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative similar to endoxyloglucan transferase EXGT-A1 GI:5533309 from [Arabidopsis thaliana]	At4g13090	136.112536	86.106	193.11376	83.214	234.746164	45.624	3.01555935	0.04884
11537	18	esterase, putative similar to ethylene-induced esterase [Citrus sinensis] GI:14279437, polyneuridine aldehyde esterase [Rauvolfia serpentina] GI:6651393; contains Pfam profile PF00561: hydrolase, alpha/beta fold family	At4g37150	230.99311	124.195	170.811486	109.248	136.964301	48.912	2.074554014	0.048384
733	2	phosphate-responsive protein, putative similar to phi-1 (phosphate-induced gene) [Nicotiana tabacum] GI:3759184; contains Pfam profile PF04674: Phosphate-induced protein 1 conserved region	At1g35140	328.59895	160.937	267.107851	166.861	402.206084	240.503	1.771640179	0.04424
1233	2	CBL-interacting protein kinase 20 (CIPK20) identical to CBL-interacting protein kinase 20 [Arabidopsis thaliana] gi|14486384|gb|AAK61493	At5g45820	319.119343	218.521	262.24332	167.245	373.054829	175.6	1.717612329	0.038808
12203	19	expressed protein	At5g03930	169.913119	100.831	206.545793	83.648	338.717875	214.241	1.911788938	0.03663
22091	34	hypothetical protein	At1g34560	171.800911	142.419	219.941179	187.243	163.849519	68.487	1.591117863	0.033288

4042	7	expressed protein	At1g68945	261.445935	157.519	307.13786	194.681	227.20989	99.16	1.84292233	0.0285
6180	10	leucine-rich repeat family protein	At3g26500	154.578679	101.428	96.5337762	61.341	287.310385	139.566	1.71878199	0.027885
17618	28	expressed protein	At1g27510	142.068977	124.584	135.950341	101.604	251.422876	122.879	1.508163122	0.027495
16921	27	leucine-rich repeat protein kinase, putative similar to light repressible receptor protein kinase, gi|2129635; contains leucine rich repeat (LRR) domains, Pfam:PF00560; contains protein kinase domain, Pfam:PF00069	At1g05700	192.703537	130.074	199.621046	154.116	179.039595	102.65	1.506977269	0.025872
1133	2	G-box binding factor 1 (GBF1) identical to G-box binding factor 1 SP:P42774 from [Arabidopsis thaliana]; contains Pfam profile: PF00170 bZIP transcription factor	At4g36730	200.358457	152.574	212.410955	189.838	1335.41121	607.551	1.543372789	0.02432
30386	47	expressed protein	At4g35430	305.476965	263.299	201.799171	104.451	147.407865	81.415	1.634254204	0.0243
1227	2	disease resistance protein (TIR-NBS-LRR class), putative (RPS4) domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein. Identical to RPS4 (GI:11357255). False intron created at intron 2 to escape a frameshift in the BAC sequence.	At5g45250	220.251408	113.827	171.179552	146.234	358.287444	171.268	1.732507467	0.02405
28208	44	expressed protein	At2g44010	215.492887	119.051	180.546922	139.018	133.867315	95.045	1.505760614	0.023667
30325	47	UDP-glucoronosyl/UDP-glucosyl transferase family protein contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase ;simalr to UDP-glucose:sinapate glucosyltransferase GI:9794913 from [Brassica napus]	At4g15490	191.631827	169.39	118.230573	86.184	512.262485	133.271	2.11563668	0.023188
4437	7	protein kinase family protein contains protein kinase domain, Pfam:PF00069	At5g20050	238.968901	130.655	181.415303	139.823	325.610326	156.765	1.734510329	0.022914
1563	3	UDP-glucoronosyl/UDP-glucosyl transferase family protein contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase	At2g43840	204.050616	123.849	149.302706	130.509	288.320719	130.916	1.664637551	0.02128
28594	44	thioesterase family protein contains Pfam profile PF03061: thioesterase family protein	At1g35290	307.70809	191.945	209.687901	132.043	119.522621	70.289	1.630526173	0.019684
27408	43	GDSL-motif lipase/hydrolase family protein similar to lipase GI:1145627 from (Arabidopsis thaliana); contains Pfam profile PF00657: Lipase/Acylhydrolase with GDSL-like motif	At1g53940	280.260759	133.49	145.134473	108.856	164.837173	61.815	2.033126681	0.019536
21214	33	zinc finger (C3HC4-type RING finger) family protein zinc finger protein, Arabidopsis thaliana, gb:L76926	At4g10160	511.843202	400.304	317.657229	273.187	212.320852	64.378	1.913151218	0.01887
780	2	MATE efflux family protein contains TIGRfam profile: TIGR00797: MATE efflux family protein, Pfam profile PF01554: Uncharacterized membrane protein family	At1g66760	281.051172	143.285	164.868249	141.866	236.370947	143.964	1.588499873	0.015708
11139	18	expressed protein similar to putative non-LTR retroelement reverse transcriptase GB:AAD21515 GI:4510429 from [Arabidopsis thaliana]; expression supported by MPSS	At1g47320	129.178507	92.626	91.4907886	60.552	119.007144	59.386	1.63651002	0.014664
8446	13	MATE efflux family protein similar to ripening regulated protein DDTFR18 [Lycopersicon esculentum] GI:12231296; contains Pfam profile PF01554: Uncharacterized membrane protein family	At1g33090	152.404241	130.642	199.527038	179.303	173.979673	60.843	1.712952395	0.01386
5486	9	expressed protein identical to unknown protein GB:AAF30301 from [Arabidopsis thaliana]	At3g06080	274.671181	162.311	109.130888	53.519	316.193592	209.634	1.746556824	0.01326
26698	42	myb family transcription factor (MYB58) contains PFAM profile: myb DNA binding domain PF00249	At1g16490	88.8514021	71.223	106.635685	63.672	345.408766	192.774	1.571352196	0.012546
4922	8	expressed protein	At3g56290	128.103588	106.125	149.549677	100.546	208.526942	100.038	1.592984654	0.010759
19234	30	glycosyl hydrolase family 1 protein contains Pfam PF00232 : Glycosyl hydrolase family 1 domain; TIGRFAM TIGR01233: 6-phospho-beta-galactosidase; similar to Cyanogenic Beta-Glucosidase (GI:1311386)(pdb:1CBG) [Trifolium Repens]; identical beta-glucosidase GI:10834547	At3g60140	163.883947	109.178	270.11293	182.171	375.652833	15.071	9.303118767	0.010248
5901	10	expressed protein	At1g19530	132.099505	61.514	58.1736101	40.551	420.629232	72.298	3.133347384	0.01005
9540	15	hypothetical protein	At4g19280	86.6159987	58.634	97.5152866	63.312	248.216609	95.777	1.869691751	0.009776
16714	26	expressed protein	At4g30790	137.501909	84.735	152.744366	135.939	117.297822	43.269	1.819083461	0.008526
22152	35	phytochrome kinase substrate-related contains weak similarity to Swiss-Prot:Q9SWI1 phytochrome kinase substrate 1 [Arabidopsis thaliana]	At1g18810	183.998299	142.503	1008.25175	56.505	78.2555943	64.938	6.779951779	0.008432
23935	37	myb family transcription factor similar to CCA1 [Arabidopsis thaliana] GI:4090569; contains Pfam profile PF00249: Myb-like DNA-binding domain	At5g17300	96.4047125	65.593	198.014938	89.288	110.21723	54.052	1.908849215	0.008424
30576	48	branched-chain amino acid aminotransferase 2 / branched-chain amino acid transaminase 2 (BCAT2) identical to SP|Q9M439 Branched-chain amino acid aminotransferase 2, chloroplast precursor (EC 2.6.1.42) (Atbcat-2) {Arabidopsis thaliana}; contains Pfam profile: PF01063 aminotransferase class IV	At1g10070	151.817047	36.508	146.573278	33.886	1110.14776	71.997	7.967767654	0.008424
11820	19	expressed protein	At1g59590	187.83485	94.422	135.980614	98.473	185.373777	158.312	1.513714745	0.00774
256	1	nucleotidyltransferase family protein contains Pfam profile: PF01909 nucleotidyltransferase domain	At2g40520	100.034836	43.817	100.980847	91.272	89.3239165	41.571	1.846031459	0.00663
2792	5	expressed protein	At2g07676	120.879706	69.933	69.9804151	57.436	329.165055	185.317	1.574380394	0.006432
10360	16	haloacid dehalogenase-like hydrolase family protein low similarity to SP|P53078 SSM1 protein {Saccharomyces cerevisiae}; contains InterPro accession IPR005834: Haloacid dehalogenase-like hydrolase	At5g59490	60.9783819	43.231	79.9978757	60.66	163.723743	73.397	1.653325178	0.00598
17478	27	expressed protein	At5g44575	199.579809	70.997	138.093411	83.727	163.888695	31.875	3.200679215	0.005883
22503	35	expressed protein contains Pfam profile PF04520: Protein of unknown function, DUF584	At4g04630	69.4889583	51.703	76.4717678	62.846	845.693628	377.844	1.599674297	0.005625
17127	27	hypothetical protein	At2g30430	98.0304604	81.705	109.309345	68.07	617.056898	257.673	1.733458562	0.00546
18014	28	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein contains Pfam protease inhibitor/seed storage/LTP family domain PF00234	At4g30880	379.733001	254.416	410.695171	268.073	156.968932	44.475	2.184656396	0.005328
14449	23	MADS-box protein (AGL60) contains Pfam profile: PF00319 SRF-type transcription factor (DNA-binding and dimerisation domain)	At1g72350	87.2716457	26.72	204.158938	142.159	1116.83041	429.967	2.433254901	0.004648
17030	27	expressed protein contains Pfam profile PF03140: Plant protein of unknown function	At1g65985	110.050299	65.886	146.372515	75.835	334.416735	138.344	2.005914144	0.0043
28	1	L-allo-threonine aldolase-related protein similar to L-allo-threonine aldolase (EC 4.1.2.-) (L-allo-TA) (L-allo-threonine acetaldehyde-lyase) (SP:O07051) {Aeromonas jandaei}; similar to ESTs gb|R30517, gb|T42772, gb|R90493, and gb|R90493	At1g08630	99.8883053	30.275	112.623536	59.297	640.486358	41.41	6.888542509	0.00414
25885	40	hydrolase, alpha/beta fold family protein low similarity to hydrolase [Terrabacter sp. DBF63] GI:14196240; contains Pfam profile PF00561: hydrolase, alpha/beta fold family	At5g19850	122.308653	107.091	251.972515	215.736	192.209002	46.647	2.143522653	0.00363
18271	29	phytochrome and flowering time regulatory protein (PFT1) PMID: 12815435	At1g25540	228.661445	165.151	102.955021	59.584	1495.5926	928.896	1.574177453	0.003621
18169	28	peptidoglycan-binding LysM domain-containing protein contains Pfam profile PF01476: LysM domain	At5g62150	164.739604	121.688	110.201627	83.868	177.480793	94.295	1.516654138	0.003528
23501	37	F-box family protein contains F-box domain Pfam:PF00646	At1g49610	108.350751	90.053	183.023005	136.61	104.718122	9.024	4.715779561	0.002714
23064	36	hypothetical protein	At3g19610	162.325582	137.48	168.856432	99.025	148.385209	90.139	1.51069782	0.002695
1004	2	cytochrome P450 71A21, putative (CYP71A21) identical to Cytochrome P450 71A21 (SP:Q9STL2) [Arabidopsis thaliana]	At3g48320	150.635171	89.772	89.7110044	48.133	85.4166008	71.3	1.57992624	0.00198
9706	15	expressed protein similar to unknown protein (pir||T05871)	At5g54150	70.0365787	49.577	72.3991371	34.368	530.61759	301.602	1.759533013	0.00196
1293	2	phosphate-responsive protein, putative similar to phi-1 (phosphate-induced gene) [Nicotiana tabacum] GI:3759184; contains Pfam profile PF04674: Phosphate-induced protein 1 conserved region	At1g35140	133.531661	52.713	83.4411288	48.618	135.613751	87.895	1.930783017	0.001848
15370	24	expressed protein	At4g14990	144.702261	129.615	135.889793	115.168	2097.92953	744.454	1.704801785	0.00182
2184	4	nodulin-related contains 14 transmembrane domains; supported by tandem duplication of nodulin -related protein (TIGR_Ath1:At2g34350) [Arabidopsis thaliana]	At2g34355	99.2112668	65.204	75.7611288	53.593	206.786691	94.714	1.706155061	0.00175
11003	17	ankyrin repeat family protein contains Pfam domain, PF00023: Ankyrin repeat	At5g54620	101.544001	80.001	121.971785	38.877	88.4641008	77.814	1.847842245	0.001566
14867	23	hypothetical protein	At5g37385	80.7108972	30.091	150.008565	113.445	178.159161	105.543	1.897517897	0.001558
16698	26	RNA recognition motif (RRM)-containing protein low similarity to tumor-rejection antigen SART3 [Mus musculus] GI:7637845; contains INTERPRO:IPR000504 RNA-binding region RNP-1 (RNA recognition motif) domain	At4g24270	115.726513	102.82	112.092946	26.084	180.008692	124.476	2.289680116	0.001458
13939	22	transcription elongation factor-related low similarity to transcription elongation factor TFIIS.h [Mus musculus] GI:3288547	At3g10820	122.163191	101.036	155.478573	120.106	139.832415	64.49	1.55729915	0.001404
22649	35	ACT domain-containing protein contains Pfam ACT domain PF01842	At5g25320	81.2734916	45.574	71.2901579	47.316	224.675805	66.762	2.218445575	0.00126
551	1	protein kinase family protein contains protein kinase domain, Pfam:PF00069	At5g25440	99.5481817	33.989	72.9584068	38.421	141.704627	107.807	2.047394705	0.000936
19615	31	pseudouridine synthase family protein low similarity to SP|P23851 Ribosomal large subunit pseudouridine synthase C (EC 4.2.1.70) (Pseudouridylate synthase) (Uracil hydrolyase) {Escherichia coli}; contains Pfam profile PF00849: RNA pseudouridylate synthase	At1g56345	113.069698	81.624	179.350308	123.085	683.66065	334.492	1.628751232	0.000864
17870	28	lipid-binding serum glycoprotein family protein similar to SP|P17213 Bactericidal permeability-increasing protein precursor (BPI) {Homo sapiens}; contains Pfam profile PF02886: LBP / BPI / CETP family, C-terminal domain	At3g20270	135.442984	102.454	98.691187	89.521	87.2826275	40.865	1.520100583	0.00084
9014	14	peroxidase, putative identical to peroxidase ATP24a [Arabidopsis thaliana] gi|1890313|emb|CAA72484	At5g39580	119.791952	76.441	122.966042	49.449	693.935137	74.349	4.462441389	0.000732
115	1	carbonic anhydrase family protein / carbonate dehydratase family protein similar to SP|P46512 Carbonic anhydrase 1 (EC 4.2.1.1) (Carbonate dehydratase 1) {Flaveria linearis}; contains Pfam profile PF00484: Carbonic anhydrase	At1g58180	110.404327	43.946	54.5439338	34.952	74.5462218	67.533	1.725553196	0.000696
20589	32	MATE efflux family protein similar to ripening regulated protein DDTFR18 [Lycopersicon esculentum] GI:12231296; contains Pfam profile PF01554: MatE	At4g21900	81.3152048	60.092	110.396017	92.295	57.5416666	15.03	2.125918017	0.000666
20476	32	glycosyl hydrolase family 17 protein similar to elicitor inducible chitinase Nt-SubE76 GI:11071974 from [Nicotiana tabacum]	At3g24330	74.7769173	65.827	76.2662243	29.178	3264.11583	1467.62	1.991291791	0.00049
13547	21	squalene monooxygenase 1,2 / squalene epoxidase 1,2 (SQP1,2) identical to SP|O65402	At5g24160	85.3688789	68.612	143.652648	91.83	118.380324	35.848	2.036948134	0.000392
27058	42	hypothetical protein	At4g07350	52.8464335	47.901	94.334938	74.259	117.114312	29.066	2.134282526	0.000344
21221	33	late embryogenesis abundant domain-containing protein / LEA domain-containing protein similar to LEA protein [Cicer arietinum] GI:2909420; contains Pfam profile PF02987: Late embryogenesis abundant protein	At4g11930	141.277494	116.876	176.856698	100.908	186.464526	86.502	1.70568112	0.000324
17540	27	miRNA gene Arabidopsis thaliana miR399f stem-loop	ath-MIR39!	121.66691	85.14	59.9470209	36.624	1690.18929	705.068	1.821015181	0.00028
17141	27	UDP-glucoronosyl/UDP-glucosyl transferase family protein contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase	At2g36750	81.9687127	44.929	86.981577	47.228	55.6467731	32.2	1.798101192	0.00027
2054	4	protein kinase family protein contains Serine/Threonine protein kinases active-site signature, PROSITE:PS00108	At1g51910	95.9490753	40.183	88.4171953	27.86	102.532499	85.772	2.252278455	0.000232
1275	2	ethylene insensitive 3 family protein contains Pfam profile: PF04873 ethylene insensitive 3	At5g65100	80.7964629	37.869	70.6783072	48.114	129.500194	76.21	1.767269488	0.000225
10676	17	acyl-[acyl-carrier-protein] desaturase, putative / stearoyl-ACP desaturase, putative similar to Acyl-[acyl-carrier protein] desaturase from Spinacia oleracea SP|P28645, Cucumis sativus SP|P32061, Ricinus communis SP|P22337; contains Pfam profile PF03405 Fatty acid desaturase	At3g02610	70.1788316	59.547	68.5527637	54.506	434.017201	140.243	1.843668959	0.000224
7726	12	hypothetical protein	At5g42785	127.440454	58.591	54.8880997	29.522	98.860241	81.544	1.748889138	0.000192
13987	22	hypothetical protein contains Pfam profile PF03384: Drosophila protein of unknown function, DUF287	At3g32080	65.4342146	37.186	94.1023073	65.911	2912.02854	1843.019	1.589132014	0.00018
8030	13	UDP-glucoronosyl/UDP-glucosyl transferase family protein contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase	At2g29750	106.729281	94.701	61.333245	42.613	864.017805	290.768	1.845941312	0.000161
20732	32	ABC transporter family protein contains Pfam profile: PF00005 ABC transporter; similar to multidrug-resistant protein CjMDR1 GI:14715462 from [Coptis japonica]	At5g46540	136.913645	110.466	59.9996018	43.236	222.857202	107.103	1.569305569	0.000144
1286	2	miRNA gene Arabidopsis thaliana miR395e stem-loop	ath-MIR39!	76.3053343	67.54	41.2584897	27.133	820.95898	334.772	1.700891527	0.00014
2949	5	hypothetical protein predicted protein, Arabidopsis thaliana	At3g43280	90.3637755	48.101	95.4263903	58.303	179.122072	50.89	2.345048993	0.000124
20365	32	expressed protein	At2g25770	347.593462	132.349	55.1525977	11.59	217.052931	142.191	2.970488336	0.00012
29620	46	yippee family protein similar to mdgl-1 [Mus musculus] GI:10441648, Yippee protein [Drosophila melanogaster] GI:5713279; contains Pfam profile PF03226: Yippee putative zinc-binding protein	At3g55890	48.3146612	25.743	94.9850293	74.616	133.644629	94.732	1.520185958	0.000117
1873	3	hypothetical protein similar to unknown protein (emb|CAB86921.1)	At5g41660	89.9616168	76.477	106.253278	89.41	111.660566	40.836	1.6996903	0.000108
2183	4	expressed protein	At2g34310	53.907448	44.334	65.7404815	48.754	112.145114	55.649	1.526524566	0.000081
4772	8	leucine-rich repeat protein kinase, putative similar to light repressible receptor protein kinase [Arabidopsis thaliana] gi|1321686|emb|CAA66376; contains leucine rich repeat (LRR) domains, Pfam:PF00560; contains protein kinase domain, Pfam:PF00069	At2g28970	77.3374703	50.637	66.1595354	36.059	136.591095	110.51	1.532685425	0.00008
14839	23	floral homeotic protein PISTILLATA (PI) contains Pfam profiles PF01486: K-box region and PF00319: SRF-type transcription factor (DNA-binding and dimerisation domain)	At5g20240	72.5821576	55.676	84.8353197	30.103	226.306774	41.153	3.206992328	0.000074
20497	32	receptor protein kinase-related similar to light repressible receptor protein kinase GI:1321686 from [Arabidopsis thaliana]	At3g45920	98.8465431	69.737	88.9461911	54.117	98.7055979	59.79	1.570626947	0.000065
16559	26	F-box family protein contains F-box domain Pfam:PF00646	At3g16580	62.4009113	28.433	51.1500748	12.322	2816.3622	1283.31	2.846796934	0.000042
29479	46	expressed protein	At2g32160	57.0509171	44.185	192.640532	132.202	68.8512319	39.262	1.500662115	0.000028
11179	18	S-adenosyl-L-methionine:carboxyl methyltransferase family protein similar to defense-related protein cjs1 [Brassica carinata][GI:14009292][Mol Plant Pathol (2001) 2(3):159-169]	At1g66690	69.8173166	46.627	42.2734607	26.566	2516.05767	578.303	2.479793363	0.000027
26303	41	auxin-responsive protein-related similar to indole-3-acetic acid induced protein arg7 (SP:P32295) [Vigna radiata]	At3g12955	65.1518479	52.375	95.4040832	73.537	102.77168	52.147	1.504039386	0.000025
25920	40	hypothetical protein	At5g42905	57.876626	46.017	128.628847	58.951	46.0650866	29.852	1.660933462	0.00002
14814	23	expressed protein ；expression supported by MPSS	At5g09580	122.102225	79.596	80.1476517	61.745	129.63628	66.866	1.590271589	0.000012
11374	18	expressed protein contains Pfam domain PF05003: protein of unknown function (DUF668); expression supported by MPSS	At3g23160	61.960248	48.348	55.2195188	23.902	3.36091004	1.611	1.892673349	0.000012
28142	44	hypothetical protein	At2g13980	185.621908	154.873	166.944399	139.668	81.3711373	33.034	1.619030472	0.00001
20277	32	MATE efflux family protein similar to ripening regulated protein DDTFR18 [Lycopersicon esculentum] GI:12231296; contains Pfam profile PF01554: Uncharacterized membrane protein family; contains 12 transmembrane domains, PMID: 11152613	At1g64820	68.4439874	59.822	61.9976765	43.642	51.772448	8.882	2.79788059	0.000008
22551	35	F-box family protein contains F-box domain Pfam:PF00646	At3g26350	52.9533906	37.243	59.8307056	31.571	604.192654	257.838	1.886751346	0.000006
9856	16	DC1 domain-containing protein contains Pfam profile PF03107: DC1 domain	At1g55430	31.5694576	19.216	47.5188051	39.071	56.5375174	34.283	1.502743922	0.000005
10600	17	expressed protein	At2g16980	89.739146	58.407	36.8719669	7.457	38.1576694	18.015	2.866387282	0.000004
9016	14	no apical meristem (NAM) family protein contains Pfam PF02365: No apical meristem (NAM) domain; NAC domain protein NAM, Arabidopsis thaliana, gb:AAD17313	At5g39820	99.2433539	39.57	69.4673529	49.843	98.8416838	75.006	1.739850793	0.000003
16291	26	expressed protein	At1g15800	65.183935	28.812	64.0148715	35.326	81.2969086	49.651	1.903957719	0.000002
23994	37	ankyrin repeat family protein contains ankyrin repeat domains, Pfam:PF00023	At5g50140	34.6872571	27.999	54.4674524	16.441	49.1600105	15.619	2.566409338	0.000002
16659	26	subtilase family protein contains similarity to subtilase; SP1 GI:9957714 from [Oryza sativa]	At4g10540	59.3676079	20.535	46.8750873	19.15	205.931	66.868	2.806164862	0.000002
11156	18	calcium-binding EF-hand family protein contains Pfam profile: PF00036 EF hand	At1g54450	48.6312542	44.04	51.0385396	42.671	32.9369184	12.569	1.640278193	0.000001
16364	26	glutathione S-transferase, putative similar to glutathione S-transferase GB:AAF29773 GI:6856103 from [Gossypium hirsutum]	At1g59670	38.6607134	23.855	42.8152034	23.179	290.675418	74.934	2.448965084	0.000001
7458	12	F-box family protein contains F-box domain Pfam:PF00646	At3g16555	36.704468	7.255	40.5510375	31.783	27.3718287	14.059	2.760664596	0.000001

Downregulated genes

SPOTNUMBER	BLOCK	NAME	AG ID	BLR-OX (1)	Col-0 (1)	BLR-OX (2)	Col-0 (2)	BLR-OX (3)	Col-0 (3)	Mean Ratio (BLR-OX:Col-0)	Spot Confidence
24301	38	expressed protein	At2g41650	1363.53617	2233.947	1010.22115	1466.435	480.42044	802.966	0.632524718	0.735816
24959	39	cold-responsive protein / cold-regulated protein (cor15b) nearly identical to cold-regulated gene cor15b [Arabidopsis thaliana] GI:456016; contains Pfam profile PF02987: Late embryogenesis abundant protein	At2g42530	2061.47403	4424.512	4093.06398	10575.54	968.905003	1914.726	0.452993517	0.7209
10518	17	disease resistance protein (CC-NBS-LRR class), putative domain signature CC-NBS-LRR exists, suggestive of a disease resistance protein.	At1g58400	2925.03817	3891.313	2128.00372	3204.954	1206.08628	2938.268	0.60871087	0.7209
5312	9	histone H1/H5 family protein contains Pfam domain, PF00538: linker histone H1 and H5 family	At1g54260	1276.22923	1551.95	596.06679	1093.608	541.413741	892.766	0.657943517	0.720099
16389	26	expressed protein	At1g70270	2132.43793	2698.786	1856.9061	3102.25	1132.4741	2351.006	0.623470762	0.711822
19576	31	stress-responsive protein, putative similar to cold acclimation WCOR413-like protein gamma form [Hordeum vulgare] gi|18449100|gb|AAL69988; similar to stress-regulated protein SAP1 [Xerophyta viscosa] gi|21360378|gb|AAM47505	At1g29390	1535.2836	2738.97	1428.4322	2345.119	948.735419	2095.259	0.54081428	0.703248
22111	35	latex-abundant family protein (AMC1) / caspase family protein contains similarity to latex-abundant protein [Hevea brasiliensis] gb:AAD13216; contains Pfam profile PF00656: ICE-like protease (caspase) p20 domain	At1g02170	2066.03468	2770.291	1730.58125	2606.191	1013.52057	2285.376	0.617763485	0.701592
22271	35	Pex2/Pex12 N-terminal domain-containing protein / zinc finger (C3HC4-type RING finger) family protein contains Pfam profiles PF00097: zinc finger C3HC4 type (RING finger), PF04757: Pex2/Pex12 amino terminal region	At1g79810	1165.21739	1725.365	1553.36605	2814.957	516.328568	710.648	0.651243838	0.6966
3133	5	hypothetical protein	At5g17120	677.697299	904.233	395.794059	812.658	623.09004	1026.722	0.614460532	0.68904
21058	33	aconitase C-terminal domain-containing protein contains Pfam profile PF00694: Aconitase C-terminal domain	At2g43100	2225.50665	2779.839	2610.70925	3969.016	819.315639	1589.865	0.657899118	0.68816
1668	3	Em-like protein GEA1 (EM1) identical to SP|Q07187 Em-like protein GEA1 (EM1) {Arabidopsis thaliana}; contains Pfam profile PF00477: Small hydrophilic plant seed protein	At3g51810	1657.25641	1847.908	998.133911	1799.548	695.122796	1631.467	0.625852926	0.679042
19285	30	S-locus protein kinase, putative (ARK3) identical to PIR|T05180|T05180 S-receptor kinase ARK3 precursor - [Arabidopsis thaliana]	At4g21380	844.002754	1247.083	921.112434	1218.567	557.900757	1127.796	0.642453979	0.673552
27575	43	expressed protein	At3g02640	1074.79051	1867.862	957.425131	1562.723	364.02161	1076.256	0.508768793	0.671416
28656	45	thaumatin, putative identical to SP|P50699 Thaumatin-like protein precursor {Arabidopsis thaliana}; strong similarity to pathogenesis-related group 5 protein GI:2749943 from [Brassica rapa]	At1g18250	510.016375	939.324	536.502176	1019.766	294.793049	822.453	0.475831928	0.667368
4191	7	lipid transfer protein 6 (LTP6) identical to GI:8571927	At3g08770	1498.4187	2576.997	1678.56279	2783.115	1248.55128	2914.676	0.537650029	0.666072
14559	23	cold-responsive protein / cold-regulated protein (cor15a) identical to cold-regulated protein cor15a [Arabidopsis thaliana] GI:507149; contains Pfam profile PF02987: Late embryogenesis abundant protein	At2g42540	1005.2117	2953.547	2631.30663	8904.34	1403.39438	1746.545	0.479791626	0.663834
19759	31	cold-responsive protein / cold-regulated protein (cor15a) identical to cold-regulated protein cor15a [Arabidopsis thaliana] GI:507149; contains Pfam profile PF02987: Late embryogenesis abundant protein	At2g42540	1394.15906	3544.164	3174.96778	9353.715	853.586612	1706.895	0.410960972	0.656656
14376	23	stress-responsive protein, putative similar to cold acclimation WCOR413-like protein gamma form [Hordeum vulgare] gi|18449100|gb|AAL69988; similar to stress-regulated protein SAP1 [Xerophyta viscosa] gi|21360378|gb|AAM47505	At1g29390	1216.7536	2028.488	1543.18766	2375.085	832.518036	1662.635	0.583431606	0.650848
29010	45	peroxidase, putative similar to peroxidase isozyme [Armoracia rusticana] gi|217932|dbj|BAA14143	At4g08780	1457.84025	1878.123	864.326641	1416.724	712.826338	1620.493	0.60873085	0.65016
3976	7	stress-responsive protein, putative similar to cold acclimation WCOR413-like protein gamma form [Hordeum vulgare] gi|18449100|gb|AAL69988; similar to stress-regulated protein SAP1 [Xerophyta viscosa] gi|21360378|gb|AAM47505	At1g29395	1447.00442	2004.122	1753.26912	3030.243	1067.7405	2321.501	0.586846605	0.649152
25722	40	copper homeostasis factor / copper chaperone (CCH) (ATX1) identical to gi:3168840 Pfam profile PF00403: Heavy-metal-associated domain	At3g56240	1524.86812	1967.272	1360.98683	2379.424	647.484474	1078.661	0.649122203	0.64881
9566	15	plastocyanin-like domain-containing protein	At4g31840	1121.53504	1849.567	753.893977	1241.57	1138.38559	2488.893	0.5569912	0.64701
14762	23	glycine-rich protein glycine-rich protein - Onobrychis viciifolia,PID:g2565429	At4g29030	969.289093	1258.401	979.289231	1522.563	439.602909	917.88	0.630790709	0.64206
23685	37	short-chain dehydrogenase/reductase (SDR) family protein contains INTERPRO family IPR002198 short-chain dehydrogenase/reductase (SDR) superfamily	At3g05260	511.351199	747.055	753.573712	1052.782	322.981393	573.094	0.654618999	0.640872

18395	29	xyloglucan fucosyltransferase, putative (FUT4) identical to SP|Q9SJP2 Probable fucosyltransferase 4 (EC 2.4.1.-) (AtFUT4) {Arabidopsis thaliana}; similar to SP|Q9SWH5 Galactoside 2-alpha-L-fucosyltransferase (EC 2.4.1.69) (Xyloglucan alpha-(1,2)-fucosyltransferase) (AtFUT1) {Arabidopsis thaliana}	At2g15390	1133.21368	1555.81	1075.49637	1449.85	481.521499	1120.857	0.633258309	0.635008
17421	27	3-isopropylmalate dehydrogenase, chloroplast, putative strong similarity to SP|P29102 3-isopropylmalate dehydrogenase, chloroplast precursor {Brassica napus}	At5g14200	1476.25291	1960.594	1084.7777	1594.785	505.536542	1272.971	0.610098799	0.63495
23354	36	pectinesterase family protein contains Pfam profile: PF01095 pectinesterase	At5g55590	1619.49949	1921.911	364.020847	651.356	566.655618	1229.065	0.620854301	0.6336
18990	30	AP2 domain-containing transcription factor, putative	At1g71130	1914.41979	2321.514	642.796881	1003.692	752.829416	1481.759	0.657713293	0.63063
29019	45	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein similar to pEARLI 1 (Accession No. L43080): an Arabidopsis member of a conserved gene family (PGF95-099), Plant Physiol. 109 (4), 1497 (1995); contains Pfam protease inhibitor/seed storage/LTP family domain PF00234	At4g12500	1375.60842	2216.844	1760.79297	3688.234	1304.93827	1798.645	0.607815197	0.62118
18490	29	expressed protein contains Pfam profile PF04862: Protein of unknown function, DUF642	At3g08030	1116.28772	1547.955	857.604251	1180.465	421.532348	974.096	0.626792046	0.61776
6153	10	seven in absentia (SINA) family protein low similarity to SP|P21461 Developmental protein seven in absentia {Drosophila melanogaster}; contains Pfam profile PF03145: Seven in absentia protein family	At3g13672	465.840953	544.613	482.844151	910.893	250.61667	444.479	0.649760963	0.61776
6624	11	aspartate aminotransferase, cytoplasmic isozyme 2 / transaminase A (ASP4) identical to aspartate aminotransferase, cytoplasmic isozyme 2 SP:P46646 [Arabidopsis thaliana]	At1g62800	478.476865	558.403	533.006342	1020.786	310.781083	644.018	0.620528426	0.613008
4419	7	sulfate transporter identical to sulfate transporter [Arabidopsis thaliana] GI:2114104	At5g10180	492.847621	695.116	385.776599	847.532	694.877429	1355.84	0.558899441	0.612
17251	27	60S acidic ribosomal protein P2 (RPP2D) acidic ribosomal protein P2, maize, PIR:S54179	At3g44590	794.930837	1208.689	387.56435	617.719	710.500506	1235.704	0.620022855	0.604824
11400	18	expressed protein	At3g45160	587.668299	787.865	177.310805	340.514	356.235845	989.931	0.54215806	0.601524
5042	8	lipid transfer protein, putative similar to lipid transfer protein 6 from Arabidopsis thaliana [gi:8571927]; contains Pfam protease inhibitor/seed storage/LTP family domain PF00234	At5g01870	313.114771	523.68	384.653279	689.26	383.778812	703.904	0.567064714	0.598752
26134	41	glycosyl hydrolase family 1 protein contains Pfam PF00232 : Glycosyl hydrolase family 1 domain; TIGRFAM TIGR01233: 6-phospho-beta-galactosidase; similar to beta-glucosidase 1 (GI:12043529) [Arabidopsis thaliana]	At1g66280	697.145308	840.614	303.892183	494.949	321.599915	670.335	0.641025182	0.598347
11824	19	aspartate aminotransferase, cytoplasmic isozyme 2 / transaminase A (ASP4) identical to aspartate aminotransferase, cytoplasmic isozyme 2 SP:P46646 [Arabidopsis thaliana]	At1g62800	596.458033	827.563	840.932915	1758.586	299.875652	752.502	0.532477366	0.595056
9572	15	expressed protein contains Pfam profile PF04862: Protein of unknown function, DUF642	At4g32460	342.853123	539.991	398.665296	651.109	513.540868	721.42	0.653019209	0.59211
23669	37	expressed protein	At2g46000	1097.70286	1435.249	1008.94487	2120.533	407.092806	865.308	0.570358262	0.588468
25092	39	expressed protein contains Pfam profile PF04396: Protein of unknown function, DUF537	At3g61100	2283.83891	3001.513	1880.64399	2961.003	1120.5439	2054.866	0.647115257	0.58608
18763	29	expressed protein	At5g36800	1323.03794	2477.41	1315.94729	2188.039	641.603912	1699.99	0.504294922	0.585316
13375	21	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein contains Pfam protease inhibitor/seed storage/LTP family domain PF00234	At3g53980	371.93155	1747.509	483.706159	3619.41	380.624093	1311.665	0.212220486	0.585144
14853	23	eukaryotic translation initiation factor 3 subunit 9 / eIF-3 eta / eIF3b (TIF3B1) nearly identical to SP|Q9C5Z1 Eukaryotic translation initiation factor 3 subunit 9 (eIF-3 eta) (eIF3 p110) (eIF3b) {Arabidopsis thaliana}	At5g27640	3927.36952	5253.568	3066.07271	4971.49	1649.12845	3906.036	0.595497828	0.58473
9216	15	nicotianamine synthase, putative similar to nicotianamine synthase [Lycopersicon esculentum][GI:4753801], nicotianamine synthase 2 [Hordeum vulgare][GI:4894912]	At1g56430	494.173889	915.084	503.299719	854.625	323.79997	736.022	0.522958859	0.582309
11507	18	GDSL-motif lipase/hydrolase family protein low similarity to family II lipases EXL3 GI:15054386, EXL1 GI:15054382 from [Arabidopsis thaliana]; contains Pfam profile PF00657: GDSL-like Lipase/Acylhydrolase	At4g30140	1067.23399	1726.25	374.31874	972.999	180.91387	1015.806	0.393681134	0.581856
5022	8	peptidyl-prolyl cis-trans isomerase / cyclophilin (CYP1) / rotamase identical to cyclophilin (CYP1) gi|992643|gb|AAA75512; similar to peptidyl-prolyl cis-trans isomerase, PPIase (cyclophilin, cyclosporin A-binding protein) [Catharanthus roseus] SWISS-PROT:Q39613	At4g34870	2204.44894	3128.739	2313.53946	3141.263	2847.46608	5394.925	0.656294993	0.578676
9277	15	plant defensin-fusion protein, putative (PDF2.1) plant defensin protein family member, personal communication, Bart Thomma (Bart.Thomma@agr.kuleuven.ac.be); contains a gamma-thionin family signature (PDOC00725)	At2g02120	908.955662	1859.646	213.800366	672.713	657.994019	2998.762	0.342006284	0.5742
30329	47	drought-responsive protein / drought-induced protein (Di21) identical to GI:469112; contains PF03242 Late embryogenesis abundant protein domain	At4g15910	1253.79177	2738.148	1572.84329	2381.044	290.64449	636.892	0.524938218	0.5733
4681	8	expressed protein	At1g67865	351.031063	635.47	186.729162	325.996	413.053782	1402.153	0.473259073	0.56848
10260	16	amino acid permease 2 (AAP2) identical to amine acid permease AAP2 [Arabidopsis thaliana] GI:510236	At5g09220	418.864325	589.08	396.139818	905.74	463.378771	897.368	0.554929877	0.5568
27815	43	expressed protein contains Pfam profile PF04654: Protein of unknown function, DUF599	At5g10580	539.729057	864.711	654.339188	1521.279	232.473941	544.776	0.493676743	0.55593
13352	21	GDSL-motif lipase, putative similar to family II lipases EXL3 GI:15054386, EXL1 GI:15054382, EXL2 GI:15054384 from [Arabidopsis thaliana]; contains Pfam profile PF00657: GDSL-like Lipase/Acylhydrolase	At3g43570	808.171056	1092.098	854.790376	1499.823	241.880366	484.504	0.603059145	0.55593
19372	30	expressed protein	At5g15860	502.501569	742.333	688.623537	1030.968	312.242976	510.158	0.652304121	0.555632
18717	29	nuclear matrix protein-related low similarity to nuclear matrix protein p84 [Homo sapiens] GI:550058	At5g09860	2369.9351	3190.201	2178.3364	3152.468	1110.03642	2371.137	0.634006246	0.5544
11885	19	expressed protein	At2g07724	587.185922	728.83	661.682989	1217.21	277.50395	603.244	0.603093739	0.5544
29679	46	NLI interacting factor (NIF) family protein contains Pfam profile PF03031: NLI interacting factor	At4g18140	951.397309	1356.064	817.067554	1317.567	670.417015	1455.117	0.594150523	0.552188
24556	38	serine carboxypeptidase S10 family protein similar to Serine carboxypeptidase II chains A and B (SP:P08819) (EC 3.4.16.6) [Triticum aestivum (Wheat)]; carboxypeptidase D - Triticum aestivum, PIR:A29639	At5g08260	359.578005	574.992	483.094308	568.647	235.632784	483.467	0.654097837	0.544896
11452	18	kinesin-like protein A, putative kinesin like protein A, Arabidopsis thaliana, gb:Q07970	At4g05190	357.99397	555.141	205.734772	271.04	349.831559	637.589	0.650868666	0.543348
18582	29	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein contains Pfam profile: PF00234 protease inhibitor/seed storage/LTP family	At3g57310	1808.29053	2433.132	1164.49036	2419.208	873.539696	1603.555	0.589766141	0.53856
11196	18	thaumatin-like protein, putative / pathogenesis-related protein, putative strong similarity to SP|P50699 Thaumatin-like protein precursor {Arabidopsis thaliana}, pathogenesis-related group 5 protein [Brassica rapa] GI:2749943; contains Pfam profile: PF00314 thaumatin family	At1g73620	314.990799	766.03	241.085079	696.227	250.864099	762.172	0.362205464	0.537342
3652	6	hypothetical protein	At4g07740	743.145418	909.828	698.061014	1530.925	515.225447	867.483	0.622234174	0.5248
20951	33	protease inhibitor, putative (DR4) identical to Dr4 GI:469114 from [Arabidopsis thaliana]; contains Pfam profile PF00197: Trypsin and protease inhibitor	At1g73330	927.28597	1533.271	346.785461	567.672	585.418981	926.99	0.615731202	0.521985
13871	22	osmotin-like protein, putative similar to SP|Q41350 Osmotin-like protein precursor {Lycopersicon esculentum}; contains Pfam profile PF00314: Thaumatin family	At2g28790	543.733531	1105.388	473.787487	780.278	314.010031	725.105	0.510717277	0.521848
12897	20	glycosyl hydrolase family 1 protein contains Pfam PF00232 : Glycosyl hydrolase family 1 domain; TIGRFAM TIGR01233: 6-phospho-beta-galactosidase; identical to thioglucosidase (GI:871992) [Arabidopsis thaliana]; similar to myrosinase precursor (EC 3.2.3.1)(Sinigrinase) (Thioglucosidase) SP|P37702 from [Arabidops	At5g25980	598.91056	1080.771	593.624168	825.061	293.256927	705.079	0.563187708	0.52065
3108	5	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein contains Pfam protease inhibitor/seed storage/LTP family domain PF00234	At5g05960	1051.94982	1265.282	145.49298	648.869	444.458703	1246.374	0.470740814	0.51901
4177	7	hydroxyproline-rich glycoprotein family protein	At3g02120	492.188765	701.509	392.898922	576.932	390.15217	681.096	0.651819506	0.5148
29306	46	cell division control protein, putative cdc2MsF [Medicago sativa] gi|1806146|emb|CAA65982	At1g20930	455.830838	713.948	378.692516	600.455	243.746392	482.075	0.591586735	0.511839
23745	37	phosphoenolpyruvate carboxylase-related / PEP carboxylase-related identical to phosphoenolpyruvate carboxylase [Arabidopsis thaliana] GP:26800701 over first 45 residues	At3g42628	978.856405	1397.72	544.480134	895.105	352.786273	904.453	0.566221615	0.51128
23775	37	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein contains Pfam protease inhibitor/seed storage/LTP family domain PF00234	At3g53980	289.973533	1284.963	305.750042	1803.251	263.229361	703.665	0.256435028	0.51051
20273	32	expressed protein	At1g64370	883.111618	1173.42	1276.21205	1971.714	627.853048	1280.71	0.630031617	0.510048
9619	15	inositol-3-phosphate synthase, putative / myo-inositol-1-phosphate synthase, putative / MI-1-P synthase, putative very strong similarity to SP|Q38862 Myo-inositol-1-phosphate synthase isozyme 2 (EC 5.5.1.4) (MI-1-P synthase 2) (IPS 2) {Arabidopsis thaliana}; identical to SP|Q9LX12| Probable inositol-3-phosphate synt	At5g10170	291.392854	425.977	282.275055	396.159	272.821357	507.596	0.644688259	0.503644
14054	22	hypothetical protein weak similarity to SP|Q13200 26S proteasome non-ATPase regulatory subunit 2 (26S proteasome regulatory subunit S2) (26S proteasome subunit p97) (Tumor necrosis factor type 1 receptor associated protein 2) {Homo sapiens}	At4g08140	361.339588	553.448	505.884151	750.272	247.552674	549.457	0.592565433	0.50184
8667	14	expressed protein contains similarity to anther-specific protein GI:1448935 from [Brassica rapa]	At2g28355	375.209785	507.529	286.354059	477.929	351.926457	573.296	0.650769545	0.495936
23595	37	xyloglucan fucosyltransferase, putative (FUT4) identical to SP|Q9SJP2 Probable fucosyltransferase 4 (EC 2.4.1.-) (AtFUT4) {Arabidopsis thaliana}; similar to SP|Q9SWH5 Galactoside 2-alpha-L-fucosyltransferase (EC 2.4.1.69) (Xyloglucan alpha-(1,2)-fucosyltransferase) (AtFUT1) {Arabidopsis thaliana}	At2g15390	586.769859	861.373	640.0324	932.297	343.761302	817.683	0.59604109	0.48708
21418	33	YT521-B-like family protein contains Pfam profile PF04146: YT521-B-like family	At5g61020	470.345986	920.834	560.561927	870.642	233.106947	417.703	0.570900061	0.484352
22637	35	chaperonin, putative similar to SWISS-PROT:P78371- T-complex protein 1, beta subunit (TCP-1-beta) [Homo sapiens]; contains Pfam:PF00118 domain, TCP-1/cpn60 chaperonin family	At5g20890	433.034002	647.133	484.149113	734.535	209.906358	513.743	0.57895445	0.48074
6762	11	glycosyl hydrolase family protein 17 similar to glucan endo-1,3-beta-glucosidase precursor SP:P52409 from [Triticum aestivum]; C terminal homology only	At2g43660	616.220497	847.724	614.6884	910.958	363.55768	888.53	0.603616897	0.472857
13442	21	pectate lyase family protein similar to pectate lyase 2 GP:6606534 from [Musa acuminata]	At4g22090	572.25899	763.364	483.608964	669.344	173.268315	446.826	0.6199806	0.4698
19305	30	beta-expansin, putative (EXPB3) similar to soybean pollen allergen (cim1) protein - soybean, PIR2:S48032; beta-expansin gene family, PMID:11641069	At4g28250	624.878674	788.971	642.208931	911.365	177.010678	455.978	0.62829481	0.463884
27422	43	flavin-containing monooxygenase family protein / FMO family protein similar to flavin-containing monooxygenase GB:AAA21178 GI:349534 SP|P32417 from [Oryctolagus cuniculus]; contains Pfam profile PF00743 Flavin-binding monooxygenase-like	At1g62560	511.252799	862.439	506.408366	1058.972	201.718522	405.229	0.522931755	0.446958
21199	33	meprin and TRAF homology domain-containing protein / MATH domain-containing protein weak similarity to ubiquitin-specific protease 12 [Arabidopsis thaliana] GI:11993471; contains Pfam profile PF00917: MATH domain	At4g01390	516.512949	878.815	532.496466	906.883	216.556012	471.764	0.54464826	0.4437
26713	42	ubiquitin extension protein, putative / 40S ribosomal protein S27A (RPS27aA) strong similarity to ubiquitin extension protein (UBQ5) GB:AAA32906 GI:166934 from (Arabidopsis thaliana)	At1g23410	377.971417	590.929	412.843022	686.467	155.824573	376.35	0.551688869	0.442953
18575	29	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein contains Pfam protease inhibitor/seed storage/LTP family domain PF00234	At3g53980	331.807663	1741.057	301.812847	2860.952	214.056979	728.039	0.196696901	0.431172
20098	31	expressed protein ; expression supported by MPSS	At5g50730	456.323911	656.154	454.201893	715.897	194.404934	353.037	0.626856128	0.430582
15183	24	glycine cleavage system H protein, mitochondrial, putative similar to SP|Q39732 Glycine cleavage system H protein, mitochondrial precursor {Flaveria anomala}; contains Pfam profile PF01597: Glycine cleavage H-protein	At2g35120	253.838077	406.273	833.162093	1133.874	311.855337	601.308	0.626072529	0.42994
27149	42	phenylalanine ammonia-lyase 3 (PAL3) nearly identical to SP|P45725	At5g04230	339.548149	438.663	343.687968	538.039	151.993548	375.996	0.605691259	0.4284
29188	45	senescence-associated protein-related similar to senescence-associated protein SAG102 (GI:22331931) [Arabidopsis thaliana];	At5g47060	165.309685	315.566	215.851021	434.021	187.198565	229.833	0.611892701	0.42484
28135	44	Ulp1 protease family protein contains Pfam profile PF02902: Ulp1 protease family, C-terminal catalytic domain; similar to At5g28270, At2g05450, At1g45090, At2g16180, At2g06750	At2g12100	737.587927	997.279	230.927403	353.465	313.366716	679.171	0.618106982	0.4059
22190	35	nodulin MtN21 family protein similar to MtN21 [Medicago truncatula] GI:2598575; contains Pfam profile PF00892: Integral membrane protein	At1g44800	284.702687	420.238	331.489196	1005.901	219.166387	451.208	0.497585561	0.4056
4159	7	protein kinase family protein contains protein kinase domain, Pfam:PF00069	At2g42550	410.620072	476.178	366.183038	621.753	181.775747	395.919	0.636800303	0.405232
14754	23	xyloglucan:xyloglucosyl transferase / xyloglucan endotransglycosylase / endo-xyloglucan transferase (XTR9) identical to xyloglucan endotransglycosylase GI:4218963 from [Arabidopsis thaliana]	At4g25820	194.046919	257.087	276.129461	551.261	259.693189	382.806	0.644696572	0.403172
24068	38	glutaredoxin family protein contains INTERPRO Domain IPR002109, Glutaredoxin (thioltransferase)	At1g06830	367.734553	701.687	409.492184	556.394	154.348247	443.537	0.536013777	0.394912
12773	20	expressed protein	At4g14590	1053.00335	1519.169	1052.31934	1422.566	482.719468	1102.321	0.623596474	0.394632
27847	43	plastocyanin-like domain-containing protein	At5g25090	620.9234	1146.757	447.939985	854.859	218.739572	544.092	0.489159983	0.393624
20620	32	expressed protein	At4g34600	317.756709	415.997	384.465262	785.524	171.245583	297.323	0.609746595	0.392445
24349	38	CCAAT-binding transcription factor (CBF-B/NF-YA) family protein contains Pfam profile: PF02045 CCAAT-binding transcription factor (CBF-B/NF-YA) subunit B	At3g14020	451.556833	633.931	712.821911	986.723	185.703682	455.764	0.614060487	0.39216
21594	34	endo-1,4-beta-glucanase (EGASE) / cellulase identical to endo-1,4-beta-glucanase GB:CAA67157 GI:2440035 from [Arabidopsis thaliana]	At1g70710	355.95109	513.735	304.462607	388.042	128.838321	369.688	0.608662376	0.39204
9335	15	meprin and TRAF homology domain-containing protein / MATH domain-containing protein low similarity to ubiquitin-specific protease 12 [Arabidopsis thaliana] GI:11993471; contains Pfam profile PF00917: MATH domain	At2g32880	264.130558	373.146	312.391171	380.781	157.938029	423.64	0.633685181	0.390432
10943	17	expressed protein	At5g22090	458.068381	737.156	421.219321	677.635	151.251261	285.908	0.590674109	0.38181
23954	37	WD-40 repeat family protein contains 5 WD-40 repeats (PF00400); similar to fizzy1 (GI:3298595) {Xenopus laevis}; similar to "Will die slowly" protein, Drosophia; putative cdc20 protein - Arabidopsis thaliana, EMBL:AF029262	At5g27570	402.367262	805.121	417.256632	600.076	115.151376	322.772	0.517285757	0.376488
15829	25	glutaredoxin family protein contains INTERPRO Domain IPR002109, Glutaredoxin (thioltransferase)	At2g30540	456.15064	791.288	442.809362	658.191	180.847889	490.621	0.539281151	0.374
1809	3	aspartyl protease family protein contains Pfam profile:PF00026 eukaryotic aspartyl protease	At5g07030	428.354629	641.316	275.820349	647.199	186.784122	616.604	0.465676706	0.368064
24351	38	expressed protein	At3g14190	372.774372	631.416	209.81537	326.527	144.758313	344.681	0.550974242	0.36421
11515	18	F-box family protein contains Pfam PF00646: F-box domain; contains TIGRFAM TIGR01640 : F-box protein interaction domain	At4g33290	460.425715	628.197	91.4987554	142.514	208.652718	427.651	0.620956567	0.363312
20091	31	pectinesterase family protein contains Pfam profile: PF01095 pectinesterase	At5g47500	460.051366	957.361	308.802922	581.653	139.032395	522.187	0.425899037	0.3608
14535	23	meprin and TRAF homology domain-containing protein / MATH domain-containing protein similar to ubiquitin-specific protease 12 [Arabidopsis thaliana] GI:11993471; contains Pfam profile PF00917: MATH domain	At2g32870	312.039852	393.195	201.698789	317.423	186.949075	555.56	0.588510762	0.355656
30922	48	speckle-type POZ protein-related contains Pfam PF00651 : BTB/POZ domain; similar to Speckle-type POZ protein (SP:O43791) [Homo sapiens]	At3g56230	519.755888	616.353	659.637114	1187.418	130.184747	294.94	0.613397522	0.353976
15294	24	hypothetical protein	At3g42600	408.265946	517.148	414.261113	633.582	213.12912	480.016	0.629100221	0.3285
22852	36	4-coumarate--CoA ligase 1 / 4-coumaroyl-CoA synthase 1 (4CL1) identical to SP|Q42524 4-coumarate--CoA ligase 1 (EC 6.2.1.12) (4CL 1) (4-coumaroyl-CoA synthase 1) {Arabidopsis thaliana}	At1g51680	387.672426	482.786	438.800466	598.281	120.466975	327.053	0.634922145	0.317856
30629	48	proton-dependent oligopeptide transport (POT) family protein contains Pfam profile: PF00854 POT family	At1g32450	536.550292	596.608	120.662042	284.602	187.730538	386.8	0.602881677	0.313728
24496	38	arginosuccinate synthase family contains Pfam profile: PF00764 arginosuccinate synthase	At4g24830	423.847457	629.11	648.056566	755.203	107.08313	287.829	0.634628391	0.310068
21825	34	expressed protein contains Pfam profile PF03759: Domain of unknown function (DUF315)	At3g55660	295.811251	488.086	324.293578	446.502	141.302555	334.728	0.584834456	0.30217
24602	38	expressed protein	At5g27330	265.760585	446.226	223.680797	326.146	109.866706	199.156	0.611021921	0.29546
29665	46	bile acid:sodium symporter family protein low similarity to SP|Q12908 Ileal sodium/bile acid cotransporter {Homo sapiens}; contains Pfam profile PF01758: Sodium Bile acid symporter family	At4g12030	258.413701	322.805	236.120167	345.043	105.107822	310.879	0.607648505	0.284746
27420	43	mitogen-activated protein kinase, putative / MAPK, putative (MPK2) identical to mitogen-activated protein kinase homolog 2 (AtMPK2)[Arabidopsis thaliana] SWISS-PROT:Q39022; PMID:12119167	At1g59580	479.800994	640.009	318.445943	575.815	132.08995	360.668	0.556316877	0.284
27891	43	formin homology 2 domain-containing protein / FH2 domain-containing protein contains formin homology 2 domain, Pfam:PF02181	At5g48360	314.446387	440.734	361.806076	499.494	110.291459	264.13	0.618456982	0.28208
25036	39	aminoalcoholphosphotransferase, putative strong similarity to aminoalcoholphosphotransferase [Arabidopsis thaliana] GI:3661593; contains Pfam profile PF01066: CDP-alcohol phosphatidyltransferase	At3g25585	239.348598	333.756	191.802424	302.924	132.236346	255.278	0.622771918	0.2772
14395	23	cyclin, putative similar to mitotic cyclin a2-type [Glycine max] GI:857397, cyclin A-like protein [Nicotiana tabacum] GI:1064927; contains Pfam profiles PF00134: Cyclin, N-terminal domain, PF02984: Cyclin, C-terminal domain	At1g44110	189.695904	322.342	249.141113	346.016	202.048427	336.446	0.636352618	0.27531
12396	20	cytochrome P450, putative similar to gb|AF069494 cytochrome P450 from Sinapis alba and is a member of the PF|00067 Cytochrome P450 family	At1g16410	220.686724	315.717	423.596615	554.702	113.002868	245.587	0.640927547	0.27255
22291	35	expressed protein	At2g11090	307.080252	380.839	311.74108	501.57	113.877117	206.711	0.659585442	0.26832
6998	11	legume lectin family protein contains Pfam domain, PF00139: Legume lectins beta domain	At5g03350	161.415377	246.834	236.403785	296.647	108.462547	210.752	0.65516932	0.264187
7510	12	peroxidase 33 (PER33) (P33) (PRXCA) / neutral peroxidase C (PERC) identical to SP|P24101 Peroxidase 33 precursor (EC 1.11.1.7) (Atperox P33) (ATPCa) (Neutral peroxidase C) (PERC) {Arabidopsis thaliana}	At3g49110	147.878886	236.745	158.676449	179.74	185.068614	409.872	0.652990815	0.261702
23324	36	expressed protein	At5g42530	376.845159	787.226	467.751835	1851.247	179.029286	330.002	0.424626103	0.25542
22615	35	expressed protein contains Pfam profile PF04654: Protein of unknown function, DUF599	At5g10580	233.191078	511.797	284.582241	632.985	96.5426564	292.272	0.411845824	0.25256
10800	17	nodulin MtN21 family protein similar to MtN21 GI:2598575 (root nodule development) from [Medicago truncatula]	At4g01450	243.821544	311.583	95.0184899	128.549	143.226315	316.98	0.657844454	0.2508
4647	8	jacalin lectin family protein similar to myrosinase-binding protein homolog [Arabidopsis thaliana] GI:2997767; contains Pfam profile PF01419 jacalin-like lectin domain	At1g52060	274.355657	344.012	70.165245	221.156	180.206635	909.797	0.437618998	0.250245
30462	47	expressed protein	At5g36710	321.008205	461.86	237.815503	344.877	101.437626	296.149	0.575707326	0.24871
28217	44	fumarate hydratase, putative / fumarase, putative similar to SP|P55250 Fumarate hydratase, mitochondrial precursor (EC 4.2.1.2) (Fumarase) {Rhizopus oryzae}; contains Pfam profile PF00206: Lyase	At2g47510	198.370125	300.638	249.453411	308.621	79.4164485	290.447	0.580514286	0.241345
20108	31	late embryogenesis abundant protein-related / LEA protein-related similar to late embryogenesis abundant protein (GI:1350543)[Picea glauca]	At5g54370	308.855739	344.411	233.602656	410.687	111.627575	451.884	0.570867186	0.236652
8829	14	expressed protein	At3g59680	196.977543	305.844	182.529063	316.071	176.047767	261.65	0.631458844	0.234423
10028	16	expressed protein	At3g04630	142.214438	197.967	168.71781	209.428	92.1260494	247.957	0.631842457	0.233472
15745	25	calmodulin-binding family protein low similarity to SF16 protein [Helianthus annuus] GI:560150; contains Pfam profile PF00612: IQ calmodulin-binding motif	At1g72670	245.650511	364.61	201.897959	266.825	106.159395	241.175	0.62352628	0.22752
27631	43	homocysteine S-methyltransferase 1 (HMT-1) identical to GB:AAF23821 from [Arabidopsis thaliana]	At3g25900	200.819442	235.057	229.537992	362.796	77.2287641	174.171	0.643480978	0.21912
26953	42	disease resistance-responsive protein-related / dirigent protein-related similar to pathogenesis-related protein [Pisum sativum] gi|4585273|gb|AAD25355; similar to dirigent protein [Forsythia x intermedia] gi|6694695|gb|AAF25358	At3g13662	245.638745	328.708	758.197645	910.458	68.7316413	176.043	0.656825323	0.217294
27199	42	hypothetical protein	At5g26050	255.256328	373.475	294.247569	398.233	67.3749058	203.288	0.584590594	0.217056
26988	42	hypothetical protein similar to hypothetical protein GB:CAB55689 GI:5881771 from [Arabidopsis thaliana]	At3g30160	136.52539	225.095	194.189279	282.637	87.3898468	172.838	0.599734332	0.213774
455	1	expressed protein weak similarity to phragmoplast-associated kinesin-related protein 1 [Arabidopsis thaliana] GI:8745333	At4g26660	139.177926	185.446	114.05756	167.135	132.271398	249.486	0.654369056	0.21216
13064	21	nodulin MtN21 family protein similar to MtN21 GI:2598575 (root nodule development) from [Medicago truncatula]	At1g21890	252.5332	564.757	166.662374	336.488	76.4967868	309.715	0.396481413	0.20655
17634	28	expressed protein	At1g35320	177.451455	267.99	323.907984	463.97	92.427088	164.793	0.640382499	0.195734
13021	21	male sterility MS5 family protein similar to male sterility MS5 [Arabidopsis thaliana] GI:3859112; contains Pfam profile PF00515 TPR Domain	At1g04770	187.823085	278.071	123.557179	194.173	105.303703	173.799	0.63922298	0.189584
22084	34	miRNA gene Arabidopsis thaliana miR397a stem-loop	ath-MIR39'	196.198896	286.5	267.01703	389.183	79.5133582	138.672	0.648100274	0.186124
28054	44	leucine-rich repeat protein kinase, putative similar to light repressible receptor protein kinase [Arabidopsis thaliana] gi|1321686|emb|CAA66376; contains leucine rich repeat (LRR) domains, Pfam:PF00560; contains protein kinase domain, Pfam:PF00069	At1g51860	171.167725	232.564	214.923685	357.197	97.2725718	167.722	0.639220293	0.173052
20140	31	peroxidase 73 (PER73) (P73) (PRXR11) identical to SP|Q43873 Peroxidase 73 precursor (EC 1.11.1.7) (Atperox P73) (PRXR11) (ATP10a) {Arabidopsis thaliana}	At5g67400	138.3458	330.899	162.78732	450.893	159.53807	350.846	0.411282597	0.171288
27851	43	expressed protein	At5g25475	251.763109	320.981	235.495569	332.573	87.3197419	182.778	0.656731224	0.167552
9386	15	formin homology 2 domain-containing protein / FH2 domain-containing protein contains formin homology 2 domain, Pfam:PF02181	At3g05470	139.229266	231.095	593.941246	1137.604	94.4127054	180.77	0.548951856	0.16384
28914	45	leucine-rich repeat transmembrane protein kinase, putative similar to receptor kinase GB:AAA33715 from [Petunia integrifolia]	At3g17840	121.469039	186.045	159.124183	199.559	79.2370625	194.169	0.6194545	0.15799
13591	21	major intrinsic family protein / MIP family protein contains Pfam profile: MIP PF00230	At5g47450	135.611977	298.31	171.21142	203.654	97.5035055	249.591	0.561983841	0.15732
12053	19	expressed protein	At3g47510	112.777705	184.261	237.718308	325.57	99.039627	220.13	0.597376249	0.156078
8017	13	serine/threonine protein kinase, putative similar to serine/threonine kinase Ayk1 [Mus musculus] gi|1763647|gb|AAB62982	At2g25880	197.83427	338.81	152.094274	224.074	107.429531	314.551	0.53473673	0.150282
26671	42	fatty acid desaturase family protein similar to delta 9 acyl-lipid desaturase (ADS1) GI:2970034 from [Arabidopsis thaliana]	At1g06360	217.992474	316.877	117.561361	220.91	47.6878082	204.071	0.484597122	0.147436
30127	47	proliferating cell nuclear antigen 2 (PCNA2) identical to SP|Q9ZW35 Proliferating cell nuclear antigen 2 (PCNA 2) {Arabidopsis thaliana}; nearly identical to SP|Q43124 Proliferating cell nuclear antigen (PCNA) {Brassica napus}; contains Pfam profiles PF00705: Proliferating cell nuclear antigen N-terminal domain, PF027	At2g29570	169.43609	302.153	172.639071	200.193	93.5673231	275.378	0.587634502	0.146615
21547	34	heavy-metal-associated domain-containing protein contains Pfam profile PF00403: Heavy-metal-associated domain	At1g51090	193.992371	291.616	157.884548	445.434	69.3089755	129.883	0.517769846	0.14592
24807	39	legume lectin family protein	At1g53060	311.619511	526.524	296.822441	525.666	66.0820895	149.763	0.532582378	0.14276
14781	23	Rac-like GTP-binding protein (ARAC3) / Rho-like GTP-binding protein (ROP6) identical to SP|Q38912 RAC-like GTP binding protein ARAC3 (GTP-binding protein ROP6) {Arabidopsis thaliana}; identical to cDNA Rho-like GTP binding protein (Rop6) GI:2645642	At4g35020	216.973173	250.697	267.925246	348.511	56.4859697	164.736	0.65904628	0.138138

27667	43	leucine-rich repeat transmembrane protein kinase, putative brassinosteroid-insensitive protein BRI1 - Arabidopsis thaliana, PIR:T09356	At3g51740	196.247026	326.862	188.418125	279.272	61.2324819	160.268	0.552378759	0.1343
24559	38	calcium-binding EF hand family protein contains INTERPRO:IPR002048 calcium-binding EF-hand domain	At5g08580	167.285183	254.159	195.361992	228.728	53.6879605	173.942	0.606989696	0.126
23410	37	nodulin MtN21 family protein similar to MtN21 GI:2598575 (root nodule development) from [Medicago truncatula]	At1g01070	273.99949	359.85	160.021245	231.997	37.7555974	129.495	0.580914298	0.125925
16995	27	cyclin, putative similar to cyclin A-like protein [Nicotiana tabacum] GI:1064931, A-type cyclin [Catharanthus roseus] GI:2190259; contains Pfam profiles PF00134: Cyclin, N-terminal domain, PF02984: Cyclin, C-terminal domain	At1g47230	330.716701	465.848	244.434324	283.571	58.1190008	158.491	0.646204198	0.123662
2349	4	pollen Ole e 1 allergen and extensin family protein contains Pfam domain, PF01190: Pollen proteins Ole e I family	At4g02270	86.9037133	134.846	175.518274	204.913	150.506913	350.04	0.643662402	0.12078
16125	25	expressed protein contains Pfam profile PF03267: Arabidopsis protein of unknown function, DUF266	At5g14550	221.634363	306.758	256.790839	374.008	54.1230231	119.538	0.620621918	0.11952
24954	39	expansin, putative (EXP4) similar to alpha-expansin 6 precursor GI:16923359 from [Cucumis sativus]; alpha-expansin gene family, PMID:11641069	At2g39700	313.122258	451.845	262.670341	431.73	41.0154739	185.05	0.507681604	0.118524
17227	27	CXC domain protein (TSO1) identical to CXC domain protein TSO1 [Arabidopsis thaliana] GI:7767425	At3g22780	190.786866	331.456	301.647138	694.989	128.908426	159.709	0.605593193	0.117612
14772	23	expressed protein contains Pfam profile PF04862: Protein of unknown function, DUF642	At4g32460	182.661335	238.157	241.045245	315.074	69.6368189	196.411	0.62885612	0.11592
22308	35	reticulon family protein non-consensus AA donor splice site at 46485 and non-consensus GG acceptor splice site at 46563, confirmed by Ceres cDNA 1885; contains Pfam profile PF02453: Reticulon	At2g20590	185.653995	271.146	168.091619	260.289	41.1185693	153.383	0.53285579	0.115425
24366	38	hypothetical protein	At3g20555	131.228875	375.267	327.811719	364.327	42.8567578	196.792	0.489081649	0.1136
29342	46	glutamine synthetase, putative similar to glutamine synthetase, cytosolic isozyme (glutamate-- ammonia ligase, GS1) [Arabidopsis thaliana] SWISS-PROT:Q9LVI8	At1g48470	177.774465	261.949	168.458092	251.445	54.90861	128.389	0.592098129	0.11297
24548	38	nicotianamine synthase, putative similar to nicotianamine synthase [Lycopersicon esculentum][GI:4753801], nicotianamine synthase 2 [Hordeum vulgare][GI:4894912]	At5g04950	530.108266	678.564	620.203022	990.784	29.8873565	106.054	0.563001781	0.11008
19467	30	proton-dependent oligopeptide transport (POT) family protein contains Pfam profile: PF00854 POT family	At5g62680	266.409814	350.197	289.445179	382.729	44.9207277	158.249	0.600290137	0.105825
16950	27	sulfotransferase family protein similar to SP|P52837 Flavonol 4'-sulfotransferase (EC 2.8.2.-) (F4-ST) {Flaveria chloraefolia}; contains Pfam profile PF00685: Sulfotransferase domain	At1g18590	205.770486	308.487	234.354723	395.637	73.0204099	108.9	0.643302109	0.105
5860	10	endo-1,4-beta-glucanase / cellulase (CEL2) identical to endo-1,4-beta glucanase; ATCEL2 GI:3132891 from [Arabidopsis thaliana]	At1g02800	99.8230614	158.293	110.276515	169.345	75.507071	162.808	0.581865445	0.104784
24272	38	Dof-type zinc finger domain-containing protein similar to zinc finger protein OBP2 GI:5059394 from [Arabidopsis thaliana]	At2g28810	239.056605	307.544	392.138889	434.701	32.2028791	110.707	0.656760418	0.104576
11671	18	AT hook motif-containing protein contains Pfam PF03479: Domain of unknown function (DUF296); contains Pfam PF02178: AT hook motif; similar to AT-Hook DNA-Binding Protein SAP1 protein (GI:4165183) [Antirrhinum majus]; similar to AT-hook protein 2, Arabidopsis thaliana, EMBL:ATAJ4119	At5g62260	98.6262115	146.604	150.958208	209.545	84.7959665	144.892	0.65946135	0.1036
27876	43	expressed protein	At5g41860	162.073163	197.187	214.208266	296.248	52.1951391	129.812	0.649026503	0.102638
27893	43	superoxide dismutase [Fe], putative / iron superoxide dismutase, putative similar to Fe-superoxide dismutase precursor [Medicago sativa] gi|16974682|gb|AAL32441	At5g51100	177.776605	224.556	135.526507	194.556	76.0782195	195.981	0.625488707	0.100768
24543	38	leucine-rich repeat transmembrane protein kinase, putative leucine-rich receptor-like protein (LRPKm1) - Malus domestica, EMBL:AF053127	At5g01890	184.979096	287.745	318.07469	373.146	35.9885422	130.682	0.590220476	0.099484
18194	28	expressed protein	At1g35320	179.219456	222.982	109.78098	236.44	86.6599313	191.097	0.573844721	0.0966
10102	16	oxidoreductase, 2OG-Fe(II) oxygenase family protein similar to hyoscyamine 6 beta-hydroxylase from Atropa belladonna [GI:4996123] and Hyoscyamus niger [SP|P24397], gibberellin 20-oxidase [GI:9791186]; contains PF03171 2OG-Fe(II) oxygenase superfamily domain	At3g46490	128.29825	142.66	74.4306724	103.679	77.9648653	224.593	0.654787542	0.09656
3880	6	GDP-D-mannose 4,6-dehydratase, putative strong similarity to GDP-D-mannose-4,6-dehydratase [Arabidopsis thaliana] GI:1764100	At5g66280	107.646973	124.61	86.9082824	162.41	60.3231804	151.515	0.599040342	0.09646
12676	20	cyclopropane-fatty-acyl-phospholipid synthase family protein similar to cyclopropane synthase [Sterculia foetida] GI:21069167; contains Pfam profile PF02353: Cyclopropane-fatty-acyl-phospholipid synthase	At3g23470	113.760641	132.701	137.895834	207.633	69.8223906	203.003	0.621783516	0.09504
17443	27	hypothetical protein	At5g22180	277.774006	379.547	276.500714	611.699	39.4071857	273.349	0.442680638	0.09296
30173	47	expressed protein	At3g01680	206.944875	266.045	121.892117	182.325	131.481687	304.764	0.625940353	0.092664
25236	39	heavy-metal-associated domain-containing protein / copper chaperone (CCH)-related similar to copper homeostasis factor [Arabidopsis thaliana][GI:3168840], and farnesylated proteins GMFP7 [Glycine max][GI:4097573], ATFP7 [GI:4097555], and ATFP6 [GI:4097553]; contains heavy-metal-associated domain PF0040	At5g17450	169.217897	205.628	246.045212	300.145	51.1848042	162.41	0.652614876	0.092416
23884	37	O-methyltransferase family 2 protein similar to caffeic acid O-methyltransferase, Pinus taeda, gb:U39301	At4g35150	157.96708	196.505	210.774573	249.083	35.0895503	116.58	0.650358864	0.091542
14569	23	WRKY family transcription factor contains Pfam profile: PF03106 WRKY DNA -binding domain	At2g46130	121.958903	170.274	126.068316	184.102	86.8166363	155.581	0.653013614	0.0912
27654	43	chitinase, putative similar to basic endochitinase CHB4 precursor SP:Q06209 from [Brassica napus]	At3g47540	156.37235	178.654	193.703303	248.895	56.4735982	175.838	0.658233953	0.090919
21173	33	DJ-1 family protein low similarity to SP|Q51732 protease I from Pyrococcus furiosus; contains Pfam profile: PF01965 DJ-1/PfpI family	At3g54600	307.969065	415.519	316.823901	441.287	55.7374971	165.593	0.598571616	0.085272
19071	30	expressed protein	At2g28780	126.874651	212.868	256.121627	377.385	33.8029198	156.604	0.496849767	0.084864
27627	43	CXC domain containing TSO1-like protein 1 (SOL1) identical to CXC domain containing TSO1-like protein 1 (SOL1) [Arabidopsis thaliana] GI:7767427; contains Pfam profile PF03638: Tesmin/TSO1-like CXC domain; supporting cDNA gi|7767426|gb|AF205142.1|AF205142	At3g22760	122.027355	165.15	104.389046	161.999	72.8740144	167.846	0.605813568	0.08294
26964	42	hypothetical protein	At3g19516	148.048948	252.22	175.81942	211.75	30.6213957	122.463	0.555781838	0.082928
28916	45	DNA-directed RNA polymerase family protein similar to SP|P38420 DNA-directed RNA polymerase II 135 kDa polypeptide (EC 2.7.7.6) (RNA polymerase II subunit 2) {Arabidopsis thaliana}; contains Pfam profiles PF04560: RNA polymerase Rpb2 domain 7, PF04561: RNA polymerase Rpb2 domain 2, PF04565: RNA pc	At3g18090	100.466943	143.183	186.840698	233.507	51.1291327	110.898	0.654288295	0.081249
2932	5	synaptobrevin-related similar to SYNAPTOBREVIN-RELATED PROTEIN GB:P47192 from [Arabidopsis thaliana] (Proc. Natl. Acad. Sci. U.S.A. (1992) 89(9), 3894-3898); contains Pfam profile PF00957: synaptobrevin	At3g24890	193.272549	248.977	93.6019919	141.107	66.2181754	136.213	0.641914727	0.079872
5227	9	syntaxin-related protein KNOLLE (KN) / syntaxin 111 (SYP111) identical to SP|Q42374 Syntaxin-related protein KNOLLE (Syntaxin 111) (AtSYP111) {Arabidopsis thaliana}; BAC F22O13 has a deletion of a cytosine at position 7887	At1g08560	320.967561	522.158	222.949445	305.697	48.8630958	208.194	0.526236426	0.079849
21511	34	expressed protein	At1g23230	153.705909	175.347	187.489196	276.495	42.2505568	103.186	0.654711349	0.07956
16311	26	caleosin-related family protein similar to caleosin GB:AAF13743 GI:6478218 from [Sesamum indicum]; similar to Ca+2-binding EF hand protein GB:AAB71227 [Glycine max]; contains Pfam profile PF05042: Caleosin related protein	At1g23240	59.4574519	115.535	139.981544	197.975	103.670672	248.093	0.546521387	0.07497
26379	41	expressed protein	At3g57860	152.740087	252.498	209.359669	236.309	48.8218576	180.922	0.586907857	0.073656
23722	37	4-coumarate--CoA ligase 2 / 4-coumaroyl-CoA synthase 2 (4CL2) identical to SP|Q9S725 4-coumarate--CoA ligase 2 (EC 6.2.1.12) (4CL 2) (4-coumaroyl-CoA synthase 2) {Arabidopsis thaliana}	At3g21240	125.994394	163.72	135.201461	259.894	32.027617	93.164	0.544522287	0.07176
18486	29	cyclin family low similarity to microtubule-binding protein TANGLED1 [Zea mays] GI:11228986; contains Pfam profile PF00134: Cyclin, N-terminal domain	At3g05330	216.643745	308.641	128.925212	150.76	73.0760814	180.629	0.653887004	0.069654
6521	11	ethylene-responsive protein, putative similar to ethylene-inducible ER33 protein [Lycopersicon esculentum] gi|5669656|gb|AAD46413; identical to bHLH transcription factor (bHLH-alpha gene)	At1g05710	128.029788	145.781	92.8467388	133.231	64.4201916	164.201	0.655814772	0.0693
22229	35	no apical meristem (NAM) family protein similar to jasmonic acid 2 GI:6175246 from [Lycopersicon esculentum]; similar to NAC2 (GI:6456751) {Arabidopsis thaliana}	At1g65910	161.743735	242.651	177.430308	283.486	81.1731941	143.909	0.61883866	0.0689
21842	34	zinc finger (C3HC4-type RING finger) family protein (ATL5) identical to RING-H2 zinc finger protein ATL5 [Arabidopsis thaliana] gi|4928401|gb|AAD33583	At3g62690	119.708525	200.404	103.200399	184.239	58.9561354	130.818	0.536051041	0.065772
13399	21	hypothetical protein	At4g00640	120.076458	191.247	181.498158	236.881	34.0070486	186.429	0.525491069	0.06555
6566	11	beta-1,3-glucanase-related similar to beta-1,3-glucanase GI:15150341 from [Camellia sinensis]; C-terminal homology only	At1g26450	74.8507177	116.843	115.317909	149.165	56.277717	174.051	0.579013107	0.065424
6522	11	jacalin lectin family protein (RTM1) identical to gi:6503088 (GB:AAF14583) from [Arabidopsis thaliana] (Proc. Natl. Acad. Sci. U.S.A. 97 (1), 489-494 (2000)); contains Pfam profile PF01419 jacalin-like lectin domain	At1g05760	65.1229695	114.062	97.0372783	121.495	85.1485528	167.95	0.625541571	0.06512
7015	11	cytochrome P450 family protein similar to Cytochrome P450 91A1 (SP:Q9FG65) {Arabidopsis thaliana} ; cytochrome P450, Helianthus tuberosus, EMBL:HTCYP81L	At5g10600	94.1104827	138.012	94.2520832	140.257	59.6118222	106.225	0.638360262	0.064288
23798	37	cyclic nucleotide-binding domain-containing protein contains Pfam profile: PF00027 cyclic nucleotide-binding domain	At4g00510	112.26645	153.144	223.82898	274.899	32.9987756	85.253	0.644789697	0.0627
30035	47	zinc knuckle (CCHC-type) family protein contains Pfam domain, PF00098: Zinc knuckle	At1g65660	191.384756	264.875	97.4403986	151.327	66.5109664	155.858	0.597731493	0.06132
6693	11	bifunctional dihydrofolate reductase-thymidylate synthase 1 / DHFR-TS (THY-1) identical to GP:289193:L08593 [SP|Q05762]	At2g16370	80.277721	132.526	86.8732284	145.828	56.5416412	172.65	0.509655835	0.060844
22041	34	disease resistance-responsive protein-related / dirigent protein-related similar to dirigent protein [Thuja plicata] gi|6694699|gb|AAF25360; similar to pathogenesis-related protein [Pisum sativum] gi|4585273|gb|AAD25355	At5g49040	95.101975	155.438	127.937328	233.798	47.1310931	96.773	0.54869087	0.058956
19650	31	COP1-interacting protein-related similar to COP1-Interacting ProteinI 7 (CIP7) [Arabidopsis thaliana] GI:3327870	At1g72410	270.755481	303.155	89.8607803	173.886	67.4511964	175.868	0.597812832	0.0585
18746	29	ferric-chelate reductase, putative similar to ferric-chelate reductase (FRO1) [Pisum sativum] GI:15341529; contains Pfam profile PF01794: Ferric reductase like transmembrane component	At5g23990	150.223386	176.89	96.3648799	208.066	56.3643171	147.181	0.565117467	0.057132
7615	12	peroxidase, putative identical to class III peroxidase ATP32 [Arabidopsis thaliana] gi|17530547|gb|AAL40837; identical to cDNA class III peroxidase ATP32 GI:17530546	At4g33420	107.818105	134.171	137.086407	218.775	88.4785342	241.966	0.598620502	0.056784
27613	43	protein kinase family protein contains protein kinase domain, Pfam:PF00069	At3g18750	150.13782	181.779	163.584	231.724	36.5431955	100.095	0.632321468	0.056576
21526	34	expressed protein	At1g31050	95.0110615	146.171	90.8932782	175.694	56.3457599	115.496	0.551732304	0.055968
6780	11	glutathione S-transferase, putative identical to glutathione S-transferase GB:AAB09584 from [Arabidopsis thaliana]	At3g03190	103.251036	130.065	69.3908716	143.049	51.4899666	115.561	0.57483057	0.05304
19953	31	ABC transporter family protein Bactrocera tryoni membrane transporter (white) gene, PID:g3676298	At4g25750	147.080986	166.085	180.511868	261.943	34.8008832	120.554	0.621125915	0.0528
25112	39	zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097: Zinc finger, C3HC4 type (RING finger)	At4g09130	184.96947	263.617	180.542142	214.699	35.8936945	172.029	0.583739041	0.052038
20033	31	expressed protein	At5g17210	156.743491	210.095	149.774341	211.843	45.6279621	133.867	0.597970626	0.050286
14721	23	gamma interferon responsive lysosomal thiol reductase family protein / GILT family protein similar to SP|P13284 Gamma-interferon inducible lysosomal thiol reductase precursor {Homo sapiens}; contains Pfam profile PF03227: Gamma interferon inducible lysosomal thiol reductase (GILT)	At4g12870	89.3230829	166.419	154.952764	199.7	67.8759495	177.258	0.565195194	0.04995
24320	38	pectate lyase family protein similar to pectate lyase P59 SP:P15722 from [Lycopersicon esculentum]	At3g01270	175.634254	224.859	228.137428	394.831	45.6052811	142.822	0.559404003	0.049284
10157	16	hypothetical protein low similarity to chaperonin-containing-TCP1 theta subunit from Tetrahymena pyriformis [GI:4959731], Homo sapiens [SP|P50990]	At4g08640	73.0805777	142.127	109.817627	170.281	39.0937757	162.357	0.466633694	0.049248
13212	21	kinesin motor protein-related	At2g22610	139.71806	197.612	97.6746227	141.012	34.4771637	103.473	0.577633583	0.047736
9055	14	expressed protein contains similarity to carboxyl-terminal proteinase contains Pfam profile PF03080: Arabidopsis proteins of unknown function	At5g56530	125.987977	212.564	131.10493	204.944	66.4697282	194.9	0.524487459	0.044733
14787	23	cyclin 2b (CYC2b) identical to cyclin 2b protein [Arabidopsis thaliana] GI:509423	At4g35620	132.279193	191.102	110.290855	169.998	45.6238383	184.585	0.529379581	0.044574
17755	28	amino acid permease, putative similar to AUX1 [Arabidopsis thaliana] GI:1531758; contains Pfam profile PF01490: Transmembrane amino acid transporter protein	At2g21050	158.007724	240.003	118.82171	171.604	37.2586776	148.479	0.533903675	0.042976
13263	21	expressed protein	At2g42860	88.7251927	154.657	134.19605	181.476	54.6261286	110.818	0.602031866	0.041292
7230	12	copper amine oxidase, putative similar to copper amine oxidase [Lens culinaris] gi|15451834|gb|AAB34918	At1g31710	75.0239882	132.517	66.7968798	126.393	67.9625496	168.348	0.499444827	0.040404
448	1	glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein weak similarity to SP|P27644 Polygalacturonase (EC 3.2.1.15) (Pectinase) {Agrobacterium tumefaciens}; contains PF00295: Glycosyl hydrolases family 28	At4g23500	136.22591	154.357	86.0367139	153.245	32.5740226	106.762	0.583026386	0.0396
25735	40	glutaredoxin family protein contains INTERPRO Domain IPR002109, Glutaredoxin (thioltransferase)	At3g62960	165.460495	308.803	152.765079	278.483	68.8532938	194.435	0.47949797	0.039072
1908	3	glycosyl hydrolase family 17 protein similar to elicitor inducible chitinase Nt-SubE76 GI:11071974 from [Nicotiana tabacum]	At5g55180	218.433137	319.098	114.757046	237.551	185.245939	464.839	0.522044417	0.037422
9611	15	beta-Ig-H3 domain-containing protein / fasciclin domain-containing protein contains Pfam profile PF02469: Fasciclin domain	At5g06390	62.0511616	160.048	85.1045977	152.401	48.9579436	172.515	0.409972797	0.03572
6938	11	disease resistance protein (TIR class), putative contains Pfam profile PF01582: TIR domain	At4g19925	73.3907533	115.391	75.2910873	113.462	52.4570014	106.175	0.597886491	0.034914
5133	8	glycine-rich protein	At5g46730	65.2780573	103.092	98.4697098	125.41	69.0038131	158.941	0.617510531	0.034452
30106	47	FAD-binding domain-containing protein / cytokinin oxidase family protein similar to cytokinin oxidase, Zea mays [SP|Q9T0N8] [gi:3441978]	At2g19500	188.718316	279.67	87.8435853	105.976	31.1018203	126.864	0.582949591	0.033152
21913	34	expressed protein hypothetical protein T29E15.27 - Arabidopsis thaliana,PID:g3738334	At4g30740	53.8582477	140.664	118.984233	171.442	47.512546	98.64	0.51952746	0.02976
21559	34	expressed protein	At1g54840	81.6178934	110.985	113.227419	137.509	40.0484391	97.697	0.656246307	0.0273
5497	9	expressed protein	At3g12320	354.810927	717.821	136.861743	177.112	115.65242	375.338	0.525052937	0.026752
6722	11	no apical meristem (NAM) family protein contains Pfam PF02365: No apical meristem (NAM) domain;	At2g27300	99.011257	224.122	55.9747719	87.157	54.572519	90.058	0.563324652	0.0265
10945	17	vegetative storage protein 2 (VSP2) identical to SP|O82122 Vegetative storage protein 2 precursor {Arabidopsis thaliana}; contains Pfam profile PF03767: HAD superfamily (subfamily IIIB) phosphatase	At5g24770	246.1254	379.255	420.532582	675.852	61.8737353	112.911	0.606394457	0.025912
3181	5	expressed protein similar to unknown protein (gb|AAD10667.1)	At5g44040	126.294944	183.578	139.750507	163.213	75.148299	174.315	0.65843863	0.02574
25661	40	expressed protein similar to GB:AAD49756 from [Arabidopsis thaliana]	At3g17680	155.102769	273.759	151.692747	282.395	106.72642	244.455	0.513440397	0.0248
10280	16	expressed protein various predicted proteins	At5g19260	53.2624967	112.293	58.9193031	118.69	45.4836286	152.962	0.422694333	0.024679
6803	11	expressed protein weak similarity to SP|Q9UKL6 Phosphatidylcholine transfer protein (PC-TP) {Homo sapiens}	At3g13062	65.7572251	88.128	71.0049462	116.217	32.9616613	72.183	0.604588258	0.022134
27373	43	expressed protein	At1g29950	257.971969	352.502	270.791702	394.071	33.3596095	122.954	0.563437927	0.021672
23540	37	expressed protein contains Pfam profile PF01027: Uncharacterized protein family UPF0005	At1g68600	234.821104	414.735	499.805478	603.316	28.8048548	88.155	0.573792856	0.021627
21972	34	paired amphipathic helix repeat-containing protein low similarity to transcriptional repressor SIN3B [Mus musculus] GI:2921547; contains Pfam profile PF02671: Paired amphipathic helix repeat	At5g15030	170.515287	201.191	198.228449	258.471	28.2893778	140.441	0.605296367	0.021
6781	11	DNA helicase (RECQI1) identical to DNA Helicase [Arabidopsis thaliana] GI:10944747	At3g05740	63.8148841	107.25	71.3443321	96.424	45.8877625	99.759	0.598299664	0.0209
7062	11	chromosome condensation family protein contains pfam profile: PF04154 chromosome condensation protein 3, C-terminal region	At5g37630	76.1438291	115.465	64.0642657	102.284	40.7123735	112.111	0.549644772	0.0198
17078	27	E3 ubiquitin ligase SCF complex subunit SKP1/ASK1 (At14), putative E3 ubiquitin ligase; similar to Skp1 homolog Skp1b GI:3068809, UIP2 GI:3719211 from [Arabidopsis thaliana]	At2g03170	287.844017	324.118	285.382109	386.254	28.8543406	100.412	0.638096404	0.01968
28995	45	zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)	At4g00305	353.662208	420.05	706.305064	849.131	21.8191105	84.939	0.643543311	0.01935
23446	37	hypothetical protein	At1g14680	237.470432	294.987	247.485611	291.389	21.3613669	85.58	0.634652548	0.019197
10769	17	cell division control protein 2 homolog B (CDC2B) identical to cell division control protein 2 homolog B [Arabidopsis thaliana] SWISS-PROT:P25859	At3g54180	95.6025343	147.14	59.1806143	131.722	37.0937249	138.212	0.455801865	0.018564
1191	2	glycosyl transferase family 2 protein similar to beta-(1-3)-glucosyl transferase GB:AAC62210 GI:3687658 from [Bradyrhizobium japonicum], cellulose synthase from Agrobacterium tumeficiens [gi:710492] and Agrobacterium radiobacter [gi:710493]; contains Pfam glycosyl transferase, group 2 family protein domain PF00	At5g22740	200.645102	244.174	138.117312	222.387	96.0704794	242.466	0.613006621	0.017958
22805	36	E3 ubiquitin ligase SCF complex subunit, putative similar to Skp1 GI:4959710 from [Medicago sativa]	At1g20140	170.562348	274.427	259.062972	358.088	89.2290687	159.788	0.634468362	0.017856
6778	11	expressed protein	At3g02950	67.1818937	82.14	36.7476847	80.008	56.2282312	143.841	0.55603352	0.017732
24448	38	expressed protein similar to A. thaliana hypothetical protein T6B20.12 (1946366)	At4g02800	129.140003	290.139	136.739054	201.158	13.8147836	205.187	0.39739475	0.01708
6908	11	equilibrative nucleoside transporter, putative (ENT6) identical to putative equilibrative nucleoside transporter ENT6 [Arabidopsis thaliana] GI:16518997; contains similarity to SWISS-PROT:O54699 equilibrative nucleoside transporter 2 (Equilibrative nitrobenzylmercaptopurine riboside-insensitive nucleoside transporter, E	At4g05110	69.1509739	90.868	56.306191	96.298	46.3063299	85.713	0.628653699	0.015824
21910	34	expansin-related similar to blight-associated protein p12 precursor [Citrus jambhiri] gi|4102727|gb|AAD03398; similar to beta-expansin [Oryza sativa] gi|8118428|gb|AAF72986; expansin-related gene, PMID:11641069, www.bio.psu.edu/expansins	At4g30380	155.811895	214.45	243.648797	294.605	26.98419	79.37	0.631193457	0.015444
6947	11	expressed protein probable membrane protein YPL012w, Saccharomyces cerevisiae, PIR2:S59681	At4g23540	51.0762935	85.598	58.587884	108.542	78.7236474	109.856	0.617692931	0.015225
7078	11	hypothetical protein	At5g44590	79.4969341	98.45	56.8001329	108.72	52.4240109	92.285	0.632665331	0.01512
14256	22	mitogen-activated protein kinase kinase (MAPKK), putative (MKK6) similar to NQK1 MAPKK [Nicotiana tabacum] gi|12718822|dbj|BAB32405; mitogen-activated protein kinase kinase (MAPKK) family, PMID:12119167	At5g56580	95.2132104	155.086	157.62961	193.281	77.0225733	191.643	0.610463667	0.01449
11716	19	importin alpha-2 subunit, putative similar to importin alpha-2 subunit (Karyopherin alpha-2 subunit) (KAP alpha) SP:O04294 from [Arabidopsis thaliana]	At1g02690	144.651991	189.694	93.8569297	158.542	110.27084	192.559	0.642404937	0.014268
7476	12	cyclopropane fatty acid synthase-related similar to cyclopropane synthase [Sterculia foetida] GI:21069167	At3g23480	55.9289372	90.07	64.4737595	89.054	45.5021857	102.712	0.59598072	0.014112
3195	5	expressed protein	At5g50335	95.5426383	227.299	165.932615	367.436	64.6531872	82.071	0.553235463	0.01332
22216	35	expressed protein	At1g58280	156.193731	203.41	146.122357	204.623	22.9242931	85.649	0.583211853	0.013248
23623	37	heme oxygenase 2 (HO2) similar to heme oxygenase 2 [Arabidopsis thaliana] gi|4530595|gb|AAD22109	At2g26550	210.24878	265.998	104.749146	127.82	21.5036385	78.176	0.62832901	0.013104
15680	25	subtilase family protein Strong similarity to gb|U80583 proteinase TMP from Lycopersicon esculentum and is a member of the PF|00082 subtilase family	At1g30600	160.588599	229.807	159.070009	180.779	27.8790581	102.245	0.617127012	0.013041
28861	45	expressed protein contains Pfam profile PF04852: Protein of unknown function (DUF640)	At2g42610	104.331303	191.435	127.637776	153.887	22.6067593	134.947	0.513981515	0.012992
22436	35	expressed protein contains Pfam PF03138: Plant protein family. The function of this family of plant proteins is unknown;	At3g26370	165.150319	251.87	135.548814	178.267	46.39293	112.194	0.609857546	0.012264
27941	43	cytochrome P450, putative similar to SP|O64636 Cytochrome P450 76C1 (EC 1.14.-.-) {Arabidopsis thaliana}; contains Pfam profile PF00067: Cytochrome P450	At1g33720	98.6176549	119.425	79.7923322	129.831	70.7420016	152.28	0.634969631	0.011914
6644	11	hypothetical protein	At1g70020	64.919751	77.079	39.6746889	98.869	59.279855	92.619	0.627858282	0.011687
30367	47	hypothetical protein	At4g31960	147.89386	165.453	91.57205	132.103	31.5142019	121.903	0.61519259	0.011648
7477	12	phragmoplast-associated kinesin-related protein, putative similar to kinesin like protein GB:CAB10194 from [Arabidopsis thaliana]	At3g23670	51.2025029	87.009	57.3657761	85.833	65.3727931	124.961	0.593320314	0.011616
9387	15	epoxide hydrolase, putative similar to epoxide hydrolase from [Glycine max] GI:2764806, [Arabidopsis thaliana] GI:1109600; contains Pfam profile PF00561: hydrolase, alpha/beta fold family	At3g05600	81.9515996	140.091	47.1953528	93.364	45.2856854	117.099	0.492405545	0.01161
11973	19	ABA-responsive protein-related similar to ABA-inducible protein [Fagus sylvatica] GI:3901016, cold-induced protein kin1 [Brassica napus] GI:167146	At3g02480	105.527084	190.548	113.789876	467.732	56.4674125	96.589	0.460567944	0.011468
6865	11	disease resistance protein (TIR-NBS-LRR class), putative domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.	At3g51560	44.3454832	70.984	72.0246973	84.865	33.3204333	77.651	0.634175792	0.011088
6916	11	subtilase family protein contains similarity to subtilase; SP1 GI:9957714 from [Oryza sativa]	At4g10510	51.7094796	76.174	64.4371122	94.298	35.7328656	66.359	0.633548885	0.010948
8670	14	kinesin motor protein-related	At2g28620	158.287951	244.591	80.1301247	152.634	110.161559	283.68	0.520155378	0.01081
895	2	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein contains Pfam protease inhibitor/seed storage/LTP family domain PF00234	At2g37870	122.890499	275.433	84.8018591	577.631	93.1631892	164.366	0.386595019	0.010656
1540	3	xanthine/uracil permease family protein contains Pfam profile: PF00860 permease family	At2g34190	167.608193	218.253	97.3161164	179.354	65.869713	202.591	0.545227497	0.01053
6933	11	pentatricopeptide (PPR) repeat-containing protein contains Pfam profile PF01535: PPR repeat	At4g19440	86.4512848	141.921	60.8361163	117.982	76.9730875	132.43	0.568675251	0.01045
22391	35	pectate lyase family protein simliar to style development-specific protein 9612 SP:P24396 from [Lycopersicon esculentum]	At3g09540	116.011019	148.474	160.66815	222.776	25.9449884	124.197	0.570489032	0.01026
7103	11	DegP protease family contains similarity to DegP2 protease [Arabidopsis thaliana] gi|13172275|gb|AAK14061	At5g54745	59.0007451	96.608	47.4821578	99.982	37.9246738	77.547	0.524894762	0.009828
19463	30	myb family transcription factor (MYB59) contains PFAM profile: myb DNA binding domain PF00249	At5g59780	123.776104	169.514	134.425494	198.19	29.8791088	109.255	0.560642813	0.009828
20470	32	zinc finger (GATA type) family protein similar to zinc finger protein ZIM gi:8918533 from [Arabidopsis thaliana]; contains Pfam PF00320: GATA zinc finger	At3g21175	106.937848	119.955	151.832963	246.975	60.8572146	134.405	0.653014475	0.009792
24237	38	hypothetical protein	At2g14340	91.4044681	128.979	179.662606	204.254	27.5986386	86.403	0.635899529	0.009729

15014	24	lysine and histidine specific transporter, putative similar to lysine and histidine specific transporter GI:2576361 from [Arabidopsis thaliana]; contains Pfam profile PF01490: Transmembrane amino acid transporter protein	At1g24400	79.9889368	124.85	109.275884	180.913	59.0262403	128.955	0.567477412	0.00966
9912	16	phosphoglycerate/bisphosphoglycerate mutase family protein similar to SP|P31217 Phosphoglycerate mutase 1 (EC 5.4.2.1) {Escherichia coli O157:H7}; contains Pfam profile PF00300: phosphoglycerate mutase family	At1g78050	50.6559521	69.412	31.3621246	132.688	43.0773819	84.601	0.491776492	0.0096
15551	24	actin-related protein, putative (ARP8) strong similarity to actin-related protein 8A (ARP8) [Arabidopsis thaliana] GI:21427473; contains Pfam profile PF00022: Actin; supporting cDNA gi|21427470|gb|AF507916.1|	At5g56180	218.014935	272.876	243.280731	273.006	35.1885219	144.774	0.64437644	0.00957
15316	24	pectate lyase family protein similar to pectate lyase 2 GP:6606534 from [Musa acuminata]	At3g53190	77.8604905	133.296	160.789245	260.618	53.205474	159.786	0.511350176	0.009177
6986	11	zinc finger protein-related similar to lateral root primordium 1 (LRP1) [Arabidopsis thaliana] GI:882341; contains Pfam profile PF05142: Domain of unknown function (DUF702), TIGR01624: LRP1 C-terminal domain, TIGR01623: putative zinc finger domain, LRP1 type	At4g36260	57.8862521	68.025	35.5112366	106.854	32.7039228	71.288	0.547349166	0.009072
6646	11	disease resistance protein (TIR-NBS-LRR class), putative domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.	At1g72860	39.2853428	70.368	67.2031869	94.542	46.4053014	80.171	0.615980712	0.008892
7086	11	forkhead-associated domain-containing protein / FHA domain-containing protein	At5g47790	59.9344806	93.966	66.0591537	94.096	40.9041309	98.363	0.585240097	0.0084
24599	38	kinesin motor protein-related non-consensus AT donor splice site at exon 12; non-consensus AC acceptor splice site at exon 13	At5g27000	125.652132	157.286	133.115751	188.077	23.2108984	68.363	0.615391224	0.008184
18964	30	leucine-rich repeat family protein similar to receptor kinase GI:498278 from [Petunia integrifolia]; contains protein kinase domain, Pfam:PF00069; contains leucine-rich repeats, Pfam:PF00560	At1g60630	136.938245	194.052	175.111967	227.166	39.535024	105.612	0.616958299	0.008052
22923	36	methyladenine glycosylase family protein similar to SP|P05100 DNA-3-methyladenine glycosylase I (EC 3.2.2.20) (3-methyladenine-DNA glycosylase I, constitutive) {Escherichia coli}; contains Pfam profile PF03352: Methyladenine glycosylase	At1g80850	149.613731	197.331	227.809196	309.33	30.3966477	113.401	0.587564136	0.007808
20847	33	cyclin, putative similar to cyclin A2 [Lycopersicon esculentum] GI:5420276, cyclin [Medicago sativa] GI:1050559; contains Pfam profiles PF00134: Cyclin, N-terminal domain, PF02984: Cyclin, C-terminal domain	At1g15570	196.373236	322.28	201.053478	293.256	44.7805179	122.918	0.553075792	0.007626
7535	12	basic helix-loop-helix (bHLH) protein, putative very strong similarity to PIF3 like basic Helix Loop Helix protein 2 (PIL2) [Arabidopsis thaliana] GI:22535494	At3g62090	36.2969615	81.652	53.4604483	70.28	94.2271337	130.192	0.642988525	0.00759
30366	47	WRKY family transcription factor identical to WRKY DNA-binding protein 18 (WRKY18) GI:13506730 from [Arabidopsis thaliana]	At4g31805	189.944044	295.707	93.2689795	143.731	53.9848753	92.271	0.625440282	0.007524
14799	23	ankyrin repeat family protein contains ankyrin repeat domains, Pfam:PF00023	At5g02620	181.266615	255.695	163.961627	192.828	27.8563771	85.679	0.62811404	0.007473
22358	35	ribonuclease P family protein similar to Ribonuclease P protein subunit p29 (EC 3.1.26.5) (hPOP4) (Swiss-Prot:O95707) [Homo sapiens]	At2g43190	126.569823	140.725	126.13683	158.733	24.1552522	90.262	0.653890981	0.00708
15811	25	transport protein-related contains Pfam PF05911: Plant protein of unknown function (DUF869) profile; weak similarity to Intracellular protein transport protein USO1 (Swiss-Prot:P25386) [Saccharomyces cerevisiae]	At2g23360	81.7890248	138.126	119.80322	142.906	41.9598278	94.608	0.624660583	0.006837
9034	14	CHP-rich zinc finger protein, putative contains similarity to CHP-rich zinc finger protein	At5g46660	308.289936	367.956	71.0925811	97.676	65.8408463	293.528	0.596664657	0.006624
20139	31	expressed protein	At5g67350	147.682085	304.365	113.753229	160.95	19.4458543	83.513	0.474941091	0.0066
19550	31	prenylated rab acceptor (PRA1) family protein weak similarity to prenylated Rab acceptor 1 (PRA1) [Homo sapiens] GI:4877285; contains Pfam profile PF03208: Prenylated rab acceptor (PRA1)	At1g17700	102.59432	140.242	101.772747	136.596	39.1453234	99.276	0.623641315	0.00648
11733	19	expressed protein contains Pfam profile PF04520: Protein of unknown function, DUF584	At1g11700	101.315113	137.516	78.4570956	145.686	63.5954284	95.657	0.646704932	0.006384
25327	39	amino acid transporter 4, putative (AAP4) identical to amino acid transporter GI:608671 from [Arabidopsis thaliana];	At5g63850	123.441328	154.909	101.857195	192.899	21.8500391	72.649	0.54188635	0.006272
24835	39	cytochrome P450 family protein similar to Cytochrome P450 90A1 (SP:Q42569) [Arabidopsis thaliana]	At1g65670	802.646722	1019.197	286.115055	343.317	32.7781515	92.183	0.65882999	0.00616
27444	43	CLE26, putative CLAVATA3/ESR-Related 26 (CLE26);	At1g69970	122.09046	154.473	88.0507222	113.509	23.7222515	89.903	0.609982792	0.006138
20711	32	calmodulin-binding protein-related has weak similarity to calmodulin-binding proteins	At5g39380	325.092897	410.248	279.994955	391.366	20.5943371	54.865	0.627741321	0.00568
27431	43	zinc finger (C2H2 type) family protein contains Pfam domain, PF00096: Zinc finger, C2H2 type	At1g66140	125.098094	261.386	107.68093	149.955	27.7759627	89.86	0.50192872	0.005544
20201	32	cyclin, putative similar to SP|Q40671 G2/mitotic-specific cyclin 2 (B-like cyclin) (CYCOS2) {Oryza sativa}; contains Pfam profiles PF00134: Cyclin, N-terminal domain, PF02984: Cyclin, C-terminal domain	At1g20590	96.5940266	159.653	65.1620915	105.929	27.633691	108.108	0.491928486	0.005376
21036	33	DNA-binding family protein / AT-hook protein 1 (AHP1) identical to AT-hook protein 1 [Arabidopsis thaliana] gi|2598227|emb|CAA10857	At2g33620	192.761294	312.447	236.687403	260.438	36.8751627	128.085	0.604547327	0.005368
24733	39	expressed protein similar to hypothetical protein GB:AAB71979	At1g10820	182.862415	238.826	220.030407	275.344	22.7572786	90.837	0.605103944	0.005313
20760	32	haloacid dehalogenase-like hydrolase family protein low similarity to SP|P53078 SSM1 protein {Saccharomyces cerevisiae}; contains InterPro accession IPR005834: Haloacid dehalogenase-like hydrolase	At5g59480	262.895204	346.488	346.183171	404.445	23.9676186	68.945	0.65410757	0.005293
23382	36	ankyrin repeat family protein contains ankyrin repeats, Pfam:PF00023	At5g65860	185.876466	274.115	275.020482	404.686	39.4628572	97.738	0.587149377	0.005106
7061	11	pentatricopeptide (PPR) repeat-containing protein contains Pfam profile PF01535: PPR repeat	At5g37570	42.511169	72.455	55.6513196	92.419	40.3907158	65.557	0.6016681	0.005096
15521	24	cysteine proteinase, putative / thiol protease, putative similar to cysteine proteinase RD21A precursor (thiol protease) GI:435619, SP:P43297 from [Arabidopsis thaliana]	At5g43060	79.0017228	120.664	164.34244	189.231	25.281054	105.357	0.587718741	0.005088
24986	39	C2 domain-containing protein similar to cold-regulated gene SRC2 [Glycine max] GI:2055230; contains Pfam profile PF00168: C2 domain	At3g05440	178.776654	203.739	194.783602	248.09	29.3966224	101.694	0.650560338	0.00507
26990	42	hypothetical protein similar to At2g04970, At2g15200, At1g32830, At2g14140, At4g03990, At5g34895, At3g47270, At2g02200	At3g30450	64.3368348	114.247	126.038042	140.773	20.8087755	79.606	0.573287793	0.00504
2363	4	high mobility group (HMG1/2) family protein similar to SP|P40618 High mobility group protein HMG2A {Gallus gallus}; contains Pfam profile PF00505: HMG (high mobility group) box	At4g11080	103.325906	143.882	73.7327803	117.464	25.6439498	142.706	0.508510865	0.005031
18663	29	auxin-responsive AUX/IAA family protein similar to SP|Q38826 Auxin-responsive protein IAA8, SP|Q38827 Auxin-responsive protein IAA9 from Arabidopsis thaliana; contains Pfam profile: PF02309: AUX/IAA family	At4g29080	115.670895	162.14	105.110838	167.446	23.5366798	92.202	0.532134701	0.005016
25960	40	haloacid dehalogenase-like hydrolase family protein low similarity to SP|P53078 SSM1 protein {Saccharomyces cerevisiae}; contains InterPro accession IPR005834: Haloacid dehalogenase-like hydrolase	At5g59480	129.180646	172.087	245.904996	346.369	25.5367306	80.417	0.59272513	0.00494
30011	47	mechanosensitive ion channel domain-containing protein / MS ion channel domain-containing protein contains Pfam profile PF00924: Mechanosensitive ion channel	At1g53470	283.186035	401.892	269.716183	322.129	11.4394656	43.385	0.601865976	0.00494
22962	36	expressed protein	At2g24440	135.023713	208.671	137.717378	194.72	34.6998497	65.44	0.628192666	0.004872
2463	4	transducin family protein / WD-40 repeat family protein contains 3 WD-40 repeats (PF00400); similar to uncharacterized protein KIAA0007 (GI:1663708) {Homo sapiens} 1.2e-11	At5g11240	57.4263366	124.309	64.9995686	75.55	79.6638775	154.377	0.612783576	0.004805
21730	34	adenylylsulfate kinase, putative similar to adenylylsulfate kinase 1, chloroplast precursor (APS kinase, Adenosine-5'phosphosulfate kinase, ATP adenosine-5'- phosphosulfate 3'-phosphotransferase) [Arabidopsis thaliana] SWISS-PROT:Q43295	At3g03900	59.8842107	98.485	131.329594	186.433	31.5946163	76.767	0.574684133	0.004416
22701	35	expressed protein contains Pfam profile PF04398: Protein of unknown function, DUF538	At5g54530	81.8564078	105.377	131.490523	180.974	22.4521162	75.119	0.600751477	0.004408
7058	11	Ca+2-binding EF hand family protein contains similarity to Ca+2-binding EF hand protein GI:2270994 from [Glycine max]	At5g29560	71.1500021	95.781	46.5309213	85.886	38.8607801	71.917	0.608323939	0.004257
27038	42	F-box family protein contains Pfam:PF00646 F-box domain	At3g62230	91.6354954	122.597	85.6638674	95.638	25.281054	86.672	0.644949681	0.00392
20583	32	kinesin-like protein A (KATA)	At4g21270	125.689566	174.488	121.14483	153.67	22.2933493	86.445	0.588856064	0.00384
14055	22	nodulin MtN21 family protein similar to MtN21 GI:2598575 (root nodule development) from [Medicago truncatula]	At4g08290	66.2096536	127.699	117.433892	156.295	60.848967	107.367	0.612193586	0.003726
7068	11	disease resistance protein (TIR-NBS-LRR class), putative domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.	At5g38340	78.6380686	99.189	35.7789213	92.375	43.1928488	90.951	0.551678448	0.003696
23168	36	F-box family protein contains F-box domain Pfam:PF00646	At4g14096	100.558926	142.611	162.61205	209.609	77.0473162	166.633	0.647764085	0.003572
25933	40	basic helix-loop-helix (bHLH) family protein contains similarity to bHLH DNA-binding protein	At5g46690	90.1241916	135.31	164.068382	279.85	32.8008325	65.418	0.584577834	0.0031
15639	25	expressed protein	At1g12180	90.9712918	119.688	88.5159836	114.194	26.1078791	81.118	0.619019271	0.003034
18015	28	dem protein-related / defective embryo and meristems protein-related identical to dem GI:2190419 from [Lycopersicon esculentum]	At4g33400	89.6268411	108.459	75.077577	113.68	31.4131684	75.178	0.634881907	0.002944
2263	4	WD-40 repeat family protein / mitotic checkpoint protein, putative contains 5 WD-40 repeats (PF00400) (1 weak); similar to testis mitotic checkpoint protein BUB3 (GB:AAC28439,SP|O43684)[Homo sapiens]	At3g19590	73.3447618	110.963	67.2462076	78.134	32.5101034	154.13	0.577520924	0.002904
3822	6	leucine-rich repeat transmembrane protein kinase, putative	At5g43020	57.779295	91.091	88.6769131	118.423	31.153368	78.615	0.593131871	0.00285
25932	40	AWPM-19-like membrane family protein similar to ABA induced plasma membrane protein PM 19 [Triticum aestivum] GI:1724112; contains Pfam profile PF05512: AWPM-19-like family	At5g46530	92.706136	118.248	169.696133	192.654	20.955171	72.565	0.65120304	0.002784
19862	31	leucine-rich repeat transmembrane protein kinase, putative receptor-like protein kinase (RKL1), Arabidopsis thaliana, EMBL:AF084034	At3g50230	126.701381	143.361	97.389411	131.103	18.7303723	80.375	0.619892123	0.002728
24152	38	caldesmon-related weak similarity to Caldesmon (CDM) (Swiss-Prot:P12957) [Gallus gallus]	At1g52410	91.1606059	126.087	152.965843	179.606	4.73001695	34.048	0.571198046	0.002684
20682	32	calcium-dependent protein kinase 19 (CDPK19) identical to calcium-dependent protein kinase [Arabidopsis thaliana] gi|836942|gb|AAA67655	At5g19450	84.1025069	107.181	175.825793	205.765	18.309743	57.306	0.652894584	0.002684
24819	39	expressed protein contains Pfam domain, PF04678: Protein of unknown function, DUF607	At1g57610	103.99118	140.678	125.011917	141.322	13.1529111	66.203	0.607492968	0.002655
7094	11	expressed protein	At5g51180	34.1171758	85.291	35.0396018	78.703	38.3514888	75.338	0.451427053	0.002576
6607	11	ubiquitin family protein contains Pfam profile: PF00240 ubiquitin family	At1g53930	48.1659908	92.07	38.2151702	59.955	30.367781	91.055	0.498017731	0.002508
18592	29	expressed protein	At3g60990	127.294993	186.843	132.612249	162.047	29.5698226	69.099	0.64252825	0.002394
27384	43	light stress-responsive one-helix protein (OHP2) contains similarity to photosystem II 22 kDa protein GI:6006279 from [Arabidopsis thaliana]	At1g34000	84.6897014	103.751	85.2193197	117.979	33.0400138	84.702	0.642892727	0.00234
27294	42	hypothetical protein	At1g35150	83.6072955	102.946	94.3190044	112.142	4.34031634	19.203	0.626412514	0.002322
6775	11	hypothetical protein	At3g02680	43.9401158	74.987	67.7210292	98.527	27.4151288	63.442	0.568477841	0.002268
3085	5	nucleotide-sugar transporter family protein similar to SP|O77592 UDP N-acetylglucosamine transporter (Golgi UDP-GlcNAc transporter) {Canis familiaris}, SP|P78382 CMP-sialic acid transporter {Homo sapiens}; contains Pfam profile PF04142: Nucleotide-sugar transporter	At4g35335	71.5724826	99.48	56.6360167	96.265	43.1309915	94.654	0.587823515	0.00221
15868	25	hypothetical protein and genefinder; expression supported by MPSS	At2g46640	51.6474444	99.8	69.6697097	81.175	53.2322788	99.154	0.637546574	0.002187
30564	48	zinc finger (C3HC4-type RING finger) family protein / BRCT domain-containing protein contains Pfam domain, PF00533: BRCA1 C Terminus (BRCT) domain	At1g04020	110.959435	158.139	140.351204	174.793	9.55900549	72.96	0.545210451	0.002162
6829	11	F-box family protein contains F-box domain Pfam:PF00646	At3g25750	57.734373	69.535	81.6661247	106.345	19.6025594	62.676	0.636996071	0.00216
30683	48	glycosyl transferase family 20 protein / trehalose-phosphatase family protein similar to SP|Q00764 Alpha,alpha-trehalose-phosphate synthase [UDP-forming] 56 kDa subunit (EC 2.4.1.15) (Trehalose-6-phosphate synthase) {Saccharomyces cerevisiae}; contains Pfam profile: PF02358 trehalose-phosphatase	At1g68020	125.383669	172.514	100.713162	153.283	58.5973635	106.271	0.64507971	0.002145
21937	34	hydroxyproline-rich glycoprotein family protein	At4g37130	52.3897267	70.385	86.6007637	119.302	28.2027776	68.207	0.627904731	0.002142
16183	25	expressed protein	At5g45030	87.2352803	108.998	98.7294276	119.447	16.1035015	47.988	0.654155378	0.002112
6621	11	hypothetical protein	At1g62530	60.7997635	71.115	71.4016931	102.098	20.530418	51.021	0.652228708	0.0021
7127	11	transducin family protein / WD-40 repeat family protein Similar to (SP:Q13112) Chromatin assembly factor 1 subunit B (CAF-1 subunit B) (CAF-Ip60) [Homo sapiens]	At5g64630	69.0386689	86.359	51.5292947	92.935	15.8643202	82.252	0.51559286	0.00208
24917	39	jacalin lectin family protein similar to myrosinase-binding protein homolog [Arabidopsis thaliana] GI:2997767; contains Pfam profile PF01419 jacalin-like lectin domain	At2g25980	139.620729	236.246	166.727702	322.318	41.7247703	145.16	0.465238041	0.002025
17924	28	delta 1-pyrroline-5-carboxylate synthetase B / P5CS B (P5CS2) identical to SP|P54888	At3g55610	96.33626	116.9	76.2216102	109.467	29.5595131	92.117	0.613759921	0.002024
5568	9	expressed protein contains Pfam PF05701: Plant protein of unknown function (DUF827)	At3g51720	146.078798	199.506	70.7420417	95.086	62.9892275	157.167	0.62565369	0.002016
24469	38	expressed protein	At4g14840	56.5578449	79.21	128.518905	150.098	19.8005025	77.552	0.608525462	0.001998
24742	39	myb family transcription factor (MYB124) contains PFAM profile: PF00249 myb-like DNA binding domain	At1g14350	97.338448	120.085	106.516183	127.016	10.2023208	33.56	0.651062143	0.001911
21486	34	protein kinase family protein contains protein kinase domain, Pfam:PF00069	At1g12680	55.1000196	72.974	98.3533944	116.907	26.7573801	85.828	0.636038527	0.00188
6969	11	expressed protein low similarity to SP|Q13061 Triadin {Homo sapiens}	At4g32970	35.3375563	64.775	40.5749379	80.419	81.2927848	98.287	0.625727769	0.001872
21453	34	Control: Stratagene Spotreport Alien Oligo	Alien1	78.8423567	102.945	91.1976102	100.545	18.1839667	74.569	0.638918581	0.001848
16506	26	strictosidine synthase family protein similar to strictosidine synthase [Rauvolfia serpentina][SP|P15324]; contains strictosidine synthase domain PF03088; protein alignments support a CG non-consensus donor splice site.	At2g41300	109.447061	143.174	101.528963	113.387	19.0355347	60.562	0.658056175	0.001833
15047	24	jacalin lectin family protein nearly identical to myrosinase-binding protein homolog GI:2997767 from [Arabidopsis thaliana]; contains Pfam profile PF01419 jacalin-like lectin domain; identical to cDNA myrosinase-binding protein homolog GI:2997766	At1g52040	50.9126492	124.118	294.065926	469.386	47.1929503	65.314	0.586413682	0.001722
22012	34	F-box family protein contains F-box domain Pfam:PF00646	At5g38396	62.6715127	94.72	107.672963	130.305	15.1715191	47.708	0.601991007	0.00171
17468	27	expressed protein ; expression supported by MPSS	At5g38320	119.806926	149.071	69.6458093	87.677	12.1673191	47.008	0.618956898	0.001692
30196	47	phytochromobilin:ferredoxin oxidoreductase, chloroplast / phytochromobilin synthase (HY2) identical to SP|Q9SR43 Phytochromobilin:ferredoxin oxidoreductase, chloroplast precursor (EC 1.3.7.4) (Phytochromobilin synthase) (PFB synthase) (PPhiB synthase) {Arabidopsis thaliana}; identical to cDNA for phytochromobili	At3g09150	70.6269818	105.237	41.4018922	67.04	62.6098364	147.257	0.571289005	0.001596
26399	41	plastocyanin-like domain-containing protein	At4g01380	82.5045678	95.715	118.909345	178.265	21.4314718	68.288	0.614286018	0.001596
21499	34	pentatricopeptide (PPR) repeat-containing protein contains Pfam profile PF01535: PPR repeat	At1g19290	48.5403407	98.638	94.891021	114.277	23.0686267	81.93	0.534676905	0.0015
20160	32	expressed protein contains 2 predicted transmembrane domains; expression supported by MPSS	At1g03660	73.1500998	107.413	125.405478	150.767	30.8523294	104.016	0.603137302	0.001488
12027	19	kinase interacting family protein similar to kinase interacting protein 1 (GI:13936326) [Petunia integrifolia]	At3g22790	77.3898793	112.016	28.3634192	118.758	117.811237	219.699	0.488651807	0.001485
9800	16	expressed protein	At1g20460	67.3166596	88.824	16.4020581	45.223	73.9214637	129.475	0.563830277	0.00147
15560	24	haloacid dehalogenase-like hydrolase family protein low similarity to SP|P53078 SSM1 protein {Saccharomyces cerevisiae}; contains InterPro accession IPR005834: Haloacid dehalogenase-like hydrolase	At5g59480	89.3369873	123.995	128.950706	189.084	35.3637841	83.536	0.608600083	0.00144
6551	11	zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)	At1g18780	34.6530308	55.672	48.9066225	66.422	30.8440818	70.469	0.598816211	0.001404
25057	39	leucine-rich repeat transmembrane protein kinase, putative protein kinase Xa21 receptor type precursor, Oryza sativa, PIR:A57676	At3g47110	76.550266	111.247	98.2832866	114.297	30.0791139	85.285	0.633564686	0.001344
7710	12	methyl-CpG-binding domain-containing protein contains Pfam profile PF01429:Methyl-CpG binding domain	At5g35338	67.0268059	88.421	93.6689131	131.828	23.5387417	60.183	0.619899996	0.00132
6700	11	expressed protein contains Pfam profile PF03087: Arabidopsis protein of unknown function; expression supported by MPSS	At2g17070	46.9648626	55.354	31.6282159	82.121	33.281257	67.637	0.575214762	0.00128
31158	48	CwfJ-like family protein / zinc finger (CCCH-type) family protein contains Pfam domain, PF00642: Zinc finger C-x8-C-x5-C-x3-H type (and similar), PF04677: Protein similar to CwfJ C-terminus 1, PF04676: Protein similar to CwfJ C-terminus 2	At5g56900	96.4646085	125.145	112.755785	130.244	10.5301642	46.281	0.621358906	0.001225
23952	37	copper-binding family protein similar to copper homeostasis factor gi:3168840 from Arabidopsis thaliana; contains Pfam profile PF00403: Heavy-metal-associated domain	At5g24580	43.7016015	104.319	49.5407802	78.934	27.8275104	72.742	0.476365457	0.001188
22606	35	expressed protein contains Pfam profile PF04788: Protein of unknown function (DUF620)	At5g06610	60.1462556	93.189	71.0288467	114.968	24.182057	57.557	0.561125784	0.001178
10792	17	Dof zinc finger protein DAG1 / Dof affecting germination 1 (DAG1) / transcription factor BBFa (BBFA) identical to SP|Q43385 DOF zinc finger protein DAG1 (Dof affecting germination 1) (Transcription factor BBFa) (AtBBFa) (rolB domain B factor a) {Arabidopsis thaliana}	At3g61850	63.044793	107.247	350.496399	475.807	48.2630806	119.481	0.576140569	0.001144
6856	11	ABC transporter family protein contains Pfam domain, PF00005: ABC transporter	At3g47790	53.2004615	59.437	43.1657429	76.787	21.51601	66.568	0.593480247	0.001131
7011	11	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein identical to tapetum-specific protein A9 [Precursor] SP| Q00762; contains Pfam protease inhibitor/seed storage/LTP family domain PF00234	At5g07230	56.8241681	64.995	31.3812449	82.146	32.2915412	88.516	0.540371124	0.001056
16326	26	expressed protein similar to EST gb|T43267	At1g31060	86.6555728	116.85	104.427287	122.227	18.5159338	73.158	0.616354498	0.001056
27493	43	F-box family protein contains Pfam:PF00646 F-box domain	At2g16300	68.9980252	116.863	73.2930126	112.546	28.9718693	77.087	0.539159541	0.00104
7056	11	calcium-binding EF hand family protein contains INTERPRO:IPR002048 calcium-binding EF-hand domain	At5g28830	33.6187557	48.362	29.7831038	91.482	68.3233835	89.132	0.595750729	0.001008
20455	32	expressed protein	At3g17120	66.7412304	88.522	91.262938	151.481	7.26410188	42.111	0.509640293	0.001008
11708	19	Control: Stratagene Spotreport Alien Oligo	Alien1	64.3079564	79.077	79.3669048	136.744	43.4773921	116.15	0.589319405	0.00099
24942	39	harpin-induced family protein (YLS9) / HIN1 family protein / harpin-responsive family protein similar to harpin-induced protein hin1 (GI:1619321) [Nicotiana tabacum]; identical to cDNA YLS9 mRNA for hin1 homolog GI:13122295	At2g35980	65.6620333	94.618	301.167536	399.398	57.8756957	139.739	0.620731145	0.00099
21864	34	ankyrin repeat family protein contains ankyrin repeats, Pfam:PF00023	At4g11000	58.0071136	101.826	67.6429545	99.026	23.3366747	76.218	0.519645	0.000986
24844	39	transcription factor CRC (CRABS CLAW) identical to transcription factor CRC (CRABS CLAW) GI:4836698 [Arabidopsis thaliana]	At1g69180	61.3784014	78.323	111.391868	122.743	19.9510218	79.418	0.647464648	0.000924
6845	11	DC1 domain-containing protein contains Pfam profile PF03107: DC1 domain	At3g43890	56.9632123	70.512	59.1152865	73.632	20.3592796	62.835	0.644903618	0.000918
21742	34	kinesin motor protein-related similar to carboxy-terminal kinesin 2 GB:P79955 [Xenopus laevis]	At3g10310	40.0607818	75.246	55.6560997	82.648	19.5819403	69.033	0.496489799	0.000864
20295	32	bHLH family protein contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	At1g74500	86.0063433	104.21	104.773046	196.756	34.2709729	114.054	0.552766739	0.000854
27345	43	expressed protein	At1g15430	96.3822515	233.914	94.736465	122.957	48.6218525	87.979	0.57839295	0.00084
14495	23	zinc finger (C3HC4-type RING finger) family protein similar to Pfam domain, PF00097: Zinc finger, C3HC4 type (RING finger)	At2g15530	72.62601	119.946	85.3786558	102.895	32.7389752	68.985	0.636611719	0.00078
6730	11	expressed protein	At2g30695	68.7263542	89.281	24.3720499	83.34	39.9247246	80.487	0.519418811	0.00076
10023	16	expressed protein ; expression supported by MPSS	At3g04160	48.5991671	65.193	59.5439006	85.292	21.4417813	70.073	0.583192108	0.000754
21218	33	hypothetical protein late embryogenesis abundant protein -Picea glauca,PID:g1161171	At4g13235	198.490986	281.574	96.3361994	205.33	41.8959087	157.703	0.479924808	0.000744
11861	19	protein kinase, putative similar to protein kinase APK1B [Arabidopsis thaliana] SWISS-PROT:P46573; contains Pfam profile: PF00069 Eukaryotic protein kinase domain	At1g76370	61.4800107	77.838	63.6786724	103.903	31.959574	76.099	0.607561965	0.00072
14876	23	TCP family transcription factor, putative similar to PCF1 (GI:2580438) and PCF2 [(GI:2580440) Oryza sativa] ; similar to unknown protein (emb|CAB61988.1)	At5g41030	72.8559678	92.856	95.8215438	138.223	32.6358798	73.353	0.640922191	0.000672
12460	20	plant defensin-fusion protein, putative (PDF1.5) plant defensin protein family member, personal communication, Bart Thomma (Bart.Thomma@agr.kuleuven.ac.be); similar to antifungal protein 4 [Raphanus sativus] gi|1655683|emb|CAA65983	At1g55010	32.1673478	79.358	112.037179	148.427	25.3429112	106.936	0.465722102	0.00066
10932	17	AAA-type ATPase family protein contains Pfam profile: ATPase family PF00004	At5g17760	175.99363	251.005	103.47605	127.492	18.9654298	48.738	0.633971301	0.00066
19123	30	myb family transcription factor contains Pfam profile: PF00249 myb-like DNA-binding domain	At3g04030	52.1458645	84.384	74.583635	82.189	19.1468777	50.745	0.634246542	0.000616
6628	11	hypothetical protein	At1g63205	61.4907064	79.62	38.9465229	61.469	18.400467	54.603	0.580961603	0.000558
18700	29	expressed protein	At5g02580	105.369857	162.985	65.4616433	93.985	43.5619303	90.034	0.608950201	0.00055
18620	29	ubiquitin-protein ligase, putative similar to SP|P39940 Ubiquitin--protein ligase RSP5 (EC 6.3.2.-) {Saccharomyces cerevisiae}; contains Pfam profiles PF00240: Ubiquitin family, PF00632: HECT-domain (ubiquitin-transferase)	At4g12570	74.3030974	109.186	78.3375936	93.027	19.3427589	78.551	0.589619456	0.00054
15497	24	WD-40 repeat family protein contains 5 WD-40 repeats (PF00400); similar to fizzy1 (GI:3298595) {Xenopus laevis}; WD-repeat protein, carrot, PIR:T14352	At5g26900	39.7473975	106.215	75.0552699	125.838	95.2580877	140.778	0.54910489	0.000528
25100	39	F-box family protein ; similar to SKP1 interacting partner 2 (SKIP2) TIGR_Ath1:At5g67250	At4g00755	93.1585645	103.883	76.9545562	105.273	12.4312433	100.316	0.583895022	0.000528
18164	28	subtilase family protein contains similarity to prepro-cucumisin GI:807698 from [Cucumis melo]	At5g59090	117.069894	134.69	57.9951537	91.182	46.7248972	133.303	0.618578024	0.000522
30913	48	expressed protein contains Pfam profile PF04949: Family of unknown function (DUF662)	At3g52900	71.5457433	98.2	47.4216101	76.947	41.3206363	156.846	0.536102723	0.00051
27590	43	transcription factor IIB (TFIIB) family protein contains Pfam domain, PF00382: Transcription factor TFIIB repeat	At3g09360	90.5081676	145.058	116.847536	170.447	22.0191155	67.571	0.545115642	0.000486

19572	31	phosphoribulokinase/uridine kinase family protein weak similarity to SP|Q59190 Uridine kinase (EC 2.7.1.48) (Uridine monophosphokinase) (Cytidine monophosphokinase) {Borrelia burgdorferi}; contains Pfam profile PF00485: Phosphoribulokinase / Uridine kinase family	At1g26190	130.854525	221.497	50.9891454	99.945	28.3223683	64.703	0.512891409	0.000473
1322	3	jacalin lectin family protein similar to gi:6503088 (GB:AAF14583) from [Arabidopsis thaliana] (Proc. Natl. Acad. Sci. U.S.A. 97 (1), 489-494 (2000)); contains Pfam profile PF01419 jacalin-like lectin domain	At1g05770	65.7957296	75.463	57.2367138	111.566	80.1937878	151.905	0.637614881	0.000468
22249	35	sugar transporter family protein contains Pfam profile: PF00083 sugar (and other) transporter	At1g73220	50.2816023	79.005	53.4445147	87.116	15.6601913	25.396	0.622187518	0.000442
30183	47	sugar transporter family protein similar to sugar-porter family proteins 1 and 2 [Arabidopsis thaliana] GI:14585699, GI:14585701; contains Pfam profile PF00083: major facilitator superfamily protein	At3g05150	97.0806814	134.96	50.9190375	83.503	42.2258139	105.971	0.575860655	0.00044
22590	35	expressed protein ; expression supported by MPSS	At4g39190	1331.23727	1890.812	74.6346226	120.965	42.1495233	83.424	0.608764655	0.000416
24146	38	endo-1,4-beta-glucanase, putative / cellulase, putative similar to endo-beta-1,4-glucanase GI:4972236 from [Fragaria x ananassa]	At1g48930	61.583759	90.776	118.891818	153.895	24.3800002	63.877	0.610879035	0.000396
20076	31	myb family transcription factor contains Pfam profile: PF00249 Myb DNA binding domain	At5g41020	60.0767335	84.099	69.092913	119.892	43.2402727	97.542	0.577983081	0.000396
14607	23	phosphoesterase identical to phosphoesterase [Arabidopsis thaliana] GI:21630064; contains Pfam profile PF00645: Poly(ADP-ribose) polymerase and DNA-Ligase Zn-finger region	At3g14890	66.1486881	93.211	75.214606	90.754	13.1013634	59.825	0.58581182	0.00039
6941	11	WD-40 repeat family protein contains 6 WD-40 repeats (PF00400); similar to fizzy-related protein (GI:5813825) Drosophila melanogaster, PID:g2326419;	At4g22910	31.0132807	54.554	39.9901744	69.058	29.1223886	71.343	0.518590399	0.000384
17856	28	expressed protein	At3g16330	46.3883638	69.609	59.5040665	92.001	46.8609831	84.856	0.621810285	0.000378
6790	11	protein phosphatase 2C family protein / PP2C family protein similar to protein phosphatase-2c (GI:3608412) [Mesembryanthemum crystallinum]; contains Pfam PF00481 : Protein phosphatase 2C domain	At3g09400	46.3498593	63.417	29.1186723	76.937	24.4480432	51.104	0.529248812	0.000368
21360	33	hypothetical protein	At5g32070	188.998544	268.017	153.035951	209.812	37.4360016	90.756	0.615686657	0.000336
6341	10	serine/threonine protein kinase, putative similar to serine-threonine protein kinase [Triticum aestivum] gi|2055374|gb|AAB58348	At4g40010	19.8758379	60.797	57.6286806	81.769	11.161108	49.549	0.418983166	0.000322
18281	29	late embryogenesis abundant group 1 domain-containing protein / LEA group 1 domain-containing protein contains Pfam domain, PF03760: Late embryogenesis abundant (LEA) group 1	At1g32560	78.8402176	108.119	106.16883	157.665	27.7285388	64.873	0.61000298	0.000312
28299	44	SIT4 phosphatase-associated family protein contains Pfam profile: PF04499 SIT4 phosphatase-associated protein	At3g45190	37.1611748	64.892	46.07522	78.24	48.5599953	80.562	0.588107786	0.0003
19528	31	LOB domain protein 1 / lateral organ boundaries domain protein 1 (LBD1) identical to SP|Q9LQR0 LOB domain protein 1 {Arabidopsis thaliana}	At1g07900	79.0092098	90.462	103.914224	148.447	24.4315479	70.164	0.640537303	0.00028
23331	36	NLI interacting factor (NIF) family protein contains Pfam profile PF03031: NLI interacting factor	At5g45700	85.1752866	180.082	78.2451786	184.547	51.0734612	222.721	0.375427182	0.00027
3015	5	beta-fructofuranosidase, putative / invertase, putative / saccharase, putative / beta-fructosidase, putative similar to neutral invertase [Daucus carota] GI:4200165; contains Pfam profile PF04853: Plant neutral invertase	At4g09510	120.682905	134.51	55.4505562	88.842	14.0560268	69.735	0.574305133	0.000261
10020	16	vacuolar ATP synthase subunit G 1 (VATG1) / V-ATPase G subunit 1 (VAG1) / vacuolar proton pump G subunit 1 (VMA10) identical to SWISS-PROT:O82628 vacuolar ATP synthase subunit G 1 (V-ATPase G subunit 1, Vacuolar proton pump G subunit 1) [Arabidopsis thaliana]	At3g01390	42.6191956	63.733	20.5288631	67.988	40.8649547	96.573	0.464604662	0.00026
17200	27	protein kinase, putative similar to viroid symptom modulation protein [Lycopersicon esculentum] gi|7672777|gb|AAF66637	At3g12690	43.7379669	93.923	73.157577	122.736	14.4745942	76.076	0.41733343	0.000258
10311	16	pollen specific phosphatase, putative / phosphatase and tensin, putative (PTEN1) identical to phosphatase and tensin homolog [Arabidopsis thaliana] GI:21535746	At5g39400	35.8819679	51.163	68.0795354	79.868	31.3286302	100.918	0.621387884	0.00024
2942	5	pentatricopeptide (PPR) repeat-containing protein contains Pfam profile PF01535: PPR repeat	At3g28660	108.85131	136.284	39.8929794	65.025	20.7860945	53.569	0.600078753	0.00021
10207	16	expressed protein	At4g31010	41.050135	46.043	45.1893113	67.592	15.5674054	51.527	0.620747401	0.000208
21355	33	SSXT protein-related / glycine-rich protein contains weak hit to Pfam profile PF05030: SSXT protein (N-terminal region)	At5g28640	96.622905	220.242	100.915519	160.835	37.1432107	113.959	0.4640316	0.000204
31148	48	seed maturation family protein similar to SP|P09444 Late embryogenesis abundant protein D-34 (LEA D-34) {Gossypium hirsutum}; contains Pfam profile PF04927: Seed maturation protein	At5g53270	44.8567382	70.279	195.424133	226.64	37.6958021	87.878	0.643163137	0.000201
18615	29	glycosyltransferase family protein contains Pfam profile: PF00201 UDP-glucoronosyl and UDP-glucosyl transferase	At4g09500	68.6589712	110.189	67.8915188	95.391	14.9117187	34.444	0.589248866	0.0002
24353	38	protein kinase family protein contains protein kinase domain, Pfam:PF00069	At3g14370	39.0970983	89.679	112.425959	129.639	36.5328859	58.28	0.6433472	0.000188
1744	3	protein kinase family protein contains Pfam domain, PF00069: Protein kinase domain	At4g23210	88.1893377	111.423	89.9611621	122.058	30.8255246	90.264	0.623340871	0.000177
23353	36	expressed protein	At5g55540	88.2588598	111.602	98.5382243	113.137	24.2872143	86.168	0.647886141	0.000174
23279	36	expressed protein similar to p53 inducible protein [Homo sapiens] GI:5616320	At5g18410	85.3581832	109.986	111.164017	138.419	5.36714652	63.209	0.554697111	0.000168
30523	47	regulator of chromosome condensation (RCC1) family protein weak similarity to UVB-resistance protein UVR8 [Arabidopsis thaliana] GI:5478530; contains Pfam profile PF00415: Regulator of chromosome condensation (RCC1)	At5g60870	56.2262779	71.086	60.7978757	84.985	12.5590816	53.947	0.579720264	0.00016
4404	7	lectin protein kinase family protein contains Pfam domains, PF00138: Legume lectins alpha domain, PF00139: Legume lectins beta domain and PF00069: Protein kinase domain	At5g03140	75.5512867	100.48	64.4498591	94.557	90.455904	192.138	0.634762607	0.00016
5249	9	actin-related protein 4 (ARP4) neary identical to actin-related protein 4 (ARP4) [Arabidopsis thaliana] GI:21427463; contains Pfam profile PF00022: Actin; supporting cDNA gi|21427462|gb|AF507912.1|	At1g18450	211.737623	239.18	53.5162159	89.589	37.2174394	99.917	0.618366946	0.000142
7043	11	harpin-induced family protein / HIN1 family protein / harpin-responsive family protein similar to harpin-induced protein hin1 (GI:1619321) [Nicotiana tabacum]	At5g22200	34.0005925	65.473	28.6964316	47.536	37.9349834	53.296	0.611588048	0.00013
10352	16	expressed protein	At5g56250	29.7971785	57.733	39.9248466	74.238	29.4667272	64.974	0.502477116	0.000126
5273	9	acetyltransferase-related low similarity to O-acetyltransferase [Cryptococcus neoformans var. neoformans] GI:17063556	At1g29890	158.145698	231.217	43.8317677	60.066	54.4096283	97.708	0.656852387	0.000126
23003	36	basic helix-loop-helix (bHLH) family protein contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	At2g41130	70.8612179	110.931	64.714357	150.526	14.208608	39.935	0.474833751	0.00012
6506	11	D-3-phosphoglycerate dehydrogenase / 3-PGDH identical to SP|O04130	At1g17745	48.9382211	57.754	33.6772781	64.38	19.656169	33.029	0.655192149	0.000114
27740	43	pentatricopeptide (PPR) repeat-containing protein contains Pfam profile PF01535: PPR repeat	At4g20090	29.8923703	62.525	39.9583072	59.227	187.80889	229.468	0.657067968	0.000114
19519	31	ribonuclease P family protein / Rpp14 family protein contains Pfam profile: PF01900 Rpp14 family	At1g04635	91.6900435	110.938	43.6596848	116.766	39.2051187	68.195	0.591767617	0.000112
30349	47	DNA-binding protein-related contains Pfam domain PF03479: Domain of unknown function (DUF296), found in AT-hook motifs Pfam:PF02178	At4g25320	109.070572	194.664	53.538523	67.863	21.9139582	69.541	0.554781742	0.000111
1623	3	expressed protein	At3g22415	65.2224396	98.927	37.7499088	87.185	24.2934001	114.724	0.43468004	0.000106
11940	19	expressed protein contains Pfam profile: PF05097 protein of unknown function (DUF688)	At2g34170	73.1800478	88.422	41.2776101	97.169	23.9098852	84.845	0.511410509	0.000105
6514	11	glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein similar to polygalacturonase PG1 GI:5669846, PG2 GI:5669848 from (Glycine max); contains PF00295: Glycosyl hydrolases family 28 (polygalacturonases)	At1g02460	38.172989	48.435	63.2245645	96.482	20.2025746	52.579	0.609220008	0.000104
20009	31	expressed protein similar to unknown protein (sp|Q9ZE28)	At5g06180	55.632666	80.142	69.860913	89.787	13.1632207	61.169	0.562481427	0.000102
13899	22	apurinic endonuclease-redox protein / DNA-(apurinic or apyrimidinic site) lyase identical to apurinic endonuclease-redox protein SP: P45951 from [Arabidopsis thaliana]	At2g41460	70.1210748	103.539	65.4664234	83.227	25.4109542	99.42	0.573145291	0.0001
6581	11	protein kinase family protein contains Pfam domain, PF00069: Protein kinase domain	At1g33770	26.5863263	56.038	32.8710374	70.314	13.1920874	51.652	0.39910878	0.000099
30888	48	hypothetical protein	At3g32394	51.5779223	97.756	50.2896599	102.97	15.8931869	35.019	0.489951683	0.000084
12078	19	leucine-rich repeat transmembrane protein kinase, putative several receptor-like protein kinases	At3g57830	77.9781433	114.894	33.231137	85.009	19.7798834	50.622	0.486782152	0.00008
15392	24	clathrin adaptor complexes medium subunit family protein contains Pfam profile: PF00928 adaptor complexes medium subunit family	At4g24550	65.2716398	99.627	114.591336	139.145	38.3370554	79.929	0.652779345	0.00008
28377	44	farnesyl pyrophosphate synthetase 2 (FPS2) / FPP synthetase 2 / farnesyl diphosphate synthase 2 identical to SP|Q43315 Farnesyl pyrophosphate synthetase 2 (FPP synthetase 2) (FPS 2) (Farnesyl diphosphate synthetase 2) [Includes: Dimethylallyltransferase (EC 2.5.1.1); Geranyltranstransferase (EC 2.5.1.10)] {Aral	At4g17190	73.4453014	94.746	49.8514856	80.395	16.6828976	68.491	0.546280298	0.000078
5870	10	VHS domain-containing protein / GAT domain-containing protein weak similarity to SP|Q9UJY5 ADP-ribosylation factor binding protein GGA1 {Homo sapiens}; contains Pfam profiles PF00790: VHS domain, PF03127: GAT domain	At1g06210	62.9153749	76.81	41.4241993	47.711	5.68674226	57.454	0.595438212	0.000076
12000	19	protein kinase, putative similar to viroid symptom modulation protein [Lycopersicon esculentum] gi|7672777|gb|AAF66637	At3g12690	47.3862736	67.247	67.2127471	80.6	29.4131176	70.331	0.652258316	0.000075
13443	21	hypothetical protein	At4g22217	29.683804	75.308	82.1648467	96.119	11.4683323	52.967	0.488502661	0.000074
3008	5	Ulp1 protease family protein contains Pfam profile PF02902: Ulp1 protease family, C-terminal catalytic domain; similar to At1g32840, At2g06430, At2g15140, At2g04980, At2g14130, At3g44500, At2g15190, At3g47260, At5g34900, At3g29210, At2g02210, At3g32900	At4g04010	50.1746452	69.215	35.2403652	53.166	46.4176729	89.105	0.636226265	0.000072
8800	14	calcineurin-like phosphoesterase family protein contains Pfam profile: PF00149 calcineurin-like phosphoesterase	At3g46120	90.5691331	141.307	69.4386724	90.957	56.3498837	101.341	0.653468047	0.000068
19997	31	expressed protein	At5g02440	63.8619453	84.574	55.1701246	121.273	31.376054	92.771	0.516078719	0.000066
6666	11	eukaryotic translation initiation factor 2 family protein / eIF-2 family protein similar to SP|O60841 Translation initiation factor IF-2 {Homo sapiens}; contains Pfam profile PF00009: Elongation factor Tu GTP binding domain	At1g76825	28.7607642	59.523	15.3823071	62.245	31.1904823	52.847	0.440172018	0.000063
28485	44	speckle-type POZ protein-related contains Pfam PF00651 : BTB/POZ domain; contains Pfam PF00917: MATH domain; similar to Speckle-type POZ protein (SP:O43791) [Homo sapiens]	At5g19000	148.907814	213.247	63.866689	91.439	12.8992964	31.552	0.601858931	0.000059
3236	5	disease resistance protein (CC-NBS-LRR class), putative domain signature CC-NBS-LRR exists, suggestive of a disease resistance protein.	At5g66910	68.2396994	89.164	64.4004649	74.647	14.8560471	47.941	0.64598109	0.000056
5816	9	peroxidase, putative similar to peroxidase [Nicotiana tabacum] gi|5381253|dbj|BAA82306	At5g58390	68.2450472	105.839	75.7611288	86.533	19.0437823	84.081	0.582270348	0.000054
7065	11	hypothetical protein	At5g38050	33.2946757	52.715	14.6637013	48.255	28.4234018	91.187	0.415727237	0.000052
21539	34	F-box family protein similar to hypothetical protein GB:AAD22295 GI:4544385 from [Arabidopsis thaliana]	At1g47300	37.8403524	56.732	67.7019089	78.547	17.7303469	50.378	0.626958925	0.000052
1580	3	no apical meristem (NAM) family protein similar to NAC2 (GI:6456751) {Arabidopsis thaliana}	At3g03200	43.0705546	78.03	21.578888	149.716	26.938828	36.168	0.480310457	0.000048
7394	12	DC1 domain-containing protein contains Pfam profile PF03107: DC1 domain	At2g37800	42.4095597	50.517	54.1806474	80.871	21.6789007	57.295	0.62928262	0.000048
2554	4	expressed protein	At5g55610	37.9868836	50.179	48.6405312	79.115	6.8558441	58.253	0.496508767	0.000046
21659	34	expressed protein and genefinder	At2g24030	29.8677702	38.37	76.9577429	96.448	3.66194861	45.053	0.552538362	0.000044
20147	31	galactosyltransferase family protein contains Pfam profile: PF01762 galactosyltransferase	At1g33430	69.0365298	97.206	68.496996	105.096	5.70323753	34.265	0.509469988	0.00004
21647	34	DC1 domain-containing protein contains Pfam profile PF03107: DC1 domain	At2g17590	57.0006473	69.097	45.7963819	84.233	30.4935574	65.176	0.6121628	0.00004
28432	44	expressed protein	At4g36630	83.5142428	114.569	79.8831537	102.078	23.6047228	62.747	0.629233787	0.000037
7093	11	expressed protein contains similarity to unknown protein (pir||T26512)	At5g51130	20.2148919	55.607	22.1094772	57.815	25.3965208	57.587	0.395653481	0.000036
7024	11	armadillo/beta-catenin repeat family protein contains Pfam profile: PF00514 armadillo/beta-catenin-like repeat	At5g14510	35.3118866	79.926	32.1556183	56.547	30.2873666	62.209	0.499108304	0.000036
1445	3	CCAAT-binding transcription factor (CBF-B/NF-YA) family protein contains Pfam profile: PF02045 CCAAT-binding transcription factor (CBF-B/NF-YA) subunit B	At1g72830	53.6806989	60.918	31.3254773	69.174	20.7242373	56.772	0.566363251	0.000035
15491	24	hypothetical protein	At5g23640	33.819835	62.192	1990.88704	3319.302	34.4111826	65.936	0.555158564	0.000034
1787	3	hypothetical protein	At4g36460	71.0409058	100.365	39.0341578	68.698	40.990731	96.351	0.567152042	0.000034
4013	7	transcription factor, putative similar to Transcription factor GB:CAA74053 GI:2398533 from [Arabidopsis thaliana] similarity to transcription factor Hap5a similar to transcription factor Hap5a [Arabidopsis thaliana](GI:6523090)	At1g56170	63.0105668	91.284	79.0482326	117.074	48.7352575	89.471	0.636724315	0.000032
6917	11	cytochrome P450 71A19, putative (CYP71A19) Identical to Cytochrome P450 (SP:Q9T0K0) [Arabidopsis thaliana]; similar to cytochrome P450LIA1, Persea americana, M32885	At4g13290	28.6163721	54.136	23.2949378	50.535	21.6809626	55.703	0.459597422	0.00003
11828	19	hypothetical protein	At1g63200	66.6353429	77.296	40.848996	84.63	18.1365428	44.866	0.582998532	0.00003
23184	36	transcription initiation factor-related contains weak similarity to Transcription initiation factor IIE, beta subunit (TFIIE-beta) (Swiss-Prot:P29084) [Homo sapiens]	At4g20330	68.3038736	98.815	104.605743	127.26	20.3840225	64.992	0.608951074	0.00003
14218	22	protein kinase, putative similar to stpk1 protein kinase [Solanum tuberosum] gi|1200256|emb|CAA62476	At5g40030	41.780652	68	61.8494939	97.833	47.4816174	77.835	0.618881693	0.00003
27963	44	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein contains Pfam profile PF00234:Protease inhibitor/seed storage/LTP family; low similarity to SP:Q42978 Nonspecific lipid-transfer protein 2 precursor (LTP 2) {Oryza sativa}	At1g03103	58.4135506	97.851	66.2057429	115.296	20.4953655	47.511	0.534189953	0.000028
8706	14	DNA polymerase delta small subunit-related similar to DNA polymerase delta small subunit SP:Q9LRE5 from [Oryza sativa]	At2g42120	52.9523211	86.996	73.7311869	113.415	18.7881057	95.422	0.4852237	0.000024
14314	23	speckle-type POZ protein-related contains Pfam profile:PF00651 BTB/POZ domain; similar to Speckle-type POZ protein (SP:O43791) [Homo sapiens]	At1g01640	49.636651	81.298	70.0154691	111.624	21.4376575	86.664	0.495053664	0.000024
28459	44	myosin heavy chain-related contains weak similarity to Myosin heavy chain, cardiac muscle alpha isoform (MyHC-alpha) (Alpha isomyosin) (Fragment) (Swiss-Prot:P04460) [Oryctolagus cuniculus]	At5g07890	166.679805	239.104	27.2640001	113.019	11.7858661	43.484	0.403124874	0.000024
9941	16	hypothetical protein	At2g15045	31.5427184	52.634	37.9777594	48.781	15.5570959	46.416	0.570995546	0.000024
28169	44	expressed protein	At2g27790	53.9555787	96.655	69.3096101	79.392	12.7858915	39.715	0.584391538	0.000024
12012	19	dynein light chain, putative similar to SP|O02414 Dynein light chain LC6, flagellar outer arm {Anthocidaris crassispina}; contains Pfam profile PF01221: Dynein light chain type 1	At3g16120	56.4434008	86.858	27.6878341	46.139	29.5327083	71.635	0.554065981	0.000023
6879	11	DNAJ heat shock N-terminal domain-containing protein contains Pfam profile PF00226 DnaJ domain	At3g58020	21.3229675	44.961	19.4820249	37.336	16.5715546	51.966	0.438316558	0.000022
27468	43	glycine-rich protein	At1g76965	46.7648528	63.106	57.3323155	65.349	18.7963533	60.77	0.642560209	0.000021
21582	34	protein kinase-related	At1g66940	14.9130285	57.093	57.0550707	64.892	4.68053116	42.133	0.41717551	0.00002
27718	43	cytochrome P450 71A20, putative (CYP71A20) Identical to Cytochrome P450 (SP:Q9T0K2) [Arabidopsis thaliana]; similar to cytochrome P450 71A4, Solanum melongena, PIR2:S36805	At4g13310	57.8488171	64.259	52.8246972	82.464	1.80004568	61.238	0.523405912	0.00002
7156	12	D-3-phosphoglycerate dehydrogenase / 3-PGDH identical to SP|O04130	At1g17745	30.3982774	50.494	58.9639172	86.932	33.887458	79.568	0.568728994	0.00002
25808	40	expressed protein	At4g31020	40.5303235	57.693	83.3471205	92.851	13.6993168	40.034	0.647450997	0.00002
6870	11	expressed protein DNA-binding Mel-18 protein, Homo sapiens, PIR:JN0717	At3g54360	21.6759259	80.303	32.0743569	61.123	19.0912062	32.961	0.457961222	0.000016
6270	10	expressed protein	At4g14200	30.2774159	55.899	36.3238507	43.555	9.44766246	39.809	0.537648807	0.000016
15394	24	protein kinase (AFC2) identical to protein kinase AFC2 [Arabidopsis thaliana] SWISS-PROT:P51567	At4g24740	48.1285559	72.714	91.1625563	104.214	17.9324139	86.881	0.581017835	0.000015
30772	48	zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)	At2g28920	61.8907259	81.12	59.5072533	76.967	11.631223	48.746	0.591571442	0.000015
28319	44	expressed protein	At3g55070	30.8228971	55.103	57.2112201	73.586	123.469113	210.712	0.640934828	0.000015
31041	48	VHS domain-containing protein / GAT domain-containing protein weak similarity to Hrs [Rattus norvegicus] GI:8547026; contains Pfam profiles PF00790: VHS domain, PF03127: GAT domain	At5g01760	36.622111	56.014	48.7504732	58.063	36.7452625	154.919	0.576868795	0.000014
12097	19	myb family transcription factor contains PFAM profile: PF00249 myb-like DNA binding domain	At4g01280	36.6830766	68.187	39.4611785	71.556	28.9512502	57.088	0.532194657	0.000012
27492	43	hypothetical protein	At2g11360	41.0116304	53.42	58.2086641	92.405	23.8500898	65.085	0.588031865	0.000012
14526	23	glutathione S-transferase, putative	At2g29440	61.3580796	69.429	40.6307055	60.135	26.8192374	121.705	0.593257915	0.000012
5607	9	callose synthase, putative / 1,3-beta-glucan synthase, putative similar to callose synthase 1 catalytic subunit GI:13649388 from [Arabidopsis thaliana]	At4g04970	75.1544759	99.908	37.6925478	66.101	36.7308291	72.776	0.60905805	0.000012
14817	23	cytochrome P450 family protein	At5g09970	63.4940128	120.771	86.7903737	103.863	19.6211165	36.682	0.632086725	0.000012
7403	12	expressed protein an isoform contains a GA donor splice site supported by FL-cDNA alignment which truncates the ORF.	At2g41150	45.8503696	54.492	33.2120167	40.673	28.7141308	90.097	0.658892956	0.000012
6533	11	pentatricopeptide (PPR) repeat-containing protein contains Pfam profile PF01535: PPR repeat	At1g11710	43.4267217	56.344	23.8510208	69.346	20.2932985	44.643	0.523084439	0.000011
15079	24	peptidase M3 family protein / thimet oligopeptidase family protein similar to SP|P42676 Neurolysin, mitochondrial precursor (EC 3.4.24.16) (Mitochondrial oligopeptidase M) {Rattus norvegicus}; contains Pfam profile PF01432: Peptidase family M3	At1g67690	36.3258399	74.499	92.8531123	115.914	38.5453082	65.685	0.625158005	0.00001
6806	11	expressed protein contains Pfam profile: PF03398 eukaryotic protein of unknown function, DUF292	At3g15490	28.3596751	59.858	37.0328964	72.845	23.8129755	44.62	0.50528194	0.000009
1312	3	no apical meristem (NAM) family protein contains Pfam PF02365 : No apical meristem (NAM) protein; similar to NAC1 (GI:21554126) (Arabidopsis thaliana)	At1g02250	25.2055102	37.128	40.1017096	68.726	20.9572329	40.275	0.594245375	0.000009
28049	44	cinnamyl-alcohol dehydrogenase, putative (CAD) similar to GB:X88797 from [Eucalyptus gunnii] (Plant Mol. Biol. 36 (5), 755-765 (1998))	At1g51410	65.7326249	77.332	53.481162	75.151	15.3096669	44.146	0.63615037	0.000009
30399	47	heavy-metal-associated domain-containing protein low similarity to gi:3168840 copper homeostasis factor; contains Pfam heavy-metal-associated domain PF00403; predicted proteins, Arabidopsis thaliana	At5g02600	52.5095187	65.338	21.3319171	44.649	6.11149531	43.794	0.473659964	0.000008
17580	28	kinase interacting family protein similar to kinase interacting protein 1 (GI:13936326) [Petunia integrifolia]	At1g09720	36.2509699	47.976	53.4110541	64.959	10.3425305	46.365	0.600300377	0.000008
30084	47	expressed protein contains Pfam profile: PF04765 protein of unknown function (DUF616)	At2g02910	44.4952232	64.056	37.1603652	47.957	17.5695181	45.238	0.619292709	0.000006
15411	24	expressed protein	At4g31430	26.3745513	57.974	99.5978094	123.652	41.6773464	94.595	0.566997811	0.000005
23325	36	transcriptional factor B3 family protein contains Pfam profile PF02362: B3 DNA binding domain	At5g42700	25.5424251	86.689	45.1781578	106.632	25.2088872	33.778	0.488212706	0.000004
23071	36	elongation factor Tu family protein similar to eukaryotic translation elongation factor 2 GB:NP_001952 [Homo sapiens]	At3g22980	63.1239413	83.778	35.2594856	54.204	45.4341428	111.121	0.6042779	0.000004
9029	14	expressed protein contains similarity to carboxyl-terminal proteinase contains Pfam profile PF03080: Arabidopsis proteins of unknown function; expression supported by MPSS	At5g46200	48.6654805	77.919	88.7613612	99.005	18.7283104	63.298	0.60565812	0.000004
30345	47	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein similar to hydroxyproline-rich glycoprotein DZ-HRGP from Volvox carteri f. nagariensis GP|6523547; contains Pfam profile PF00234 Protease inhibitor/seed storage/LTP family	At4g22470	30.9234368	72.897	44.3735105	61.764	38.5803606	49.609	0.640110825	0.000004
6963	11	aspartyl protease family protein contains Pfam domain, PF00026: eukaryotic aspartyl protease	At4g30040	22.7668883	32.211	12.3342075	59.307	11.2827606	50.907	0.378803909	0.000003
6597	11	protein kinase family protein contains protein kinase domain, Pfam:PF00069	At1g50230	26.7574577	33.395	18.1515685	77.1	18.7448056	50.334	0.469692921	0.000003
14089	22	calmodulin-binding family protein contains IQ calmodulin-binding motif, Pfam:PF00612	At4g21820	28.7971296	82.08	15.916083	67.832	28.2048395	69.847	0.329763618	0.000002
6904	11	calcium-dependent protein kinase, putative / CDPK, putative similar to calcium-dependent protein kinase [Nicotiana tabacum] gi|3283996|gb|AAC25423; contains protein kinase domain, Pfam:PF00069; contains EF hand domain (calcium-binding EF-hand), Pfam:PF00036, INTERPRO:IPR002048	At4g04710	15.7408764	36.985	20.6515519	52.02	13.5632308	43.829	0.377350695	0.000002
7391	12	origin recognition complex subunit 2 (ORC2) identical to origin recognition complex subunit 2 (ORC2) SP:Q38899 from [Arabidopsis thaliana]	At2g37560	37.2595754	46.784	31.9118341	73.675	20.5139227	76.336	0.499430776	0.000002
14984	24	serine/threonine protein phosphatase 2A (PP2A) regulatory subunit B', putative similar to SWISS-PROT:Q28653 serine/threonine protein phosphatase 2A, 56 kDa regulatory subunit, delta isoform (PP2A, B subunit, B' delta isoform, PP2A, B subunit, B56 delta isoform, PP2A, B subunit, PR61 delta isoform, PP2A, B subu	At1g13460	14.1172676	72.421	53.7647802	71.672	53.9642562	95.425	0.503532873	0.000002
7224	12	F-box family protein contains F-box domain Pfam:PF00646	At1g30930	28.8473994	52.17	35.3742076	50.056	16.4684592	46.671	0.537501801	0.000002
3428	6	hypothetical protein	At2g05087	41.3335713	51.5	34.4946723	70.524	11.9570045	36.358	0.540193946	0.000002
20024	31	expressed protein	At5g13590	59.6114701	72.976	36.4608798	84.481	28.5553639	57.13	0.582760705	0.000002
6635	11	cox19 family protein contains Pfam profile PF05490: Cox19 protein	At1g66590	14.0423977	27.973	5.09238176	23.479	2.42892762	25.564	0.271300928	0.000001
6632	11	subtilase family protein contains similarity to subtilase; SP1 GI:9957714 from [Oryza sativa]	At1g66210	9.19724103	40.53	19.0773113	44.152	12.2745383	45.891	0.308826156	0.000001
6810	11	hypothetical protein	At3g15910	9.12344063	25.059	9.90911206	41.518	23.7696754	50.756	0.357020429	0.000001
6603	11	expressed protein ; expression supported by MPSS	At1g51000	9.00257911	30.864	20.7216598	64.187	2.06396991	4.4	0.361200719	0.000001

12055	19	expressed protein	At3g47720	15.5975539	32.185	23.4463071	71.655	18.9674917	60.802	0.374595981	0.000001
15696	25	F-box protein-related contains weak hit to Pfam PF00646: F-box domain; contains weak hit to TIGRFAM TIGR01640 : F-box protein interaction domain	At1g46984	13.8691272	58.055	14.0231702	39.462	16.8829027	29.042	0.39186077	0.000001
24163	38	SWIM zinc finger family protein contains Pfam domain PF04434: SWIM zinc finger	At1g60560	30.9555239	59.674	47.8645644	70.278	8.46413234	47.269	0.45962721	0.000001
19868	31	AAA-type ATPase family protein contains Pfam profile: ATPase family PF00004	At3g50930	37.7002386	55.134	36.1995686	76.83	11.5961706	42.261	0.476450517	0.000001
24579	38	heavy-metal-associated domain-containing protein contains Pfam heavy-metal-associated domain PF00403; glycine-rich protein GRP22, rape, PIR:S31415; isoform contains a non-consensus TG-acceptor splice site at intron 3	At5g19090	22.777584	40.335	45.6545727	56.602	7.50328321	42.525	0.515914531	0.000001
22198	35	C2 domain-containing protein low similarity to CLB1 [Lycopersicon esculentum] GI:2789434; contains Pfam profile PF00168: C2 domain	At1g50260	39.0404111	54.587	31.7604648	64.137	16.6767119	47.494	0.520508795	0.000001
28287	44	myosin heavy chain-related similar to Myosin heavy chain, non-muscle (Zipper protein) (Myosin II)(SP:Q99323) {Drosophila melanogaster}	At3g30230	24.7295511	53.068	69.0690126	122.056	8.12185561	12.918	0.55353368	0.000001
20290	32	expressed protein contains Pfam profile: PF04842 plant protein of unknown function (DUF639)	At1g71240	35.6990713	58.498	31.0609793	68.931	25.1800205	41.874	0.55406647	0.000001
6846	11	hypothetical protein	At3g43950	18.8693716	21.306	4.16026557	32.622	6.78161541	10.436	0.554331652	0.000001
3173	5	nitrate-responsive NOI protein, putative similar to nitrate-induced NOI protein [Zea mays] GI:2642213	At5g40645	44.1829084	49.373	19.8150374	43.344	14.1611841	43.452	0.559313869	0.000001
7240	12	endonuclease/exonuclease/phosphatase family protein similar to SP|P32019 Type II inositol-1,4,5-trisphosphate 5-phosphatase precursor (EC 3.1.3.56) {Homo sapiens}; contains Pfam profile PF03372: Endonuclease/Exonuclease/phosphatase family	At1g47510	31.7833718	52.203	47.9872532	64.656	26.0130313	73.073	0.569007374	0.000001
21813	34	serine carboxypeptidase S10 family protein similar to SP|P52711 Serine carboxypeptidase II-3 precursor (EC 3.4.16.6) Hordeum vulgare; contains Pfam profile PF0450 serine carboxypeptidase	At3g52020	25.0889269	38.353	22.0505229	79.81	17.7468422	22.203	0.576581715	0.000001
5047	8	expressed protein	At5g05020	39.9923293	45.788	40.2674192	67.749	27.7862722	63.65	0.634777835	0.000001
15081	24	hypothetical protein hypothetical protein	At1g67855	28.4484495	56.915	56.3157512	62.594	22.2871636	39.1	0.656514679	0.000001
23131	36	DC1 domain-containing protein contains Pfam profile PF03107: DC1 domain	At3g59130	51.2335205	63.632	41.1469545	48.072	20.1819555	64.2	0.658486123	0.000001